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Correlation and Path Coefficient Analysis for Agro-morphological important traits in Aman rice Genotypes (*Oryza sativa* L.)

Golam Sarwar1, Md. Harun-Ur-Rashid 2*, Shahanaz Parveen3, Md. Sarowar Hossain4
1 Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Bangladesh
2 Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Bangladesh
3 Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Bangladesh
4 Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Bangladesh
*Corresponding author email:sumonsau@gmail.com

ABSTRACT

The experiment was conducted with forty two genotypes of rice at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period of July 2013- December 2013 to estimate the correlation and path coefficient analysis among 42 Aman rice genotypes. Correlation analysis revealed that significant and positive correlation of total tillers per plant and effective tillers per plant with yield per plant at both genotypic and phenotypic level whereas significant and positive correlation of days to maturity with yield per plant at genotypic level only. This indicates the relative utility of these traits for selection with respect to yield per plant. On the other hand it revealed significant and negative association of unfilled grains per panicle with yield per plant at both genotypic and phenotypic level. From the result of path analysis it was evident that direct positive effect was contributed by filled grains per panicle, total tillers per plant, thousand grains weight, and effective tillers per plant, plant height, days to 50% flowering and days to maturity. From the correlation and path analysis it was revealed that total tillers per plant, effective tillers per plant and days to maturity showed significantly positive genotypic correlation with yield as well as employed positive direct effect on yield per plant and this suggested that the selection for total tillers per plant, effective tillers per plant and days to maturity would likely the best parameter for improvement in yield per plant.
Key words: Correlation analysis, Path coefficient analysis, Agro-morphological, Traits, Aman rice.

INTRODUCTION

Rice is a cereal crop belonging to genus *Oryza* of family Poaceae. The genus *Oryza* has twenty two wild and two cultivated species viz., *O. sativa* and *O. glaberrima*. All the germplasms found in Asia, America and Europe belong to *O. sativa*, while those in West Africa belong to *O. glaberrima*. *O. sativa* is a cultivated diploid species having 24 chromosomes of AA genome.

Rice is the staple food crop of more than half of the world's population [1]. By 2030, the world must have to produce 60% more rice than it produce in 1995 to meet the demands [2]. Bangladesh is the fourth largest producer of rice in the world with production of 33.8 million tons in 2012 [3]. It occupies 74.77% total cropped areas and it alone constitutes 90% of the total food grain produced annually in the country [4]. Bangladesh needs to 2.7% increases in rice production per year due to increasing population [5].

Grain yield, being a quantitative trait is a complex character of any crop. Various morphological and physiological plant characters contribute to yield. These yield contributing components are interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions [6]. Measurement of correlation coefficient helps to identify the relative contribution of component characters toward yield [7]. Path coefficient analysis partitions the genetic correlation between yield and its component traits into direct and indirect effects and hence has effectively been used in identifying useful traits as selection criteria to improve grain yield in rice [8, 9, 10, and 11]. The present

investigation was undertaken to study correlation among agro-morphological important traits in the 42 Aman rice genotypes and the direct and indirect effect of these characters towards seed yield.

MATERIALS AND METHODS
Experimental site
The research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University, Dhaka during July 2013-December 2013. The location of the site is 23° 74' N latitude and 90° 35' E longitude with an elevation of 8.2 meter above sea level. It was situated in the sub-tropical zone. The soil of the experimental site lies in Agroecological region of "Madhupur Tract" (AEZ No. 28). Its top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 6.1 and organic carbon content is 0.82%.

Plant materials

Table 1: List of the genotypes used in the experiment with their source

Sl. No.	Genotypes	Source
1	G1: AL-17 (iii) B	
2	G2: AL-17 (iii)	
3	G3: AL-42	
4	G4: From IR-25B (Yellow)	
5	G5: From IR-25B	
6	G6: Special (Early)	
7	G7: Richer	
8	G8: AL-35	
9	G9: Special-130	
10	G10: IR-25B (Dwarf)	
11	G11: AL-36(C)	
12	G12: Special from AL-36(D)	
13	G13: P-5B (i)	
14	G14: Hira	
15	G15: AL-17(iii) (Tall)	
16	G16: Aloron	
17	G17: IR-25B (Tall)	
18	G18: AL-36(iii)	
19	G19: Special from AL-33	
20	G20: Special from AL-29 (Basmoti type)	
21	G21:S-1 (Basmoti type)	
22	G22: S-2 (Basmoti type)	
23	G23; S-5 (Basmoti type)	Sher-e-Bangla Agricultural University
24	G24: AL-33(ii) (Basmoti type)	
25	G25: AL-36 (Basmoti type)	
26	G26: AL-42(ii) (Basmoti-Yellow type)	
27	G27: AL-44(i) (Basmoti-Yellow type)	
28	G28: AL-17(ii) A	
29	G29: AL-47	
30	G30: PP-48	
31	G31: PP-4B(i)	
32	G32: Special from-129	
33	G33: P-5B (ii)	
34	G34: AL-36	
35	G35: Special stigma color	
36	G36: IR-25B	
37	G37: Special from-17(iv)	
38	G38: Special from S-2	
39	G39: Special from AL-33	
40	G40: AL-44(i)	
41	G41: AL-17	
42	G42: AL-104	

Field experiment
The experimental plot was prepared by plugging with proper tiller. The weeds and other unwanted plant materials were removed from the field during the land preparation. Proper laddering was done to bring the soil at proper tilth condition.

A Randomized Complete Block Design was used in the experiment with three replications. The field was divided into three blocks; the blocks were subdivided into 42 plots. Genotypes were randomly assigned into 42 plots in each block. The plot size was 2m × 1m. Block to block and plot to plot distance were 1 m and .5 m respectively.

The seeds were sown on 22nd July 2013 and one seedling per hill was transplanted to the main plot on 24th August 2013. Intra and inter row distance were maintained @ 20 cm and 25 cm respectively.

Urea, Triple Super Phosphate, Muriate of Potash, Gypsum @ 180, 55, 80, 60 kg per hectare respectively were used in the experiment. Total TSP, MP and Gypsum were applied in final land preparation. Total urea was applied in three installments, at 15 days after transplanting (DAT), 35 DAT and 55 DAT respectively.

Weeding, during first two top dressing of urea, was done to break the soil crust, to keep the plots free from weed and to incorporate the urea fertilizer into the soil for reducing the loss of urea through denitrification. Irrigation with regular interval was given to maintain 5-7 cm water up to hard dough stage of rice.

Proper control measures were taken against rice stem borer during tillering and heading stage of rice. Furadan 5G (carbofuran) @ 1 g per square meter were applied at active tillering stage and panicle initiation stage of rice for controlling the stem borer. Lani rate and malathion (organophosphates) were applied to protect from rat and rice bug respectively.

Two-three cm of water level was maintained at the time of transplanting. 5 cm depth of water was given at the time of maximum tillering stage. Then field was irrigated as and when required up to physiological maturity. Harvesting was started when 80% of the plant population of each plot reached maturity.

Data were recorded on individual plant basis from 10 randomly selected plants. Observations were recorded on various plant traits i.e. days to 50% flowering, days to maturity, plant height, total tillers per plant, effective tillers per plant, panicle length, fertile grains per panicle, and unfertile grains per panicle, 1000 grains weight and yield per plant.

Statistical analysis

The genotypic and phenotypic correlation coefficients between yield and different yield contributing characters were estimated as:

Genotypic correlation = $\dfrac{Cov(g)1.2}{\sqrt{\sigma^2(g)1.\sigma^2(g)2}}$

Where, $Cov_{g\,(xy)}$ = Genotypic covariance between the variables X and Y

$\sigma^2_{(g)1}$ = Genotypic variance of the variable X_1

$\sigma^2_{(g)2}$ = Genotypic variance of the variable X_2

Similarly, phenotypic correlation $r_{p(xy)}$ = $\dfrac{Cov(ph)1.2}{\sqrt{\sigma^2(ph)1.\sigma^2(ph)2}}$

Where, $Cov_{ph(xy)}$ = phenotypic covariance between the variables X and Y

$\sigma^2_{(ph)1}$ = phenotypic variance of the variable X_1

$\sigma^2_{(ph)2}$ = phenotypic variance of the variable X_2

Path coefficient analysis was done according to the procedure employed by [12] also quoted in [13], using genotypic 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. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3..................and 10 on yield y, a set of simultaneous equations (one equations in this example) is required to be formulated as shown below:

$r_{1.y} = P_{1.y} + r_{1.2}\,P_{2.y} + r_{1.3}\,P_{3.y} + r_{1.4}\,P_{4.y} + r_{1.5}\,P_{5.y} + r_{1.6}\,P_{6.y} + r_{1.7}\,P_{7.y} + r_{1.8}\,P_{8.y} + r_{1.9}\,P_{9.y} + r_{1.10}\,P_{10.y}$

Where, r_{1y} = Genotypic correlation coefficients between y and I th character (y= Grain yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,..........,10)

Here, 1 = Plant height, 2 = Total tillers/plant, 3 = Effective tillers/plant, 4 = Panicle length,   5 = Filled grains/panicle, 6 = Unfilled grains/panicle, 7 = Days to 50% flowering, 8 = 1000 grains weight, 9 = Days to maturity and 10 = Yield/plant

Total correlation, say between 1 and y i. e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y, $r_{1.2}\,P_{2.y}$ = indirect effect of 1 via 2 on y and so on.

Where, $P_{1.y},\ P_{2.y},\ P_{3.y}\ ...\ P_{10.y}$ = Path coefficient of the independent variables 1, 2,..., 10 on the dependent variable y, respectively.

$r_{1.y},\ r_{2.y},\ r_{3.y}...\ r_{10.y}$ = Correlation coefficient of 1, 2, 3... 10 with y, respectively.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985)-

$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots + r_{10.y}P_{10.y})$

Where, $P^2_{RY} = R^2$

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

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y

RESULTS AND DISCUSSION
Correlation study

The correlation coefficient between yield and yield contributing characters in rice are presented in Table 2. Correlation analysis among yield and its contributing character revealed that the genotypic correlation in most cases were higher than their phenotypic correlation coefficients indicating the association is largely due to genetic reason. In some cases phenotypic correlation coefficients were higher than genotypic correlation indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level.

Plant height was positively and significantly correlated with panicle length at both genotypic and phenotypic level. It was positively and significantly correlated with filled grains per panicle at the genotypic level only. It was negatively and significantly correlated with total tillers per plant and effective tillers per plant at the genotypic level. Days to 50% flowering, unfilled grains per panicle, 1000 grains weight and yield per plant were positively and non-significantly correlated with plant height at both genotypic and phenotypic level.

Total tillers per plant showed positive and significant correlation with effective tillers per plant and yield per plant at both genotypic and phenotypic level. This indicates relative utility of total tillers per plant for selection with respect to yield per plant. Total tillers per plant showed negative and significant association with panicle length and thousand grains weight at genotypic level only. Filled grains per panicle, unfilled grains per panicle, days to 50% flowering and days to maturity was positively and non significantly correlated with total tillers per plant at both genotypic and phenotypic level. Total tillers per plant showed non-significant negative association with filled grains per panicle at both genotypic and phenotypic level. Reference [14, 15, 16] also reported positive and significant correlation of yield with total tillers per plant at both genotypic and phenotypic level.

Effective tillers per plant showed positive and significant correlation with days to 50% flowering and yield per plant at both genotypic and phenotypic level. This indicates relative utility of effective tillers per plant for selection with respect to yield per plant. It showed positive and non significant association with days to maturity at both genotypic and phenotypic levels. Effective tillers per plant were negatively and non significantly correlated with panicle length, filled grains per panicle, unfilled grains per panicle and thousand grains weight at both genotypic and phenotypic level. Reference [14, 17] also found positive and significant correlation of yield with effective tillers per plant at both genotypic and phenotypic level and [15, 18] found positive and significant correlation of yield with effective tillers per plant at genotypic level only.

Days to 50% flowering showed positive and non significant correlation with unfilled grain, days to maturity and yield per plant at both genotypic and phenotypic level. It was negatively and non-significantly associated with panicle length, filled grains per panicle and thousand grains weight at both genotypic and phenotypic level.

Panicle length showed significant and positive association with filled grains per panicle at both genotypic and phenotypic level whereas it was positively and significantly associated with thousand grains weight at genotypic level only. It showed non-significant positive association with unfilled grains per panicle at both genotypic and phenotypic level. It showed non significant negative association with yield per plant at genotypic level whereas non significantly and positively correlated with yield per plant at phenotypic level.

Filled grains per panicle showed significant positive association with unfilled grains per panicle at both genotypic and phenotypic level. It showed positive and non-significant association with days to maturity and yield per plant at both genotypic and phenotypic level. It was negatively and non-significantly correlated with thousand grain weight at both genotypic and phenotypic level.

Unfilled grains per panicle showed negative and significant association with yield per plant at both genotypic and phenotypic level. It showed positive and non-significant association with days to maturity and days to 50% flowering at both genotypic and phenotypic level whereas it showed negative and non-significant association with 1000 grains weight at both genotypic and phenotypic level.

Table 2: Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of rice

Parameters		TTP	ETP	DFF	PL	FG	UFG	DM	TGW	YPP
PH	rg	-0.357*	-0.316*	0.067	0.373*	0.309*	0.068	-0.018	0.131	0.111
	rp	-0.215	-0.198	0.045	0.359*	0.285	0.101	-0.047	0.123	0.167
TTP	rg		0.501**	0.257	-0.312*	-0.119	0.009	0.271	-0.313*	0.416**
	rp		0.499**	0.204	-0.177	-0.097	-0.013	0.223	-0.259	0.458**
ETP	rg			0.449**	-0.261	-0.030	-0.026	0.276	-0.265	0.461**
	rp			0.376*	-0.142	-0.034	-0.049	0.236	-0.230	0.499**
DFF	rg				-0.111	-0.161	0.048	0.277	-0.162	0.262
	rp				-0.098	-0.141	0.019	0.261	-0.138	0.208
PL	rg					0.483**	0.222	-0.019	0.309*	-0.025
	rp					0.419**	0.247	-0.033	0.218	0.078
FG	rg						0.385**	0.017	-0.012	0.205
	rp						0.318*	0.013	-0.006	0.173
UFG	rg							0.050	-0.026	-0.340*
	rp							0.031	-0.015	-0.309*
DM	rg								0.085	0.360*
	rp								0.066	0.281
TGW	rg									0.187
	rp									0.137

** = Significant at 1%, * = Significant at 5%
Here, PH = Plant height (cm), TTP = Total tillers per plant, ET = Effective tillers per plant, DF = Days to 50% flowering, PL = Panicle length (cm), FG = Filled grains per panicle, UFG = Unfilled grains per panicle, DM = Days to maturity, TGW = Thousand grains weight (g), YPP = Yield per plant (g)

Days to maturity showed positive and significant association with yield per plant at genotypic level only. This indicates relative utility of days to maturity for selection with respect to yield per plant. It showed positive and non-significant association with 1000 grains weight at both genotypic and phenotypic level. Reference [14] reported positive and significant correlation of days to maturity with yield at both genotypic and phenotypic level. Thousand grains weight showed non-significant positive association with yield per plant at both genotypic and phenotypic level.

Pleiotropy or linkage relations among genes controlling the traits are some of the reasons of genetic trait correlations. Directions and rates of short term evolution are effected by genetic trait correlations [19, 20, 21]. Much of dissimilarity phenotypic and genetic correlation estimates seems to be due to imprecise estimates of genetic correlations. In many situations, phenotypic correlations are likely to be fair estimates of their genetic counterparts [22]. Genetic correlations between morphological traits are more often positive than correlation between other traits [20, 23]. Competition between processes for a resource may result in negative correlations [24].

Path coefficient analysis

Plant height employed positive direct effect on yield per plant (0.243) as well as positive indirect effect via filled grains per panicle, days to 50% flowering and thousand grain weights. It also showed negative indirect effect of total tillers per plant, effective tillers per plant, panicle length, unfilled grains per panicle and days to maturity. Reference [9, 25, 15] also found positive direct effect of plant height on yield per plant. But Reference [26] found negative direct effect of plant height on yield per plant.

Total tillers per plant employed positive direct effect on yield per plant (0.440) and exhibited significant positive correlation with yield per plant at both genotypic and phenotypic level, indicating true relationship between these traits. This may indicate that the direct selection for total tillers per plant would likely be effective in increasing yield per plant. Total tillers per plant employed positive indirect effect via panicle length, effective tillers per plant, days to maturity and days to 50% flowering. But it showed negative indirect effect of plant height, filled grains per panicle and unfilled grains per panicle and thousand grains weight. Reference [27, 25, 15, 16] also found positive direct effect of total tillers per plant on yield per plant.

Effective tillers per plant employed positive direct effect on yield per plant (0.318) and exhibited significant positive correlation with yield per plant at both genotypic and phenotypic level, indicating true relationship between these traits. This may indicate that the direct selection for effective tillers per plant would likely be effective in increasing yield per plant. Effective tillers per plant employed indirect positive effect via total tillers per plant, panicle length, unfilled grains per panicle, days to maturity and days to 50% flowering. On the other hand it showed negative indirect effect of plant height, filled grains per

panicle and thousand grains weight. Reference [18] also found positive direct effect of effective tillers per plant on yield per plant. But reference [14, 26, 15] found negative direct effect of effective tillers per plant on yield per plant.

Days to 50% flowering employed positive direct effect on yield per plant (0.113) as well as positive indirect effect via plant height, total tillers per plant, and effective tillers per plant, panicle length and days to maturity. It also showed negative indirect effect of filled grains per panicle, unfilled grains per panicle and thousand grains weight. Reference [15, 28] also reported positive direct effects of days to 50% flowering on yield per plant. But reference [29] also reported negative direct effect of days to 50% flowering on yield per plant.

Panicle length employed negative direct effect on yield per plant (-0.122) as well as indirect positive effect via total tillers per plant, unfilled grains per panicle, effective tillers per plant, days to 50% flowering and days to maturity. It also showed positive indirect effect of plant height, filled grains per panicle and thousand grains weight. But reference [25, 15] found direct positive effect of panicle length on yield per plant.

Filled grains per panicle employed positive direct effect on yield per plant (0.466) as well as indirect positive effect via plant height and days to maturity. It also showed negative indirect effect of effective tillers per plant, days to 50% flowering, total tillers per plant, panicle length, unfilled grains per panicle and thousand grains weight. Reference [29, 26, 15, 18] also found positive direct effect of filled grains per panicle on yield per plant.

Unfilled grains per panicle employed negative direct effect on yield per plant (-0.505) as well as indirect negative effect via, panicle length, effective tillers per plant and thousand grains weight. It also showed positive indirect effect of plant height, total tillers per plant, days to 50% flowering, filled grains per panicle and days to maturity.

Days to maturity employed direct positive effect on yield per plant (0.106) and exhibited significant positive correlation with yield per plant at genotypic level only, indicating true relationship between these traits. This may indicate that the direct selection for days to maturity would likely be effective in increasing yield per plant. Days to maturity employed indirect positive effect via total tillers per plant, panicle length, filled grains per panicle, effective tillers per plant, days to 50% flowering and thousand grains weight. It also showed negative indirect effect of plant height and unfilled grains per panicle.

Table 2: Path coefficient analysis showing direct and indirect effects of different characters on yield of rice genotypes

Trait	Direct (Bold) and Indirect effect									Genotypic correlation with yield
	PH	TTP	ETP	DF	PL	FG	UFG	DM	TGW	
PH	**0.243**	-0.157	-0.100	0.008	-0.046	0.144	-0.034	-0.002	0.055	0.111
TTP	-0.087	**0.440**	0.159	0.029	0.038	-0.056	-0.005	0.029	-0.131	0.416**
ETP	-0.077	0.220	**0.318**	0.051	0.032	-0.014	0.013	0.029	-0.111	0.461**
DFF	0.016	0.113	0.143	**-0.122**	0.014	-0.075	-0.024	0.029	-0.067	0.262
PL	0.091	-0.137	-0.083	-0.013	**0.466**	0.225	-0.112	-0.002	0.129	-0.025
FG	0.075	-0.053	-0.009	-0.018	-0.059	**-0.505**	-0.195	0.002	-0.005	0.205
UFG	0.016	0.004	-0.008	0.005	-0.027	0.180	**0.113**	0.005	-0.011	-0.340*
DM	-0.005	0.119	0.088	0.031	0.002	0.008	-0.025	**0.106**	0.035	0.360*
TGW	0.032	-0.138	-0.084	-0.018	-0.038	-0.005	0.013	0.009	**0.417**	0.187
R	0.47									

** = Significant at 1% and * = Significant at 5%, R= Residual effect

Here, PH = Plant height (cm), TTP = Total tillers per plant, ETP= Effective tillers, DFF= Days to 50% flowering, PL= Panicle length (cm), FG=Filled grains per panicle, UFG = Unfilled grains per panicle, DM = Days to maturity, TGW = Thousand grains weight (g), YPP = Yield per plant (g)

Thousand grains weight employed direct positive effect on yield per plant (0.417) but exhibited non significant positive association with yield per plant at both genotypic and phenotypic level. It may be due to higher indirect negative effect of total tillers per plant (-0.138) and effective tillers per plant (-0.084). Thousand grains weight showed indirect positive effect via plant height, unfilled grains per panicle and days to maturity. It also showed negative indirect effect of days to 50% flowering, total tillers per plant, effective tillers per plant, panicle length and filled grains per panicle. Reference [14] also found positive direct effect of thousand grains weight on yield per plant.

Here, the correlation coefficient is positive but the direct effect is negative. Therefore, the indirect effects seem to be the cause of correlation. In such situation the indirect causal factors are to be considered simultaneously. When correlation coefficient is negative and the direct effect is positive and high, a restricted simultaneous selection model is to be followed, i.e. restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect [30, 31]. Residual effects (0.47) indicated that the characters which were selected in this study contributed 53% to the yield. It is suggested that more emphasis should be given on the above characters for selecting rape seed genotypes with higher yield and other traits.

From the above discussion of correlation and path analysis it was revealed that total tillers per plant, effective tillers per plant and days to maturity showed significantly positive genotypic correlation with yield as well as employed positive direct effect on yield suggesting that the selection for these traits would helpful for the improvement of yield per plant.

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