

**GENETIC VARIABILITY AND CHARACTER ASSOCIATION OF
YIELD AND YIELD CONTRIBUTING TRAITS IN BORO RICE
(*Oryza sativa* L.)**

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YIELD AND YIELD CONTRIBUTING TRAITS IN BORO RICE**

(Oryza sativa L.)

By

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A Thesis

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CERTIFICATE

This is to certify that the thesis entitled '*Genetic variability and character association of yield and yield contributing traits in Boro rice (*Oryza sativa* L.)*' submitted to the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **Master of Science in Genetics and Plant Breeding**, embodies the result of a piece of bona fide research work carried out by **Tanjina Islam**, Registration number: **15-06383** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that any help or source of information, received during the course of this investigation has duly been acknowledged.

Dated: June, 2022
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TO

MY BELOVED PARENTS

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LISTS OF SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviation
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
Food and Agricultural Organization	FAO
Bangladesh Agricultural Research Institute	BARI
Bangladesh Agricultural University	BAU
Bangladesh Institute of Nuclear Agriculture	BINA
Centimeter	Cm
Degree	$^{\circ}\text{C}$
Co-efficient of variation	CV
Days after sowing	DAS
Degrees of Freedom	Df
Environmental variance	σ_e^2
And others	et al.
At the rate	@
Et cetera	etc.
Mean sum of square	MS
Heritability in broad sense	h^2_b
Genetic Advance	GA
Genotypic correlation	r_g
Genotypic variance	σ_g^2
Genotypic Co-efficient of variation	GCV
Gram	G
Kilogram	Kg
Meter	M
Milliliter	mL
Metric ton	MT
Triple Super Phosphate	TSP
Muriate of Potash	MOP
Number	No.
Percent	(%)
Percentage of Co-efficient of Variation	CV%
Phenotypic variances	σ_p^2
Phenotypic Co-efficient of variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Species	<i>sp.</i>
Square meter	m^2
Standard error	SE

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ABSTRACT

Twenty three Boro rice genotypes were used in this experiment to evaluate the variability, heritability, genetic advance in percent of mean, correlation of co-efficient and path analysis. The present experiment was laid on randomized complete block design in the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 with three replications. Analysis of variance revealed that; mean sum of square of genotype was recorded highly significant for all the studied characters. PCV were noted greater than the GCV for all the observed traits. The highest value of PCV and GCV were found for number of unfilled grains per tiller 48.90% and 47.72% respectively. High heritability associated with high genetic advance in percent of mean were found for leaf sheath length, number of unfilled grains per tiller, number of primary branches per panicle, panicle length, and thousand seed weight. Through the correlation co-efficient analysis, it was observed that, yield per plant had significant positive association with number of effective tillers ($P= 0.535$), number of total tiller ($G= 0.461$), number of filled grain per tiller ($G= 0.504$, $P= 0.379$), number of unfilled grains per tiller ($G= 0.604$, $P= 0.365$), number of secondary branches per panicle ($G= 0.388$), and thousand seeds weight ($G= 0.821$, $P= 0.673$). Path analysis exhibited that, leaf blade (1.733), stem length (1.338), number of effective tillers, number of unfilled grains per tiller (4.413), number of primary branches per panicle (16.909), number of secondary branches per panicle (0.698), panicle length (16.929) was recorded to show positive and direct effect on yield per plant. From this observation, it was found that G20 (BRRI dhan96) gave early flowering with maximum number of filled grain and maximum yield per plant, G1 (BR1) was found to produce maximum number of effective tillers, G3 (BR5) was found to give highest number of total tillers, and G5 (BR14) exhibited maximum weight for thousand seeds. So, these genotypes of Boro rice could be used for future breeding programs.

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.), which is locally known as “Dhan” in Bangladesh, is the principal staple crop of Asia including Bangladesh. It is self-pollinated, monocotyle and its chromosome number is $2n = 24$. It belongs to the Gramineae family and subfamily *Oryzoidea* under the genus *Oryza* and order Cyperales (Hooker, 1979). The genus *Oryza* has twenty-five species, twenty three of them are wild species and other two namely viz., *O. glaberrima* and *O. sativa* are cultivated species (Brar and Khush, 2003). Among these two, *O. sativa* is cultivated all around the world, while *O. glaberrima* has been produced in the West Africa for the last ~3500 years (IRRI, 2001). Rice can survive as perennial crop and able to produce ratoon crops for up to 30 years, but it is cultivated as annual crop. It is the only cereal crop that are grown for the longest periods under standing water (IYR, 2004). Approximately 57% of the rice is cultivated in the irrigated land; almost 25% in the rainfed lowland, upland includes 10% of rice, 6% in the deep water, and only 2% of rice in the tidal wetland (Chopra and Prakash, 2002).

Rice is believed to originate in Asia. Although it is produced all through the world, there are four type rice that are now-a-days grown worldwide namely viz., Indica, Aromatic, Japonica, and Glutinous and other specialty rices. Among them Indica is mostly grown in the tropical and sub-tropical areas such as South Asia and Southeast Asia, and placing at the of global rice trade, which is 70-72%. The aromatic rice like Basmati rice and Jasmine rice is mostly cultivated in Thailand, Cambodia, Vietnam, Pakistan, and India. Whereas, Japonica is grown well in the cooler climate, so Korea, Japan, some parts of China, Europe, California, and Australia primarily cultivate it. Southeast Asia grows the glutinous rice (USDA, 2022).

Rice is grown under the diverse cultural situations and over wide ranges of geographical conditions. Asia produces and consumes most of the world’s rice. About 11% of world’s cultivable land is used for annual rice production and ranked next to wheat In Bangladesh, rice is the main staple food of almost 135 million people (Chakravarthi and Naravaneni, 2006). It provides employment to rural people about

48%. Rice sector contributes one-sixth of the national income and one-half of the agricultural GDP is contributed by rice sector in Bangladesh. Here, almost 13 million farm families grow rice. Approximately 75% of the cropped area and more than 80 % of the total irrigated land is under rice cultivation. Thus, a vital role is played by rice in the livelihood of the Bangladeshi people (BRKB, 2012). In 2021, total production of rice was 518.8 million tones and area under it was around 165.25 million hectares all through the world (FAO, 2022). Bangladesh placing third in rice production and in 2021, the production was about 35.5-million tonnes on 11.42 million hectares (BBS, 2022).

Rice is a good source of nutrients and energy. Rice (brown or white) contain mainly carbohydrate, almost 80 % of its total dry weight and some sort of proteins with no fat. Cooked rice contains huge amount of water which is almost 70% of total weight. Rice is a good source of energy, from 100 g of rice one can get 130 calories, 28.7 g of carbohydrate, and protein 2.36 g fiber 1.6 g. Basmati rice is high in amylose, so that after cooking it doesn't stick together; whereas glutinous rice or sticky rice is rich in amylopectin and low in amylose. Brown rice contains more nutrients than white rice and it's good for diabetic people. Brown rice is also containing some minerals, antioxidants, lignans and dietary fiber which are good for heart health (Kathy and Anderson, 2022). Rice helps to maintain optimum weight and protects against chronic disease.

Rice is grown in temperate and tropical countries over the wide ranges of climatic and soil condition. In Bangladesh, it is cultivated under the diverse condition viz., deep water, irrigated and rain fed in three different seasons namely, Aus, Aman and Boro (Rashid, 1994). Here, Boro season covers the maximum area than the other two. So, it is important to improve some Boro rice varieties which will fit our desire characters and satisfy the food demand.

Various qualitative and quantitative characters contribute to the yield of crops. These contributing traits are interrelated to each other and they exhibited different results because of their complex interrelationship. The expression of them also highly influenced by the environmental conditions (Prasad *et al.*2001). The existence of genetic variability in a population is the pre-requisite of a breeding program. To make a breeding program more efficient, knowledge of genotypic and phenotypic co-

efficient of variation and heritability with genetic advance among the genotypes for desirable character is essential (Mishra *et al.*1988). Evaluation of heritability is vital for the selection-based improvement, as it suggests the transmissibility of a trait into future generations (Sabesan *et al.*2009). High heritability in a relationship with high genetic advance as a percent of mean is very helpful in predicting the suitable trait for selection (Thomas and Lal, 2012). Estimated data from the analysis of correlation indicates the contribution of the characters toward the final production (panse and Maurya, 1992). Evaluation of path represents the direct and indirect effects of the traits. Thus, these measurement helps to identify the best characters for selection criteria for the improvement of yield (Mustafa and Elsheikh, 2007; Akinwale *et al.* 2011).

Therefore, following objectives were undertaken in this experiment:

1. To evaluate the genetic variability among the twenty three genotypes of Boro rice,
2. To study the contribution of the yield related characters on yield of the twenty three genotypes of Boro rice, and
3. To measure the direct and indirect effects of yield and yield contributing traits of twenty three Boro rice genotypes.

CHAPTER II

REVIEW OF LITERATURE

2.1 Variability, heritability and genetic advance

Vennila *et al.*(2022) conducted a study to investigate the variability in thirty-three rice germplasm lines for quantitative traits. Analysis of variance revealed extremely significant differences for all eight characters, indicating the presence of genetic variability among the studied genotypes. High PCV and GCV were found for traits such as grain yield per plant (39.83%), plant height (34.00%), 1000 grain weight (22.59%), and days to 50% flowering (21.77%), indicating a smaller environmental influence on trait expression, implying that genetic improvement through direct selection is possible for these traits. High heritability associated with genetic advancement suggests the influence of additive gene actions, and selection would be effective in such characters as 1000 grain weight (99.38%), plant height (97.24%), days to 50% flowering (95.24%), grain yield (87.65%), total number of tillers per plant (86.55%), and productive tillers per plant (73.42%).

Singh *et al.*(2021) conducted an experiment with fifty advanced breeding lines along with five checks for eleven yield and nineteen quality traits for estimating genetic variability, heritability and genetic advance was studied in during Kharif 2020. They found significant variations among all the advanced breeding lines for all the yield and quality characters, suggesting presence of significant amount of variance. High value for GCV and PCV were observed in number of unfilled grains/panicle (49.20), amylose% (30.36), alkali spreading value (32.24), gel consistency (27.05), grain yield/plant (g) (22.40), number of filled grains/panicle (24.48), head rice recovery % (22.20), biological yield per plant (g) (20.53) and harvest index % (19.16). High estimates for genetic advance as % of mean associated with high heritability were number of filled grains per panicle, number of unfilled grains per panicle, biological yield/plant (g), 100 seed weight (g), grain yield per plant (g), paddy L: B ratio, amylose percent, kernel breadth (mm), brown rice L: B ratio, gel consistency, cooked rice L: B ratio, alkali spreading value and head rice recovery percent was found by them.

Yashwanth *et al.*(2021) evaluated forty-four rice genotypes which includes 40 advanced breeding lines and four check varieties to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as per cent of mean for 15 quantitative characters in randomized block design. High phenotypic and genotypic co-efficient of variation were noted for the traits viz., number of chaffy grains per panicle, grain yield per plant, number of filled grains per plant, harvest index, 100 grain weight (g) and biological yield per plant indicating the presence of large amount of variation among the genotypes for studied characters. High heritability along with high genetic advance in per cent of mean was observed for number of chaffy grains per panicle, grain yield per plant, number of filled grains per panicle, 100 grain weight (g), harvest index, biological yield per plant, plant height (cm), number of panicles per plant, days to maturity and days to 50% flowering, indicating that these characters were controlled by additive gene effects and may be chosen as selection criteria for further breeding strategies in rice

In 2021, Limbongan *et al.* had an experiment for estimating genetic diversity, heritability, and genetic advance on specific agronomic characters of cross-breed red rice genotypes (Toraja red rice Pare Lea' x Inpari-4). It was conducted in RCBD design in Tallunglipu, North Toraja, South Sulawesi, Indonesia. Results exhibited existence of a considerably high level of diversity among studied genotypes, where the highest value for genetic advance was recorded in filled-grain weight per hill of F2 plants, followed by plant height (cm), and filled-grain weight per hill of F1 (g). The maximum estimate of broad-sense heritability was noted in 1000-grain weight (g), number of productive tillers, plant height (cm), flag leaf length (cm), filled-grain weight per hill (g), and harvest age. Genetic advance of agronomic characters between genotypes varied from 1.631-38%, where the highest estimate was found in filled-grain weight per hill (38%) and plant height (24.648%). The above-mentioned characters could be used for selection in further breeding programs of rice to obtain plants with superior genotypes.

Hoque *et al.*(2021) evaluated eight rice genotypes for grain length, grain width, grain length width ratio, 1000 grain weight, grain thickness, seed germination percent, root length, shoot length and root shoot ratio. The genetic variance, phenotypic variance, phenotypic covariance (PCV), genotypic co-efficient of variation (GCV), heritability,

genetic advance (GA), genetic advance in percent of mean and correlation co-efficient were evaluated. For all of the studied characters, analysis of variance showed a significant difference in genotypes. PCV values greater than GCV were recorded in all of the characteristics, indicating that the influence of non-additive gene action rather than environmental factors and that selection for improving these traits would be effective. The PCV and GCV estimated for the root shoot ratio were both high, indicating a wide range of variability for the two characteristics, shoot length and root length. PCV and GCV values were found moderate for grain length width ratio, seed germination percent, shoot length, and root length. The PCV and GCV were found low for most of the characters. High heritability, ranging from 90.77% to 99.81% was observed for all traits except for 1000 grain weight (g). Seed germination percent, shoot length, root length and root shoot ratio all had high heritability and high genetic advance in percent of mean. Grain thickness and seed germination percent had the lowest GA%.

In 2018, Sandeep *et al.* conducted an experimental at Indian Institute of Rice Research Farm, India, during Boro, 2014-2015, to estimate genetic variability, heritability and genetic advance in two hundred genotypes of rice. ANOVA revealed highly significant differences for all the characters among the genotypes, indicating variability existed in the selected material for the study. Environmental effect was very meagre on the expression of all the traits as there is a low difference between genotypic and phenotypic co-efficient of variation. A genotypic and phenotypic co-efficient of variability was high for single plant yield (g), number of tillers per hill, number of grains per panicle, pollen viability and spikelet fertility. The characters viz., spikelet fertility, plant height (cm), single plant yield (g), number of grains per panicle, number of tillers per hill, pollen viability, number of productive tillers per hill, panicle length and 1000 grain weight (g) showed high heritability estimates combined with high genetic advance as per cent of mean which suggested that these traits were amenable for further improvement by simple selection methods.

Kishore *et al.* (2018) studied thirteen quantitative traits in twenty rice genotypes for the evaluation of significant difference for all the quantitative traits was observed among the genotypes. They found phenotypic co-efficient of variation (PCV) higher than genotypic co-efficient of variation (GCV) for all the characters, reflected the

influence of environmental factors on these traits. The characters fertile spikelets per panicles, yield per plant, test weight, harvest index, biological yield per plant and flag leaf width exhibited greater influence of environment and reflecting scope of improvement of these characters. Plant height, effective tillers per plant, test weight, flag leaf length, and biological yield per plant expressed high estimates of heritability along with genetic advance indicating the additive genetic components and can be used for selection in segregating generations.

Singh and Verma (2018) carried out an investigation during Kharif season with twenty-two parents (19 lines and 3 testers) along with fifty-seven F1 hybrid grown in Randomized Block Design with three replications to evaluate variability, heritability and genetic advance. Total fifteen quantitative characters viz., days to 50 % flowering, plant height, flag leaf area, panicle bearing tillers per plant, panicle length, spikelets per panicle, grains per panicle, spikelet fertility (%), L:B ratio, biological yield per plant, harvest index (%), 1000-grains weight, Kernel width, Kernel length, and grain yield per plant were used for evaluation under salt affected soil. Analysis of variance revealed the existence of significant genotypic differences among the parents of rice and their hybrids for the yield, its components for all the traits. High value of GCV and PCV were found for flag leaf area and panicle bearing tillers per plant. High heritability coupled with high genetic advance (% mean) was observed for flag leaf area, grains per panicle, spikelet per panicle, panicle bearing tillers per plant, and plant height which indicated that these traits were controlled by additive type of gene action.

Prasad *et al.* (2017) examined fifty Boro rice genotypes to estimate variability, heritability and genetic advance in yield and yield contributing traits at Hyderabad, India, during Rabi 2013-14. Analysis of variance exhibited the existence of significant genotypic differences among the genotypes for all the characters. High GCV and PCV values were recorded for number of filled grains per panicle, number of unfilled grains per panicle, grain yield per plant. High heritability associated with high genetic advance as per cent of mean was observed for plant height (cm), number of tillers per plant, number of filled grains per panicle, number of productive tillers per plant, 1000- grain weight, number of unfilled grains per panicle, and grain yield per plant which suggested that these traits were governed by additive type of gene action. The

remaining characters were mostly under the influence of non-additive gene effects as they were found to express low to moderate estimates of genetic advance. It was concluded that variation exists in the germplasm and this provides the opportunities for this collection to be useful for genetic improvement.

Yadav *et al.*(2017) carried out an experiment with thirty-five diverse genotypes of rice with two checks for twelve quantitative traits under sodic soil. The variability analysis indicated that high PCV (phenotypic co-efficient of variability) and GCV (genotypic co-efficient of variability) was recorded in case of biological yield per plant indicating greater scope of improvement through simple selection in the environment. Moderate PCV and GCV was found in case of plant height (PCV =18.80%, GCV =18.52%), grain yield per plant (18.67%, 18.15%) effective tillers per plant and flag leaf area (PCV =17.47%, GCV = 14.07%). While spikelets/panicle followed by 1000 grain weight, days to 50% flowering, harvest index, days to maturity, panicle length and spikelet fertility (%) showed lower PCV and GCV. High broad sense heritability was noted for plant height followed by days to 50% flowering, days to maturity, grain yield per plant, biological yield per plant, 1000-grain weight, and spikelet per panicle whereas, spikelet fertility, flag leaf area per plant, and harvest index showed moderate heritability. Panicle length and effective tillers per plant recorded low heritability among all the traits under study. While high genetic advance as percent of mean was noticed for biological yield per plant, panicle length had smallest value for this parameter. High heritability along with high genetic advance as % of mean was observed for plant height and grain yield/ plant indicating the involvement of additive gene action. Hence, emphasis should be given to select these quantitative characters to enhance the yield potential of rice in sodic soil.

Das *et al.*(2015) conducted an experiment to estimate genetic variability for twenty-one morpho-physiological characters in thirty rice (*Oryza sativa* L.) genotypes during Boro season 2012- 13. Highly significant variation was recorded among the genotypes for all the traits. The genotypes namely Kala Boro, Boro 1, and Tepi Boro were noticed tolerant to low temperature at seedling stage. The mean yield performance of the genotypes exhibited that Dinanath (36.1 g/plant) had significant superiority over all other genotypes, followed by Joymoti (30.0 g), IR-62266-42-6-2 (29.1 g), and Jhum Kamrung (28.5 g). The highest estimates of PCV and GCV were noted for grain

yield per plant (46.6%, 41.3%), booting to heading duration (41.0%, 35.8%), followed by grains per panicle (44.6%, 40.7 %), effective tillers (38.7%, 32.3%), and biological yield (35.0%, 28.1%). High heritability combined with high genetic advance was recorded for seedling emergence (97.3%, 71.2%), seedling vigor index (91.8%, 70.7%), seedling establishment (96.4%, 67.7%), and grains per panicle (83.4%, 76.6%) indicating the preponderance of additive gene action for these traits. The results of the present investigation provide evidence for the presence of exploitable level of genetic variability for important adaptive characters like seedling emergence, grains per panicle, seedling vigor index, and grain yield in the Boro season.

Sharma *et al.* (2014) carried out an investigation on one hundred and twenty genotypes of Rice to examine the nature and magnitude of genetic variability during the Kharif season of 2012-13. Analysis of variance exhibited that there was maximum amount of variability present in the genotypes for all the traits because mean sums of squares were highly significant. High estimates of heritability and genetic advance were found for culm length (cm), plant height (cm), total number of filled spikelet's per panicle, total number of spikelets per panicle, ligule length (cm), plant weight (g), biological yield (g), spikelet density, leaf width (cm), panicle weight (g), grain yield (kg), 1000 seed weight (g), total number of tillers per plant, total number of productive tillers per plant, and single panicle weight (g). It indicates that heritability was because of additive gene effects and the direct selection of these characters may be effective. High heritability with medium genetic advance was found for Flag leaf width (cm), flag leaf length (cm), seed width and harvest index, whereas high heritability with low genetic advance was observed for, panicle length (cm), spikelet fertility, seed length (cm), days to 50% flowering and days to maturity. It is indicative of non-additive gene effect. The high heritability is being exhibited due to influence of environment.

Rahman *et al.* (2012) evaluated ten physiological characters along with yield in T. Aman season 2008. ANOVA revealed significant differences among the genotypes for all the characters. Flag leaf area, CGR at flowering, LAI at flowering, RGR at flowering, NAR at flowering, and harvest index showed that they were governed by additive gene action, so that selection for the improvement of these characters would be rewarding. Genotypic co-efficient of variation and phenotypic co-efficient of variation was found the highest for NAR at flowering (41.21 and 45.75, respectively),

followed by CGR at flowering and the lowest for panicle exertion rate (3.75 and 4.05, respectively). Growth duration exhibited the highest heritability (98.97), followed by days to flowering (98.00) and flag leaf area (92.29). The highest genetic advance was found for NAR at flowering and the lowest for panicle exertion rate.

In 2010, Yadav *et al.* did a field experiment to evaluate the association between yields and yield relevant components and others traits in Boro rice. They reported high heritability associated with high to moderate genetic advance as (% mean) on plant height, biological yield, seed yield per plant, test weight, harvest index, and number of spikelets per panicle; indicating existence of additive gene action in the expression of these parameters.

Jayasudha *et al.* (2010) conducted a study on forty-seven rice genotypes and found that high genotypic as well as phenotypic co-efficient of variation for grain yield per plant, pollen fertility, harvest index, and spikelet fertility. Characters like pollen fertility, spikelet fertility, days to 50% flowering, and grain yield per plant exhibited high value of heritability along with high genetic advance in percent of mean.

2. 2 Analysis of Correlation of co-efficient

In 2022, Vennila *et al.* evaluated thirty-three genotypes and found plant height (cm), number of grains per panicle, number of productive tillers per plant, and thousand grain weights (g) positively correlated with grain yield per plant (kg). Grain yield per plant was directly affected by characters such as 1000 grain weight (g) and the number of productive tillers per plant.

Hoque *et al.* (2021) estimated variability and relationship of eight rice genotypes among the yield and yield contributing traits. Grain length with grain length width ratio, 1000 grain weight with grain width, grain width with root shoot ratio, root shoot ratio, grain thickness, and root length were found to have positive and significant correlations in a character association study. At the genotypic level, the maximum positive significant correlation was observed between 1000 grain weight and root shoot ratio ($r_g = 0.908$) and grain length and grain width ratio ($r_p = 0.900$). According to genetic variability and correlation analysis, grain length, grain length width ratio, 1000 grain weight, root length and root shoot ratio could be used as selection indices for further improvement of seed and seedling characters of rice genotypes.

Singh *et al.*(2021) conducted a study with eighty rice genotypes during Kharif season to assess the variability and trait associations in a crop helps to enhance selection. For all of the traits studied, the results revealed significant variance in all the genotypes. PCV was found to be slightly more than the corresponding GCV for all the characters, indicating the role of environment in the expression of these traits. However, high GCV and high PCV were found for number of effective tillers/ plant, grain yield per plot, number of filled grains/ panicle, number of unfilled grains per panicle, biomass yield, harvest index, grain yield per plant and grain yield per hectare. Furthermore, high heritability and high genetic progress as a percentage of mean was observed for all the traits, with the exception of days to days to maturity, 50% blooming, and kernel breadth. Days to first flowering, days to maturity, days to 50% flowering, spikelet fertility percentage, number of filled grains per panicle, harvest index, and kernel length showed highly significant and positive association with grain yield per plot. Highest direct contribution to grain yield per plot was found by kernel length, harvest index and spikelet fertility percent. Days to first flowering, number of effective tillers, days to maturity, number of unfilled grains per panicle, test weight, biomass yield were also found to exert a positive effect on yield. Thus it can be considered as desirable traits for selection high yielding genotypes.

Bagudam *et al.*(2018) conducted an experiment to analysis the association between yield and its component traits by using forty-six rice genotypes including tropical japonica accessions, indica land races and elite indica cultivars. The data was observed for twelve quantitative traits viz., plant height, days to 50% flowering, number of tillers, panicle length, number of panicles, panicle weight, grain number, single plant yield, test weight, plot yield, biomass, and harvest index. Correlation studies expressed highly significant positive association of yield per plant with days to 50% flowering, productive tillers per plant, tillers per plant, and biomass, that indicating, these characters are very important for yield improvement and selection will directly lead to high yield.

Panigrahi *et al.*(2018) carried out an experiment to find out the genetic variability, heritability, genetic advance and character association among the genotypes homozygous dominant for gall midge resistance genes G1 and G4 in the genetic background of ADT 38 variety of rice in advanced backcrossed (BC1F5) generation

of rice. The Phenotypic co-efficient of variation (PCV) was slightly higher than the genotypic co-efficient of variation (GCV) for all the studied traits. High heritability coupled with high genetic advance as percent of mean was found for character like hundred grains weight. Highly significant and positive correlation with single plant yield was expressed by traits like number of tillers, number of productive tillers, and number of filled grain per panicle. Positive direct effect was showed by number of tillers, number of filled grains per panicle, and hundred grain weights towards single plant yield. These characters will be useful for further breeding.

Islam *et al.*(2018) conducted a study with forty Boro rice germplasm to estimate the extent of genetic variability and relation between yield and related traits of rice. Analysis of variance revealed significant differences among the genotypes for the fourteen quantitative characters. The presence of slightly higher PCV than GCV are suggesting the negligible effect of environment on the expression these traits. Days to flowering, leaf length, days to maturity, and 1000 grain weight exhibited highly positive significant correlation with yield per hill. High heritability had been recorded for yield contributing characters during the study, indicating that these characters would respond to selection to their high genetic variability and transmissibility. Therefore, a thorough understanding of the inheritance of characters, their heritability and relationship with other characteristics is important for the selection of breeding and selection methods for crop improvement

Sudeepthi *et al.*(2017) carried out an investigation in rice to evaluate the characters association and direct or indirect effects of them on yield by using thirty-three genotypes. They found that the genotypic correlations were generally higher than the phenotypic correlations and thus, suggested that the observed relationships among the traits were due to genetic factors. Grain yield per plant showed significant positive association with days to 50% flowering, plant height, days to maturity, number of productive tillers per plant, and number of filled grains per panicle; while, non-significant and positive association with panicle length and test weight.

Guru *et al.*(2016) carried out a research work with fifty-eight rice germplasm lines including twenty indica genotypes, twenty-five tropical japonica varieties and thirteen hybrid genotypes for eleven qualitative characters. Through the correlation analysis they observed highly significant positive association of total dry matter at flowering

and harvesting stage, panicle length, panicle number, panicle weight, number of filled grains per panicle, number of grains per panicle, grain filling, and harvest index with grain yield per plant.

Das and Sarma (2015) carried out an experiment with thirty rice genotypes of local and exotic origin to ascertain the genotypic and phenotypic correlation among 21 morpho-physiological and yield characters and their direct or indirect contributions to grain yield. The result showed that yield per plant had significant positive correlation with harvest index (0.748**, 0.658**), biological yield (0.927**, 0.766**), days to first flowering (0.459*, 0.377*), grains per panicle (0.576**, 0.484**), panicle length (0.501**, 0.445*), and 1000 grain weight (0.573**, 0.460*) at both genotypic and phenotypic levels.

Moosavi *et al.*(2015) carried out an investigation to find out relationships of morphological and physiological characters and association of these traits with yield by using thirty breeding line of rice in order to breeding of rice genotypes that can be tolerant to warm conditions in Khuzestan. CRBD design was used for this experiment. Correlation analysis revealed that the correlation between grain yield/ plant and number of panicles ($r = 0.55$) was the highest. Stepwise regression for yield as dependent variable (Y) and other characters as independent variables (X) exhibited that panicle number, dry weight, harvest index and panicle length were able to explain a large quantity of the variance ($R^2 = 0.65$). Due to high levels of direct effects of harvest index and number of panicles and also significant correlation between these characters with grain yield per plant, these characters can be used as indicators for indirect selection.

Rahman *et al.*(2014) evaluated twenty-one rice varieties for thirteen morphological characters during T. Aman season. Analysis of variance expressed the significant differences among the genotypes for all the traits. Plant height, number of spikelets per panicle, number of effective tillers per square meter, number of effective spikelets per panicle, 1000 grains weight, number of ineffective spikelets per panicle, straw yield and grain yield showed that they were governed by additive gene action and selection for the improvement of these characters would be productive. The phenotypic variance was slightly higher than the corresponding genotypic variance for all the parameters. All the characters showed moderate-low phenotypic and genotypic

co-efficient of variation. Genotypic co-efficient of variation was found the highest for number of ineffective spikelets per panicle (39.96), followed by 1000 grains weight (24.33) and number of spikelets per panicle (18.61). Plant height and 1000 grains weight (95.30) had the highest heritability.

2.3 Analysis of Path co-efficient

Islam *et al.*(2021) carried out a study to evaluate the correlation co-efficient, path analysis, direct and indirect effects of ten popular upland rice genotypes to determine nature of relation between the grain yield with the other yield contributing traits. They noticed that, plant height, panicle length, effective tiller, panicle number, flag leaf width, flag leaf length, harvest index, filled grain, unfilled grain, seed fertility, seed length, and seed width was found positively significant and phenotypically correlated with the grain yield per genotypes. Path analysis revealed that plant height, effective tiller, panicle number, panicle length, internode length, and filled grain showed the positive direct effect on grain yield. Among these parameters, filled grain, seed width, seed fertility, panicle number, and effective tiller possessed high positive and direct effects. Thus, selection of these characters like can bring improvement to the yield performance of upland rice.

Chakrabarty *et al.*(2019) conducted a study to assess the genetic variations in yield and yield contributing traits, their associations and also direct and indirect effects on yield. They observed the following parameters viz., number of effective tillers, filled grains per panicle, unfilled grains per panicle, harvest index, days to maturity, and grain yield. Traits association analysis revealed that the days to flowering, days to maturity, and filled grain/panicle could significantly improve the rice germplasm. Path analysis estimated that the direct selection based on the days to flowering, days to maturity, and filled grain per panicle would be important for improvement of rice germplasm. G5 had highest yield combined with filled grain/ plant, harvest index and 1000 grain weight and it could be used as potential variety for the improvement of yield. The germplasm G7, G19, G9 and G33 could be used in the further breeding program.

Islam *et al.*(2019) investigated twenty nine Boro rice genotypes with fourteen agromorphological traits. They found that, analysis of variance expressed the significant

differences among the restorer lines for all the traits. The phenotypic co-efficient of variation (PCV) was slightly higher than genotypic co-efficient of variation (GCV) for all the traits, indicating the presence of little environmental influence in phenotypic expression. Heritability was found high for all the yield contributing traits. High heritability along with high genetic advance as % of mean was recorded for secondary branches per panicle followed by number of effective tillers, flag leaf area, and panicle weight. Contrary, days to flowering and days to maturity exhibited high heritability coupled with low genetic advance as % of mean. Pearson correlation revealed grain yield had positive association with the number of effective tillers per hill, panicle length, flag leaf area, spikelet fertility, plant height, and thousand grain weights. Mentioned characters also observed to present positive association with yield in both genotypic and phenotypic levels. Spikelet fertility, thousand grain weights, number of secondary branches per panicle, and number of effective tillers possessed higher positive and direct effect on grain yield of rice. It indicated the importance of these characters as selection criteria of yield improvement in the hybrid rice program.

Jomadder *et al.*(2019) evaluated eighteen Boro rice genotypes by using randomized complete block design with three replications. Significant variations were noticed among the studied genotypes both in irrigated and rainfed conditions. The genotypes BRRI dhan55, Gopal Deshi, and Soilerpona showed superior performance in terms of grain yield and qualitative characters under rainfed condition. Based on the stress tolerance index (STI) value, the genotypes BRRI dhan55, BRRI dhan58, Soilerpuna and Gopaldeshi were graded as the drought tolerant genotypes. Under rainfed condition, yield per plant expressed the positive and significant correlation with the flag leaf length, number of primary branches per panicle, number of grains per panicle, number of secondary branches per panicle, and thousand-seed weight. Path analysis showed that the number of primary/ secondary branches per panicle, and number of unfilled grains per panicle showed the highest positive and direct effect on the grain yield under the irrigated condition; while, Plant height, panicle length and thousand-seed weight had the highest direct but negative effect on grain yield. Thousand seeds weight, number of primary branches per panicle and number of unfilled grains per panicle exhibited the highest positive and direct effect on the grain yield under rainfed condition. Based on the results, seven genotypes among the eighteen studied genotypes namely, BRRI dhan36, BRRI dhan55, BRRI dhan58,

BRR1 dhan59, Soilerpona, Gopal Deshi, and Borail were identified as drought tolerance genotypes with high yield potential.

Bagudam *et al.*(2018) carried out an experiment to assess the direct and indirect effect of the qualitative characters with single plant yield. Through the path co-efficient analysis, they observed that, productive tillers per plant expressed highest positive direct effect; followed by panicle length, test weight, number of grains per panicle, panicle weight, harvest index, and biomass on single plant yield. That suggesting selection for these characters is likely to bring about an overall improvement in grain yield per plant directly.

Gour *et al.*(2017) carried out an experiment to measure the variability, correlation and analysis of path in eighty-three genotypes of rice. Analysis of variance exhibited the significant differences among the genotypes for different morphological traits. High GCV and PCV were found for grain yield per plant, panicle weight per plant, biological yield per plant, filled spikletes per plant, harvest index, number of tillers per plant, and 1000 seed weight, whereas moderate GCV and PCV was noted for Plant height. High heritability along with high genetic advance as % of mean were found for grain yield per plant, panicle weigh per plant, biological yield per plant, filled spikletes per plant, harvest index, number of tillers per plant, 1000 seed weight, panicle length per plant, where as high heritability coupled with moderate genetic advance as % of mean for days to 50% flowering and days to maturity. The filled spikletes per plant, harvest index, biological yield per plant exhibited high genetic advance that helped in effective and reliable selection through these characters for the crop improvement. Grain yield per plant express positive association with panicle weight per plant, biological yield per plant, number of tillers per plant and harvest index; while, negative association with plant height. The biological yield per plant had the maximum direct effect on grain yield per plant, followed by panicle length per plant, harvest index, filled spikletes for single plant, panicle length in a single plant and days to maturity. Hence, biological yield per plant, harvest index and number of seeds per plant are identified as the key traits for the development of high yielding genotypes of rice for future breeding program.

Sudeepthi *et al.*(2017) studied thirty-three rice genotypes to measure the direct and indirect effects of yield contributing characters on yield. Though the path analysis

studies they found grain yield per plant had direct relationship with plant height, number of productive tillers per plant and number of filled grains per panicle. Therefore, direct selection for any of these traits would be effective for yield improvement in rice.

Guru *et al.*(2016) observe fifty eight genotypes of rice and through the path analysis they found that, total dry matter at harvesting stage, panicle weight, harvest index, grain filling, total dry matter at flowering, and number of grains per panicle was the main yield component characters which were noted to produce maximum positive direct effect on grain yield.

In 2015, Das and Sarma evaluated thirty rice genotypes for twenty-one yield contributing characters. Through the path co-efficient analyses they found high positive and direct effect of biological yield (0.7181) and harvest index (0.6382) on grain yield per plant at both genotypic and phenotypic levels. Thus, direct selection for grain yield per plant and indirect selection through these characters would be effective for improvement of yield in Boro rice.

CHAPTER III

MATERIALS AND METHODS

The experimental work was entitled as “Genetic variability and character association of yield and yield contributing traits in Boro rice (*Oryza sativa* L.)”. It was conducted in the research field of Sher-e-Bangla Agricultural University, Dhaka during the Boro season from December, 2020 to May, 2021. Information about the materials and methods used for conducting this experiment is discussed below:

3.1 Site of Experiment

The experimental plot of Sher-e-Bangla Agricultural University, Dhaka- 1207 was used for carrying the research work, which is under the Agro-ecological Zone of Madhupur Tract (AEZ-28) (www.banglapedia.com). It was at 90° 22" E longitude and 23° 41" N latitude at an altitude of 8.6 meters from the sea level (www.distancesfrom.com) (Appendix I).

3.2 Soil and Climate

There are eleven different types of soil in that experimental area, with shallow red brown terrace, deep red brown terrace, and acid basin clays being the most common. Dark grey thick clays make up the soil. The soil has a high acidity level, clay loam texture with limited moisture retention capacity, and medium fertility level. The experimental location was shown in the map of AEZ of Bangladesh in Appendix I. The site is under subtropical climate zone with dry winter and moist summer. Generally, rainfalls were moderate, high temperature and moderate humidity was recorded during the Boro season. This climatic data is shown in Appendix II.

3.3. Planting materials for the experimental

Twenty three genotypes (Table 1) of Boro rice were used in this experiment and those samples were collected from GEPB, SAU.

Table 1. List of the genotypes used in the study and their sources

Sl. NO.	Genotype No.	Genotypes Name	Source
1.	G1	BR1	GEPB, SAU
2.	G2	BR2	GEPB, SAU
3.	G3	BR5	GEPB, SAU
4.	G4	BR9	GEPB, SAU

Cont'd.

Sl. NO.	Genotype No.	Genotypes Name	Source
5.	G5	BR14	GEPB, SAU
6.	G6	BR16	GEPB, SAU
7.	G7	BRRRI dhan28	GEPB, SAU
8.	G8	BRRRI dhan29	GEPB, SAU
9.	G9	BRRRI dhan50	GEPB, SAU
10.	G10	BRRRI dhan55	GEPB, SAU
11.	G11	BRRRI dhan63	GEPB, SAU
12.	G12	BRRRI dhan64	GEPB, SAU
13.	G13	BRRRI dhan67	GEPB, SAU
14.	G14	BRRRI dhan68	GEPB, SAU
15.	G15	BRRRI dhan74	GEPB, SAU
16.	G16	BRRRI dhan81	GEPB, SAU
17.	G17	BRRRI dhan88	GEPB, SAU
18.	G18	BRRRI dhan89	GEPB, SAU
19.	G19	BRRRI dhan92	GEPB, SAU
20.	G20	BRRRI dhan96	GEPB, SAU
21.	G21	BRRRI dhan97	GEPB, SAU
22.	G22	BRRRI dhan99	GEPB, SAU
23.	G23	SAU Purple1	GEPB, SAU

3.4 Experimental design and layout

Randomized complete Block Design was used for the experiment with three replications. Total area for the experiment was 392 m². The field was grouped into three different blocks for maintaining three replications. Seedlings were transplanted with (25cm × 20cm) spacing from plant-plant and row-row.

3.5 Seed germination

Seeds of the studied genotypes were soaked separately in water containing pot with cloth bags in for 48 hours. They were kept in an increased temperature. Straw heat was used for increasing the germination (Plate 1).

3.6 Seedbed preparation and raising of seedlings

Seedbed was ready by giving two ploughing and laddering. Weeding was done and irrigation was given. Twenty three lines were made and sprouted seed were sown in 24 December, 2020. The seedlings were grown with proper care and management such as by maintaining the irrigation, controlling the weeds, and protecting from the birds and insect pests.



Plate 1. Preparation for seed sowing

3.7 Preparation of experimental land

Land was prepared by giving 2-3 ploughing and cross ploughing and organic matter was added properly (Table 2). Then harrowing was done with the help of tractor. After three days, final ploughing was given. Field was cleaned by removing the weeds and stubbles. Urea is splitted into three portions. One portion of Urea and full portion of all other fertilizers were applied at the final land preparation. Other two doses of urea were applied in 30 and 45 days after transplanting respectively.

Table 2. Doses of fertilizers used in the study

Fertilizers	Dose (kg/ha)
Urea	150
TSP	60
MoP	60
Gypsum	50

Source: BIRRI, 2012

3.8 Transplanting of seedlings

Seedlings were transplanted to the main field when they are thirty-nine days old in 2 February 2021(Plate 2). Spacing was 25cm × 20cm spacing from row - row and plant – plant.



3.9 Intercultural operations

After transplanting the seedlings different intercultural activities were conducted for better growth and development such as -

i. Irrigation

As Boro rice requires standing water for growth and development so that, flood irrigation is given to maintain the standing level up to 6 cm. 15 days before harvesting field was drained out.

ii. Weeding

To keep the plot free from weeds and allow the all nutrient and water for rice plants only, regular weeding was conducted, that also minimized the disease and insect infestation rate.

iii. Gap filling

After ten days of transplanting, gap filing was done.

iv. Top dressing

After the basal dose, the remaining doses of urea fertilizer were top-dressed into two equal installments. The fertilizers were applied on both sides of seedlings rows.

v. Protection of plant

Insecticides and pesticides were applied when necessary.

3.10 Harvesting

After the plants get matured harvesting was done. When the 80% of plant exhibited the maturity symptoms such as, color of panicles turns into straw color, tiller color turns into straw color etc. Ten matured plants were randomly selected from each replication for collecting data. Plants were uprooted and tagged properly. Additionally, seeds were also collected properly.

3.11 Data Collection

Data were collected on the following fourteen parameters –

- **50% flowering**

Data was recorded as days from sowing to 50% flowering of plant in each genotype.

- **Flag leaf length (cm)**

With the help of measuring tape length of flag leaf of desirable plant is recorded in centimeter.

- **Leaf blade length (cm)**

Length of leaf blade of desirable plant of every genotype was recorded by using measuring tape and expressed in centimeter.

- **Leaf sheath length (cm)**

Leaf sheath length was measure with the help of measuring tape in centimeters.

- **Stem length (cm)**

Stem of each studied plant of every genotype measure and expressed in centimeter.

- **Number of effective tillers**

The number of effective tillers per plant was counted for each desirable plant and average value was recorded.

- **Number of total tillers**

- The total number of panicles bearing tillers was counted from each of the plant and average was taken.

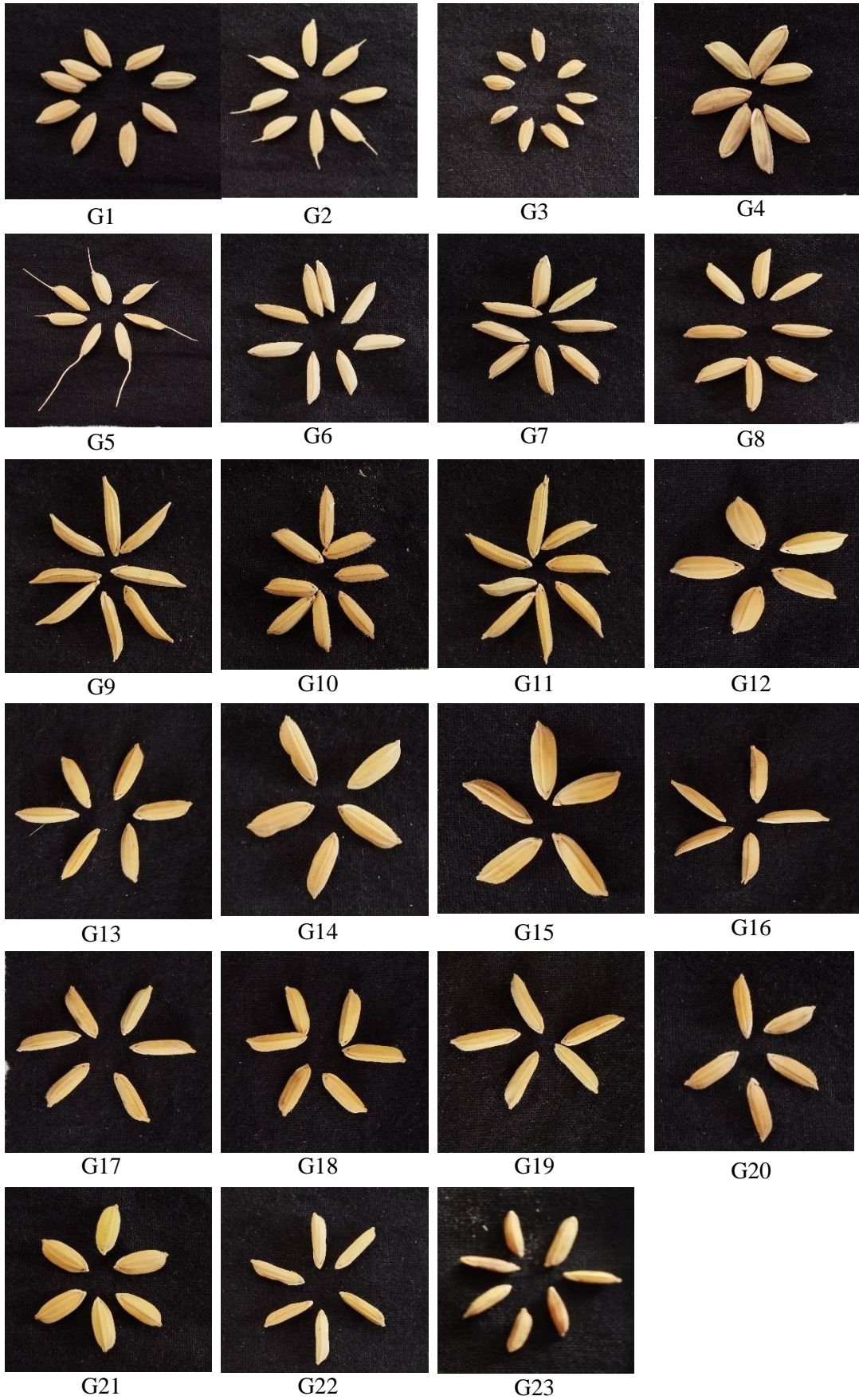


Plate 3. Rice grains of twenty three genotypes

- **Number of filled grains per tiller**
Presence of endosperm in spikelet was considered as filled grain and total number of filled grains present on main panicle was counted and average was taken.
- **Number of unfilled grains per tiller**
Number of unfilled spikelets was counted and average was considered as total number of unfilled grains per tillers.
- **Number of primary branches per panicle**
Primary branches of studied ten plants were counted from panicle of and the average value was recorded.
- **Number of secondary branches per panicle**
Secondary branches from one panicle of each of them were counted from randomly selected plants and the average value was recorded.
- **Panicle length (cm)**
With the help of meter scale panicle length of randomly selected plant is measure and average is taken in centimeter.
- **Thousand seed weight (g)**
One thousand seeds from selected plant were counted and weight was recorded in gram.
- **Yield per plant**
Grains obtained from each plant were sun dried and weighted carefully and average data was collected in gram.



Plate 4. Field of rice plant bearing grains

3.12 Statistical analysis

Data which were collected for different characters for all the studied genotypes were statistically analyzed to find out the variance, phenotypic and genotypic co-efficient of variation, heritability, genetic advance, correlation and path analysis. Significance of difference among the genotypes was computed by using statistix 10 software program. Analysis of variance was found out by the F test. The significant differences among the genotypes achieved at 5% level of probability by the least significant difference (LSD) test (Gomez and Gomez, 1984). The genotypic variance and phenotypic variance was estimated by the formula of Johnson *et al.*(1955). According to Burton's (1952) PCV and GCV were estimated. Broad sense heritability was computed by using the formula provided by Singh and Chaudhary (1985). Allard (1960) formula was used for computing genetic advance, whereas genetic advance (% mean) was estimated by the procedure given by Comstock and Robinson (1952). Correlation co-efficient analysis was done by the formula of Al-Jibouri *et al.*(1958). Path analysis was obtained by following the method of Dewey and Lu (1959).

- **Analysis of variance:**

For fourteen different studied characters of the all genotypes, analysis of variance was carried out. Significant level was tested by using the F test at 1% and 5%. According to Cochran and Cox (1957), the model ANOVA was -

Sources of variation	Degrees of freedom (D.F.)	Mean sum of squares (MS)	Expected MS
Replication	(r-1)	Mr	$p \sigma_r^2 + \sigma_e^2$
Genotype	(g-1)	Mg	$r \sigma_p^2 + \sigma_e^2$
Error	(p-1) (r-1)	Me	σ_e^2
Total	(rp-1)		

Here,

- g = number of genotypes;
- r = number of replications;
- σ_r^2 = variance due to replications;
- σ_g^2 = variance due to genotypes; and
- σ_e^2 = variances due to error.

To test the significance of the difference between the any two-adjusted genotypic mean, the standard error of mean was calculated by using the formula:

$$S. E = \sqrt{\frac{2Me}{r} \left(1 + \frac{rqu}{q+1}\right)}$$

Here,

S. E = Standard error of mean;

Me = Mean sum of square for error (Intra block);

r = No. of replications;

q = No. of populations in each sub-block; and

u = Weightage factor computed.

Genotypic and phenotypic variance

Genotypic and phenotypic variances were computed by the formula of Johnson *et al.*(1955).

a. Genotypic variance, $\sigma_g^2 = \frac{MSG-MSE}{r}$

Here,

MSG = Mean sum of square for genotypes;

MSE = Mean sum of square for error; and

r = Number of replications.

b. Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Here,

σ_p^2 = Phenotypic variance;

σ_g^2 = Genotypic variance; and

σ_e^2 = Environmental variance = Mean square of error (MSE).

Phenotypic and genotypic co-efficient of variation

By using the following formula given by Burton (1952), phenotypic co-efficient of variation (GCV) and genotypic co-efficient of variation (PCV) for all the traits of studied genotypes were estimated -

$$PCV = \frac{\sigma_p \times 100}{\bar{x}}$$

$$GCV = \frac{\sigma_g \times 100}{\bar{x}}$$

Here,

σ_g = Genotypic standard deviation;

σ_p = Phenotypic standard deviation; and

\bar{x} = Population mean.

According to Sivasubramanian and Madhavamenon (1973), PCV and GCV were categorized as -

Low (0-10%);

Moderate (10-20%); and

High (>20%).

Broad sense heritability

Following formula was used for estimating heritability in broad sense for all the characters. The formula was provided by Singh and Chaudhary in 1985.

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Here,

h_b^2 = Heritability in broad sense

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

Following categories were suggested by Robinson *et al.* in 1966 for estimated heritability.

Low: 0-30%, moderate: 30-60%, and high: >60%.

Genetic Advance

Genetic advance was calculated by the following procedure which was suggested by Allard in 1960 for all the studied traits.

$$GA = \frac{\sigma_g^2}{\sigma_p^2} \cdot K \cdot \sigma_p$$

Here,

GA = Genetic advance;

σ_g^2 = Genotypic variance;

σ_p^2 = Phenotypic variance;

K = Standard selection differential which is 2.06 at 5% selection intensity; and

σ_p = Phenotypic standard deviation.

Categories for genetic advance:

Low (<10%), moderate (10-20%), and high (>20%)

Genetic advance in percent of mean

Comstock and Robinson (1952) suggested the following formula for calculating genetic advance in percent of mean –

$$\text{GA in percent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

Johnson *et al.*(1955) categorized the genetic advance in percent of mean as following

Less than 10% - Low; 10-20% -Moderate and More than 20% -High

- **Correlation co-efficient analysis**

Al-Jibouri *et al.*(1958) suggested the following procedure for estimating the relationship of yield contributing traits with the yield and among themselves.

$$r_{gxy} = \frac{\text{Cov}_{gxy}}{\sqrt{\sigma_{gx}^2} \cdot \sqrt{\sigma_{gy}^2}}$$

$$r_{pxy} = \frac{\text{Cov}_{pxy}}{\sqrt{\sigma_{px}^2} \cdot \sqrt{\sigma_{py}^2}}$$

Here,

$r_g(xy)$ = The genotypic correlation co-efficient of x and y;

$r_p(xy)$ = The phenotypic correlation co-efficient of x and y;

Cov_{gxy} = The genotypic covariance of x and y;

Cov_{pxy} = The phenotypic covariance of x and y;

σ_{gx}^2 = Genotypic variance of the trait x;

σ_{gy}^2 = Genotypic variance of the trait y.

σ_{px}^2 = Phenotypic variance of the trait x; and

σ_{py}^2 = Phenotypic variance of the trait y.

The calculated value of 'r' was compared with Table 'r' value with n-2 degrees of freedom at 5% and 1% level of significance,

Here, n was referring to the number of pairs of observation. Thus, the data obtained from various experimental objectives were subjected to pertinent statistical analysis to draw meaningful inference towards the genetic divergence of mustard populations.

- **Path analysis**

According to the procedure provided by Dewey and Lu (1959) also noted in Singh and Chaudhary (1985). Path co-efficient analysis was done utilizing the simple correlation values. In path analysis, the correlation co-efficient is divided into direct and indirect independent variables on the dependent variable.

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3} + \dots + P_{yx11} \cdot r_{x1x11}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3} + \dots + P_{yx11} \cdot r_{x2x11}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3} + \dots + P_{yx11} \cdot r_{x3x11}$$

To estimate direct and indirect effect of the correlated traits, say x_1 , x_2 and x_3 yield y , a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

Where r 's denoted simple correlation co-efficient and P 's indicate path co-efficient (unknown).

P 's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x_1 on y ;

$P_{yx2}r_{x1x2}$ = the indirect effect of x_1 via x_2 on y ; and

$P_{yx3}r_{x1x3}$ = the indirect effect of x_1 via x_3 on y .

After estimating the direct and indirect effect of the traits, the residual effect (R) was computed by using the following formula given by Singh and Chaudhary in 1985.

$$P_{RY}^2 = 1 - \sum P_{iy} \cdot r_{iy}$$

Here,

$$P_{RY}^2 = (R^2);$$

$$\text{Hence, residual effect, } R = (P_{RY}^2)^{1/2};$$

P_{iy} = Direct effect of the character on yield; and

r_{iy} = Correlation of the character with yield.

Categories:

Negligible (0.00 - 0.09); low (0.10 - 0.19); moderate (0.20 - 0.29); high (0.30 - 1.0); and very high (>1.00).

CHAPTER IV

RESULTS AND DISCUSSION

The experimental work was carried out in the experimental field of Sher-e-Bangla Agricultural University, Dhaka during the Boro season from December, 2020 to May, 2021 to conclude the performance of some characters of twenty three Boro rice genotypes. Genetic variation is fundamentally most important for introducing new cultivars in breeding programs. Thus, authentic information of the parents on the nature and degree of diversity is the prerequisite for an effective breeding program. The knowledge of genotypic variation within genotypes in relation to morphology, phenology, and yield would help to screen out better genotypes for the hybridization or further breeding programs. The accessibility of transgressive sergeants in the breeding methods relies upon the dissimilarities of the parents. So, appropriate data on the degree of diversity of the parent is important for an effective breeding program. The results on different parameters have been interpreted, discussed and presented in following sub-headings:

4.1 Estimation of genetic variability, heritability and genetic advance

4.1.1 50% flowering

Analysis of variance in Table 3 showed that, there are highly significant differences (68.02**) for 50% flowering among the genotypes. Maximum days for 50% flowering are observed in G19 (76.67), followed by G23 (74.33) and G18 (72.67), while minimum days were recorded in G20 (59.33), followed by G5 (60.33), G10 (60.33), and G17 (60.33). The mean value was 64.27 (Table 4). Yashwanth *et al.*(2021) found minimum days for 50% flowering 82.67 days. The genotypic and phenotypic variances for 50% flowering were 22.32 and 23.39, respectively. The phenotypic variance was little bit higher than the genotypic variance indicating slight influence of environment on the expression of genes for expressing this trait. For 50% flowering, the PCV and GCV were recorded 7.52% and 7.35% respectively. It was observed that PCV is slightly higher than GCV, suggesting variation exists among the genotypes (Table 5). The less value of GCV indicating that the less possibility of improving this trait through selection. Yashwanth *et al.*(2021) found that PCV is higher than GCV for 50% flowering.

Table 3. Analysis of variance of 14 characters of 23 rice genotypes

Source of variation	df	FFL	FLL	LBL	LSL	SL	NET	NTT
Replication	2	0.10	6.18	126.57	9.06	134.00	0.41	0.88
Genotype	22	68.02**	11.92**	25.79**	27.43**	161.18**	8.62**	8.14**
Error	44	1.07	5.47	10.74	2.36	21.57	3.28	2.75
CV (%)		1.62	9.15	10.23	5.99	7.82	16.65	9.07

Cont'd.

Source of variation	df	NFG	NUnFG	NPB	NSB	PL	TSW	YPP
Replication	2	3.96	3.93	0.93	10.01	0.22	4.01	4.07
Genotype	22	290.51**	108.64**	94.49**	16.54**	78.33**	40.58**	92.78**
Error	44	42.81	1.79	2.96	5.38	3.61	4.96	31.52
CV (%)		5.77	11.22	9.43	5.98	12.01	9.79	20.03

Here, *= Significant at 5 % level of probability, **= Significant at 1 % level of probability, and df = Degree of freedom

FFL=50% flowering;
 FLL= Flag leaf length (cm);
 LBL= Leaf blade length (cm);
 LSL= Leaf sheath length (cm);
 SL= Stem length (cm);

NET= Number of effective tillers;
 NTT= Number of total tillers;
 NFG= Number of filled grains per tiller;
 NUnFG= Number of unfilled grains per tiller;

NPB= Number of primary branches per panicle;
 NSB= Number of secondary branches per panicle;
 PL = Panicle length (cm);
 TSW= Thousand seed weight (g); and
 YPP= Yield per plant (g)

Table 4. Mean performance of 14 characters of 23 rice genotypes

Genotypes	FFL	FLL	LBL	LSL	SL	NET	NTT
G1	61.67g-i	21.37g	29.23d-g	19.40m	46.37h	17.00a	19.33a-d
G2	65.33cd	28.27ab	32.13bcd-g	26.57c-g	65.83a-c	10.00c-e	20.00a-c
G3	59.33k	27.30a-d	36.53ab	26.37d-h	64.10b-d	9.33de	21.33a
G4	62.33f-h	23.40e-g	28.67fg	22.43j-l	51.13f-h	13.33b	16.33e-g
G5	60.33i-k	23.53d-g	30.53cd-g	27.27b-f	58.73c-f	9.00e	17.67b-f
G6	65.67c	21.70fg	28.33g	23.23i-l	58.53c-f	10.00c-e	15.67fg
G7	59.67jk	27.77ab	33.37a—g	27.93b-e	56.87d-g	12.00b-d	19.33a-d
G8	63.67d-f	23.80cd-g	30.37c-g	25.73e-i	57.50d-f	11.00b-e	17.67b-f
G9	64.67c-e	26.20a-e	32.10b-g	21.83km	53.43e-h	11.00b-e	17.67b-f
G10	60.33i-k	24.63b-g	29.83d-g	23.73i-l	56.37e-g	10.00c-e	17.67b-f
G11	63.33e-g	26.80a-e	31.73b-g	24.03h-k	52.67e-h	9.67c-e	18.67a-e
G12	61.33h-j	25.30b-f	34.23a-d	28.53b-d	69.13ab	10.00c-e	17.33c-f
G13	64.67c-e	26.27a-e	32.83a-g	29.67ab	67.17ab	9.33de	16.67d-g
G14	61.33h-j	26.30a-e	29.07d-g	24.40g-j	56.67d-g	10.33c-e	19.67a-c
G15	60.67h-k	26.20a-e	34.07a-e	25.33f-i	67.10ab	10.33c-e	19.00a-e
G16	61.33h-j	25.20b-g	31.60b-g	25.10f-i	55.80efg	10.33c-e	20.33ab
G17	60.33i-k	25.93a-e	28.70e-g	23.23i-l	48.13h	10.33c-e	19.33a-d

Cont'd.

Genotypes	FFL	FLL	LBL	LSL	SL	NET	NTT
G18	72.67b	23.87c-g	33.77a-f	25.17f-i	66.87ab	11.33b-e	18.33b-f
G19	76.67a	25.77a-e	37.60a	28.73b-d	71.83a	11.33b-e	19.00a-e
G20	59.33k	25.60b-e	28.07g	21.47lm	49.23gh	11.33b-e	19.67a-c
G21	65.33cd	25.47b-f	31.07c-g	29.27ab	66.10a-c	12.33-c	18.33b-f
G22	66.33c	27.57a-c	35.47a-c	31.33a	67.03ab	11.33b-e	17.33c-f
G23	74.33b	29.60a	37.70a	28.97a-c	58.80c-e	9.67c-e	14.00g
Min	59.33	21.37	28.07	19.40	46.37	9.00	14.00
Max	76.67	29.60	37.70	31.33	71.83	17.00	21.33
Average	64.27	25.55	32.11	25.62	59.34	11.05	18.23
SE	0.85	1.91	2.68	1.25	3.79	1.48	1.35
LSD	1.70	3.85	5.39	2.53	7.64	2.98	2.73

Here,

FFL=50% flowering;
 FLL= Flag leaf length (cm);
 LBL= Leaf blade length (cm);
 LSL= Leaf sheath length (cm);
 SL= Stem length (cm);

NET= Number of effective tillers;
 NTT= Number of total tillers;
 NFG= Number of filled grains per tiller;
 NUnFG= Number of unfilled grains per tiller;

NPB= Number of primary branches per panicle;
 NSB= Number of secondary branches per panicle;
 PL = Panicle length (cm);
 TSW= Thousand seed weight (g); and
 YPP= Yield per plant (g)

Table 4. Mean performance of 14 characters of 23 rice genotypes

Genotypes	NFG	NUnFG	NPB	NSB	PL	TSW	YPP
G1	90.33f	9.00e-g	11.67e	42.00ab	18.32c	19.45hi	30.38b-d
G2	113.00c-e	11.67c	11.00e	40.33a-e	22.20a	21.40e-i	24.26cd
G3	118.67cd	10.67c-e	10.67e	41.33a-d	24.06a	27.18a	31.84bc
G4	106.33e	11.33cd	22.33a-c	39.33a-g	12.14de	23.90a-f	33.86b
G5	107.67e	8.33fg	12.00e	41.00a-e	21.89ab	27.45a	26.60b-d
G6	111.33c-e	9.67c-f	15.00d	38.00cd-i	18.79bc	25.10a-d	27.93b-d
G7	113.67c-e	11.33cd	23.33ab	37.67d-i	12.12de	20.45f-i	27.81b-d
G8	111.67c-e	9.00efg	11.33e	38.33b-i	23.54a	24.80a-e	30.61bcd
G9	110.33de	7.33g	10.33e	40.00a-e	22.79 a	20.05g-i	24.28cd
G10	114.67c-e	11.67c	23.67a	36.00f-i	11.91de	26.60ab	30.56bcd
G11	112.33c-e	11.67c	20.33c	37.67d-i	14.97d	12.05j	14.29e
G12	113.00c-e	10.33c-f	23.00a-c	35.67g-i	11.73e	25.70a-c	29.09bcd
G13	114.33c-e	11.67c	23.00a-c	34.67i	11.91de	22.65c-h	24.11cd
G14	111.67c-e	11.33cd	22.00a-c	38.33b-i	12.03de	26.50ab	30.54bcd
G15	122.00bc	11.00c-e	11.00e	39.00a-h	22.03a	20.65f-i	25.82bcd
G16	132.33b	29.00a	23.00a-c	41.67a-c	11.37e	23.35b-g	32.10bc
G17	107.67e	16.00b	21.33a-c	42.33a	11.17e	19.45hi	21.69de

Cont'd.

Genotypes	NFG	NUnFG	NPB	NSB	PL	TSW	YPP
G18	111.00de	9.00e-g	23.33ab	37.33e-i	11.77e	24.00a-f	30.04b-d
G19	111.33c-e	8.33fg	22.67a-c	35.33hi	11.78e	25.90a-c	32.77bc
G20	144.00a	31.00a	20.67bc	41.67a-c	11.27e	26.50ab	43.17a
G21	110.00de	9.33d-g	23.00a-c	39.67a-f	11.43e	18.50i	25.09b-d
G22	107.33e	8.33fg	11.00e	40.00a-e	22.83a	22.00d-i	26.35b-d
G23	111.33c-e	7.33g	24.00a	35.33hi	12.05de	20.00g-i	21.53de
Min	90.33	7.33	10.33	34.67	11.17	12.05	14.29
Max	144.00	31.00	24.00	42.33	24.06	27.45	43.17
Average	113.61	12.51	18.16	38.79	15.97	22.53	28.09
SE	5.34	1.09	1.40	1.89	1.55	1.82	4.58
LSD	10.77	2.20	2.83	3.82	3.13	3.67	9.24

Here,

FFL=50% flowering;
 FLL= Flag leaf length (cm);
 LBL= Leaf blade length (cm);
 LSL= Leaf sheath length (cm);
 SL= Stem length (cm);

NET= Number of effective tillers;
 NTT= Number of total tillers;
 NFG= Number of filled grains per tiller;
 NUnFG= Number of unfilled grains per tiller;

NPB= Number of primary branches per panicle;
 NSB= Number of secondary branches per panicle;
 PL =Panicle length (cm);
 TSW= Thousand seed weight (g); and
 YPP= Yield per plant (g)

Table 5. Estimation of genetic parameters of twenty three rice genotypes

Character	Phenotypic variance	Genotypic variance	PCV	GCV	Heritability (%)	GA	GA (%)
FFL	23.39	22.32	7.52	7.35	95.42	9.51	14.79
FLL	7.62	2.15	10.81	5.74	28.20	1.60	6.28
LBL	15.75	5.02	12.36	6.98	31.86	2.60	8.11
LSL	10.71	8.36	12.78	11.29	78.01	5.26	20.53
SL	68.10	46.54	13.91	11.50	68.33	11.62	19.57
NET	5.06	1.78	20.36	12.07	35.15	1.63	14.74
NTT	4.55	1.80	11.70	7.36	39.55	1.74	9.53
NFG	125.37	82.57	9.86	8.00	65.86	15.19	13.37
NUnFG	37.41	35.61	48.90	47.72	95.21	12.00	95.92
NPB	33.47	30.51	31.86	30.42	91.16	10.86	59.83
NSB	9.10	3.72	7.78	4.97	40.89	2.54	6.55
PL	28.52	24.90	33.43	31.24	87.33	9.61	60.14
TSW	16.83	11.87	18.22	15.30	70.51	5.96	26.46
YPP	51.94	20.42	25.66	16.09	39.31	5.84	20.78

Here, PCV= Phenotypic co-efficient variation; GCV= Genotypic co-efficient variation; GA= Genetic Advance and GA (%) = Genetic Advance in percent

FFL=50% flowering;

CD= Culm diameter (cm);

FLL= Flag leaf length (cm);

LBL= Leaf blade length (cm);

LSL= Leaf sheath length (cm);

SL= Stem length (cm);

NET= Number of effective tillers;

NTT= Number of total tillers;

NFG= Number of filled grains per tiller;

NUnFG= Number of unfilled grains per tiller;

NPB= Number of primary branches per panicle;

NSB= Number of secondary branches per panicle;

PL =Panicle length (cm);

TSW= Thousand seed weight (g); and

YPP= Yield per plant (g).

4.1.2 Flag leaf length (cm)

Highly significant mean sum of square 11.92** for flag leaf length (cm) among the twenty three genotypes was observed in Table 3. Maximum length for flag leaf was recorded in G23 (29.60cm), followed by G2 (28.27cm) and G7 (27.77cm), while smallest length of flag leaf was found in G1 (21.37cm), followed by G6 (21.70cm) and G4 (23.40 cm), and average flag leaf length was 25.55 cm (Table 4). The phenotypic and genotypic variances were found 7.62 and 2.15, respectively. Phenotypic variance is higher than the genotypic variance which suggested that there was environmental influence for gene expression of this character. PCV and GCV was recorded 10.81% and 5.74% respectively. The difference between the PCV and GCV indicates less variability (Table 5). Similar result was also recorded by Limbongan *et al.*(2021).

4.1.3 Leaf blade length (cm)

Analysis of variance (Table 3) expressed highly significant differences among the twenty three genotypes (25.79**) for leaf blade length (cm). The highest length of leaf blade (cm) was recorded in G23 (37.70 cm), followed by G19 (37.60cm) and G3 (36.53 cm), whereas the minimum leaf blade length was found in G20 (28.07cm), followed by G6 (28.33cm) and G4 (28.67cm) and mean value for leaf blade length was 32.11 cm (Table 4). Phenotypic variance (15.75) is higher than the genotypic variance (5.02), indicating expression of this character is influenced by environment. PCV and GCV were found 12.36% and 6.98%, respectively (Table 5). High level of PCV (21.07) and moderate level of GCV (17.87) were recorded by Akshaya *et al.* in 2020.

4.1.4 Leaf sheath length (cm)

Highly significant (27.43**) for leaf sheath length (cm) was recorded in analysis of variance (Table 3). Maximum length for leaf sheath was found in G22 (31.33cm), followed by G13 (29.67cm) and G21 (29.27cm), while minimum length for leaf sheath was observed in G1 (19.40cm), followed by G20 (21.47cm) and G9 (21.83cm), and mean value for leaf sheath length was recorded 25.62 cm in Table 4. In Table 5, phenotypic and genotypic variance for leaf sheath length was recorded 10.71 and 8.36, respectively. Additionally, PCV and GCV were noted 12.78% and 11.29% respectively. There was a slight difference between phenotypic and genotypic

variance and phenotypic variance was a bit higher than the genotypic variance, indicating the expression of this character is influenced by environment. Akshaya *et al.* (2020) found high level of PCV (33.56) and GCV (28.85).

4.1.5 Stem length (cm)

Analysis of variance for stem length was found highly significant (161.18**) among the twenty three genotypes in Table 3. Highest stem length was observed in G19 (71.83cm), followed by G12 (69.13cm) and G13 (67.17cm), whereas smallest length for stem was noted in G1 (46.37cm), followed by G17 (48.13cm) and G20 (49.23cm), and average mean value for stem length was 59.34cm in Table 4. Phenotypic variance 68.10 was highly higher than genotypic variance 46.54, indicating there was large influence of environment for expression of gene for controlling this character. PCV and GCV were recorded 13.91% and 11.50% respectively (Table 5). Less difference between PCV and GCV indicates less variability. PCV and GCV levels were relatively low for culm length according to the findings by Chakravorty *et al.* in 2011.

4.1.6 Number of effective tillers

From Table 3, it was found that number of effective tillers exhibited highly significant variations 8.62** among the twenty three genotypes. Maximum effective tillers were recorded in G1 (17.00), followed by G4 (13.33) and G21 (12.33), whereas number of effective tillers were recorded minimum in G5 (9.00), followed by G3 (9.33) and G13 (9.33), and average effective tillers were found 11.05 (Table 4). Genotypic and phenotypic variances were found 1.78 and 5.06, respectively. PCV 20.36% was recorded higher than GCV 12.07%, indicating higher environmental influence for expressing this character (Table 5). Dhurai *et al.* (2014) recorded moderate values of PCV and GCV for the number of effective tillers per plant.

4.1.7 Number of total tillers

Highly significant variations (8.14**) were observed among the genotypes for number of total tillers in Table 3. Maximum number of total tillers were noted in G3 (21.33), followed by G2 (20.00), G14 (19.67) and G20 (19.6), while lowest number of total tillers were found in G23 (14.00), followed by G6 (15.67) and G4 (16.34), and mean value for total tiller number was 18.23 (Table 4). It was found that genotypic variance (1.80) was lower than phenotypic variance (4.55). PCV (11.70%)

was found higher than GCV (7.36%) (Table 5). The difference between them indicates the slight influence of environment in the expression of this trait. Ghosal *et al.*(2010) revealed similar estimation for this character.

4.1.8 Number of filled grains per tiller

From the ANOVA (Table 3), it was observed that number of filled grains per tiller showed highly significant variations (290.51**) among the rice genotypes. Highest number of filled grains per tiller were observed in G20 (144.00), followed by G16 (132.33) and G15 (122.00), whereas minimum number of filled grains per plant were found in G1 (90.33), followed by G (107.33); and mean value was 113.61 (Table 4). Phenotypic variance (125.37) is higher than the genotypic variance (82.57), that indicating the presence of environment for the expression of the trait. GCV and PCV were also recorded 8.00% and 9.86% respectively in Table 5. Karim *et al.*(2007) found high PCV (31.71) and GCV (24.41).

4.1.9 Number of unfilled grains per tiller

Highly significant variation 108.64** was observed among the twenty three genotypes for number of unfilled gains per tiller (Table 3). Lowest number of unfilled grains per tiller was recorded in G23 (7.33) and G 9 (7.33), followed by G5 (8.33), G19 (8.33) and G22 (8.33), while maximum number of unfilled grains per tiller were noted in G20 (31.00), followed by G16 (29.00) and G17 (16.00). The average number of unfilled grains per tiller was recorded 12.51 in Table 4. It was observed that, Genotypic variance 35.61 was slightly smaller than phenotypic variance. PCV (48.90%) was observed slightly higher than the GCV (47.72%) in Table 5. this suggesting that there is little influence of environment in expression of this character. Dhanwani *et al.*(2013) found higher GCV than PCV.

4.1.10 Number of primary branches per panicle

Analysis o variation exhibited highly significant difference 94.49** for number of primary branches per panicle in Table 3. Maximum number of primary brunches per panicle were recorded in G23 (24.00), followed by G10 (23.67), G7 (23.33) and G18 (23.33), while lowest number of primary brunches per panicle was observed in G9 (10.33), followed by G3 (10.67), G2 (11.00), G15 (11.00) and G22 (11.00), and mean value for number of primary branches was 18.16 (Table 4). Phenotypic variance

(33.47) was slightly higher than the genotypic variance (30.51). GCV (30.42%) was found slightly lower than the PCV (31.86%) in Table 5. This indicating there is little influence of environment for revealing this character. Karim *et al.*(2007) revealed that PCV (8.06) was higher than the GCV (5.47) for this character.

4.1.11 Number of secondary branches per panicle

It was observed that, analysis of variation in Table 3 exhibited that number of secondary branches per panicle had highly significant differences 16.54** among the rice genotypes. Minimum number of secondary branches per panicle were recorded in G13 (34.67), followed by G19 (35.33) and G23 (35.33), while Highest number of secondary branches per panicle were noted in G17 (42.33), followed by G1 (42.00), G16 (41.67) and G20 (41.67). The average number of secondary branches per panicle was 38.79 (Table 4). Phenotypic variance (9.10) was found higher than the genotypic variance (3.72), suggesting environmental effect on this trait's expression. Additionally, PCV and GCV were observed 7.78% and 4.97% respectively in Table 5. Ogunbayo *et al.*(2014) revealed that PCV (12.23) was higher than the GCV (10.26) for this character.

4.1.12 Panicle length (cm)

Highly significant variance (78.33**) was noted among the twenty-three Boro rice genotype for panicle length in Table 3. Highest panicle length was found in G3 (24.06cm), followed by G8 (23.54cm) and G22 (22.83), while lowest length for panicle (cm) was found in G17 (11.17cm), followed by G20 (11.27cm) and G16 (11.38cm), and mean value was 15.97 cm (Table 4). Yashwanth *et al.*(2021) found the largest panicle, which was 29.66 cm. Genotypic variance (24.90) was observed lower than the phenotypic variance (28.52). PCV (33.43%) was recorded slightly higher than the GCV (31.24%) in Table 5, indicating slight influence of environment for the expression of the character. Yashwanth *et al.*(2021) observed greater PCV than the GCV for panicle length.

4.1.13 Thousand seeds weight (g)

It was found in ANOVA (Table 3) that, thousand seed weight exhibited highly significant variation (40.58**) among the genotypes. Maximum weight for thousand seed were found in G5 (27.45g), followed by G3 (27.18g), G10 (26.60g) G14(26.50g)and G20 (26.50g). On the other hand, minimum thousand seed weight

was recorded in G11 (12.05 g), and mean weight for thousand seed was 22.53g (Table 4). Phenotypic and genotypic variances were 16.83 and 11.87, respectively. GCV (15.30%) is lower than the PCV (18.22%) in Table 5, indicating the influence of environment on this trait expression. Hoque *et al.*(2021) found similar type of result for this trait.

4.1.14 Yield per plant (g)

Highly significant variation (92.78**) for yield per plant (g) among the twenty three rice genotypes has been shown in Table 3. Maximum yield per plant was noted in G20 (43.17g), followed by G4 (33.86g) and G19 (32.76g). Whereas, lowest yield per plant (g) was recorded in G11 (14.29g), followed by G23 (21.5g) and G17 (21.69g). Average yield per plant was 28.09 g (Table 4). In 2018, Kishore *et al.* reported similar estimation for this trait. Phenotypic variance (51.94) is highly higher than the genotypic variance (20.42), and PCV (25.66%) is higher than the GCV (16.09%) (Table 5). Those indicating that, there was environmental effect for controlling the gene for expressing the character.

4.2 Heritability and Genetic Advance

4.2.1. 50% flowering

50% flowering exhibited high heritability (95.42%) coupled with low genetic advance (9.51) and moderate genetic advance in percentage of mean (14.79%) in Table 5 which indicating that, this character was controlled by additive genes and the selection based on this trait would be effective. Yashwanth *et al.*(2021) found similar heritability for this character.

4.2.2 Flag leaf length (cm)

Flag leaf length (cm) showed low heritability (28.20%) coupled with low genetic advance (1.60) and low genetic advance in percent of mean (6.28%) (Table 5), so simple selection is not possible for this character. Similar result was observed by Sandeep *et al.* in 2018.

4.2.3 Leaf blade length (cm)

In Table 5, it was observed that, leaf blade length (cm) exhibited moderate heritability (31.86%). Genetic advance and genetic advance in percent of mean was 2.60 and 8.11% respectively. In 2019, Longjam *et al.* found that leaf length has high heritability (95.78%) with moderate level of genetic advance by percent of mean (18.54).

4.2.4 Leaf sheath length (cm)

High heritability (78.01%) combined with low genetic (5.26) advance and high genetic advance (% mean) (20.53%) was observed in Table 5, which suggesting the presence of additive gene action for expressing this trait, so that simple selection would be effective for this character. In 2020, Akshaya *et al.* found high heritability with high genetic advance by percent of mean.

4.2.5 Stem length (cm)

Stem length showed high heritability (68.33%) combined with moderate genetic advance (11.62) and moderate genetic advance in percent of mean (19.57%) in Table 5. These findings expressed that, this character was controlled by additive gene and selection of this character would be effective. Surjaye *et al.* in 2022 found that stem length has high heritability with high genetic advance.

4.2.6 Number of effective tillers

The magnitude of heritability in broad sense of number of effective tillers was moderate (35.15%) associated with low genetic advance (1.63) and moderate genetic advance in percentage of mean (14.74%) (Table 5). Singh *et al.* (2021) observed moderate heritability coupled with moderate genetic advance in percent of mean.

4.2.7 Number of total tillers

Moderate heritability (39.55%) associated with low genetic advance (1.74) and low genetic advance (% mean) (9.53%) was recorded in Table 5, indicating presence of non-additive gene action and selection of the trait might not be effective. Longjam *et al.* (2019) found moderate heritability (76.89) with high level of genetic advance by percent of mean (25.39).

4.2.8 Number of filled grains per tiller

Number of filled grains per tiller exhibited high heritability (65.86%) combined with moderate genetic advance (15.19) and genetic advance in percent mean (13.37%) in Table 5. These indicating the presence of additive gene, so selection of this character might be effective for future program. In 2021, Singh *et al.* observed high heritability associated with high genetic advance in percent of mean.

4.2.9 Number of unfilled grains per tiller

High heritability (95.21%) coupled with moderate genetic advance (12.00) and high genetic advance in percent of mean (95.92%) (Table 5), which suggests that there was presence of additive gene action for expressing this trait. So that for future program selection of this character would be effective. Limbani *et al.* (2017) observed high heritability coupled with high genetic advance.

4.2.10 Number of primary branches per panicle

It was observed in Table 5 that, number of primary branches per panicle showed high heritability (91.16%). Moreover, the genetic advance and the genetic advance in percent of mean were 10.86 and 59.83%, respectively. High heritability coupled with high genetic advance in percent of mean suggesting that additive gene action presence and selection of this trait would be effective. Ketan *et al.* (2014) reported number of unfilled grains per panicle had moderate level of heritability coupled with high genetic advance.

4.2.11 Number of secondary branches per panicle

Number of secondary branches per panicle revealed moderate heritability (40.89%) associated with low genetic advance (2.54) and low genetic advance in percent of mean (6.55%) in Table 5. These indicate the presence of non-additive gene so selection of this character might not be productive. Ketan *et al.* (2014) found high heritability with high genetic advance in number of secondary branches per panicle.

4.2.12 Panicle length (cm)

High heritability (87.33%) was observed for panicle length. Genetic advance and genetic advance (% mean) were 9.61 and 60.14% respectively (Table 5). High heritability coupled with high genetic advance in percent of mean expressed the

presence of additive gene action, and effective selection of this trait was possible. In 2021, Singh *et al.* reported moderate heritability associated with low genetic advance.

4.2.13 Thousand seed weight (g)

Thousand seed weight showed high heritability (70.51%) associated with low genetic advance (5.96) and high genetic advance in percent of mean (26.46%) (Table 5), indicating additive gene action and selection for further program selection of this character might be productive. In 2021, Hoque *et al.* reported moderate heritability associated with low genetic advance for yield of rice.

4.2.14 Yield per plant (g)

Moderate heritability (39.31%) coupled with low genetic advance (5.84) and high genetic advance in percent of mean (20.78%) was observed for yield per plant in Table 3. In 2021, Yashwanth *et al.* found high heritability coupled with high genetic advance in percent mean.

4.3 Analysis of correlation co-efficient

Yield of product depends on the different yield contributing characters. Determination of co-efficient of correlation provided the information how several inter-dependable quantitative characters influencing the yield. For improving a particular character in the plant breeding program, it is important to estimate the association of different yield contributing traits with the yield and among themselves. It provides a plant breeder a good guideline to make improvement through selection. The effect of every trait on yield could be well-known through analysis of correlation with a view to see the extent and nature of relationships among yield and yield attributing parameters. So, the genotypic and phenotypic correlation co-efficient values for twenty-three characters of rice genotypes are given in Table 6.

Table 6. Correlation co-efficient analysis of 23 rice genotypes

Characters		FFL	FLL	LBL	LSL	SL	NET	NTT	NFG	NUnFG	NPB	NSB	PL	TSW
FLL	r _g	0.246*												
	r _p	0.098												
LBL	r _g	0.765**	0.748**											
	r _p	0.380**	0.522**											
LSL	r _g	0.397**	0.737**	0.905**										
	r _p	0.347**	0.382**	0.506**										
SL	r _g	0.513**	0.327**	0.819**	0.853**									
	r _p	0.392**	0.287*	0.600**	0.693**									
NET	r _g	-0.023	-0.759**	-0.252*	-0.579**	-0.471**								
	r _p	0.007	-0.259*	-0.267*	-0.252*	-0.278*								
NTT	r _g	-0.529**	0.067	-0.165	-0.255*	-0.125	0.184							
	r _p	-0.320**	0.101	-0.006	-0.182	0.002	0.041							
NFG	r _g	-0.232	0.315**	-0.190	-0.028	0.005	-0.586**	0.399**						
	r _p	-0.213	0.255*	0.162	0.025	0.080	-0.297*	0.201						
NUnFG	r _g	-0.396**	0.013	-0.508**	-0.322**	-0.404**	-0.060	0.521**	0.853**					
	r _p	-0.381**	-0.001	-0.220	-0.281*	-0.311**	-0.055	0.327**	0.721**					
NPB	r _g	0.212	0.143	0.023	0.166	0.002	-0.143	-0.249*	0.219	0.278*				
	r _p	0.207	0.089	-0.028	0.135	-0.002	0.028	-0.100	0.177	0.260*				
NSB	r _g	-0.641**	-0.491**	-0.846**	-0.651**	-0.688**	0.580**	0.791**	0.092	0.497**	-0.581**			
	r _p	-0.386**	0.023	-0.127	-0.256*	-0.305*	0.077	0.360**	0.098	0.329**	-0.411**			
PL	r _g	-0.149	-0.016	0.142	-0.028	0.114	-0.075	0.153	-0.212	-0.369**	-0.981**	0.423**		
	r _p	-0.155	-0.030	0.102	-0.000	0.103	-0.089	0.045	-0.161	-0.348**	-0.958**	0.307*		
TSW	r _g	-0.092	-0.439**	-0.039	0.048	0.259*	-0.350**	0.117	0.304*	0.147	-0.017	-0.057	0.039	
	r _p	-0.072	-0.148	-0.046	0.054	0.178	-0.071	-0.021	0.223	0.117	-0.007	-0.055	0.020	
YPP	r _g	-0.210	-0.654**	-0.280*	-0.380**	-0.102	-0.019	0.461**	0.504**	0.604**	0.037	0.388**	-0.154	0.821**
	r _p	-0.118	-0.162	-0.167	-0.148	-0.071	0.535**	0.113	0.379**	0.365**	0.126	0.047	-0.146	0.673**

Here,

* = Correlation is significant at the 0.05 level;

** = Correlation is significant at the 0.01 level.

FFL=50% flowering;

FLL= Flag leaf length (cm);

LBL= Leaf blade length (cm);

LSL= Leaf sheath length (cm);

SL= Stem length (cm);

NET= Number of effective tillers;

NTT= Number of total tillers;

NFG= Number of filled grains per tiller;

NUnFG= Number of unfilled grains per tiller

NPB= Number of primary branches per panicle;

NSB= Number of secondary branches per panicle;

PL =Panicle length (cm);

TSW= Thousand seed weight (g); and

YPP= Yield per plant (g)

4.3.1. 50% flowering

50% flowering showed significant and positive correlation with flag leaf length ($G=0.246$), leaf blade length ($G=0.765$, $P=0.380$), leaf sheath length ($G=0.397$, $P=0.347$), and stem length ($G=0.513$, $P=0.392$), whereas, it exhibited non-significant and positive correlation with flag leaf length ($P=0.098$), number of effective tillers ($P=0.007$), number of primary branches per panicle ($G=0.212$, $P=0.207$). On the other hand, 50% flowering was observed to show highly significant and negative correlation with number of total tillers ($G=-0.529$, $P=-0.320$), number of unfilled grains per tiller ($G=-0.396$, $P=-0.381$), and number of secondary branches per panicle ($G=-0.641$, $P=-0.386$). While, it also expressed non-significant and negative correlation with number of effective tillers ($G=-0.023$), number of filled grain per tiller ($G=-0.232$, $P=-0.213$), panicle length ($G=-0.149$, $P=-0.155$), thousand seeds weight ($G=-0.092$, $P=-0.072$), and yield per plant ($G=-0.210$, $P=-0.118$). Das and Sarma (2015) recorded similar result.

4.3.2 Flag leaf length (cm)

Flag leaf length exhibited highly significant and positive correlation with leaf blade length ($G=0.748$, $P=0.522$), leaf sheath length ($G=0.737$, $P=0.382$), stem length number ($G=0.327$, $P=0.287$), and number of filled grain per tiller ($G=0.315$, $P=0.255$). Moreover, there was observed non-significant but positive correlation with number of total tillers ($G=0.067$, $P=0.101$), number of unfilled grain per tiller ($G=0.013$), number of primary branches per panicle ($G=0.143$, $P=0.089$), and number of secondary branches per panicle ($P=0.023$). On the contrary, flag leaf length showed negative but highly significant relation with number of effective tillers ($G=-0.759$, $P=-0.259$), number of secondary branches per panicle ($G=-0.491^{**}$) thousand seed weight ($G=-0.439$), and yield per plant ($G=-0.654$). Besides, there was also observed negative but non-significant relationship with number of unfilled grain per tiller ($P=-0.001$), panicle length ($G=-0.016$, $P=-0.030$), thousand seeds weight ($P=-0.148$), and yield per plant ($P=-0.162$). Rahman *et al.* (2013) in his statistical analysis indicated that flag leaf length was positively correlated with panicle length.

4.3.3 Leaf blade length (cm)

Leaf blade length was observed to present highly significant and positive correlation with leaf sheath length ($G=0.905$, $P=0.506$) and stem length ($G=0.819$, $P=0.600$).

Moreover, it showed positive and non-significant relation with number of filled grain per tiller ($P=0.162$) number of primary branches per panicle ($G=0.023$), and panicle length ($G=0.142$, $P=0.102$). Whereas, it exhibited highly significant but negative correlation with number of effective tillers ($G=-0.252$, $P=-0.267$), number of unfilled grains per tiller ($G=-0.508$), number of secondary branches per panicle ($G=-0.846$), and yield per plant ($G=-0.280$). Furthermore, it expressed non-significant but negative correlation with number of total tillers ($G=-0.165$, $P=-0.006$), number of filled grains per tiller ($G=-0.190$), number of unfilled grains per tiller ($P=-0.220$), number of primary branches per panicle ($P=-0.028$), number of secondary branches per panicle ($P=-0.127$), thousand seeds weight ($G=-0.039$, $P=-0.046$), and yield per plant ($P=-0.167$). In 2013 Ranawake *et al.* found that leaf blade length has significantly positive correlation with seed weight.

4.3.4 Leaf sheath length (cm)

Leaf sheath length showed positive and significant relationship with stem length ($G=0.853$, $P=0.693$). It was also recorded positive and non-significant relationship with number of filled grains per tiller ($P=0.025$), number of primary branches per panicle ($G=0.166$, $P=0.135$), and thousand seeds weight ($G=0.048$, $P=0.054$). On the other hand leaf sheath length showed negative but significant correlation with number of effective tillers ($G=-0.579$, $P=-0.252$), number of total tillers ($G=-0.255$), number of unfilled grains per tiller ($G=-0.322$, $P=-0.281$), number of secondary branches per panicle ($G=-0.651$, $P=-0.256$) and yield per plant ($G=-0.380$). It also showed non-significant and negative correlation with number of total tillers ($P=-0.182$), number of filled grains per tiller ($G=-0.028$), panicle length ($G=-0.028$, $P=-0.000$), and yield per plant ($P=-0.148$). Similar result was observed by Islam *et al.* (2018).

4.3.5 Stem length (cm)

Stem length exhibited significant and positive correlation with thousand seeds weight ($G=0.259$) only. It showed positive but non-significant relation with number of total tillers ($P=0.002$), number of filled grains per tiller ($G=0.005$, $P=0.080$), number of primary branches per panicle ($G=0.002$), panicle length ($G=0.114$, $P=0.103$), and thousand seeds weight ($P=0.178$). It was also observed that, stem length had highly significant and negative relationship with number of effective tillers ($G=-0.471$, $P=-0.278$), number of unfilled grains per tiller ($G=-0.404$, $P=-0.311$), and number of

secondary branches per panicle ($G=-0.688$, $P=-0.305$), while negative but non-significant relation was found with number of total tillers ($G=-0.125$), number of primary branches per panicle ($P=-0.002$), and yield per plant ($G=-0.102$, $P=-0.071$). Rahman *et al.*(2014) got similar result.

4.3.6 Number of effective tillers

Number of effective tillers was found to show positive and highly significant relationship with number of secondary branches per panicle ($G=0.580$) and yield per plant ($P=0.535$). Moreover, it showed positive and no-significant relationship with number of total tillers ($G=0.184$, $P=0.041$), number of primary branches per panicle ($P=0.028$), and number of secondary branches per panicle ($P=0.077$). On the other hand, number of effective tillers showed negative but significant correlation with number of filled grains per tiller ($G=-0.586$, $P=-0.297$) and thousand seeds weight ($G=-0.350$), furthermore it represented non-significant and negative correlation with number of unfilled grains per tiller, ($G=-0.060$, $P=-0.055$), number of primary branches per panicle ($G=-0.143$), panicle length ($G=-0.075$, $P=-0.089$), thousand seeds weight ($P=-0.071$), and yield per plant ($G=-0.019$). In 2008, similar result was noted by Rokonuzzaman *et al.*

4.3.7 Number of total tillers

Number of total tillers exhibited highly significant and positive correlation with number of filled grains per tiller ($G=0.399$), number of unfilled grains per tiller ($G=0.521$, $P=0.327$), number of secondary branches per panicle ($G=0.791$, $P=0.360$), and yield per plant ($G=0.461$). Additionally positive but non-significant relation was found with number of filled grains per tiller ($P=0.201$), panicle length ($G=0.153$, $P=0.045$), thousand seeds weight ($G=0.117$), and yield per plant ($P=0.113$). Whereas, it showed significant but negative correlation with number of primary branches per panicle ($G=-0.249$) only. Moreover, non-significant and negative relation was noted with number of primary branches per panicle ($P=-0.100$) and thousand seeds weight ($P=-0.021$). Similar estimation was reported by Panigrahi *et al.*(2018).

4.3.8 Number of filled grains per tiller

Number of filled grains per tiller presented significant and positive relationship with number of unfilled grains per tiller ($G=0.853$, $P=0.721$), thousand seeds weight ($G=0.304$), and yield per plant ($G=0.504$, $P=0.379$). Moreover, it exhibited non-

significant and positive relationship with number of primary branches per panicle ($G=0.219$, $P=0.177$), number of secondary branches per panicle ($G=0.092$, $P=0.098$), and thousand seeds weight ($P=0.223$). On the other hand, it showed negative and non-significant correlation with panicle length ($G=-0.212$, $P=-0.161$). Chakrabarty *et al.*(2019) found positive and significant correlation between number of filled grains per tiller and yield per plant.

4.3.9 Number of unfilled grains per tiller

Number of unfilled grains per tiller exhibited positively significant correlation with number of primary branches per panicle ($G=0.278$, $P=0.260$), number of secondary branches per panicle ($G=0.497$, $P=0.329$), and yield per plant ($G=0.604$, $P=0.365$). Additionally, it presented non-significant but positive correlation with thousand seeds weight ($G=0.147$, $P=0.117$). On the contrary, number of unfilled grains per tiller showed highly significant but negative correlation with panicle length ($G=-0.369$, $P=-0.348$). Non-significant and negative correlation on yield per plant was reported by Chakrabarty *et al.*(2019).

4.3.10 Number of primary branches per panicle

Number of primary branches per panicle showed non-significant but positive relationship with yield per plant ($G=0.037$, $P=0.126$). On the other hand, it exhibited highly significant but negative relation with number of secondary branches per panicle ($G=-0.581$, $P=-0.411$) and panicle length ($G=-0.981$, $P=-0.958$), while it showed negative and non-significant correlation with thousand seeds weight ($G=-0.017$, $P=-0.007$). K. Tsuneo *et al.*(1996) found that the number of primary branches per panicle did not show positive genetic correlations with the traits for number of spikelets on secondary branches per panicle.

4.3.11 Number of secondary branches per panicle

Number of secondary branches per panicle was recorded to present significant and positive relation with panicle length ($G=0.423$, $P=0.307$) and yield per plant ($G=0.388$), while non-significant and positive relation was found with yield per plant ($P=0.047$). On the other hand, negative and non-significant correlation was observed with thousand seeds weight ($G=-0.057$, $P=-0.055$). In 1996 K. Tsuneo *et al.*found that secondary branches per panicle showed negative correlations with the traits of filled grain percentage.

4.3.12 Panicle length (cm)

Panicle length showed non-significant and positive correlation with thousand seeds weight ($G=0.039$, $P=0.020$). Whereas, it exhibited negative and non-significant correlation with yield per plant ($G=-0.154$, $P=-0.146$). In 2001, Chakraborty *et al.* reported similar result.

4.3.13 Thousand seeds weight (g)

Thousand seeds weight exhibited highly significant and positive correlation with yield per plant ($G=0.821$, $P=0.673$). Rokonzaman *et al.* (2008) observed the non-significant but positive correlation between thousand seeds weight and yield per plant.

4.4 Analysis of path co-efficient

Path analysis reveals the direct and indirect effects of the traits on yield and among themselves. this technique was discovered by Wright (2207) and demonstrated by Dewey and Lu (1959). it evaluates the direct effect of one variable upon the another. Such kind of data would be a good value in enabling the breeders to specifically identify the necessary traits of yield and utilize the genetic stocks for the improvement. Estimation of direct and indirect influence of path co-efficient analysis is presented in Table 7.

4.4.1 50% flowering

From the path analysis, it was observed that 50% flowering had direct but negative effect (-0.535) on yield per plant. Moreover, it showed positive indirect effect on number of effective tillers (0.013), number of total tillers (0.283), number of filled grains per tiller (0.124), number of unfilled grains per tiller (0.212), number of secondary branches per panicle (0.343), panicle length (0.080), and thousand seeds weight (0.049), while negative indirect effect on flag leaf length (-0.131), leaf blade length (-0.409), leaf sheath length (-0.213), stem length (-0.274), and number of primary branches per panicle (-0.114) with yield per plant. In 2015, Das and Sarma reported similar result.

4.4.2 Flag leaf length (cm)

Path analysis revealed that, flag leaf length had negatively direct effect (-2.521) on yield per plant. It expressed positive indirect effect on number of effective tillers (1.914), number of secondary branches per panicle (1.237), panicle length (0.041),

and thousand seeds weight (1.108). On the other hand, it presented negative indirect effect on 50% flowering (-0.619), leaf blade length (-1.885), leaf sheath length (-1.859), stem length (-0.824), number of total tillers (-0.170), number of filled grains per tiller (-0.795), number of unfilled grains per tiller (-0.033), and number of primary branches per panicle (-0.361) with yield per plant. In 2013, Reddy *et al.* recorded negative direct effect on grain yield by flag leaf length.

4.4.3 Leaf blade length (cm)

Leaf blade length had positive and direct effect (1.733) on yield per plant. It was also observed that, leaf blade length had positive indirect effect on 50% flowering (1.325), flag leaf length (1.296), leaf sheath length (1.568), stem length (1.419), number of primary branches per panicle (0.039), and panicle length (0.247); while, negative direct effect was recorded on number of effective tillers (-0.438), number of total tillers (-0.285), number of filled grains per tiller (-0.330), number of unfilled grains per tiller (-0.880), number of secondary branches per panicle (-1.465), and thousand seeds weight (-0.068) with yield per plant. Chhangte *et al.* in 2019 found similar result on aromatic rice that length of leaf blade has positive direct effect on grain yield per plant.

4.4.4 Leaf sheath length (cm)

Leaf sheath length was found to show negative direct effect (-1.064) on yield per plant. Moreover, it was also recorded that, leaf sheath length had positive indirect effect on number of effective tillers (0.616), number of total tillers (0.271), number of filled grains per tiller (0.029), number of unfilled grains per tiller (0.342), number of secondary branches per panicle (0.692), and panicle length (0.030), whereas it had negative and indirect effect on 50% flowering (-0.423), flag leaf length (-0.784), leaf blade length (-0.962), stem length (-0.908), number of primary branches per panicle (-0.177), and thousand seeds weight (-0.051) with yield per plant.

4.4.5 Stem length (cm)

Analysis of path expressed that, stem length had positive and direct effect (1.338) on yield per plant. Additionally, it had positive indirect effect on 50% flowering (0.686), flag leaf length (0.437), leaf blade length (1.096), leaf sheath length (1.142), number

Table 7. Partitioning of genotypic into direct (bold) and indirect effects of morphological characters of 23 rice genotypes by path co-efficient analysis

Traits	FFL	FLL	LBL	LSL	SL	NET	NTT	NFG	NUnFG	NPB	NSB	PL	TSW	Genotypic correlation with YPP
FFL	-0.535	-0.619	1.325	-0.423	0.686	-0.018	0.021	0.414	-1.749	3.591	-0.447	-2.524	0.068	-0.210
FLL	-0.131	-2.521	1.296	-0.784	0.437	-0.571	-0.003	-0.563	0.058	2.420	-0.342	-0.273	0.323	-0.654**
LBL	-0.409	-1.885	1.733	-0.962	1.096	-0.190	0.007	0.340	-2.240	0.381	-0.590	2.412	0.029	-0.280*
LSL	-0.213	-1.859	1.568	-1.064	1.142	-0.435	0.010	0.049	-1.420	2.807	-0.454	-0.477	-0.035	-0.380**
SL	-0.274	-0.824	1.419	-0.908	1.338	-0.354	0.005	-0.010	-1.781	0.026	-0.480	1.931	-0.190	-0.102
NET	0.013	1.914	-0.438	0.616	-0.631	0.751	-0.007	1.047	-0.263	-2.418	0.405	-1.265	0.257	-0.019
NTT	0.283	-0.170	-0.285	0.271	-0.167	0.139	-0.040	-0.712	2.298	-4.216	0.552	2.594	-0.086	0.461**
NFG	0.124	-0.795	-0.330	0.029	0.007	-0.441	-0.016	-1.786	3.765	3.701	0.064	-3.596	-0.224	0.504**
NUnFG	0.212	-0.033	-0.880	0.342	-0.540	-0.045	-0.021	-1.524	4.413	4.695	0.347	-6.255	-0.108	0.604**
NPB	-0.114	-0.361	0.039	-0.177	0.002	-0.107	0.010	-0.391	1.225	16.909	-0.406	-16.606	0.013	0.037
NSB	0.343	1.237	-1.465	0.692	-0.920	0.436	-0.031	-0.165	2.193	-9.829	0.698	7.157	0.042	0.388**
PL	0.080	0.041	0.247	0.030	0.153	-0.056	-0.006	0.379	-1.630	-16.586	0.295	16.929	-0.029	-0.154
TSW	0.049	1.108	-0.068	-0.051	0.346	-0.263	-0.005	-0.544	0.649	-0.292	-0.040	0.666	-0.736	0.821**
Residual effect = 0.04434														

Here,

* = Correlation is significant at the 0.05 level;
 ** = Correlation is significant at the 0.01 level.

FFL=50% flowering;
 FLL= Flag leaf length (cm);
 LBL= Leaf blade length (cm);
 LSL= Leaf sheath length (cm)
 SL= Stem length (cm);

NET= Number of effective tillers;
 NTT= Number of total tillers;
 NFG= Number of filled grains per tiller;
 NUnFG= Number of unfilled grains per tiller;

NPB= Number of primary branches per panicle;
 NSB= Number of secondary branches per panicle;
 PL =Panicle length (cm);
 TSW= Thousand seed weight (g); and
 YPP= Yield per plant (g)

of filled grains per tiller (0.007), number of primary branches per panicle (0.002), panicle length (0.153), and thousand seeds weight (0.346); while negative indirect effect was found on number of effective tillers (-0.631), number of total tillers (-0.167), number of unfilled grains per tiller (-0.540), and number of secondary branches per panicle (-0.920). Surjaye *et al.* in 2022 observed stem length was shown positive direct effect towards grain yield/plant (1.2384).

4.4.6 Number of effective tillers

Through the path analysis it was observed that, number of effective tillers had positive and direct effect (0.751) on yield per plant. It also exhibited negative in direct effect on 50% flowering (-0.018), flag leaf length (-0.571), leaf blade length (-0.190), leaf sheath length (-0.435), stem length (-0.354), number of filled grains per tiller (-0.441), number of unfilled grains per tiller (-0.045), number of primary branches per panicle (-0.107), panicle length (-0.056), and thousand seeds weight (-0.263); while positive indirect effect on number of total tillers (0.139) and number of secondary branches per panicle (0.436) with yield per plant. Rokonuzzaman *et al.* (2008) reported positive and direct effect on yield per plant by the number of effective tillers.

4.4.7 Number of total tillers

Number of total tillers had negative but direct effect (-0.040) on yield per plant. Moreover, positive indirect effect was recorded on 50% flowering (0.021), leaf blade length (0.007), leaf sheath length (0.010), stem length (0.005), and number of primary branches per panicle (0.010); whereas, negative indirect effect was found on flag leaf length (-0.003), number of effective tillers (-0.007), number of filled grains per tiller (-0.016), number of unfilled grains per tiller (-0.021), number of secondary branches per panicle (-0.031), panicle length (-0.006), and thousand seeds weight (-0.005) with yield per plant. In 2018, Panigrahi *et al.* observed positive and direct effect on yield per plant.

4.4.8 Number of filled grains per tiller

Number of filled grains per tiller showed negative but direct effect (-1.786) on yield per plant. Additionally, it exhibited positive indirect effect on 50% flowering (0.414), leaf blade length (0.340), leaf sheath length (0.049), number of effective tillers (1.047), and panicle length (0.379); while negative indirect influence was found on

flag leaf length (-0.563), stem length (-0.010), number of total tillers (-0.712), number of unfilled grains per tiller (-1.524), number of primary branches per panicle (-0.391), number of secondary branches per panicle (-0.165), and thousand seeds weight (-0.544) with yield per plant. In 2019, Chakrabarty *et al.* reported positive direct effect by the number of filled grain per tiller on yield per plant.

4.4.9 Number of unfilled grains per tiller

Analysis of path reveals that, number of unfilled grains per tiller had positive direct effect (4.413) on yield per plant. It was also estimated that, it had positive indirect effect on flag leaf length (0.058), number of total tillers (2.298), number of filled grains per tiller (3.765), number of primary branches per panicle (1.225), number of secondary branches per panicle (2.193), and thousand seeds weight (0.649); while, negative and indirect effect was noted on 50% flowering (-1.749), leaf blade length (-2.240), leaf sheath length (-1.420), stem length (-1.781), number of effective tillers (-0.263), panicle length (-1.630) with yield per plant. Chakrabarty *et al.* (2019) observed negative but direct effect by the number of unfilled grains per tiller on yield per plant.

4.4.10 Number of primary branches per panicle

By evaluating path co-efficient analysis, it was observed that, number of primary branches per panicle had positive and direct effect (16.909) on yield per plant. Moreover, it had positive indirect effect on 50% flowering (3.591), flag leaf length (2.420), leaf blade length (0.381), leaf sheath length (2.807), stem length (0.026), number of filled grains per tiller (3.701), and number of unfilled grains per tiller (4.695); whereas negative indirect effect was found on number of effective tillers (-2.418), number of total tillers (-4.216), number of secondary branches per panicle (-9.829), panicle length (-16.586), and thousand seeds weight (-0.292) with yield per plant. Chakraborty *et al.* (2001) noted similar finding.

4.4.11 Number of secondary branches per panicle

Through the path analysis, number of secondary branches per panicle showed positive and direct effect (0.698) on yield per plant. Additionally, it had positive but indirect influence on number of effective tillers (0.405), number of total tillers (0.552), number of filled grains per tiller (0.064), number of unfilled grains per tiller (0.347), and panicle length (0.295); while it had negative and indirect effect on 50% flowering

(-0.447), flag leaf length (-0.342), leaf blade length (-0.590), leaf sheath length (-0.454), stem length (-0.480), number of primary branches per panicle (-0.406), and thousand seeds weight (-0.040) with yield per plant. Similar result was reported by Hairmanis *et al.*(2011).

4.4.12 Panicle length (cm)

Panicle length was found to express positive and direct effect (16.929) on yield per plant. Moreover, it had negative indirect effect on 50% flowering (-2.524), flag leaf length (-0.273), leaf sheath length (-0.477), number of effective tillers (-1.265), number of filled grains per tiller (-3.596), number of unfilled grains per tiller (-6.255), and number of primary branches per panicle (-16.606); while positive indirect effect was recorded on leaf blade length (2.412), stem length (1.931), number of total tillers (2.594), number of secondary branches per panicle (7.157), and thousand seeds weight (0.666) with yield per plant. In 2010, Chakraborty *et al.*observed similar estimation for panicle length.

4.4.13 Thousand seed weight (g)

Evaluation of path reveals that, thousand seeds weight had negative but direct effect (-0.736) on yield per plant. Additionally, it had positive and indirect effect on 50% flowering (0.068), flag leaf length (0.323), leaf blade length (0.029), number of effective tillers (0.257), number of primary branches per panicle (0.013), and number of secondary branches per panicle (0.042); while negative indirect effect was recorded on leaf sheath length (-0.035), stem length (-0.190), number of total tillers (-0.086), number of filled grains per tiller (-0.224), number of unfilled grains per tiller (-0.108), and panicle length (-0.029) with yield per plant. In 2008, Rokonuzzaman *et al.*observed positive direct effect by the thousand seeds weight on yield per plant.

CHAPTER IV

SUMMARY AND CONCLUSION

The present experiment was conducted with twenty three genotypes of Boro rice (*O. sativa* L.) at the experimental area of the Sher-e-Bangla Agricultural University, Bangladesh during the December, 2020 to May, 2021. Seedlings were transplanted in the main farm by following the Randomized Complete Block Design with three replications. Data different yield contributing traits were collected such as, 50% flowering, flag leaf length, leaf blade length, leaf sheath length, stem length, number of effective tillers, number of total tillers, number of filled grains per tiller, number of unfilled grains per tiller, number of primary branches per panicle, number of secondary branches per panicle, panicle length, thousand seeds weight, and yield per plant.

From variability analysis of twenty three genotypes, it was found that, highly significant variation among all the genotypes were observed for all the studied traits. The minimum days for flowering were noted in G20 (59.33 days), while a highest day to flowering was found in G19 (76.67 days). The largest flag leaf length was observed in G23 (29.60 cm), whereas smallest length for flag leaf was recorded in G1 (21.37 cm). The maximum length for leaf blade was found in G23 (37.70 cm), while minimum was noted in G20 (28.07 cm). The smallest leaf sheath length was observed in G1 (19.40 cm), while longest one was noted in G22 (31.33 cm). Maximum stem length was recorded in G19 (71.83 cm), whereas smallest stem was observed in G1 (46.37 cm). The maximum number effective tillers were found in G1 (17.00), while lowest numbers of effective tillers were noted in G5 (9.00). The highest number of total tillers was noted in G3 (21.33), while lowest number of total tillers was found in G23 (14.00). The highest number of filled grains per tiller was observed in G20 (144.00), while smallest number of filled grains per tiller was noted in G1 (90.33). The lowest number of unfilled grains per tiller was recorded in G23 (7.33) while highest number was found in G20 (31.00). The maximum number of primary branches per panicle was recorded in G23 (24.00), while minimum number of primary branches per panicle was noted in G9 (10.33). The highest number of secondary branches per panicle was observed in G17 (42.33), while the minimum number was recorded in G13 (34.67). The longest length for panicle was found in G3 (24.06 cm), while the smallest length for panicle was found in G17 (11.17 cm). The maximum

weight for thousand seeds was observed in G5 (27.45 g), while minimum thousand seeds weight was noted in G11 (12.05 g). The highest yield per plant was found in G20 (43.17 g), while the lowest yield per plant was recorded in G11 (14.29 g).

The phenotypic variance for all the traits was higher than the genotypic variance. Similarly, phenotypic co-efficient of variation were also found higher than the genotypic co-efficient of variation for all of the studied characters, indicating the influence of environment for the expression of the characters. High heritability coupled with high genetic advance in a percent of mean was found for leaf sheath length, number of unfilled grains per tiller, number of primary branches per panicle, panicle length, and thousand seeds weight, suggesting that there was the existence of additive gene action for the expression these traits; so that, simple selection for these characters could be possible for future breeding program.

Evaluation of correlation analysis revealed that, yield per plant had significant positive association with number of effective tillers ($P= 0.535$), number of total tiller ($G= 0.461$), number of filled grain per tiller ($G= 0.504$, $P= 0.379$), number of unfilled grain per tiller ($G= 0.604$, $P= 0.365$), number of primary branches per panicle ($G= 0.388$), and thousand seeds weight ($G= 0.821$, $P= 0.673$).

Path co-efficient analysis exhibited that, leaf blade length (1.733), stem length (1.338), number of effective tillers (0.751), number of unfilled grains per tiller (4.413), number of primary branches per panicle (16.909), number of secondary branches per panicle (0.698), panicle length (16.929) had positive and direct effect toward yield per plant.

The traits which had high ranges of genetic variability, high heritability, high genetic advance percent in mean, highest degree of significant and positive association, and direct positive effect on yield per plant would be very effective and excellent tool for improving yield potential. Moreover, G1 for producing maximum number of effective tillers, G3 for highest number of total tillers, G5 for highest thousand seeds weight, and G20 for maximum yield per plant and early flowering could be used for further breeding programs.

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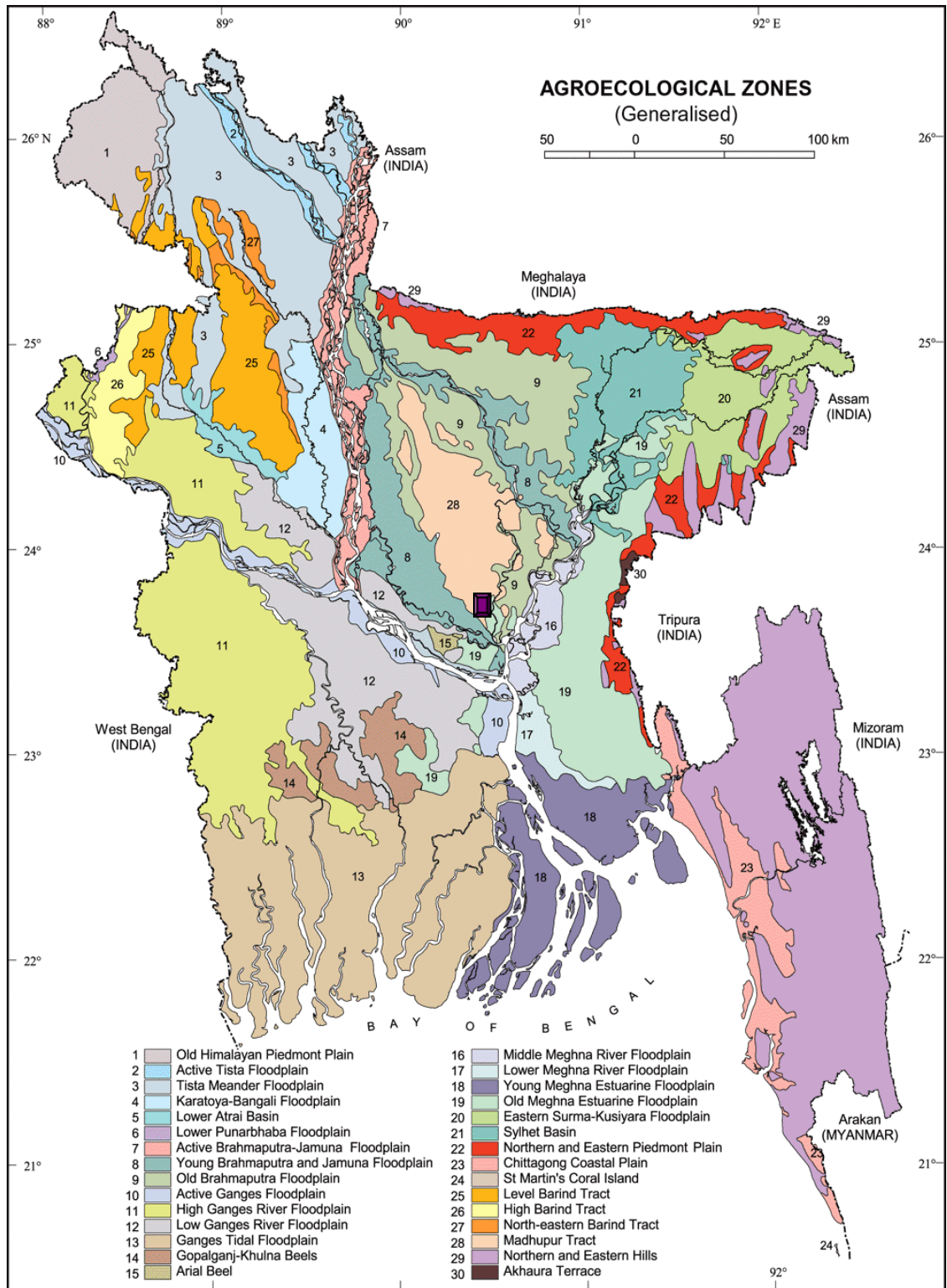
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APPENDICES

Appendix I. Map exhibiting the experimental location under the experiment



 The experimental site under the research

Appendix II. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from December, 2020 to May, 2021

MONTH	AVG. TEMPERATURE (°C)	RELATIVE HUMIDITY (%)	TOTAL RAINFALL (MM)
DECEMBER, 2020	21.4	63	8
JANUARY, 2021	20.7	69	18
FEBRUARY, 2021	23.6	57	2
MARCH, 2021	26.7	56	27
APRIL, 2021	28.4	59	58
MAY, 2021	30.5	68	204

Source: Bangladesh Meteorological Department (Climate Division, Dhaka Station), Agargaon, Dhaka – 1207

Appendix III. Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil particles	Percentage
Sand	37
Clay	36.7
Silt	26.40
Texture Class	Loamy clay

B. Chemical composition of the soil

Soil Chemicals	Amount
Organic Carbon	0.82 %
Total N	1790.00 (kg/ha)
Available N	55.00 (kg/ha)
Total P	841.00 (kg/ha)
Available P	70.00 (kg/ha)
Exchangeable K	89.50 (kg/ha)
Total S	225.00 (ppm)
Available S	16.01 (ppm)
pH	5.55

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka