

Variability and Genetic Gain Prediction for Maintainer Line Improvement of Hybrid Rice in Bangladesh

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ABSTRACT

Assessment of genetic variability in the nursery of the breeding population is essential for crop improvement successfully. Thirteen maintainer lines of hybrid rice were evaluated to estimate the level of their genetic diversity and heritability of grain yield influencing parameters in the transplanted Aman 2020 season. The studied traits were days to 50% flowering, total effective tillers plant⁻¹, plant tallness (cm), length of flag leaf (cm), breadth of flag leaf (cm), panicle size (cm), filled grains panicle⁻¹, unfilled grains panicle⁻¹, growth duration (days) and grain yield (tha⁻¹). Coefficient of variation (genotypic and phenotypic) was noticed high for most traits that revealed high variability among the studied genotypes. Broad-sense heritability (h_{bs}^2) was high in all traits except flag leaf breadth. Analysis of the cluster and its mean comparison showed that cluster 2 (i.e. BRRI 11B, BRRI 99B, IR 79125B and IR 79156B) represented the best agronomic traits and yield potentials. Therefore, selection of genotypes with valuable attributes from cluster 2 will be considered for maintainer line improvement programmes. The use and estimation of predicted genetic gain will provide a visionary insight of the future genotypes produced after the crossing of the genotypes under study.

Key words: Maintainer line, genetic advance, heritability, predicted genetic gain, hybrid rice

INTRODUCTION

Ever growing and dense population allied with yield ceiling of the staple food rice has become a curse for Bangladesh. Here rice takes up 75% (BBS, 2017) to 78% (Kabir *et al.*, 2020) of the total cropped area. Commercial exploitation of heterosis in rice was the weapon to feed the people of China and 55% rice area was used to produce 66% of overall rice production (Virmani *et al.*, 1998). Promising and potential hybrids out yielded modern and best rice varieties (conventional varieties) by 15-20% and 20-30%, respectively (Yuan, 1998). Polygenic trait like grain yield is impacted by environments where the genotypes grow and is estimated by the nature and degree of genetic variation (Selvaraj *et al.*,

2011). Variability among the genotypes expressed as genetic divergence used for gene pool broadening and needs trustworthy heritability estimates to design breeding strategy with high efficiency (Akinwale *et al.*, 2011). Broad sense-heritability provides knowledge about the overall variability accounted for by genotypic effect (Allard, 1960). Maintainer lines (B lines) are the key genotypes that are used to supply yield boosting genes to the female parent (A line) during new female line development. Maintainer lines (B lines) are mainly developed using B×B crossing method (Virmani *et al.*, 1998). Hybrid rice breeders have to select new and better B×B

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combinations to develop new elite maintainers for CMS lines multiplication and as well hybrid rice production. Heritability, genetic distance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV); environmental coefficient of variation (ECV), coefficient of variation (CV), genetic advance (GA), clustering of genotypes help the breeder to effectively select cross combinations e.g. B×B cross combination selection in case of maintainer line improvement. Previous studies suggested that superior rice genotypes should measure and achieve genetic gain with sensory perception and grain quality attributes (Anacleto *et al.*, 2015). Empirical evaluation plus genetic prediction will need to be complemented by the future plant breeders (Cooper *et al.*, 2014). So the present investigation was conducted to estimate genetic variability, heritability, genetic advance and predicted genetic gain of the studied maintainer lines.

MATERIALS AND METHODS

During T. Aman, 2020 (July - December, 2020) season; 13 maintainer lines (enlisted in Table 2) of hybrid rice were assessed in three replications using RCB design at the research field (West Byed) of Bangladesh Rice Research Institute (BRRI). The experimental plots were monocrop area where rice is grown throughout the year. Chemical fertilizers @ 194-82-52-60 kg/ha for urea-MoP-TSP-gypsum, respectively were used in the field to ensure nutrient supply to plants. Complete urea was administered in three splits i.e. 10 days after transplantation (DAT), 30 DAT and 45 DAT. At the time of final land preparation, complete TSP, MoP, and gypsum were applied. Thirty-days-old seedlings were transplanted with a spacing of (25 cm × 15 cm). Data from each replication were obtained from randomly selected 10 plants. Data collection on 50% flowering (days), total effective tillers hill⁻¹, plant height (cm),

length of flag leaf (cm), breadth of flag leaf (cm), filled grains panicle⁻¹, length of panicle (cm), unfilled grains panicle⁻¹, growth duration (days) and grain yield (tha⁻¹).

STATISTICAL ANALYSIS

Variance analysis was conducted with the collected data from the RCB design of this experiment using the STAR Version: 2.0.1 (Statistical Tool for Agricultural Research) software for genetic divergence and cluster analysis. Mean sum of squares were utilized to assess genetic parameters e.g. genotypic variance (σ_g^2), phenotypic variance (σ_p^2) environmental variance (σ_e^2), Genotypic coefficient of variation (GCV), genetic advance (GA), coefficient of variation (CV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV) to display variability among maintainer line genotypes. Multivariate cluster analysis using the method of Agglomerative Cluster Analysis (Ward's method) was done. Ten yield and yield-contributing traits were used for genetic divergence and cluster analysis.

Total variation of each character was divided into non-genetic and genetic parts and GCV, PCV, ECV, %CV were assessed in line with Burton (1952) and Sharma (1988):

$$\sigma_g^2 = \frac{MS_g + MS_e}{r}, \sigma_e^2 = MS_e, \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

where σ_p^2 = phenotypic variance, σ_g^2 = genotypic variance, and σ_e^2 = environmental variance and MS_g = mean squares of genotypes, MS_e = mean squares of error, and r = number of blocks .

$$\%CV = \frac{\sqrt{MS_g}}{\bar{x}} \times 100, PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100, GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100, ECV = \frac{\sqrt{\sigma_e^2}}{\bar{x}} \times 100$$

Where, \bar{x} = grand mean for each measured traits . h_{bs}^2 = Broad sense heritability which is expressed as the proportion of the genotypic variance (σ_g^2) to phenotypic variance (σ_p^2) ratio and was assessed as stated by Burton (1952). Genetic advance (GA) was projected by the technique

defined by Fehr (1987) $\Delta G = \frac{i r \sigma_A}{t}$, where at 5% pressure of selection the value of constant K is 2.06, $(\sqrt{\sigma_p^2}) =$ phenotypic standard deviation and $h_{bs}^2 =$ broad sense heritability, GA = genetic advance was also assessed as proportion of the average. We have used **RStudio Version 1.1.463** to calculate the predicted genetic gain/year. The expected or predicted genetic gain/year was estimated as:

$$\Delta G = \frac{i r \sigma_A}{t}$$

Here, $\Delta G =$ predicted genetic gain/year, $i =$ selection intensity (mean deviance of carefully chosen entries in units of σ_A (phenotypic standard deviation), $r =$ accuracy of selection, $\sigma_A =$ standard deviation of breeding values (Falconer and Mackay, 1996) or genetic standard deviation ($\sqrt{\text{additive genetic variance}}$), and $t =$ time or duration per breeding cycle (Yunbi *et al.* 2017). In genomic selection (GS) analysis, $r =$ the correlation between TBVs (true breeding values) and GEBVs (genomic-estimated breeding values), while in case of phenotypic selection, $r = h_{ns}^2$

and thus $\Delta G = \frac{i h \sigma_A}{t}$ (Bassi *et al.*, 2016; Heffner *et al.*, 2010; Meuwissen, 2003). In our experiment, we used the expected accuracy, $r = \sqrt{1 - \frac{PEV}{V_g}}$ (where, $V_g =$ Genetic variance, and PEV = unexplained part of V_g by the predictions) that is supported by Pszczola *et al.* 2012, Hayes *et al.* 2009, VanRaden 2008. In this article, genotypes were presumed to be unrelated.

RESULT AND DISCUSSION

Genetic variability

Diverse breeding materials with high genetic variability are a prerequisite to guide a breeding program towards success. Understanding the variability and magnitude in maintainer lines (B Line) is crucial as it delivers the foundation of parent selection for B \times B improvement in hybrid rice breeding. Table 3 presents the genetic parameters and mean squares of 13 maintainer lines of hybrid rice are presented in Table 3.

Table 1. Quantitative traits related mean square with genetic parameters of 13 maintainer lines in T. Aman, 2020.

Traits	MS _g	σ_e^2	σ_g^2	σ_p^2	Mean	GCV	PCV	ECV	%CV	H ² _{bs} (%)	GA
50%F	94.92***	1.09	31.28	32.37	77.82	7.19	7.31	1.40	12.52	96.63	11.33
GD	61.37***	1.09	20.09	21.18	102.51	4.37	4.49	1.06	7.64	94.87	8.99
Etil	5.09***	0.56	1.51	2.07	7.87	15.61	18.27	7.11	28.65	72.94	2.16
Yield	0.72***	0.11	0.20	0.32	3.45	13.02	16.29	3.31	24.59	63.86	0.74
FGP	3041.3***	151.39	963.30	1114.69	127.77	24.29	26.13	118.49	43.16	86.42	59.44
UFGP	2721.63***	36.89	894.91	931.80	58.28	51.33	52.38	63.30	89.51	96.04	60.39
PL	9.29***	0.10	3.06	3.16	21.93	7.98	8.11	0.47	13.89	96.73	3.54
PH	223.35***	2.18	73.72	75.90	87.81	9.78	9.92	2.48	17.02	97.13	17.43
FLL	39.62***	1.60	12.67	14.27	34.96	10.18	10.81	4.58	18.00	88.78	6.91
FLB	0.04*	0.02	0.01	0.02	1.58	5.74	9.87	1.02	12.78	33.84	0.11

Legends: 50%F=days to 50% flowering, Etil=total effective tillers hill⁻¹), PH=plant height (cm), FLL=flag leaf length (cm), FLB=flag leaf breadth (cm), PL=panicle length (cm), FGP=filled grains panicle⁻¹), UFGP=unfilled grains panicle⁻¹), GD=growth duration (days), Yield=grain yield (tha⁻¹), MS_g = mean squares of genotypes, σ_p^2 = phenotypic variance, σ_g^2 =genotypic variance, σ_e^2 =environmental variance genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), environmental coefficient of variation (ECV), coefficient of variation (%CV), h_{bs}^2 =broad sense heritability, GA=genetic advance, * and ***= significant at the 5% and the 0.1% level.

ANOVA exhibited significant ($p < 0.001$) differences for all the studied characters in the maintainer lines except flag leaf breadth that was significant ($p < 0.05$) marginally (Table 1). The significant variations detected among the maintainer lines for all the traits influenced the presence of intrinsic genetic variability among the studied maintainers. Akter *et al.* (2019) described the presence of genetic difference among hybrid rice genotypes. Breeding programs related to the betterment of yield requires genetic variation in the selected mating populations to effectively select and achieve yield upgrading (Ndukauba *et al.*, 2015 ; Idahosa *et al.*, 2010). Percentage of CV relates the relative quantity of variability in the traits of crop plant (Sharma, 1988). The highest percentage of CV obtained by the unfilled grains panicle⁻¹ followed by filled grains panicle⁻¹, effective tiller hill⁻¹ and yield (tha⁻¹) (Table 1). These results indicated that the unfilled grains panicle⁻¹ followed by filled grains panicle⁻¹, effective tiller hill⁻¹ and yield (tha⁻¹), respectively, had greater quantities of accessible genetic variability amongst the studied maintainer lines. It also implied the bigger prospect of yield improvement in choosing these traits compared to rest of the traits (Ndukauba *et al.*, 2015; Eid, 2009). On the contrary, the

lowest coefficient of variation was noted for growth duration, days required to flower 50% and flag leaf breadth exhibited low utilizable genetic variability that has less potential of satisfactory advancement in selecting these traits contrasted with other traits. The phenotypic variance (σ_p^2) of the studied traits was separated into genotypic variance (heritable) and environmental variance (non-heritable) constituents (Table 1). Genotypic variances were greater than their related environmental variances in all the traits, except flag leaf breadth which was negligible (Table 1). This specified that the total variation was contributed mainly by the component of genotypic variation in the considered traits. The maximum PCV was found for the unfilled grains panicle⁻¹ followed by filled grains panicle⁻¹, effective tiller hill⁻¹, and yield while the smallest PCV was recorded for growth duration, panicle length, flag leaf breadth and plant height. High PCV specifies the presence of a bigger scope of choice for the characters of interest, which was determined by the quantity of variability exist (Naik *et al.*, 2020; Khan *et al.*, 2009). Thus, ample potential for selecting the filled grains panicle⁻¹, effective tiller hill⁻¹, yield and flag leaf length among the tested maintainer lines is predicted. In contrast, there was a minor scope of choice for growth duration, panicle length, flag leaf breadth, plant height as a consequence of low variability. Diverse quantitative traits exhibited genetic variability in plants and estimated by GCV. Unfilled grains panicle⁻¹, filled grains panicle⁻¹, effective tiller hill⁻¹, yield (tha⁻¹) and flag leaf length showed the highest amount of GCV, respectively. Growth duration, flag leaf breadth, 50% flowering and panicle length contrariwise, showed the least amount of GCV (Table 1). The existence of utilizable genetic variability for different traits is indicated by high GCV, which can simplify selection effectively (Naik *et al.*, 2020; Yadav *et al.*, 2009). The range obtained for environmental coefficient of variation

(ECV) was 0.47 (panicle length) to 118.49 (filled grain panicle⁻¹). Though estimates for phenotypic coefficient of variation (PCV) were higher than those estimates for genotypic coefficient of variation (GCV), they were close; inferring that trait expression is governed mainly by lines compared to environment and phenotypic value based selection is therefore feasible. Whereas, a large inequality between GCV and PCV estimations for flag leaf breadth specified a greater amount of environmental regulation for these traits. Variation governed by polygene can be phenotypic, genotypic or environmental and the relative estimates of GCV, PCV and ECV for a trait provides knowledge about the degree of variability (Ndukauba *et al.*, 2015; Nausherwan *et al.*, 2008).

HERITABILITY ESTIMATES

Heritability estimates offer a vision into the degree of genetic regulation to express individual characteristics and phenotypical reliability of breeding value prediction (Ndukauba *et al.*, 2015). High heritability estimate of a trait indicates low environmental effect in the detected variation (Eid, 2009). h_{bs}^2 only shows whether there is adequate genetic variation in any population, which infers about the population response to selection pressure (Gatti *et al.*, 2005; Milatovic *et al.*, 2010; Ullah *et al.*, 2012). Heritability of the studied traits ranged from 33.84% (flag leaf b) to 97.13% (plant height). Heritability of all the traits

except plant height was above 60% (Table 1). GCV, PCV, ECV and heritability results of this experiment explained the existence of considerable extent of genetic variation in these traits to permit parent assortment for the development of better maintainer line. These traits should be under special consideration when choosing parents of maintainer line improvement programme. To achieve more effective character selection, heritability supplemented with genetic advance is more suitable than heritability on its own (Ullah *et al.*, 2012). For most of the traits, high h_{bs}^2 was reported in the current study, but were associated with low genetic advance except unfilled grains panicle⁻¹ (Genetic advance= 60.39) and filled grains panicle⁻¹ (Genetic advance= 59.44) (Table 1). High heritability connected with high genetic advance for a certain trait resulted due to the actions of additive gene and offers an effective situation for selection (Rashid *et al.*, 2017; Gyawali *et al.*, 2018; Ndukauba *et al.*, 2015; Tazeen *et al.*, 2009).

Genetic divergence of the maintainer lines

Narrow distance indicates the most similar genotype pairs and long distance shows diverse genotype pairs. The longest Euclidean distance was 7.0 (between IR79125B and BRRI50B) and the shortest distance was 1.8 (between BRRI97B and BRRI35B) (Table 2). The genotype pairs that exhibited long distance will be used for new elite parental line development (Table 2).

Table 2. Euclidean distances of maintainer line genotypes under study.

	BRR1 10B	BRR1 11B	BRR1 35B	BRR1 48B	BRR1 50B	BRR1 7B	BRR1 97B	BRR1 99B	IR 105687B	IR 105688B	IR 58025B	IR 79125B	IR 79156B
BRR1 10B	0.0	4.1	2.3	2.8	4.2	3.3	2.5	3.7	3.9	3.7	4.3	4.5	5.2
BRR1 11B	4.1	0.0	3.5	4.4	5.0	4.3	3.2	2.9	6.0	5.0	5.1	4.8	3.8
BRR1 35B	2.3	3.5	0.0	2.6	3.8	2.3	1.8	3.0	4.2	3.6	4.9	5.4	5.3
BRR1 48B	2.8	4.4	2.6	0.0	4.3	2.5	2.3	4.2	4.6	4.1	5.0	6.0	6.2
BRR1 50B	4.2	5.0	3.8	4.3	0.0	4.6	4.4	5.8	5.0	4.6	4.9	7.1	6.7
BRR1 7B	3.3	4.3	2.3	2.5	4.6	0.0	2.7	4.2	4.7	4.1	5.1	5.7	6.3
BRR1 97B	2.5	3.2	1.8	2.3	4.4	2.7	0.0	2.8	4.1	3.4	4.6	5.2	5.1
BRR1 99B	3.7	2.9	3.0	4.2	5.8	4.2	2.8	0.0	5.6	4.5	5.9	4.7	4.6
IR 105687B	3.9	6.0	4.2	4.6	5.0	4.7	4.1	5.6	0.0	2.3	3.2	5.3	5.6
IR 105688B	3.7	5.0	3.6	4.1	4.6	4.1	3.4	4.5	2.3	0.0	3.8	5.1	5.5
IR 58025B	4.3	5.1	4.9	5.0	4.9	5.1	4.6	5.9	3.2	3.8	0.0	4.1	4.3
IR 79125B	4.5	4.8	5.4	6.0	7.1	5.7	5.2	4.7	5.3	5.1	4.1	0.0	3.4
IR 79156B	5.2	3.8	5.3	6.2	6.7	6.3	5.1	4.6	5.6	5.5	4.3	3.4	0.0

Three clusters were formed at distance coefficient 7 having 6, 4 and 3 entries in cluster 1, cluster 2, and cluster 3, respectively (Fig 1). Cluster 1 showed the moderate value for yield, filled grain panicle-1, panicle length, flag leaf breadth; and the lowest value for 50% flowering date, growth duration, effective tiller hill⁻¹ and unfilled grains panicle-1 (Table 3). Cluster 2 occupied the highest value for 50% flowering date, growth duration, yield, filled grains panicle⁻¹, flag leaf length, plant height; moderate value for effective tiller

hill⁻¹, unfilled grains panicle⁻¹; and the lowest value for flag leaf breadth. Cluster 3 contained the highest value for effective tiller hill⁻¹, unfilled grains panicle⁻¹ and flag leaf breadth; moderate value for 50% flowering date, growth duration, flag leaf length and the lowest value for yield, panicle length, plant height and filled grains panicle⁻¹. Similar method of Euclidean distance based clustering was applied to select parent for hybridization programme of rice crop by breeders (Adhikary *et al.*, 2018, Nitesh *et al.*, 2014).

Table 3. Cluster mean of ten traits utilized in the grouping of 13 maintainer lines in T. Aman, 2020.

Traits	Cluster 1	Cluster 2	Cluster 3
50%F	73.80	81.60	80.90
GD	100.23	106.00	102.47
Etil	7.05	7.85	9.57
Yield	3.50	3.70	3.00
FGP	130.85	137.75	108.33
UFGP	33.85	57.53	96.80
PL	21.03	24.02	20.83
PH	84.45	98.05	81.00
FLL	32.53	39.30	34.03
FLB	1.62	1.50	1.63

Legends: 50%F=days to 50% flowering, Etil=total effective tillers hill⁻¹, PH=plant height (cm), FLL=flag leaf length (cm), FLB=flag leaf breadth (cm), PL=panicle length (cm), FGP=filled grains panicle⁻¹, UFGP = unfilled grains panicle⁻¹, GD = growth duration (days), Yield=grain yield (tha⁻¹)

The cluster 1 contained six lines viz. BRRI

10B, BRRI 35B, BRRI 48B, BRRI 50B, BRRI 7B and BRRI 97B. Four maintainers BRRI 11B, BRRI 99B, IR 79125B and IR 79156B formed cluster 2. The smallest cluster contained only three maintainers i.e. IR 105687B, IR 105688B and IR 58025B. Maintainers in the same cluster had more similarity than the maintainers in different cluster.

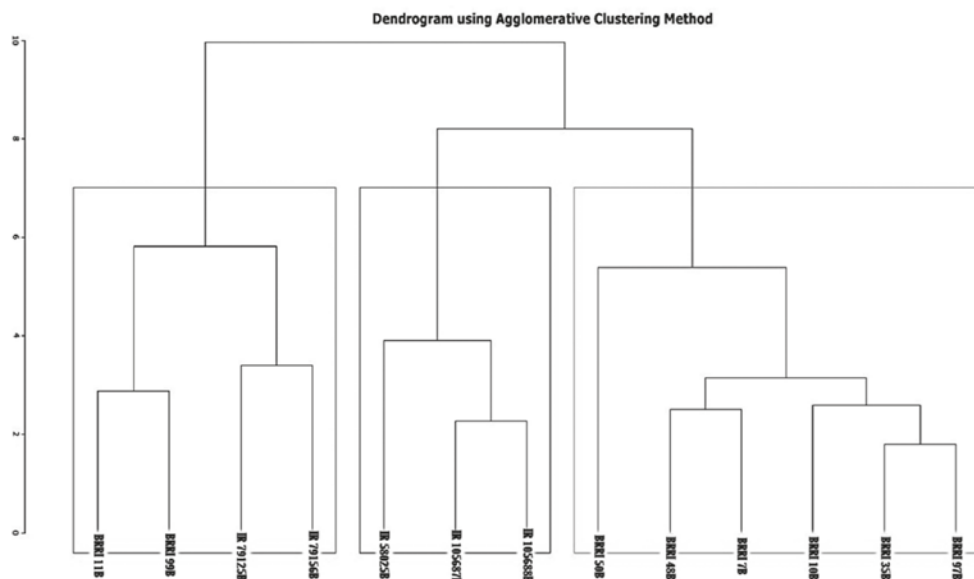


Fig. 1. Dendrogram showing clusters of 13 maintainer lines of hybrid rice genotypes obtained using a set of 10 characters.

Predicted genetic gain:

At present hybrid rice division, BRRI needs six years to complete a breeding cycle for B×B improvement. About 0.084 $\text{tha}^{-1} \text{year}^{-1}$ genetic gains can be achieved from the genotypes used in this experiment at 30% selection intensity and six year breeding cycle length. At the same time, 10% selection intensity and 6 year breeding cycle length will produce 0.117 $\text{tha}^{-1} \text{year}^{-1}$ genetic gain (Table 4). The

population size will be needed to increase 10-fold to double genetic gain and rising selection intensity from 0.1% to 0.01% only raises the projected gains by 20% (approximately) (Yunbi *et al.* 2017). We're concentrating on shortening the breeding cycle using field rapid generation advance. If the length of breeding cycle is reduced compared to the present; it will escalate the genetic gain for the studied genotypes also and table 4 presents the conditions.

Table 4. Predicted genetic gain ($\text{tha}^{-1} \text{year}^{-1}$) in different situations for the studied maintainers.

Breeding cycle length (Year)	Selection intensity	Predicted genetic gain ($\text{tha}^{-1} \text{year}^{-1}$)	Breeding cycle length (Year)	Selection intensity	Predicted genetic gain ($\text{tha}^{-1} \text{year}^{-1}$)
3	5%	0.275	3	10%	0.234
4	5%	0.206	4	10%	0.176
5	5%	0.165	5	10%	0.141
6	5%	0.138	6	10%	0.117

CONCLUSION

Four promising maintainer lines (viz BRRI 11B, BRRI 99B, IR 79125B and IR 79156B) were selected for the transplanted Aman rice (Wet season). The best maintainer lines will be further used in cyclic breeding to develop new elite maintainer lines. Genotype clustering into several clusters (3) advocates moderate genetic variation among genotypes to warrant improvement through breeding for transplanted Aman season.

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