Estimation of genetic variability, direct and indirect effects of yield contributing characters on grain yield of upland rice (*Oryza sativa* L.) germplasm

ABSTRACT

A study was carried out ~~with the experimental materials consisting~~ using ~~of~~ 24 u~~U~~pland r~~R~~ice genotypes grown in r~~R~~andomized 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 ,~~was identified for~~ 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 ~~will~~ 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.

Key Words : ~~Rice,~~ Genetic variability, Heritability, Genetic advance, Correlation coefficient analysis and Path coefficient analysis

INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the family Poaceae (Graminae) with ~~a Chromosome~~ chromosome no. ~~of~~ 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~~.~~ **(Akinola *et al.*, 2019).** Approximately 90% of the ~~worlds~~ world's rice is grown and consumed in Asia, whereas 50% of the population depends on rice for food~~.~~ **(Tenorio *et al.*, 2013).** It is one of the world's largest cereal crops providing the caloric need ~~for~~ of millions of people. It plays a pivotal role in Indian economy ~~also is the staple food for two third of the population.~~ 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(only Indias?) 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, ~~the~~ moisture stress and blast are the major abiotic and biotic constraint, respectively

~~constraints and~~ with productivity ~~is~~ 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 ~~with~~ the environment~~ and is the product of many factors called yield components~~. 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 provides adequate information about the contribution of each factor towards the yield. Therefore, ~~a techniques of~~ 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.

MATERIALS AND METHODS

Twenty four upland rice genotypes collected from SHUATS(expand) were ~~sowing~~ sown in ~~the~~ randomized block design with three replications, at the ~~e~~Experimental ~~f~~Farm of the Department of ~~the~~ Genetics and Plant ~~breeding~~Breeding, Sam Higginbottom Institute of Agriculture ~~technology~~ Technology and Sciences, Allahabad, during *Kharif* 2021.~~ The university is situated on the left side of Allahabd Rewa National Highway, about 5km from Prayagraj city~~. All types of facilities necessary for cultivation of successful crop including field preparation inputs, irrigation facilities were provided ~~from tht Department of Genetics and Plant Breeding, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Prayagraj (Allahabad), U.P~~during the crop growth period. In each replication, two to three seedling ~~was sowed~~were sown per hill with 20x10 cm spacing. The observations were recorded on five randomly selected plants from each plot ~~for~~ 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(expand) and PCV(expand) were calculated by formula given by Burton (1952), heritability in broad sense (h^2) by Burton and de Vane (1953) and genetic advance *i.e.*, the expected genetic gain was calculated using the procedure given by Johnson et al., (1955). The correlation coefficient and path coefficient were worked ~~out as for~~based on the method recommended by Al-Jibouri et al., (1958) and Deway and Lu (1959) ~~respectievely~~respectively, the estimated values were compared with table values of the correlation coefficient to test the ~~significanceof~~ significance of the ~~corellation~~correlation coefficient prescribed by Fisher and Yates (1967).

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Table 1 : Experimental material used in the present study~~:~~

Sl~~r~~. 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

RESULTS AND DISCUSSION

Analysis of ~~variamce~~ variance indicated highly significant differences among the genotypes for all the traits studied. This indicates that there is~~was~~ ~~an~~ ample scope for selection of promising lines from the present gene pool for yield and its components. All the characters ~~shown~~ showed significant differences at 1% level of significance.

Mean ~~performnace~~ performance of grain yield per plant was high for ~~the Rice genotypes~~ **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).**

In the present investigation, it is depicted that the estimates of ~~the phenotypic coefficient of variance~~PCV ~~was found~~were higher than the~~ir~~ corresponding ~~genotypic coefficient of variations~~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 ~~phenotypic and genotypic coefficient of variation~~PCV and GCV were recorded for grain yield per hill, number of tillers per hill, number of panicles per hill and flag leaf length ~~indicated~~ indicating the presence of variation for all the characters under study.

Heritability

~~Heritability varied from 30.74 (days to 50% flowering) to 94.84 (grain yield per hill).~~ 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 p~~P~~anicle 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 ~~the traits~~ 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~~ panicle indicates the scope of genetic improvement ~~of these characters~~ 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~~high-yielding varieties through desirable selection in succeeding generations.

Genetic advance as a percentage mean (5%)

The estimation of genetic advance as ~~percent~~ 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*. (1955)**.

~~Genetic advance as percent mean varied from 3.26 (days to maturity) to 59.00 (grain yield per hill).~~ H~~h~~igh genetic advance as ~~percent~~ 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 ~~percent~~ 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). W~~w~~hereas, test weight (8.78), days to 50% flowering (4.27), days to maturity (3.26) recorded low genetic advance as ~~percen~~per centt mean.

In the present investigation, high genetic advance as ~~percent~~ 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~~improvement of these traits.~~

Correlation and path coefficient

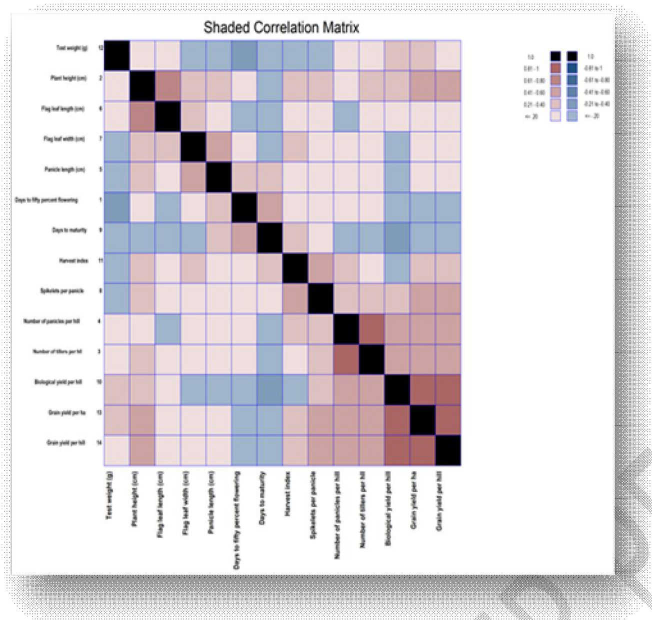
In the present investigation, the path coefficient analysis at genotypic level revealed that ~~the characters~~ number of tillers per hill, panicle length, biological yield per hill, harvest index had positive direct effect on grain yield per hill. Therefore, selection ~~programme~~ should be based on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

Correlation and path coefficient studies suggest that selection based on ~~characters~~ d~~D~~ays to 50% flowering, biological yield per hill and harvest index had positive correlation and direct effect~~s~~ with grain yield per hill and would bring out desired improvement in yield and crop improvement programme based on these traits in upland rice.

Table 2 : Estimates of ~~Correaltion~~Correlation c~~C~~oefficient ~~Analysis~~ for various traits

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**	-0.0.785	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



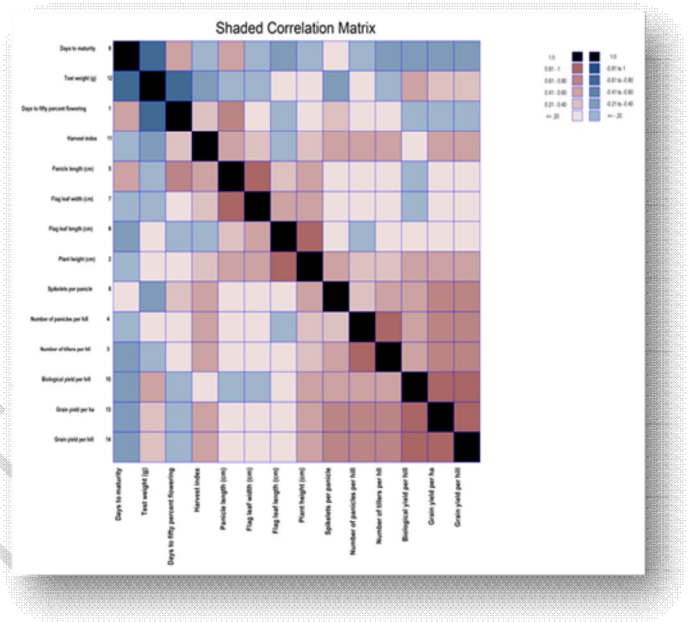


Fig.1 **Genotypic Correlation ~~Diagram~~ co-efficients for various traits under the present investigation**

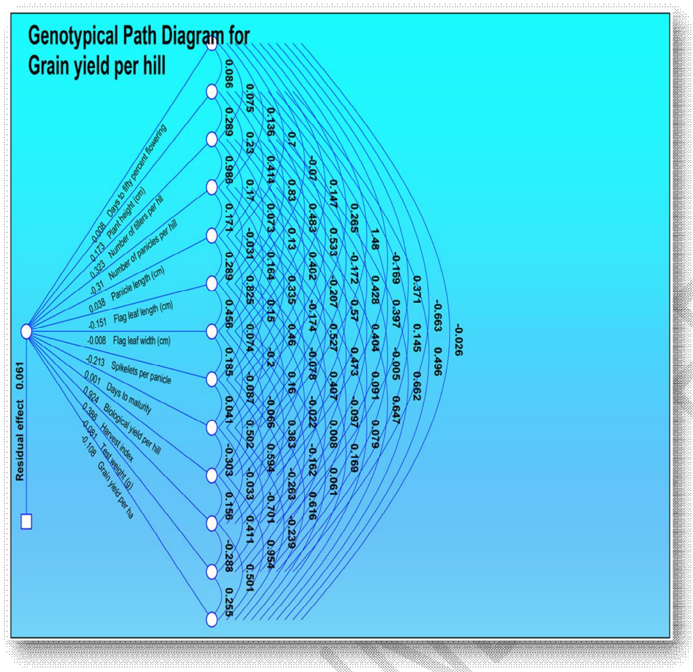
F~~f~~ig.2 **Phenotypic Correlation ~~Diagram~~ co-efficients of various traits under the present investigation**

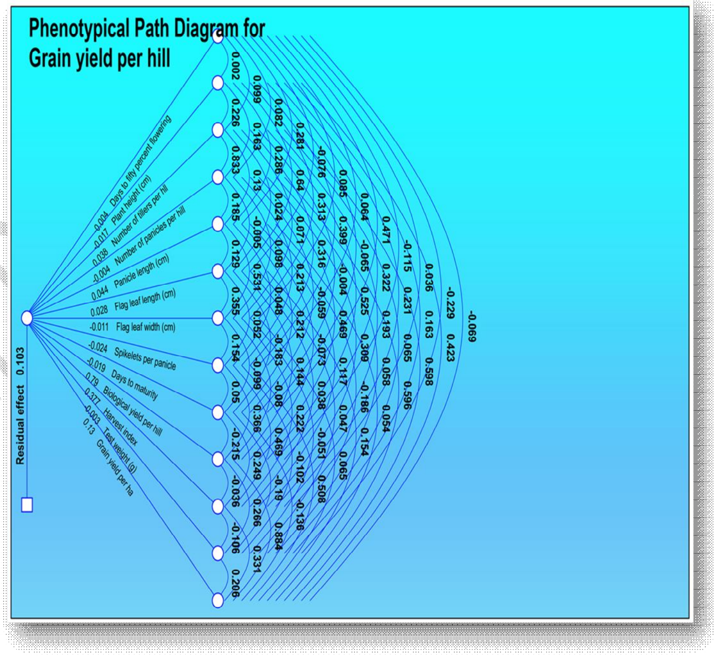
Table 3 : Estimates of p~~P~~ath c~~C~~oefficient for various traits studied in 24 rice genotypes in the present investigation~~Analysis~~

DF: Days to 50% flowering**, PT** :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

Traits		**DF50**	**PH**	**NT/H**	**NP/H**	**PL**	**FLL**	**FLW**	**S/P**	**DM**	**BY/H**	**HI**	**TW**	**GY/H**
DF50	P	-0.0036	0	-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.3 ~~Genotypic Path Coefficient~~ Renamefig.4 ~~Phenotypic Path Coefficient~~Rename





Conclusion

From the present investigation, it is concluded that the genotype SHUATS UPR – 13 (9.41 g) was found superior for~~in~~ grain yield per hectare followed by SHUATS UPR – 11 (6.60 g) over the check variety SAHBHAGI DHAN (4.37g). Among the 24 genotypes of upland rice, ~~Analysis of variance revealed that~~ 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 ~~percent~~ per cent mean was recorded for ~~characters like~~ grain yield per hill, biological yield per hill, number of panicles per hill and number of tillers per hill. 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 ~~will~~ 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~~will~~ be rewarding for yield improvement in u~~U~~pland rice.

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