

Diversity Assessment of Yield, Yield Contributing Traits, and Earliness of Advanced T-aman Rice (*Oryza sativa* L.) Lines

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Abstract

Thirty advanced T-aman rice (*Oryza sativa* L.) breeding lines along with four checks were studied at the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. The experiment was conducted following Randomized Complete Block Design (RCBD) with three replications. The objective of the study was to know variability in yield, yield contributing characters and earliness of studied lines, and to identify short duration rice genotypes at F_9 generation. The genotypes differed significantly for plant height (cm), length of panicle, total number of tiller per hill, effective tiller number per hill, filled grains per panicle, unfilled grains per panicle, days to 50% flowering, days to maturity, 1000 grains weight and yield per plot (Kg plot⁻¹). Considering all the traits genotype R7 was the earliest compared to all other genotypes which took 113 days for maturity. The genotype R16 recorded the highest yield, took 118 days for maturity, and that was significantly higher than check varieties. Phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits studied indicating that the measured traits interacted with the environment to some extent. All the studied traits expressed moderate to high heritability estimates. High heritability along with high genetic advance was noticed for the following traits: number of filled grain per panicle, number of unfilled grain per panicle and plant height. Data suggests a few promising breeding lines might be potential as short duration and high yielding T-aman variety.

Key words: *Oryza sativa*, variability, GCV, PCV, heritability, genetic advance, F_9 generation, advanced breeding lines

Introduction

Rice (*Oryza sativa* L.) is a crop belongs to Poaceae family, serve as a major carbohydrate sources for many nations all over the world. Bangladesh is mainly a rice growing country and majority of the arable lands are used only for rice cultivation. But nowadays, we are losing huge amount of cultivable land every year for infrastructure, garment industries and accommodation of ever-growing population (Mahmud, 2003). 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 (Williams et al., 2006). Generally rice in boro season is late maturing compared to aman season. Early maturing crops are comparatively low yielding in any season but it may be balanced by less standing duration in the field. Moreover, short duration aman rice provides a window just enough for next short duration vegetable cultivation in the same piece of land. Thus, helps in increasing cropping intensity.

So, it is crucial to select short duration lines of aman without much sacrificing yield. In a successful rice improvement program, breeders provide efforts to accommodate the desirable characters to

improve grain yield. 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 (Doehlert et al., 2001). Magnitude and nature of variation as well as interrelationship of plant traits in a plant population lead to the progress of breeding.

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 (Ye et al., 2013; Peyman, 2012; Chakravorty et al., 2013). Estimation of heritability measures the information on flow of traits from parents to offspring. Estimation of heritability along with genetic advance is more helpful in selection than single heritability estimation. On the other hand, estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) also play vital role in selection practice for an effective rice breeding program. The present study therefore was planned to estimate variability, heritability and genetic advance of selected advanced rice breeding lines at F₉ generation with a vision to develop short duration and high yielding rice varieties in future.

Materials and Method

Thirty advanced breeding lines along with four check varieties viz. BINA dhan7, BRRI dhan 39, BRRI dhan 49, BRRI dhan 57 were used in the present study (Table 1). The advanced breeding lines were originated from the hybridization programme carried out at International Rice Research Institute using different breeding lines under PETRA (Poverty Elimination through Rice Research Activities) project. A Randomized Complete Block Design with three replications was used to carry out the experiment. The individual plot size was 2.5m × 2m (5 square m). Data were recorded to estimate the traits viz., plant height (cm), length of panicle (cm), total number of tiller per hill, effective tiller number per hill, filled grains per panicle, unfilled grains per panicle, days to 50% flowering, days to maturity, 1000 grains weight (g) and yield per plot (kg).

Table 1. A list of the genotypes used in the experiment

Sl.	Designation	Pedigree	Source
1	R1	Hy-23-29-32	GPB, BAU
2	R2	Hy-3-281	GPB, BAU
3	R3	Hy-5-407	GPB, BAU
4	R4	Hy-7-435	GPB, BAU
5	R5	Hy-9-755	GPB, BAU
6	R6	Hy-10-584	GPB, BAU
7	R7	Hy-10-648	GPB, BAU
8	R8	Hy-11-818	GPB, BAU
9	R9	Hy-15-926	GPB, BAU
10	R10	Hy-15-927	GPB, BAU
11	R11	Hy-17-1093	GPB, BAU
12	R12	Hy-17-1059	GPB, BAU
13	R13	Hy-17-1065	GPB, BAU
14	R14	Hy-16-1192-7	GPB, BAU
15	R15	IR 58082-126-1-2R	IRRI, Philippines
16	R16	BR 6017-3-1-1-3	GPB, BAU
17	R17	BR 6017-3-3-4-1	GPB, BAU
18	R18	IR 68926-61-2R	IRRI, Philippines
19	R19	IR 58082-126-1-2R	IRRI, Philippines
20	R20	BAU 94026-6-4-5-3-7-2-3-5	GPB, BAU

21	R21	IR 68926-61-2R	IRRI, Philippines
22	R22	BR 4839-17-5-2-2HR5	GPB, BAU
23	R23	Hy-8-554-54	GPB, BAU
24	R24	BAU 94012-4-1-3-2-6-7-1-5	GPB, BAU
25	R25	Hy-5-427-33	GPB, BAU
26	R26	Hy-4-377-48	GPB, BAU
27	R27	IR 72	IRRI, Philippines
28	R28	BAU 92089-4-2-4-6-5-4-9-2	GPB, BAU
29	R29	BR(BE) 6158-RWBC-7-11	GPB, BAU
30	R30	Hy-9-765-10	GPB, BAU
31	R31	BINA dhan7	BINA, Mymensingh
32	R32	BRRI dhan39	BRRI, Gazipur
33	R33	BRRI dhan49	BRRI, Gazipur
34	R34	BRRI dhan57	BRRI, Gazipur

GPB= Department of Genetics and Plant Breeding, BAU= Bangladesh Agricultural University, BRRI= Bangladesh Rice Research Institute, BINA= Bangladesh Institute of Nuclear Agriculture

Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955).

$$\text{Genotypic variance, } \sigma_g^2 = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean square

EMS = Error mean square

r = Number of replication

$$\text{Phenotypic variance, } \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where, σ_g^2 = Genotypic variance

σ_e^2 = Error mean square

Genotypic and phenotypic co-efficient of variations were estimated according to Burton (1952) and Singh and Chaudhary (1985).

$$\text{Genotypic co-efficient of variations, GCV} = \frac{\sigma_g^2}{\bar{X}} \times 100$$

Where, σ_g^2 = Genotypic variance; and

\bar{X} = Population mean

$$\text{Phenotypic co-efficient of variations, PCV} = \frac{\sigma_p^2}{\bar{X}} \times 100$$

Where, σ_p^2 = Phenotypic variance; and

\bar{X} = Population mean

Heritability in broad sense (h_b^2) was estimated according to the formula suggested by Johnson *et al.*

(1955) and Hanson et al. (1956).

$$\text{Heritability, } h^2_b = \frac{\delta^2_g}{\delta^2_p} \times 100$$

Where,

δ^2_g = Genotypic variance; and

δ^2_p = Phenotypic variance.

Estimation of genetic advance was done following formula given by Allard (1960).

$$\text{Genetic advance, GA} = h^2_b \cdot K \cdot \sigma_p$$

Where,

h^2_b = Heritability

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

σ_p = Phenotypic standard deviation

Statistical analysis

Analyses of variances of the data were carried out using Minitab 17 statistical software package (Minitab Inc. State College, Pennsylvania).

Results and Discussion

Analysis of variance

Analysis of variance indicated that the difference among genotypes for all the traits under study viz., plant height (cm), panicle length (cm), tiller number per hill, effective tiller number per hill, filled grain per panicle, unfilled grain per panicle, days to 50% flowering, days to maturity and yield per plot (kg) were highly significant (Table 2). Minimum days to maturity was approximately 113 days for genotype R7 (Table 2). These results suggested that these experimental materials might be used as precious germplasm to breed for earliness. Plant height, length of panicle, total tillers/hill, effective tillers/hill, filled grains/panicle, unfilled grains/panicle, days to 50% flowering, days to maturity, weight of 1000 grains (g) and yield/plot (kg) differed significantly across 34 rice genotypes (Table 3). Significant variation in yield contributing characters as observed, were also reported in some previous studies (e.g., Rahman et al. 2014; Seyoum et al. 2012; Bhadru et al. 2012; Courtois et al. 2012; Hossain et al. 2012; Peyman, 2012).

Table 2. Mean sum of squares for different plant traits of 34 rice genotypes

Traits	Source of variation		
	Replication (d.f.= 2)	Genotype (d.f.=33)	Error (d.f.=66)
PH	3.59	164.5**	6.95
LP	0.198	6.98**	1.337
TT	1.032	3.6**	1.017
ET	0.082	3.2**	0.586
FG	24.55	674**	25.18
UFG	9.199	192**	10.02
DF	--	45.5**	5.735
DM	--	9.18**	5.980
WT	--	38.2**	0.627
YD (Kg)	--	0.401**	0.035

** indicates significant at 0.01 probability

PH= plant height (cm), LP= length of panicle (cm), TT= total tillers/hill, ET= effective tillers/hill, FG= filled grains/panicle, UFG= unfilled grains/panicle, DF= days to 50% flowering, DM= days to maturity, WT= weight of 1000 grains (g), YD= yield/plot (Kg).

Genotypic and phenotypic variability

A wide range of variation was observed among 34 rice genotypes for nine yield contributing traits (Table 4). Data revealed that variance due to genotype was highly significant for all the traits (Table 4). The higher phenotypic variance values compared to genotypic variances indicated influences of environmental factor on these traits (Rahman et al., 2014). PCV were always higher than the corresponding GCV for all the traits indicating that they all have major environmental influences for regulating the traits (Table 4). Number unfilled grain per panicle had the highest estimates of GCV and PCV compared to any other traits (Table 4). Total tiller per panicle accounted for similar values of GCV and PCV with number effective tiller number per hill (Table 4). On the other hand, seed weight had very close GCV and PCV values with filled grain (Table 4). Plant height, length of panicle, days to flowering and days to maturity exhibited lower level of GCV and PCV (Table 4). The high values of GCV and PCV for these traits suggested the potential of yield improvement through selection of these traits. 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., 2012).

Table 3. Mean performances of 34 rice genotypes based on different morphological traits related to yield

Genotypes	PH	LP	TT	ET	IT	FG	UFG	DF	DM	WT(gm)	YD(gm)
R1	120	26.75	10.77	9.77	1.00	102	36.77	87.00	116.7	33.57	2040
R2	120	27.37	7.77	7.00	0.77	122	21.22	86.67	116.3	25.10	2093
R3	105	25.14	10.33	9.44	0.77	109	33.88	87.00	116.0	24.93	1740
R4	105	27.28	8.44	7.66	0.77	97	23.88	86.67	115.7	24.20	2657
R5	110	25.02	7.33	6.66	0.66	85	10.11	86.66	118.0	23.10	2333
R6	101	28.18	7.33	6.66	0.66	83	11.88	84.00	115.0	25.63	1613
R7	106	25.48	9.55	8.66	0.88	126	31.44	84.00	112.7	22.30	1570
R8	96	23.42	9.88	8.55	1.33	99	20.11	86.66	115.3	28.83	2257
R9	113	24.27	8.44	7.33	1.11	133	22.11	92.66	118.0	31.93	2270
R10	104	25.77	8.00	7.00	1.00	77	12.00	85.66	114.3	24.83	1967
R11	112	24.83	7.66	6.77	0.88	106	31.66	86.00	114.7	29.30	1970
R12	114	25.43	9.88	8.88	1.00	103	33.55	94.33	118.7	27.17	1973
R13	104	28.53	8.00	7.33	0.66	110	21.33	84.66	114.3	25.73	1813
R14	107	24.52	8.22	7.44	0.77	116	31.22	93.33	115.3	27.17	2003
R15	102	26.00	6.66	5.88	0.77	113	21.11	97.00	119.3	29.30	1810
R16	108	25.76	9.44	8.22	1.22	117	16.11	94.33	118.0	24.83	2757
R17	109	25.41	10.00	9.00	1.00	132	32.44	88.33	116.0	31.97	1897
R18	117	24.43	8.66	7.88	0.77	121	29.22	92.00	117.0	31.60	1613
R19	98	25.31	9.44	8.44	1.00	107	13.44	93.00	117.7	25.13	2727
R20	124	28.20	9.44	8.00	1.22	109	27.55	96.66	115.7	33.60	1977
R21	100	25.35	10.11	9.22	0.88	108	35.11	93.33	116	24.90	1103
R22	109	25.97	8.11	7.11	1.00	112	14.33	93.00	118	28.13	2230
R23	103	26.63	9.11	7.88	1.22	81	32.77	88.33	115	18.40	1563
R24	103	21.48	7.66	7.11	0.55	112	17.77	92.66	120.3	22.50	1920
R25	104	24.82	9.22	8.11	1.11	110	11.66	94.33	117.7	25.13	2117
R26	102	23.72	7.44	6.77	0.66	104	14.88	94.66	116.3	24.10	2097
R27	115	24.63	9.77	8.55	1.22	125	21.44	92.66	114.3	21.70	2703
R28	97	26.00	7.66	6.88	0.77	121	18.55	85.66	115.7	27.10	1733
R29	122	24.41	9.88	9.22	0.66	135	12.00	90.00	113.3	25.93	1903

R30	111	22.67	9.88	8.88	1.00	111	26.11	88.33	115	26.73	2070
R31	101	25.87	8.22	7.22	1.00	102	19.11	88.33	115	23.40	1967
R32	112	24.63	9.88	9.22	0.66	130	29.55	87.00	114.7	20.00	2153
R33	100	26.10	9.55	8.55	1.00	123	26.55	85.00	113.7	26.50	1853
R34	102	23.64	10.44	9.88	0.55	88	20.66	92.00	115.7	26.63	2563
Minimum	96	21.48	6.66	5.88	0.55	77	10.11	84.00	112.7	18.40	1103
Maximum	124	28.53	10.77	9.88	1.33	135	36.77	97.00	120.3	33.60	2757
Mean	108	25.38	8.88	7.98	0.90	110	22.99	89.76	116.0	26.21	2031
SEM	1.52	0.66	0.58	0.44	0.29	2.89	1.82	1.38	1.41	0.42	107.9
P value	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01	<0.01

PH= plant height (cm), LP= length of panicle (cm), TT= total tillers/hill, ET= effective tillers/hill, FG= filled grains/panicle, UFG= unfilled grains/panicle, DF= days to 50% flowering, DM= days to maturity, WT= weight of 1000 grains (g), YD= yield/plot (Kg).

SEM= Standard error of mean, P= probability of statistical significance in generalized linear model

Table 4. Genetic parameters of 34 rice genotypes based on different yield related morphological traits

Traits	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_{ph})	Grand mean	Heritability, h^2_b (%)	GCV(%)	PCV(%)	GA	GA(%)
PH	52.5	59.5	108	88.3	6.74	7.17	14.0	13.1
LP	1.88	3.22	25.4	58.4	5.40	7.07	2.16	8.50
TT	0.86	1.88	8.89	45.8	10.5	15.4	1.30	14.6
ET	0.87	1.46	7.98	59.6	11.7	15.1	1.48	18.6
FG	216	241	110	89.6	13.4	14.2	28.7	26.2
UFG	60.8	70.9	22.9	85.9	33.9	36.6	14.9	64.8
DF	13.3	18.9	89.8	69.8	4.06	4.86	6.27	6.98
DM	1.07	7.05	116	15.2	0.89	2.29	0.83	0.72
WT	12.6	13.2	26.2	95.9	13.6	13.8	7.17	27.4

PH= plant height (cm), LP= length of panicle (cm), TT= total tillers/hill, ET= effective tillers/hill, FG= filled grains/panicle, UFG= unfilled grains/panicle, DF= days to 50% flowering, DM= days to maturity, WT= weight of 1000 grains (g), PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, GA= Genetic advance, GA (%) = Genetic advance as percent of mean

Heritability

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait. The traits studied in the present investigation expressed low to high heritability estimates ranging from 15 to 96 percent (Table 4). The highest heritability was recorded for weight of 1000 seeds (95.9%) followed by number of filled grain per panicle, plant height, unfilled grain per panicle, days to 50% flowering, effective tiller per hill, length of panicle, total number of tiller. The lowest heritability value was recorded for days to maturity (Table 4). High heritability values indicate that the traits under study are less influenced by environment in their expression (Akinwale et al., 2011). It also indicates the scope of genetic improvement of these traits through selection. Thus, a breeder may make his selection securely on the basis of phenotypic expression of these traits on the individual plant.

Genetic advance

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of better selection value (Akinwale et al. 2011). In the present study genetic advance was the highest for number of filled grains per panicle (28.7) followed by unfilled grain per panicle and the lowest for days to maturity (0.83) among yield contributing traits (Table 4). The genetic advance as percent of mean was the highest in case of unfilled grain per panicle while it was the lowest for days to maturity (Table 4). If selection is made for improving the particular trait under study; one should focus on heritability and genetic advance. The information on genetic variation, heritability and genetic advance help to predict the genetic gain that could be obtained in later generations. High heritability with high genetic advance exhibited by the traits, controlled by additive gene action (Panse, 1957; Hasan et al. 2013; Prasad et al. 2001; Singh et al. 2013) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability associated with high genetic advance leads to

accumulate more additive genes. It can enhance the opportunities for further improvements of their performance. In the present study, high heritability along with high genetic advance was noticed for the traits: number of filled grain per panicle, unfilled grain per panicle and plant height. Other traits showed high heritability along with moderate or low genetic advance which can be improved by intermating superior genotypes of segregating population (Prajapati et al., 2011).

Conclusions

The phenotypic coefficients of variation of all studied traits were higher than genotypic coefficient of variation which indicating that they all interacted with the environment to some extent. The traits studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among all of the traits, unfilled grain per panicle exhibited the highest estimates of GCV and PCV followed by seed weight and number of filled grain per panicle. The lowest PCV and GCV values were recorded for days to maturity.

The studied traits expressed low to high heritability estimates ranging from 15 to 96 percent. Among the traits, the highest heritability was recorded for 1000 seed weight followed by number of filled grain per panicle, plant height, unfilled grain per panicle, days to 50% flowering, effective tiller per plant, length of panicle, total tiller per hill and days to maturity. The lowest heritability value was recorded for days to maturity. High heritability values indicated that the traits under study were less influenced by environment in their expression.

Genetic advance was the highest for number of filled grains per panicle followed by unfilled grain per panicle and plant height. The lowest genetic advance was obtained in days to maturity. In this study, high heritability along with high genetic advance was noticed for filled grain per panicle, unfilled grain per panicle and plant height. These traits can be improved through simple or progeny selection methods. Other traits showed high heritability along with moderate or low genetic advance. These traits can be improved by inter-mating superior genotypes of segregating population developed from combination breeding.

In this study 30 advanced rice breeding lines at F₉ exhibited high variability. The results therefore suggested that selecting a line for shorter growth duration of 113 days with comparatively higher yield would be possible from those genotypes.

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