



Estimation of Genetic Variability, Heritability and Genetic Advances for Short Duration and High Yielding Rice Genotypes

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ABSTRACT: The goal of the study was to find genotypes of 18 different rice varieties that would yield a lot of rice in a short amount of time. With this in mind, the study genotypes' field performance as well as the relationships between various morpho-physiological and yield-contributing traits among the genotypes was assessed. The experiments were conducted from July to December 2018 at the Agronomy Field, Department of Agronomy and Agricultural Extension, Faculty of Agriculture, Rajshahi University. In genotype BRR1 dhan 51, the maximum number of days to 50% flowering was discovered. The genotype BRR1 dhan 56 had the lowest number of days required for 50% flowering. Genotypes showed a wide range of days to maturity (92.00–109.00), with an average of 98.96 days. The genotypes DRR 46, BINA 7, and DRR 44 are followed by the genotypes BRR1 dhan 66, BRR1 dhan 56, and BRR1 dhan 57, which have shorter maturity periods (i.e., 92.00 days), indicating earliness. The traits investigated in this study showed high heritabilities, with estimates ranging from 67.00 to 96.00 percent. Days to flowering and unfilled grain panicle-1 had the highest heritability among the traits (96.00%). The presence of high heritability values suggests that the expression of the traits under study is less influenced by the external environment. The unfilled grain panicle-1 had the highest genetic advance as a percentage of the mean (144.80%), while panicle length had the lowest genetic advance (10.48%) among the traits that affected yield.

Keywords: Wheat Genotype, Variability, Heritability, Genetic Advance, PCV (Phenotypic Co-Efficient of Variation), GCV (Genotypic Co-Efficient of Variation).



1. Introduction

The cultivated rice plant, *Oryza sativa* L., has chromosome number $2n=2x=24$ and is an annual self-pollinated short-day monocotyledonous grass of the Poaceae (Graminae) family. It is a warm-season crop that was first domesticated in South East Asia and is now widely grown throughout the world's humid tropical and subtropical regions. More than half of the world's population consumes rice as a staple food, and its cultivation takes up about 9% of the planet's arable land. About 49% of the calories consumed by the human population come from rice, maize, and wheat, with 23% coming from rice. As a result, nearly one-fourth of the calories consumed globally come from rice. (S. K. Singh V. P., August 2020).

Two million hectares of indigenous rice cultivars are grown in Bangladesh, compared to eight million hectares of HYV and one million hectares of hybrids. (S. P. Chakma¹, 2012).

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Plant breeding is based on genetic diversity. Genetic diversity in the parent generation is assumed when yield in each generation is segregated (or yield component traits are segregated) for selective breeding. As a result, it's crucial to estimate the genetic diversity in yield traits (a population statistic describing its genotypes) for the policies that choose parents in crossing programs.(Al, 6 March 2017).

Any crop's ability to improve genetically is largely dependent on the population's genetic diversity. The type and degree of genetic divergence would guide the plant breeder in selecting the appropriate parents and breeding strategy to produce high levels of heterotic expression in F₁s and a wide range of variability in succeeding generations. (GHOSH, 30-11-2012).

Other crucial selection criteria include heritability and genetic advancement. The plant breeder can identify the character for which selection would be fruitful using the heritability estimates. Based on their phenotypic expression, breeders are interested in selecting superior genotypes. Heritability estimates' main purpose is to inform people about how traits are passed down from one generation to the next. Estimates of heritability can predict improvement by choosing useful characters. In general, genetic advance and heritability estimates work better together to predict the gain under selection than heritability estimates alone.(Paikhomba N, 2014)

A trait's heritability (h^2) is crucial in determining how well a cultivar responds to selection. It is well known that grain yield has a low heritability and is greatly influenced by the environment (BESER, 2005).



Crop improvement breeding programs require the genetic advance prediction, especially when large populations are subjected to selection. facilitated by obtaining phenotypic and genotypic coefficients of variation, without which it would be physically more difficult to evaluate each genotype in the field. Therefore, it is necessary to research variability. Crop improvement requires the presence of variability for various traits in the source population because breeding and selection efforts would be ineffective without a significant amount of heritable variability.(Sedeek & all, 2009).

By identifying the traits that will be passed down to the following generation, heritability can be used to estimate the population's structures. (Ahmad F, 2015 September 22,).

An important factor in the successful selection of parents for a hybridization program is genetic divergence. An important factor in the successful selection of parents for a hybridization program is genetic divergence.(Sneha Gupta*, 08 January 2020).

Physiological or morphological traits have traditionally been used to measure genetic diversity in plants. Phenotype evaluation may not be a valid indicator of genetic differences because gene expression is influenced by the environment.(L.V. Subba Rao, 2015).

Studies on genetic diversity, relationships, and population structure are helpful for a variety of reasons, including choosing parental combinations to produce offspring with significantly higher yield potential and phenotypically superior traits than their parents. (Marie Noelle Ndjiondjop1*, 09 April 2018).

The genetic improvement in yield that can be achieved through selection can be measured by correlation coefficient analysis, which identifies the component characters on which selection can be based.(all, 2010).



2. MATERIALS AND METHODS

2.1. Location and duration of the experiment

2.2. The experimental field was located on the western side of the University of Rajshahi's Department of Agronomy and Agricultural Extension. The experimental field was situated 20 meters above sea level in the High Ganges River Flood Plain AEZ-11 at 24°22'362" N latitude and 88°38'27" E longitude.

2.3. Experimental design

2.4. The experiment was conducted using a Randomized Complete Block Design (RCBD) with three replications. The size of each plot was 2.5 m by 2 m. (5 m²). There were: 18 x 3 = 54 total plots.

2.5. Recording of data

Ten randomly selected plants from each of the TEN rows of each plot in each block were used to collect data on each individual plant. Days to 50% flowering and days to physiological maturity were two of the studied characters that were noted in the field. After harvesting, the remaining characters were recorded.

The data were recorded on the following traits:

- a) **Days to 50% flowering:** Recorded as days from sowing to flowering when 50% of the plant of each plot flowered.
- b) **Days to maturity:** Recorded as days on plot basis from sowing to the time when about 90% of the plant were ready for harvesting.
- c) **Plant height (cm):** The length of five main culms of five randomly selected plants from the ground level to tip of its panicle was measured and average was taken.
- d) **Number of total tillers m⁻²:** Number of tillers (effective or non effective) was counted from each hill and average from the collected five hills.
- e) **Effective tiller number m⁻²:** The number of panicle bearing tillers were counted from each of the five sample randomly selected plants and the average was taken.
- f) **Number of non-effective tillers m⁻²:** The panicles, which had no grain, were regarded as non effective tillers.
- g) **Panicle length (cm):** Recorded as the distance (cm) from the last node of the rachis to tip of the main panicle which was randomly selected from each plant and the average was taken.
- h) **Grain panicle⁻¹:** the number of grains per panicle



- i) Number of filled grain panicle⁻¹:** The spikelet's with kernel was considered as filled grain and counted from one randomly selected panicle from each plant and the average was taken.
- j) Number of unfilled grain panicle⁻¹:** The spikelet without kernel was considered as unfilled grain and counted from one randomly selected panicle from each plant and the average was taken.
- k) Thousand grain weight (g):** Thousand grain weight of each plot was taken proper cleaning and sun drying.
- l) Grain Yield per m⁻² (kg):** Total gain weight of each plot was taken after proper cleaning and drying for at least two days.
- m) Straw weight.** Straw weight of each plot was taken.

2.6. Statistical analysis

Analysis of variance was performed using the plant breeding statistical program (PLABSTAT, Version 2N, Utz, 2007) with the following model:

$$Y_{ij} = g_i + r_j + \epsilon_{ij}$$

Where,

Y_{ij} = observation of genotype i in replication j ,

g_i = effects of genotype i

r_j = effects of replication j ,

ϵ_{ij} = the residual error of genotype i in replicate j .

The replicates were considered as random variable. Multiple mean comparisons were made with Fisher's least significant difference (LSD) procedure using Stat Graphics Plus for Windows 3.0 (Statistical Graphics Crop. Rockville, USA).

2.6.1. Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were estimated according to the formula given by (MA Islam, Analysis of genetic variability, heritability and genetic advance for yield, 2015)

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



Where,

GMS = Genotypic mean square

EMS = Error mean square

r = Number of replication

Phenotypic variance, $\sigma_{ph}^2 = \sigma_g^2 + EMS$

Where,

σ_g^2 = Genotypic variance

EMS = Error mean square

2.6.2. Estimation of genotypic and phenotypic co-efficient of variations

The estimated co-efficient of variation for both genotypes and phenotypes was Burton (1952) and Singh and Chaudhary (1985).

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

Where,

σ_p^2 = Phenotypic variance; and

\bar{X} = Population mean

2.6.3. Estimation of heritability

Heritability in broad sense (h_b^2) was estimated according to the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956).

$$\text{Heritability, } h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$



Where,

δ^2_g = Genotypic variance; and

δ^2_p = Phenotypic variance.

2.6.4. Estimation of genetic advance

Estimation of genetic advance was done following formula given by Johnson *et al.* (1955) and Allard (1960).

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.

2.6.5. Experimental material

Eighteen rice varieties were used in the present study. The list of varieties is presented below table 1.

TABLE 1: the list of the genotypes used in the experiment with their sources

SL. NO	VARIETIES	lines	SOURCES
1.	BR11		BRR1
2.	DRR46		BRR1
3.	BRR1 dhan79		BRR1
4.	CR DHAN 405		BRR1
5.	BRR1 dhan 51		BRR1
6.	BRR1 dhan78		BRR1
7.	CSR 43		BRR1
8.	BRR1 dhan66		BRR1
9.	DRR 42		BRR1



10.	BRR1 dhan52	BRR1
11.	DRR 39	BRR1
12.	BRR1 dhan56	BRR1
13.	CR dhan801	BRR1
14.	BINA 11	BRR1
15.	BINA 7	BRR1
16.	BRR1 dhan57	BRR1
17.	DRR 44	BRR1
18.	BRR1 dhan71	BRR1

BRR1= Bangladesh Rice Research Institute

3. Result

3.1. Evaluation of performance of rice genotypes

3.1.1. Analysis of variance

Table 2 displays the analyses of variance of various advanced lines for morphological traits. In nine of the thirteen traits under study—days to flowering, days to maturity, plant height, effective tiller, panicle length, grain panicle, effective grain panicle-1, thousand grain yield, and grain yield per hectare—the difference between genotypes is highly significant, according to the analysis of variance. This suggests that all of these genotypes for these traits are variable. Significant variation for these traits was also found in rice in earlier research. (Selvaraj, 2011). Although some attempts also revealed non-significant variation for these traits in rice, genotypes showed that all are significant. similar outcome is discovered by (M. Y. Rafii, 2018). These show how important each grain is for increasing yield. The hypothesis is therefore supported by the significant genotype-based variations for grain length-width and weight traits in the current study.



Table 2: Analysis of variance (mean square values for various traits across 18 genotypes of rice).

Traits	Source of variations		
	Replication (df =2)	Genotype (df =17)	Error (df =34)
DF	512.46	237.67**	2.81
MD	224.01	113.95**	2.01
PH	94.08	244.04**	28.85
TT	1104.35	2037.85**	35.02
ETM ²	867.94	2081.74**	78.57
NETM ²	14.88	697.64**	40.35
PL	0.24	8.65**	1.20
GP ¹	79.26	2402.48**	67.25
EGP ¹	129.74	1528.47**	43.63
UFGP ¹	7.62	636.78**	6.76
THGW	161.44	15.25**	0.52
GY	0.12	6.14**	0.15
STW	0.53	6.76**	0.34

DF= days to flowering, MD= maturity day, PH= plant height, TT= total tiller ETM²= effective tiller m², NETM²= non effective tiller m², PL= panicle length GP= grain panicle, EGP=effective grain panicle, UFGP¹= unfilled grain per panicle THW= thousand grain weight, GY= grain yield, STW= straw weight .

3.1.2. Performance of the genotypes for yield and yield contributing traits

An excellent opportunity to identify and classify the genotypes according to various traits individually was provided by univariate statistical analysis. Table 4 displays the average traits performances of the 18 rice genotypes.

The genotypes' varying days to 50% flowering ranged from 55.33 to 83.00 days, with a mean of 66.57 days. The genotype BRR1 dhan 51 has the highest number of days to 50% flowering, followed by BR 11, BRR1 dhan 79, and BIRRI dhan 52. The genotype BRR1 dhan 56 has the shortest days to 50% flowering, followed by BRR1 dhan 57, DRR 42, and BRR1 dhan 66.

Genotypes showed a wide range of days to maturity (92.00–109.00), with an average of 98.96 days. The genotypes DRR 46, BINA 7, and DRR 44 are followed by the genotypes BRR1 dhan 66, BRR1 dhan 56, and BRR1 dhan 57, which have shorter



maturity periods (i.e., 92.00 days), indicating earliness. Under various agro-ecological conditions and breeding programs, variations in crop duration could be used directly.

The genotypes' average plant height was 96.64 cm, with genotypes ranging from 74.59 cm to 108.90 cm in height. The genotype DRR39 has the tallest plants (108.90 cm), followed by BRR1 dhan 52, BR11, and BIRRI dhan 66, and the genotype CSR43 has the shortest plants (74.59 cm). Rice plant height is a complex trait that results from a number of genetically controlled factors.(NABEELA ZAFAR, 2004). Reducing plant height may increase the plants' resistance to lodging and lessen the significant yield losses brought on by this trait. (Abbasi, 1995/01/01)).

The genotype BRR1 dhan 51 achieved the highest total tiller value (306.67), followed by BINA 7 and BRR1 dhan 52. By using BRR1 Dhan 71, the minimum value of 209.00 is obtained. Total's median value is 258.22.

The genotype BRR1 dhan 57, which is followed by BRR1 dhan 51 and BINA 7, has the highest effective tiller value (257.00), while genotype CSR 43, which is followed by DRR 42 BRR1 dhan 71, has the lowest effective tiller value (167.31). Effective tiller has a mean value of 210.89.

The highest non-effective tiller value (80.00) was found in CSR 43, and the lowest value (26.33) was found in BRR1 Dhan 57. The average non-productive tiller value was 47.33.

In terms of panicle length, genotype DRR 39 recorded the highest value (29.86 cm). It showed a respectable amount of variation, ranging from 21.71 cm to 29.86 cm, with a 25.08 cm average. The genotype CSR 43 panicle had the shortest length (21.71 cm).

The genotypes' grain panicle-1 measurements ranged from 80.22 cm to 184.11 cm, with 134.93 cm serving as the mean. The genotype DRR 39, which is followed by BR 11 and BRR1 dhan 71, had the highest grain width measurement (184.11 cm), while genotype CSR 43, which is followed by BINA 7 and DRR 42, had the lowest grain panicle measurement (80.22 cm).

The range of variation for the number of filled grains panicle-1 was high, ranging from 65.67 to 153.22, with a mean value of 114.92. The genotype DRR 39 had the most filled grains per panicle, followed by BRR1 dhan 66, BR 11, and BRR1 dhan 78, while genotype DRR 42 had the fewest filled grains per panicle, followed by CR dhan 405, BINA 7, and DRR 42. This could be used in future programs as having more filled grains per panicle is one of the key factors that contribute to higher grain yield.

Unfilled grain panicle -1 has a maximum value of 70.11, which was discovered by BRR1 dhan 71, followed by DRR 39 and BRR 1, and a minimum value of 6.56, which was discovered by DRR 42. Unfilled grain panicle-1 had a mean value of 20.02.



The weight of a thousand grains varied from 22.71g to 31.61g, with a mean of 26.78g. The genotype CSR 43 showed the highest value of thousand grain weight (31.61g), which was followed by BRR1 dhan 51 and BINA 11, while genotype BRR1 dhan71 showed the lowest value of thousand grain weight (22.71g), which was followed by BRR1 dhan 57 and BRR1 dhan 78.

Grain yield at its highest point (t ha⁻¹), 7.97 g, was recorded for genotype BRR1 dhan 51. It had a respectable range of variation between 3.40 g and 7.97 g, with an average of 5.50 g. The genotype CR dhan 405 had the shortest panicle length (3.40 g).

The lowest value was (4.60 g) obtained from DRR 42 followed by CR dhan405 and CSR 43, and the highest value straw weight was (9.73) obtained from BRR1 dhan51, followed by BRR1 dhan79, and BRR1 dhan 66. The average weight of a straw is 6.91.

Table 4: Mean performance of the rice genotypes for yield components and yield

Genoty pes	DF (50%)	MD	PH (cm)	TT	ETM ²	NET M ²	PL (cm)	GP ⁻¹	EGP ⁻¹	UFG P ⁻¹	THW (g)	Grain Yield (t ha ⁻¹)	Straw yield (t ha ⁻¹)
BR 11	82.00 a	109.0 0 a	104.3 7 ab	243.3 3 efg	194.0 0efgh	49.33 cdefg h	26.37 b	173.7 8 ab	145.0 0 a-c	28.78 bc	25.23 fg	6.90 abc	8.37 abcd
DR 46	61.00 de	95.00 cd	102.5 0 ab	240.0 0 fg	210.6 7 def	29.33 i	26.07 bc	140.6 7 cd	128.4 5 a-d	12.22 ghi	27.04 d-f	5.00 efg	6.67 cdef
BRR1 dhan 79	78.00 ab	109.0 0 a	97.17 ab	285.6 7 b	229.6 7bcd	56.00 bcdef	24.27 b-d	150.2 3bcd	127.4 3 a-d	22.80 cde	26.48 d-f	7.37 ab	9.40 a
CR dhan 405	62.00 d	97.00 c	96.25 a-c	256.0 0cdef	203.3 3defg	52.67 bcdef g	26.11 b	102.3 3 fgh	91.33 de	11.00 ghi	27.97 b-e	3.40 h	5.17 fg
BRR1 dhan 51	83.00 a	109.0 0 a	88.03 a-c	306.6 7 a	247.3 4 ab	59.33 bcde	22.73 cd	125.4 3defg	109.0 0 b-e	16.43 efg	30.00 ab	7.97 a	9.73 a
BRR1 dhan 78	74.00 bc	102.0 0 b	92.50 a-c	236.0 0 g	194.0 0efgh	42.00 defghi	25.57 bc	149.5 7bcd	129.2 0 a-d	20.37 def	25.11 fg	5.43 def	6.63 cdef
CSR 43	63.00 d	97.00 c	74.59 c	247.3 1defg	167.3 1 h	80.00 a	21.71 d	80.22 h	65.67 -g	14.56 fgh	31.61 a	4.17 gh	5.37 fg
BRR1 dhan 66	60.00 d-f	92.00 b	105.8 6 ab	248.6 7defg	219.3 4cde	29.33 i	24.84 b-d	158.7 8 bc	148.8 9 ab	9.89 ghi	26.22 ef	7.50 ab	8.53 ab
DRR 42	59.00 d-f	97.33 c	90.87 a-c	210.0 0 h	171.0 0 h	39.00 fghi	25.86 bc	102.2 2fgh	95.67 de	6.56 i	28.61 b-d	3.47 h	4.60 g



BRRIdhan 52	78.00 ab	109.0 0 a	107.3 3 ab	286.0 0 b	223.3 3 bcd	62.67 abc	25.73 bc	141.1 0 cd	116.4 3 a-e	24.67 bcd	27.68 c-e	7.07 ab	8.40 abc
DRR 39	70.00 c	97.00 c	108.9 0 a	251.6 7defg	190.3 4 fgh	61.33 abcd	29.86 a	184.1 1 a	153.2 2 a	30.89 b	26.98 d-f	6.63 bcd	8.00 abcde
BRRIdhan 56	55.33 f	92.00 d	101.4 2 ab	262.0 0 cd	191.3 3 fgh	70.67 ab	23.96 b-d	127.0 0def	109.8 9 b-e	17.11 defg	25.38 fg	5.13 efg	5.83 fg
CR dhan 801	70.00 c	102.0 0 b	89.41 a-c	260.0 0 cde	220.0 0 cde	40.00 efghi	24.10 b-d	139.4 3 cd	127.8 7 a-d	11.57 ghi	26.20 ef	5.43 def	6.57 def
BINA 11	63.00 d	96.00 cd	90.47 a-c	270.0 0 bc	225.6 7 bcd	44.33c defghi	24.22 b-d	108.4 4efg	98.89 c-e	9.56 ghi	29.48 a-c	4.83 efg	6.23 efg
BINA 7	61.00 de	95.00 cd	85.08 bc	287.6 7 b	245.3 4 abc	42.33 defghi	24.94 b-d	100.2 2 gh	91.89 de	8.34 hi	26.86 df	4.50 fgh	6.70 cdef
BRRIdhan 57	56.00 ef	92.00 d	99.73 ab	283.3 3 b	257.0 0 a	26.33 i	24.86 b-d	144.2 2 cd	127.2 2 a-d	17.00 defg	23.18 gh	5.77 cde	6.93 bcdef
DRR 44	61.00 de	95.00 cd	103.3 3 ab	264.0 0 cd	228.0 0 bcd	36.00 ghi	24.61 b-d	130.2 2 de	101.7 8 e-f	28.45 bc	25.25 fg	4.23 fgh	5.83 fg
BRRIdhan 71	62.00 d	96.00 cd	101.7 4 ab	209.6 7 h	178.3 4 gh	31.33 hi	25.67 bc	170.7 8 ab	100.6 7 ab	70.11 a	22.71 h	4.20 gh	5.43 fg
CV (%)	2.52	1.44	5.56	2.29	4.20	13.42	4.37	6.08	5.75	12.99	2.70	7.16	8.51
Standard error	1.37	1.16	4.39	4.83	7.24	5.19	0.89	6.70	5.39	2.12	0.59	0.32	0.4801
Mean value	66.57	98.96	96.64	258.2 2	210.8 9	47.33	25.08	134.9 3	114.9 2	20.02	26.78	5.50	6.91

DF= days to flowering, MD= maturity day, PH= plant height, ETM²= effective tiller per meter square, GP= grain panicle, EGP=effective grain panicle, THW= thousand grain weight, GY= grain yield.



3.2. Estimation of genetic parameters of rice genotypes

The genetic advance and genetic advance as a percent of mean, GA (%) for all the traits that contribute to yield are shown in Table 5 along with heritability, genotypic variances, phenotypic variances, genotypic co-efficient of variation (GCV), and phenotypic co-efficient of variation (PCV).

3.2.1. Variability parameters

Nine yield-contributing traits and yield both show a wide range of variation among 18 rice genotypes. Data analysis showed that variance is highly significant for all traits (Table 5). This implied that the genotypes varied genetically from one another. The genotypes showed significant genetic variation in a number of component traits, suggesting that these traits might be useful for further rice improvement. For all traits, phenotypic variance is higher than genotypic variance, indicating that environmental factors have an impact on these traits. Similar findings were reported earlier by Devi *et al.* (2006) and Prajapatiet *al.* (2011).

Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits (Table 5) indicating that they all interacted with the environment to some extent. Bhadrue *et al.* (2012) also mentioned the same result in rice. Among the all traits, high GCV and PCV were found for unfilled grain ⁻¹ (1048.95 and 1082.71%, respectively) followed by for grain⁻¹ (576.89 and 626.73%), non effective tiller (462.89 and 548.15%) and effective grain panicle⁻¹ (446.34 and 484.31%).

The high GCV and PCV values for these traits indicated the possibility of increasing yield by selecting for these traits. Low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation were observed for panicle length (9.88% and 14.67%), grain panicle-1 (576.89% and 626.73%), filled grain panicle-1 (446.34 and 484.31%), thousand grain yield ha⁻¹ (18.33 and 20.27%), and grain yield (36.18 and 38.90%). (PCV). Days to maturity estimates with low PCV and GCV have also been reported by (K. Rajendra Prasad, (2017)).

3.2.2. Heritability

The reliability of phenotypic value is expressed using heritability estimates as a predictive tool. High heritability therefore aids in efficient selection for a given trait. According to research, heritability is categorized as low (below 30%), medium (30-60%), and high (above 60%). (MA Islam, Analysis of genetic variability, heritability and genetic advance for yield, 2015).

The traits investigated in this study showed high heritabilities, with estimates ranging from 67.00 to 96.00 percent. Days to flowering and unfilled grain panicle-1 have the highest heritability among the traits (96.00%), followed by total tiller and days to maturity (95.00 and 94.00%, respectively).



The lowest heritability value was recorded by panicle length (67.00%), followed by thousand grain weight (90.00%), grain panicle (92.00%), and grain yield (92.00%), plant height (71.00%), effective tiller (89.00%), non-effective tiller (84.00%), straw weight (86.00%), and effective tiller (84.00%). (Table 5).

The presence of high heritability values suggests that the expression of the traits under study is less influenced by the external environment. Therefore, the plant breeder may safely make his selection by using straightforward selection methods based on the phenotypic expression of these traits in the particular plant. According to a study by Patel *et al.* (2012), the days to 50% flowering, total tillers, days to maturity, grain panicle-1, filled grain panicle-1, grain yield, and thousand grain weights had the highest heritabilities.

3.2.3. Genetic advance

A helpful indicator of the progress that can be anticipated as a result of applying selection to the relevant population is genetic advancement. A more accurate indicator of selection value would be provided by heritability in conjunction with genetic advancement (Johnson *et al.* 1955). In the current study, among yield-contributing traits, grain panicle genetic advance is highest (54.96), total tiller is second (51.67), and panicle length is lowest (2.63). (Table 5).

The unfilled grain panicle-1 has the highest genetic advance as a percentage of the mean (144.80%), while panicle length has the lowest genetic advance (10.48%) among the traits that affect yield. Additionally, the number of filled grains in panicle-1 and the highest genetic advance as a percentage of the mean for grain width were found by Babu *et al.* (2012).

If selection is used to improve the specific trait under study, knowledge of genetic variation, heritability, and genetic advance can be used to predict the genetic gain that may be attained in subsequent generations.

In general, additive gene action controls traits with high heritability and high genetic advance (Panse and Sukhatme, 1957). These traits can be improved using simple or progeny selection techniques.

It is likely that selection for traits with high heritability and genetic advance will accumulate more additive genes, further enhancing their performance. Days to flowering and unfilled grain panicle-1 are traits that are observed in the current study to have high heritability and high genetic advance. Other characteristics showed high or moderate heritability and moderate or low genetic advance, which can be enhanced by crossing superior genotypes of segregating populations created through combination breeding, as suggested by Samadia (2005).



Table 5: Estimation of genetic parameters of eighteen rice genotypes

Traits	(δ^2p)	(δ^2g)	PCV	GCV	H ² b %	GA	GA (%)
DF	80.87	78.06	121.48	117.26	96.	17.71	26.6
MD	39.52	37.31	39.73	37.7	94	12.1	12.22
PH	100.58	71.73	104.07	74.22	71	14.62	15.12
TT	702.63	667.61	272.1	258.54	95	51.67	20.01
ETM ²	746.29	667.72	353.87	316.62	89	49.97	23.69
NET ²	259.44	2.19.09	548.15	462.89	84	27.85	58.84
PL	3.68	2.48	14.67	9.88	67	2.63	10.48
GP ⁻¹	845.66	778.41	626.73	576.89	92	54.96	40.73
EGP ⁻¹	556.57	512.94	484.31	446.34	92	44.58	38.79
UFGP ⁻¹	216.76	210	1082.71	1048.9 5	96	28.99	144.8
THGW	5.43	4.91	20.27	18.33	90	4.31	16.01
GY	2.14	1.99	38.9	36.18	92	2.75	50.00
STW	2.48	2.14	35.89	30.96	86	2.77	40.08

Note: (δ^2p) = Genotypic variance, (δ^2g) = Phenotypic variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, H²b = Heritability,

GA= Genetic advance, GA (%) = Genetic advance as percent of mean.

DF= days to flowering, MD= maturity day, PH= plant height, TT= total tiller ETM⁻²= effective tiller m², NETM²= non effective tiller m², PL= panicle length GP= grain panicle, EGP=effective grain panicle, UFGP⁻¹= unfiled grain per panicle THW= thousand grain weight, GY= grain yield, STW= straw weight .



4. Discussion

4.1. Evaluation of performance of rice genotypes

4.1.1. Analysis of variance

Table 2 displays the analyses of variance of various advanced lines for morphological traits. In nine of the thirteen traits under study—days to flowering, days to maturity, plant height, effective tiller, panicle length, grain panicle, effective grain panicle-1, thousand grain yield, and grain yield per hectare—the difference between genotypes is highly significant, according to the analysis of variance. This suggests that all of these genotypes for these traits are variable.

4.1.2. Performance of the genotypes for yield and yield contributing traits

An excellent opportunity to identify and classify the genotypes according to various traits individually was provided by univariate statistical analysis. Table 4 displays the average traits performances of the 18 rice genotypes. The genotypes' days to 50% flowering varied from 55.33 to 83.00 days, with a mean value of 66.57 days. The genotype BRR1 dhan 51 has the highest number of days to 50% flowering, followed by BR 11, BRR1 dhan 79, and BIRRI dhan 52. The genotype BRR1 dhan 56 has the shortest days to 50% flowering, followed by BRR1 dhan 57, DRR 42, and BRR1 dhan 66.

Genotypes showed a wide range of days to maturity (92.00–109.00), with an average of 98.96 days. The genotypes DRR 46, BINA 7, and DRR 44 are followed by the genotypes BRR1 dhan 66, BRR1 dhan 56, and BRR1 dhan 57, which have shorter maturity periods (i.e., 92.00 days), indicating earliness. Under various agro-ecological conditions and breeding programs, variations in crop duration could be used directly.

The genotypes' average plant height was 96.64 cm, with genotypes ranging from 74.59 cm to 108.90 cm in height. The genotype DRR39 has the tallest plants (108.90 cm), followed by BRR1 dhan 52, BR11, and BIRRI dhan 66, and the genotype CSR43 has the shortest plants (74.59 cm). Rice plant height is a complex trait that results from a number of genetically controlled factors.(NABEELA ZAFAR, 2004). Reduction in plant height may improve their resistance to lodging and reduce substantial yield losses associated with this trait(Abbasi, 1995/01/01)).

The genotype BRR1 dhan 51 achieved the highest total tiller value (306.67), followed by BINA 7 and BRR1 dhan 52. By using BRR1 Dhan 71, the minimum value of 209.00 is obtained. Total's median value is 258.22.

The genotype BRR1 dhan 57, which is followed by BRR1 dhan 51 and BINA 7, has the highest effective tiller value (257.00), while genotype CSR 43, which is followed by DRR 42 BRR1 dhan 71, has the lowest effective tiller value (167.31). Effective tiller has a mean value of 210.89.



The highest non-effective tiller value (80.00) was found in CSR 43, and the lowest value (26.33) was found in BRR1 Dhan 57. The average non-productive tiller value was 47.33.

In terms of panicle length, genotype DRR 39 recorded the highest value (29.86 cm). It showed a respectable amount of variation, ranging from 21.71 cm to 29.86 cm, with a 25.08 cm average. The genotype CSR 43 panicle had the shortest length (21.71 cm).

The genotypes' grain panicle-1 measurements ranged from 80.22 cm to 184.11 cm, with 134.93 cm serving as the mean. The genotype DRR 39, which is followed by BR 11 and BRR1 dhan 71, had the highest grain width measurement (184.11 cm), while genotype CSR 43, which is followed by BINA 7 and DRR 42, had the lowest grain panicle measurement (80.22 cm).

The range of variation for the number of filled grains panicle-1 was high, ranging from 65.67 to 153.22, with a mean value of 114.92. The genotype DRR 39 had the most filled grains per panicle, followed by BRR1 dhan 66, BR 11, and BRR1 dhan 78, while genotype DRR 42 had the fewest filled grains per panicle, followed by CR dhan 405, BINA 7, and DRR 42. This could be used in future programs as having more filled grains per panicle is one of the key factors that contribute to higher grain yield.

Unfilled grain panicle -1 has a maximum value of 70.11, which was discovered by BRR1 dhan 71, followed by DRR 39 and BRR 1, and a minimum value of 6.56, which was discovered by DRR 42. Unfilled grain panicle-1 had a mean value of 20.02.

The weight of a thousand grains varied from 22.71g to 31.61g, with a mean of 26.78g. The genotype CSR 43 showed the highest value of thousand grain weight (31.61g), which was followed by BRR1 dhan 51 and BINA 11, while genotype BRR1 dhan71 showed the lowest value of thousand grain weight (22.71g), which was followed by BRR1 dhan 57 and BRR1 dhan 78.

Grain yield at its highest point (t ha⁻¹), 7.97 g, was recorded for genotype BRR1 dhan 51. It had a respectable range of variation between 3.40 g and 7.97 g, with an average of 5.50 g. The genotype CR dhan 405 had the shortest panicle length (3.40 g).

The lowest value was (4.60 g) obtained from DRR 42 followed by CR dhan405 and CSR 43, and the highest value straw weight was (9.73) obtained from BRR1 dhan51, followed by BRR1 dhan79, and BRR1 dhan 66. The average weight of a straw is 6.91g.



4.2. Estimation of genetic parameters of rice genotypes

The genetic advance and genetic advance as a percent of mean, GA (%) for all the traits that contribute to yield are shown in Table 5 along with heritability, genotypic variances, phenotypic variances, genotypic co-efficient of variation (GCV), and phenotypic co-efficient of variation (PCV).

4.2.1. Variability parameters

Nine yield-contributing traits and yield both show a wide range of variation among 18 rice genotypes. Data analysis showed that variance is highly significant for all traits (Table 5). This implied that the genotypes varied genetically from one another. The genotypes showed significant genetic variation in a number of component traits, suggesting that these traits might be useful for further rice improvement.

For all traits, phenotypic variance is higher than genotypic variance, indicating that environmental factors have an impact on these traits. Similar results were previously reported by Prajapatiet al. and Devi et al. (2006). (2011). According to the study on coefficients of variation, all of the traits had phenotypic coefficients of variation (PCV) that were higher than the corresponding genotypic coefficients of variation (GCV) (Table 5), indicating that all of the traits had some degree of environmental interaction. The same outcome in rice was mentioned by Bhadrueet al. (2012).

Unfilled grain 1 (1048.95 and 1082.71%, respectively) had the highest GCV and PCV of all the traits, followed by grain-1 (576.89 and 626.73%), non-effective tiller (462.89 and 548.15%), and effective grain panicle-1 (446.34 and 484.31%). The high GCV and PCV values for these traits indicated the possibility of increasing yield by selecting for these traits. Low genotypic coefficient of variation (GCV) and phenotypic coefficient of variation were observed for panicle length (9.88% and 14.67%), grain panicle-1 (576.89% and 626.73%), filled grain panicle-1 (446.34 and 484.31%), thousand grain yield ha-1 (18.33 and 20.27%), and grain yield (36.18 and 38.90%). (PCV). Days to maturity estimates with low PCV and GCV have also been reported by(K. Rajendra Prasad, (2017)).

4.2.2. Heritability

The reliability of phenotypic value is expressed using heritability estimates as a predictive tool. High heritability therefore aids in efficient selection for a given trait. According to research, heritability is categorized as low (below 30%), medium (30-60%), and high (above 60%). (MA Islam, Analysis of genetic variability, heritability and genetic advance for yield, 2015). The traits investigated in this study showed high heritabilities, with estimates ranging from 67.00 to 96.00 percent. Days to flowering and unfilled grain panicle-1 have the highest heritability among the traits (96.00%), followed by total tiller and days to maturity (95.00 and 94.00%, respectively), thousand grain weight (90.00%), grain panicle (92.00%) and grain yield (92.00%), plant height (71.00%), effective tiller (89.00%), non-effective tiller (84.00%), and straw weight. (86.00%) and



Panicle length had the lowest heritability percentage (67.00%). (Table 5). The presence of high heritability values suggests that the expression of the traits under study is less influenced by the external environment. Therefore, the plant breeder may safely make his selection by using straightforward selection methods based on the phenotypic expression of these traits in the particular plant. According to a study by Patel et al. (2012), the days to 50% flowering, total tillers, days to maturity, grain panicle-1, filled grain panicle-1, grain yield, and thousand grain weights had the highest heritabilities.

4.2.3. Genetic advance

A helpful indicator of the progress that can be anticipated as a result of applying selection to the relevant population is genetic advancement. A more accurate indicator of selection value would be provided by heritability in conjunction with genetic advancement (Johnson et al. 1955). In the current study, among yield-contributing traits, grain panicle genetic advance is highest (54.96), total tiller is second (51.67), and panicle length is lowest (2.63). (Table 5).

The unfilled grain panicle-1 has the highest genetic advance as a percentage of the mean (144.80%), while panicle length has the lowest genetic advance (10.48%) among the traits that affect yield. Additionally, the number of filled grains in panicle-1 and the highest genetic advance as a percentage of the mean for grain width were found by Babu et al. (2012).

If selection is used to improve the specific trait under study, knowledge of genetic variation, heritability, and genetic advance can be used to predict the genetic gain that may be attained in subsequent generations.

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It is likely that selection for traits with high heritability and genetic advance will accumulate more additive genes, further enhancing their performance. Days to flowering and unfilled grain panicle-1 are traits that are observed in the current study to have high heritability and high genetic advance.

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5. Conclusion

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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