TITLE

CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS IN UPLAND RICE (*Oryza sativa* L.) FOR GRAIN YIELD AND QUALITY CHARACTERS

Article type: *Original Research Article*

ABSTRACT

The present investigation was undertaken to evaluate Twenty Five Upland Rice genotypes. There are various aspects to move up rice yield, such as creating of irrigation work, development of rice ecosystems, soil conditions, traditional practices, and breeding of high yielding genotypes. Among them, it seems that the most effective and economic way available is to develop different rice ecosystems especially Upland Rice Genotypes. High to moderate phenotypic and genotypic coefficient of variation were observed for number of panicles per hill and number of tillers per hill. High heritability coupled with high genetic advance as percent of mean was observed for number of panicles per hill, number of tillers per hill, grain yield per hill, test weight and flag leaf length, indicating that these traits are most probably under the control of additive gene action and hence these traits can be fixed by proper selection**.**Days to 50% flowering, plant height, number of panicles per hill, flag leaf width, spikelets per panicle, days to maturity, biological yield per hill, harvest index and test weight, exhibited positive significant correlation with grain yield per hill at both genotypic and phenotypic levels, indicating selection based on these traits could be more effective to maximize grain yield. Days to 50% flowering, biological yield per hill and harvest index had positive direct effect on grain yield per hill. Therefore, selection program should be based on these traits for crop improvement with high yielding genotypes in Upland rice.

Key Words: UplandRice, Genetic variability, Heritability, Genetic advance, Correlation coefficient analysis, Path coefficient analysis.

1. INTRODUCTION

Drought is one of the most known limiting factors of crop cultivation leading to unstable food security. Osmolyte like proline helps the plants to escape from drought stress by protecting from dehydration rapidly. Deep rooted plants show greater drought avoidance capacity than shallow-rooted plants. It has also been reported that drought resistant upland rice varieties remained tall and generally have low tillering capacity [1].Rice cultivation consumes about 30% of all fresh water used worldwide. In Asia, flood irrigated rice consumes more than 45% of total fresh water used [2]. By 2025, 15 out of 75millions hectare of Asia's flood irrigated rice crop will experience water shortage[3]. With increasing water scarcity, the sustainability, food production, and ecosystem services of rice fields are threatened [4]. To overcome the water scarcity problem upland is an important system of rice culture and constitutes about one sixth of the world's total rice land. Direct seeding rice, a common practice before green revolution in India, is once again became popular because of its potential to save water and labour [5].Upland rice is also called autumn rice. The study of genetic variability in any crop would help in the genetic improvement of yield and desirable characters. It will facilitate the identification of proper genotypes for a particular agro-climate zone.Heritability along with the genetic advance would be more useful tool in predicting the resultant effect from selection of the best genotypes for yield and some of its components in rice [6].Correlation and genetic variability analysis leads us to a clear understanding of the genetic association of various plant traits and their contribution to yield.correlation coefficients are generally employed to determine the relation of grain yield and yield components [7]. Path coefficient analysis is an efficient statistical technique specially designed to quantify the interrelationship of different components and their direct and indirect effects on grain yield [8].The information on relative direct and indirect contribution of each component character toward yield will help breeders to formulate the effective criteria in selecting desirable genotypes in early segregating populations [9]. In view of this, the present study was planned to determine the genetic variability, heritability, genetic advance, correlation coefficients and direct and indirect contribution of twenty five upland rice genotypes yield and yield attributing traits on grain yield.

1.1Objectives

1. To estimate genetic variability, heritability and genetic advance for yield and it's related traits in rice cultivars.
2. To study the nature of character association among yield and grain yield attributing traits.
3. To assess the direct and indirect contribution of yield attributing traits on grain yield.

2. MATERIALS AND METHODS

Twenty five upland rice genotypes(Table 1) collected from SHUATSwere sownin the randomized block design with three replicationsat the Crop Research Farm of the Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture technology and Sciences, Prayagraj, U.P during Kharif - 2021. In each replication, two to three seedling were sowed per hill with 20x10 cm spacing. The observations were recorded on five randomly selected plants from each plot for days to 50 percent flowering, plant height, number of tillers per hill, number of panicles per hill, panicle length, number of spikelets per panicle, spikelet fertility, flag leaf length, flag leaf width, test weight, days to maturity, biological yield per hill, harvest index and grain yield per hill. As per established methods, data were analysed to determine Analysis of variance [10]. The statistical and biometrical analysis of GCV and PCV were calculated by formula given by Burton (1952), [11]. Heritability in broad sense (h^2) by Burton and de Vane (1953), [12].The expected genetic gain was calculated using the procedure given by Johnson et al.(1955), [13]. The correlation coefficient and path coefficient were worked out as for the method recommended by Al-Jibouri et al.(1958) and Deway and Lu (1959), [14] respectively, the estimated values were compared with table values of the correlation coefficient to test the significance of the correlation coefficient prescribed by Fisher and Yates (1963), [15].

2.1 Layout Description

Season: *Kharif* - 2021

Crop: Upland Rice (*Oryza sativa L.)*

Number of genotypes : 24+1 check

Experimental design : Randomized Block Design

Gross experimental area : 240 sq.m

Net experimental area : 210 sq.m

Row to row distance :20 cm

Plant to plant spacing :10cm

Date of sowing : 3-8-2021

Fertilizer dose : N:P:K @ 120:60:50 kg/ha

Date of Harvesting: 15-11-2021

Recommended package of practice were followed to raise a healthy crop

Table 1.List of Experimental Materials

Sr. No.	Advanced breeding lines	Cross combination	Grain type
1.	SHUATS UPR-25	IR82589-B-B-121-3 X NDR-97 (P2)	Medium bold
2	SHUATS UPR-26	IR82589-B-B-121-3 X NDR-97 (P3)	Medium bold
3.	SHUATS UPR-27	IR82589-B-B-121-3 X NDR-97 (P5)	Medium bold
4.	SHUATS UPR-28	IR82589-B-B-121-3 X NDR-97 (P7)	Medium bold
5.	SHUATS UPR-29	IR82589-B-B-121-3 X Sahbhagidhan	Medium slender
6.	SHUATS UPR-30	IR82589-B-B-121-3 X Sahbhagidhan	Medium slender
7.	SHUATS UPR-31	IR82589-B-B-121-3 X Sahbhagidhan	Medium slender
8.	SHUATS UPR-32	IR82589-B-B-121-3 X Sahbhagidhan	Medium slender
9.	SHUATS UPR-33	IR82589-B-B-121-3 X Sahbhagidhan	Medium slender
10.	SHUATS UPR-34	IR82589-B-B-121-3 X Sahbhagidhan	Medium slender
11.	SHUATS UPR-35	IR82589-B-B-121-3 X Sahbhagidhan	Long slender
12.	SHUATS UPR-36	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
13.	SHUATS UPR-37	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
14.	SHUATS UPR-38	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
15.	SHUATS UPR-39	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
16.	SHUATS UPR-40	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
17.	SHUATS UPR-41	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
18.	SHUATS UPR-42	IR82639-B-B-200-4 X Sahbhagidhan	Long slender
19.	SHUATS UPR-43	IR83750-B-B-131-1 X NDR-97 (P1)	Long slender
20.	SHUATS UPR-44	IR83750-B-B-131-1 X NDR-97 (P3)	Long slender
21.	SHUATS UPR-45	IR83750-B-B-131-1 X NDR-97 (P4)	Long slender
22.	SHUATS UPR-46	IR83750-B-B-131-1 X NDR-97 (P5)	Medium bold
23.	SHUATS UPR-47	IR83750-B-B-131-1 X NDR-97 (P7)	Medium bold
24.	SHUATS UPR-48	IR83750-B-B-131-1 X Sahbhagidhan	Medium slender
25.	SAHBHAGIDHAN (CHECK-1)		Medium slender

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

Analysis of Variance revealed existence of sufficient genetic variability among all the genotypes (Table 3). The mean sum of squares for fifteen quantitative traits of 25 upland rice genotypes reported high significant differences among the genotypes for all the traits at 1% level of significance. This indicates that there was an ample scope for selection of promising lines for yield and its components.The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. Similar results have been reported by Girma et al. [29] and Magar et al. [30].

Table 3. Analysis of Variance for fifteen quantitative traits of 25 Upland rice genotypes

Characters	**Mean Sum of Squares**		
	Replication	**Treatments**	**Error**
	(df=02)	(df= 24)	(df=48)
Days to 50% flowering	28.47	33.43**	14.19
Plant height	28.98	326.79**	55.64
No. of tillers per hill	0.40	5.73**	0.14
No. of Panicles per hill	0.13	4.84**	0.16
Panicle length	4.94	6.25**	1.87
Flag leaf length	8.71	68.45**	4.27
Flag leaf width	0.01	0.01**	0.01
Spikelets per panicle	96.27	977.92**	67.16
Spikelet fertility	47.41	52.88**	23.74
Days to maturity	21.07	27.89**	10.57
Biological yield per hill	1.29	23.6**	4.49
Harvest index	2.33	64.84**	22.94
Test weight	2.70	31.32**	1.78
Grain yield per hill	0.18	9.42**	0.56
Grain yield per ha	0.01	1.02**	0.06

** Significant 1% level of significance

3.1.1. Genotypic andPhenotypic variance

Wide range of Genotypic and Phenotypic coefficient of variance were observed in the experimental material for all the traits (Table 4). The higher phenotypic coefficient of variation was recorded for number of panicles per hill (24.10) followed by number of tillers per hill (22.28). And higher genotypic coefficient of variation was observed for number of panicles per hill (22.92) followed by number of tillers per hill (21.44). it is evident that phenotypic coefficient of variation values were higher than genotypic coefficient of variation for all the traits under study indicating the influence of environment on studied characters. The results are parallel with the findings of Kumar et al. [16], Khatunet al. [17], Chandra et al. [18], Anjaneyulu et al. [19].

3.1.2. Heritability

Estimation of genotypic coefficient of variation reflect the total amount of genotypic variability, the proportion of this genotypic variability, which transmittedfrom parents to the progeny, is reflected through heritability. Lush (1949), [20], gave the concept of broad sense heritability, which is the ratio of genotypic variance (VG) to phenotypic variance (VP). It determines efficiency with which we can utilize the genotypic variability in breeding programs. Burton (1952) suggested that genetic variation along with heritability will give better idea about expected efficiency of selection.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 recorded for the traits (Table 4),Number of tillers per hill (92.62) followed by number of panicles per hill (90.43), test weight (84.67), grain yield per hill (84.03), flag leaf length (83.34), spikelets per panicle (81.88), plant height (61.89)these characters are less influenced by environmental effects and selection on the basis of phenotypic performance of genotypes would be more efficient in further improvement of these traits.Similar results have been reported by Tiwari et al. [21] and Pratap et al. [22].

3.1.3. Mean performance of superior genotypes for quality parameters based on grain yield

According to the above (Table 2), Among 25 accessions SHUATS UPR –33 had highest kernellength before cooking (6.37), L/B ratio (3.76) and kernel length after cooking (7.90). SHUATS UPR – 31 had highest mean values for kernel width after cooking (2.97) and elongation ratio

(1.25). SHUATS UPR – 34 exhibited highest values for alkali spreading value (6.52) and hulling percentage (73.4).SHUATS UPR-43 (25.04) was found to be highest in amylose content and SHUATS UPR-30 (76.00) was found to be highest in gel consistency.

Table 2. Mean performance of superior five genotypes for quality parameters

S.No.	Characters	SHUATS UPR - 34	SHUATS UPR - 33	SHUATS UPR - 43	SHUATS UPR - 31	SHUATS UPR - 30

1.	Kernellength Before Cooking	6.24	6.37	5.68	5.65	6.11
2.	Kernel width Before Cooking	1.76	1.69	2.26	1.75	1.99
3.	Kernellength After Cooking	7.40	7.90	6.86	7.09	7.12
4.	Kernel width After Cooking	2.36	2.78	2.86	2.97	2.81
5.	L/B Ratio	3.54	3.76	1.98	3.22	3.07
6.	Elongation Ratio	1.18	1.24	1.20	1.25	1.16
7.	Gel Consistency	54.33	72.66	65.00	70.66	76.00
8.	Amylose content	21.77	22.61	25.04	24.89	23.82
9.	Alkali spreading value	6.52	5.25	6.15	5.81	2.01
10.	Hulling(%)	73.4	68.5	71.3	65.8	70.2

3.1.4. Genetic Advance

In present study (Table 4), Estimates of genetic advance ranged from (0.08) flag leaf widthto (32.48) spikelet per panicle. High genetic advance was recorded for spikelet per panicle (32.48).). Moderate genetic advance was recorded for plant height (15.40). Traits such as flag leaf length (8.69), test weight (5.94), harvest index (4.73), biological yield (3.97), spikelet fertility (3.45), grain yield per hill (3.24), days to maturity (2.94), days to 50% flowering (2.91), panicle length (1.64), number of tillers per hill (2.70), number of panicles per hill (2.44) and flag leaf width (0.08) exhibited low genetic advance. High to Moderate estimates of genetic advance for the traits, Spikelets per panicle and plant height suggested that these parameters were under the control of additive genetic effects and selection at early segregating generation for these traits will prove beneficial for selecting superior varieties of upland rice. Similar results were reported by Longjam and Singh [23]and Singh et al. [31].

3.1.5. Genetic advance as % of mean

The estimation of genetic advance as percent 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.* [24].In present study, the estimates of genetic advance as % of mean varied from (2.89) days to maturityto (44.91) number of paniclesper hill. High GAM recorded for number of panicles per hill(44.91) followed by number of tillers per hill (42.52), grain yield per hill (29.45), test weight (26.58), flag leaf length (25.40) and spikelets per panicle (24.8). Highgenetic advance as percent of mean coupled with high heritability was recorded for number of tillers per hill followed by number of panicles per hill, flag leaf length, test weight and grain yield per hill indicating that these traits are most probably under the control of additive gene action and hence these traits can be fixed by proper selection. Similar results have been reported by Rashmi et al. [25].

Table 4. Genetic Variability parameters for 15 quantitative characters

Characteristics	GCV	PCV	h^2 (bs)	GA	GAM
Days to 50% flowering	3.451	6.185	31.126	2.911	3.966
Plant height	9.122	11.595	61.897	15.408	14.784
No. of tillers per hill	21.448	22.285	92.625	2.706	42.522
No. of Panicles per hill	22.925	24.108	90.43	2.445	44.91
Panicle length	5.284	7.982	43.826	1.648	7.206
Flag leaf length	13.51	14.798	83.348	8.698	25.408
Flag leaf width	7.555	11.28	44.856	0.086	10.423
Spikelets per panicle	13.304	14.702	81.885	32.48	24.8
Spikelet fertility	3.48	6.459	29.031	3.459	3.863
Days to maturity	2.365	3.98	35.309	2.941	2.895
Biological yield per hill	10.567	13.805	58.593	3.979	16.663
Harvest index	8.074	13.125	37.843	4.736	10.232
Test weight	14.025	15.242	84.665	5.948	26.584
Grain yield per hill	15.596	17.013	84.037	3.246	29.452
Grain yield per ha	15.618	17.035	84.052	1.071	29.496

GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation, h2(bs): Heritability (broad sense),GA: Genetic Advance, GAM: Genetic Advance as Percent ofmean

3.2.Correlation Coefficient analysis

Correlation study indicates the degree of interdependence of plant characters, which is an important toll in selection of a pertinent genotype. Therefore, information on association between characters is quite useful to plant breeders to formulate their breeding and selection strategies.At present study, Grain yield per plant showed the positive significant phenotypic association with(Table 5) days to 50% flowering(0.311*),plant height(0.337*), number of tillers per plant(0.312*), Number of panicles per hill(0.472**), flag leaf width(0.426**), spikelets per panicle(0.346*), days to maturity(0.305*), biological yield perhill(0.659**), harvest index(0.638**) and test weight(0.274*) while, it exhibited positive non-significant association with panicle length (0.1589) and flag leaf length(0.2035).Grain yield per hill showed positive significant genotypic association with days to 50% flowering (0.392**), plant height (0.501**), number of tillers per plant (0.333*), number of panicles per hill (0.505**), panicle length (0.294*), flag leaf length (0.311*), flag leaf width (0.649**), spikelets per panicle (0.459**), days to maturity (0.412**), biological yield per hill (0.879**), harvest index (0.849**) and Test weight (0.343*). Thus, days to 50% flowering, plant height, Number of panicles per hill, flag leaf width, spikelets per panicle, days to maturity, biological yield per hill, harvest index, test weight were found to possess positive significant association with grain yield per hill at both genotypic and phenotypic level indicating selection based on these traits could be more effective to maximize grain yield.similar with the findings ofSingh et al. [32] and Srijan et al. [33].

3.3.Path Coefficient Analysis

Correlation gives only the relation between two variables whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlation (Wright, 1921), [26]. In the present investigation, the path coefficient analysis at phenotypic level revealed that the characters such as (Table 6) days to 50% flowering(0.0448), plant height(0.0119), number of tillers per hill(0.0176), number of panicles per hill(0.0080), flag leaf width(0.0030), biological yield per hill(0.7419) and harvest index(0.7292)had positive direct effect on grain yield per hill. At the Genotypic level path coefficient analysis based on yield as dependent variable showed that days to 50% flowering(0.0562), panicle length(0.1732), flag leaf length(0.0714), spikelet fertility(0.0612), days to maturity(0.0711), biological yield per hill(0.4685), harvest index(0.5446) revealed positive direct effect on grain yield per hill.Therefore, selection program should be based on these traits for crop improvement with high yielding genotypes in Upland rice. These findings of path Coefficient analysis in upland rice were found to be similar with the findings of Sharma et al. [27], Mishu et al. [28] and Belete et al. [34].

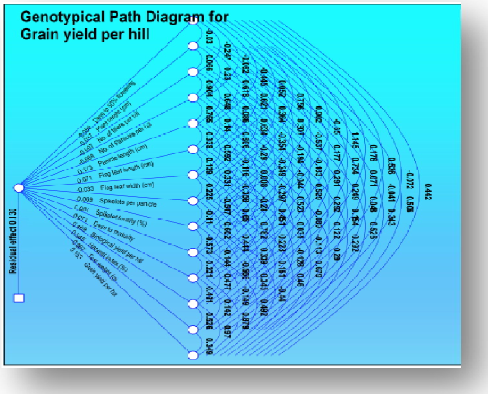

Fig. 1. Genotypic Path Coefficient

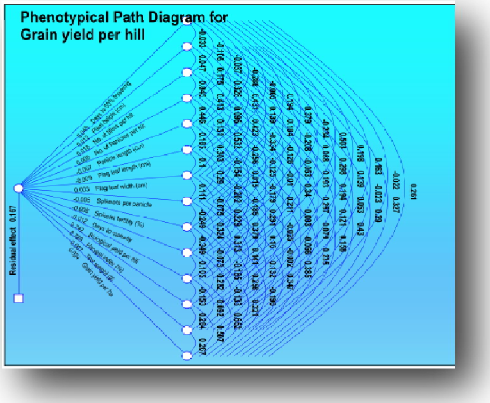

Fig. 2. Phenotypic Path Coefficient

Table 5. Phenotypic and Genotypic correlation coefficient for grain yield and its component characters in 25 Upland rice genotypes

		PH	NT/H	NP/H	PL	FLL	FLW	S/P	SF	DM	BY/H	HI	TW	GY/H
DF50	P	-0.0330	-0.1065	-0.0369	-0.288*	-0.0065	0.1936	0.379**	-0.234*	0.508**	0.1979	0.1633	-0.0217	0.311*
	G	-0.0299	-0.247*	-0.0817	-0.445**	0.0518	0.756**	0.902**	-0.650**	0.824**	0.1759	0.536**	-0.0722	0.392**
PH	P	1	0.0471	0.1752	0.328*	0.431**	0.1387	0.1843	-0.2082	0.0683	0.298*	0.1390	-0.0227	0.337*
	G	1	0.0663	0.230*	0.618**	0.621**	0.364*	0.307*	-0.537**	0.1765	0.724**	0.0709	-0.0410	0.501**
NT/H	P		1	0.845**	0.413**	0.0964	0.423**	-0.334*	-0.1281	-0.0531	0.1928	0.1944	0.0528	0.312*
	G		1	0.904**	0.648**	0.0856	0.634**	-0.354*	-0.1938	-0.1825	0.291*	0.249*	0.0477	0.333*
NP/H	P			1	0.446**	0.1310	0.532**	-0.256*	-0.1249	-0.0095	0.340*	0.257*	0.1206	0.472**
	G			1	0.755**	0.1404	0.807**	-0.290*	-0.249*	0.0441	0.529**	0.292*	0.1538	0.505**
PL	P				1	0.1848	0.303*	-0.1537	0.0147	-0.1788	0.2112	0.0030	0.0785	0.1589
	G				1	0.338*	0.592**	-0.1160	0.0075	-0.297*	0.523**	-0.0885	0.1223	0.294*
FLL	P					1	0.0998	0.290*	-0.2015	-0.1855	0.291*	-0.0250	-0.0557	0.2035
	G					1	0.1386	0.331*	0.358*	-0.280*	0.451**	0.0310	-0.1126	0.311*
FLW	P						1	0.1109	-0.0745	0.229	0.379**	0.1598	-0.0018	0.426**
	G						1	0.2250	-0.507**	0.650**	0.782**	0.2233	-0.1283	0.649**
S/P	P							1	-0.249*	0.324*	0.313*	0.1411	0.1317	0.346*
	G							1	-0.410**	0.602**	0.444**	0.339*	0.1614	0.459**
SF	P								1	0.349I*	-0.0726	-0.1851	0.258*	-0.2125
	G								1	-0.573**	-0.1442	-0.568**	0.345*	-0.424**
DM	P									1	0.1050	0.282*	-0.1330	0.305*
	G									1	0.2213	0.477**	-0.1486	0.412**
BY/H	P										1	-0.1532	0.0922	0.659**
	G										1	0.491**	0.1425	0.879**
HI	P											1	0.284*	0.638**
	G											1	0.526**	0.849**
TW	P												1	0.274*
	G												1	0.343*

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.Direct and indirect effects of yield component traits on grain yield in 25 Upland rice genotypes at both phenotypic and genotypic level

		DF50	PH	NT/H	NP/H	PL	FLL	FLW	S/P	SF	DM	BY/H	HI	TW	GY/H
DF50	P	0.0448	-0.0015	-0.0048	-0.0017	-0.0129	-0.0003	0.0087	0.0170	-0.0105	0.0227	0.0089	0.0073	-0.0010	0.311*
	G	0.0562	-0.0017	-0.0139	-0.0046	-0.0250	0.0029	0.0425	0.0507	-0.0365	0.0643	0.0099	0.0301	-0.0041	0.392*
PH	P	-0.0004	0.0119	0.0006	0.0021	0.0039	0.0051	0.0017	0.0022	-0.0025	0.0008	0.0035	0.0017	-0.0003	0.337*
	G	0.001	-0.0370	-0.0025	-0.0085	-0.0228	-0.0230	-0.0135	-0.0114	0.0199	-0.0065	-0.0268	-0.0026	0.0015	0,501*
NT/H	P	-0.0019	0.0008	0.0176	0.0149	0.0073	0.0017	0.0074	-0.0059	-0.0023	-0.0009	0.0034	0.0034	0.0009	0.312*
	G	0.0017	-0.0005	-0.0070	-0.0063	-0.0045	-0.0006	-0.0044	0.0025	0.0013	0.0013	-0.0020	-0.0017	-0.0003	0.333*
NP/H	P	-0.0003	0.0014	0.0068	0.0080	0.0036	0.0010	0.0043	-0.0021	-0.0010	-0.0001	0.0027	0.0021	0.0010	0.472*
	G	0.0056	-0.0157	-0.0616	-0.0682	-0.0515	-0.0096	-0.0550	0.0198	0.0170	0.0030	-0.0360	-0.0199	-0.0105	0.505*
PL	P	0.0021	-0.0024	-0.0030	-0.0032	-0.0072	-0.0013	-0.0022	0.0011	-0.0001	0.0013	-0.0015	0.000	-0.0006	0.1589
	G	-0.0771	0.1071	0.1122	0.1308	0.1732	0.0585	0.1026	-0.0201	0.0013	-0.0514	0.0906	-0.0153	0.0212	0.294*
FLL	P	0.0001	-0.0039	-0.0009	-0.0012	-0.0017	-0.0092	-0.0009	-0.0027	0.0018	0.0017	-0.0027	0.0002	0.0005	0.2035
	G	0.0037	0.0443	0.0061	0.0100	0.0241	0.0714	0.0099	0.0236	-0.0256	-0.0200	0.0322	0.0022	-0.0080	0.311*
FLW	P	0.0006	0.0004	0.0012	0.0016	0.0009	0.0003	0.0030	0.0003	-0.0002	0.0007	0.0011	0.0005	0.000	0.426**
	G	-0.0252	-0.0121	-0.0211	-0.0268	-0.0197	-0.0046	-0.0333	-0.0075	0.0169	-0.0216	-0.0260	-0.0074	0.0043	0.649**
S/P	P	-0.0017	-0.0008	0.0015	0.0012	0.0007	-0.0013	-0.0005	-0.0046	0.0011	-0.0015	-0.0014	-0.0006	-0.0006	0.346*
	G	-0.0621	-0.0212	0.0244	0.0200	0.0080	-0.0228	-0.0155	-0.0689	0.0282	-0.0415	-0.0306	-0.0233	-0.0111	0.459**
SF	P	0.0018	0.0016	0.0010	0.0010	-0.0001	0.0016	0.0006	0.0019	-0.0077	0.0027	0.0006	0.0014	-0.0020	-0.2125
	G	-0.0398	-0.0329	-0.0119	-0.0152	0.0005	-0.0219	-0.0311	-0.0251	0.0612	-0.0351	-0.0088	-0.0348	0.0211	-0.424**
DM	P	-0.0063	-0.0009	0.0007	0.0001	0.0022	0.0023	-0.0028	-0.0040	0.0044	-0.0125	-0.0013	-0.0035	0.0017	0.305*
	G	0.0814	0.0126	-0.0130	-0.0031	-0.0211	-0.0199	0.0462	0.0428	-0.0407	0.0711	0.0157	0.0339	-0.0106	0.412**
BY/H	P	0.1468	0.2208	0.1430	0.2522	0.1567	0.2156	0.2810	0.2319	-0.0539	0.0779	0.7419	-0.1137	0.0684	0.659**
	G	0.0824	0.3391	0.1361	0.2477	0.2450	0.2114	0.3664	0.2081	-0.0675	0.1037	0.4685	0.2299	0.0668	0.879**
HI	P	0.1190	0.1013	0.1418	0.1877	0.0022	-0.0182	0.1162	0.1029	-0.1350	0.2059	-0.1117	0.7292	0.2067	0.638**
	G	0.2917	0.0386	0.1357	0.1588	-0.0482	0.0169	0.1216	0.1846	-0.3094	0.2599	0.2673	0.5446	0.2865	0.849**
TW	P	0.0002	0.0002	-0.0004	-0.0009	-0.0006	0.0004	0.0000	-0.0010	-0.0019	-0.0010	-0.0007	-0.0021	-0.0074	0.274*
	G	0.0048	0.0027	-0.0032	-0.0103	-0.0082	0.0075	0.0086	-0.0108	-0.0231	0.0099	-0.0095	-0.0352	-0.0669	0.343*

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

4. Conclusion

From the present investigation, it is concluded that studied advanced breeding lines of upland rice showed significant variation to all the characters. On the basis of mean performance among 25 genotypes of upland rice, SHUATS UPR – 34 (4.52 tons/ha) was found to be superior in grain yield per hectare followed by SHUATS UPR – 33 (4.38 tons/ha) over the check variety SAHBHAGIDHAN (4.37 tons/ha).Estimation of genetic variability parameters, correlation analysis and path coefficient analysis revealed that, number of tillers per hill, number of panicles per hill, days to 50% flowering, plant height, biological yield per hill were most reliable traits for yield improvement. So, the utmost importance should be given to these characters during the selection for yield improvement in upland rice.

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