



Estimation of Genetic Variability, Direct and Indirect Effects of Yield Contributing Characters on Grain Yield of Upland Rice (*Oryza sativa* L.) Germplasm

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

A study was carried out using 24 upland rice genotypes grown in randomized block design with three replications to estimate genetic variability, correlation and path coefficient analysis. Based on the mean performance, of high grain yield per hill, the genotype SHUATS UPR-13 followed by SHUATS UPR-11 were identified to be superior. High phenotypic and genotypic coefficient of variation were observed for grain yield per hill, biological yield per hill and number of panicles per hill. High heritability coupled with high genetic advance as percent of mean was observed for grain yield per hill, biological yield per hill, number of panicles per hill, number of tillers per hill indicating that genotypic variation present in the genetic material studied is probably due to additive genetic variance, which can be effectively exploited in crop improvement programme. The traits biological yield per hill, number of tillers per hill, number of panicles per hill, plant height, harvest index were found to have positive significant association with grain yield per hill at both genotypic and phenotypic level. Hence, selection of these traits shall help in selecting the genotypes with high grain yield per hill. Number of tillers per hill, panicle length, biological yield per hill, harvest index had positively direct effect on grain yield per hill at both genotypic and phenotypic level. Therefore, effective selection must be attempted for these traits which would help in the improvement of grain yield in rice genotypes suitable for different environments.

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1. INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the family Poaceae (Graminae) with chromosome no. $2n = 24$. It is the second most important cereal crop after Wheat. It is the staple food in many parts of the world including many developing countries [1]. Approximately 90% of the world's rice is grown and consumed in Asia, whereas 50% of the population depends on rice for food. It is one of the world's largest cereal crops providing the caloric need of millions of people. It plays a pivotal role in Indian economy. Thus, to meet the challenge of producing more rice from suitable lands, need of rice varieties with higher yield potential and greater yield stability to ensure food and nutritional security of India's ever-increasing population is the need of the hour.

In India, most of the upland rice is grown in the eastern and northern central states and along the south-western coast. Upland rice is grown in around 6.00 million hectares of well-drained soil where moisture stress and blast are the major abiotic and biotic constraint, respectively with the productivity of around 1 t/ha (ICAR-NRRI, Cuttack 2019). Principal upland rice growing states are Madhya Pradesh (1.30 million ha), West Bengal (0.88 million ha), Uttar Pradesh (0.70 million ha), Orissa (0.70 million ha), and Bihar (0.53 million ha). Globally rice is cultivated in 162.00 million hectares with an annual production of around 503.17 million metric tonnes (United States, Department of Agriculture, Annual Report 2020).

Grain yield is a complex polygenic character controlled by many genes interacting not just with other genetic elements but also the environment. The selection of parents based on yield alone is often misleading (Selvaraj et al. 2011). Knowledge regarding the relative contribution of individual traits to yield may be accomplished by correlation but it does not provide adequate information about the contribution of each factor towards the yield. Therefore, path coefficient analysis is utilized to have an idea of direct and indirect contribution of traits on yield. The present paper deals with genetic variability, character association and path analysis in a set of 24 rice genotypes.

1.1 Justification

- Research results over the years indicated that indiscriminate consumption of rice with

little or no attention to its nutritional value poses threat to the human health.

- Maintaining rice grain quality to meet the diverse interest groups in the rice sub-sector currently represents a major challenge of rice development in many rice producing areas of the world.
- To charter the needs of food security in world keeping the above points in view, an investigation was planned with the following objectives.

1.2 Objectives

1. To estimate the genetic variability parameters for grain yield and its attributing characters among upland rice germplasm.
2. To access the relationship between yield and yield attributing traits on grain yield.
3. To measure the direct and indirect effects of yield contributing traits on grain yield.

2. MATERIALS AND METHODS

Twenty four upland rice genotypes collected from Sam Higginbottom University of Agriculture and Technology (SHUATS) were sown in randomized block design with three replications, at the experimental farm of the Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture Technology and Sciences, Allahabad, during *Kharif* 2021. The site is located at 25.28 N latitude, 81.54 E longitude and 98 meters above the sea level. All types of facilities necessary for cultivation of successful crop including field preparation inputs, irrigation facilities were provided during the crop growing period. In each replication, two to three seedlings were sown per hill with 20x10 cm spacing. The observations were recorded on five randomly selected plants from each plot on days to 50 percent flowering, plant height (cm), number of tillers per hill, number of panicles per hill, panicle length (cm), number of spikelets per panicle, flag leaf length (cm), flag leaf width (cm), test weight (g), days to maturity, biological yield per hill (g), harvest index and grain yield per hill (g). The statistical and biometrical analysis of GCV Genotypic Coefficient of Variation and PCV Phenotypic Coefficient of Variation were calculated by formula given by Burton [2], heritability in broad sense (h^2) by Burton and de Vane [3] and genetic advance *i.e.*, the expected

Table 1. Experimental material used in the present study

Sl. No.	Advanced breeding lines	Cross combination	Grain type
1	SHUATS UPR-2	IR82589-B-B-95-2 X Vandana (P5)	Long slender
2	SHUATS UPR-3	IR82589-B-B-95-2 X Vandana (P6)	Long slender
3.	SHUATS UPR-4	IR82589-B-B-95-2 X Vandana (P7)	Long slender
4.	SHUATS UPR-5	IR82589-B-B-95-2 X NDR-97 (P1)	Long slender
5.	SHUATS UPR-6	IR82589-B-B-95-2 X NDR-97 (P3)	Long slender
6.	SHUATS UPR-7	IR82589-B-B-95-2 X NDR-97 (P5)	Long slender
7.	SHUATS UPR-8	IR82589-B-B-95-2 X NDR-97 (P6)	Long slender
8.	SHUATS UPR-9	IR82589-B-B-95-2 X NDR-97 (P7)	Long slender
9.	SHUATS UPR-10	IR82589-B-B-95-2 X NDR-97 (P8)	Long slender
10.	SHUATS UPR-11	IR82589-B-B-95-2 X NDR-97 (P9)	Long slender
11.	SHUATS UPR-12	IR82589-B-B-2-3 X NDR-97 (P1)	Medium bold
12.	SHUATS UPR-13	IR82589-B-B-2-3 X NDR-97 (P2)	Medium bold
13.	SHUATS UPR-14	IR82589-B-B-2-3 X NDR-97 (P3)	Medium bold
14.	SHUATS UPR-15	IR82589-B-B-2-3 X NDR-97 (P4)	Medium bold
15.	SHUATS UPR-16	IR82589-B-B-2-3 X NDR-97 (P5)	Medium bold
16.	SHUATS UPR-17	IR82589-B-B-2-3 X NDR-97 (P6)	Medium bold
17.	SHUATS UPR-18	IR82589-B-B-2-3 X NDR-97 (P7)	Medium bold
18.	SHUATS UPR-19	IR82589-B-B-2-3 X NDR-97 (P8)	Medium bold
19.	SHUATS UPR-20	IR82589-B-B-2-3 X NDR-97 (P9)	Medium bold
20.	SHUATS UPR-21	IR82589-B-B-2-3 X NDR-97 (P10)	Medium bold
21.	SHUATS UPR-22	IR82589-B-B-2-3 X Sahbhagidhan (P1)	Medium slender
22.	SHUATS UPR-23	IR82589-B-B-2-3 X Sahbhagidhan (P2)	Medium slender
23.	SHUATS UPR-24	IR82589-B-B-2-3 X Sahbhagidhan (P5)	Medium slender
24.	SAHBHAGI DHAN		Medium slender

Cross combination: (P1): Plant 1, NDR-97: Narendradhan-97

genetic gain was calculated using the procedure given by Johnson et al. [4]. The correlation coefficient and path coefficient were worked based on method recommended by Al-Jibouri et al. [5] and Deway and Lu [6] respectively.

3. RESULTS AND DISCUSSION

Analysis of variance for yield and yield contributing are presented in Table 2. Analysis of variance indicated highly significant differences among the genotypes for all the traits studied. This indicates that there is ample scope for selection of promising lines from the present gene pool for yield and its components. All the characters showed significant differences at 1% level of significance.

The mean squares due to genotypes showed highly significant differences ($\alpha=0.01$) for all the characters indicating the presence of substantial amount of genetic variability among the rice genotypes, which revealed a wide range of variation for all traits studies the mean values, the coefficient of variation (C.V.), standard error of the mean ($SEm\pm$), the critical difference (C.D.)

at 5% and 1%, range of 24 genotypes for 14 quantitative characters are presented.

Mean performance of grain yield per plant was high for SHUATS UPR-13 (28.53g) followed by SHUATS UPR-11 (20.00g), SHUATS UPR-3 (19.53g), SHUATS UPR-5 (18.46g) and SHUATS UPR-16 (18.33g).

3.1 Genotypic and Phenotypic Coefficient of Variation

The estimates of variability parameters for various yield and yield related traits are presented in Table 4. It is depicted the estimates of PCV were found higher than their corresponding GCV estimates, indicating that the apparent variation is not only due to genotypes but, also due to the influence of environment. On an average, high GCV and PCV coefficient of variation were recorded for grain yield per hill, number of tillers per hill, number of panicles per hill and flag leaf length indicating the presence of variation for all the characters under study.

Heritability: High magnitude of heritability was recorded for grain yield per hill (94.84), biological yield per hill (92.78), number of tillers per hill

(85.38), number of panicles per hill (84.14), flag leaf length (82.62), flag leaf width (75.49), plant height (69.70) and spikelet per panicle (69.41). Whereas, moderate heritability was recorded for panicle length (54.11), test weight (47.09), harvest index (42.77), days to maturity (34.08) and days to 50% flowering (30.74).

In the present study, estimates of broad sense heritability are computed which includes both additive and non-additive gene effects. Higher values of broad sense heritability for, grain yield per hill, biological yield per hill, number of tillers per hill, number of panicles per hill, flag leaf length, flag leaf width, plant height and spikelet per panicle indicates the scope of genetic improvement through selection. High to moderate heritability for most of the traits in the present study indicated the considerable potential for the development of high-yielding varieties through desirable selection in succeeding generations.

3.2 Genetic Advance as a Percentage Mean (5%)

The estimation of genetic advance as per cent mean helps to understand the type of gene action involved in the expression of a trait. It is classified as low (less than 10%), moderate (10-20%) and high (more than 20%) as proposed by Johnson et al. [4].

High genetic advance as per cent mean was recorded for grain yield per hill (59.00) followed by biological yield per hill (52.68), number of panicles per hill (36.77), number of tillers per hill

(35.90) and flag leaf length (28.41). Moderate genetic advance as per cent mean was observed for flag leaf width (19.56), spikelets per panicle (18.62), plant height (14.98), panicle length (12.49) and harvest index (11.08). Whereas, test weight (8.78), days to 50% flowering (4.27), days to maturity (3.26) recorded low genetic advance as per cent mean.

In the present investigation, high genetic advance as per cent of mean coupled with high heritability was recorded for grain yield per hill, biological yield per hill, number of panicles per hill, number of tillers per hill indicating most likely the heritability might be due to additive gene effect and selection may be effective in segregating generations to improve these traits.

3.3 Correlation Analysis

The estimation of Correlation coefficient analysis is presented in Table 5. In the improvement of any crop, the knowledge of association of one or more of these characters associated with yield is useful in selecting the individual with high yield on the basis of their phenotypic values. Such association between plant characters is statistically elaborated by correlation coefficients. But the correlation between the dependent and independent character and the direct and indirect effects of the independent character on the dependent character are completely separate things. Sometime the correlation between two characters may be highly positive but the direct effect of the independent characters on the

Table 2. Analysis of variance for 14 quantitative characters of upland rice

Characters	Mean Sum of Squares		
	Replication (df=02)	Treatments (df= 23)	Error (df=46)
Days to 50% flowering	32.3880	37.946**	16.272
Plant height	15.1650	339.357**	42.949
Number of tillers per hill	0.7060	6.019**	0.325
Number of panicles per hill	0.0050	5.051**	0.299
Panicle length	4.3680	12.636**	2.784
Flag leaf length	4.180	97.352**	6.376
Flag leaf width	0.0160	0.052**	0.005
Spikelets per panicle	192.810	755.484**	96.755
Days to maturity	29.4920	37.768**	14.805
Biological yield per hill	4.5120	225.457**	5.696
Harvest index	13.7860	65.943**	20.339
Test weight	5.4460	8.778**	2.391
Grain yield per hill	1.3240	61.529**	1.094
Grain yield per hectare	0.0180	6.697**	0.136

** indicates 1% level of significance

Table 3. Mean performance of 24 upland rice genotypes for 14 quantitative traits during *Kharif*-2021

Sl. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of tillers per hill	No. of Panicles per hill	Panicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Spikelets per panicle	Days to maturity	Biological yield per hill	Harvest index (%)	Test weight (g)	Grain yield per hill	Grain yield per ha
1	SHUATS UPR-2	71.33	94.60	8.19	6.66	22.66	30.96	1.06	104.73	103.33	19.80	44.45	23.00	8.79	2.90
2	SHUATS UPR-3	71.00	101.46	7.86	6.45	22.40	30.10	1.14	146.66	101.32	39.00	50.19	21.99	19.53	6.44
3	SHUATS UPR-4	73.33	120.53	5.66	4.93	25.51	33.80	1.29	148.26	105.00	29.33	48.46	22.99	14.20	4.67
4	SHUATS UPR-5	71.65	108.73	8.52	7.86	22.06	31.46	1.18	147.73	98.00	36.66	50.40	22.00	18.46	6.09
5	SHUATS UPR-6	70.00	127.26	8.60	7.46	23.09	35.53	1.07	168.53	99.00	35.41	48.26	24.00	17.06	5.61
6	SHUATS UPR-7	75.00	121.86	7.00	6.53	22.73	42.46	1.22	151.40	105.33	29.32	50.24	21.00	14.53	4.79
7	SHUATS UPR-8	71.00	108.03	8.10	6.99	21.26	33.72	1.08	146.60	105.00	30.53	51.32	22.00	15.53	5.15
8	SHUATS UPR-9	72.66	122.93	7.06	6.13	22.85	37.06	1.05	123.72	104.33	42.20	41.84	25.00	17.66	5.82
9	SHUATS UPR-10	73.66	117.90	7.66	7.33	24.13	41.83	1.28	133.85	101.00	34.03	47.94	26.00	16.32	5.38
10	SHUATS UPR-11	74.99	138.13	9.00	6.39	23.09	47.85	1.32	170.25	103.33	39.66	50.43	21.99	20.00	6.60
11	SHUATS UPR-12	73.00	101.80	8.80	7.93	20.76	28.98	1.10	125.00	102.66	24.73	43.16	23.00	10.66	3.51
12	SHUATS UPR-13	72.33	125.23	9.93	9.33	22.76	40.35	1.11	145.20	100.66	54.06	52.79	23.99	28.53	9.41
13	SHUATS UPR-14	75.00	127.13	7.33	6.53	25.00	42.92	1.36	127.40	104.33	31.33	50.01	24.00	15.56	5.13
14	SHUATS UPR-15	68.66	111.66	7.65	7.26	21.90	32.73	1.15	125.40	99.00	36.53	47.8	24.00	17.46	5.75
15	SHUATS UPR-16	66.00	115.93	6.79	6.26	20.03	36.36	1.14	139.06	97.66	37.80	48.49	27.00	18.33	6.04
16	SHUATS UPR-17	69.00	113.50	4.53	4.00	17.23	35.56	0.87	130.33	100.32	20.73	51.06	23.00	10.46	3.45
17	SHUATS UPR-18	72.00	124.56	9.46	8.46	20.63	39.70	1.10	133.26	100.00	37.53	48.11	26.00	18.06	5.95
18	SHUATS UPR-19	71.00	100.83	6.32	5.60	18.30	33.50	1.08	137.00	100.32	40.00	39.22	23.00	15.59	5.14
19	SHUATS UPR-20	67.00	106.53	6.00	4.53	18.60	35.73	0.93	124.99	98.65	37.86	34.21	25.99	12.86	4.24

Sl. No.	Genotypes	Days to 50% flowering	Plant height (cm)	No. of tillers per hill	No. of Panicles per hill	Panicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Spikelets per panicle	Days to maturity	Biological yield per hill	Harvest index (%)	Test weight (g)	Grain yield per hill	Grain yield per ha
20	SHUATS UPR-21	68.65	109.40	5.93	5.53	21.26	36.10	1.15	131.53	101.33	27.93	51.72	25.00	14.46	4.77
21	SHUATS UPR-22	67.00	116.53	7.06	6.59	22.43	36.43	1.45	138.00	96.00	23.93	50.99	23.00	12.06	3.97
22	SHUATS UPR-23	73.00	114.66	6.66	5.92	21.39	45.40	1.12	121.93	104.00	24.46	43.86	20.00	10.73	3.54
23	SHUATS UPR-24	74.00	109.93	4.46	4.13	25.00	40.20	1.26	108.26	102.33	15.06	40.84	23.00	6.13	2.02
24	Sahbhagi Dhan (C)	83.33	99.66	6.66	6.36	22.46	22.34	1.02	147.33	113.33	25.70	51.59	22.25	13.26	4.37
Range	Mean	71.86	114.12	7.30	6.47	21.98	36.30	1.15	136.52	101.93	32.24	47.40	23.47	15.26	5.03
	Max	83.33	138.13	9.93	9.33	25.51	47.86	1.45	170.26	113.33	54.06	52.79	27.00	28.53	9.41
	Min	66.00	94.60	4.46	4.00	17.23	22.34	0.87	104.73	96.00	15.06	34.21	20.00	6.13	2.02
	CV	5.61	5.74	7.80	8.45	7.59	6.96	6.23	7.21	3.77	7.40	9.51	6.59	6.85	7.33
	SEM	2.33	3.78	0.33	0.32	0.96	1.46	0.04	5.68	2.22	1.38	2.60	0.89	0.60	0.21
	CD (at 5%)	6.63	10.77	0.94	0.90	2.74	4.15	0.12	16.17	6.32	3.92	7.41	2.54	1.72	0.61

dependent characters may be negative. Hence, mere correlation cannot serve the purpose of selection in crop improvement programme. In a complex situation, selection for an optimum advance should be based on judiciously computed index. Therefore, the method of partitioning the direct and indirect effects of the independent character on the dependent character i.e. path coefficient analysis was detailed by Wright [7]. Li (1954) emphasized great use of this technique in genetics and plant breeding. Further, Dewey and Lu [6] gave the detail procedure for path analysis of replicated trials which was quite different technique in eliminating the environmental variances [8-15].

In the present investigation, at the both genotypic and phenotypic levels, significant positive correlations were observed for plant height, number of tillers per plant, number of panicles per plant, number of spikelets per panicle, biological yield per hill, harvest index and test weight [16-20].

3.4 Path Coefficient Analysis

The estimation of Path coefficient analysis is presented in Table 6.

Path coefficient analysis is an important tool for partitioning the correlation coefficient in to direct and indirect effects of an independent variable and dependent variable through correlation gives information about the component traits associated with the characters, they could not provide an exact picture of relative importance of the direct and indirect contribution of the component character.

In the present investigation, the path coefficient analysis at genotypic level revealed that number of tillers per hill, panicle length, biological yield per hill, harvest index had positive direct effect on grain yield per hill. Therefore, selection should be based on these traits for obtaining high yielding genotypes in upland rice using pureline method of breeding [21-25].

Correlation and path coefficient studies suggest that selection based on days to 50% flowering, biological yield per hill and harvest index had positive correlation and direct effect with grain yield per hill and would bring out desired improvement in yield and crop improvement programme based on these traits in upland rice [26-30].

Table 4. Genetic variability parameters for 14 quantitative characters in upland rice genotypes

Characteristics	GCV	PCV	h^2 (bs)	GA	GAM
Days to 50% flowering	3.74	6.746	30.748	3.07	4.273
Plant height	8.71	10.433	69.701	17.095	14.98
No. of tillers per hill	18.863	20.414	85.385	2.622	35.906
No. of panicles per hill	19.462	21.217	84.143	2.378	36.777
Panicle length	8.244	11.206	54.118	2.746	12.493
Flag leaf length	15.172	16.691	82.628	10.312	28.411
Flag leaf width	10.931	12.581	75.49	0.225	19.564
Spikelets per panicle	10.854	13.028	69.413	25.432	18.629
Days to maturity	2.714	4.649	34.082	3.327	3.264
Biological yield per hill	26.551	27.564	92.785	16.983	52.685
Harvest index	8.226	12.578	42.773	5.253	11.082
Test weight	6.217	9.059	47.096	2.063	8.789
Grain yield per hill	29.41	30.198	94.849	9.005	59.003
Grain yield per hector	29.388	30.288	94.147	2.956	58.741

PCV: Phenotypic Coefficient of Variation, GCV: Genotypic Coefficient of Variation, h^2 (bs): Heritability (broad sense), GA: Genetic Advance, GAM: Genetic Advance as Percent Mean

Table 5. Estimation of Phenotypic and Genotypic Correlation Coefficient for different quantitative characters in upland rice

Traits		PH	NT/H	NP/H	PL	FLL	FLW	S/P	DM	BY/H	HI	TW	GY/H
DF	P	0.0022	0.0993	0.0817	0.281*	-0.0760	0.0854	0.0638	0.471*	-0.1148	0.0355	-0.2285	-0.0870
	G	0.0857	0.0752	0.1363	0.700*	-0.0697	0.1470	0.265*	0.822**	-0.1693	0.371*	-0.663**	-0.0100
PH	P	1	0.2261	0.1633	0.286*	0.640**	0.313*	0.399**	-0.0649	0.322*	0.2315	0.1628	0.406**
	G	1	0.289*	0.2302	0.415**	0.830**	0.483**	0.533**	-0.1722	0.428**	0.397**	0.1453	0.508**
NT/H	P		1	0.833**	0.1296	0.0236	0.0715	0.316*	-0.0039	0.525**	0.1927	0.0655	0.594**
	G		1	0.986**	0.1697	0.0731	0.1304	0.402**	-0.2072	0.570**	0.404**	-0.0052	0.664**
NP/H	P			1	0.1846	-0.0054	0.0979	0.2127	-0.0586	0.469**	0.309*	0.0576	0.592**
	G			1	0.1708	-0.0309	0.1640	0.335*	-0.1737	0.527**	0.473**	0.0912	0.650**
PL	P				1	0.1293	0.531**	0.0480	0.2118	-0.0730	0.1171	-0.1862	0.0290
	G				1	0.289*	0.825**	0.1504	0.460**	-0.0785	0.407**	-0.0975	0.0977
FLL	P					1	0.355*	0.0515	-0.1831	0.1440	0.0385	0.0473	0.1710
	G					1	0.456**	0.0736	-0.2001	0.1599	-0.0217	0.0083	0.1598
FLW	P						1	0.1537	-0.0993	-0.0795	0.2217	-0.0511	0.0467
	G						1	0.1850	-0.0867	-0.0663	0.383**	-0.1619	0.0733
S/P	P							1	0.0499	0.366*	0.469**	-0.1018	0.513**
	G							1	0.0408	0.502**	0.594**	-0.263*	0.613**
DM	P								1	-0.2154	0.249*	-0.1900	-0.1087
	G								1	-0.303*	-0.0332	-0.701**	-0.266*
BY/H	P									1	-0.0361	0.266**	0.901**
	G									1	0.1562	0.411**	0.945**
HI	P										1	-0.1064	0.382**
	G										1	-0.288*	0.460**
TW	P											1	0.1940
	G											1	0.268*

DF50: Days to 50% Flowering, DM:Days to Maturity, PH: Plant Height, NT/H: Number of Tillers per Hill, NP/H: Number of Panicles per Hill, PL: Panicle Length, FLL: Flag Leaf Length, FLW: Flag leaf width, S/P: Spikelets per Panicle, DM: Days to Maturity, BY/H: Biological Yield per Hill, HI: Harvest index, TW: Test weight, P: Phenotypic, G: Genotypic

Table 6. Estimation of direct and indirect effects of yield component traits on seed yield of upland rice genotypes at Phenotypic and Genotypic level

Traits		DF50	PH	NT/H	NP/H	PL	FLL	FLW	S/P	DM	BY/H	HI	TW	GY/H
DF50	P	-0.0036	0.0000	-0.0004	-0.0003	-0.0010	0.0003	-0.0003	-0.0002	-0.0017	0.0004	-0.0001	0.0008	-0.0870
	G	-0.0081	-0.0007	-0.0006	-0.0011	-0.0057	0.0006	-0.0012	-0.0022	-0.0120	0.0014	-0.0030	0.0054	-0.0100
PH	P	0.0000	-0.0168	-0.0038	-0.0027	-0.0048	-0.0108	-0.0053	-0.0067	0.0011	-0.0054	-0.0039	-0.0027	0.406**
	G	0.0148	0.1729	0.0499	0.0398	0.0717	0.1435	0.0835	0.0922	-0.0298	0.0740	0.0687	0.0251	0.508**
NT/H	P	0.0038	0.0087	0.0384	0.0320	0.0050	0.0009	0.0027	0.0121	-0.0001	0.0202	0.0074	0.0025	0.594**
	G	0.0243	0.0931	0.3227	0.3181	0.0548	0.0236	0.0421	0.1298	-0.0669	0.1840	0.1340	-0.0017	0.664**
NP/H	P	-0.0004	-0.0007	-0.0037	-0.0044	-0.0008	0.0000	-0.0004	-0.0009	0.0003	-0.0021	-0.0014	-0.0003	0.592**
	G	-0.0422	-0.0713	-0.3053	-0.3097	-0.0529	0.0096	-0.0508	-0.1037	0.0538	-0.1633	-0.1466	-0.0282	0.650**
PL	P	0.0123	0.0125	0.0057	0.0081	0.0438	0.0057	0.0233	0.0021	0.0093	-0.0032	0.0051	-0.0082	0.0290
	G	0.0269	0.0159	0.0065	0.0066	0.0384	0.0111	0.0316	0.0058	0.0177	-0.0030	0.0156	-0.0037	0.0977
FLL	P	-0.0022	0.0182	0.0007	-0.0002	0.0037	0.0284	0.0101	0.0015	-0.0052	0.0041	0.0011	0.0013	0.1710
	G	0.0105	-0.1253	-0.0110	0.0047	-0.0437	-0.1510	-0.0688	-0.0111	0.0302	-0.0241	0.0033	-0.0013	0.1598
FLW	P	-0.0009	-0.0034	-0.0008	-0.0011	-0.0057	-0.0038	-0.0108	-0.0017	0.0011	0.0009	-0.0024	0.0006	0.0467
	G	-0.0012	-0.0039	-0.0010	-0.0013	-0.0066	-0.0036	-0.0080	-0.0015	0.0007	0.0005	-0.0031	0.0013	0.0733
S/P	P	-0.0015	-0.0097	-0.0077	-0.0052	-0.0012	-0.0013	-0.0037	-0.0243	-0.0012	-0.0089	-0.0114	0.0025	0.513**
	G	-0.0566	-0.1137	-0.0858	-0.0714	-0.0321	-0.0157	-0.0395	0.2133	-0.0087	-0.1071	-0.1267	0.0562	0.613**
DM	P	-0.0089	0.0012	0.0001	0.0011	-0.0040	0.0035	0.0019	-0.0009	-0.0189	0.0041	-0.0047	0.0036	-0.1087
	G	0.0010	-0.0001	-0.0001	-0.0001	0.0003	-0.0001	-0.0001	0.0000	0.0007	-0.0002	0.0000	-0.0005	-0.266*
BY/H	P	-0.0907	0.2544	0.4150	0.3709	-0.0577	0.1138	-0.0628	0.2888	-0.1701	0.7901	-0.0285	0.2103	0.901**
	G	-0.1793	0.4529	0.6040	0.5584	-0.0831	0.1693	-0.0703	0.5319	-0.3212	0.9240	0.1654	0.4350	0.945**
HI	P	0.0134	0.0873	0.0727	0.1164	0.0441	0.0145	0.0836	0.1767	0.0940	-0.0136	0.3770	-0.0401	0.382**
	G	0.1434	0.1534	0.1561	0.1829	0.1572	-0.0084	0.1481	0.2296	-0.0128	0.0604	0.3864	-0.1113	0.460**
TW	P	0.0008	-0.0005	-0.0002	-0.0002	0.0006	-0.0002	0.0002	0.0003	0.0006	-0.0009	0.0004	-0.0033	0.1940
	G	0.0537	-0.0118	0.0004	-0.0074	0.0079	-0.0007	0.0131	0.0213	0.0568	-0.0333	0.0233	-0.0810	0.268*
GY/H	P	-0.0870	0.406*	0.594**	0.592**	0.0290	0.1710	0.0467	0.513**	-0.1087	0.901**	0.382**	0.1940	1.0000
	G	-0.0100	0.508**	0.664**	0.650**	0.0977	0.1598	0.0733	0.613**	-0.266*	0.945**	0.460**	0.268*	1.0000

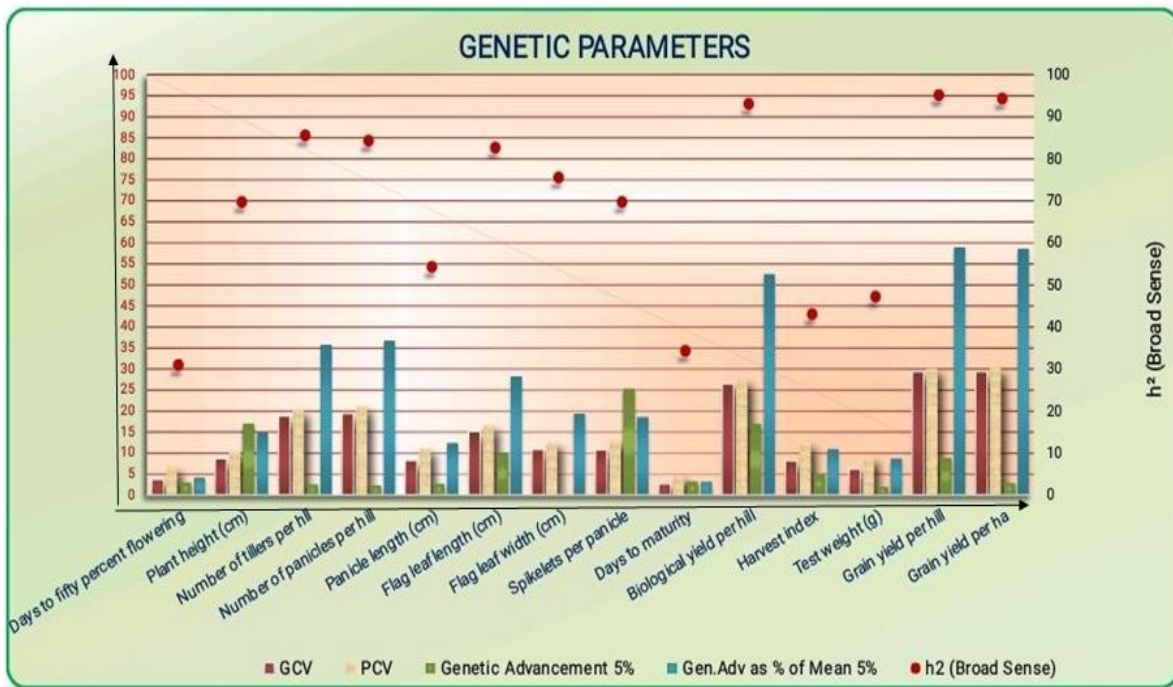


Fig. 1. Histogram depicting GCV, PCV, heritability and genetic advance for 14 quantitative characters of rice genotypes

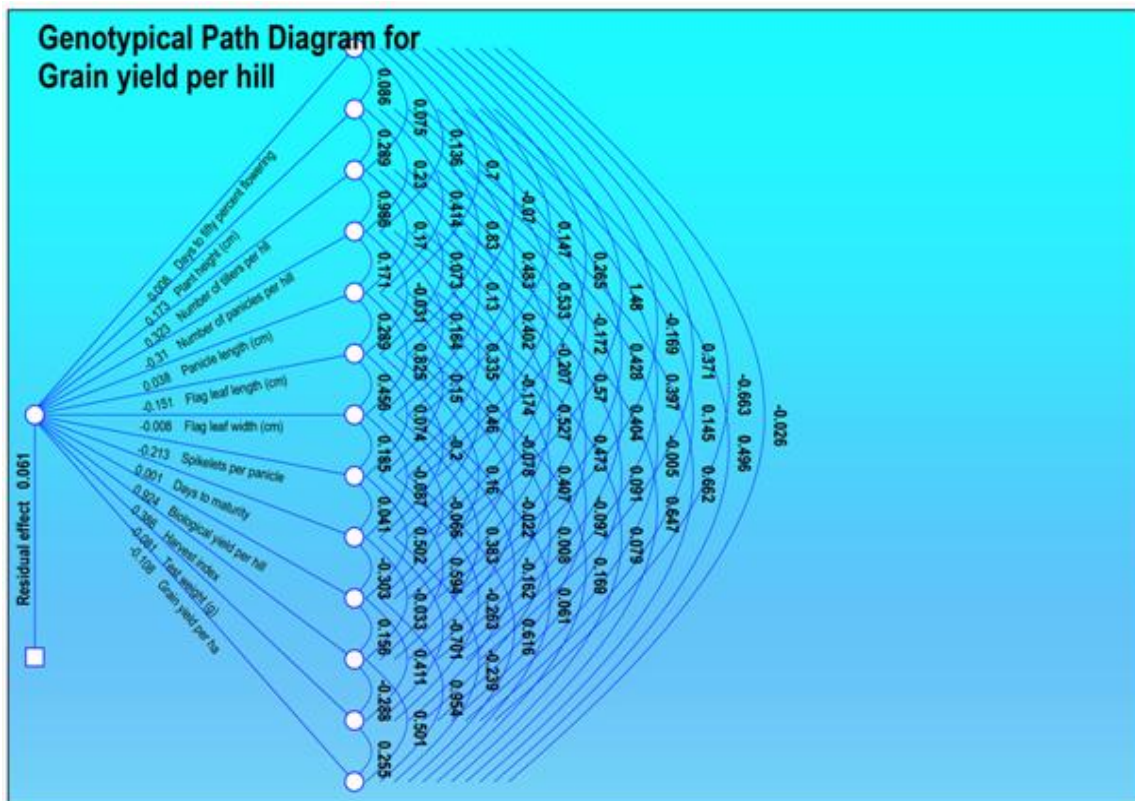


Fig. 2. Genotypical path diagram for grain yield per hill (g)

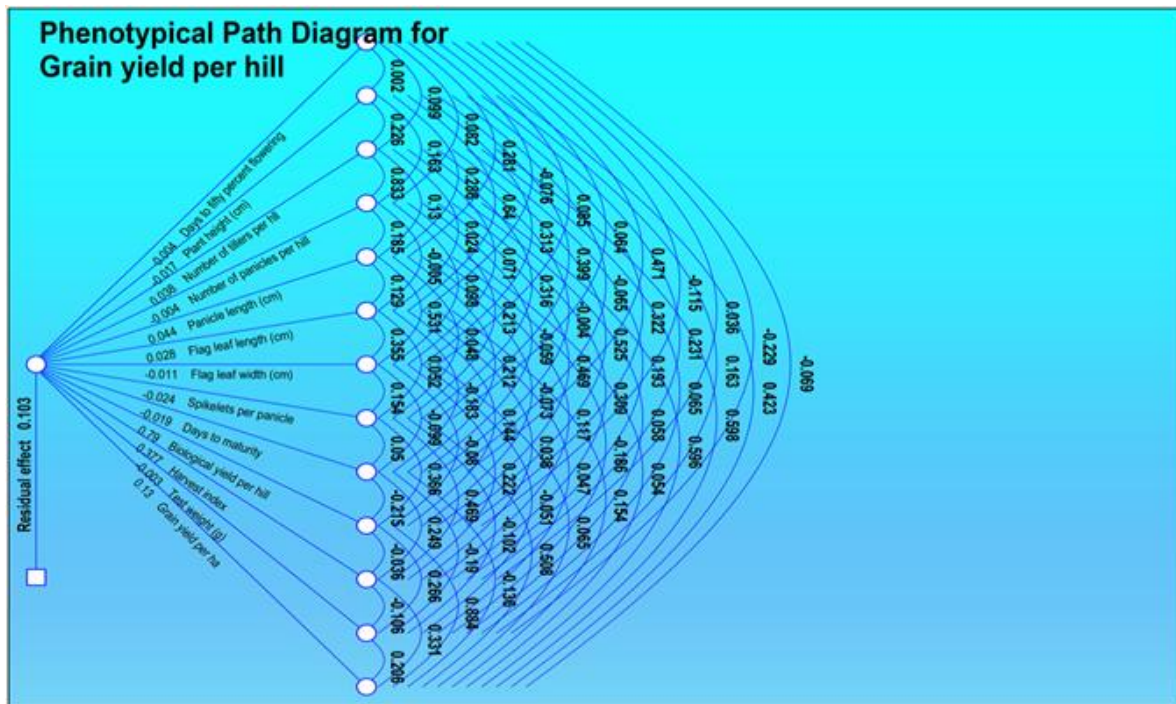


Fig. 3. Phenotypic path diagram for grain yield per hill (g)

4. CONCLUSION

- From the present investigation, it is concluded that the genotype SHUATS UPR – 13 (9.41 t/ha) was found superior for grain yield per hectare followed by SHUATS UPR – 11 (6.60 t/ha) over the check variety SAHBHAGI DHAN (4.37 t/ha).
- Among the 24 genotypes of upland rice, mean sum of squares due to genotypes were significant for all the characters studied, suggesting the existence of high genetic variability among the genotypes for all the traits. High GCV and PCV were recorded for grain yield per hill followed by biological yield per hill and number of panicles per hill. High heritability coupled with high genetic advance as per cent mean was recorded for grain yield per hill, biological yield per hill, number of panicles per hill and number of tillers per hill [31-34].
- The traits, biological yield per hill, number of tillers per hill and number of panicles per hill recorded positive significant association with grain yield per hill at both genotypic and phenotypic level. Hence, these characters emerged as most important associate of grain yield per hill and

selection of these traits shall help in selecting genotypes with high grain yield.

- Number of tillers per hill, panicle length and biological yield per hill had a high positive direct effect on grain yield per hill. Therefore, direct selection for these traits shall be rewarding for yield improvement in upland rice.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Akinola TF, Odiyl AC, Ohunakin AO. Genetic variability and genetic diversity of 13 upland rice genotypes for agronomic traits and nutritional qualities. *Crop Res.* 2019;45(1):63-8.
- Burton GW. Estimating heritability in tall fescue from replicated clonal material. *Agron J.* 1952;45(3):474-81.
- Turner JH, GW, De vane EH, Agron J. Estimating heritability in Tall Fescue (*Festuca arundinacea*) from replicated clonal material. 1953;45(10):487-90.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental

- variability in soybeans 1. Agron J. 1955; 47(7):314-8.
5. Jibouri A. Genetic variability and Correlation Studies in Chillies. Prog Hortic. 1958;36:113-7.
 6. Dewey DR, Lu KH. A correlation and path-coefficient analysis of components of crested wheatgrass seed production 1. Agron J. 1959;51(9):515-8.
 7. Wright S. Correlation causation. J Agric Res. 1921;20:557-86.
 8. Ahamed S, Chowdhury R. Atik, Ahmed S, Hossain S, Matin, M.N. Pak J Agric Res; 2021. Analysis of Genetic Variability, Heritability and Correlation among Bangladeshi Local Rice Cultivars (*Oryza sativa* L.);34(2):356-61.
 9. Alam MS, Hassan L, Islam MM, Begum SN, Islam SN. Evaluation of habitual rice (*Oryza sativa* L.) landraces of Bangladesh through different genetic parameters. Int J Innov Sci Res. 2014;11(2):494-502.
 10. Anjaneyulu M, Reddy DR, Reddy KHP. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). Res Crops. 2010;11(2):415-6.
 11. Anyacha C, Adegbehingbe F, Uba U, Popoola B, Gracen V, Mande S, Fofana, M. Genetic diversity of selected upland rice genotypes (*Oryza sativa* L.) for grain yield and related traits. Journal of Plant Nutrition and Soil Sciences. 2018;22(5):1-9.
 12. Bhargavi M, Shanthi P, Reddy V, Reddy DM, Reddy BR. Estimates of genetic variability, heritability and genetic advance for grain yield and other yield attributing traits in rice (*Oryza sativa* L.). The Pharm Innov J. 2021;10(5):507-11.
 13. Ekka R, Sarawgi AK, Raja R. Correlation and path analysis in traditional rice accessions of Chhattisgarh. Rice Res. 2011;4(1&2):11-7.
 14. Immanuel SC, Pothiraj N, Thiyagarajan K, Bharathi M, Rabindran R. Genetic parameters of variability, correlation and pathcoefficient studies of grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). Afr J Biotechnol. 2011;10(17):3322-34.
 15. Islam MZ, Khalequzzaman M, Bashar MK, Ivy NA, Haque MM, Mian MAK. Variability assessment of aromatic and fine rice germplasm in Bangladesh based on quantitative traits. Sci World J. 2016:14.
 16. Jahan N, Rahman M, Khan NA, Hasan M, Habib M. Genetic variability, heritability and genetic advance of some prominent advanced lines of upland rice (broadcast Aus) genotypes. Int J Bus Soc Sci Res; 2020. ISSN: 2309-7892
 17. Jayasudha S, Deepak S. Genetic parameters of variability, correlation and path-coefficient for grain yield and physiological traits in rice (*Oryza sativa* L.) under shallow lowland situation. Electron J Plant Breed. 2010;1(5):1332-8.
 18. Muthuramu S, Sakthivel S. Genetic variability studies in rainfed rice (*Oryza sativa* L.). Rice Res. 2016;9(2).
 19. Osman KA, Mustafa AM, Ali F. Genetic Variability for yield and related attributes of upland rice genotypes in semi-arid zones (Sudan). Afr J Agric Res. 2012;7(33):4613-9.
 20. Paul A, Suresh BG, Lavanya GR. Variation and association among yield and yield components in upland rice (*Oryza sativa* L.). Environ Ecol. 2011;29(2):690-5.
 21. Pratap A, Bisen P, Loitongbam B, Singh PK. Assessment of genetic variability for yield and yield components in rice (*Oryza sativa* L.) germplasms. Int J Bio-Resource Stress Manag. 2018;9(1):87-92.
 22. Prasad GSV, Prasad ASR, Sastry MVS, Srinivasan TE. Genetic relationship among yield components in rice. Indian J Agric Sci. 2013;58(6):470-2.
 23. Rahman SS, Mishra SB, Ali F. Estimation of grain yield and inter-relationship with yield components in upland rice. Mysore J Agric Sci. 2012;34:142-6.
 24. Rashmi D, Saha S, Loitongbam B, Singh S, Singh PK. Genetic variability study for yield and yield components in rice (*Oryza sativa* L.). Int J Agric Environ Biotechnol. 2017;10(2):171.
 25. Rathi S, Yadav RNS, Sarma RN. Variability in grain quality characters of upland rice of Assam, India. Rice Sci. 2010;17(4):330-3.
 26. Saidaiah P, Sudheer S, Ramesha MS. Variability for yield and yield component attributes in rice. Crop Res. 2010;39:(1,2&3):91-93.
 27. Samudin S, Labalado S. Genetic diversity, heritability, correlation and path analysis yields and yield component local rice variety. Int J Vet Sci Agric Res. 2019;1(3):39-48.
 28. Sravan T, Rangare NR, Suresh BG, Kumar S. Genetic variability and characters

- association in rainfed upland rice. Rice Res. 2012;5(1&2):24-9.
29. Srivastava N, Babu GS, Singh ON, Verma R, Pathak SK, Behra M et al. Genetic variation, heritability and diversity analysis of rice (*Oryza sativa* L.) germplasm based on quantitative traits. J Pharm Innov. 2017;6(12):316-20.
 30. Prasad K, Chakraborty M, Singh D, Kumari P, Ekka JP. Genetic variability, correlation and path coefficient studies in F₂ generation of rice (*Oryza sativa* L.). Int J Chem Stud. 2020;8(4):3116-20.
 31. Tiruneh A, Gebrselassie W, Tesfaye A. Genetic diversity study on upland rice (*Oryza sativa* L.) genotypes based on morphological traits in South-western Ethiopia. Asian J Crop Sci. 2019;11(1): 17-24.
 32. Tiwari GC. Variability, heritability and genetic advance analysis for grain yield in rice. J Eng Res Appl. 2015;5:46-9.
 33. Totok ADH, Riyanto A, Susanti D, Farid N, Kantun IN, Shao-Hui Z. Variability of grain protein content in improved upland rice genotypes and its response to locations. Electron J Plant Breed. 2011;2(2): 200-8.
 34. Tripathi A, Kumar S, Singh MK, Kumar A, Karnwal MK. Phenotypic assessment of rice (*Oryza sativa* L.) genotypes for genetic variability and varietal diversity under direct seeded condition. J Appl Nat Sci. 2017;9(1):6-9.

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