Character Association of T. Aman Rice
(*Oryza sativa* L.) Varieties of Bangladesh

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Abstract: A field experiment was conducted during June 2013 to December 2013 to study the character association of T. Aman rice varieties of Bangladesh (*Oryza sativa* L.). Twenty eight genotypes were evaluated for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield. The experiment was laid out in RCBD with three replications. Plant height (cm), Flag leaf blade length (cm), Tillers per hill (No.), Panicle length (cm), Primary branches per panicle (No.), Secondary branches per panicle (No.), Panicle per m^2(No.), Filled grains per panicle (No.), 1000 grains weight (g) and Grain yield (t/ha) data were recorded. Genotypic variance (σ^2g), Phenotypic variance (σ^2p), Genotypic Coefficient of Variation (GCV %), Phenotypic Coefficient of Variation (PCV %), heritability and genetic advance (GA), Genotypic and phenotypic correlation coefficients and Path coefficient analysis were estimated. Analysis of variance raveled significant differences among the varieties for all the traits. Plant height, flag leaf blade length, tillers per hill, panicle length, secondary branches per panicle, 1000 grains weight and grain yield exhibited that they were controlled by additive gene action and improvement of these traits for selection. The phenotypic variance was higher than the corresponding genotypic variance in most of the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation. Genotypic coefficient of variation was the highest for primary branches per panicle (16.74) followed by secondary branches per panicle (14.12), tillers per hill (14.09), plant height (13.95) and grain yield (13.32). Highest heritability was found flag leaf blade length (99.23), plant height (98.04) and 1000 grains weight. Considering the character association and path analysis showed that panicles per m^2, tillers per hill, panicle length and filled grains per panicle are the most important yield components in rice. Emphasize should be given on these characters for the selection of genotypes for future breeding program to improve the yield in transplanted aman rice.

Key words: Genetic Advance · Genetic Variability · GCV · PCV and Rice (*Oryza sativa* L.)

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INTRODUCTION

Rice (*Oryza sativa* L.) is a self-pollinated cereal crop having chromosome number 2n=24 under the family Gramineae [1]. It is the staple food for more than half of the global population [2, 3].

The production of rice in Bangladesh of over 155 million people was around 33.8 million tons. The production of Aman which constitutes 40 per cent of the total rice production [4]. Total area under Aman crop has been estimated at 5.61 million hectares in 2012-13 as compared to 5.58 million hectares in 2011-12 which is 0.54 percent higher [4]. Total Aman production of 2012-2013 has been estimated at 12.897 million metric tons as compared to 12.798 million metric tons in 2011-12 which is 0.77 percent higher than that of last year [4]. Basically, aman season provides lower yield potential than boro seasons but large amount of arable lands are utilized in aman rice cultivation in our country because of sufficient precipitation compared to boro season [5]. Rice is a semi aquatic plant. It is required for the rainy season but flood or submergence condition can hampered the expected production. Sometimes, rice plants may be damaged due to submergence for long time which affects the production of rice. So, we should improve the production of rice vertically utilizing every resources and opportunity judiciously. Rice yield is dependent on many yield contributing characters as well as on the environmental influence. Yield is a complex polygenic character where many of yield contributing characters form a complex chain of relationship with grain yield. Those yield contributing characters are highly influenced by environmental conditions [6]. Association of different characters is essential to determine their contribution towards yield. Yield component analysis is of fundamental importance to determine the direct and indirect contributions towards yield. As the yield is polygenic ally controlled and also influenced by its component characters, direct selection for yield is often misleading. Knowledge about genetic variability of yield contributing characters, interrelationship among them and their relation with yield are necessary for a successful breeding program. As the yield potential of modern varieties has reached to a certain level, selection based on related characters to yield can help to get progenies having high yield potential. Genetic diversity in the available gene pool is the foundation of all plant improvement programs. It is source of variation, which is raw material for the improvement work. This genetic diversity is essential to decrease crop vulnerability to abiotic and biotic stress, ensure long-term selection grain in genetic improvement and promote rational use of genetic resource [7]. Genetically distant parents usually able to produce higher heterosis. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm [8]. A systematic and efficient breeding program involves the steps like creation of genetic variation, selection practices and utilization of selected genotypes to develop promising varieties and all of those steps involves biometrical and multivariate analyses [9-11].

Therefore, the present study was conducted to explore the characters highly responsible for high yield potential of transplanted aman rice. To determine the pattern of variability exist in the T. Aman rice genotypes for different traits and to assess the magnitude of diversity and classify them under different groups based on genetic divergence.

MATERIALS AND METHODS

Twenty eight rice varieties were collected from the gene bank of Bangladesh Rice Research Institute (BRRI) (Table 1). The experiment was conducted at the experimental field of BRRI, Gazipur during T. Aman 2013 using Randomized Complete Block Design (RCBD) with three replications. The soil type of the experimental field belongs to the Shallow Red Brown Terrace type under Salna Series of Madhupur Tract of Agro ecological Zone (AEZ) 28 which is characterized by silty clay with pH value of 5.92. Twenty six days old seedlings from each entry were planted in 5 m x 4 m plot with 25 cm x 15 cm spacing using single seedling per hill. Fertilizer doses were 195:53:83:60:1 kg Urea, TSP, MP, Gypsum and Zinc sulphate per hectare. Except urea all other fertilizers were used as basal dose and urea fertilizer was top dressed in three equal splits at 15, 30 and 45 days after transplant. All necessary cultural operations and management practices were employed whenever needed. At maturity, 10 m^2 area was harvested for estimating grain yield excluding border area and yield was adjusted at 14% moisture level and converted it to ton per hectare. Observations were made from ten randomly selected plants.

data were recorded on Plant height (cm), Flag leaf blade length (cm), Tillers per hill (No.), Panicle length (cm), Primary branches per panicle (No.), Secondary branches per panicle (No.), Panicle per m^2 (No.), Filled grains per panicle (No.), 1000 grain weight (g), Grain yield (t/ha).

Table 1: List of rice (*Oryza sativa* L.) varieties used in this study

SL. No.	Name of variety	Year of release	Parents/crosses
1.	BR3	1973	IR506-1-133 × Latishil
2.	BR4	1975	IR20 × IR5-114-3-1
3.	BR5	1976	Badshavog
4.	BR10	1980	IR20 × IR5-114-3-1
5.	BR11	1980	IR20 × IR5-47-2
6.	BR 22	1988	Nazirshil × BR51-46-5
7.	BR 23	1988	DA29 × BR4
8.	BR 25	1992	Pajam2 × IR26
9.	BRRI dhan30	1994	IR2058-78-1-3-2-3 × BR4
10.	BRRI dhan31	1994	BR11 × ARC10550
11.	BRRI dhan32	1994	BR4 × BR2662
12.	BRRI dhan33	1997	BG388 × BG367-4
13.	BRRI dhan34	1997	Selection (Acc. No 4341)
14.	BRRI dhan37	1998	Bashmati (D) × BR5
15.	BRRI dhan38	1998	Bashmati (D) × BR5
16.	BRRI dhan39	1999	BR1185-2B-56-2-1-1×BR1674-28-3-1-1
17.	BRRI dhan40	2003	BR10 × IR4595-4-1-15
18.	BRRI dhan41	2003	BR23 × BR1185-2B-16-1
19.	BRRI dhan44	2005	BR10 × BRRI dhan31
20.	BRRI dhan46	2007	BR11 × ARC14766 × Swarnolota
21.	BRRI dhan49	2008	BR4962-12-4-1 × IR33380-7-2-1-3
22.	BRRI dhan51	2010	Swarna× IR49830-7-1-2-3
23.	BRRI dhan52	2010	BR11 × IR 40931-33-1-3-2
24.	BRRI dhan53	2010	BR10 × BR23 × BR847-76-1-1
25.	BRRI dhan54	2010	BR1185-2B-16-1 × BR548-128-1-3
26.	BRRI dhan55	2011	IR64×Oryza rufipogon
27.	BRRI dhan56	2011	IR55419-4×WAY RAREM
28.	BINA dhan-7	2007	Ain guen 250 γ ray

The data were analyzed by MSTAT program for ANOVA, Basic for Correlation coefficient and Path coefficient analysis. Genotypic variance (σ^2g) and Phenotypic variance (σ^2p) were estimated following Johnson *et al*., Genotypic Coefficient of Variation (GCV %) and Phenotypic Coefficient of Variation (PCV %) were estimated according to Burton. Board sense heritability and genetic advance (GA) were estimated using the formula suggested by Johnson *et al*. [12] and Hanson [13]. Genotypic and phenotypic correlation coefficients were carried out using formula suggested by Miller [14], Hanson [13] and Johnson *et al.* [12], The correlation coefficients were further partitioned into components of direct and indirect effects by path coefficient analysis developed by Wright [15] and later described by Lu and Snow [16]. The estimate of GCV and PCV were classified as low, medium and high as per Sivasubramanian [17]. The heritability was categorized as suggested by Robinson *et al.* [18]. Again, genetic advance was classified by adopting the method Johnson *et al.* [12].

RESULTS AND DISCUSSION

Variability: Mean sum of square, variance components, heritability estimates, genetic advance, genetic advance in percent of mean and coefficient of genotypic and phenotypic variations are presented in Table 2. Mean sum of square for all the characters were highly significant due to genotypes indicated wide range of variability among the genotypes for these traits. The Genotypic variance (σ^2g), Phenotypic variance (σ^2p), Genotypic Coefficient of Variation (GCV %), Phenotypic Coefficient of Variation (PCV %) were close to each other for all the traits, except primary branches per panicle, filled grain per panicle and panicle per m^2 which indicated less environmental influence and non-additive gene action for these traits.

Plant height, flag leaf blade length, tillers per hill, panicle length, secondary branches per panicle, 1000 grains weight and grain yield showed moderately high genetic advance in percent of mean along with high heritability. Those seven characters exhibited that they were controlled by additive gene action and selection

Table 2: Estimation of statistical and genetic parameters of yield and its contributing traits of 28 rice genotypes

Parameters	MSSG	Gen.var. ($\sigma2g$)	Env.var ($\sigma2e$)	Phn.var. ($\sigma2p$)	Herit.	G.Ad (5%)	G.Ad (5%) in % mean	GCV	PCV	ECV
PH	849.9**	281.42	5.62	287.04	98.04	34.22	28.46	13.95	14.09	1.97
FLBL	47.76**	15.88	0.12	16.00	99.23	8.18	23.80	11.60	11.65	1.02
TH	14.91**	4.46	1.53	5.99	74.41	3.75	25.04	14.09	16.34	8.26
PL	4.19**	1.24	0.47	1.71	72.75	1.96	7.50	4.27	5.01	2.61
PBP	3.16**	0.82	0.70	1.52	53.89	1.37	12.23	8.09	11.02	7.48
SBP	4.84**	1.47	0.43	1.90	77.26	2.20	25.57	14.12	16.06	7.66
PPM	5960.96**	1793.95	579.11	2373.05	75.60	75.86	29.99	16.74	19.26	9.51
FGP	720.25**	205.66	117.32	226.50	59.54	14.75	16.83	10.59	13.72	8.73
TGW	15.05**	4.96	0.17	5.13	96.74	4.51	19.19	9.47	9.63	1.74
GY	1.03**	0.32	0.07	0.39	82.23	1.06	24.88	13.32	14.69	6.19

**Significant at 1% level of probability * Significant at 5% level of probability

PH=Plant height, FLBL=Flag leaf blade length, TH=Tillers per Hill, PL=Panicle length (cm), PBP=Primary branches per panicle, SBP=Secondary branches per panicle, PPM= Panicles per m^2, FGP=Filled grains per panicle, TGW=Thousand grain weight, GY=Grain yield (t/ha)

Table 3: Genotypic (r_g) and phenotypic (r_p) correlation coefficient among yield and its contributing traits of 28 rice genotypes

		FLBL	TH	PL	PBP	SBP	PPM	FGP	TGW	GY
PH	r_g	0.421**	-0.775**	-0.023	-0.170	-0.214	-0.736**	-0.185	0.512**	-0.652**
	r_p	0.415**	-0.652**	-0.007	-0.110	-0.166	-0.633**	-0.125	0.507**	-0.560**
FLBL	r_g		-0.387*	0.430**	0.298*	0.171	-0.257	0.137	0.598**	0.008
	r_p		-0.329*	0.374*	0.202	0.165	-0.226	0.105	0.582**	0.014
TH	r_g			0.332*	0.124	0.195	0.649**	0.220	-0.569**	0.625**
	r_p			0.247	0.177	0.071	0.628**	0.115	-0.475**	0.527**
PL	r_g				0.637**	-0.098	-0.229	0.249	0.483**	0.522**
	r_p				0.440**	-0.052	-0.145	0.188	0.396**	0.581**
PBP	r_g					0.554**	-0.274	0.911**	0.110	0.709**
	r_p					0.241	-0.115	0.601**	0.095	0.520**
SBP	r_g						0.445**	0.836**	-0.334*	0.307*
	r_p						0.258	0.648**	-0.277	0.264
PPM	r_g							0.150	-0.692**	0.443**
	r_p							-0.011	-0.583**	0.375**
FGP	r_g								-0.316*	0.545**
	r_p								-0.209	0.383**
TGW	r_g									-0.211
	r_p									-0.183

**Significant at 1% level of probability * Significant at 5% level of probability

for the improvement of these traits for increasing yield in future. Rahman *et al*. [19], Ganapati *et al*. [20], Hossain *et al*. [21] and Iftekharuddaula *et al*. [22] reported similar results for one or more characters.

The highest GCV was found in panicle per m^2 (16.74), Secondary branch per panicle (14.12) and tillers per hill (14.09) indicated wide range of variability for these traits. Very little GCV was found in panicle length (cm) (4.27) followed by primary branch per panicle (8.09) and seed size (9.47) indicating lack of inherent variability and limited scope for improvement through selection for these traits among the tested genotypes. High h^{2}b values were observed in all the characters except primary branch per panicle. Broad sense heritability (h^{2}b) indicates the effectiveness of selection is not always accompanied by high GA Sinha TS [23]. High h^{2}b estimate with high GA for panicles per m^2, plant height, flag leaf blade length,

tiller per hill, secondary branch per panicle and grain yield suggested that they were simply inherited traits governed by a few major genes or additive gene effects. While, high h^{2}b estimates with low GA for panicle length, primary branches per panicle, flag leaf blade length and thousand grain weight indicated non additive type of gene action and genotype x environment (g x e) interaction plays a significant role in the expression of the trait. Panicle per m^2, tillers per hill, secondary branches per panicle and grain yield showed high GCV and h^{2}b suggesting better scope for selection. Characters with high values of GCV and heritability indicating that they might transmit to their progenies and therefore, phenotypic selection based on these characters would be effective Akand *et al*. [24].The estimates of PCV were always higher than GCV for all the traits (Table 4) which indicates all traits interacted with the environment to some extent Bhadru *et al*. [25].

Table 4: Partitioning of genotypic correlation with grain yield into direct (bold) and indirect effect of yield contributing traits in 28 rice genotypes

	PH	FLBL	TH	PL	PBP	SBP	PPM	FGH	SS	Grain yield (t/ha)
PH	-0.739	-0.026	0.450	-0.018	0.054	0.085	-0.247	-0.165	-0.046	-0.652**
FLBL	-0.311	-0.063	0.225	0.337	-0.094	-0.068	-0.086	0.122	-0.053	0.008
TH	0.573	0.024	-0.581	0.261	-0.039	-0.078	0.218	0.196	0.051	0.625**
PL	0.017	-0.027	-0.193	0.785	-0.201	0.039	-0.077	0.221	-0.043	0.522**
PBP	0.125	-0.019	-0.072	0.500	-0.316	-0.221	-0.092	0.812	-0.010	0.709**
SBP	0.158	-0.011	-0.113	-0.077	-0.175	-0.398	0.149	0.744	0.030	0.307*
PPM	0.544	0.016	-0.377	-0.180	0.086	-0.177	0.336	0.134	0.061	0.443**
FGH	0.137	-0.009	-0.128	0.195	-0.288	-0.333	0.050	0.891	0.028	0.545**
SS	-0.379	-0.038	0.330	0.379	-0.035	0.133	-0.232	-0.282	-0.089	-0.211

**Significant at 1% level of probability * Significant at 5% level of probability

Character Associations: Genotypic and phenotypic correlation co-efficient between pairs of characters for rice is presented in Table 3. It is evident that in majority to the case, the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient. This indicated 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 co-efficient were same with or higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. Grain yield per plant had highest significant positive correlation with primary branches per panicle (G = 0.709 and P = 0.520) which indicating that, if primary branch per panicle increase, grain yield per plant also increase (Table 3).

Grain yield was found positively and significantly associated with tillers per hill, panicle length, primary branches per panicle, plant height, panicles per m² and filled grain per panicle both at genotypic and phenotypic levels and secondary branch per panicle had positive and significant association at only genotypic level and plant height show negatively and highly significant both at genotypic and phenotypic levels. Similar associations in rice were also reported by Singh *et al.* [26]. Plant height showed positive significant interaction with flag leaf blade length (G = 0.421, P=0.415) and thousand seed weight (G = 0.512, P=0.507), where as negative interaction were found in tillers per hill (G = -0.775, P = -0.652) and number of panicles per m2 (G = -0.736, P = -0.633) (Table 3). Similar associations in rice were also reported by Mirza *et al.* [27]. Flag leaf blade length trait showed highly significant positive correlation with panicle length (G = 0.403) and Thousand grains weight (G = 0.598) at genotypic level (Table 3) and significant positive

correlation with panicle length (P = 0.374) and thousand grains weight (P = 0.582) at the phenotypic level. Significant negative correlation was found in tillers per hill (G = -0. 387, P = -0. 329) at genotypic and phenotypic level Table 3. Tiller per hill showed positive significant interaction with panicle per m² (G= 0.649, P=0.628), grain yield (G= 0.625, P=0.527) at genotypic level and phenotypic level and showed significant negative interaction with thousand grains weight (G=-0.569, P=-0.475) (Table 3). Length of panicle showed positive significant interaction with primary branches per panicle (G= 0.637, P = 0.440), thousand grains weight (G= 0.483, P= 0.396) and grain yield (G= 0.522, P= 0. 581) at both genotypic level and phenotypic level and showed negative interaction with secondary branches per panicle (G = -0.098, P=-0. 052) and panicles per m² (G = -0.229, P=-0. 145) at both genotypic level and phenotypic level (Table 3). Primary branches per panicle showed positive significant interaction with filled grains per panicle (G = 0.911, P = 0.601) and grain yield (G = 0.709, P = 0.520) at both genotypic level and phenotypic level. Whereas, the negative interaction was found in primary branches per panicle (G= -0.274, P = -0. 115) at both genotypic level and phenotypic level (Table 3). Secondary branches per panicle showed positive significant interaction with found filled grains per panicle (G = 0.836, P= 0.648) at both genotypic level and phenotypic level, whereas negative significant interaction were found thousand grain weight (G =-0.334) at genotypic level (Table 3). Panicles per m² showed positive significant interaction with grain yield (G = 0.443, P= 0.375) at genotypic level and phenotypic level and showed negative interaction with thousand grains weight (G=-692, P=-0. 583) (Table 3). Filled grains per panicle showed positive interaction with grain yield (G=0.545, P=0. 383) and negative significant interaction with thousand grain weight (G = -0.316) at genotypic level (Table 3). Thousand grains weight showed no significant negative interaction with yield per plant (G =-0. 211, P =-0.

183) (Table 3). However, the correlation study revealed that tillers per hill, panicle length, primary branches per panicle, panicles per m² and field grains per plant were the important characters to be considered in the selection for improvement of T. Aman rice genotypes.

Path Coefficient Analysis: In correlation studies, with increasing number of variables, the indirect association becomes complex and important. In such situation, path coefficient analysis is useful to find out direct and indirect causes of associations. Path coefficient analysis permits a critical examination to specific factors acting to produce a given correlation and measures the relative importance of each factor. From the results of path analysis (Table 4) it was evident that direct positive effects contributed by panicle length, panicles per m² and filled grains per panicle was high indicating that among the component traits, these three characters contributed maximum for grain yield in rice. These three characters also showed significantly positive genotypic correlation with yield which indicates that selection based on these characters would to be effective.

Plant height showed negative direct effect (-0.739) on grain yield and positive indirect effect through tillers per hill (0.450), number of primary branches per panicle (0.054), number of secondary branches per panicle (0.085). On the other hand, plant height showed negative indirect effect on grain yield via flag leaf blade length (-0.026), panicle length (-0.018), panicles per square meter (-0.247), filled grains per plant (-0.165) and thousand grains weight (-0.046). Flag leaf blade length showed negative direct (-0.063) effect on grain yield (t/ha) and positive indirect effects through tillers per hill (0.225), panicle length (0.337) and filled grains per plant (0.122). Flag leaf blade length had negative indirect effect on all other characters. Tillers per hill had negative direct effect -0.581) on grain yield and positive indirect effect on plant height (0.573), flag leaf blade length (0.024), panicle length (0.261), panicle per square meter (0.218), filled grains per plant (0.196) and thousand grains weight (0.051). On the other hand, this trait showed negative indirect effect on primary branch per plant (-0.039) and secondary branch per plant (-0.078). Panicle length showed the direct positive effect (0.785) on grain yield (t/ha). This trait had also indirect positive effect on plant height (0.017), secondary branches per plant (0.039) and filled grains per plant (0.221). Panicle length had negative indirect effect on all other characters. Primary branches per panicle had negative direct effect (-0.316) on grain yield and positive indirect effect on plant height (0.125), panicle length

(0.500) and field grain per plant (0.812). On the other hand, this trait showed negative indirect effect on all other parameters. Secondary branches per panicle had negative direct effect (-0.398) on grain yield and positive indirect effect on plant height (0.158), panicle per m2 (0.149), field grains per plant (0.744) and thousand grains weight (0.030). On the other hand, this trait showed negative indirect effect on all other parameters. Panicles per m2 had positive direct effect (0.336) on grain yield and negative indirect effect on tillers per hill (-0.377), panicle length (-0.180) and secondary branches per panicle (-0.177). On the other hand, this trait showed positive indirect effect on all other parameters. Filled grains per panicle had positive direct effect (0.891) on grain yield and negative indirect effect on tiller per hill (-0.128), primary branches per panicle (-0.288) and secondary branches per panicle (-0.333). On the other hand this trait showed positive indirect effect on all other parameters.

The residual effect of the present study was R=0.406, indicating that 40.6 percent of the variability in grain yield was contributed by the ten component characters studied in this path analysis. Similar findings (R=0.766) was found by Mojumder [28].This gave an impression that a more other characters than those involved in the present study might also contributed to yield. The genetic variability, correlation and path analysis showed that panicles per m², tillers per hill, panicle length and filled grains per panicle are the most important yield components in rice. Therefore, emphasis should be given on these characters for the selection of genotypes for higher grain yield in rice.

CONCLUSION

Seven genetic variability traits viz. plant height, flag leaf blade length, tillers per hill, panicle length, secondary branches per panicle, 1000 grains weight and grain yield exhibited that they were controlled by additive gene action and improvement of these traits for selection. Considering the character association and path analysis showed that panicles per m², tillers per hill, panicle length and filled grains per panicle are the most important yield components in rice. Emphasis should be given on these characters for the selection of genotypes for higher grain yield in rice.

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