

# COMPARATIVE TRIAL AMONG TEN ADVANCED LINES OF BORO RICE

THESIS

BY

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**COMPARATIVE TRIAL AMONG TEN ADVANCED LINES  
OF BORO RICE**

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## *CERTIFICATE*

*This is to certify that the thesis entitled, “COMPARATIVE TRIAL AMONG TEN ADVANCED LINES OF BORO RICE” submitted to the Department of Genetics and Plant Breeding, Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE (MS) IN GENETICS AND PLANT BREEDING, embodies the result of a piece of Bonafede research work carried out by Jannatul Afroze Registration No. 18-09316 under my supervision and my guidance. No part of the thesis has been submitted for any other degree or diploma.*

*I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.*

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**DEDICATED TO  
MY  
BELOVED PARENTS**

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## ABSTRACT

The investigation was carried out under the field condition to characterize and study variability among the ten advanced boro rice lines (F9 genotypes) during the period of boro season (2017-2018) at the experimental field of Sher-e-Bangla Agricultural University, Dhaka. Variability study are carried out on twelve parameters to select the best lines for further trial. Among all the quantitative character number of effective tillers per plant, time of maturity, thousand grain weight and yield showed difference in all the lines which showed better agronomic performance. The highest days to maturity was observed in L8 (141 days) and the minimum days to maturity was observed in L5 (134 days). Phenotypic variance for number of total tillers per plant showed (3.26) was higher than genotypic variance (0.68) indicating moderate environmental influence on these characters and high difference between the phenotypic coefficient of variation (12.94%) and the genotypic coefficient of variation (6.71%) value indicating that this trait was highly influenced by the environment. L5 showed the maximum (9.21 t/ha) yield per hectare and the minimum by in L10 (7.07 t/ha). Days to maturity showed high heritability (72.25%) coupled with low genetic advance (3.26) and moderate genetic advance in percentage of mean (2.38%). Yield per hectare exhibited high heritability (55.05%) conjunction with very low genetic advance (0.86) and genetic advance in percentage of mean (10.94%). Days to maturity showed significant and positive correlation with plant height ( $G=0.375^*$ ) at genotypic level suggested that if days to maturity increased the plant height also increased. It also exhibited significant and positive contribution with plant height ( $G=0.375$ ,  $P=0.327$ ) at both genotypic and phenotypic level and with number of effective tiller ( $P=0.034$ ), total number of filled grain per panicle ( $P=0.001$ ) at phenotypic level. Days to maturity showed significant negative association with thousand seed weight ( $G=-0.062$ ,  $P=-0.141$ ) at both genotypic and phenotypic level. Path coefficient analysis revealed that days to maturity was negatively correlated ( $-0.548^{**}$ ) and had negative direct effect ( $-0.422$ ) on yield per hectare. Thus, the lines L5, L8 and L9 would be suitable for release as high yielding boro rice variety for their short duration and high yielding characters.

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## ABBREVIATION AND ACRONYMS

AEZ	=	Agro-Ecological Zone
BARI	=	Bangladesh Agricultural Research Institute
HRC	=	Horticulture Research Centre
BBS	=	Bangladesh Bureau of Statistics
FAO	=	Food and Agricultural Organization
N	=	Nitrogen
<i>et al.</i>	=	And others
TSP	=	Triple Super Phosphate
MOP	=	Murate of Potash
RCBD	=	Randomized Complete Block Design
DAT	=	Days after Transplanting
ha <sup>-1</sup>	=	Per hectare
g	=	gram (g)
kg	=	Kilogram
SAU	=	Sher-e-Bangla Agricultural University
SRDI	=	Soil Resources and Development Institute
wt	=	Weight
LSD	=	Least Significant Difference
°C	=	Degree Celsius
NS	=	Not significant
Max	=	Maximum
Min	=	Minimum
%	=	Percent
NPK	=	Nitrogen, Phosphorus and Potassium
CV%	=	Percentage of Coefficient of Variance

## CHAPTER 1

### INTRODUCTION

Rice is a self-pollinated cereal crop belong to genus *Oryza* of family *Poaceae* under the order *Cyperales* and class *Monocotyledon* (Hooker, 1979). Rice plays a dominant role in the agriculture sector of Bangladesh and it is the staple food for Bangladeshi people. In Bangladesh, majority of food grain comes from rice (*O. sativa* L.). Rice is the most important food crop in terms of area, production and its contribution to the national income and national economic development. Rice provides 21% energy and 15% of per capita protein for global human (Maclean *et al.*, 2002). Various morphological and physiological characters contribute the yield of rice, and the yield contributing characters are interrelated with each other with a complex chain relationship and it is also highly influenced by the environmental conditions. Developing country like Bangladesh is striving hard for rapid development of its economy. The economic development of our country is mainly based on agriculture. The contribution of agriculture sector in Gross Domestic Product (GDP) is 14.23% (GoB, 2021). In Bangladesh almost 66% of the labor force depends on agriculture for employment.

Almost 80% of the total cropped area is planted with rice, which accounts for more than 90% of total grain production (Asaduzzaman *et al.*, 2010). There are thousands of rice varieties, genotypes, land races and wild species which differ with respect to plant and grain characteristics like plant type, height, nature of leaves, grain size, texture, glutinous nature, aroma and cooking quality of Boro is the dry-season irrigated rice planted from mid-November mid-December to early February and harvested between April and May. Earlier, boro was grown in the very low-lying areas with residual water from the wet season and irrigated manually using surface water in times of water shortage (Fujita, 2010). Such traditional boro rice was transplanted after the recession of floodwater in November and harvested from April to May. In the mid-1960s, the modern high

yielding rice variety IR-8 was introduced into Bangladesh agriculture, primarily for boro season using irrigation. Boro covers the largest production area and produces the highest amount of rice in Bangladesh. Alternatively, early rice varieties in Boro season might also help to create a gap between Boro and Aus, which can be utilized to grow minor crops in between to promote crop diversification. The continuous growing of rice in the same land decreases soil fertility and soil health. Therefore, the land can be kept fallow or grown with green manuring crops in the gap period before the Aus starts, which might be also helpful for improving soil health and nutrition status. BRRI dhan 28 and BRRI dhan 29 are the two popular rice variety. The duration of BRRI dhan 28 is 140 days and BRRI dhan 29 is 160 days.

A breeding program was carried out using boro and aus rice varieties. The generation have been advanced and selection was carried out for short duration and higher yielding rice varieties suitable for boro season and to find out some suitable rice lines for future trial and release if found suitable. The available variability in a population can be partitioned into genetic parameters such as coefficients of variation, heritability and genetic advance to serve as basis for selection of desirable genotypes. Thus, the identification of important components and information about their association with yield and other traits are very useful for developing efficient selection strategy for developing high yielding varieties. Genetic diversity is an important tool for a crop improvement program, as it helps in the development of superior recombinants (Manonmani and Fazlullah, 2003). Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different traits (Nayak *et al.*, 2004).

For the better understand of growth, physiological and yield related characters; investigation on their genetic system is vitally important. Studies on character association and components of genetic variance would serve the above purpose. Genotypic and phenotypic interrelationships of morphological and physiological

characters and their possible influence on yield attributes needs to be analyzed for interpreting the results of breeding works meaningfully.

**OBJECTIVES:**

1. To characterize various traits among the advanced rice lines.
2. To evaluate the performance of ten advanced lines of boro rice meaningful comparison, and
3. To select better and promising boro rice lines for future use.

## CHAPTER 2

### REVIEW OF LITERATURE

Due to application of different techniques in breeding process remarkable improvement has been brought in both productivity and quality of rice. A large number of literatures are available on variability, genetic diversity, correlation and path analysis of yield and yield contributing characters of rice grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely-

- Genetic variability, heritability and genetic advance
- Correlation among different characters
- Path coefficient analysis
- Genetic diversity analysis

#### **2.1 Genetic Variability, heritability and genetic advance**

Austin *et al.* (1980) reported that yield potential is determined by the total dry matter or biomass and the harvest index (HI, the grain-to-straw ratio). Harvestable yield is the product of total biomass produced times HI. For cereal crops, genetic gain in yield potential usually resulted from improved HI. For cereal crops, genetic gain in yield potential usually resulted from improved HI through modified canopy architecture.

Sinha *et al.* (1985) investigated on gene systems governing yield and its component characters in rice. Analysis was performed, by Griffing's methods, of data on some botanical characters, yield and various components of yield and some aspects of grain quality from a 6-variety complete diallel cross and a 7-variety half diallel cross. Additive effects were found more important than non-additive in every character except height and number of tillers, indicating the suitability of the pedigree method in breeding, though the use of recurrent



selection and biparental mating would make it possible to exploit the dominance effects which in some characters were not negligible. The best general combiners for yield and for some components were T141, ASDI and Vijaya, but for protein percentage SLO16 and ADY27 were the best. Vijaya  $\times$  T141 and Vijaya  $\times$  ASDI showed high specific combining ability for yield.

Agarwal and Sharma (1987) conducted diallel analysis for growth duration involving diverse genotypes of rice. Results indicated partial dominance for 50% flowering and days to maturity and the importance of additive and dominance effects in the inheritance of these characters. Asymmetrical distributions of dominant and recessive genes were observed in the parents. Narrow-sense heritability was high for both characters.

Kalaimani *et al.* (1988) reported combining ability for yield and yield components in rice. Results from a 7 $\times$ 7 diallel cross indicated that GCA variance than SCA for yield and characters related to yield. The best combiners were IR8 for all characters, 340 and ADT3 for earliness and grain weight, Co37 for yield and IR20 for grains per panicle. The progeny of cross between 340 and IR8 gave the highest yield (36.23 g per plant) and involved local and exotic germplasm in the percentage. A total of populations of crosses involving six cultivars in a diallel set and data for four quantitative traits were analyzed for combining ability (Mishra and Khare, 1991). The length/breadth ratio (LBR) of grain was governed by additive gene effects, whereas number of fertile spikelet's/panicle (FSP), 1000-seed weight (GW) and grain yield/plant (GYP), were controlled by nonadditive effects. Good general combines were Poorva for FSP, Rasi for GW, IR36 for LBR and IR50 for GYP of the crosses, best specific combiners were Poorva $\times$  Tripti for FSP, IR50  $\times$  Rasi for GW and GYP and Anupama  $\times$  IR50 for LBR.

Das *et al.* (1992); evaluated 30 rice genotypes for variability analysis and found that plant height, days to 50% flowering, number of filled grains per panicle, panicle length, 1000-grains weight and days to maturity had high genetic coefficient of variation.

Vivekzuradan and Subramanian (1993) evaluated 28 rice genotypes for the magnitude of genetic divergence using Mahalanobis's  $D^2$  statistics. The population was grouped into five clusters. Plant height and grain yield contributed considerably, accounting for 85% of total divergence. The geographic diversity has not been found related to genetic diversity.

Sing *et al.* (1993) studied genetics of earliness in an eight-parent half-diallel cross in rice. Days to heading appeared to be controlled by both additive and dominance gene effects. Parents carried an abundance of dominant alleles operating towards lateness and displaying overdominance. Heritability in the narrow sense reflected preponderance of additive genetic variance. *Per se* performance was closely associated with general combining ability effects of parents and specific combining ability effects of crosses. Pusa 33, Saket 4, Prasanna and Sujata were good general combiners for earliness. The cross Pusa 33  $\times$  Pankaj appeared promising for isolating high yielding lines of short duration.

Surek and Korkut (1996) determined combining ability for yield and its contributing characters in rice. Eight rice cultivars were crossed in diallel fashion excluding reciprocals. They reported significant variances for GCA for all the studied traits except grain yield/plant. The ratios of the components (GCA/SCA) revealed that magnitude of GCA was greater than SCA for days to flowering, plant height, panicle length, panicles/plant, spikelet sterility, 1000 grain weight, grain length and grain breadth. Whereas, this ratio indicated the higher magnitude of nonadditive gene effects for biological yield/plant, grain yield/plant, and harvest index. Parents and crosses with high general and specific combining ability for various characters were identified.

Pandey and Awasthy (2001), studied genetic variability of 21 genotypes of aromatic rice and reported significant genetic variability for plant height, days to 50% flowering, panicle per hill, panicle length, grains per panicle, grain length and breadth. They concluded that these traits play a major role in the

enhancement of production of grain yield and serve as important criteria for screening germplasm to identify the suitable aromatic rice cultivars.

Basher (2002), studied genetic divergence among 36 genotypes by using  $D^2$  statistics for 15 characters related to yield and its contributing characters. The genotypes were grouped into six clusters. The results revealed that the harvest index had the highest contribution followed by tillers per plant, panicle length, 1000-grains weight, filled grains per panicle, days to maturity and leaf photosynthetic rate towards genetic divergence.

Roy *et al.* (2002); evaluated 50 rice cultivars for genetic diversity and responded that plant height, tiller numbers, panicle length, 100-grains weight, 100-kernel weight, filled grains/panicle and kernel-grain ratio contributed most towards divergence.

Mishra *et al.* (2003); evaluated 16 rice cultivars and their 72  $F_1$  hybrids for genetic diversity and grouped in twelve clusters using Mahalanobis's  $D^2$  statistics. The values revealed that plant height, ear bearing tillers per plant, panicle length, 1000-grain weight, hulling and milling percentage, biological yield, harvest index, kernel length after cooking, gelatinization temperature and grain yield were the main factors for differentiation.

Souresh *et al.* (2004); studied the genetic diversity of quantitative and qualitative traits of 36 lines and cultivars of rice using 17 traits including grain yield, number of particles per plant, number of filled grains per panicle, 1000-grains weight, leaf length, leaf width, leaf area, plant height, culm length, amylose content of the grain, gel consistency, panicle weight, grain length, grain width, grain shape, days to 50% flowering and maturity.

Madhaviatha *et al.* (2005) were evaluated fifty-four elite rice genotypes for their variability with regards to grain yield, yield components (plant height, number of effective tillers per plant, panicle length, number of grains per panicle, fertility percentage, days to 50% flowering, days to maturity and harvest index) and quality parameters (hulling recovery, kernel length (L), breadth (B), L/B ratio

and elongation ratio, volume expansion ratio and 1000-grains weight). Estimation of heritability and genetic advance were also obtained for the above traits.

Houque *et al.* (2020) studied 43 rice genotypes including some released varieties and advanced lines were evaluated based on morpho-genetic parameters. A field experiment was conducted at the field laboratory of Genetics and Plant Breeding Department, Bangladesh Agricultural University using a randomized complete block design with three replications. Analysis of variance revealed that all genotypes exhibited significant variations ( $P \leq 0.001$ ) for all considered traits except leaf length indicating a wider extent of variability for selection. Greater phenotypic coefficient of variation (PCV) compared to corresponding genotypic coefficient of variation (GCV) for all the traits representing environmental influence on the studied traits. High GCV and PCV values were observed for the most important yield related traits like seedling height, leaf length, flag leaf area, flag leaf angle, number of effective tiller hill<sup>-1</sup>, 1000-grain weight and yield plant<sup>-1</sup>. These results suggested that selecting genotypes with these traits could be way for attaining enhancement in rice yield. Majority of the traits displayed high heritability (>60%) with high genetic advance (>20%) pointing towards non-additive gene action suggesting selection should be practiced carefully. Correlation study explored significant positive and negative association among yield and related attributes. Principal component analysis revealed the most important traits contributing to the variations among the genotypes. According to cluster analysis, 43 genotypes were grouped into 4 clusters among which genotypes within cluster I and cluster III might be selected for future rice breeding programs regarding yield potentiality and other related traits.

Regularly the inter-cluster distances were greater than the intra-cluster distances suggesting wider diversity among the genotypes. Maximum inter cluster distance was observed between cluster III and VII followed by cluster II and VII indicating the possibility to obtain the heterotic progenies, by attempting the crosses among the genotypes of these groups. The results of principal component

analysis (PCA) revealed that first three components accounted for more than 80% of total variation. The highest variability was observed in days to 50% flowering, number of filled grain per panicle, number of unfilled grain per panicle, yield per plot, flag leaf area and plant height.

## **2.2. Correlation coefficient**

Rai and Murty (1978) investigated correlations between specific leaf weight (SLW) and 4 physiological characters of 18 rice cv. at the mid tillering, max. tillering and flowering stages. The results showed that SLW was negatively correlated with LAI at all the growth stages and with leaf length at the tillering stage and that tillering stage and that SLW was positively correlated with leaf length at the flowering stage. The relationship between SLW and photosynthetic efficiency of the crops at different growth stages was discussed.

Singh (1980) conducted an experiment on association of grain yield and its components in  $F_1$  and  $F_2$  populations of rice. Correlation analysis of data from segregating and nonsegregating populations from a  $6 \times 6$  diallel, excluding reciprocals, revealed that grain yield per plant was positively correlated with number of fertile tillers, grain weight and number of fertile grains per panicle in both  $F_1$  and  $F_2$ .

Subramaninan and Rathinam (1984) studied association of grain yield attributes in the hybrids of crosses between tall and semi-dwarf varieties of rice. Genotypic associations between grain yield/plant and eight related characters were evaluated in a diallel cross of 10 varieties conducted during three seasons. Grain yield was correlated positively with 100-grain weight, tiller number and grain: straw ratio, and length: width ratio of the grain.

Choi (1985) reported that genotypic correlations between the characters were mostly higher than phenotypic correlations in 15  $F_1$ 's derived from a  $6 \times 6$  diallel cross in rice. In this study, grain yield was positively correlated with spikelet number/panicle.

Kim (1987) analyzed correlation among six panicle characters in rice. Analysis of a diallel cross involving Raekyung, Yeongnamjosaeng, Nongbaek, Yushin and Honenwase showed that all the panicle traits investigated were correlated with each other, apart from the number of grains per primary branch, and that the number of secondary branches per primary branch influenced the number of grains per panicle most.

Rahangdale *et al.* (1987) investigated the physiological basis of varietal differences in productivity of early tall and late dwarf upland rice (*Oryza sativa* L.). Higher yields in late dwarf cv. Were ascribed to the higher RGR, NAR and LAI during the post-flowering period. Dwarf cv. Contained higher chlorophyll contents during the tillering and flag leaf stages. Yield was positively correlated with leaf angle, panicles/plant, chlorophyll content at the flag leaf stage and harvest index.

Gomathinayagam *et al.* (1988) obtained positive and significant correlation of grain yield with growth duration and plant height in upland varieties of rice.

Manuel and Palanisamy (1989) derived correlation coefficients on nine yield components in six cultivars and their F<sub>1</sub> hybrids. Grain yield was significantly and positively correlated with days to flowering, plant height, flag leaf area, panicles/plant, panicle length and grains/panicle.

Sampath *et al.* (1989) generated information on yield correlations which was derived from data on grain yield and 12 related traits in 14 intervarietal hybrids and their parents grown in 1983. Yield was correlated significantly with 100-grain weight, panicle length and number of grains/panicle in the parents but not the hybrids in which yield was correlated with the number of primary and secondary branches/panicle, number of days to panicle emergence and tiller number. F<sub>1</sub> mean performance was correlated with the mid parental and better parent values, the correlation being less marked with the better parent value, suggesting that the high performance of the F<sub>1</sub>'s was not due to the better parent alone.

Mirza *et al.* (1992) carried out correlation studies and path analysis of plant height, yield and yield components in rice (*O. sativa* L.). Six crosses and five parental rice genotypes were compared in field experiments at Kala Shah Kuku, Pakistan in the Kharif (rainy) season of 1989, in order to develop selection criteria for rice breeding. Plant height was positively correlated with panicle length and 1000-grain weight. Grain yield was positively correlated with 1000-grain weight and number of grains/panicle and number of panicles/plant should be used as selection criteria.

Bai *et al.* (1992) studied correlation of yield and yield components in medium duration rice cultivars. Fifty-eight medium durated rice cultivars were sown in wet and dry seasons of 1990, in kerala, India. Grain yield per plant positively correlated with numbers of productive tillers, plant height, panicle length and numbers of productive tillers, plant height, panicle length and number of grains/panicle at genotypic and phenotypic levels. Flag leaf area and panicle exertion were positively correlated with yield only at genotypic level. The genotypic correlations were greater than the phenotypic ones.

Manomani *et al.* (1999) studied relationship between earliness and other yield components were analyzed in 20 crosses involving four early and five very early lines in India rice. Earliness (days to flowering), had significant and positive correlation with most of the characters studied. Positive significant association was observed among the yield components. Correlation studies revealed that selection for very early types obviously resulted in reduction in panicle length, number of grains and 100-grain weight which in turn reduced the yield.

Meenakshi *et al.* (1999) carried out experiment on correlation of yield and some physiological characters in rainfed rice. Yield correlations were derived from data on yield and physiological components in 10 genotypes and their 21 hybrids grown at Madurai. Productive tillers/plant, dry matter production (DMP) and harvest index was positively correlated with grain yield. Path analysis revealed that DMP was the most important character influencing yield.

Govindarasu *et al.* (1999) investigated in rice (*Oryza sativa*) to study the components of yield sink capacity. Among 17 component characters analyzed by correlation study, spikelets, grains, high density grains/panicle, secondary branches/panicle, spikelets, and grains and high-density grains on secondary branches were found to be important contributing characters for grain yield/panicle. The varieties which registered high values for these traits also recorded higher grain yield/ panicle. Inter-correlation among these important contributing characters indicated strong correlation among themselves suggesting simultaneous improvement of these characters through a simple selection. The study suggested that while handling a large germplasm or segregating populations by the breeders, secondary branches/panicle might be used as a criterion for selection for higher grain yield in rice, as recording of this character is simple and easy compared with other contributing characters.

Cui *et al.* (2000) carried out experiments to find out the relationship between harvest index and morphological characteristics in rice using 60 Japanese varieties (J group) and 20 high yielding varieties bred in Asian countries (H group). In the J group, HI showed a positive correlation with varieties bred in Asian countries (H group). In the J group, HI showed a positive correlation with leaf color (SPAD value, SV) and a negative correlation with plant length [height] (PL) at the heading time. In the H group, HI showed a positive correlation with SV, but the correlation coefficient between HI and PL was not significant. The correlation between HI and culm length (CL) was similar to that between HI and PL. HI showed a negative correlation with ear length (EL) in the J group, but significantly positive correlation in the H group. There was a significantly positive correlation between EL/CL and HI in the H group. A significant multiple correlation coefficient was obtained between HI and SV(X1), PL(X2) or EL/CL (X3). Consequently, it is considered that these morphological characteristics are useful indexes to select varieties with a high harvest index.



### 2.3 Path coefficient analysis

Prasad *et al.* (2001) studied genetic variability and selection criteria of eight fine rice genotypes for some yield contributing characters through correlation and path analysis. Path coefficient analysis revealed maximum contribution of fertile grains per panicle to grain yield.

Iftekharuddaula *et al.* (2001) studied twenty-four modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for grain yield and its component characters. Path analysis revealed that higher number of grains/panicle, bold grains, more panicles/m<sup>2</sup> and higher harvest index had positive and higher direct effect on grain yield.

Moreover, days to maturity, days to flowering, plant height and spikelet/panicle had positive and higher indirect effect on grain yield through grains/panicle.

Mahto *et al.* (2003); evaluated twenty-six early maturing upland rice genotypes for genetic variation, character association and path analysis based on days to 50% flowering. Plant height, number of panicle per plant, panicle length, number of branches per panicle. Number of filled grains per panicle, 1000-grain weight and grain yield. The genotypic variance ranged from 5.36 for panicle length to 24.83 for grain yield. The difference between phenotypic and genotypic coefficient of variation was minimum for 1000-grain weight (0.12) and days to 50% flowering (0.13). High values of heritability were observed for 1000-grains weight (98.30%) and days to 50% flowering (97.33%). The number of grains per panicle and panicle length showed a significant difference between phenotypic and genotypic coefficient of variation. The association of high heritability with high genetic advance was observed for 1000-grain weight, days to 50% flowering, grain yield, number of branches per panicle and plant height. Grain yield was positively and significantly correlated with days to 50% flowering, number of panicles per plant, number of branches per panicle and number of filled grains per panicle.

Habib *et al.* (2005) evaluated path coefficient through the experiment using 10 local birion rice varieties. Path analysis revealed that plant height, days to maturity, 1000-grain weight and chlorophyll content had positive and highest direct effect on grain yields. Moreover, panicle length had highest indirect effect on grain yield through plant height and filled grains per panicle had positive and higher effect on grain yield through days to maturity, panicles per hill and panicle length.

Agahi *et al.* (2007) investigated path coefficient of grain yield and sixteen yield-related traits among 25 lines. Genotypic and phenotypic path coefficient analysis revealed that the number of productive tillers had the highest positive direct effect on grain yield (pp = 1.034, pg = 1.196). The second and third traits were the number of grain per panicle (pp = 0.665, pg = 0.813) and 100-grain weight (pp = 0.440, pg = 0.425) respectively.

Rokonuzzaman *et al.* (2008) evaluated the variability and genetic association for grain yield component characters of twenty Boro rice varieties. Path coefficient showed that number of effective tillers per plant and plant heights were the characters that contribute largely to grain yield.

Kole *et al.* (2008) studied path coefficient for twelve morphological characters were studied on 18 morphologically distinct mutants in M4 generation along with their two mother genotypes (IET 14142 and IET 14143), which were developed from Tulaipanja, an aromatic non-basmati rice cultivar of West Bengal. The results of genotypic path analysis revealed that panicle number had the highest positive direct effect followed by grain number, test weight, plant height, days to flower and straw weight.

Yadav *et al.* (2010) carried out a field experiment was to establish the extent of association between yield and yield components and others characters in rice. They found that the path coefficient at genotypic level revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of

spikelets per panicle, plant height and test weight had direct positive effect on seed yield per hill, indicating these are the main contributors to yield.

Chakraborty *et al.* (2010) studied on the path analysis of 29 genotypes of rice. Path analysis based on genotypic correlation coefficients elucidated high positive direct effect of harvest index (0.86), panicle length (0.2560) and 100-grain weight (0.1632) on yield per plant with a residual effect of 0.33. Plant height and panicles per plant recorded high positive indirect effect on yield per plant via harvest index whereas effective grains per panicle on yield per plant via harvest index and panicle length.

Sadeghi (2011) used 49 rice varieties (*Oryza sativa* L.) in an experiment to determine variability, heritability and correlation between yield and yield components for 2 years. Result of the phenotypic path analysis revealed that the numbers of productive tillers had the highest positive direct effect followed by days to maturity, grains per panicle and 1000-grain weight.

Satheeshkumar *et al.* (2012) carried out estimation of path analysis in fifty-three genotypes of rice for fifteen characters. The maximum positive direct effects were observed for kernel L/B ratio, kernel length, filled grains per panicle, total number of grains, and number of productive tillers per plant.

Rangare *et al.* (2012) evaluated forty exotic and Indian rice germplasm including one local check for their efficiency with respect to eleven yield and yield contributing characters from Kharif 2009 under normal conditions. This study for improvement of yield was used through path coefficient analysis, and results revealed that biological yield per plant, harvest index, number of fertile tiller per plant, days to 50% flowering, test weight, days to maturity and panicle length all had important role in the improvement of grain yield in rice at genotypic and phenotypic levels.

Ganapati *et al.* (2014) evaluated twenty-five genotypes of rice for yield and yield contributing characters to observe their direct and indirect effect on yield during Aman season, 2010. From the results of path analysis, it was evident that direct

positive effects contributed by tiller per hill, number of filled grain per panicle and thousand grain weights were high indicating that among the component traits, these four characters contributed maximum for grain yield in rice.

## CHAPTER 3

### MATERIALS AND METHODS

In this chapter the details of the different experimental materials and methodologies followed during the course of research were presented. A brief description of the experimental site and duration, experimental treatment, materials used for the study, the procedure of data collection, recording and statistical analysis were explained under the following headings:

#### **3.1 Experimental Site**

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2018 to April 2019. The location of the site was situated at 23°41' N latitude and 90°22' E longitude. Geographically the experimental field is located at 8.4 meter above sea level. The experimental site was shown in the map in Appendix I.

#### **3.2 Climate and Soil**

The experimental site was medium high land belonging to old Madhupur tract (AEZ-28). The soil of the experimental plot was clay loam in texture having pH around 5.6 and organic carbon content is 0.45%. The experiment area was above flood level and having available irrigation and drainage system. The experimental site was under the subtropical climate. The experimental site can be characterized by three distinct seasons, winter season from November to February and the pre-monsoon or hot season from March to April and the monsoon period from May to October. Details of the metrological data of air temperature, relative humidity, rainfall and sunshine hour at the time of experiment was collected from the weather station of Bangladesh, Sher-e-Bangla Nagar, Dhaka.

### 3.3 Planting Materials (Lines)

Ten advance rice genotypes were used for the present study. Ten advance line genotypes were F9 materials from the previously continued studies, used as experimental materials in the study. Descriptions of the lines are given in Table 1.

**Table 1. List of materials used for the experiment**

<b>Lines</b>	<b>Pedigree</b>	<b>Source</b>
<b>L1</b>	BRR I dhan 29 × BRR I dhan 36 S <sub>5</sub> P <sub>2</sub> P <sub>4</sub> S <sub>6</sub>	GEPB, SAU
<b>L2</b>	BRR I dhan 29 × BRR I dhan 36 S <sub>2</sub> P <sub>2</sub> P <sub>4</sub> S <sub>6</sub>	GEPB, SAU
<b>L3</b>	BRR I dhan 21 × BRR I dhan 29 S <sub>2</sub> P <sub>1</sub> S <sub>1</sub>	GEPB, SAU
<b>L4</b>	BRR I dhan 29 × BRR I dhan 36 S <sub>5</sub> P <sub>2</sub> P <sub>4</sub> S <sub>3</sub>	GEPB, SAU
<b>L5</b>	BRR I dhan 21 × BRR I dhan 29 S <sub>6</sub> P <sub>1</sub> P <sub>1</sub> S <sub>2</sub>	GEPB, SAU
<b>L6</b>	BRR I dhan 26 × BRR I dhan 28 S <sub>1</sub> P <sub>9</sub> P <sub>4</sub> S <sub>1</sub>	GEPB, SAU
<b>L7</b>	BRR I dhan 28 × BRR I dhan 29 S <sub>2</sub> P <sub>4</sub> P <sub>3</sub> S <sub>2</sub>	GEPB, SAU
<b>L8</b>	BRR I dhan 28 × BRR I dhan 29 S <sub>2</sub> P <sub>4</sub> P <sub>3</sub> S <sub>3</sub>	GEPB, SAU
<b>L9</b>	BRR I dhan 21 × BRR I dhan 29 S <sub>6</sub> P <sub>1</sub> P <sub>1</sub> S <sub>1</sub>	GEPB, SAU
<b>L10</b>	BRR I dhan 29 × BRR I dhan 36 S <sub>5</sub> P <sub>2</sub> P <sub>4</sub> S <sub>5</sub>	GEPB, SAU

**L=Lines**

**SAU= Sher-e-Bangla Agricultural University**

**BRR I= Bangladesh Rice Research Institute**

**GEPB=Genetics and Plant Breeding**



a



b



c



d

**Plate 1. Showing a. Seed soaking for germination, b. Seed sowing in seed bed, c. transplanting in main field and d. Field view of experimental plots.**

### 3.4 Design and layout

The experiment was laid out in Randomized Complete Block Design (RCBD). The field was divided into three blocks; the blocks were sub-divided into 10 plots (lines) where genotypes were randomly assigned. The experimental field size was  $27 \text{ m} \times 14 \text{ m} = 378 \text{ m}^2$  where 1m border was maintained surrounding the field and every block. The experimental field was designed such a way where

row to row distance was 25 cm and plant to plant distance was 20 cm. The 10 genotypes (F9) were distributed to each plot within each block randomly.

### **3.5 Collection of seed**

The seeds of ten boro lines (F9 genotypes) were collected from germplasm center of Sher-e-Bangla Agricultural University.

### **3.6 Germination of seed**

Seeds of all collected boro lines soaked separately for 48 hours in bag. Soaked seeds were picked out from water and wrapped with straw and gunny bag to increase the temperature for facilitating germination. After 72 hours seeds were sprouted properly.

### **3.7 Seedbed preparation and seedling raising**

The seed bed was prepared well by puddling the wetland with repeated ploughing following by laddering. Sprouted seeds were sown separately in the previously wet seedbed on 19 November, 2018. Proper care was taken so that there was no infestation of pest and diseases and no damage by birds

### **3.8 Preparation of main field**

The experimental plot was prepared by ploughing with power tiller followed by laddering. Weeds and stubbles were removed from the field. The land was mudded and leveled well before transplanting. First split of urea and full portion of all other fertilizers recommended by BRRRI were added to the main land before final ploughing

### **3.9 Application of fertilizers**

The fertilizers N, P, K, S and B in the form of Urea, TSP and MP respectively were applied. The entire amount of TSP and MP were applied during final land preparation. Urea was applied in three equal installments 5-7 days after ploughing, vegetative stage and before panicle initiation. The dose and method of application of fertilizer are shown in Table 2.



**Table 2. Dose and method of application of fertilizers in rice field**

Fertilizers	Dose (kg/ha)	Application (%)		
		Basal	1 <sup>st</sup> installment	2 <sup>nd</sup> installment
Urea	127	33.33	33.33	33.33
TSP	52	100	-	-
MP	60	100	-	-

Source: BRRRI (2015), Joydebpur, Gazipur

### **3.10 Transplanting of seedling**

Healthy seedlings of 33 days old were transplanted on 22 December 2018 in separate strip of experimental field (2-3 seedling per hill). Water level was maintained properly after transplanting.

### **3.11 Intercultural operation and after care**

After establishment of seedlings, various intercultural operations were done for better growth and development of the rice seedlings.

#### **3.11.1. Irrigation and drainage**

Flood irrigation was given to maintain a constant level of standing water up to 6 cm in the early stages to enhance tillering, proper growth and development of the seedlings and 10-12 cm in the later stage to discourage late tillering. The field was finally dried out 15 days before harvesting.

#### **3.11.2. Gap filling**

First gap filling was done for all of the plots at 10 days after transplanting (DAT).

#### **3.11.3. Weeding**

Weddings were done to keep the plots free from weeds, which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully at tillering stage and at panicle initiation stage by mechanical means.

#### **3.11.4. Top dressing**

After basal dose, the remaining doses of urea were top dressed in 2 equal installments.

#### **3.11.5. Plant protection measure**

Diazinon 57 EC and Malathion 57 EC was applied at the time of final land preparation and later on other insecticides were applied as and when necessary.

#### **3.11.6. Harvesting, threshing and cleaning**

The rice was harvested depending upon the maturity of plant and harvesting was done manually from each plot. The harvested crop of each plot was bundled separately. Properly tagged and brought to threshing floor. Enough care was taken for threshing and also cleaning of rice seed. Fresh weight of grain was recorded. The grains were cleaned and finally the weight was adjusted to 14% moisture content.

### **3.12 Data collection for estimation of variability**

Some quantitative data were recorded on ten selected plants for each advanced line on the following characters:

#### **I. Days to 80% maturity**

Days to 80% maturity of the crops of different combination were recorded considering the symptom such as moisture content of rice, color and hardness of the grain.

#### **II. Plant height (cm)**

The plant height was recorded in centimeter (cm) at the time of harvesting. The height was recorded from the ground level to the tip of the panicle.

#### **III. Number of total tillers per hill**

The number of panicles bearing total tillers were counted from each of the sample hills and average was taken.

#### **IV.Number of effective tillers per hill**

The number of effective tillers per hill was recorded as the number of panicles bearing tillers per plant and average value was recorded from ten plants.

#### **V.Panicle length (cm)**

The panicle length was measured with a meter scale from 10 selected plants and the average value was recorded as per plant. The height was measured from the ground level to the tip of the panicle.

#### **VI.Number of primary branches per panicle**

Primary branches were counted from one panicle of each of the randomly selected 10 plants and the average value was calculated.

#### **VII.Number of secondary branches per panicle**

Secondary branches were counted from one panicle of each of the randomly selected 10 plants and the average value was recorded.

#### **VIII.Number of filled grains per panicle**

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.

#### **IX.Number of unfilled grains per panicle**

Absence of endosperm in spikelet was considered as unfilled grain and total number of unfilled grains present on main panicle was counted and average was taken.

#### **X.Total number of spikelets per panicle**

The total number of filled grains and unfilled grains were collected randomly from selected 10 plants of a plot and then average numbers of total spikelet per panicle was counted.

#### **XI.1000-grain weight (g)**

One thousand grain were counted randomly cleaned grains and then weighted in grams and recorded.

## XII. Yield per hectare (ton)

Grains taken from each unit plot were sun dried and weighted carefully and converted to ton per hectare.

### 3.12 Estimation of variability and statistical analysis

Collected data on the ten lines were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTAT-C a software and then phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Genotypic and phenotypic coefficient of variation were calculated was done following the method outlined by Dewey and Lu (1959).

#### Analysis of variance (ANOVA)

The analysis of variance (ANOVA) for all characters was carried out individually.

Source of variation	d.f.	M.S.S.	EMSS	F-Ratio
Replication (r)	r-1	M1	-	M1/M3
Genotypes (g)	g- 1	M2	$\delta^2e + \delta^2g$	M2/M3
Error(e)	(r-1) (g-1)	M3	$\delta^2e$	-

Where.

r = Number of replications

g = Number of genotypes

d.f. = degree of freedom

M.S.S. = Mean sum of square

EMSS = Expected values of M.S.S.

## ii. Estimation of variance components

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

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

Where,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error and

r = Number of replications

b. Phenotypic variance,  $\delta^2p = \delta^2g + \delta^2e$

Where,

$\delta^2g$  = Genotypic variance,

$\delta^2e$  = Environmental variance = Mean square of error.

## iii. Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following formula;

Genotypic coefficient of variance (GCV) (%) =  $\frac{\sqrt{\delta^2g}}{\bar{x}} \times 100$

Where,  $\delta^2g$  = genotypic variance

$\bar{x}$  = population mean

Phenotypic coefficient of variance (PCV) (%) =  $\frac{\sqrt{\delta^2p}}{\bar{x}} \times 100$

Where,

$\delta^2p$  = phenotypic variance

$\bar{x}$  = population mean

### iii) Estimation of heritability:

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985).

$$h^2b (\%) = \frac{\delta^2g}{\delta^2p} \times 100$$

Where,

$h^2b (\%)$  = Heritability in broad sense

$\delta^2g$  = Genotypic variance

$\delta^2p$  = Phenotypic variance

### iv) Estimation of genetic advance:

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960).

$$\text{Genetic Advance GA} = K.h^2$$

Where,

K- constant = 2.06 at 5% selection intensity,

$\delta^2p$  = phenotypic variance,

$h^2$  = heritability in broad sense.

### v) Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952).

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{X}} \times 100$$

### vi) Estimation of simple correlation co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{[\sum x^2 - \frac{(\sum x)^2}{N}] [\sum y^2 - \frac{(\sum y)^2}{N}]}}$$

Where,

$\sum$  = Summation

x and y are the two variables correlated

N = Number of observations

**vii) Path co-efficient analysis:**

Path co-efficient analysis was done according to the procedure of Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) and Dabholkar (1992), using simple correlation values. In path analysis, correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} \times P_{yx2} r_{x1x2} \times P_{yx3} r_{x1x3}$$

$$r_{yx2} = P_{yx1} r_{x1x2} \times P_{yx2} \times P_{yx3} r_{x2x3}$$

$$r_{yx3} = P_{yx1} r_{x1x3} \times P_{yx2} r_{x2x3} \times P_{yx3}$$

Where,

r's denotes simple correlation co-efficient and P's denote path co-efficient.

P's in the above equations may be conveniently solved by arranging them in matrix form.

Total correlation, say between x1 and y is thus partitioned as follows:

$P_{yx1}$  = The direct effect of x1 on y.

$P_{yx2} r_{x1x2}$  = The indirect effect of x1 via x2 on y.

$P_{yx3} r_{x1x3}$  = The indirect effect of x1 via x3 on y.

After calculating the direct and indirect effect of the characters, residual effect (R) was calculated by using the formula given below (Singh and Chaudhary, 1985):

$$P^2_{RY1} = 1 - \sum P_{iy} \cdot r_{iy}$$

Where,

$P^2_{RY} = (R^2)$ ; and hence residual effect,  $R (P^2_{RY})^{1/2}$

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

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



## CHAPTER 4

### RESULTS AND DISCUSSION

The present study was conducted with a view to determine the comparative trial among ten advance boro rice lines (F9 genotypes) and also to study the correlation and path coefficient for yield and different yield contributing characters. The data were recorded on different characters such as days to maturity, plant height (cm), number of tillers/hill, number of effective tillers/hill, panicle length, number of primary branches/panicle, number of secondary branches/panicle, total number of spikelet/panicle, number of filled grain of main tiller, number of unfilled grain of main tiller, thousand grain weight and yield per hectare (t/ha). The data were statistically analyzed and results are described below under the following heads:

- Variability study in rice
- Correlation coefficient of characters
- Path coefficient analysis

The analysis of variance (ANOVA) of the data on different yield components and yield of ten F9 genotypes as advance boro rice lines of *O. sativa* were given in Table 4. The mean performance, range and CV% over three replications for all the characters of ten 10 boro rice lines are presented in Table 4 and Table 5. Phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters are presented in Table 6 to 9.

#### 4.1 Variability among the ten lines of rice

Genetic variability among these traits is important for selecting desirable types and best lines for further trial. The analysis of variance (ANOVA) of the data on different yield components and yield of ten advance boro lines of rice (F9 genotypes). are given in Table 3. Phenotypic variance, genotypic variance,

phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters are presented in Table 5.

#### **4.1.1 Days to maturity**

Significant variations were observed among the ten lines (11.78) for days to maturity (Table 3). The highest days to maturity was resulted in L8 (141 days) and the minimum days to maturity was found in L5 was 134 days (Table 4, Plate 2). The phenotypic and genotypic variance for days to maturity was observed 5.50 and 2.5 respectively suggested that the environment had significant role in the expression of trait. The phenotypic coefficient of variation (1.60%) was higher than genotypic coefficient of variation (1.36%) (Table 5) suggested that environment influenced on the expression of the genes controlling the trait. Similar result for this trait was also observed by Ketan and Sarkar (2014) in Aman rice.



**Plate 2. Photograph showing variation at 80% maturity stage**

#### **4.1.2 Plant height (cm)**

The highest plant height was observed in L3 (112.5 cm) whereas the minimum plant height was observed in L2 (87.64 cm) which is close to L10 (89.93 cm) (Table 4). Phenotypic variance and genotypic variance were observed as 85.75 and 79.09 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (9.83%) and the genotypic coefficient of variation (9.54%) also indicated presence of variability among the lines for this trait (Table 5). The highest variation in plant height among 14 upland rice genotypes was observed by Seyoum *et al.* (2012).

#### **4.1.3 Number of total tillers per hill**

Significant variations were observed among ten lines (4.32) for number of total tillers per hill (Table 3). Among the ten lines L2 (14.6 tillers) showed the maximum number of total tillers per hill and the minimum number of total tillers per hill showed by L3 (11.87 tillers) (Table 4). Phenotypic variance (3.26) is higher than genotypic variance (0.68) indicating moderate environmental influence on these characters and high difference between the phenotypic coefficient of variation (12.94%) and the genotypic coefficient of variation (6.71%) value indicating that this trait is highly influenced by the environment (Table 5). Ghosal *et al.* (2010) reported similar result for this trait in irrigated rice.

**Table 3. Analysis of variances for twelve important characters of ten advanced lines of boro rice.**

Source of variance	Df	Mean sum of square											
		Character											
		DM	PH (cm)	NTT	NET	PL	NPBP	NSBP	NFGP	NUFGP	TSP	TGW	Y/H
<b>Replication</b>	<b>2</b>	12.63	83.44	0.98	0.23	1.29	0.26	1.20	59.97	4.76	35.13	0.65	0.62
<b>Line</b>	<b>9</b>	11.78**	279.71**	4.32**	3.72**	3.38**	3.86**	36.95**	542.37**	66.83**	541.84**	3.05**	1.23**
<b>Error</b>	<b>18</b>	1.34	5.61	2.05	2.09	0.91	0.45	1.86	47.73	6.45	48.67	0.72	0.26

\*\*=Significant at 5%; DM = days to maturity, PH = plant height, NTT = number of total tillers per hill, NET = number of effective tillers per hill, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUFG/P = number of filled grains per panicle, TGW = thousand grain weight, Y/H = yield per hectare

**Table 4. Mean performance of ten advanced lines of boro rice in respect of twelve important characters**

Line	DM	PH	NTT	NET	LP	NPBP	NSBP	NFG/P	NUFG/P	TSP	TGW	Y/H
<b>L1</b>	136 bcd	92.40 c	13.73 abc	13 a-d	25.67 ab	8.80 d	30.23 bc	153.73 d	20.30 b	174.03 cd	22.47 bc	7.53 bcd
<b>L2</b>	137 bcd	87.64 c	14.60 a	14 a	25.34 ab	9.77 cd	31.77 bc	159.50 cd	12.93 cd	172.43 cd	22.57 abc	7.91 a-d
<b>L3</b>	136 bcd	112.50 a	11.87 c	11 cd	24.20 ab	11.17 a	37.07 ab	169.83 bc	11.83 d	181.67 b	23.52 ab	8.65 ab
<b>L4</b>	137 bc	90.05 c	14.43 a	14 a	24.67 b	8.63 d	32.83 b	153.97 cd	10.33 d	164.30 c	21.23 c	7.91 a-d
<b>L5</b>	134 cd	105.90 b	11.97 abc	12 a-d	26.67 a	12.13 a	36.97 ab	192.73 b	16.67 cd	209.40 a	24.67 bc	9.21 a
<b>L6</b>	139 ab	102.86 b	12.20 abc	12 a-d	24.04 b	9.50 bcd	28.77 c	168.33 bcd	18.96 b	187.30 b	22.68 bc	7.96 a-d
<b>L7</b>	138 ab	100.80 b	11.90 bc	11 cd	23.61 b	9.77 cd	36.70 c	177.93 b	19.06 b	197.00 ab	23.01 abc	7.18 cd
<b>L8</b>	141 a	111.50 a	11.90 abc	11 cd	24.07 ab	10.57 abc	30.57 c	162.13 bcd	18.56 b	180.70 bc	24.00 a	7.75 bcd
<b>L9</b>	138 ab	109.17 ab	12.40 abc	12 a-d	26.17 ab	11.20 ab	38.73 a	182.10 a	13.86 bc	195.97 ab	21.89 c	7.99 ab
<b>L10</b>	135 d	89.33 c	14.43 a	13 a-d	23.97 b	9.43 cd	31.66 c	153.47 d	26.03 a	179.50 b	22.37 bc	7.08 d
<b>DMRT</b>	2.97	4.42	2.75	2.57	1.78	1.70	3.61	18.09	4.35	17.54	2.12	1.215
<b>CV%</b>	0.84	2.36	11.06	11.69	3.84	6.60	4.07	4.13	15.07	3.79	3.72	6.47

[In a column means having similar letter(s) are statistically similar and those having dissimilar letter(s) differ significantly at 0.05 level of probability, CV%= Coefficient of Variance]

DM = days to maturity, PH = plant height, NTT = number of total tillers per hill, NET = number of effective tillers per hill, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUFG/P = number of filled grains per panicle, TGW = thousand grain weight, Y/H = yield per hectare

**Table 5. Estimates of genetic parameters in twelve important characters of ten advanced lines of boro rice**

Character	$\delta^2P$	$\delta^2G$	PCV (%)	GCV (%)
DM	5.50	2.50	1.60	1.36
PH	85.75	79.09	9.83	9.54
NTT	3.26	0.68	12.94	6.71
NET	2.90	0.66	13.11	5.92
PL	1.34	0.26	5.30	3.65
NPBP	1.92	0.93	12.48	10.55
NSBP	11.05	6.60	10.98	10.20
NFG	270.59	159.26	8.71	7.67
NUFG	37.56	23.58	30.58	26.61
TSP	346.43	133.66	7.92	6.96
TGW	2.04	0.51	5.36	3.86
Y/H	0.76	0.26	9.65	7.16

$\sigma^2p$  = Phenotypic variance,  $\sigma^2g$  = Genotypic variance;

DM = days to maturity, PH = plant height, NTT = number of total tillers per hill, NET = number of effective tillers per hill, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, NFG/P = number of filled grains per panicle, NUGF/P = number of unfilled grains per panicle, TSP = total number of spikelet per panicle, TGW = thousand grain weight, Y/H = yield per hectare

#### **4.1.4 Number of effective tillers per hill**

Analysis of variance (Table 3) revealed significant differences among the ten lines (3.71) for number of effective tillers per plant. The highest number of effective tillers per hill was recorded in L10 (13.83 tillers) whereas the minimum number of effective tillers per hill was recorded in L3 (11.13 tillers) (Table 4). Phenotypic variance (2.90) was different from the genotypic variance (0.66) that indicated high environmental effect over the trait. Large difference between the phenotypic coefficient of variation (13.11%) and the genotypic coefficient of variation (5.92%) values indicated that high influence of environment on this character (Table 5). Ghosal *et al.* (2010) reported similar result for this trait in rice.

#### **4.1.5 Panicle length (cm)**

From ANOVA table (Table 3) significant difference were observed among ten lines (3.4) for panicle length. Among the ten lines the highest panicle length was observed in L5 (26.67 cm) and the lowest panicle length was observed in L7 (23.6 cm) (Table 4). Panicle length showed less difference between phenotypic variance (1.34) and genotypic variance (0.26) indicating less environmental influence on these character and low difference between PCV (5.30%) and GCV (3.65%) (Table 5). Low phenotypic coefficient of variation than genotypic coefficient of variation for panicle length was reported by Kole *et al.* (2008) in rice.

#### **4.1.6 Number of primary branches per panicle**

From ANOVA table (Table 3) significant difference were observed among ten boro rice lines (3.86) for number of primary branches per panicle. From the mean table value, it was found that the highest number of primary branches per panicle was recorded in L5 (12.13) which is very close to L9 (11.20) while the minimum number of primary branches per panicle was recorded in L1 (8.8) (Table 4). Number of primary branches per panicle showed the low phenotypic variance (1.92) and genotypic variance (0.93) which indicated less environmental influence. The phenotypic coefficient (12.47%) values was recorded for number of primary branches per panicle very close to genotypic coefficient of variability (10.55%) which indicated a less extent of the environment influences on the character. Elayaraja *et al.* (2005) found similar result.

#### **4.1.7 Number of secondary branches per panicle**

Significant variations were observed among ten lines (36.95) for number of secondary branches per panicle (Table 3). Among ten lines, the highest number of secondary branches per panicle was recorded in L9 (38.73) whereas the minimum number of secondary branches per panicle was observed in L6 (28.77) (Table 4). The value of phenotypic and genotypic variance (11.05) and (6.60), respectively for number of secondary branches per panicle with high difference

between them indicates high effect of environment on this character (Table 5). According to Table 5, PCV (10.98%) and GCV (10.20%) for number of secondary branches per panicle which indicate that sufficient variation exists among genotypes for this trait. Low PCV, GCV for this trait was also recorded by Kumar *et al.* (2007) in segregating generation of rice.

#### **4.1.8 Number of filled grains per panicle**

Significant variations were observed among ten lines (542.37) for number of filled grain per panicle (Table 3). In the ten boro rice lines under trial, the number of filled grains per panicle was recorded highest in L5 (192.73) and minimum was recorded in L10 (153.46) (Table 4). The magnitude of difference between phenotypic variances (270.59) and genotypic variances (159.26) were higher for number of filled grains per panicle suggested that large environmental influence on this character (Table 5). The high value of phenotypic (8.7%) and genotypic coefficient of variance (7.6%) respectively for this character indicated that the existence of high variation among the population with possibility of high potential for the selection. High genotypic, phenotypic variance and high GCV, PCV for this trait was also reported by Akter (2010).

#### **4.1.9 Number of unfilled grains per panicle**

Significant variation (66.83) among ten lines for number of unfilled grains per panicle (Table 3). The L10 showed the highest (26.03) number of unfilled grains per panicle among ten genotypes whereas the L4 showed the minimum (10.33) number of unfilled grains per panicle (Table 4). The high value of phenotypic (37.56) and genotypic (23.58) variance for number of unfilled grains per panicle with high difference between them suggests significant role of environment on the character. The difference between phenotypic (30.58%) and genotypic (26.61%) coefficient of variances were high for number of unfilled grains per panicle which indicates the existence of adequate variation among the lines (Table 5). The highest phenotypic variance, genotypic variance and phenotypic



coefficient of variance, genotypic coefficient of variance was also observed by Iftekharrudduauula *et al.* (2001).

#### **4.1.10 Total number of spikelet per panicle**

From the ANOVA (Table 3), it was found that total number of spikelet per panicle showed significant variations among the lines (541.84). The total number of spikelet per panicle was the maximum in L5 (209.04) and the minimum was observed in L4 (164.3) (Table 4). The phenotypic and genotypic variances for total number of spikelet per panicle were 346.43 and 133.66 respectively. The phenotypic variance was higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 7.92% and 6.96% respectively for total number of spikelet per panicle which indicating that high variation exists among different lines (Table 5). High genotypic, phenotypic variance and high GCV, PCV for this trait was also reported by Satish *et al.* (2003).

#### **4.1.11 Thousand grain weight (gm)**

From the ANOVA (Table 3), it was found that thousand grain weight showed significant variations among the lines (3.05). Thousand grain weight was found the maximum in L5 (24.67 gm) whereas the minimum thousand seed weight was found in L4 (21.23 gm) (Table 4). The phenotypic variance (2.04) was higher than genotypic variance (0.51) indicating that environment has influence on expression of this character. The values of phenotypic coefficient of variation and genotypic coefficient of variation were 5.36% and 3.86% indicating that the line has considerable variation for this trait (Table 5). Bidhan *et al.* (2001) reported similar result for this trait.

#### **4.1.12 Yield per hectare (t/ha)**

From the ANOVA (Table 3) revealed that the yield per hectare showed significant differences among the ten lines (1.23). Among the ten lines L5 showed the maximum (9.21 t/ha) yield per hectare and the minimum by in L10 (7.07 t/ha) (Table 4). Yield per hectare showed phenotypic variance (0.76) is

moderately higher than genotypic variance (0.26) indicating moderate environmental influence on this character. The value of phenotypic coefficient of variation (9.65%) and genotypic coefficient of variation (7.16%) indicates that this trait is influenced by the environment (Table 5). Pandey *et al.* (2010) reported low value of PCV and GCV for this trait.

## **4.2 Heritability and genetic advance**

### **4.2.1 Days to maturity**

Days to maturity showed high heritability (72.25%) coupled with low genetic advance (3.27) and moderate genetic advance in percentage of mean (2.38%) (Table 6). The result showed that due to presence of additive gene effect and medium scope of selection of this trait. High heritability coupled with low genetic advance for this trait was also observed by Akhtar *et al.* (2011).

### **4.2.2 Plant height (cm)**

Plant height of 10 boro rice lines showed high heritability (94.25%) associated with high genetic advance (19.13) and high genetic advance in percentage of mean of 19.07% (Table 6). This finding revealed that presence of additive gene action and scope of improvement of the character through selection may be rewarding. High heritability in plant height with high genetic advance in percentage of mean was also observed by Sabesan *et al.* (2009).

### **4.2.3 Total no. of tillers per hill**

Total no. of tillers per hill exhibited high heritability (26.92%) conjunction with low genetic advance (0.98) and genetic advance in percentage of mean (7.17%) (Table 6). These findings revealed that it was indicative of non-additive gene action. Selection for this trait may not be wise.

**Table 6. Estimation of heritability, genetic advance and genetic advance in percent mean twelve important characters.**

Parameters	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to maturity	72.25	3.27	2.38
Plant height	94.25	19.13	19.07
Total no of tiller/hill	26.92	0.98	7.17
Number of effective tiller/hill	20.42	0.68	5.51
Panicle length	47.46	1.28	5.18
Number of primary branches/panicle	71.56	1.85	18.37
Number of secondary branches/panicle	86.27	6.54	19.52
Number of filled grain per panicle	77.55	23.29	13.92
Number of unfilled grain per panicle	75.72	8.04	47.71
Total no of spikelets/panicle	77.15	23.20	12.59
Thousand grain weight	51.88	1.30	5.73
Yield per hectare	55.05	0.87	10.95

#### **4.2.4 Number of effective tillers per hill**

Relatively low heritability (20.42%) accompanied with low genetic advance (0.68) and genetic advance in percentage of mean (5.52%) was calculated in respect of number of effective tillers per hill (Table 6). These findings discovered the action of non-additive gene effects on the expression of this trait. The high heritability is being exhibited due to high environmental effects. Selection may not be effective in such character.

#### **4.2.5 Panicle length (cm)**

Panicle length exhibited moderate heritability (47.5%) along with low genetic advance (1.28) and genetic advance (5.28%) (Table 6). These results revealed the presence of additive gene. Selection for this trait may not be effective.

#### **4.2.6 Number of primary branches per panicle**

High heritability (71.5%) along with low genetic advance (1.86) and genetic advance in percentage of mean (18.38%) was calculated in number of primary branches per panicle (Table 6). It is indicated that environmental effect was more than the genotypic effect and due to non-additive gene action; selection for further improvement of the trait might not be wise. Similar results were also found by Biswas *et al.* (2000).

#### **4.2.7 Number of secondary branches per panicle**

Number of secondary branches per panicle showed high heritability (86.27%) coupled with low genetic advance (6.54) and genetic advance in percent mean (19.52%) (Table 6), which indicating the roles of non-additive gene action and selection of this trait will be not effective.

#### **4.2.8 Number of filled grains per panicle**

The effectiveness of heritability in broad sense of number of filled grains per panicle was high (77.55%) with high genetic advance (23.29) and high genetic advance in percentage of mean (13.92%) (Table 6). These findings revealed that this trait was controlled by additive gene and selection for this character would be effective. Prasad *et al.* (2001) also found high heritability coupled with high genetic advance as percent of mean for the trait filled grains per panicle.

#### **4.2.9 Number of unfilled grains per panicle**

Number of unfilled grains per panicle showed high heritability (75.72%) accompanied with low genetic advance (8.04) and high genetic advance in percentage of mean (47.71%) (Table 6). These finding revealed that the additive gene effect on the expression of this character and selection for this character would be effective.

#### **4.2.10 Total number of spikelet per panicle**

Total number of spikelet per panicle showed heritability (77.15%) coupled with high genetic advance (23.20) and genetic advance in percentage of mean

(12.59%) (Table 6). These findings exposed the predominance of additive genes for controlling total number of spikelet per panicle. Thus, selection based on this character will be rewarding for improvement.

#### **4.2.11 Thousand grain weight (gm)**

Thousand grain weight of 10 boro rice lines showed high heritability (51.88%) associated with low genetic advance (1.30) and genetic advance in percentage of mean (5.73%) (Table 6), revealed that thousand seed weight is highly influenced by environmental effects and scope of improvement through selection may not be rewarding.

#### **4.2.12 Yield per hectare (t/ ha)**

Yield per hectare exhibited high heritability (55.05%) conjunction with very low genetic advance (0.87) and genetic advance in percentage of mean (10.95%) (Table 6). These findings revealed that it was indicative of non-additive gene action.

### **4.3 Correlation coefficient**

When selection pressure is exercised for the trial of any line highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection vis-à-vis provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). In our study, both genotypic and phenotypic correlation co-efficient of different characters of 10 boro rice lines are determined (Table 7 and 9). Most of the characters showed the genotypic correlation coefficients were higher than their respective phenotypic ones. These values indicated that these traits were strongly associated genetically and the phenotypic expression of these traits was less influenced by the environment. In few cases, phenotypic correlation coefficient were higher than their corresponding genotypic correlation coefficient suggesting that both environmental and genotypic

correlation acted in the same direction and finally maximized their expression at phenotypic level.

#### **4.3.1 Days to maturity**

Days to maturity showed significant and positive correlation with plant height ( $G=0.375^*$ ) at genotypic level suggested that if days to maturity increased the plant height also increased. It also exhibited positive interaction with plant height ( $G=0.375$ ,  $P=0.327$ ) at both genotypic and phenotypic level and with number of effective tiller ( $P=0.034$ ), total number of filled grain per panicle ( $P=0.001$ ) at phenotypic level. Days to maturity showed negative association with thousand seed weight ( $G=-0.062$ ,  $P=-0.141$ ) at both genotypic and phenotypic level (Table 7 and 9). Sadeghi (2011) also revealed that days to maturity had non-significant and positive interaction with yield per hectare.

**Table 7. Genotypic correlation coefficients among different pairs of yield and yield contributing characters of ten advanced lines of boro rice**

	DM	PH	NT	NET	PL	NPB/P	NSB/P	NFG/P	NUG/P	TS/P	TGW	Y(t/ha.)
<b>DM</b>	1											
<b>PH</b>	0.375*	1										
<b>NT</b>	-0.743**	-0.990**	1									
<b>NET</b>	-0.855**	-0.929**	0.957**	1								
<b>PL</b>	-0.624**	0.034 <sup>NS</sup>	0.037 <sup>NS</sup>	0.043 <sup>NS</sup>	1							
<b>NPB/P</b>	-0.222 <sup>NS</sup>	0.799**	-0.988**	-0.980**	0.453*	1						
<b>NSB/P</b>	-0.300 <sup>NS</sup>	0.479**	-0.616**	-0.772**	0.323 <sup>NS</sup>	0.708**	1					
<b>NFG/P</b>	-0.146 <sup>NS</sup>	0.656**	-0.086**	-0.916**	0.478**	0.906**	0.752**	1				
<b>NUG/P</b>	-0.049 <sup>NS</sup>	-0.183 <sup>NS</sup>	0.068 <sup>NS</sup>	0.257 <sup>NS</sup>	-0.342 <sup>NS</sup>	-0.238 <sup>NS</sup>	-0.417*	-0.179 <sup>NS</sup>	1			
<b>TS/P</b>	-0.163 <sup>NS</sup>	0.593**	-0.964**	-0.928**	0.359 <sup>NS</sup>	0.824**	0.607**	0.939**	0.171 <sup>NS</sup>	1		
<b>TGW</b>	-0.062 <sup>NS</sup>	0.669**	0.929**	0.995**	0.099 <sup>NS</sup>	0.822**	0.196 <sup>NS</sup>	0.633**	0.215 <sup>NS</sup>	0.709**	1	
<b>Y/ha</b>	-0.548**	0.559**	0.813**	0.978**	0.689**	0.842**	0.452*	0.650**	-0.632**	0.429*	0.728**	1

NS= Not significant; \*=Significant at 5% level; \*\*= Significant at 1% level; DM = days to maturity, PH = plant height, NTT = number of total tillers per hill, NET = number of effective tillers per hill, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUG/P = number of filled grains per panicle, TGW = thousand grain weight, Y/H = yield per hectare

**Table 8. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters of ten advanced lines of boro rice.**

	DM	PH	NT	NET	PL	NPB/P	NSB/P	NFG/P	NUG/P	TS/P	TGW	Y(t/ha.)
<b>DM</b>	1											
<b>PH</b>	0.327 <sup>NS</sup>	1										
<b>NT</b>	-0.037 <sup>NS</sup>	-0.649 <sup>**</sup>	1									
<b>NET</b>	0.034 <sup>NS</sup>	-0.629 <sup>**</sup>	0.959 <sup>**</sup>	1								
<b>PL</b>	-0.249 <sup>NS</sup>	0.025 <sup>NS</sup>	0.064 <sup>NS</sup>	0.106 <sup>NS</sup>	1							
<b>NPB/P</b>	-0.064 <sup>NS</sup>	0.690 <sup>**</sup>	-0.338 <sup>NS</sup>	-0.313 <sup>NS</sup>	0.435 <sup>*</sup>	1						
<b>NSB/P</b>	-0.141 <sup>NS</sup>	0.430 <sup>*</sup>	-0.272 <sup>NS</sup>	-0.267 <sup>NS</sup>	0.384 <sup>*</sup>	0.615 <sup>**</sup>	1					
<b>NFG/P</b>	0.001 <sup>NS</sup>	0.618 <sup>**</sup>	-0.457 <sup>*</sup>	-0.439 <sup>*</sup>	0.398 <sup>*</sup>	0.704 <sup>**</sup>	0.701 <sup>**</sup>	1				
<b>NUG/P</b>	-0.121 <sup>NS</sup>	-0.180 <sup>NS</sup>	0.005 <sup>NS</sup>	0.024 <sup>NS</sup>	-0.234 <sup>NS</sup>	-0.161 <sup>NS</sup>	-0.363 <sup>*</sup>	-0.174 <sup>NS</sup>	1			
<b>TS/P</b>	-0.041 <sup>NS</sup>	0.554 <sup>**</sup>	-0.454 <sup>*</sup>	-0.430 <sup>*</sup>	0.314 <sup>NS</sup>	0.647 <sup>**</sup>	0.572 <sup>**</sup>	0.938 <sup>**</sup>	0.180 <sup>NS</sup>	1		
<b>TGW</b>	-0.141 <sup>NS</sup>	0.480 <sup>**</sup>	0.469 <sup>**</sup>	0.489 <sup>**</sup>	0.111 <sup>NS</sup>	0.572 <sup>**</sup>	0.141 <sup>NS</sup>	0.421 <sup>*</sup>	0.095 <sup>NS</sup>	0.454 <sup>*</sup>	1	
<b>Y/ha</b>	-0.120 <sup>NS</sup>	0.406 <sup>*</sup>	0.092 <sup>NS</sup>	0.041 <sup>NS</sup>	0.459 <sup>*</sup>	0.582 <sup>**</sup>	0.345 <sup>NS</sup>	0.519 <sup>**</sup>	-0.453 <sup>*</sup>	0.359 <sup>NS</sup>	0.303 <sup>NS</sup>	1

NS= Not significant; \*=Significant at 5% level; \*\*= Significant at 1% level; DM = days to maturity, PH = plant height, NTT = number of total tillers per hill, NET = number of effective tillers per hill, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUG/P = number of filled grains per panicle, TGW = thousand grain weight, Y/H = yield per hectare



### 4.3.2 Plant height

Plant height showed positive interaction with number of filled grain per panicle ( $G = 0.656$ ,  $P = 0.618$ ), panicle length  $P$  ( $G=0.034$ ,  $P=0.025$ ) and number of primary and secondary branches per panicle ( $G =0.799$ ,  $P =0.690$ ); ( $G =0.479$ ,  $P =0.430$ ), negative interaction with total no. of tiller ( $G =-0.290$ ,  $P =-0.649$ ). The results tend to emphasize that if plant height increased the number of primary and secondary branches per panicle also increased. It was negatively associated with number of total tillers ( $G =-0.290^{**}$ ,  $P =-0.649^{**}$ ). (Table 7 and 8). Prasad *et al.* (2001), Iftekharudduauula *et al.* (2001) also observed that plant height was negative associated with tiller number.

### 4.3.3 Total no. of tillers per hill

Total no. of tillers per hill showed significant and positive correlation with number of effective tillers ( $G=0.057$ ,  $P= 0.959$ ) and yield per plot ( $G=0.813$ ,  $P=0.092$ ) indicated that yield per plot can be improved if total number of tillers per hill and number of effective tillers increased. It also exhibited non-significant and positive interaction with panicle length ( $G= 0.037^{NS}$ ,  $P=0.064^{NS}$ ) and yield per hectare ( $G=0.195$ ,  $P=0.134$ ). Number of total tillers per hill had non-significant and positive interaction with number of unfilled grains per panicle ( $G=0.813^{NS}$ ,  $P=0.092^{NS}$ ). (Table 7 and 8). Agahi *et al.* (2007), Selvaraj *et al.* (2011) and Ganapati *et al.* (2014) also reported positive correlation of yield per hectare with total number of tillers per hill at both genotypic and phenotypic level.

### 4.3.4 Number of effective tillers per hill

The number of effective tillers per hill showed positive correlation with Thousand grain weight ( $G=0.995$ ,  $P= 0.489$ ) at both genotypic and phenotypic level but positively significant with yield per hectare at genotypic level and yield per plant ( $G=0.078$ ) indicated that the traits were governed by same gene and simultaneous improvement would be effective. (Table 7 and 8). Non-significant association of these traits indicated that the association between these traits is

largely influenced by environmental factors. Agahi *et al.* (2007) and Babu *et al.* (2012) also found positive and significant correlation of yield with effective tillers per plant at both genotypic and phenotypic level. Selvaraj *et al.* (2011) and Satheeshkumar *et al.* (2012) found positive and significant correlation of yield per hectare with effective tillers per plant at phenotypic level only.

#### **4.3.5 Panicle length**

Panicle length showed negative correlation with number of unfilled grain per panicle ( $G=-0.342$ ,  $P=-0.23$ ), suggested that yield per plot can be increased by improving panicle length, number of secondary branches per panicle, total number of spikelet. (Table 7 and 8). Ullah *et al.* (2011) reported that Positive and significant correlation for Panicle length was found with yield per hectare.

#### **4.3.6 Number of primary branches per panicle**

Number of primary branches per panicle showed negative correlation with number of unfilled grains per panicle ( $G=-0.238$ ,  $P=-0.161$ ), at both genotypic and phenotypic level indicated that if number of primary branches per panicle increased then this character also increased. (Table 7 and 8).

#### **4.3.7 Number of secondary branches per panicle**

Negative correlation was found between number of secondary branches per panicle and with number of unfilled grain per panicle ( $G=-0.417$ ,  $P=-0.363$ ) at both genotypic and phenotypic level and yield per plant ( $G= 0.437$ ) at genotypic level. This result suggested that yield per plant and yield per hectare can be increased through improvement of total number of spikelet, number of filled grain per panicle (Table 7 and 9). Mustafa *et al.* (2007) found that this significant and positive correlation with yield per hectare.

#### **4.3.8 Number of filled grains per panicle**

Number of filled grains per panicle showed significant and positive correlation yield per hectare ( $G=0.650^{**}$ ,  $P=0.519^{**}$ ) indicated that if number of filled grains per panicle increased then yield per plot also increased.

#### **4.3.9 Number of unfilled grains per panicle**

Number of unfilled grains per panicle showed negative correlation with yield per plant ( $G=-0.632$ ,  $P=-0.453$ ) at both genotypic and phenotypic level. This result expressed that yield per plot can be increased by decreasing the number of unfilled grains per panicle. (Table 7 and 8). Same result for this trait was reported by Iftakharuddaula *et al.* (2001).

#### **4.3.10 Total number of spikelet per panicle**

Total number of spikelet per panicle showed positive correlation with yield per hectare ( $G= 0.429$ ,  $P=0.359$ ) indicated that improvement of yield per plot can be improved number of filled grain per panicle and total number of spikelet per panicle.

#### **4.3.11 Thousand grain weight**

Thousand seed weight showed non-significant and negative correlation with days maturity ( $G= -0.062^{NS}$ ,  $P=-0.141^{NS}$ ) (Table 7 and 9) indicated that very little contribution of thousand grain weight toward increase in yield per plot.

### **4.4 Path Coefficient analysis**

Path coefficient analysis splits the correlation coefficient into direct and indirect effects. It reveals whether the association of the traits with yield is due to their direct effect or is a consequence of their indirect effect via other traits. Path coefficient analysis was done with days to maturity, plant height (cm), total number of tillers per hill, number of effective tillers per hill, panicle length (cm), number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, number of unfilled grains of per panicle, total number of spikelet per panicle, thousand grain weight and yield. Estimation of direct and indirect effect of path co- efficient analysis for *O. sativa* L. is presented in Table 9.

#### **4.4.1 Days to maturity**

Path coefficient analysis revealed that, days to maturity was negative correlated (-0.548\*\*) and had negative direct effect (-0.422) on yield per plot. It had positive indirect influence on the yield per hectare through number of tillers per plant (0.015), panicle length (0.105), number of primary and secondary branches per panicle (0.027, 0.059), and number of unfilled grains per panicle (0.050). The indirect negative effect of this trait through plant height (-0.138) (Table 9). Similar result also recorded by Habib *et al.* (2005), sadeghi (2011).

#### **4.4.2 Plant height (cm)**

Plant height was positively correlated (0.559\*\*) and had positive direct effect (0.487) on yield per hectare. Plant height had negative indirect influence on yield per hectare through number of effective tillers per plant (-0.306), number of unfilled grains per panicle (-0.087), total no. of tiller per hill (-0.316) (Table 9).

**Table 9. Partitioning of genotypic correlations into direct (bold) and indirect effects of yield of ten advanced lines of boro rice by path analysis**

	<b>DM</b>	<b>PH</b>	<b>NT</b>	<b>NET</b>	<b>PL</b>	<b>NPB/P</b>	<b>NSB/P</b>	<b>NFG/P</b>	<b>NUG/P</b>	<b>TS/P</b>	<b>TSW</b>	Correlated response with yield
<b>DM</b>	<b>-0.422</b>	0.159	0.023	0.035	-0.019	-0.008	0.061	-0.001	0.131	-0.071	-0.007	-0.548**
<b>PH</b>	-0.138	<b>0.487</b>	0.409	-0.655	0.001	0.088	-0.187	-0.774	0.196	0.953	0.025	0.559**
<b>NT</b>	0.015	-0.316	<b>-0.631</b>	0.999	0.005	-0.043	0.118	0.571	-0.005	-0.782	-0.025	0.813**
<b>NET</b>	-0.014	-0.306	-0.604	<b>1.043</b>	0.008	-0.040	0.115	0.550	-0.026	-0.740	-0.026	0.078**
<b>PL</b>	0.105	0.011	-0.040	0.110	<b>0.079</b>	0.055	-0.167	-0.497	0.254	0.541	0.005	0.689**
<b>NPB/P</b>	0.027	0.336	0.213	-0.326	0.034	<b>0.128</b>	-0.267	-0.881	0.175	1.113	0.030	0.842**
<b>NSB/P</b>	0.059	0.209	0.171	-0.277	0.030	0.078	<b>0.435</b>	-0.877	0.394	0.984	0.007	0.452*
<b>NFG/P</b>	-0.000	0.301	0.288	-0.458	0.031	0.090	-0.304	<b>1.252</b>	0.189	1.614	0.022	0.650**
<b>NUG/P</b>	0.050	-0.087	-0.003	0.025	-0.018	-0.020	0.157	0.217	<b>-1.088</b>	0.309	0.005	-0.632**
<b>TS/P</b>	0.017	0.269	0.286	-0.448	0.024	0.082	-0.248	-1.173	-0.195	<b>1.722</b>	0.024	0.429*
<b>TSW</b>	0.059	0.233	0.295	0.510	0.008	0.073	-0.061	0.526	-0.103	0.780	<b>0.054</b>	0.728**

Residual = 0.297, NS= Not significant, \*=Significant at 5% level, \*\*= Significant at 1% level; DM = days to maturity, PH = plant height, NTT = number of total tillers per hill, NET = number of effective tillers per hill, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUG/P = number of filled grains per panicle, TGW = thousand grain weight, Y/H = yield per hectare

#### **4.4.3 Number of total tillers per plant**

Number of total tillers per plant had negative direct (-0.631) effect on yield per hectare. It had positive indirect effect on yield per hectare via days maturity (0.023) plant height (0.409), number of primary and secondary branches per plant (0.213, 0.171), total number of spikelet per panicle (0.017), number of spikelet per panicle (0.286), and thousand seed weight (0.295). Whereas, it had negative indirect effect through panicle length (-0.040), number of unfilled grain (-0.003) on yield per hectare. Number of total tillers per plant finally made significant positive genotypic correlation (0.813\*\*) with yield per hectare (Table 9).

#### **4.4.4 Number of effective tillers per plant**

The positive direct effect (1.043) of number of effective tillers per plant was found on yield per hectare. Number of effective tillers per plant had positive indirect effect on yield per hectare through days maturity (0.035), panicle length (0.110), thousand seed weight (0.510). The indirect effect of this trait on yield per hectare via number of primary and secondary branches per panicle (-0.326, -0.277), total number of spikelet per panicle (-0.448) was negative. Finally, number of effective tillers per plant made significant positive genotypic correlation (0.078\*\*) with yield per hectare (Table 9). Rokonuzzaman *et al.* (2008), Agahi *et al.* (2007), Sadeghi (2011) found similar findings for this character.

#### **4.4.5 Panicle length (cm)**

Panicle length had positive direct effect (0.079) on yield per hectare. Negative indirect effect on yield per hectare was found through number of unfilled grains per panicle (-0.018) (Table 9). Its correlation with yield per hectare was positive and significant (0.689\*\*). Selvaraj *et al.* (2011) found positive and significant correlation of this trait with yield per hectare.

#### **4.4.6 Number of primary branches per panicle**

Path analysis revealed that, number of primary branches per panicle had direct positive effect (0.128) on yield per hectare. Number of primary branches per panicle

had negative indirect effect on yield per hectare through days to maturity (-0.008), number of total tiller per plant (-0.043), total number of spikelet per panicle (0.082), thousand seed weight (-0.073). The genotypic correlation with yield per hectare was significant and positive (0.842\*\*). This result exposed that yield per hectare will be increased by direct selection of number of primary branches per panicle. Chakraborty *et al.* (2010) found similar finding.

#### **4.4.7 Number of secondary branches per panicle**

Number of secondary branches per panicle had positive direct effect (0.437) on yield per hectare. It had positive indirect effect through days maturity (0.061), number of effective tillers per plant (0.115), number of unfilled grains per panicle (0.157). This trait had significant positive genotypic correlation (0.452\*\*) with yield per hectare (Table 9). Hence, selection should be practiced for this trait which had a greater number of secondary branches per panicle in order to improve seed yield. Chakraborty *et al.* (2010) found similar finding.

#### **4.4.8 Number of filled grains per panicle**

Path co-efficient analysis revealed that number of filled grains per panicle exhibited positive direct effect on yield per hectare (1.252) followed by positive indirect effect through number of effective tillers per plant (0.571), panicle length (0.031) and thousand seed weight (0.526). Number of filled grains per panicle had highly significant and positive correlation with yield per plant (0.650\*\*) (Table 9) indicated that direct selection of this trait will improve yield per hectare. kumar *et al* (2007) also found positive direct effect of filled grains per panicle on yield per hectare.

#### **4.4.9 Number of unfilled grains per panicle**

Number of unfilled grains per panicle had negative direct effect (-1.088) on yield per hectare. It had negative indirect effect through number of effective tillers per plant (-0.026), total number of spikelet per panicle (-0.195), thousand seed weight (-0.103) on yield per hectare. Number of unfilled grains per panicle finally made

significant negative genotypic correlation (0.632\*\*) with yield per hectare (Table 9).

#### **4.4.10 Total number of spikelet per panicle**

Total number of spikelet per panicle had direct positive effect (1.722) on yield per hectare. This trait had also indirect negative effect of this trait showed on yield per hectare through number of effective tiller (-0.740), number of tiller (-0.782). Finally, this trait had significant positive correlation (0.429\*) with yield per plant (Table 9).

#### **4.4.11 Thousand grain weight**

Thousand grain weight had positive direct effect (0.054) on yield per plot. It had positive indirect effect on yield per hectare through days maturity (0.059), total number of tillers per hill (0.295). Thousand grain weight made positive genotypic correlation (0.728\*\*) with yield per hectare (Table 9). Yield per hectare may be improved through direct selection of thousand seeds weight. Agahi *et al.* (2007) also found positive direct effect of thousand grains weight on yield per hectare.



## CHAPTER 5

### SUMMARY AND CONCLUSION

The present study was undertaken with ten advanced boro lines (F9 genotypes) of *O. sativa* L. at the Sher-e-Bangla Agricultural University Farm, Dhaka, during November 2018 to April 2019. Seedlings were transplanted in the main field in Randomized Complete Block Design with three replications. Data on various yield attributing characters such as, days to maturity, number of total tillers per hill, number of effective tillers per hill, panicle length (cm), number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, number of unfilled grains of per panicle, total number of spikelet per panicle, thousand grain weight and yield were recorded.

Significant variations were observed among the ten lines (11.78) for days to maturity, the highest days to maturity was resulted in L8 (141 days) and the minimum days to maturity was found in L5 was 134 days. The phenotypic and genotypic variance for days to maturity was observed 5.50 and 2.5 respectively suggested that the environment had significant role in the expression of trait. The highest plant height was observed in L3 (112.5 cm) whereas the minimum plant height was observed in L2 (87.64 cm) which is close to L10 (89.93 cm), phenotypic variance and genotypic variance were observed as 85.75 and 79.09 respectively. Among the ten lines L2 (14.6 tillers) showed the maximum number of total tillers per hill and the minimum number of total tillers per hill showed by L3 (11.87 tillers). The highest number of effective tillers per hill was recorded in L10 (13.83 tillers) whereas the minimum number of effective tillers per hill was recorded in L3 (11.13 tillers), phenotypic variance (2.90) was different from the genotypic variance (0.66) that indicated high environmental effect over the trait.

The L10 showed the highest (26.03) number of unfilled grains per panicle among ten genotypes whereas the L4 showed the minimum (10.33) number of unfilled grains per panicle. Thousand grain weight was found the maximum in L5 (24.67

gm) whereas the minimum thousand seed weight was found in L4 (21.23 gm), the phenotypic variance (2.04) was higher than genotypic variance (0.51) indicating that environment has influence on expression of this character. Among the ten lines L5 showed the maximum (9.21 t/ha) yield per hectare and the minimum by in L10 (7.07 t/ha), yield per hectare showed phenotypic variance (0.76) is 38 moderately higher than genotypic variance (0.26) indicating moderate environmental influence on this character. The value of phenotypic coefficient of variation (9.65%) and genotypic coefficient of variation (7.16%).

Days to maturity showed high heritability (72.25%) coupled with low genetic advance (3.27) and moderate genetic advance in percentage of mean (2.38%). Total no. of tillers per hill exhibited high heritability (26.92%) conjunction with low genetic advance (0.98) and genetic advance in percentage of mean (7.17%). Relatively low heritability (20.42%) accompanied with low genetic advance (0.68) and genetic advance in percentage of mean (5.52%) was calculated in respect of number of effective tillers per hill. Number of unfilled grains per panicle showed high heritability (75.72%) accompanied with low genetic advance (8.04) and high genetic advance in percentage of mean (47.71%). Thousand grain weight of 10 boro rice lines showed high heritability (51.88%) associated with low genetic advance (1.30) and genetic advance in percentage of mean (5.73%). Yield per hectare exhibited high heritability (55.05%) conjunction with very low genetic advance (0.87) and genetic advance in percentage of mean (10.95%).

Correlation coefficients among the characters were studied to determine the association between yield and yield components. Study on correlation revealed that yield had significant positive association with days to maturity, plant height, number of effective tiller per hill, number of primary branch per panicle number of secondary branches per panicle, total number of spikelet per panicle, number of filled grain per panicle, yield at both genotypic and phenotypic level. In addition, there were non-significant positive correlation with yield was also found in number of total tiller per hill, panicle length, number of unfilled grain per panicle.

Path coefficient analysis expressed that the days maturity, number of effective tillers per hill, panicle length, number of secondary branches per panicle, number of filled grain per panicle had the positive direct effect on yield. Among these characters number of effective tillers per hill, number of filled grain per panicle showed high direct effect and highly significant correlation with yield. Days to maturity and number of unfilled grain per panicle had the negative direct effect on yield.

Results based on Mean Data of F<sub>9</sub> lines, the following conclusions and recommendations may be drawn:

- High heritability with high genetic advance and genetic advance in percent of mean was observed for days to maturity, plant height, total number of spikelet per panicle, and number of filled grain per panicle indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective.
- significant positive association with days to maturity, plant height, number of effective tiller per plant, number of primary branch per panicle number of secondary branches per panicle, total number of spikelet per panicle, number of filled grain per panicle at both genotypic and phenotypic level. These results suggested that yield could be increased by improving these characters.
- The number of effective tillers per hill, panicle length, number of secondary branches per panicle, number of filled grain per panicle had the positive direct effect on yield per hectare. So yield improvement was associated with these characters.

### **Recommendations:**

By the Consideration of morphological, genotypic and phenotypic coefficient of variation and degree of variability of different important yield and yield contributing characters the most promising lines L5, L8 and L9 could be selected and suitable for released as high yielding boro rice line. Thus, the lines

L5, L8 and L9 would be suitable for release as high yielding boro rice variety for their short duration and high yielding characters.

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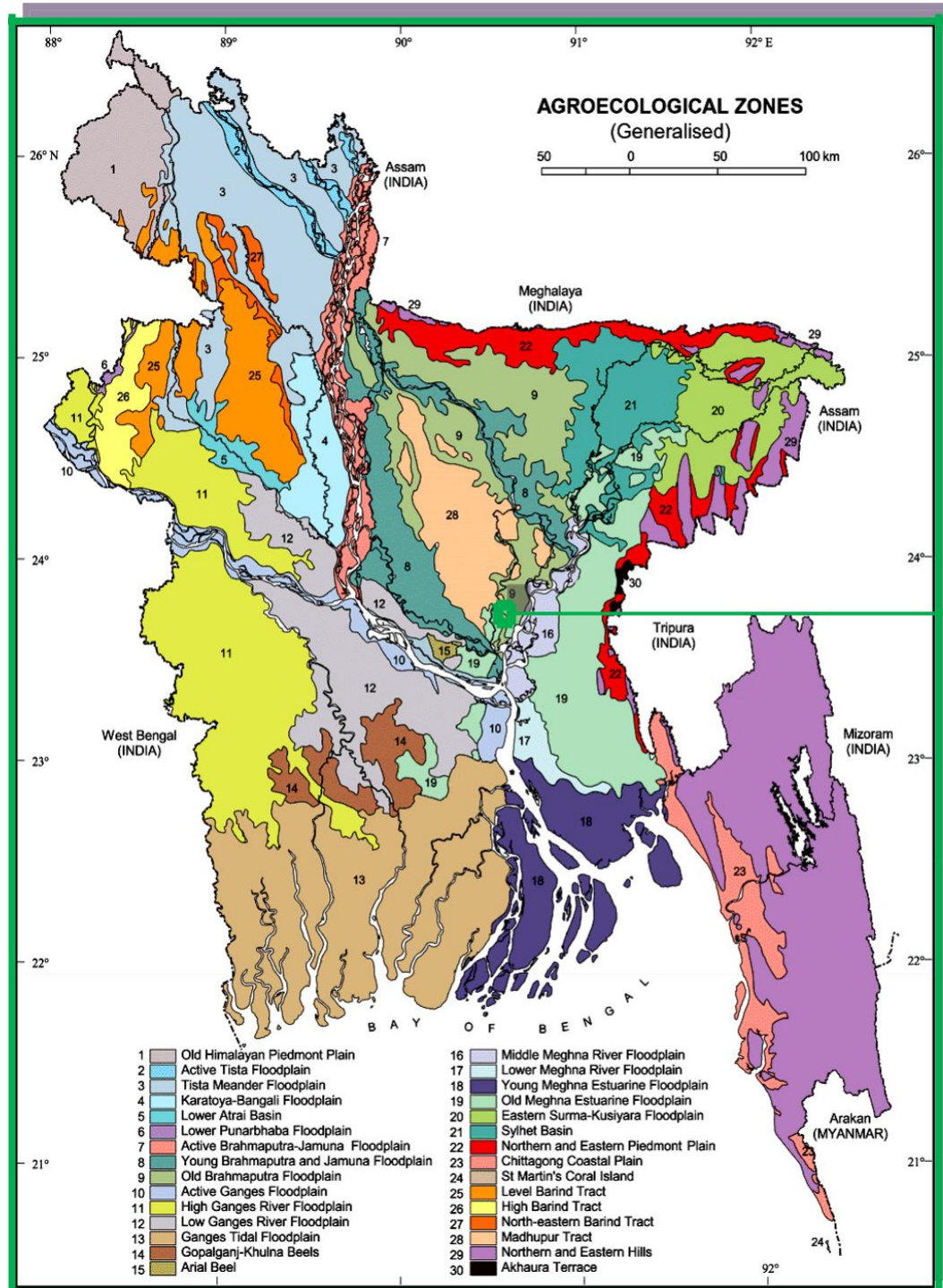
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# APPENDICES

Appendix I. Map showing the experimental site under study



**Experiment site**

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

Physical characteristics	
Constituents	Percent
Sand	26
Silt	45
Clay	29
Textural class	Silty clay
Chemical characteristics	
Soil characters	Value
pH	5.6
Organic carbon (%)	0.45
Organic matter (%)	0.78
Total nitrogen (%)	0.03
Available P (ppm)	20.54
Exchangeable K (me/100 g soil)	0.10

**Source:** Central Library, Sher-e-Bangla Agricultural University, Dhaka.

**Appendix III. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from November 2018 to March 2019**

Year	Month	Air temperature (°C)		Relative humidity (%)	Total rainfall (mm)
		Maximum	Minimum		
2018	November	28.10	11.83	58.18	47
	December	25.00	9.46	69.53	00
2019	January	25.2	12.8	69	00
	February	27.3	16.9	66	39
	March	31.7	19.2	57	23

**Source:** Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka -1207