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Genetic Variability, Correlation and Path Coefficient Analysis of Morphological Traits in some Extinct Local Aman Rice (*Oryza sativa* L)

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Abstract

Thirty five local aman rice varieties were evaluated for their variability with regards to yield and yield components. Estimates of heritability and genetic advance in per cent of mean were also obtained for the above traits. In addition, studies on character associations and path coefficients were also undertaken. The highest σ^2g was found for number of root hair (103415.40) and the lowest magnitude of σ^2g was observed in number of primary branches per panicle (1.97). The highest σ^2p was found for number of root hair (109410.31) and the lowest magnitude of σ^2p was observed in number of primary branches per panicle (2.61). High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield per hill (g) indicated that selection of these traits would be effective. Correlation of Grain yield per hill was found to be highly significant and positive for number of root hair, days to flowering and plant height at both genotypic and phenotypic level and negatively significant for number of secondary branches per panicle at both level. Significant positive correlation of grain yield per hill with number of root hair, days to flowering and plant height implied that selection for these characters would lead to simultaneous improvement of grain yield in rice. Further, yield was observed to be positively associated with panicle bearing tillers and number of filled grains per panicle and these characters were noticed to exert high direct effects on grain yield per plant. High indirect effects of most of the traits were noticed mostly through panicle bearing tillers per hill indicating importance of the trait as selection criteria in crop yield improvement programs.

Keywords: Correlation, Genetic advance, Heritability, Path co-efficients, Rice (*Oryza sativa* L)

Introduction

Rice is a self-pollinated cereal crop belonging to the family Gramineae (synomym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number 2n=24 [1]. The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild species and two, *Oryza sativa* and *Oryza glaberrima* are cultivated [2]. It can survive as a perennial crop and can produce a ratoon crop for up to 30 years but cultivated as annual crop and grown in tropical and temperate countries over a wide range of soil and climatic condition.

Rice and agriculture are still fundamental to the economic development of most of the Asian countries. In much of Asia, rice plays a central role in politics, society and culture, directly or indirectly employs more people than any other sector. A healthy rice industry, especially in Asia's poorer countries, is crucial to the livelihoods of rice producers and consumers alike. Farmers need to achieve good yields without harming the environment so that they can make a good living while providing the rice-eating people with a high-quality, affordable staple. Underpinning this, a strong rice research sector can help to reduce costs, improve production and ensure environmental sustainability. Indeed, rice research has been a key to productivity and livelihood.

Rice is the second largest produce cereal in the world in 158.3 million hectare area with annual production of about 685.24 million metric tons [3] and also the staple food for over one third of the world's population [4] and more than 90% to 95% of rice is produced and consumed is Asia [5]. Rice (*Oryza sativa* L) is the staple food in Bangladesh, and grown in a wide range of environments ranging from the upland areas like Chittagong Hill Tracts, Sylhet and Garo Hills, with little moisture, to situations where the water is 3-4 meter deep [6]. Bangladesh is ranked as fourth in rice production with annual production of 47.72 million metric ton in the world [3]. Bangladesh has a population density of 977/square km [7] which is the highest in the world. The land scarcity therefore, usually calls for vertical increased in yield or total production. To solve this problem, the production must be increase from less land, with less labor, less water and fewer pesticides.

Rice is the most consumed cereal grain in the world. It is staple food crop for more than half of the world's human population. Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement. A critical analysis of the genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programs. Further, information on correlation co-efficients between grain yield and its component characters is essential for yield improvement, since grain yield in rice is a complex entity and is highly influenced by several component characters. Studies on

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path co-efficient also provide useful information regarding the direct and indirect effects of different yield component characters on grain yield and thus aid in the identification of effective selection criteria for effective yield improvement. The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance, character associations and path of effect in promising rice genotypes. A good knowledge of genetic resources might also help in identifying desirable genotypes for future hybridization program.

Materials and Methods

The study was conducted at the experimental farm of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207 during the period from July 2012 to December 2012. The experimental field was located at 90° 33.5′ E longitude and 23° 77.4′ N latitude at an altitude of 9 meter above the sea level. The soil of the experiment site was a medium high land, clay loam in texture and having pH 5.47-5.63. The land was located in Agro-ecological Zone of 'Madhupur Tract' (AEZ No. 28). The climate of the experimental site is sub-tropical characterized by heavy rainfall during April to July and sporadic during the rest of the year. The experimental plots were laid out in randomized complete block design (RCBD). The field was divided into three blocks; representing three replications. Thirty five genotypes were distributed to each plot within each block randomly. The experimental materials of the study comprised of 35 rice genotypes. Thirty five separate strips were made and sprouted seeds were sown on each strip in 14th July of 2012. The experimental plot was fertilized by applying urea, TSP, MP and Gypsum @180,100,70&60 Kg/ha, respectively. Total TSP, MP and Gypsum were applied at final land preparation. Total urea was applied in three installments, at 15 days after transplanting (DAT), 30 DAT and 50 DAT. The seeds were collected from Bangladesh Institute of Nuclear Agriculture, Mymensingh (BINA). The details of these genotypes are given in (Table 1).

Statistical Analysis of Data

Estimation of genotypic and phenotypic variance

Genotypic and Phenotypic Variances were estimated according to the formula given by [8]

Genotypic variance ($\sigma^2 g$)= $\frac{\text{GMS - EMS}}{\text{r}}$ Where,

GMS=Genotypic mean square

EMS=Error mean square

R=Number of replication

Phenotypic Variance ($\sigma^2 p$)=$\sigma^2 g$+EMS Where,

$\sigma^2 g$=Genotypic variance

EMS=Error mean square

Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and Phenotypic co-efficient of variation were estimated according to [9,10]

Genotypic co-efficient of variation,

(GCV)=$\frac{\sigma^2 g}{\bar{\text{x}}} \times 100$ Where,

$\sigma^2 g$=Genotypic variance

x=Population mean

Phenotypic co-efficient of variation,

(PCV)=$\frac{\sigma^2 p}{\bar{\text{x}}} \times 100$ Where,

$\sigma^2 p$=Phenotypic variance

x=Population mean

Estimation of heritability

Heritability was estimated in broad sense by the formula suggested by [8].

Heritability ($h^2 b$)=$\frac{\sigma^2 g}{\sigma^2 p} \times 100$ Where,

Sl. No.	Indicating Symbol	Genotypes	Source
1	G-1	KathiGoccha	BINA
2	G-2	Hamai	BINA
3	G-3	KhakShail	BINA
4	G-4	Hari	BINA
5	G-5	Tal Mugur	BINA
6	G-6	DakhShail	BINA
7	G-7	MoinaMoti	BINA
8	G-8	Nona Bokhra	BINA
9	G-9	Bogi	BINA
10	G-10	Patnai	BINA
11	G-11	LedraBinni	BINA
12	G-12	Lalanamia	BINA
13	G-13	Hogla	BINA
14	G-14	JamaiNaru	BINA
15	G-15	Jota Balam	BINA
16	G-16	KhejurChori	BINA
17	G-17	Ghunshai	BINA
18	G-18	Malagoti	BINA
19	G-19	BazraMuri	BINA
20	G-20	Nona Kochi	BINA
21	G-21	MoghaiBalam	BINA
22	G-22	Ghocca	BINA
23	G-23	Mondeshor	BINA
24	G-24	MotaAman	BINA
25	G-25	Golapi	BINA
26	G-26	BhuteShelot	BINA
27	G-27	Mowbinni	BINA
28	G-28	KaloMota	BINA
29	G-29	Ponkhiraj	BINA
30	G-30	Jolkumri	BINA
31	G-31	Lalbiroi-31	BINA
32	G-32	Karengal	BINA
33	G-33	SadaGotal	BINA
34	G-34	HoldeGotal	BINA
35	G-35	BRRI Dhan-33	BRRI

BINA: Bangladesh Institute of Nuclear Agriculture
BRRI: Bangladesh Rice Research Institute
Data were collected from 5 hills of each genotype on the following parameters: Plant height at maturity (cm), Number of effective tillers, Length of panicle (cm), Days to flowering (DAS), Number of primary branches per panicle, Number of secondary branches per panicle, Number of unfilled grain per panicle, Number of filled grain per panicle, 1000 grain weight, Root length, Number of root hair, Root weight and Grain yield per hill (g).

Table 1: List of thirty five rice genotypes along with their sources.

$\sigma^2 g$=Genotypic variance

$\sigma^2 p$=Phenotypic variance

Estimation of genetic advance

Estimation of Genetic Advance was done following formula given by [8].

Genetic Advance (GA)=$h^2b.K.\sigma p$ Where,

h^2b=Heritability

K=Selection differential, the value of which is 2.06 at 5% selection intensity; and

σp=Phenotypic standard deviation.

Estimation of correlation coefficients

The Genotypic and Phenotypic correlation coefficients between yield and different yield contributing characters were estimated as:

$$\text{Genotypic correlation}=\frac{\mathrm{Cov}(g)1.2}{\sqrt{\sigma^2(g)1.\sigma^2(g)2}}$$ Where,

Cov(g)(xy)=Genotypic covariance between the variables X and Y

$\sigma 2(g)1$=Genotypic variance of the variable X1

$\sigma 2(g)2$=Genotypic variance of the variable X2

Similarly,

$$\text{Phenotypic correlation}=\frac{\mathrm{Cov(ph)}\ 1.2}{\sqrt{\sigma^2(\mathrm{ph})1.\sigma^2(\mathrm{ph})2}}$$ Where,

Cov(ph)(xy)=Phenotypic covariance between the variables X and Y

$\sigma 2(ph)1$=Phenotypic variance of the variable X1

$\sigma 2(ph)2$=Phenotypic variance of the variable X2

Estimation of path coefficients

Path coefficient analysis was done according to the procedure employed by [11] also quoted in [10], using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on grain yield per hectare.

After calculating the direct and indirect effect of the characters, residual effects (R) was calculated by using the formula given below [10].

$$P^2_{RY}=1-(r_{1.y}P_{1.y}+r_{2.y}P_{2.y}+\ldots\ldots\ldots\ldots\ldots\ldots+r_{12.y}P_{12.y})$$

Where,

$P^2_{RY}=R^2$ and hence residual effect, $R=(P^2_{RY})^{1/2}$

$P_{I.y}$= Direct effect of the i th character on yield y.

$r_{I.y}$= Correlation of the i th character with yield y.

Result and Discussion

The extent of variability for any character is very important for the improvement of a crop through breeding. The estimates of genotypic variation ($\sigma^2 g$), phenotypic variation ($\sigma^2 p$), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) for different characters have been presented in Table 2. The highest $\sigma^2 g$ was found for number of root hair (103415.40) and the lowest magnitude of $\sigma^2 g$ was observed in number of primary branches per panicle (1.97). The highest $\sigma^2 p$ was found for number of root hair (109410.31) and the lowest magnitude of $\sigma^2 p$ was observed in number of primary branches per panicle (2.61). Wide variability existed in anther length, stigma length and percent exerted stigma. The genetic variation constituted a high proportion of the total variation for these traits. Thus, selection for these characters is expected to be highly effective.

The GCV and PCV were the highest for number of effective tiller (54.39and 56.33) followed by root weight (50.97and 51.26), number of root hair (28.00 and 28.80) and grain yield per hill (g) (26.51 and 26.57). High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield per hill (g) indicated that selection of these traits would be effective. The GCV and PCV were the lowest for days to flowering (3.28and 3.43) and plant height (cm) (5.69 and 5.76). PCV were slightly higher than GCV in case of all the traits, indicating presence of environmental influence to some degrees in the phenotypic expression of the characters [12] also reported similar result (Table 2 and Figure 1).

Characters	Grand mean	(σ^2g)	(σ^2p)	(σ^2 e)	h^2_b (%)	GCV (%)	PCV (%)	GA	GA (%)
PH	161.54	84.47	86.71	2.24	97.42	5.69	5.76	18.69	11.57
NET	5.04	7.50	8.05	0.54	93.25	54.39	56.33	5.45	108.20
LP	28.95	4.93	6.07	1.14	81.28	7.67	8.51	4.12	14.24
DF	108.66	12.71	13.92	1.20	91.35	3.28	3.43	7.02	6.46
NPBP	10.71	1.97	2.61	0.64	75.52	13.10	15.08	2.51	23.46
NSBP	27.25	42.99	43.96	0.97	97.79	24.06	24.33	13.36	49.02
NFGP	120.36	181.79	187.50	5.71	96.96	11.20	11.38	27.35	22.72
NUFGP	31.38	31.04	32.16	1.11	96.54	17.75	18.07	11.28	35.93
1000GW	22.91	2.19	3.08	0.89	71.00	6.46	7.67	2.57	11.21
RL	9.85	2.57	4.54	1.98	56.46	16.26	21.64	2.48	25.17
NRH	1148.66	103415.40	109410.31	5994.91	94.52	28.00	28.80	644.06	56.07
RW	57.05	845.41	855.07	9.66	98.87	50.97	51.26	59.56	104.40
GYH	23.56	39.02	39.20	0.18	99.53	26.51	26.57	12.84	54.48

PH: Plant height (cm); NET: Number of effective tiller; LP: Length of panicle; DF: Days to flowering; NPBP: Number of primary branches per panicle, NSBP: Number of secondary branches per panicle; NFGP: Number of filled grain per panicle; NUFGP: Number of unfilled grain per panicle; 1000 GW: 1000 grain weight; RL: Root length; NRH: Number of root hair; RW: Root weight, GYH: Grain yield per hill (g); **σ^2g:** Genotypic variance; **σ^2p:** Phenotypic variance; σ^2 e: Environmental variance; **h^2_b**: Heritability (broad sense); GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; GA: Genetic Advance

Table 2: Estimation of genetic parameters in thirteen characters of 35 genotypes in rice.

Heritability estimates were high for all the characters studied except root length, 1000 grain weight and number of primary branches per panicle. The values were especially high for grain yield per hill (g), root weight and number of secondary branches per panicle [8] suggested that high heritability combined with high genetic advance is an indicative of additive gene action and selection based on these parameters would be more reliable. In the present investigation, high heritability estimates in conjunction with high genetic advance in present of mean were observed for number of effective tiller, root weight and number of root hair (Figure 2).

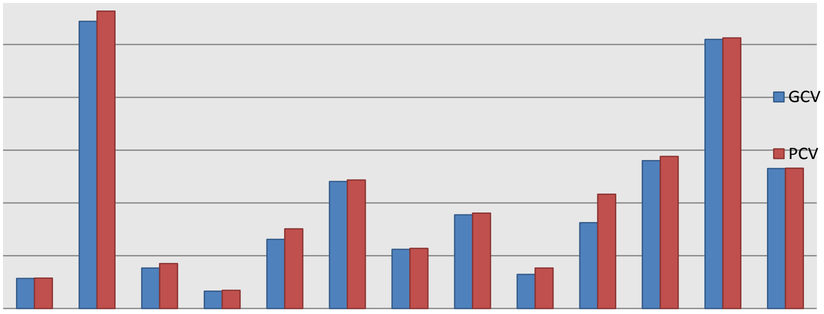
Yield is a complex product being influenced by several independent quantitative characters. Breeders always look for variation among traits to select desirable types. Some of these characters are highly associated among themselves and with seed yield. The analysis of the relationships among these characters and their associations with seed yield is essential to establish selection criteria. When more characters are involved in correlation study it becomes difficult to ascertain the characters which really contribute toward yield. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters. Selection for yield *per se* may not be effective unless the other yield components were having direct or indirect influence on it and are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Genotypic and phenotypic correlation coefficients were calculated as according to [13].

Correlation coefficient

The genotypic and phenotypic correlations among yield and yield contributing characters in rice are shown in Table 3. It is evident that in majority of the cases, the genotypic correlation coefficients were higher than their phenotypic correlation coefficients indicating that of a strong inherent association between the characters studied and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, however, phenotypic correlation coefficients were same with or higher than their corresponding genotypic correlation coefficients suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. Accordingly, [14] reported that the genotypic correlations were greater than the phenotypic values in medium duration rice varieties (Table 3).

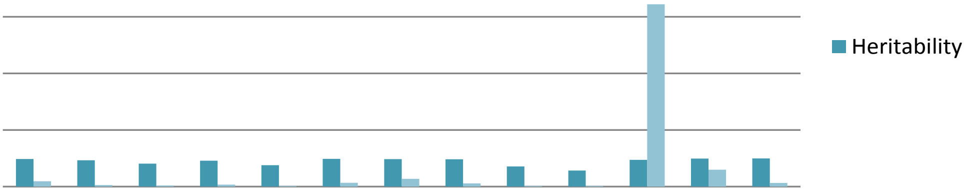
Character association

Correlation of grain yield per hill was found to be highly significant and positive for number of root hair, days to flowering and plant height at both genotypic and phenotypic level and negatively significant for Number of secondary branches per panicle at both level. Significant positive correlation of grain yield per hill with number of root hair, days to flowering and plant height imply that selection for these characters would lead to simultaneous improvement of grain yield in rice. Plant height recorded significant negative correlation with number of secondary branches per panicle followed by number of primary branches per panicle and number of root hair at genotypic and phenotypic level. Number of effective tiller showed significant positive correlation with number of root hair at both genotypic and phenotypic level. It is observed that length of panicle was significantly and positively associated with root length followed by root weight at both genotypic and phenotypic level.



PH: Plant height (cm); NET: Number of effective tiller; LP: Length of panicle; DF: Days to flowering; NPBP: Number of primary branches per panicle; NSBP: Number of secondary branches per panicle; NFGP: Number of filled grain per panicle; NUFGP: Number of unfilled grain per panicle; 1000 GW: 1000 grain weight; RL: Root length; NRH: Number of root hair; RW: Root weight; GYH: Grain yield per hill (g)

Figure 1: Graphical representation of genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV).



PH: Plant height (cm); NET: Number of effective tiller; LP: Length of panicle; DF: Days to flowering; NPBP: Number of primary branches per panicle; NSBP: Number of secondary branches per panicle; NFGP: Number of filled grain per panicle; NUFGP: Number of unfilled grain per panicle; 1000 GW: 1000 grain weight; RL: Root length; NRH: Number of root hair; RW: Root weight; GYH: Grain yield per hill (g)

Figure 2: Graph showing heritability and genetic advance.

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Characters		NET	LP	DF	NPBP	NSBP	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
PH	Rg	0.201	0.985**	0.648**	-0.624**	-0.996**	-0.158	-0.314	0.030	0.983**	-0.616**	0.151	0.772**
	Rp	0.192	0.882**	0.620**	-0.539	-0.970**	-0.157	-0.302	0.041	0.955**	-0.590**	0.145	0.763**
NET	Rg		-0.638**	-0.427**	-0.851**	-0.044	-0.728**	0.038	0.165	0.303	0.802**	0.309	0.161
	Rp		-0.577**	-0.382**	-0.810**	-0.041	-0.691**	0.037	0.134	0.209	0.753**	0.289	0.161
LP	Rg			0.103	0.442**	0.110	-0.323	0.235*	0.111	0.829**	0.038	0.514**	0.039
	Rp			0.102	0.325	0.098	-0.281	0.204	0.061	0.565**	0.032	0.459**	0.035
DF	Rg				0.200	-0.543**	0.663**	0.186	-0.516**	0.233	0.598**	-0.309	0.846**
	Rp				0.140	-0.503**	0.614**	0.171	-0.432**	0.157	0.528**	-0.295	0.809**
NPBP	Rg					0.543**	0.817**	0.921**	0.515**	0.426*	0.114	-0.446**	0.060
	Rp					0.470**	0.686**	0.789**	0.403*	0.308	0.106	-0.369*	0.051
NSBP	Rg						0.563**	0.770**	-0.124	-0.127	0.152	-0.214	-0.218
	Rp						0.545**	0.747**	-0.118	-0.081	0.133	-0.210	-0.215
NFGP	Rg							-0.071	0.433**	0.831**	0.182	-0.162	0.288
	Rp							-0.069	0.353*	0.612**	0.175	-0.160	0.282
NUFGP	Rg								0.531**	0.290	0.505**	0.091	0.517**
	Rp								0.442**	0.239	0.478**	0.089	0.507**
1000GW	Rg									0.963**	-0.038	-0.283	0.176
	Rp									0.630**	-0.025	-0.232	0.151
RL	Rg										0.839**	-0.125	0.645**
	Rp										0.630**	-0.088	0.479**
NRH	Rg											-0.094	0.888**
	Rp											-0.092	0.859**
RW	Rg												0.031
	Rp												0.030

**: Significant at 1%. *: Significant at 5%.

PH: Plant height (cm); NET: Number of effective tiller; LP: Length of panicle; DF: Days to flowering; NPBP: Number of primary branches per panicle; NSBP: Number of secondary branches per panicle; NFGP: Number of filled grain per panicle; NUFGP: Number of unfilled grain per panicle; 1000 GW: 1000 grain weight; RL: Root length , NRH: Number of root hair; RW: Root weight; GYH: Grain yield per hill (g); Rg: Genotypic correlation; Rp: Phenotypic correlation.

Table 3: Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of rice.

Characters	PH	NET	LP	DF	NPBP	NSBP	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
PH	0.240	0.127	-0.184	0.466	-0.110	0.092	-0.027	-0.170	-0.005	0.182	0.144	0.016	0.772**
NET	0.048	0.635	0.119	-0.307	-0.150	0.004	-0.128	0.020	-0.027	0.056	-0.141	0.033	0.161
LP	0.236	-0.405	-0.186	0.074	0.078	-0.010	-0.057	0.127	-0.018	0.153	-0.008	0.055	0.039
DF	0.155	-0.271	-0.019	0.719	0.035	0.050	0.117	0.101	0.087	0.043	-0.140	-0.033	0.846**
NPBP	-0.149	-0.540	-0.082	0.143	0.177	-0.050	0.144	0.501	-0.087	0.079	-0.026	-0.048	0.060
NSBP	-0.239	-0.027	-0.020	-0.390	0.096	-0.093	0.099	0.419	0.021	-0.023	-0.035	-0.023	-0.218
NFGP	-0.037	-0.462	0.060	0.477	0.144	-0.052	0.176	-0.038	-0.073	0.154	-0.042	-0.017	0.288
NUFGP	-0.075	0.024	-0.043	0.133	0.163	-0.071	-0.012	0.544	-0.090	0.053	-0.118	0.009	0.517**
1000GW	0.007	0.104	-0.020	-0.371	0.091	0.011	0.076	0.289	-0.169	0.178	0.008	-0.030	0.176
RL	0.236	0.192	-0.154	0.167	0.075	0.011	0.146	0.157	-0.163	0.185	-0.197	-0.013	0.645**
NRH	-0.147	0.382	-0.007	0.430	0.020	-0.014	0.032	0.274	0.006	0.155	-0.235	-0.010	0.888**
RW	0.036	0.196	0.096	-0.222	-0.079	0.019	-0.028	0.049	0.048	-0.023	0.022	0.108	0.031

Residual effect: 0.137. **: Significant at 1%. *: Significant at 5%.

PH: Plant height (cm); NET: Number of effective tiller; LP: Length of panicle; DF: Days to flowering; NPBP: Number of primary branches per panicle; NSBP: Number of secondary branches per panicle; NFGP: Number of filled grain per panicle; NUFGP: Number of unfilled grain per panicle; 1000 GW: 1000 grain weight; RL: Root length; NRH: Number of root hair; RW: Root weight; GYH: Grain yield per hill (g).

Table 4: Genotypic path coefficient analysis showing direct and indirect effects of different characters on yield of 35 rice genotypes.

Path analysis

Associations of characters determined by correlation coefficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on grain yield per plant. As a matter of fact, in order to find out a clear picture of the interrelationship between grain yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at both genotypic and phenotypic level.

Genotypic path coefficient analysis showing direct and indirect effects of different characters and the results are presented in Table 4. From the path coefficient analysis showed that days to flowering had maximum direct effect (0.719) on yield followed by number of effective tiller (0.635), number of unfilled grain per panicle (0.544). [13] reported that the number of branches per panicle (0.424) had the highest positive direct effect on grain yield followed by number of filled grains per panicle (0.411), and days to 50% flowering (0.07).The lowest direct effect on grain yield was exhibited by root weight(0.108) followed by number of filled grain per panicle(0.176). The highest negative indirect effects on grain yield were obtained by number of root hair (-0.235). [15] worked out on path co-efficient in 128 aromatic rice accessions for seven traits and observed greatest positive direct effect of 1000-grain

Characters	PH	NET	LP	DF	NPBP	NSBP	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
PH	0.247	0.110	-0.461	0.329	-0.278	0.274	-0.004	-0.188	-0.020	0.519	0.206	0.029	0.763**
NET	0.047	0.575	0.302	-0.203	-0.418	0.011	-0.018	0.023	-0.067	0.113	-0.263	0.058	0.161
LP	0.218	-0.332	-0.523	0.054	0.168	-0.027	-0.007	0.127	-0.030	0.307	-0.011	0.093	0.035
DF	0.153	-0.219	-0.053	0.531	0.072	0.142	0.016	0.106	0.218	0.085	-0.184	-0.060	0.809**
NPBP	-0.133	-0.466	-0.170	0.074	0.517	-0.132	0.018	0.492	-0.203	0.167	-0.037	-0.075	0.051
NSBP	-0.239	-0.023	-0.051	-0.267	0.243	-0.282	0.014	0.466	0.059	-0.044	-0.046	-0.042	-0.215
NFGP	-0.038	-0.397	0.147	0.326	0.354	-0.154	0.027	-0.043	-0.178	0.332	-0.061	-0.032	0.282
NUFGP	-0.074	0.021	-0.106	0.090	0.407	-0.211	-0.001	0.623	-0.223	0.129	-0.167	0.018	0.507**
1000GW	0.010	0.077	-0.031	-0.229	0.208	0.033	0.009	0.275	-0.505	0.342	0.008	-0.047	0.151
RL	0.236	0.120	-0.295	0.083	0.159	0.022	0.016	0.149	-0.318	0.543	-0.220	-0.017	0.479**
NRH	-0.145	0.433	-0.016	0.280	0.054	-0.037	0.004	0.298	0.012	0.342	-0.349	-0.018	0.859**
RW	0.035	0.166	-0.240	-0.156	-0.190	0.059	-0.004	0.055	0.117	-0.047	0.032	0.203	0.030

Residual effect: 0.0055

PH: Plant height (cm); NET: Number of effective tiller; LP: Length of panicle; DF: Days to flowering; NPBP: Number of primary branches per panicle; NSBP: Number of secondary branches per panicle; NFGP: Number of filled grain per panicle; NUFGP: Number of unfilled grain per panicle; 1000 GW: 1000 grain weight; RL: Root length; NRH: Number of root hair; RW: Root weight; GYH: Grain yield per hill (g).

Table 5: Phenotypic path coefficient analysis showing direct and indirect effects of different characters on yield of rice.

weight followed by number of ear-bearing tillers per plant, number of filled grains per panicle and number of days to 50% flowering on grain yield. However, 1000-grain weight had on significant correlation with grain yield per plant due to its negative indirect on grain yield plant through number of filled grain per panicle and plant height. The results prescribed that highly significant positive correlation with positive direct effect was observed in days to flowering, number of effective tiller, number of unfilled grain per panicle, number of filled grain per panicle and root weight. The residual effect of the present study was 0.137 [16] (Table 4).

Phenotypic path coefficient analysis showing direct and indirect effects of different characters and the results are presented in Table 5. From the path coefficient analysis showed that number of unfilled grain per panicle had maximum direct effect (0.623) on yield followed by number of effective tiller (0.575), root length (0.543). The lowest direct effect on grain yield was exhibited by number of filled grain per panicle (0.027) followed by root weight (0.203). The highest negative indirect effects on grain yield were obtained by length of panicle (-0.523). The results prescribed that highly significant positive correlation with positive direct effect was observed in number of unfilled grain per panicle, number of effective tiller, root length, root weight and number of filled grain per panicle. The residual effect of the present study was 0.0055 (Table 5).

Conclusion

Thirty-four local varieties of rice along with one standard check were evaluated for thirteen yield and yield attributing traits. Results of the present investigation on variability, heritability and genetic advance indicated a scope for improvement of grain yield through selection. Further, studies on character association and path co-efficient revealed the importance of panicle bearing tillers per hill and number of filled grains per panicle as selection criteria for effective yield improvement. The study also indicated the need for balanced selection in light of negative association of panicle bearing tillers per hill with number of filled grains per panicle; and number of filled grains per panicle with 1000-grain weight in crop yield improvement programs.

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