



## Genetic variability, character association and path coefficient analysis in rice (*Oryza sativa*) genotypes of semi-arid region of India

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### ABSTRACT

A field experiment was conducted during rainy (*kharif*) seasons of 2021 and 2022 at research farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh to find out genetic variations, trait association and path coefficient among 116 rice (*Oryza sativa* L.) genotypes based on grain yield and yield attributes. Variance analysis displayed extensive trait-wise variations across genotypes, indicated variability and opportunity for genetic selection of desirable traits. All the studied characters showed minimum influence of environment on the expression of trait and genetic factors. High heritability in broad sense ( $h^2$  b) and high to moderate genetic advance in per cent of the mean were recorded for all the characters. Genetic factors showed significant influence on the expression of traits, with high heritability and moderate genetic advance. Genotypic correlation with grain yield and path analysis revealed selection based on plant height, harvest index, biological yield per plant, flag leaf area, spikelet fertility, number of spikelets per panicle and seedling vigour will be more effective for increasing grain yield.

**Keywords:** Correlation, Genetic variability, Heritability, Path coefficient

Rice (*Oryza sativa* L.) cultivation not only helps to food security, but also secures economic state and work prospects. It accounts for 75% of total cultivated land in India and employs 48% of farm labourer, contributing 70% of agricultural GDP. Rice increasing demand needs the creation of exceptional genotypes that can survive in a variety of environments. A lot of variations exists in rice germplasm that serve as the vital source of crop improvement endeavour to fulfil the near-future demand of food security and adapt to climate change. Genetic variations provide opportunities to integrate favourable alleles to meet desirable changes (Pandey *et al.* 2021). Grain yield (GY) is a multidimensional trait that is influenced by a combination of genes, the environment in which they grow, and the degree and kind of genetic variation. Furthermore, GY is linked to other yield attributes like primary and secondary branches per panicle, filled grains per panicle, panicle length, plant growth, plant height and tiller per plant (Asante *et al.* 2019). Plant breeders' principal attention is on selecting desired traits in the mix and to consider each economic benefit

based on GY to build a preference index (Saroj *et al.* 2021).

In spite of the fact that GY has a poor genetic inheritance, it is feasible to boost GY through various yield-related characters. Combining genetic advance and heritability may be more favourable than selecting features just based on heredity. Most efforts to identify plant selection criteria require knowledge of the relationship between yield and related causative factors (Singh *et al.* 2022). GY and related variables may be classified as having direct or indirect effects on seed yield. As a result, it is critical to connect component attributes to yield and to one another. Earlier researches have also analyzed the effect of phenotypic traits on rice GY and other yield attributes (Asante *et al.* 2019). Path coefficient (PC) study breaks the genetic relationship between GY and its paying qualities into direct and indirect PCs, providing important features as selection criteria to increase rice GY (Hasan-Ud-Daula and Sarker 2020). Therefore, the present study was designed to investigate genotype variability, quantify the proportional contribution of each character to yield and their inter-relationships, and identify the direct and indirect PCs of component characteristics to GY.

### MATERIALS AND METHODS

The field experiment was conducted during rainy (*kharif*) seasons of 2021 and 2022 at research farm of Acharya Narendra Deva University of Agriculture and

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Technology, Kumarganj, Ayodhya, Uttar Pradesh with 116 rice genotypes in an augmented randomized block design (Federer 1956) consisting of 3 biological replications of each genotype. At 30 days, one seedling per hill was transplanted with 35 cm spacing of row to row and 10 cm spacing of plant to plant. Each replication was maintained in two rows of 3 m each consisting 30 plants per row for each genotype. Urea was applied at 15-days interval (15, 30 and 45 days) after transplanting. To maintain the optimum plant growth, all management inputs were taken care including intercultural activities like weeding, gap filling, insecticide application and fertigation. Observations were recorded by random selection of 10 hills per genotype in each replication. Data collected during both *kharif* seasons of 2021 and 2022 included 13 individual traits i.e., days to 50% flowering (DFF), seedling vigor (SV), plant height (PH), flag leaf area (FLA), panicles bearing tillers per plant (PTP), panicle length (PL), number of spikelets per panicle (NSP), number of grains per panicle (NGP), spikelet fertility (SF), biological yield per plant (BYP), harvest index (HI), test weight (TW) and grain yield per plant (GYP).

*Statistical analysis:* The pooled data of both years for each agronomic trait were subjected to data analysis through SPSS statistical tool. Analysis of variance was done as per Federer (1956) and estimates were made for square root of the error mean to get the error variance ( $\sigma^2 e$ ). The G and P components of variance ( $\sigma^2 g$  and  $\sigma^2 p$ ), phenotypic and genotypic coefficients of variation (PCV, GCV), broad-sense heritability ( $h^2 b$ ) (Burton and devane 1953), genetic advance (GA) (Johnson *et al.* 1955), and genetic advance as per cent of the mean (GAM) (Comstock and Robinson 1952) were estimated. Correlation coefficients (Searle 1961) were further partitioned into components of direct and indirect effects by PC analysis (Dewey and Lu 1959).

## RESULTS AND DISCUSSION

*Genetic variability:* The grain yield (GY) is the ultimate product of agronomic traits that impacted by many interdependent variables. Improving one trait directly related to yield has a knock-on impact on several other closely related traits (Hasan-Ud-Daulla and Sakrer 2020). To address these complicated interactions, we must develop high-yielding varieties by introducing quality traits from existing cultivated genotypes. Under study, genotypes revealed extremely significant variance among all analyzed attributes (Table 1). GA is measure for genetic divergence, genotypic and phenotypic variations, coefficient of variation, and  $h^2 b$  (Shilpashree *et al.* 2021). Germplasm variations may be modified by characteristics with  $\sigma^2 g$  and  $\sigma^2 p$  (Shilpashree *et al.* 2021).

The extent of variation in GY and related yield traits was observed with a wide genetic divergence for days of 50% flowering (DFF) among genotypes (Table 1). The phenotypic variance ( $\sigma^2 p$ ) for DFF (95.03) was somewhat higher than the genotypic variance ( $\sigma^2 g$ ) (93.72). The GCV (25.96) and PCV (26.98) was found nearby similar for SV. The  $h^2 b$  (92.57) value was the highest while GA

(16.62) and GAM (51.45) found with moderate values that indicated large extent of variation among rice accessions. Variations in morphological features and yield-contributing traits of several crops have been observed by Saroj *et al.* (2021). It is important to divide  $\sigma^2 p$  into genotypic and environmental impacts when genotype selection is based on  $\sigma^2 p$  (Zaid *et al.* 2022).

The plant height (PH) revealed a wide variability among genotypes (Table 1), with marginal difference between  $\sigma^2 p$  (226.44) and  $\sigma^2 g$  (225.48). The variation of GCV (12.67) and PCV (12.70) was the smallest. Flag leaf area (FLA) phenotypic expression was impacted by the environment to some extent with  $\sigma^2 p$  (10.36), slightly greater than  $\sigma^2 g$  (7.49) and equivalent to GCV (10.49) and PCV (12.33). Researches have previously established environmental influences on yield-contributing properties of rice (Pratap *et al.* 2018, Zaid *et al.* 2022). Panicle bearing tillers per plant (PTP) had a closer value of  $\sigma^2 p$  (2.07) and  $\sigma^2 g$  (1.98). GCV (17.06) and PCV (17.46) deviations indicated less environmental effect. PTP had a greater heritability  $h^2 b$  (95.57) and a higher GAM (34.37). Low PCV and GCV values indicate low genetic variability, while high PCV and GCV indicate high genetic variability (Hasan-Ud-Daulla and Sarker 2020). The presence of significant diversity suggests the possibility of successful selection for character enrichment.

Panicle length (PL) showed evident variance in  $\sigma^2 g$  (7.65) and  $\sigma^2 p$  (8.12), as well as GCV (10.06) and PCV (10.36) (Table 1). PL showed with high  $h^2 b$  (94.30) but a very low GA (5.53) and GAM (20.12). The number of spikelets per panicle (NSP) exhibited a discernible difference between  $\sigma^2 g$  (554.43) and  $\sigma^2 p$  (615.66), with practically equal values of GCV (20.65) and PCV (21.76) for NSP. However, number of grains per panicle (NGP) differed significantly between  $\sigma^2 g$  (54.39) and  $\sigma^2 p$  (71.64). The study found a significant environmental effect on the expressivity of spikelets fertility (SF). SF had a high  $h^2 b$  (73.05) but a low GA (18.38) and GAM (30.94) (Table 1). High  $h^2 b$  along with high GA of a trait is critical for trait selection in any breeding programme. Previous research found strong heritability and high genetic advance in per cent of the mean for many yield-related parameters (Hasan-Ud-Daulla and Sarker 2020).

The  $\sigma^2 p$  (69.92) was slightly higher than  $\sigma^2 g$  (64.48) for biological yield per plant (BYP). GCV (26.94) was close to PCV (28.05), indicating a minor environmental influence on trait manifestation. The value of  $h^2 b$  for BYP was fairly high (92.22), although the GA (15.89) and GAM (53.29) were modest. The variation in  $\sigma^2 g$  (28.91) and  $\sigma^2 p$  (31.94) and GCV (18.86) and PCV (19.82) showed a strong environment effect on the expressivity of harvest index (HI%). The test weight (TW) was found to vary somewhat in  $\sigma^2 g$  (6.94),  $\sigma^2 p$  (9.29), GCV (11.81) and PCV (13.66) with a high  $h^2 b$  (74.73) (Table 1). This conclusion is similar with prior findings (Dhurai *et al.* 2014), which found very minor variations between  $\sigma^2 p$  and  $\sigma^2 g$  for PH, NFS.

GYP, like TW has a robust genetic control among

Table 1 Estimation of genetic parameters for yield and its component characters in 116 genotypes of rice

Genetic parameter	DFF	SV	PH (cm)	FLA (cm <sup>2</sup> )	PTP	PL (cm)	NSP	NGP	SF	BYP (g)	HI (%)	TW (g)	GYP (g)
$\sigma^2 e$	1.32	5.65	0.97	2.87	0.09	0.46	61.23	17.25	40.22	5.44	3.03	2.35	0.40
$\sigma^2 g$	93.72	70.32	225.48	7.49	1.98	7.65	554.43	54.39	109.01	64.48	28.91	6.94	12.09
$\sigma^2 p$	95.03	75.97	226.44	10.36	2.07	8.12	615.66	71.64	149.23	69.92	31.94	9.29	12.49
GCV	8.99	25.96	12.67	10.49	17.06	10.06	20.65	8.66	17.57	26.94	18.86	11.81	29.75
PCV	9.06	26.98	12.70	12.33	17.46	10.36	21.76	9.93	20.56	28.05	19.82	13.66	30.24
h <sup>2</sup> b	98.61	92.57	99.57	72.34	95.57	94.30	90.05	75.92	73.05	92.22	90.53	74.73	96.79
GA	19.80	16.62	30.87	4.80	2.83	5.53	46.03	13.24	18.38	15.89	10.54	4.69	7.05
GAM	18.40	51.45	26.05	18.38	34.37	20.12	40.37	15.54	30.94	53.29	36.97	21.03	60.30

$\sigma^2 e$ , environmental variance;  $\sigma^2 g$ , genotypic variance;  $\sigma^2 p$ , phenotypic variance; GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; h<sup>2</sup> b, heritability in broad sense; GA, genetic advance; GAM, genetic advance in per cent of mean. Trait details are given under Materials and Methods.

the chosen lines, with near values of  $\sigma^2 g$  (12.09) and  $\sigma^2 p$  (12.49), GCV (29.75) and PCV (30.24) with high h<sup>2</sup> b (96.79). The GYP had a low GA (7.05) but a high GAM (60.30). Several researchers have also observed similar findings (Hasan-ud-Daula and Sarker 2020), showing that there is lot of space for improvement in GY.

**Character association:** Due of the susceptibility of quantitative features to environmental effect, selecting acceptable phenotypes only on yield may not be feasible. In addition to h<sup>2</sup> b and GA, selection should be based on the correlation coefficient analysis of GY and its component traits to increase yield genetically. The link between GY and yield-related qualities makes it easier to identify traits that, through indirect selection, may increase seed yield (Hasan-Ud-Daula and Sarker 2020). To determine the character link between yield and yield characteristics, genotypic and phenotypic correlation was done (Table 2). DFF exhibited no significant positive connection with any of the examined agronomic parameters at both the genotypic level (GL) and phenotypic level (PL).

At GL, SV has significant (P<0.05) positive correlation with NSP (0.284), NGP (0.261), while negatively linked with GYP (-0.199) and SF (-0.329). At the PL, only SV had significantly negative (P<0.05) connection with HI% (-0.221). Plant height (PH) had a substantial (P<0.01) positive connection with PL (0.612 and 0.600) at both the GL and PL, but no other agronomic characteristics were found to be correlated. FLA at GL showed significant (P<0.05) positive relationship with NSP (0.207) and HI% (0.259), as well as a negative link with SF (-0.197), BYP (-0.251), while highly significant (P<0.01) link with TW (-0.405), same time PL showed negative association (P<0.05) with NGP (-0.198 cm<sup>2</sup>). Other studies observed similar findings (Hasan-Ud-Daula and Sarker 2020). PTP observed insignificant association with examined traits, while panicle length (PL) had significant (P<0.05) positive link with GYP (0.211, 0.194). NSP showed substantial (P<0.01) negative link with SF

(-0.847, -0.832) at both GL and PL, while it favours only (P<0.05) BYP (0.233) at GL.

At the GL, NGP showed significant (P<0.05) positive connection with SF (0.203), but not found associated with any other trait examined. At both the GL and PL, BYP had significantly (P<0.01) negative association with HI% (-0.445, -0.474) and positive link with GYP (0.549, 0.538). At the GL, it exhibits significantly (P<0.05) negative relationship with TW (-0.211). At the PL, HI% was positively connected with only GYP (0.454), but at the GL, it found positively linked with both TW (0.339) and GYP (0.470). No relationship between TW and GYP at any level in agronomic characteristics was evaluated. According to Pratap *et al.* (2018), grain yield has a substantial positive connection with full grains panicle, number of effective tillers per hill, plant height and 1000-grain weight in rice. Fentie *et al.* (2021) discovered a significant positive correlation between grain yield and number of filled spikelets per panicle, harvest index, panicle length and plant height. Previous studies found no correlation between days to 50% flowering and spikelet sterility of rice (Asante *et al.* 2019, Hasan-Ud-Daula and Sarker 2020).

**Path coefficient analysis:** Path coefficient analysis is a method used to assess the direct and indirect effects of traits linked with other traits, allowing for the evaluation of selection criteria in various species. It segments G and P correlation coefficients into direct and indirect effects through substitute features, providing insights into essential component qualities that may be used in the indirect selection of multifarious attributes like yield (Hasan-Ud-Daula and Sarker 2020). The study used GY as the outcome character, while yield characteristics (DFF, SV, PH, FLA, PTP, PL, NSP, SF, BYP, HI%, TW and GYP) were used as the independent characters. Each component has two paths of action: direct effects on yield and indirect effects via component characteristics. The genotypic correlation was classified as having direct or indirect effects on GY (Table 3 and Fig 1).

Table 2 Genotypic vs phenotypic correlation coefficient among agronomic traits of 116 rice genotypes

Trait	CC	DFE	SV	PH (cm)	FLA (cm <sup>2</sup> )	PTP	PL (cm)	NSP	NGP	SF	BYP (g)	HI (%)	TW (g)	GYP (g)
DFE	GL	1.0000	-0.0597	0.0871	0.0006	-0.1124	0.1049	0.0465	0.0145	-0.0439	0.0724	-0.1324	-0.1080	-0.0865
	PL	1.0000	-0.0540	0.0844	0.0146	-0.1071	0.1064	0.0464	0.0097	-0.0257	0.0663	-0.1170	-0.0812	-0.0810
SV	GL	1.0000	1.0000	-0.0806	-0.1307	-0.0196	-0.1710	0.284*	0.261*	-0.329**	-0.0289	-0.1720	-0.0854	-0.199*
	PL	1.0000	1.0000	-0.0784	0.0173	-0.0680	-0.1562	0.1803	0.1757	-0.1506	0.0456	-0.221*	0.0557	-0.1727
PH (cm)	GL			1.0000	-0.1271	0.1326	0.612**	-0.0971	-0.0245	0.0369	-0.0329	0.1013	-0.1274	0.0866
	PL			1.0000	-0.1074	0.1305	0.600**	-0.0914	-0.0216	0.0204	-0.0341	0.0897	-0.1158	0.0780
FLA (cm <sup>2</sup> )	GL			1.0000	1.0000	0.0039	-0.1545	0.207*	-0.0656	-0.197*	-0.251*	0.259*	-0.405**	0.0370
	PL			1.0000	1.0000	-0.0567	-0.0855	0.0170	-0.198*	0.0992	-0.0962	0.1174	-0.0503	0.0517
PTP	GL				1.0000	1.0000	0.0664	-0.0289	-0.1703	0.0700	0.1389	-0.0822	0.0018	0.0401
	PL				1.0000	1.0000	0.0759	0.0210	-0.1423	-0.0079	0.0757	-0.0202	-0.0769	0.0320
PL (cm)	GL						1.0000	-0.0658	0.0314	-0.0715	0.0903	0.1224	-0.0453	0.211*
	PL						1.0000	-0.0604	-0.0222	-0.0507	0.0780	0.1124	-0.0339	0.194*
NSP	GL							1.0000	-0.1585	-0.847**	0.233*	-0.1621	0.0809	0.0732
	PL							1.0000	-0.0600	-0.832**	0.1356	-0.0797	-0.0826	0.0524
NGP	GL								1.0000	0.203*	0.1173	-0.0495	0.0249	0.0529
	PL								1.0000	-0.0021	0.0600	-0.0238	-0.0937	0.0274
SF	GL									1.0000	-0.315**	0.1338	-0.253*	-0.1577
	PL									1.0000	-0.1379	0.0366	0.0546	-0.0809
BYP (g)	GL										1.0000	-0.445**	-0.211*	0.549**
	PL										1.0000	-0.474**	-0.0527	0.538**
HI (%)	GL											1.0000	0.339**	0.470**
	PL											1.0000	0.1742	0.454**
TW (g)	GL												1.0000	0.1015
	PL												1.0000	0.1100
GYP (g)	GL													1.0000
	PL													1.0000

CC, Correlation coefficient; GL, Genotypic level; PL, Phenotypic level. Trait details are given under Materials and Methods.

\*Indicates significant at 5% level and \*\* Indicates significant at 1% level.

Table 3 Partitioning of genotypic correlation with grain yield per plant (g) into direct (bold) and indirect PCs in 116 genotypes of rice

Trait	DFF	SV	PH	FLA	PTP	PL	NSP	NGP	SF	BYP	HI	TW	GYP	Partial R <sup>2</sup>
			(cm)	(cm <sup>2</sup> )						(g)	(%)	(g)	(g)	
DFF	-0.052	0.003	-0.005	0.000	0.006	-0.005	-0.002	-0.001	0.002	-0.004	0.007	0.006	-0.087	0.005
SV	0.015	-0.247	0.020	0.032	0.005	0.042	-0.070	-0.065	0.081	0.007	0.043	0.021	-0.199*	0.049
PH (cm)	-0.002	0.002	-0.022	0.003	-0.003	-0.014	0.002	0.001	-0.001	0.001	-0.002	0.003	0.087	-0.002
FLA (cm <sup>2</sup> )	0.000	0.037	0.036	-0.282	-0.001	0.044	-0.059	0.019	0.055	0.071	-0.073	0.114	0.037	-0.010
PTP	-0.009	-0.002	0.011	0.000	0.079	0.005	-0.002	-0.014	0.006	0.011	-0.007	0.000	0.040	0.003
PL	-0.012	0.019	-0.067	0.017	-0.007	-0.110	0.007	-0.004	0.008	-0.010	-0.014	0.005	0.211*	-0.023
NSP	-0.007	-0.041	0.014	-0.030	0.004	0.010	-0.145	0.023	0.123	-0.034	0.023	-0.012	0.073	-0.011
NGP	0.002	0.042	-0.004	-0.011	-0.027	0.005	-0.026	0.161	0.033	0.019	-0.008	0.004	0.053	0.009
SF	0.020	0.151	-0.017	0.090	-0.032	0.033	0.390	-0.094	-0.460	0.145	-0.062	0.116	-0.158	0.073
BYP (g)	0.052	-0.021	-0.024	-0.179	0.099	0.065	0.167	0.084	-0.225	0.714	-0.318	-0.150	0.549**	0.392
HI (%)	-0.132	-0.171	0.101	0.257	-0.082	0.122	-0.161	-0.049	0.133	-0.443	0.996	0.337	0.470**	0.468
TW (g)	0.037	0.029	0.044	0.139	-0.001	0.016	-0.028	-0.009	0.087	0.072	-0.116	-0.343	0.102	-0.035

Trait details are given under Materials and Methods.

\*Indicates significant at 5% level and \*\*Indicates significant at 1% level.

The results showed that PTP, NGP, BYP and HI% had direct PC in a positive direction, while DFF, SV, PH, FLA, PL, NSP, SF and TW had direct PC in a negative direction. The significant indirect PC was negative via SV with GYP (-0.199), but positive via PL (0.211), BYP (0.549), and HI% (0.470). The overall correlation between GY and other agronomic traits became favourable, with positive partial R<sup>2</sup> values for DFF, SV, PTP, NGP, SF, BYP, and HI%. However, partial R<sup>2</sup> values for PH, FLA, PL, NSP, and TW were all negative.

The positive association between features highlights the need for explicitly selecting these qualities to increase

GY. These findings are consistent with previous studies of Immanuel *et al.* (2011), Hasan-Ud-Daula and Sarker (2020) and Takele *et al.* (2022). The genotypic route with the least residual effect for GY suggested that all significant features were included in the current investigation.

The study found that BYP, HI%, SF and SV are the primary components of yield and should be given high importance in selection for future breeding programmes. High heritability and GAM suggest superior genotypes can be used as cultivars and middling yielder genotypes can be used as parent materials. All of the traits have high heritability in the broad sense (h<sup>2</sup> b) and high to moderate genetic advance in per cent of the mean (GAM). The genotypic coefficient of correlation was often larger than the matching phenotypic coefficient of correlation, indicating that the apparent link might be attributable to genetic factors.

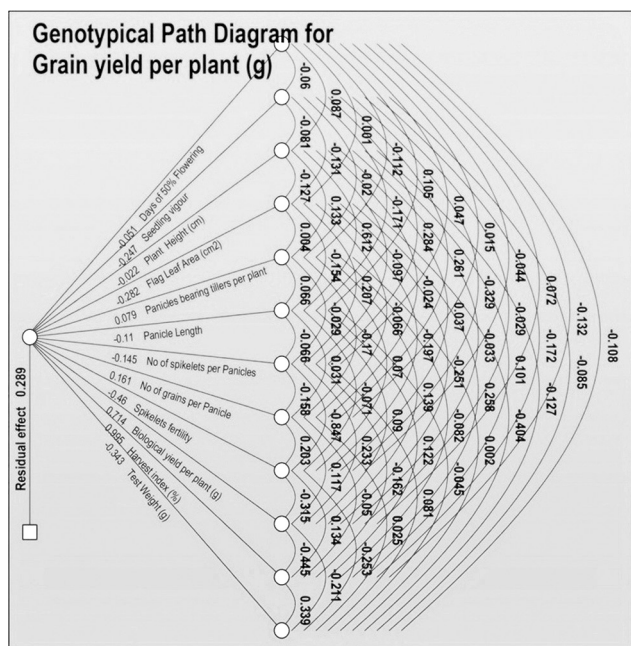


Fig 1 The path coefficient (PC) diagram representing cause and effect relationships among quantitative traits and grain yield.

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