Research Article

Study on Genetic Variability and Heritability in F4 Population of Irrigated Rice

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Article Information

Abstract

Population establishment, selection, and evaluation are key components of plant breeding program. This study was designed to observe the genetic variability and the heritability of the selected yield component traits in F4 rice population. A field experiment was carried out with 16 F4 materials and 4 check varieties of *Oryza sativa L.* at Sher-e-Bangla Agricultural University, Dhaka to identify the suitable traits for the augmentation of rice yield. The F4 populations obtained from BR21×BR26, BR21× BRRI dhan28, BR 21× BRRI dhan29, BR24× BRRI dhan29, BR24× BRRI dhan36, BR26× BRRI dhan36 were utilized as breeding materials. Nine characters were considered i.e., days to 50% flowering, 80% maturity, plant height, tiller per panicle, panicle length(cm), filled grain per panicle, yield per plant(g), thousand-grain weight(g) and yield (t/ha). The selected genotypes were found significantly variable for all of the characters. The lowest days to maturity (92.00 days) were observed in G11 (BR21 × BRRI dhan29, F4, S7P2) following as G4 (BR21 × BRRI dhan29, F4, S1P2) (95.33 days) and G5 (BR21 ×BRRI dhan29, F4, S1P5) (96 days). The highest yield among F4 population was recorded in G6 (BR21 × BRRI dhan29, F4, S6P3) (6.08 t/ha) followed by G10 (BR21× BRRI dhan29, F4, S7P1) (5.30 t/ha) and G7 (BR21 × BRRI dhan29, F4, S6P8) (4.68ton/ha). All the traits showed remarkably higher phenotypic variances than the genotypic variances. Besides, all characters showed high heritability and higher PCV than the GCV. High heritability along with moderate to high genetic advance in percent mean is controlled by additive gene action which is better for selection.

Introduction

Rice is mostly a self-fertilizing cereal crop from the family Gramineae (synonym-Poaceae) belongs to the class Monocotyledon and order Cyperales, made up of chromosome number 2n=24 (Hooker, 1979). It can thrive well in both annual and perennial conditions. Rice and agriculture are still basic to the economic progress of many Asian countries. The livelihood of rice producers and consumers significantly depends on the sound rice industry.

Intending to provide the rice-eating people with a high-quality, affordable staple, farmers need to secure good yields without harming the environment while making a good living while. Indeed, rice research has been imperative to productivity and subsistence. Rice is the second largest produced cereal in the world with an annual production of about 755.47 million metric tons (FAO, 2021) and is also the staple food for over one-third of the world's population. More than 90% to 95% of rice is produced and consumed in Asia. Rice is central to Bangladesh's economy and staple

food for the people since ancient times and has grown in a wide range of environments. Rice continues to dominate the cropping system; three-quarters of the total cultivated area is used for rice production. More than half of the world's human population takes it as a staple food. Enhancement of the grain yield is the primary breeding target in rice breeding programs and knowledge of the nature and significance of the genetic variation determining the inheritance of quantitative traits like yield and its components is a prerequisite for functional genetic advancement. A critical analysis of the genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different characteristics of economic importance is mandatory for the plant breeder to work with crop improvement programs. However, knowledge of correlation coefficients between grain yield and its component characters is vital for yield improvement, since complex entity like grain yield in rice is highly governed by several component characters. The present investigation was conducted to evaluate segregating F4 population of aus-boro crosses. Most promising lines from segregating populations were selected based on the earliness of maturity and higher yield for future trials. Grain yield is a complicated polygenic quantitative trait that is remarkably affected by the environment and determined by the magnitude and nature of its genetic variability (Singh *et al.*, 2000). According to Yoshida (1981), grain yield generally depends on other parameters such as plant type, growth duration, and yield contributing components. Estimates of heritability and genetic advance will help in knowing the nature of gene action affecting the concerned trait (Sravan, 2012). In view of the above discussion, the present study was undertaken to elucidate information on variability, heritability and genetic advance in promising rice genotypes. in thousand grain yield among twenty rice genotypes.

Materials and Methods

The experiment was carried out in experimental Field of Sher-e-Bangla Agricultural University, Dhaka from March 2014 to July 2014. The position of experimental field was 90º 33.5´ E longitude and 23º 77.4´ N latitude with 9 meters of elevation above the sea level. So, the soilexture of the experiment site was medium high land, clay loam, having pH 5.46-5.67. This site was cothe vered by Agro-ecological Zone (AEZ no.28) the of 'Madhupur tract'. The climatic condition of the experimental site was sub-tropical characterized by significant precipitation during April to July and sporadic during the remainder of the year. The experimental materials comprised of 16 rice genotypes and 4 check varieties (Table 1). All the genotypes were transplanted in RCBD design with 3 replications having spacing of 20cm×20 cm. The fertilizer doses applied in experimental plot were N-P-K-Zn @60, 11, 30 & 11 Kg/ha, respective total dose of, TSP, MP and Gypsum were

incorporated during final land preparation. On the other hand, urea was applied in three installments, at 10 days after transplanting (DAT,), 25 DAT and 40 DAT. Data were recorded on 10 randomly selected plants in each plot for the characteristics viz.; days to 50% flowering, days to maturity, plant height, effective tiller/m^2 and yield t/ha. Analysis of variance (ANOVA) was carried out using MSTAT-C. The genetic parameters consisted of phenotypic variances (Vp) and genotypic variances (Vg), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability (%), genetic advance (GA) and genetic advance as percent of the mean (GAM) were estimated following the formula given by Burton and Vane (1953) and Johnson *et al.* (1955).

Table 1: Number of genotypes

SL No.	Genotype number	Genotype name
1.	G1	BR21× BR26 F5 S6 P6
2.	G2	BR21× BRRI dhan28 F5 S5 P8
3.	G3	BR21× BRRI dhan28 F5 S5 P9
4.	G4	BR21× BRRI dhan29 F5 S1 P2
5.	G5	BR21× BRRI dhan29 F5 S1 P5
6.	G6	BR21× BRRI dhan29 F5 S6 P3
7.	G7	BR21× BRRI dhan29 F5 S6 P8
8.	G8	BR21× BRRI dhan29 F5 S6 P9
9.	G9	BR21× BRRI dhan29 F5 S6 P10
10.	G10	BR21× BRRI dhan29 F5 S7 P1
11.	G11	BR21× BRRI dhan29 F5 S7 P2
12.	G12	BR24× BRRI dhan29 F5 S5 P8
13.	G13	BR24× BRRI dhan29 F5 S5 P9
14.	G14	BR24× BRRI dhan29 F5 S5 P10
15.	G15	BR24× BRRI dhan36 F5 S7 P8
16.	G16	BR 26×BRRI dhan36 F5 S7 P10
17.	G17	BR21(Check)
18.	G18	BR26(Check)
19.	G19	BRRI dhan42 (Check)
20.	G20	BRRI dhan43(Check)

Results and Discussion

Analysis of Variance (ANOVA)

The analysis of variance (ANOVA) showed (Table 2) a significant mean sum of squares due to genotypes difference (191.62**) for days to 50% flowering (Table 3). Highly significant differences in days to 50% heading were recorded among rice genotypes ranging from 66.33 to 97.67 days. Analysis of variance for days to 80% maturity expressed a significant mean sum of square (178.67**) due to genotypes disparity. Genotypes significantly varied in plant height range ranging 108.82 to 151.63 cm. Sabouri *et al.* (2008) recommended plant height as an essential trait for the selection of high-yielding rice plants. KC *et al.* (2020), significant differences in plant height among the twenty-five rice genotypes. Mohammad *et al.* (2002) described

those differences in plant height depends the on genetic makeup of a plant and environmental conditions. Sharma (2002) reported significant difference in panicle length among fine grain rice genotypes. The significant differences were found in number of tillers/plants. Similar results were achieved by Kusutani *et al*. (2000) and Dutta *et al*. (2002) who reported differences in number of effective tillers among genotypes. Dhungana *et al*. (2020) reported a significant difference r number of effective tillers per plant, panicle length, number of filled grains per panicle, total number of spikelets per panicle, thousand seed weight, yield (t/ha) significantly significant (6.43**) mean sum of square due to genotypes differ clearly imply that the presence of satisfactory variability in the experimental material.

Table 2: ANOVA table for 20 rice genotypes for different characteristics

Sl No.	Traits	Treatment	Replication	Error
1	Days to 50% flowering	191.62**	8.15	0.68
2	Days to maturity	178.67**	0.52	2.24
3	Plant height(cm)	334.77**	20.37	14.06
4	Effective tiller/plant	6.43**	0.07	0.14
5	Panicle length (cm)	10.58**	0.25	1.47
6	Filled grain	1138.28**	107.01	25.38
7	Yield per plant (gm)	34.33**	3.14	0.75
8	Thousand seed weight (gm)	14.74**	3.81	1.60
9	Yield(t/ha).	2.09**	0.08	0.03

Significant at 1% level of probability, *= Significant at 1% level of probability

Table 3: Agronomic performances of tested genotypes

Genotypes	D50F	DM	PH	ETILL	PL	FG	GYP	TSW	YIELD
G1	82.67	104.67	126.04	9.57	22.71	99.13	20.99	19.93	4.08
G2	78.33	104.67	116.64	9.73	21.60	72.43	17.40	22.50	3.45
G3	92.33	118.67	151.63	8.87	23.64	83.43	17.49	25.27	4.13
G4	73.00	95.33	112.76	10.57	20.52	102.10	23.43	19.40	2.52
G5	72.67	96.00	113.02	9.20	21.03	82.67	19.96	22.93	3.37
G6	79.00	104.00	125.49	14.10	23.58	135.33	27.54	23.67	6.08
G7	75.33	101.00	119.84	11.63	22.49	125.13	23.55	21.70	4.68
G8	75.67	99.67	124.56	10.27	21.63	107.73	22.35	22.27	3.61
G9	77.00	100.33	123.21	10.20	21.52	115.33	23.48	22.50	4.24
G10	84.00	108.33	129.31	12.27	23.40	135.90	24.81	21.37	5.30
G11	66.33	92.00	124.38	9.57	24.46	112.23	22.45	22.16	3.93
G12	78.67	103.67	129.57	11.43	26.31	127.60	24.13	27.43	4.37
G13	98.33	118.33	138.98	9.77	26.21	84.67	16.89	18.87	2.69
G14	81.33	105.67	116.85	9.77	25.13	109.27	18.33	19.33	3.34
G15	97.67	122.33	145.60	9.57	25.41	71.30	16.60	22.87	3.50
G16	84.00	107.33	124.28	9.43	26.22	113.63	27.12	23.66	3.26
G17	86.33	109.67	123.24	8.17	22.31	114.27	25.00	23.00	4.21
G18	85.67	109.00	108.82	7.37	23.89	118.30	24.14	25.00	3.44
G19	81.33	103.33	122.12	9.43	21.38	93.23	23.36	24.53	3.36
G20	81.33	104.67	120.86	10.30	21.33	93.10	25.35	25.10	4.10
LSD$_{0.05}$	1.36	2.47	6.20	0.63	2.00	8.33	1.43	2.09	0.27
CV%	1.01	1.42	3.00	3.78	5.22	4.81	3.89	5.57	4.23
Mean	81.55	105.43	124.86	10.06	23.24	104.84	22.22	22.67	3.88

D50F= Days to 50% flowering, DM= Days to maturity, PH= Plant height(cm), ETILL= Total number of effective tiller/plants, PL= Panicle length (cm), FG= Number of filled grain of main tiller, GYP= Yield per plant (gm), TSW= Thousand seed weight (gm) and YIELD=Yield(t/ha), CV: Coefficient of variation

Agronomic Performances

Coefficient of variation (CV) for days to 50% flowering, days to maturity, plant height, No. of effective tillers/plant, panicle length, filled grain/panicle, grain yield per plant, thousand-grain weight and grain yield were 1.01, 1.42, 3.00, 3.78, 5.22, 4.81, 3.89, 5.57 and 4.23 % respectively (Table 3). It was observed that mean values for the examined characters ranged from 72 to 98 days for 50% flowering, 9 to 14 for the number of tillers/plants, 18.87 to 25.10 g for thousand-grain weight, 21.33 to 25.13 cm for panicle length and 2.52 to 6.08 t/ha for grain yield. The maximum grain yield was observed in G6 (6.08 t/ha), which was followed by G10 (5.30 t/ha), and G7 (4.68 t/ha) (Table 2). The lowest yield was reported in G4 (2.52 t/ha). These findings are similar to those of Poudel *et al*. (2014) and Gyawali *et al*. (2018), who found differences in rice growth and yield traits. Shrestha *et al*. (2021), Gyawali *et al*. (2018), Bekele *et al*. (2013), Rashid *et al*. (2017), Summanth *et al*. (2017), Abebe *et al*. (2017), Bandi *et al*. (2018) and Poudel *et al*. (2014) documented significant genetic variability among rice genotypes for grain yield. Similar outcomes were supported by Zahid *et al*. (2005), who assessed the yield performance of twelve genotypes of coarse rice. They observed that different traits exhibited lot of variation. The contribution of environmental factors could be the reason for these variations (Mahapatra,1993) or due to the correlation of grain yield per plant and different yield contributing parameters such as a number of grains per panicle, and grain weight.

Genetic Variability

The phenotypic and genotypic coefficient of variation were acquired for all examined traits (Table 4). The highest genotypic coefficient of variation and phenotypic coefficient of variation were obtained from grain yield of 26.51 t/ha, filled grain per panicle (23.01) and yield per plant (18.85 g). High GCV along with marginally high PCV values showed that inter-genotypic variation was high which were less affected by environmental factor and less gap between GCV and PCV value exhibited sufficient variation in the materials under examination. These results are analogous to the findings of Khan *et al*. (2009), Akinwale *et al*. (2011) and Ketan and Sarkar (2015).

Shrestha *et al*. (2021), Manjutha *et al*. (2020) & Abebe *et al*. (2017), also reported a high PCV on grain yield, which is similar to the findings of this study. The difference between phenotypic and genotypic variance was higher in the number of tillers/plants, indicating that the environment had a significant impact on these traits. The findings on plant 188 height variation were similar to those of Ojo *et al*. (2006) and Kashiani *et al*. (2010).

Heritability

Heritability is an important tool for selection as it enables a plant breeder to understand the possibilities to which extent improvement can take place, while genetic advance measures the true gain under selection. According to Johnson *et al*. (1955), heritability was classified as low (below 30%), medium (30-60%) and high (above 60%). High heritability was recorded for all the traits ranging from 75.58 for panicle length to 99.30 % for days to 50% flowering. This Heritability Burton (1952) reported that genotypic coefficient of variation along with high heritability estimates would depict an expected genetic gain through phenotypic selection. High heritability does not invariably indicate high genetic gain; high heritability in conjunction with high genetic advance should be used to choose desired varieties. Estimation of broad sense heritability showed the relative contribution of the heritable portion.
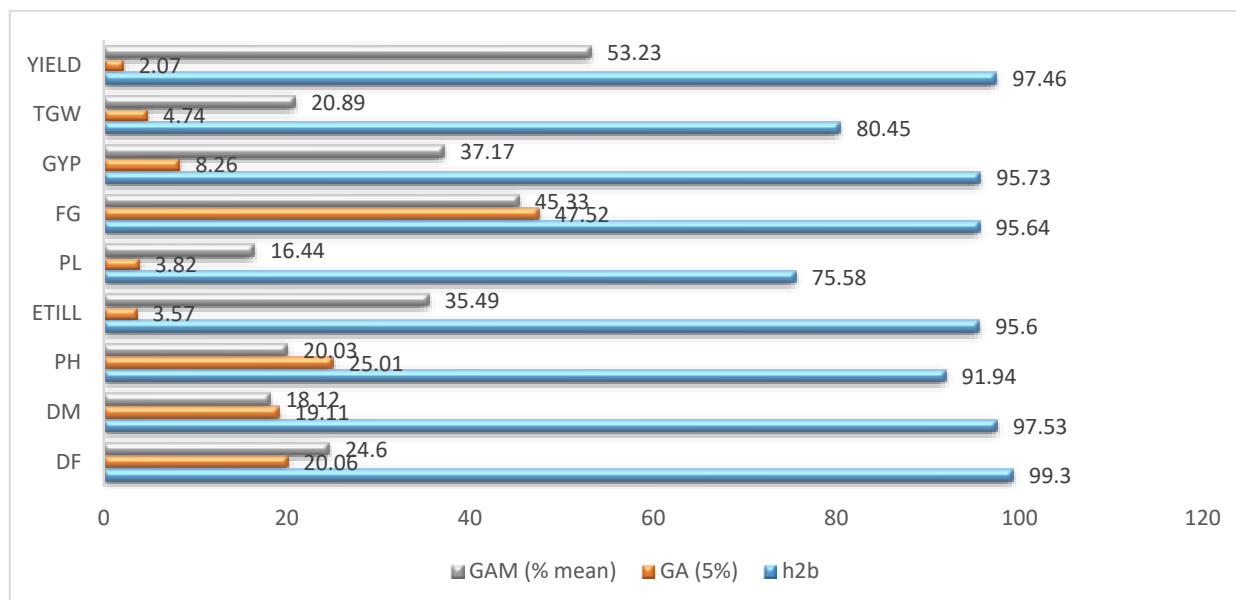
Genetic Advance

The effect of both additive and non-additive genes is included in the heritability estimates, but it cannot provide a complete picture of practical significance until it is assessed with genetic advance. Estimates of the genetic advance can aid in determining the degree of gene action exhibited by different polygenic features. In this study, high heritability along with high genetic advance was observed for the traits, viz., days to 50% flowering (20.6), filled grain per panicle (47.52), plant height (25.01) indicated that the characters (Table 4) were mostly governed by additive gene effects means less influence of the environment (Panse and Sukhatme, 1957). Earlier research backed up these findings by many workers (Manjutha *et al*., 2020; Gyawali *et al*., 2018; Bandhi *et al*., 2018; Abebe *et al*., 2017; Subbaiah *et al*., 2011; Lipi *et al*., 2020).

Table 4: Phenotypic ($\sigma^2 p$) and genotypic variance ($\sigma^2 g$), phenotypic coefficient (PCV) and genotypic coefficient of variance (GCV), genetic advance (GA) at 5% selection intensity, genetic advance as percent of the mean (GAM) and broad sense heritability ($h^2 b$) for studied traits in rice genotypes

Traits	Mean	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	h^2_b	GA (5%)
Days to 50% flowering	81.55	95.47	96.15	11.98	12.02	99.30	20.06
80%Maturity	105.43	88.22	90.45	8.91	9.02	97.53	19.11
Plant Height	124.86	160.36	174.42	10.14	10.58	91.94	25.01
Tiller per plant	10.06	3.14	3.29	17.62	18.02	95.60	3.57
Panicle length	23.24	4.55	6.02	9.18	10.56	75.58	3.82
Filled grain per panicle	104.84	556.45	581.83	22.50	23.01	95.64	47.52
Yield per plant(g)	22.22	16.79	17.54	18.44	18.85	95.73	8.26
Thousand-grain weight(g)	22.67	6.57	8.17	11.31	12.61	80.45	4.74
Yield (t/ha)	3.88	1.03	1.06	26.18	26.51	97.46	2.07

Fig. 1: Graphical depiction of heritability as broad sense (h^{2}b), genetic advance (GA), and genetic advance as mean percent (GAM % mean)

Heritability Coupled with Genetic Advance as Percent of Mean (GAM)

Genetic advance as a percentage of the mean (GAM) gives a more precise result in comparison to genetic advance. Therefore, heritability estimation coupled with genetic advance as percent of mean is more effective for selection. In comparison to genetic advance, genetic advance as a percentage of the mean (GAM) provides a more exact result. As a result, for selection, heritability assessment combined with genetic advance as a percentage of mean is more successful. Genetic advance as percent mean was classified as low (0-10 %), moderate (10-20 %) and high (≥20 %).

Days to 80% maturity exhibited high heritability with moderate genetic advance and genetic advance in the percentage of the mean (18.12%). A number of effective tillers per plant, yield per plant, and yield per hectare showed high heritability with low genetic advance and high genetic advance in the percentage of the mean (Fig. 1). These results indicated the possibility of the predominance of additive gene action in the inheritance of these characters. Both environmental and genotypic factors influenced the trait. As a result, selection to increase grain yield would be effective.

The degree of heritability of panicle length and thousand seed weight (g) were high with very low genetic advance and moderate genetic advance in percent of the mean (Fig. 1). Which depicted that the environmental effect was more than the genotypic effect and due to additive gene action, selection for further improvement of the trait might be effective. A similar result was revealed by Ullah *et al.* (2011).

Low genetic advance as percent of mean coupled with low estimates of heritability was observed for panicle length, thousand-grain weight, the results indicated involvement of non-additive gene effect for expression of these traits and hence, population improvement approach would be most effective for improvement of these characters. These findings conform with Patel *et al.*, (2018), while Ketan and Sarkar (2014) reported only low genetic advance as percent of the mean for grain length. Thus, direct selection of these characters depending on phenotypic expression by a simple selection procedure would be useful due to the accumulation of more additive genes directing to advance improvement. The similar outcome for a number of grains per panicle and the number of filled grains per panicle were formally documented by Edukondalu *et al*; (2017).

Conclusions

In conclusion, this article has discussed mean, variance, heritability, genetic advance and genetic advance as percent mean. The number of filled grain per panicle and yield per plant (g) displayed significant phenotypic and genotypic variance, high heritability and high genetic advance. According to the estimation of genetic parameters in some promising F4 lines of rice days to flowering, plant height, tiller per plant, yield per plant(g), thousand seed weight (g) and grain yield (t/ha) all demonstrated substantial phenotypic and genotypic variance, as well as heritability and genetic advance. This research also identifies the most promising F4 rice genotypes G6 (BR21 × BRRI dhan29, F4, S6P3), G7(BR 21 × BRRI dhan29, F4, S6P3) and G9 (BR21 × BRRI dhan29, F4, S7P1). These lines could be introduced as improved materials for the further breeding program based on yield and other contributing parameters.

Authors' Contribution

Conflict of Interest

Acknowledgements

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