EVALUATION OF NINE ADVANCED LINES OF AUS RICE (*Oryza sativa* L.)

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JUNE, 2016

EVALUATION OF NINE ADVANCED LINES OF AUS RICE (*Oryza sativa* L.)

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A Thesis
Submitted to the Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka,
in partial fulfilment of the requirements
for the degree of

MASTER OF SCIENCE

IN

GENETICS AND PLANT BREEDING

SEMESTER: January-June, 2016

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CERTIFICATE

This is to certify that thesis entitled, "EVALUATION OF NINE ADVANCED LINES OF AUS RICE (Oryza sativa L.)" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,** embodies the result of a piece of bona fide research work carried out by **MITA RANI DAS**, Registration No. **10-03864**, under my supervision and 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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Dated: June, 2016
Place: Dhaka, Bangladesh

DEDICATED

TO

MY BELOVED PARENTS
AND

TEACHERS

ACKNOWLEDGEMENTS

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ABSTRACT

A field experiment was conducted with nine aus F_5 materials along with parents as checks at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period from April 2015 to September 2015 to compare among the 9 F_5 lines in order to select high yielding and short duration aus line(s). Fourteen characters were studied to find out the suitable traits and three replications were conducted at Randomized Complete Block Design for the improvement of rice yield. The selected genotypes were found significantly variable. Comparatively phenotypic variances were higher than the genotypic variances and PCV were higher than GCV. All characters showed high heritability. All characters except panicle length showed moderate to high genetic advance in percent mean. High heritability coupled with moderate to high genetic advance in percent mean is governed by additive gene action which is better for selection. On the other hand, the significant positive correlation with seed yield per hectare was found in days to flowering (G = 0.924, P = 0.872), days to maturity (G = 0.983, P = 0.892), plant height (G = 0.771, P= 0.657), panicle length (G = 0.503, P = 0.367), number of primary branches per panicle (G = 0.940, P = 0.669), number of secondary branches per panicle (G = 0.653, P = 0.587), total no of spikelets per panicle (G = 1.085, P = 0.535), number of filled grain (G = 1.101, P = 0.600), yield per plant (G = 0.965, P = 0.844). Path co-efficient analysis revealed that days to maturity (0.332), total number of tiller per plant (0.336), panicle length (0.973), number of primary branches per panicle (0.436), number of filled grain (1.25), number of unfilled grain (0.21) and yield per plant (1.11) had the positive direct effect on yield per hectare. Number of filled grain per panicle was important for selection. The residual effect was found 0.10737 which indicated that 89.3% of the variability was accounted for fourteen yield and yield contributing traits in the present studies. Genotype G1 and G9 took longest period for days to maturity (130.3 days) which produce higher yield G1 (5.0 t) and G9 (4.88 t) with compare to their checks. Plant height in G1 (120.3cm), total number tiller per plant in G7 (18.33), number of effective tiller in G7 (15.39), panicle length in G8 (24.67) number of primary and secondary branches per panicle in G9, number of filled grain in G9 (136.10) and yield per plant in G1 (31.0) were higher than their checks.

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SOME COMMONLY USED ABBREVIATIONS

Full word	Abbreviations
Agriculture	Agric.
Agro Chemical Industries	ACI
Agro-Ecological Zone	AEZ
Agricultural	Agril.
And others	*et al.*
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Bangladesh Rice	BR
Centimeter	cm
Co-efficient of Variance	CV
Degree Celsius	^{o}C
Date After Transplanting	DAT
Degree of freedom	df
Environmental Co-efficient of Variance	ECV
Food and Agricultural Organization	FAO
The fifth generation of a cross between two dissimilar homozygous parents	F_5
Gram	g
Genotype	G
Genotypic Coefficient of Variance	GCV
Hectare	Ha
Journal	J.
Kilogram	Kg
Meter	M
Murate Potash	MP
Ministry of Agriculture	MOA
Percent	%
Randomized Complete Block Design	RCBD
Square meter	m2
Sher-e-Bangla Agricultural University	SAU
Ton	t
Triple Super Phosphate	TSP

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.*)* is the most important crop of tropical world. It is grown in warm tropical, sub-tropical and temperate countries over a wide range of soil and climatic condition. It is a self pollinated cereal food crop belonging to the family Gramineae (Poaceae) under the order Cyperales and class monocotyledons having chromosome number $2n = 24$ (Hooker,1979). There are two cultivated species of rice and 18 valid wild species. Of the two cultivated species *Oryza sativa* and *Oryza glaberrima* were originated from South and South east Asia, 90% of this crop is grown here and consumed them (Nanda, 2002).

Rice is the staple food for approximately 340 million poor people in South Asia and 140 million each in Southeast Asia and sub-Saharan Africa (IRRI, 2006).It is the most important cereal crop providing energy, protein and vitamins for half of the world's population (Tiwari *et al.,*2011). Rice grain contains 75 to 80% starch, 12% water and 7% protein (Oko *et al.,*2012;   Hossain *et al*., 2015).

The aus crop is either directly seeded or transplanted under rainfed and/or irrigated conditions. It is sown in March or April and harvested in late July to mid-August (Xiao *et al.*, 2006).Rice is grown in three overlapping season, namely aus, aman and boro (Rashid, 1994). Annual average rainfall varies from 1,500 mm to 5,000 mm. It is the fundamental food crop of Asia, providing over 30% of the calories consumed in the region. Overall, there is an estimated global need for an additional 116 million tons of rice by 2035 as compared to 439 million tons production in 2010. The estimated annual increase is expected to be 13% for the first 10 years and 12% in the next 15 years as population growth drops and people

diversify from rice to another crops. To meet the projected demands due to increasing global population, the world's rice production has to increase by 25% or more by 2030 (Seck *et al*., 2012).

Rice production in 2016 is estimated at 224 million cwt, down 5 percent from the previous forecast but up 16 percent from the revised 2015 total. Planted area for 2016 is estimated at 3.15 million acres, up 20 percent from 2015 (Anonymous, 2016). In Bangladesh about 76% of the household live in rural areas, and 47.5% of the total manpower is involved in agriculture. In Bangladesh, agriculture contributes 19.3% of the gross domestic product (GDP) of the country (Anonymous, 2014). Bangladesh has a immense history of rice cultivation. Rice is grown throughout the country except in the south eastern hilly areas. The agro-climatic conditions of the country are suitable for growing rice year-round. However, the national average rice yield is much lower (2.94 t/ha) than that of other rice-growing countries (Anonymous, 2012).

Breeding method for rice high yield include conventional hybridization and selection, F_1 hybrid breeding, ideotype (ideal plant type) breeding and enhancement of photosynthesis (Jeon *et al*., 2011). Genetic variability, character association and path coefficients are pre-requisites for improvement of any crop including rice for selection of superior genotypes and improvement of any trait (Krishnaveni *et al*., 2006).The knowledge about genetic variability can help to know if these variations are heritable or non-heritable. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement. Genetic variability for agronomic traits is the key component of breeding programme for broadening the gene pool of rice (Dutta *et al.*, 2013).

However, heritability in broad sense alone may not be helpful for selection based on phenotype, because it's influenced by environment. Thus, estimate heritability along with genetic advance conjointly are reliable helpful in predicting the gain under selection than heritability alone. Positives correlated between yield and yield components are requires for effective yield component breeding increasing grain yield in rice (Ogunbayo *et al*., 2014). Moosavi *et al*. (2015) reported that grain yield is a complex trait, quantitative in nature and a combined function of a number of constituent traits.

Considering the above idea the present investigation was studied with the following objectives:

- To select short duration Aus rice lines utilize them directly in varietal improvement program
- To characterize the F_5 Aus lines
- To select high yielding short duration lines for further yield trial

CHAPTER II

REVIEW OF LITERATURE

Rice (*Oryza sativa* L.) is one of the most important staple food crops. About 3 billion people, nearly half the world's population, depend on rice for survival. The morphological parameters such as plant height, number of effective tiller, number of spikelet per panicle, number of filled grain and yield per plant determine yield of rice variety. The present research work has aimed at studying the variability, heritability, genetic advance, interrelationship and path co-efficient analysis among the F_5 generation of rice genotypes. The review of literature regarding the studies presented under the following head:

2.1. Genetic parameters

Devi *et al*. (2017) studied on 27 rice genotypes. High heritability in broad sense coupled with high genetic advance as percent of mean exhibited by effective tillers, plant height, flag leaf length, filled grains per panicle, test weight, yield per plant, head rice recovery and length/breadth ratio indicating preponderance of additive gene action which provide good scope for further improvement by selection. Grain yield per plant had highest significant positive association with filled seeds per panicle, plant height, flag leaf length, effective tillers, flag leaf width and panicle length indicating importance of these characters for yield improvement..

An experiment was conducted Nuruzzaman *et al.* (2016) to evaluate thirty one NERICA mutant rice genotypes (twenty eight NERICA mutant lines along with three parental lines) of advanced (M_4 and M_5)generations for morphological characters and genetic parameters assessment in aus season, 2014 at the

experimental field of Biotechnology division, BINA, BAU Campus, Mymensingh. The genotypes differed significantly for all the traits *viz.,* days to flowering (1st, 50%, 80%), days to maturity, plant height, total tillers and effective tillers hill^{-1}, filled and unfilled grains panicle^{-1}, 100-seed weight (g) and yield plant-1(g).N1/300/P-9-5 had maximum yield plant^{-1} and N$_4$ parent had minimum yield plant^{-1}. All the parental lines showed less yield compared to other mutant lines. The phenotypic coefficient of variations (PCV) were higher than genotypic co-efficient of variations (GCV) for all the traits studied indicating that they all interacted with the environment to some extent. All the traits studied expressed moderate to high heritability estimates ranging from 43.68 to 92.87%. High heritability along with high genetic advance was noticed for the traits, number of filled grains panicle^{-1}, number of unfilled grains panicle^{-1} and plant height.

The experiments was conducted to study the early establishment morphological characters of advanced deep water rice. The parameters such as plant height, number of leaves, and number of effective & non-effective tillers were studied with different DAS as treatment in field condition. The advanced genotype BR224-2B-2-5 is able to establish significantly at early stage as it showed vigorous growth against stress condition present at early stage. The yield of the genotype BR224-2B-2-5 and BR5915-B-7 are 3.07 t ha-1 and 2.71 t ha-1 respectively. Finally, the advanced genotype BR224-2B-2-5 may be a good source to meet the future challenge (Ahmed *et al.* 2016).

Khan *et al*. (2015) studied fifteen advance lines of rice. Data on morphological parameters (qualitative and quantitative) was collected from productive tillers of every three plants of each variety at suitable phase of growth to check variation. Findings were recorded according to IRRI description morphology and varietals characteristics. The advance rice lines such as Line-2, Line-29, Line-35, Line-54, Line-127 and Line- 86-2 showed good physical characteristics (grain length, grain width, L/B ratio, chalkiness). While grain quality traits (GT, GC) were excellent in

advance Line-95, Line-168, Line-2, Line-35, Line-54, Line-127, Line-64 and Line-71. However, highest yield/plant was recorded in Line-86-2 (162g), Line-79-L (134.9g), Line-71 (116.5g), Line-95 (114.1g), Line-168 (110.1g) and Line-149 (103.7g).

Shahriar *et al*. (2014) conveyed an experiment with 30 advanced breeding lines including four check varieties rice and found high heritability with high genetic advance for plant height.

An experiment conducted by Ketan and Sarkar (2014) to observe variability for nineteen quantitative characters in 26 indigenous aman rice cultivars. The magnitude of PCV was higher than the corresponding GCV for all the characters. High heritability was observed days to 50 per cent flowering, plant height, 1000 grain weight, panicle length, florets number per panicle, kernel length and kernel L/B ratio. Number of grains per panicle recorded the highest genetic advance followed by floret number per panicle, plant height and number of secondary branches. High heritability in conjunction with high genetic advance was registered for plant height, days to 50 per cent flowering and number of secondary branches. High heritability with low genetic advance was observed for panicle length, panicle weight, kernel length and kernel L/B ratio.

Paikhomba *et al.* (2014) reported thirty F1 rice hybrids along with complete set of 13 parents and checks were evaluated for variability, heritability and genetic advance in different yield and yield contributing traits. The data was recorded on five randomly selected plants for fifteen quantitative characters. The treatment, i.e. mean sum of squares due to genotypes showed significant differences for 14 characters studied, indicating the presence of high genetic variability among the genotypes. The estimates of GCV were lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits studied. Characters like percent pollen fertility (99.9, 33.33), grain yield hill-1 (99.2,

31.13), harvest index (98.5, 30.42) and number of filled grains panicle-1 (97.8, 30.04) showed high heritability.

An experiment was conducted by Kumar *et al.* (2014) with 40 genotypes of rice. Analysis of variance revealed significant difference among fourty rice genotypes for all characters indicating the existence of variability. High GCV and PCV were observed for grain yield per plant and biological yield per plant also observed Positive significant association of grain yield with grains per panicle, days to maturity, number of productive tillers and days to flowering was also observed by Sadeghi (2011). On the other hand, Rafiqul (2014), conducted experiment with 19 genotypes of rice, existence of variance in 14 yield contributing character including days to maturity, no. of effective tiller per plant, no. of filled grain of main tiller and yield (ton/ha) were found in analysis of variance.

Aditya *et al*. (2013) studied in eighteen rice genotypes under rainfed ecosystem for fifteen quantitative traits. The analysis of variance revealed that there were highly significant differences for all the characters among the genotypes. The estimate of GCV and PCV was found to be highest for grain yield per plot followed by fertile grains per panicle and grains per panicle. The broad sense heritability was highest for plant height and fertile grains per panicle (98.14%) followed by grains per panicle (97.74%), days to 50 per cent flowering (95.18) and days to maturity (94.71). The phenotypic correlation coefficient among fifteen traits showed that grain yield was significantly and positively correlated with plant height, days to 50 per cent flowering, days to maturity, flag leaf length, flag leaf width, panicle length, grains per panicle, fertile grains per panicle, kernel length and L/B ratio.

According to Tuwar *et al*. (2013) reported that with twenty nine genotypes of rice from diverse locations to estimate the genetic components of variability. Heritability was higher for days to 50% flowering followed by days to maturity, plant height and panicle length which suggested that these traits would respond to

selection owing to their transmissibility and high genetic variability. Analysis stated that plant height exhibited high estimates of PCV and GCV proceeded by number of tillers and grain weight per panicle. High heritability coupled with high genetic advance as percent of mean was recorded for number of spikelets and number of grains per panicle and grain weight per panicle. These characters indicate the predominance of additive gene effects in their 4 expression and would respond to selection effectively as they are least influenced by environment.

Shabir *et al.* (2013) evaluated an experiment comprising 79 rice genotypes from different countries was studied at National Institute for Biotechnology and Genetic Engineering, Faisalabad, Pakistan during the year 2009-2011. Grain yield and yield components of these rice genotypes were evaluated to check variance, correlation, cluster pattern and genetic diversity.

An experiment was carried out by Babu *et al.* (2012) to study in twenty one rice hybrids with genetic parameters for yield, yield attributing, quality and nutritional characters. Analysis of variance revealed significant differences for all the traits under study. The Characters those are, number of filled grains per panicle, number of chaffy grains per panicle and iron content exhibited high genotypic coefficient of variation and phenotypic coefficient of variation. Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. The characters namely number of filled grains per panicle and water uptake exhibited high heritability coupled with high genetic advance indicating that simple selection could be effective for improving these characters.

An experiment was estimated with variability, heritability, genetic advance in fifty three genotypes of rice for fifteen characters. The highest genotypic and phenotypic coefficient of variation was found for number of productive tillers per plant, grain L/B ratio and grain yield per plant. Days to first flower, plant height,

number of productive tillers per plant, panicle length, filled grains per panicle, total number of grains, spikelet fertility, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel L/B ratio and grain yield per plant contain high heritability. High genetic advance as percent of mean were observed for the characters, days to first flower, plant height, number of productive tillers per plant, panicle length, filled grains per panicle, total number of grains, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel L/B ratio and grain yield per plant. Hence, the study suggested the selection based on these traits could be more effective in rice (Satheesh kumar *et al.* 2012).

An experiment was carried out with a field experiments using fourteen rice genotypes during the main rainy seasons of 2009 and 2010 at three rainfed upland locations of Southwest Ethiopia to estimate the genetic variability, heritability of grain yield and yield contributing traits in upland rice. Days to 50% flowering, plant height, grains per panicle, spikelets per panicle, thousand grains weight and grain yield showed relatively high GCV and PCV estimates. High heritability was obtained for plant height (92.17%), followed by 50% flowering (90.16%), thousand grains weight (83.17%), days to 85% maturity (82.45%), panicle length (79.25%) and spikelet per panicle (60.25%) which indicates high heritable portion of variation. High to medium estimates of heritability and genetic advance were obtained for plant height, days to 50% flowering, panicles per plant, spikelets per panicle, grains per panicle and thousand grains weight, indicating the roles of additive gene action and a good scope of selection using their phenotypic performance (Seyoum *et al.* 2012).

An experiment was evaluated with twenty rice genotypes in the International Institute of Tropical Agriculture, Ibadan, Nigeria during 2008/2009 cropping season. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the traits studied, indicating considerable influence of the environment on the expression of the traits. High to medium broad sense

heritability estimates observed on days to heading, days to maturity, plant height, grain yield and number of grains per panicle, panicle weight, number of panicles per m2 and panicle length. The low broad sense heritability observed for the number of tillers per plant and 1000 grain weight is indicative of the influence of the environment on these traits. Low heritability of these traits indicates the ineffectiveness of direct selection for these traits. High to medium heritability and genetic advance were recorded for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant (Akinwale *et al.* 2011).

Selvaraj *et al.* (2011) reported variability, correlation and path coefficient on twenty one rice genotypes for grain yield and other yield attributes. The phenotypic correlation coefficient (PCV) values were slightly greater than genotypic correlation coefficient (GCV), revealing negligible influence of environment in character expression. Analysis of variance revealed considerable variability among the genotypes for all the characters. High heritability coupled with high genetic advance and high GCV were observed for number of tillers/plant followed by number of productive tillers per plant, plant height and grain yield / plant.

Prajapati *et al.* (2011) assessed thirty eight rice genotypes at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad School of Agriculture, SHIATS, Allahabad during kharif-2009. The experiment was conducted to study the 12 quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance. High estimates of heritability coupled with high genetic advance as percent of mean was observed for harvest index followed by number of spikelets per panicle, number of panicles per hill and number of tillers per hill. High estimates of heritability coupled with moderate genetic advance as percent of mean was observed for flag leaf width followed by days to 50% flowering, panicle length and biological yield per hill.

According to Akhtar *et al*. (2011), an experiment was carried out with the yield contributing traits in ten rice genotypes for variances and heritability analysis. Analysis of variance revealed significant differences among the genotypes for all the traits. Highest genotypic as well as phenotypic coefficient of variation were obtained in case of number of grains per panicle followed by number of tillers per plant, paddy yield and plant height. High heritability was found for days to maturity, number of grains per panicle, number of tiller per plant and plant height.

Ullah *et al.* (2011) reported ten traditional fine Biroin rice and noted that grain yield was positively and significantly associated with panicle length and grains per panicle and observed that the higher genotypic coefficient of variations was found in case of grains per panicle followed by grain yield/plant, 1000-grain weight and panicles per plant. High heritability was observed for all the tested characters except harvest index. High heritability with high genetic advance in percentage of mean was recorded for the characters grains per panicle, grain yield per plant and 1000-grain weight indicating role of additive gene action in the expression of these traits.

An experiment, to evaluate thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. They observed high heritability with high genetic advance as percent of mean was registered for number of effective tillers per plant, panicle weight, number of grains per panicle, number of spikelets per panicle, 1000 grain weight, kernel length before cooking (KLBC), length breadth(L/B) ratio, water uptake ratio and grain yield per plant (Nandan *et al*. 2010).

The assessment of the genetic variability, correlation and heritability of 47 bold grained rice genotypes with two locally recommended high yielding check varieties namely Ranjit and Monohar Sali of Barak Valley, Assam for eight morpho-physiological characters. Very small difference between genotypic

coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was observed for the characters like days to 50% flowering. The characters like plant height, effective branch tillers per hill, panicle length, sterility percentage and yield per plant were found wide difference between GCV and PCV. There was high heritability associated with high genetic advance was found in the characters grain yield per hill and sterility percentage. High heritability with moderate genetic advance was found for the characters effective branch tillers per hill. High heritability with low genetic advance was observed for the character days to 50% flowering (Chakraborty and Chakraborty 2010).

Hairmansis *et al*. (2010); recorded a positive and significant association of grain yield with filled grains per panicle, spikelet per panicle and spikelet fertility.

An experiment where studied four crosses of F2 generation were advanced to F3 and F4 generations to study variability, heritability and genetic advance of four crosses of rice genotypes. Among the four crosses studied, cross 1 exhibited superior *per* se performance in both F3 and F4 generations for almost all the economic characters studied including yield. This cross also recorded increased performance from F3 to F4 generations. This indicated the improvement of the genotypes as the generation progresses. High PCV and GCV values were observed for grain yield per plant for cross 1 followed by cross 2 in both F3 and F4 generations. Also cross 1 and cross 2 recorded high heritability and genetic advance for the characters *viz,* number of productive tillers per plant, 1000 grain weight and grain yield per plant in both F3 and F4 generations. This indicated that these characters are controlled by additive gene action. Hence the expected progress under selection could be obtained in the early generation itself. Genetic improvement for quantitative traits can be achieved through a clear understanding of the nature and amount of variability present in the genetic stocks and the extent to which the desirable traits are heritable. Therefore, information on the genetic parameters such as coefficient of variation, heritability, genetic advance and the

influence of environment on the expression of these characters will help the breeder to evolve suitable cultivars within a short time (Anbanandan *et al.* 2009).

Bisne *et al*. (2009) conveyed an experiment on fourty four rice genotype in Raipur, Chhattisgarh in *kharif* 2005 for 13 characters. Low, moderate, and high genotypic and phenotypic coefficient of variations were observed. Harvest index, total number of filled spikelets per panicle, 100-grain weight and spikelet fertility percentage express high genotypic and phenotypic coefficient of variations. High heritability coupled with high genetic advance was exhibited by harvest index, total number of chaffy spikelets per panicle, grain yield per plant, total number of filled spikelets per panicle and spikelet fertility percentage and selection may be effective for these characters.

Karad *et al*. (2008) performed a wide range of variability in yield and yield contributing characters. The GCV was slightly lower than PCV for almost all the characters. The parameters of genetic variability revealed high GCV values for number of mature and immature panicles mt.sq.-1, 1000 grain weight and plant height. The estimate of heritability together with genetic advance was high for 1000 grain weight, number of mature and immature panicles and plant height.

Padmaja *et al.* (2008) studied genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for eleven characters in one hundred and fifty genotypes including five check varieties of rice were studied. The analysis of variance revealed that there were highly significant differences for all the characters except leaf width and 100- seed weight among the genotypes. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were high for all the characters except days to 50% flowering and panicle length.

Vange (2008) conveyed a field experiments in 2005 in the Experimental Farm Station of the University of Agriculture. Makurdi, Nigeria to evaluate the performance and genetic diversity of some upland rice accessions. Preliminary results indicates highly significant (P <0.01)differences on all traits studied except for grain length, grain width, grain length/width ratio and 1000 grain weight, indicating genetic diversity among these accessions. Genotypic coefficient of variability (GCV) was generally lower than phenotypic coefficient of variability (PCV). Days to 50% heading, days to maturity, flag leaf area, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle, grain weight/panicle and seed yield showed very low differences between their PVC and GCV values. Also these traits had high estimates for heritability and genetic advance.

A study was conducted by Kumar *et al.* (2007) to estimate of genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean in the F2 and F3 segregating populations of six crosses of rice for six yield and yield component characters. The F2 populations of the cross P1 P3 showed high PCV, GCV coupled with high heritability estimates and high genetic advance as percentage of mean for number of filled grains per panicle, 100-grain weight, biomass per plant and grain yield per plant. Similarly, the F3 population of the cross P2 P1 exhibited high genetic parameters for number of productive tillers per plant and grain yield per plant. These populations could be subjected to simple pure line selection to improve grain yield per plant.

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 particle. Number of filled grains per panicle, 100.-seed weight and 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). The genotypic variance ranged from 5.36 for panicle length to 24.83 for grain yield. 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 particle and plant height.

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. All the characters tested were showed significant variation among the varieties. The highest genetic variability was obtained in spikelets/panicle and grains/panicle. High heritability together with high genetic advance in percentage of mean was observed in plant height, 1000-grain weight, grains/panicle and spikelets/panicle.

2.2. Correlation co-efficient

Konate *et al.* (2016) carried out an experiment to evaluate genetic variability of agro-morphological traits and also determine the correlation between grain yield with its components in rice lines, 17 recombinants inbred lines, their parents and a check variety were grown in research station of Africa rice center in Benin republic during two consecutive years 2013 and 2014. Phenotypic coefficients of variance were higher than genotypic coefficients of variance in all the characters across the two years. High heritability in broad sense (H2) estimates were obtained for biomass (68.77%), date of 50% flowering (98.11%), plant height (81.94%), number of panicles (64.40%), and yield/plant (62.23%) suggesting that the traits were primarily under genetic control. Grain yield/plant recorded positive and significant correlation with stem weight (r=0.5262) and biomass (r=0.9291). This result indicates that selection based on these two characters will be highly effective for yield improvement in rice.

Allam *et al.* (2015) carried out an experiment to study of correlation and path analysis was undertaken in 23 genotypes of basmati rice for grain yield, its component traits and grain quality traits. Yield per plant had highly significant positive genotypic and phenotypic correlation with days to maturity effective panicles, spikelets per panicle and amylose content. Correlation studies indicated that close relationship between genotypic and phenotypic correlation coefficients and magnitude of genotypic correlation were higher than their corresponding phenotypic correlation for most of the characters.

Bhati *et al*. (2015) studies on genetic variability, correlation and path coefficient analysis were conducted on 30 elite rice (*Oryza sativa* L.) genotypes. Analysis of variance among 30 genotypes showed significant difference for all characters studied. Highest genotypic coefficient of variance (GCV) phenotypic coefficient variance (PCV) was observed for grain yield per hill followed by harvest index indicating that these characters could be used as selection for crop improvement. High estimates of heritability coupled with high genetic advance were observed for plant height and spikelets per panicle. Correlation studies revealed that grain yield per hill was positively significant correlated with harvest index, biological yield per hill, test weight and plant height at both genotypic and phenotypic level.

According to Islam *et al.* (2015) a field experiment was conducted using twenty three rice genotypes including three check varieties during the period from June to December 2013 to investigate the association among eight morpho-physiological traits including yield. The experiment was laid out in a randomized complete block design with three replications. Grain yield was found to be positively and significantly correlated with filled grain per panicle, plant height, days to 50% flowering and days to maturity both at genotypic and phenotypic levels, indicating the importance of these traits for yield improvement in rice.

Kishore *et al*. (2015) studied that seventy three rice varieties were evaluated for their variability with regards to yield and yield components. Estimates of heritability and genetic advance in per cent of mean were also obtained for the above traits. The results revealed high variability, heritability and genetic advance in per cent of mean for grain yield while panicle bearing tillers and 1000 grain weight had recorded high heritability coupled with low genetic advance as per cent of mean. Further, yield was observed to be positively associated with panicle bearing tillers and number of filled grains per panicle.

Ratna *et al*. (2015)studies correlation and path coefficients analyses among fourteen morphological characters were studied in six advanced lines of Basmati rice and one commercial check namely BRRI Dhan 29. In general, genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients suggesting that the environmental influence reduces the relationship between yield and yield contributing characters of rice. Correlation coefficient analysis showed significant positive correlation between plant height and panicle length at genotypic level. Number of filled spikelets/panicle showed significant positive correlation with yield at both genotypic and phenotypic levels but significant negative correlation was observed between plant height and yield. Number of effective tillers/plant had negative significant correlation with panicle length and with number of unfilled spikelets/panicle at genotypic level. Number of ineffective tillers/plant had significant negative correlation with 1000-seed weight at both genotypic and phenotypic levels.

Bornare *et al*. (2014) reported fifteen CMS and ten restorer lines that the coefficients of phenotypic and genotypic variability were comparatively high for effective tillers/plant followed by grain yield/plant, plant height and angle of floret. High heritability accompanied with high genetic advance indicated predominance of additive gene action for the traits viz., 1,000 seed weight, plant height, anther breadth, anther length, effective tillers/plant and angle of floret

opening. Selections can be effective on the basis of correlation and path analysis for characters like effective tillers/plant, spikelet density, angle of floret opening, duration of floret opening, panicle length, 1,000 seed weight and days to 50 per cent flowering.

Ganapati *et al.* (2014) reported that twenty five genotypes were evaluated for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Amon season, 2010. Grain panicle-1 and filled grain panicle-1 had high genotypic variance, high heritability, high genetic advance and high genotypic coefficient of variation. Tiller hill-1, plant height and thousand grain weights showed significant positive association with grain yield.

Rahman *et al.* (2014) twenty one rice varieties were assessed for thirteen morphological characters. Plant height, number of effective tillers per square meter, number of spikelets per panicle, number of effective spikelets per panicle, number of ineffective spikelets per panicle, 1000 grains weight, straw yield and grain yield exhibited that they were controlled by additive gene action and selection for the improvement of these traits would be rewarding. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation. Genotypic coefficient of variation was the highest for number of ineffective spikelets per panicle (39.96) followed by 1000 grains weight (24.33) and number of spikelets per panicle (18.61). Plant height and 1000 grains weight (95.30) had the highest heritability.

Janwan *et al.* (2013) studiedrice improvement for high yield is important to increase productivity of the crop. A total of 271 recombinant inbred lines (RILs) were obtained in this program. Three lines were observed with significantly higher yield than the best check variety, CNT1. However, the frequency was higher for plant height, days to 50% flowering and number of panicles. The result of

correlation analysis revealed highly significant and positive correlation between yield and all the eleven traits under study.

Shabir *et al.* (2013) evaluated an experiment comprising 79 rice genotypes from different countries was studied at National Institute for Biotechnology and Genetic Engineering, Faisalabad, Pakistan during the year 2009-2011. Correlation analysis indicated highly positive significant association for grain yield with all other parameters such as plant height (r = 0.17**), number of tillers per plant (r = 0.24**), panicle length (r = 0.45**), panicle weight (r = 0.67**), 1000-grain weight (r = 0.36**), number of grains per panicle (r = 0.84**) and spikelet fertility (r = 0.56**) at P < 0.01 level. So selection on the basis of these characters will help breeders to achieve more paddy yield in rice.

Babu *et al*. (2012) carried out an experiment to study the correlation in twenty one popular hybrids of rice (*Oryza sativa* L.). Character association of the yield attributing traits revealed significantly positive association grain yield per plant with number of productive tillers per plant. Hence, the result suggested selection for these traits can improve the yield

Seyoum *et al.* (2012) conducted a field experiments using fourteen rice genotypes during the main rainy seasons of 2009 and 2010 at three rainfed upland locations of Southwest Ethiopia to estimate the correlation coefficient of grain yield and yield contributing traits in upland rice. Grains per panicle had highly significant (r = 0.906**) genotypic correlation coefficient with grain yield.

Satheesh kumar *et al.* (2012) estimated correlation in fifty three genotypes of rice for fifteen characters. It revealed grain yield per plant exhibited high significant and positive genotypic correlation with number of productive tillers per plant, filled grains per panicle and total number of grains.

Akinwale *et al.* (2011) evaluated twenty rice genotypes in the International Institute of Tropical Agriculture, Ibadan, Nigeria during 2008/2009 cropping season. They concluded that grain yield exhibited significantly positive correlation with the number of tillers per plant (r = 0.58**), panicle weight (r =0.60*) and number of grains per panicle (r= 0.52*). Therefore, the results suggest that these traits can be used for grain yield selection. This suggests that these traits are primarily under genetic control and selection for them can be achieved through their phenotypic performance.

Ullah *et al.* (2011) studied ten traditional fine Biroin rice and found that genotypic correlations were higher than the phenotypic correlations in most of the cases. Grains per panicle, panicle length, leaf area index, harvest index and chlorophyll content were the major characters contributing to grain yield as these traits were significantly and positively associated with grain yield per plant.

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 correlation coefficient between seed yield per plant and other quantitative attributing to yield showed that grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicle per plant, panicle length, number of spikelet's per panicle and test weight at both genotypic and phenotypic levels.

Padmaja *et al.* (2008) studied genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for eleven characters in one hundred and fifty genotypes including five check varieties of rice were studied. Heritability and genetic advance were high for all the characters except days to 50% flowering and panicle length, which had moderate genetic advance along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Vange (2008) conveyed a field experiments in 2005 in the Experimental Farm Station of the University of Agriculture. Makurdi, Nigeria to evaluate the performance and genetic diversity of some upland rice accessions. Genotypic correlation analysis of yield with other traits revealed that yield had a significantly positive correlation with flag leaf area, number of tillers, number of panicles, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle and seed weigh/panicle, grain length and 1000 seed weight. The direct and indirect effect of the rice traits on yield was assessed.

Zahid *et al*. (2006) reported phenotypic and genotypic variances, coefficient of variance, genetic advance, heritability, correlation coefficient and path coefficient analysis were conducted for yield, yield components and grain quality characteristics in 14 genotypes of Basmati rice. High heritability estimates coupled with high genetic advance were observed for plant height and 1000 grain weight. Plant height has negative correlation with yield indicating that taller Basmati plants have low yield. Grains per panicle have positive and significant genotypic and phenotypic correlation with yield. Plant height and 1000 grain weight had positive correlations with grain quality characteristics i.e. grain length and cooked grain length while tillers per plant had negative correlation with these quality traits.

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. The number of grains per panicle and panicle length showed a significant difference between phenotypic and genotypic coefficient of variation. High values of heritability were observed for 1000-grains weight (98.30%) and days to 50% flowering (97.33%). 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.

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. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Days to flowering, days to maturity, grains/panicle, 1000-grain weight and harvest index showed significant positive correlation with grain yield.

2.3 Path co-efficient

Devi *et al*. (2017) studied on 27 rice genotypes. Path analysis reveals that test weight (3.48), effective tillers (1.57), and filled grains per panicle (1.41) had positive direct effect on grain yield per plant.

Allam *et al.* (2015) carried out an experiment to study of correlation and path analysis was undertaken in 23 genotypes of basmati rice for grain yield, its component traits and grain quality traits. Yield per plant had highly significant positive genotypic and phenotypic correlation with days to maturity effective panicles, spikelets per panicle and amylose content. Path coefficient analysis revealed that the number of characters chosen for the study were very much appropriate as evident from low value of residual effect (0.1614).Effective panicles per plant imparted the highest positive direct effects (0.6169) on yield followed by test weight (0.5545), spikelets per panicle (0.5268), kernel length (0.3364) and spikelet fertility (0.2175).

Bhati *et al*. (2015) studies on genetic variability, correlation and path coefficient analysis were conducted on 30 elite rice (*Oryza sativa L.*) genotypes. Analysis of variance among 30 genotypes showed significant difference for all characters studied. Path coefficients revealed the harvest index, biological yield per hill, number of spikelets per panicle, number of tillers per hill and plant height had high positive direct effect on grain yield at both genotypic and phenotypic level.

According to Islam *et al.* (2015) a field experiment was conducted using twenty three rice genotypes including three check varieties during the period from June to December 2013 to investigate the association among eight morpho-physiological traits including yield. From the path coefficient analysis, it was revealed that days to maturity, days to 50% flowering, plant height, number of filled grain per panicle and grain length had direct positive effect on yield, indicating these are the main contributors to yield. Eventually, it was recommended that, for obtaining increased rice yield, a genotype should possess more number of filled grains per panicle.

Kishore *et al.* (2015) studied that seventy three rice varieties were evaluated for their variability with regards to yield and yield components. Further, yield was observed to be positively associated with panicle bearing tillers and number of filled grains per panicle and these characters were noticed to exert high direct effects on grain yield per plant. High indirect effects of most of the traits were noticed mostly through panicle bearing tillers per hill indicating importance of the trait as selection criteria in crop yield improvement programmes.

Ratna *et al.* (2015) studies correlation and path coefficients analyses among fourteen morphological characters were studied in six advanced lines of Basmati rice and one commercial check namely BRRI Dhan 29. Path coefficient analysis revealed highest positive direct effect of number of filled spikelets/panicle on grain yield but plant height and number of unfilled spikelets/panicle had negative direct effect on grain.

Ganapati *et al.* (2014) reported that twenty five genotypes were evaluated for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Amon season, 2010. Path coefficient analysis also revealed that, tiller hill-1, thousand grain weight and grain panicle-1 had higher direct effects on yield. Genetic variability, correlation and path analysis revealed that tiller hill-1, plant height and thousand grain weights are the most

important yield components in rice. Therefore, from the present study it could be suggested that emphasize should be given on these characters for the selection of genotypes for higher grain yield in transplanted Aman rice.

Rahman *et al.* (2014) twenty one rice varieties were assessed for thirteen morphological characters. Considering the path analysis number of effective spikelets per panicle, 1000 grain weight, number of effective spikelets per panicle, number of effective tillers per square meter and plant height are important characters for yield improvement.

Janwan *et al.* (2013) studied rice improvement for high yield is important to increase productivity of the crop. A total of 271 recombinant inbred lines (RILs) were obtained in this program. Path analysis identified panicle weight, number of panicle, days to 50% flowering, seed-setting rate and flag leaf length as traits contributing for linear increase in yield. These traits could be considered as critical criteria for selecting high-yielding lines in rice breeding programs.

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.

Seyoum *et al.* (2012) conducted a field experiments using fourteen rice genotypes during the main rainy seasons of 2009 and 2010 at three rainfed upland locations of Southwest Ethiopia to estimate the path coefficient of grain yield and yield contributing traits in upland rice. They showed that grains per panicle had maximum positive direct effect.

According to Abarshahr *et al.* (2011) revealed that with 30 varieties of rice under two irrigation regimes. Path analysis revealed for paddy yield indicated that number of spikelet per panicle and flag leaf length had positive direct effects and

days to complete maturity and plant height had negative direct effect on paddy yield under optimum irrigation condition, while flag leaf width and numbed of filled grains per panicle had positive direct effects and days to 50% flowering had negative direct effect on paddy yield under drought stress condition.

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.

Selvaraj *et al.* (2011) studied variability, correlation and path coefficient on 21 rice genotypes for grain yield and other yield attributes. Results of path-coefficient analysis revealed that, test weight exhibited maximum positive direct effect on grain yield / plant followed by filled grains / panicle, plant height, panicle length, number of tillers / plant and days to 50% flowering and they contributed primarily to yield and could be relied upon for selection of genotypes to improve genetic yield potential of rice.

Subbaiah *et al*. (2011) studied the extent of variability and genetic parameters with 16 parents and 48 hybrids for nine yield and its components and twenty five quality characters. The magnitude of difference between PCV and GCV was relatively low for all the traits, indicating less environmental influence. High GCV and PCV were recorded for harvest index, total number of productive tillers per plant and gelatinization temperature in parents and for total number of productive tillers per plant, number of grains per panicle, gelatinization temperature and amylose content in hybrids. High heritability coupled with high genetic advance as percent of mean were recorded for gelatinization temperature, harvest index, total number of productive tillers per plant, number of grains per panicle, kernel length, kernel L/B ratio and grain yield per plant in case of parents and for gelatinization

temperature, amylase content, total number of productive tillers per plant, number of grains per panicle and harvest index in case of hybrids indicating the additive gene effects in the genetic control of these traits and can be improved by simple selection in the present breeding material.

Ullah *et al.* (2011) studied ten traditional fine Biroin rice and found that maximum contribution of more chlorophyll content to grain yield was observed in path analysis, which was followed by higher harvest index and grains per panicle through higher direct effect. Leaf area index, panicle length, days to maturity, grains per panicle, harvest index, 1000-grain weight and plant height had positive but indirect effect on grain yield through chlorophyll content.

Ghosal *et al.* (2010) reported eigtheen advanced breeding lines. For observation of yield and yield contributing characters with their variability, associations and direct and indirect effect on yield and found panicle length (cm) showed significant positive association with grain yield.

Karad *et al.* (2008) conducted a wide range of variability in yield and yield contributing characters. Path coefficient analysis revealed that length of panicle had higher positive direct effect via by number of panicles, number of tillers per plant, number of mature panicles whereas the negative effect on plant height and thousand seed weight.

Zahid *et al*. (2006) reported phenotypic and genotypic variances, coefficient of variance, genetic advance, heritability, correlation coefficient and path coefficient analysis were conducted for yield, yield components and grain quality characteristics in 14 genotypes of Basmati rice. Hence, number of tillers per plant, no. of grains per panicle and 1000 grain weight contributed maximum direct effect on 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/m2 and higher harvest index had positive and higher direct effect on grain yield. Moreover, days to maturity, days to flowering, plant height and spikelets/panicle had positive and higher indirect effect on grain yield though grains/panicle.

CHAPTER III

MATERIALS AND METHODS

The present research work was conveyed during the period from April 2015 to September 2015. To study the comparative trial of characterization and to select high yielding and short duration rice *(Oryza sativa* L.) from various crosses. All the materials and methods that were used and followed for conducting the experiment have been presented below-

3.1 Experimental site

The present research work was conveyed in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during the period from April 2015 to September 2015. The location of the experimental site was situated at 23° 64" N latitude and 90°45" E longitudes with an elevation of 8.3 meter from the sea level. Experimental site was showed in (Appendix I) (Plate 1).

3.2 Soil and climate

The experimental site was situated in the subtropical zone. The soil of the experimental site lies in Agro ecological region of "Madhupur Tract" (AEZ No. 28). The top of the soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH of soil is 5.47 to 5.63 and it's organic carbon content is 0.82% (Appendix II). The record of air temperature, humidity and rainfall during the period of experiment were noted from the SAU Weather Stations, Sher-e-Bangla Nagar, Dhaka-1207. (Appendix III).

3.3 Planting materials

The healthy seeds of eleven rice genotypes were used for the present research work and out of eleven, nine rice genotypes has been developed at SAU. Two check varieties were collected from BRRI which were used as planting materials. Brief description about these nine genotypes will increase the credibility of the research. The materials used in that experiment is presented in Table 1.

Table 1: List of rice genotypes and check varieties along with their sources

Sl. No.	Genotypes	Origin of genotypes	Sources
1	G 1	BR21XBRRI dhan29 $F_5S_6P_2$	SAU
2	G 2	BR21XBRRI dhan29 $F_5S_6P_3$(a)	SAU
3	G 3	BR21XBRRI dhan29 $F_5S_6P_3$(b)	SAU
4	G 4	BR21XBRRI dhan29 $F_5S_6P_5$	SAU
5	G 5	BR21XBRRI dhan29 $F_5S_6P_8$	SAU
6	G 6	BR21XBRRI dhan29 $F_5S_6P_{10}$	SAU
7	G 7	BR21XBRRI dhan36 $F_5S_1P_9$	SAU
8	G 8	BR24XBRRI dhan 28 $F_5S_{10}P_8$	SAU
9	G 9	BR24XBRRI dhan29 $F_5S_5P_{10}$	SAU
10	G 10	BRRI dhan 48	BRRI
11	G 11	BRRI dhan 55	BRRI

3.4 Methods

The methods have been followed to carry out the experiment is following-

3.4.1 Germination of seed

Seeds of all rice genotypes soaked separately for 24 hours in clothes 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.

3.4.2 Preparation of seedbed and raising seedling

The seed bed was prepared thoroughly by 3-4 times ploughing and cross ploughing followed by laddering to attain a good puddle. Weeds and stubbles were removed from the land. Sprouted seeds were sown separately in the previously prepared wet seed bed on 25 April 2015. Seedbed was irrigated with regular interval to maintain moisture.

3.4.3 Land preparation for transplanting

The experimental plot was prepared thoroughly by several ploughing and cross ploughing followed by laddering and harrowing with a tractor drawn disc plough to attain a good puddle. Weeds and other stubbles were removed from the field. The soil is well pulverized by breaking the clods and the experiment plot was leveled properly.

3.4.4 Application of manure and fertilizer

The fertilizers Nitrogen, Phosphorous, Potassium, Sulpher and Boron in the form of Urea, TSP, MoP, Gypsum and Borax, respectively were applied. The entire amount of TSP, MoP, Gypsum, Zinc sulphate and Borax all these fertilizers recommended by BRRI were applied during the final preparation of land. Urea was applied in three equal installments. The first 1/3rd applied at 4-5 tillering, the second 1/3rd and last one third at panicle initiation stage.

3.4.5 Experimental design and layout

Field lay out was done after final land preparation. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 27 m x 14 m = 378 m^2. Each plot size was 4 m x 2.2 m

and the distance between replication to replication was 1m. The spacing between lines to lines was 25 cm. Seeds were sown in lines in the experimental plots on 25 April, 2015.

3.4.6 Transplanting

The check varieties and parents were first transplanted randomly in each block. Then experimental genotypes (nine F_5 cross lines) were tranplanted randomly to the remaining plots. Each entry was grown as single seedling per hill in the rows on 26 May, 2015 with a spacing of row to row is 25 cm and plant to plant is 25 cm.

3.4.7 Intercultural operations and after care

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

i. Irrigation and drainage

Flood irrigation was given to maintain a constant level of standing water upto 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 discourge late tillering. The field was finally dried out 15 days before harvesting.

ii. Gap filling

First gap filling was done for all of the plots at 8 days after transplanting (DAT).

iii. Weeding

Weeding was done to keep the plots free from weeds, which ultimately ensured better growth and development. Weeds are always competing with crops for all the essential elements. The newly emerged weeds were uprooted carefully at tillering stage and at panicle initiation stage by mechanical means.

iv. Top dressing

After basal dose, the remaining doses of urea were top-dressed in 2 equal installments. The fertilizers were applied on both sides of seedlings rows with the soil.

v. Plant Protection

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.

3.4.8 Crop harvesting

Harvesting was done from 16th August to 8th September, 2015depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e., straw color of panicles, leaves, stems desirable seed color, the crop was assessed to attain maturity. Ten plants were selected at random from F_5 progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants. Variation at flowering and ripening stage of different genotypes are presented in Plate no. 1.

3.4.9 Data collection

For studying different genetic parameters and inter-relationships, fourteen characters were taken into consideration. The data were recorded on ten selected plants for each cross and ten selected plants for each parent on the following traits-

i. Days to flowering

Difference between the dates of transplanting to the date of 50% flowering of a plot was counted and was recorded when 50% plant of a plot were at the flowering stage. Plate 1(a) showing variation at days to flowering.

ii. Days to maturity

Maturities of the crops of different combination were recorded considering the symptom such as moisture content of rice, color changing of the plant from greenish to straw colored appearance. Plate 1(b) showing variation at maturity stage.

iii. Plant height (cm)

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

iv. Number of total tillers per plant

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

v. Number of effective tillers per plant

The number of effective tiller per plant was counted as the number of panicle bearing tillers per plant and average value was recorded.

vi. Panicle length (cm)

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

vii. 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 recorded.

viii. 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.

ix. 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.

x. **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.

xi. Total number of spikelet 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 recorded.

xii. Yield per plant (g)

Grains obtained from each plant were sun dried and weighted carefully. The dry weight of gains per plant was then recorded.

xii. Thousand seed weight (g)

One thousand seeds were counted randomly from the total cleaned harvested seeds and then weighted in grams and recorded.

xiii. Yield per hectare (t/ha)

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

(a)

(b)

Plate 1. Photograph showing variation at (a) flowering stage and (b) ripening stage

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3.4.10 Statistical analysis

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTATC software program and then phenotypic and genotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). Genotypic and phenotypic co-efficient of variation were calculated by the formula of Burton (1952). Genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller *et al.* (1958) and Johnson *et al.* (1955); and path co efficient analysis was done following the method outlined by Dewey and Lu (1959).

i) Estimation of genotypic and phenotypic variances

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

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

Where, MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error and

r = Number of replication

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

Where, $\sigma^2 g =$ Genotypic variance,

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

ii) Estimation of genotypic co-efficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV) were calculated following formula as suggested by Burton (1952):

Genotypic coefficient of variance, (GCV) $= \frac{\sigma g \times 100}{\bar{x}}$

Phenotypic coefficient of variance, (PCV) $= \frac{\sigma p \times 100}{\bar{x}}$

Where, GCV = Genotypic coefficient of variance,

PCV = Phenotypic coefficient of variance

σg = Genotypic standard deviation

σp = Phenotypic standard deviation

x = Population mean

iii) Estimation of heritability

Broad sense heritability was estimated by the formula suggested by Singh and Chaudhary (1985). The heritability was categorized as suggested by Robinson *et al.* (1949).

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

Where, $h^2 b$ = Heritability in broad sense

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = 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) and classified by adopting the method of Johnson *et al* (1955).

$$GA = \frac{\sigma 2g}{\sigma 2p} \cdot K \cdot \sigma p$$

Where, GA = Genetic advance

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = phenotypic variance

σp = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity

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).

$$\text{Genetic advance in percentage of mean} = \frac{\text{Genetic advance}}{\overline{x}} \times 100$$

x = population mean

vi) Estimation of simple correlation co-efficient

Simple correlation was estimated with the following formula (Singh and Chaudhury, 1985).

$$r = \frac{\sum xy - \frac{\sum x \cdot \sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

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 employed by Dewey and Lu (1959) also quoted in Singh and Chaudhury (1985), using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect of independent variables on the dependable variable.

In order to estimate direct and indirect effect of the correlated characters, say independent variables x1, x2, x3 on dependent variable yield y, a set of simultaneous equations (three equations in this example) is required to

be formulated as given below:

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$

Where, r's denotes simple correlation co-efficient and P's denote path co-efficient (unknown). 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

$P_{yx1}r_{x1x2}$ = the indirect effect of x1 via x2 on y

$P_{yx1}r_{x1x3}$ = 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 Chaudhury, 1985):

$$P^2RY = 1 - \sum P_{iy}.\ riy$$

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 IV

RESULTS AND DISCUSSION

The present research work was conveyed to compare among the 9 F_5 lines in order to select high yielding and short duration aus line(s) and also to study the correlation and path co-efficient for different yield contributing characters. The data were recorded on different characters such as days to flowering, days to maturity, plant height (cm), number of total tillers per plant, number of effective tillers per plant, 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 per panicle, total number of spikelet per panicle, yield per plant (g), thousand seed weight (g), yield per hectare (t).

4.1 Analysis of variance

The analyses of variance of different advanced aus lines for morphological traits are shown in Table 2. Analysis of variance indicated that the difference among genotypes for thirteen traits among fourteen under study viz., days to 50% flowering, days to maturity, plant height, total no. of tiller per plant, number of effective tiller per plant, panicle length, number of primary branches/panicle, number of secondary branches per panicle, total no. of spikelets per panicle and number of filled grains of main tiller, yield per plant, thousand seed weight and yield per ha was highly significant. This suggests the presence of variation among the genotypes for all these traits. Previous studies in rice also found significant variation for these traits (Nuruzzaman *et al.,* 2016; Paikhomba *et al.,* 2014; Kumar *et al.,* 2014)**.** Genotypes showed no significant difference for number of unfilled grains of main tiller. Similar result was found by Seyoum *et al*. (2012) for total number of tiller. Univariate statistical analysis gave an excellent opportunity to identify and group the genotypes into different categories with respect to various

traits individually. The mean performances of the 11 rice genotypes for their traits are shown in Table 3a, Table 3b, Appendix IV and Appendix V.

4.1.1 Days to flowering

In this study out of 11 genotypes, the maximum days to 50% flowering was found in genotype G9 (BR24X BRRI dhan29, $F_5S_5P_{10}$) that took the period (96.67), which was statistically similar with G1 (96.67) and G4 (93.33) and higher than their checks. As their checks G10 (BRRI dhan 48) and G11 (BRRI dhan 55) were taken 90 days and 75 days for flowering respectively. The minimum days to 50% flowering was found in both genotypes G2 and G3 which were statistically similar with G5, G6, G7 and G11 with the same value of 75.00 days (Table 3a). There were significant variations among the genotypes (329.733**) (Table 2).Days to 50% flowering among the genotypes ranged from 70.67 to 96.67 days with a mean value of 81.33 days (Table 4). Compare at flowering among different genotypes Plate 2.Aditya *et al*. (2013) revealed similar results.

4.1.2 Days to maturity

There were significant variations among the genotypes (311.667**) for days to maturity (Table 2). In case of days to maturity, genotypes G1 (BR21 X BRRI dhan29, $F_5S_6P_2$) and G9 (BR24 X BRRI dhan29, $F_5S_5P_{10}$) showed the highest number of days to maturity (130.3 days) which were higher than their check G10 (112 days) and G11(110days). The genotype G5 performed minimum days to maturity (102.7 days), representing earliness, which was statistically similar with G2 (105.0 days) and G3 (106.3 days). (Table 3a). Genotypes exhibited high days to maturity range from 102.67 to 130.33 days with an average of 113.33 days (Table 4). Variations in maturity duration of crop could be utilized directly under varied agro-ecological situation as well as breeding program. A schematic representation of days to maturity was shown in Figure 1 and Plate 3.

Table 2. Analysis of variance for different characters in rice genotypes

Characters	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 10	Error (r-1)(g-1) = 20
Days to 50% flowering	7.848	329.733**	7.915
Days to maturity	5.121	311.667**	4.821
Plant height	59.530	527.344**	33.021
Total no of tiller/plant	1.963	11.441**	1.033
Number of effective tiller/plant	0.040	8.734**	1.064
Panicle length/plant	0.666	6.051**	1.044
Number of primary branches/panicle	0.033	1.310**	0.215
Number of secondary branches/panicle	19.592	82.806**	6.312
Total no of spikelets/panicle	54.203	1183.901**	207.294
Number of filled grain of main tiller	427.167	1162.152**	198.699
Number of unfilled grain of main tiller	96.918	145.648	75.667
Yield/plant	0.939	67.497**	9.306
Thousand seed weight	3.075	18.322**	2.505
Yield/ha	0.729	3.886**	0.430

** Denote Significant at 1% level of probability

Table 3a. Mean performance of eleven genotypes of *Oryza sativa* in respect of seven important characters

Genotype	DF	DM	PH	NTT/P	NET/P	PL/P	NPB/P
G1	96.67	130.3	120.3	13.50	12.77	24.26	8.833
G2	70.67	105.0	99.93	13.20	11.34	22.91	8.267
G3	70.67	106.3	93.27	12.23	10.27	24.12	8.467
G4	93.33	125.0	124.7	12.17	11.63	25.25	9.167
G5	75.00	102.7	104.3	10.94	9.787	24.36	7.843d
G6	75.00	108.0	102.9	11.60	9.833	23.57	7.400
G7	75.00	107.0	77.65	18.33	15.39	20.21	7.433
G8	76.67	110.0	105.8	14.00	13.27	24.67	8.367
G9	96.67	130.3	117.2	14.03	13.43	24.66	9.533
G10	90.00	112.0	101.0	12.77	12.13b	22.71	8.400
G11	75.00	110.0	96.83	12.50	11.50	22.53	8.600

DF = Days to 50% flowering,, DM = Days to maturity, PH = Plant height, NTT/P = Number of total tillers/plant, NET/P = Number of effective tiller/plant, PL/P = Panicle length/plant, NPB/P = Number of primary branches/panicle,

G1 = BR21 X BRRI dhan29 $F_5S_6P_2$, G2 = BR21X BRRI dhan29 $F_5S_6P_3$(a), G3 = BR21X BRRI dhan29 $F_5S_6P_3$(b), G4 = BR21X BRRI dhan29 $F_5S_6P_5$, G5 = BR21 X BRRI dhan29 $F_5S_6P_8$, G6 = BR21X BRRI dhan29 $F_5S_6P_{10}$, G7 = BR21 X BRRI dhan36 $F_5S_1P_9$, G8 = BR24 X BRRI dhan 28 $F_5S_{10}P_8$, G9 =BR24X BRRI dhan29 $F_5S_5P_{10,}$G10 = BRRI dhan 48 and G11= BRRI dhan 55

Table 3b. Mean performance of eleven genotypes of *Oryza sativa* in respect of seven important characters

Genotypes	NSB/P	TS/P	NFG/P	NUFG/P	Y/P	TSW	Y/ha
G1	27.70	147.00	126.30	22.99	31.00	26.27	5.000
G2	23.77	120.00	103.70	14.30	19.33	21.23	2.287
G3	23.73	121.90	104.80	17.10	18.67	23.67	2.367
G4	30.67	153.70	120.70	32.97	26.33	21.47	3.427
G5	24.21	117.30	81.08	36.04	17.00	23.00	1.900
G6	21.73	104.70c	85.13	22.92	17.00	23.03	1.807
G7	17.83	107.00	85.40	21.63	18.00	19.67	1.853
G8	19.77	115.80	87.57	29.43	21.33	24.15	2.560
G9	31.17	156.60	136.10	28.60	26.00	22.29	4.887
G10	17.10	123.60	104.80	19.00	26.67	24.60	3.167
G11	15.77	97.93	78.60	18.09	20.33	27.50	2.473

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NSB/P = Number of secondary branches per panicle, TS/P = Total number of spikelets per panicle, NFG = Number of filled grain of main tiller, NUG = Number of unfilled grain of main tiller, Y/P (Dry) = Yield per plant, TSW = Thousand seed weight, Y/ha = Yield per hectare.

G1 = BR21 X BRRI dhan29 $F_5S_6P_2$, G2= BR21 X BRRI dhan29 $F_5S_6P_3$(a), G3 = BR21 X BRRI dhan29 $F_5S_6P_3$(b), G4 = BR21 X BRRI dhan29, $F_5S_6P_5$, G5 = BR21 X BRRI dhan29 $F_5S_6P_8$, G6 = BR21 X BRRIdhan29 $F_5S_6P_{10}$, G7 = BR21 X BRRI dhan36 $F_5S_1P_9$, G8 = BR24 X BRRI dhan 28 $F_5S_{10}P_8$, G9 = BR24 X BRRI dhan29 F_5S_5P, G10 = BRRI dhan 48 and G11=BRRIdhan55.

4.1.3 Plant height (cm)

Plant height among the genotypes ranged from 77.65 cm to 124.71 cm with a mean value of 103.98 cm (Table 4). Highest plant height was observed in genotype G4 (124.7 cm) which was longer than their checks G10 (101 cm) and G11 (96.83 cm) and that was statistically similar with the genotype G1 (120.3 cm) and G9 (117.2 cm). while lowest plant height was observed in genotype G7 (77.65cm) which was shorter than BRRI dhan 48 and BRRI dhan 55. There were significant variations among the genotypes (527.344**) for plant height (Table 2).A schematic representation of plant height was shown in (Plate 4).Kumar *et al.* (2014) also reported significant variation in plant height. A schematic representation of days to maturity was shown in and Plate 4.

4.1.4 Total number of tiller per plant

There were significant variations among the genotypes (11.441**) for total number of tiller per plant (Table 2).Total no. of tiller/plant was performed with the ranged from 10.94 to 18.33. The average total no. of tiller/plant was 13.21. (Table 4).In case of total number of tiller per plant, genotypes G7 (BR21 X BRRI dhan36, $F_5S_1P_9$) showed the highest total number of tiller (18.33) which were higher than their check G10 (12.77) and G11(12.50). The genotype G5 performed minimum days to maturity (10.94), representing earliness, which was statistically similar with G6 (11.60) (Table 3a). G3 (12.23), G4 (12.17) genotypes are more or less similar to their checks as G10 (12.77) and G11 (12.50). A schematic comparison among among checks (a), (b) and genotypes (c), (d) in Plate 5.

4.1.5 Number of effective tiller per plant

There were significant variations among the genotypes (8.734**) (Table 2).The ranged from 9.79 to 15.39 were found for number of effective tiller per plant with an average of 11.94 (Table 4).The most significant number of effective tiller per plant was exhibited by genotype G7 (15.39) which was higher than their checks

Table 4. Range, mean, CV (%) standard deviation and standard error of eleven rice genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Days to 50% flowering	70.67	96.67	81.33	3.46	2.81	1.06
Days to maturity	102.67	130.33	113.33	1.94	2.20	0.83
Plant height	77.65	124.71	103.98	5.53	5.75	2.17
Total no of tiller/plant	10.94	18.33	13.21	7.70	1.02	0.38
Number of effective tiller/plant	9.79	15.39	11.94	8.64	1.03	0.39
Panical length/plant	20.21	25.25	23.57	4.33	1.02	0.39
Number of primary branches/panicle	7.40	9.53	8.39	5.53	0.46	0.18
Number of secondary branches/panicle	15.77	31.17	23.04	10.90	2.51	0.95
Total no of spikelets/panicle	97.93	156.59	124.13	11.60	14.40	5.44
Number of filled grain of main tiller	78.60	136.13	101.29	13.92	14.10	5.33
Number of unfilled grain of main tiller	14.30	36.04	23.92	36.37	8.70	3.29
Yield/plant (g)	17.00	31.00	21.97	13.89	3.05	1.15
Thousand seed weight (g)	19.67	27.50	23.90	6.62	1.58	0.60
Yield/ha (ton)	1.81	5.00	2.88	22.74	1.58	0.60

CV (%) = Coefficient of variation, SD = Standard deviation and SE = Standard error
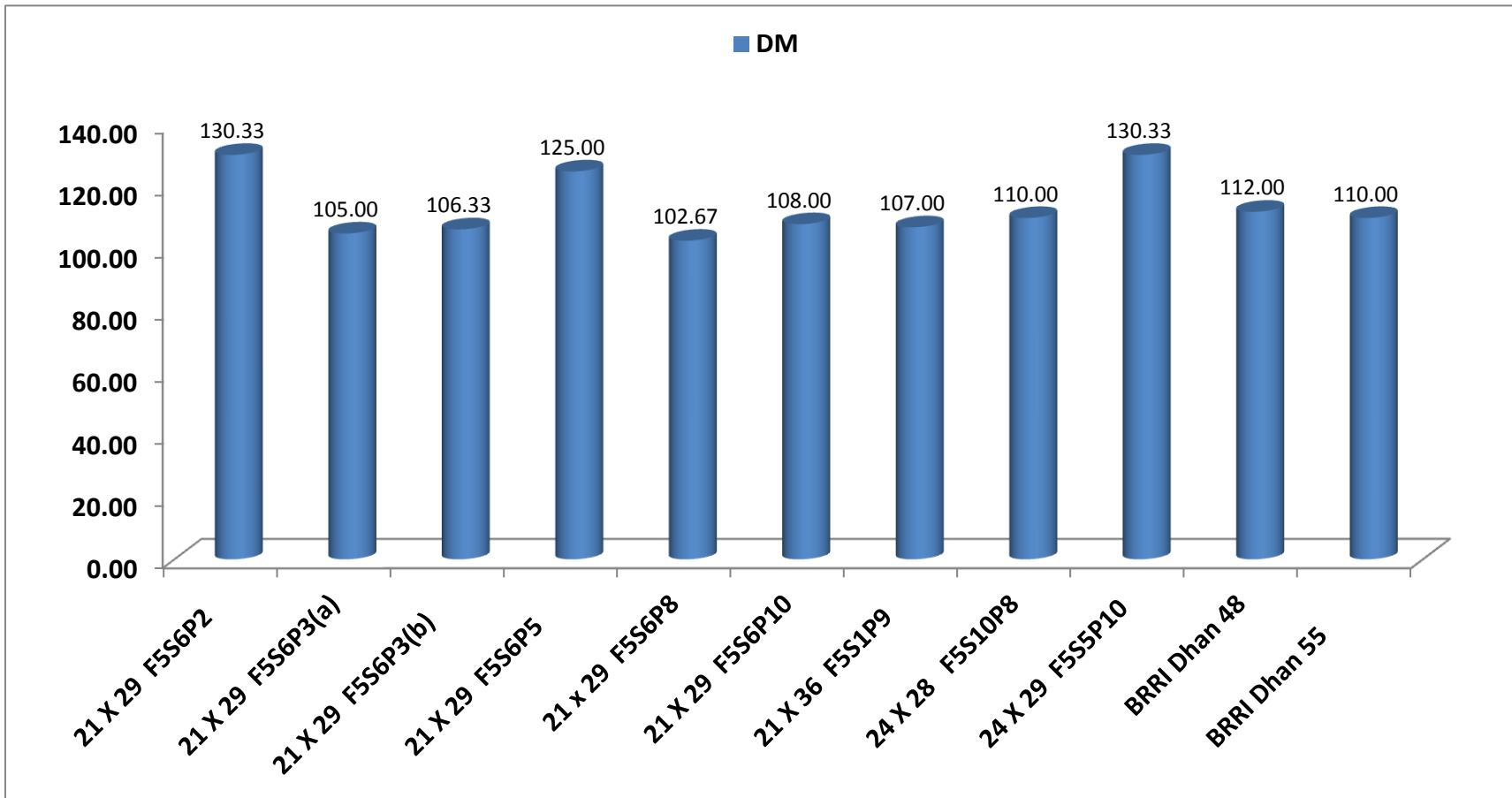
Figure 1. Variation in mean performance of 11 genotypes on days to maturity of rice

BR24 X BRRI dhan 29

$F_5S_5P_{10}$

BR21 X BRRI dhan29

$F_5S_6P_5$

BR21 X BRRI dhan 29

$F_5S_6P_2$

Plate 2. Photograph to understand differences among genotypes for days to flowering.

BR 21X BRRI dhan 29

$F_5S_6P_{10}$

BR 21X BRRI dhan 29

$F_5S_6P_3$ (a)

Plate 3. Photograph to understand differences among genotypes for days to maturity.

BR21 X BRRI dhan 29

$F_5S_6P_3$ (a)

BR21 X BRRI dhan29

$F_5S_6P_2$

BR21 X BRRI dhan29

$F_5S_6P_5$

BR21 X BRRI dhan29

$F_5S_6P_3$ (b)
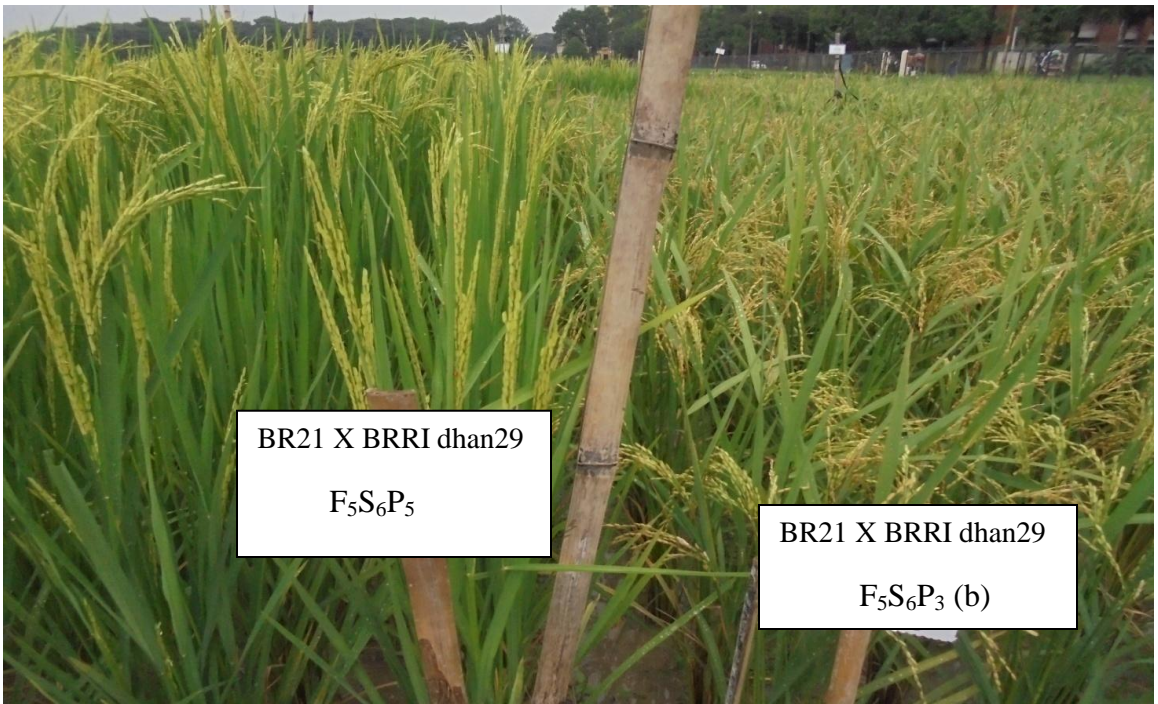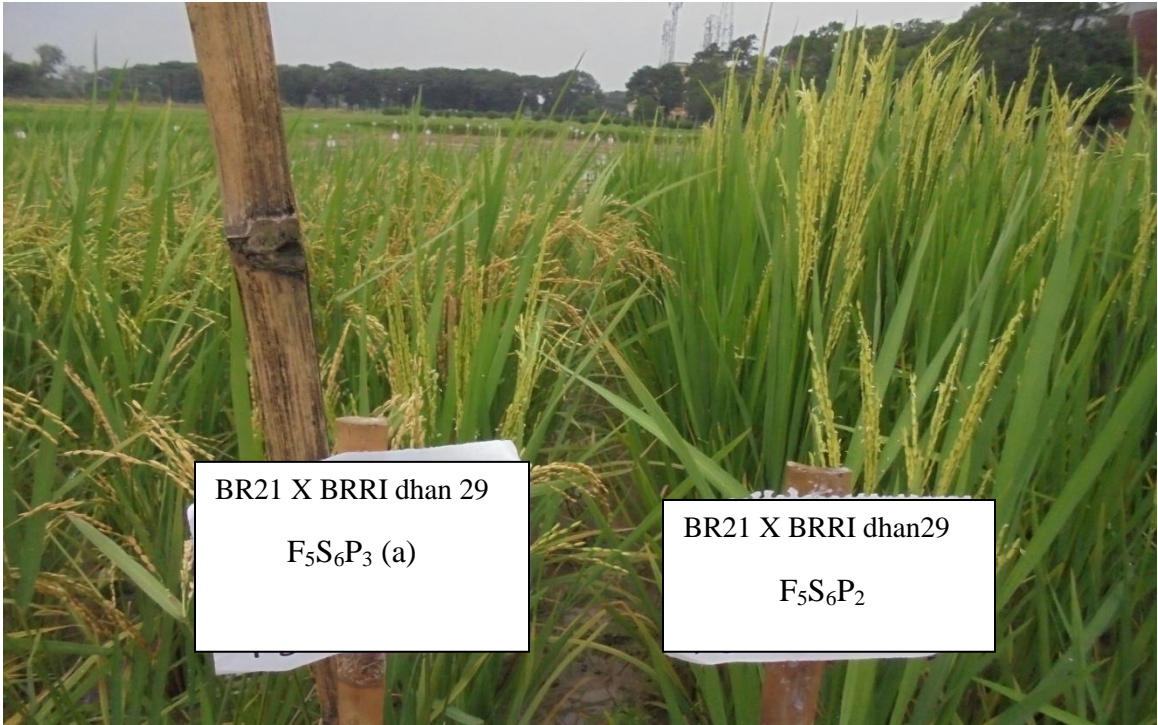
Plate 4. Photograph to understand differences among genotypes for plant height.

BRRI dhan 48

(a)

BRRI dhan 55

(b)

BR24 X BRRI dhan28

$F_5S_{10}P_8$

(c)

BR21 X BRRI dhan36

$F_5S_1P_9$
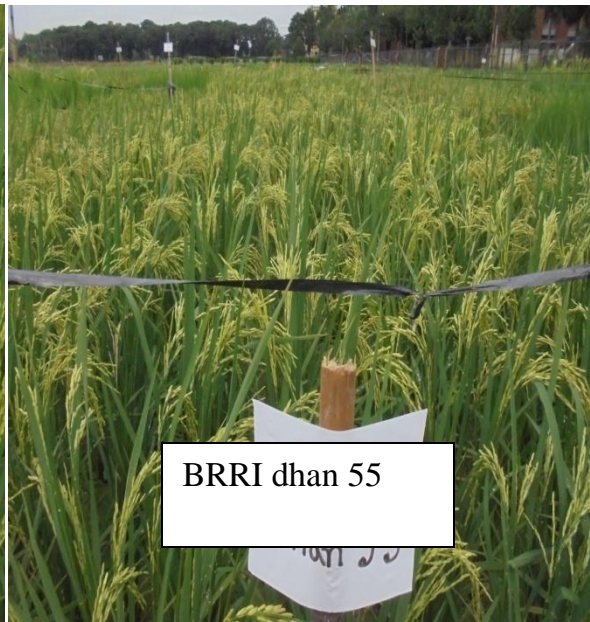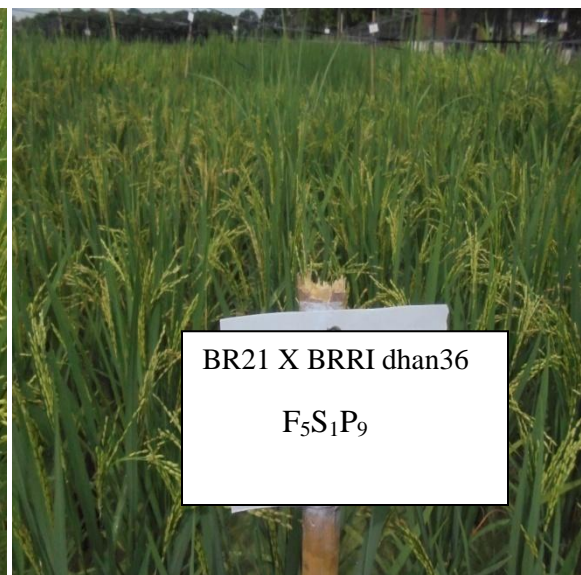
(d)

Plate 5. Photograph to understand differences among checks (a), (b) and genotypes (c), (d).

G10 (12.13) and G11 (11.50).While genotype G5 (9.787) showed the lowest number for this trait which was lower than all checks.G2, G3 and G6 had lower number of effective tiller per plant than their checks.

4.1.6 Panicle length (cm)

There were significant variations among the genotypes (6.051**) (Table 2). Panicle length per plant was exhibited the variation with the ranged from 20.21 cm to 25.25 cm with an average of 23.57 cm. The genotype G4 (BR21 X BRRI dhan29 $F_5S_6P_5$), represented the longest panicle length (25.25 cm) which was statistically similar with G5 (24.36 cm), 24.67 (24.67 cm), G9 (24.66 cm) and G1 (24.26 cm). While the significant shortest panicle length was observed by the genotype G7 (BR21X BRRI dhan36 $F_5S_1P_9$) which represented the shorter panicle length (20.21). A schematic representation of panicle length was shown in Plate 6. Ullah *et al.*(2011) reported similar result.

4.1.7 Number of primary branches/panicle

There were significant variations among the genotypes (1.310**) (Table 2). The genotypes G9 (BR24 X BRRI dhan29 $F_5S_5P_{10}$) and G6 (BR21 X BRRI dhan29 $F_5S_6P_{10}$) were produce the highest and lowest number of primary branches per panicle respectively. The height number of primary branches per panicle was recorded in G9 (9.533) which was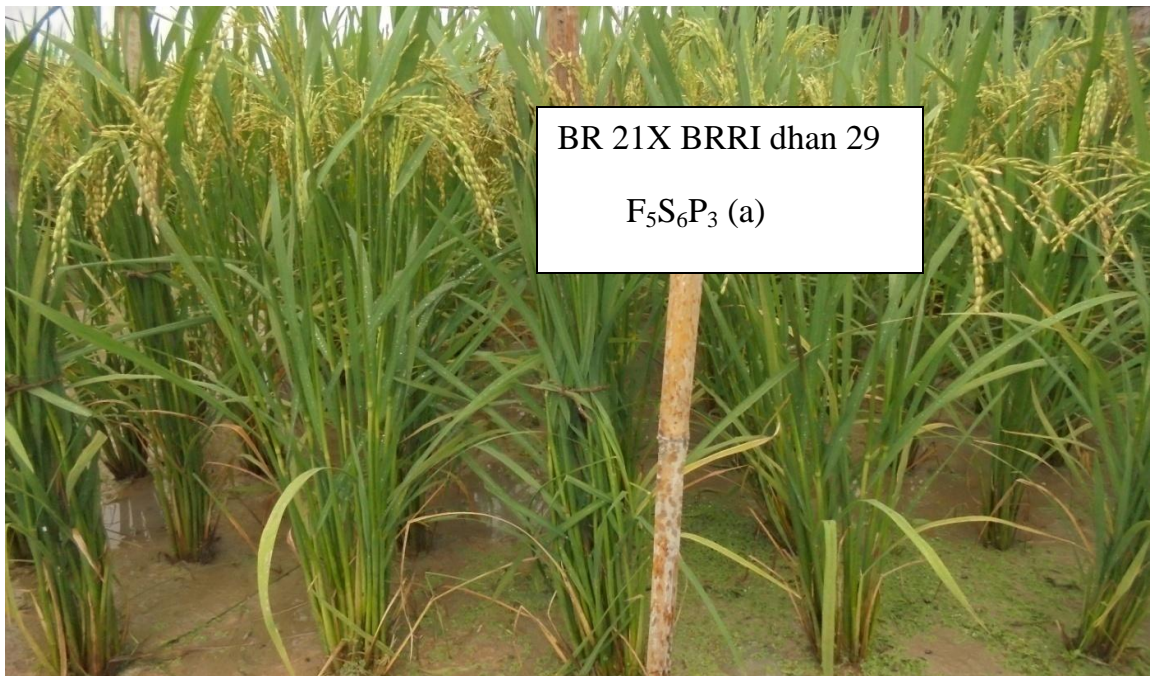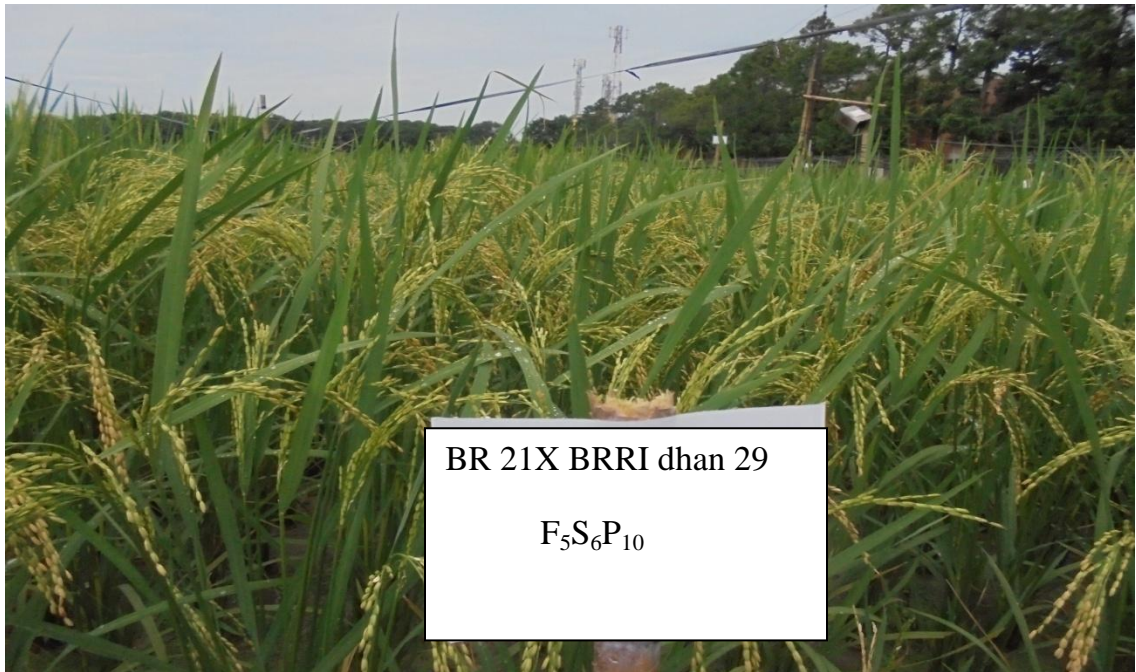 higher than their checks, as their checks BRRI dhan 48 and BRRI dhan 55 had 8.40 and 8.60 number of primary branches per panicle respectively. The lowest number of primary branches per panicle was observed in G6 (7.40), which was similar to G5, G7. Genotype G1, G2, G3 and G8 had similar number of primary branches per panicle with their checks, as their checks BRRI dhan 48 and BRRI dhan 55. Number of primary branches per panicle was varied from 7.40 to 9.53. The average of number of primary branches per panicle was 8.39 (Table 4).
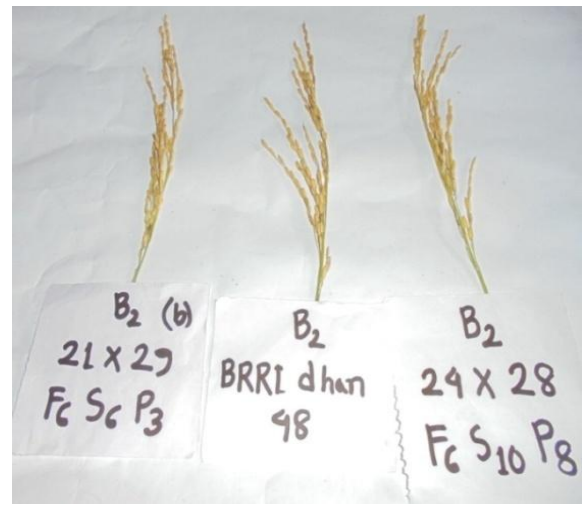
Plate 6. Comparison among different genotypes for panicle length

4.1.8 Number of secondary branches/panicle

There were significant variations among the genotypes (82.806**) (Table 2). The important yield contributing trait number of secondary branches/panicle was ranged from 15.77 to 31.17 with a mean value of 23.04 (Table 4).The highest and lowest number of secondary branches/panicle was exhibited by the genotypes G9 (BR24 X BRRI dhan29, $F_5S_5P_{10}$) and G11 (BRRI dhan 55).. The height number of secondary branches per panicle was recorded in G9 (31.17) which was higher than their checks, as their checks BRRI dhan 48 and BRRI dhan 55 had 17.10 and 15.77 number of secondary branches per panicle respectively. The lowest number of primary branches per panicle was observed in G11 (15.77). All genotypes (G1, G2, G3, G4, G5, G6, G7, G8, and G9) had higher number of secondary branches per panicle than their checks.

4.1.9 Total number of spikelets per panicle

High variation of total no. of spikelets per panicle in the present study was observed with minimum 97.93 to maximum 156.59. The average of total no. of spikelets per panicle was 124.13(Table 4). Highest total number of spikelets per panicle was observed by the genotype G9 (BR24X BRRI dhan29 $F_5S_5P_{10}$) while G11 (BRRI dhan 55) showed the lowest number of spikelets per panicle. The height total number of spikelets per panicle was recorded in G9 (156.60) which was higher than their checks, as their checks BRRI dhan 48 and BRRI dhan 55 had 123.60 and 97.93 total number of spikelets per panicle respectively. The lowest total number of spikelets per panicle was observed in G11 (97.93). Rest of the populations showed different number of total number of spikelets per panicle. A graphical presentation of total number of spikelets per panicle was shown in Figure 2. There were significant variations among the genotypes (1183.901**) (Table 2).
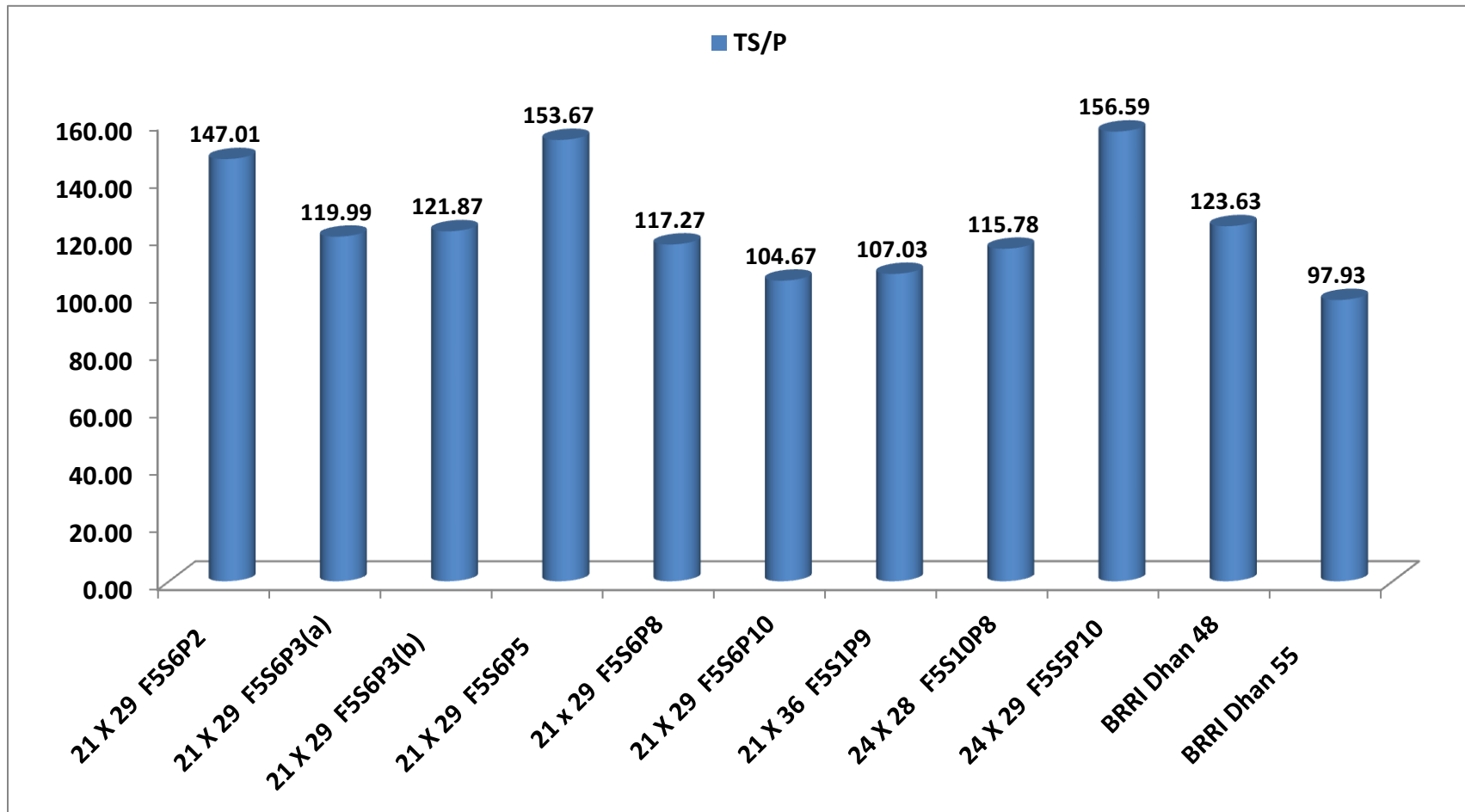
Figure 2. Variation in mean performance of 11 genotypes of total spikelets per panicle of rice

4.1.10 Number of filled grains of main tiller

There were significant variations among the genotypes (1162.152**) (Table 2). In case of number of filled grains of main tiller, they exhibited high range of variation from 78.60 to 136.13 and the mean value was 101.29 (Table 4). The maximum number of filled grains of main tiller was observed in genotype G9(136.10) which was statistically similar with G1 (126.30) and G4 (120.70) and while minimum number of filled grains of mail tiller was observed in genotype G11 (78.60) which was similar in statistical as 5% level of provability with G5 (81.08), G6 (85.13) and G7 (85.40). Since, greater number of filled grains per panicle is one of the major criteria which contribute to higher seed yield and it could be utilized in further program. Hairmansis *et al*. (2010) also reported variation in number of filled grains per panicle in respect of yield.

4.1.11 Number of unfilled grain of main tiller

There were non-significant variations among the genotypes (145.648) (Table 2).In case of number of unfilled grain of main tiller was varied from 14.30 to 36.04 with a mean of 23.92 (Table 4). The lowest number of unfilled grain of main tiller was observed by genotype G2 (14.30) which was lower than their checks as G10 (BRRI dhan 48) and G11 (BRRI dhan 55). While the highest number of this trait in G5 (36.04)which was higher than their checks, as their checks BRRI dhan 48 and BRRI dhan 55 had 19.00 and 18.09 number of unfilled grain of main tiller respectively. Except G2 and G3 all other genotypes G1, G4, G6, G7, G7 and G8 had higher number of unfilled grain of main tiller than their checks.

4.1.12 Yield per plant (g)

There were significant variations among the genotypes (67.497**) (Table 2).The most important trait yield/plant was ranged from 17.00 g to 31.00 g. The average value of yield/plant was estimated 21.97 g (Table 4). The highest yield per plant was observed by the genotype G1 (31.00g) which was statistically similar with G4 value of yield/plant was estimated 21.97 g (Table 4). The highest yield per plant

Plate No. 7: Photograph showing variation among 11 genotypes of seed grain.

was observed by the genotype G1 (31.00 g) which was statistically similar with G4 (26.33 g) and G10 (26.67 g) and higher than their checks, as their checks G10 (BRRI dhan 48) and G11 (BRRI dhan 55) had 26.67 and 20.33 yield per plant respectively. While genotype G5 (17.00) showed the lowest yield per plant which was lower than their checks and similar with G3 (18.67), G6 (17.00) and G7 (18.00). A graphical demonstration of 11 genotypes was shown for mean yield per plant in (Figure 3) and variation among 11 genotypes of seed grain in Plate 7. Kumar *et al*. (2014) also observed similar findings.

4.1.13 Thousand seed weight (g)

There were significant variations among the genotypes (18.322**) (Table 2). The thousand seed weight was ranged from 19.67 g to 27.50 g with a mean value of 23.90 g (Table 4). The maximum value of thousand seed weight was observed in genotype G11 (27.50) which was statistically similar with G1 (26.27) while minimum value of thousand grain weight was observed in genotype G7 (19.67). G3, G5, G6 andG8 had more or less thousand seed weight with their checks to G10 (BRRI dhan 48). Eleven genotypes were shown in graphically for the mean data of thousand seed weight in Figure 4.

4.1.14 Yield per ha (t)

There were significant variations among the genotypes (3.886**) (Table 2). Regarding the yield per ha, it was ranged from 1.81 ton to 5.00 ton with mean of 2.88 ton (Table 4). Maximum yield per ha was obtained in genotype G1 (5.00 t) which was statistically similar with G9 (4.887), while genotype G6 (1.80 t) showed the lowest value of this trait. The yield of G1 (5.00 t) was high may be due to long growth duration (130.3 days), high secondary branches/panicle (27.70), high filled grain per panicle (126.30), high thousand seed weight (26.27 g) and yield per plant (31.00 g). A graphical representation of variation was shown on mean performance of 11 genotypes for yield per ha of rice in Figure 5. Rafiqul (2014) found similar result for yield per ha (t).
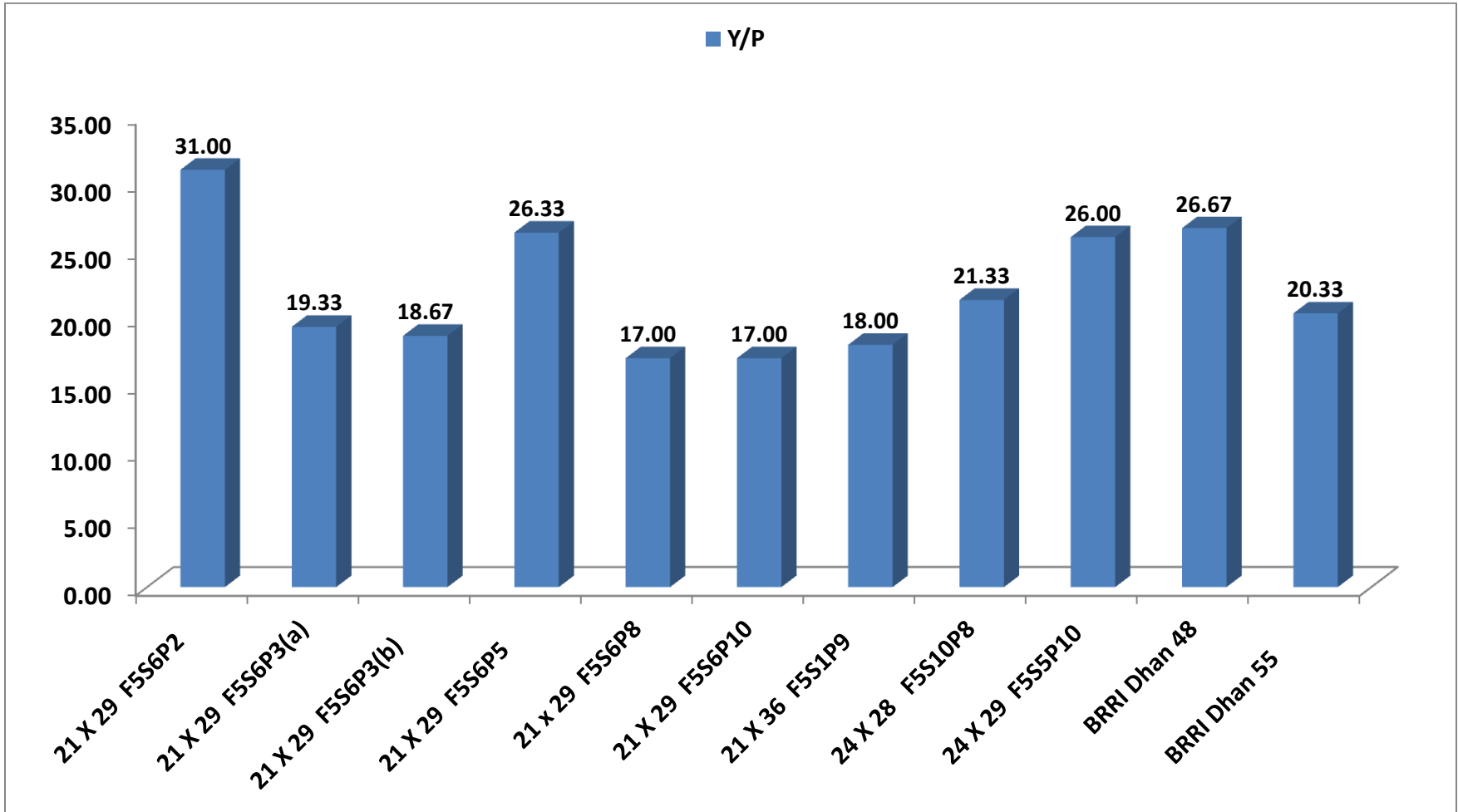
Figure 3. Variation in mean performance of 11 genotypes of yield per plant (dry) of rice
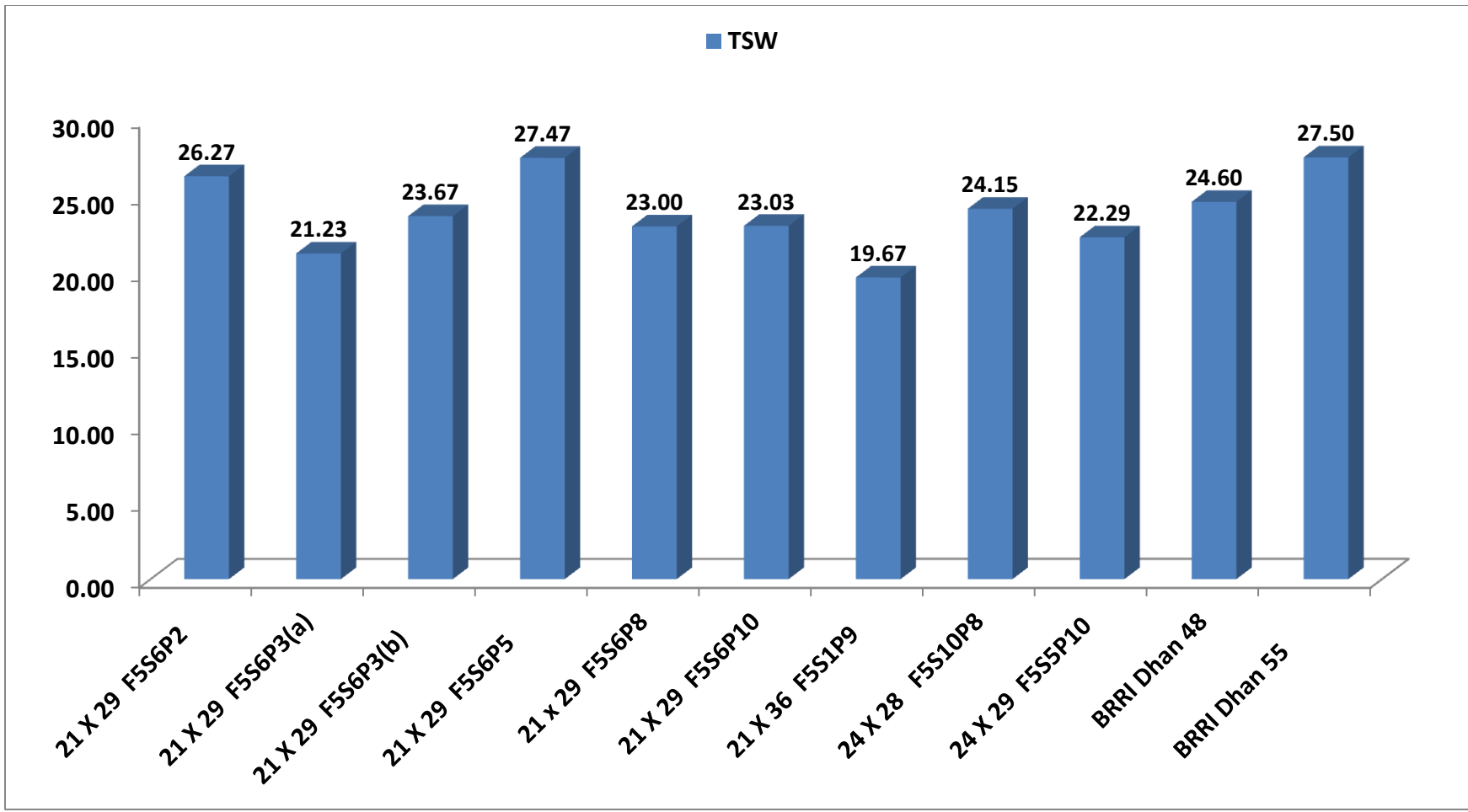
Figure 4. Variation in mean performance of 11 genotypes of thousand seed weight of rice
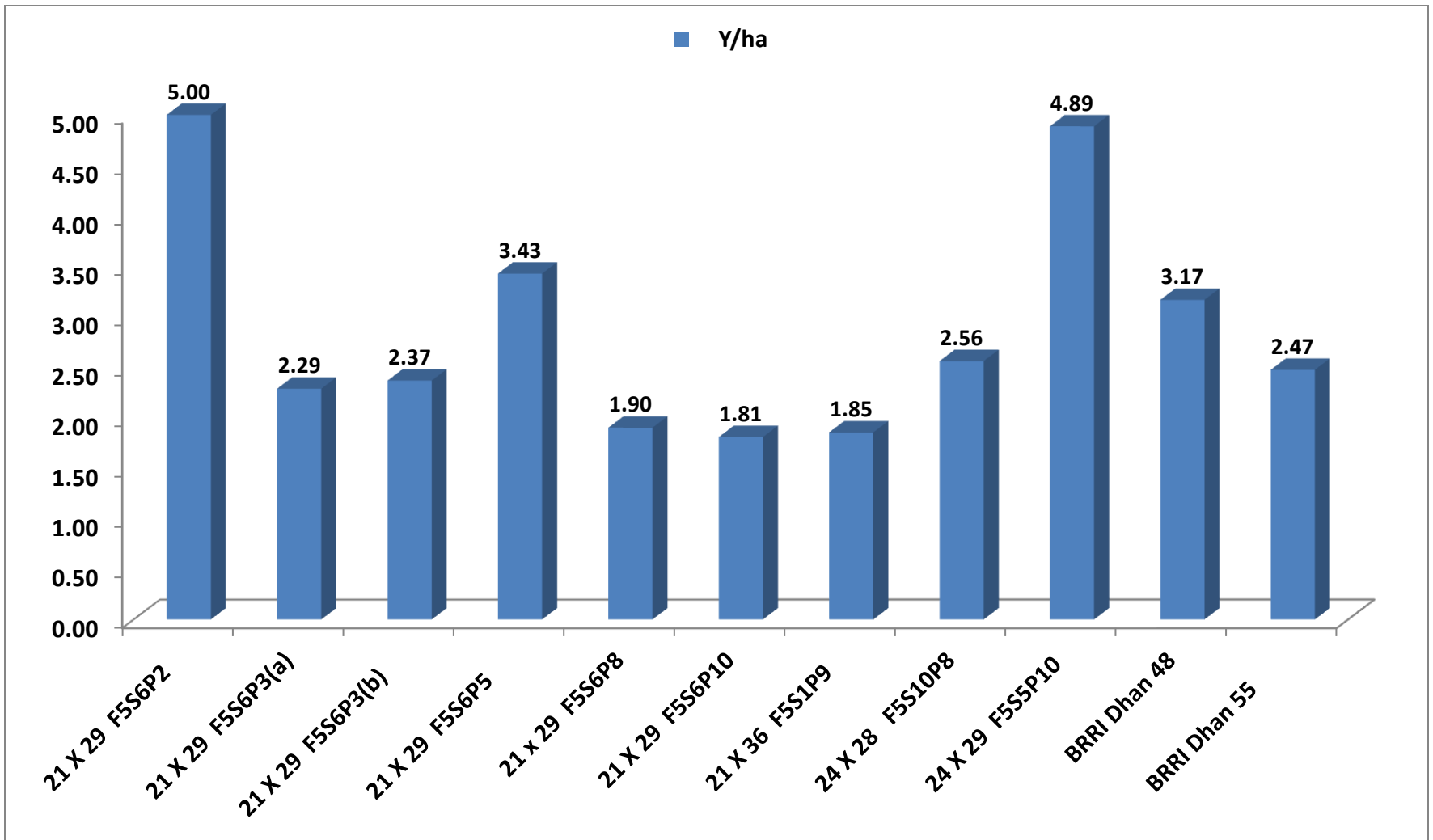
Figure 5.   Variation in mean performance of 11 genotypes of yield per hectare of rice

4.2 Estimation of genetic parameters of rice genotypes

Genotypic variances, phenotypic variances, heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance and genetic advance as percent of mean, GA (%) for all yield and the yield contributing traits are presented in Table 5.

4.2.1 Days to flowering

The phenotypic variance (115.19) was higher than genotypic variance (107.27) indicating that there was environmental effect for the expression of the days to flowering and genetic factor had low expressivity on the traits. Moderate GCV (12.73%) and PCV (13.20%) (Table 5 and Figure 6) with less difference between them indicating that environment had a significant role in the expression of this character. Similar result was found by Padmaja *et al*. (2008). Days to flowering showed high heritability (93.13%) with high genetic advance (20.59%) and genetic advance in percentage of mean (25.32%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and selection based on this character could be effective. Ketan and Sarkar (2014) and Mahto *et al*. (2003) reported high heritability with high genetic advance for days to 50% flowering.

4.2.2 Days to maturity

The phenotypic variance (107.10) was higher than genotypic variance (102.28) indicating least environmental effect for the expression of the days to maturity and genetic factor had low expressivity on the traits. Low GCV (8.92%) and PCV (9.13%) (Table 5 and Figure 6) with less difference between them indicating that environment had a significant role in the expression of this character. Vange (2008) found GCV was lower than PCV. Days to maturity showed high heritability (95.50%) with high genetic advance (20.36%) and genetic advance in percentage of mean (17.96%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and

selection based on this character could be effective. High heritability with for this trait was observed by Akhtar *et al*. (2011).

4.2.3 Plant height (cm)

The phenotypic variance (197.80) was higher than genotypic variance (164.77) indicating that environmental effect had a significant role for the expression of the plant height and genetic factor had low expressivity on the traits. Moderate GCV (12.35%) and PCV (13.53%) (Table 5 and Figure 6) with less difference between them indicating that environment had a significant role in the expression of this character. Plant height showed high heritability (83.31%) with high genetic advance (24.14%) and genetic advance in percentage of mean (23.21%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and selection based on this character could be effective. High heritability coupled with high genetic advance for plant height was observed by Shahriar *et al*. (2014), Selvaraj *et al.* (2011) and Satheesh kumar *et al. (*2012).

4.2.4 Number of total tillers per plant

The genotypic variance (3.47) and phenotypic variance (4.50) were close to each other, indicating least environmental effect had for the expression of the character and genetic factor had significant expressivity on the number of total tillers per plant. Moderate GCV (14.10%) and PCV (16.07%) (Table 5 and Figure 6) with less difference between them indicating that environment had a significant role in the expression of this character. Number of total tillers per plant showed high heritability (77.06%) with low genetic advance (3.37%) and genetic advance in percentage of mean (25.50%) (Table 5 and Figure 7) for was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of non-additive gene effect and there is a lot of scope for the improvement of this character through selection. Akhtar *et al*. (2011) reported high heritability with number of tiller per plant.

Table 5. Estimation of genetic parameters in fourteen characters of 11ricegenotypes

Parameters	$\sigma^2 p$	$\sigma^2 g$	$\sigma^2 e$	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 50% flowering	115.19	107.27	7.92	13.20	12.73	3.46	93.13	20.59	25.32
Days to maturity	107.10	102.28	4.82	9.13	8.92	1.94	95.50	20.36	17.96
Plant height	197.80	164.77	33.02	13.53	12.35	5.53	83.31	24.14	23.21
Total no of tiller/plant	4.50	3.47	1.03	16.07	14.10	7.70	77.06	3.37	25.50
Number of effective tiller/plant	3.62	2.56	1.06	15.93	13.39	8.64	70.62	2.77	23.18
Panical length/plant	2.71	1.67	1.04	6.99	5.48	4.33	61.53	2.09	8.86
Number of primary branches/panicle	0.58	0.36	0.22	9.08	7.20	5.53	62.91	0.99	11.76
Number of secondary branches/panicle	31.81	25.50	6.31	24.48	21.92	10.90	80.16	9.31	40.42
Total no of spikelets/panicle	532.83	325.54	207.29	18.60	14.54	11.60	61.10	29.05	23.40
Number of filled grain of main tiller	519.85	321.15	198.70	22.51	17.69	13.92	61.78	29.02	28.65
Number of unfilled grain of main tiller	98.99	23.33	75.67	41.60	20.19	36.37	23.56	4.83	20.19
Yield/plant	28.70	19.40	9.31	24.39	20.05	13.89	67.58	7.46	33.95
Thousand seed weight	7.78	5.27	2.50	11.67	9.61	6.62	67.80	3.89	16.30
Yield/ha	1.58	1.15	0.43	43.61	37.21	22.74	72.81	1.89	65.41

$\sigma^2 p$ = Phenotypic variance, $\sigma^2 g$ = Genotypic variance and $\sigma^2 e$ = Environmental variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, ECV = Environmental coefficient of variation.
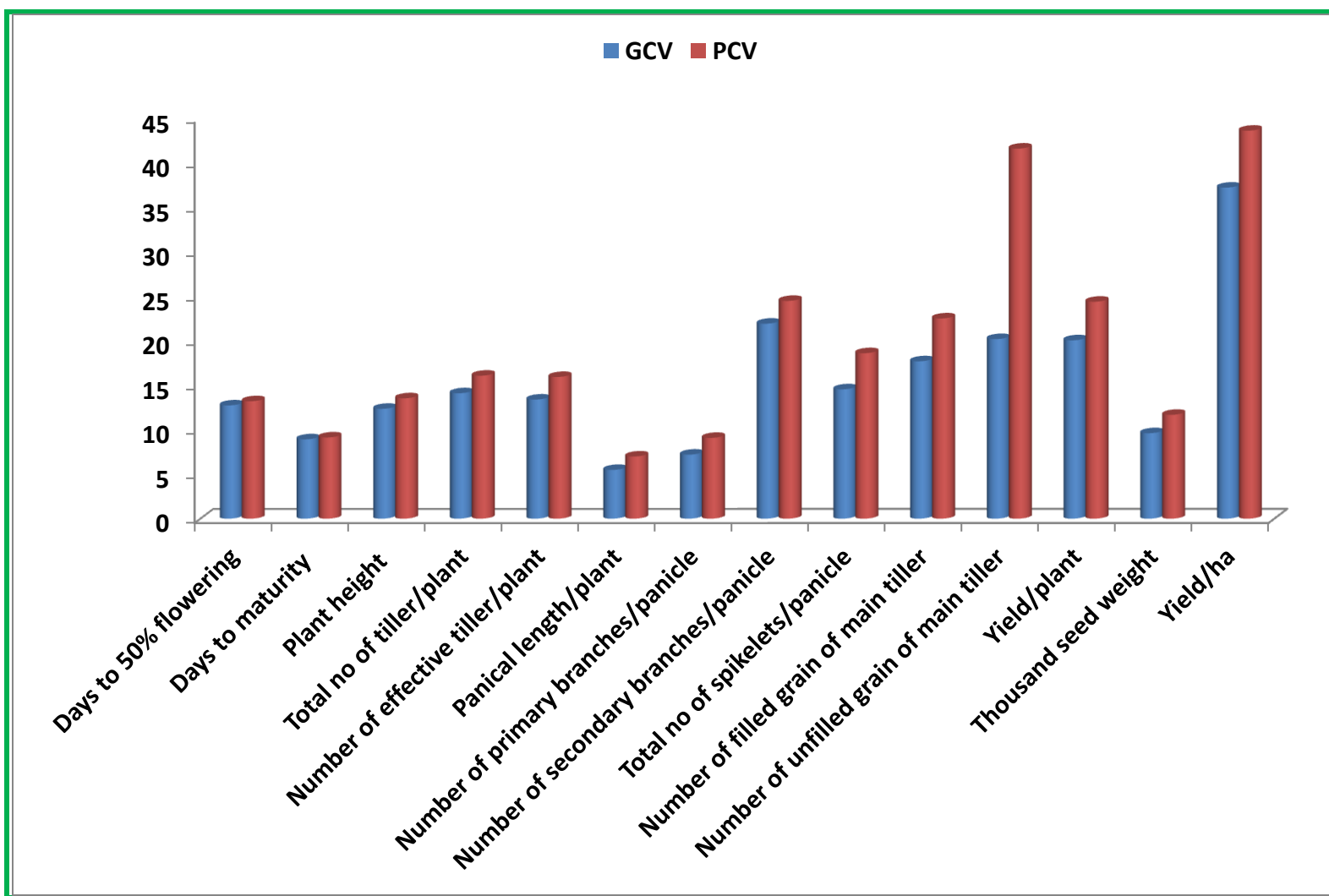
Figure 6. Genotypic and phenotypic coefficient of variability in rice
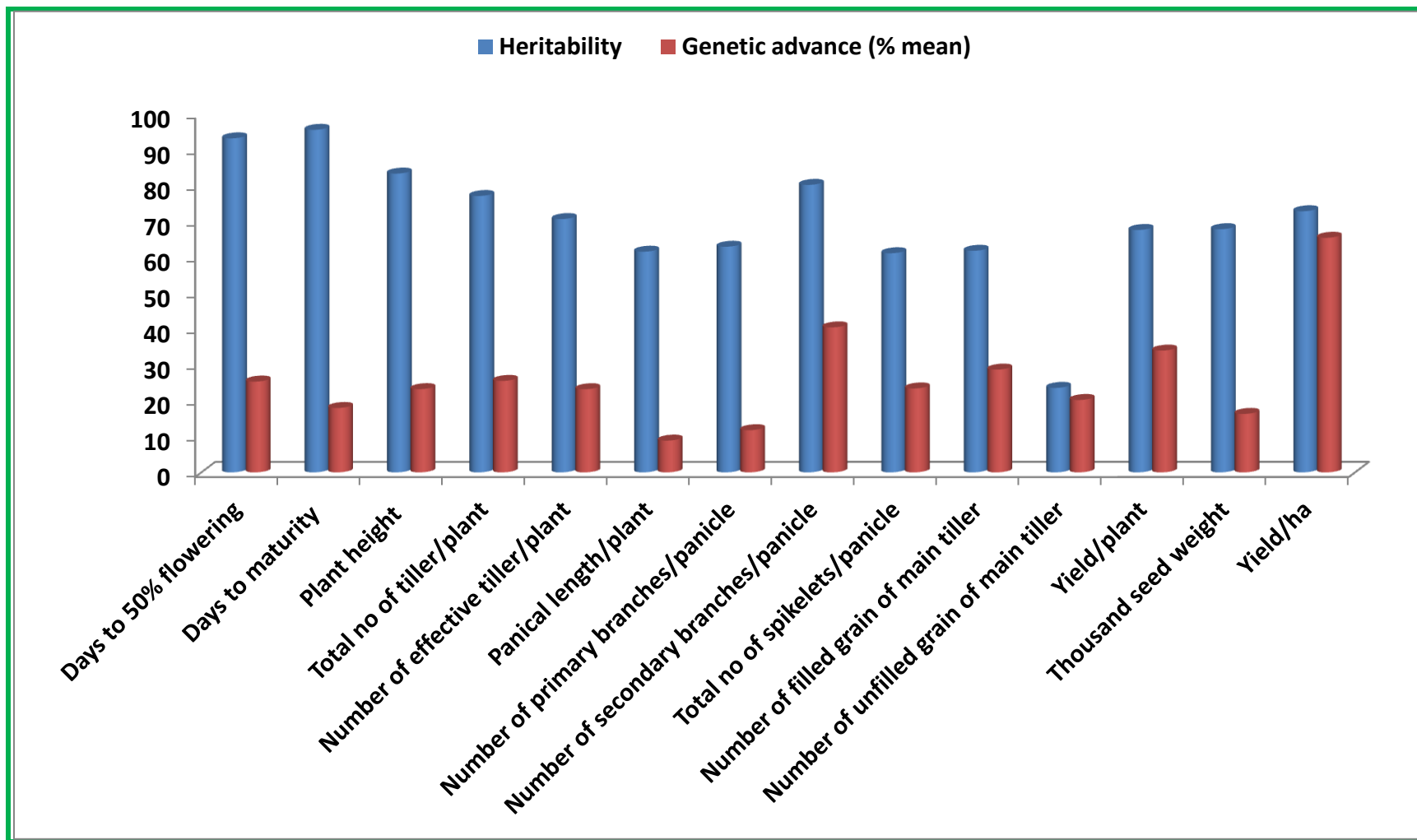
Figure 7. Heritability and genetic advance over mean in rice

4.2.5 Number of effective tillers per plant

The genotypic variance (2.56) and phenotypic variance (3.62) were close to each other, indicating least environmental effect had for the expression of the character and genetic factor had significant expressivity on the number of effective tillers per plant. Moderate GCV (13.39%) and PCV (15.93%) (Table 5 and Figure 6) with less difference between them indicating that environment had a significant role in the expression of this character. Number of effective tillers per plant showed high heritability (70.62%) with low genetic advance (2.77%) and genetic advance in percentage of mean (23.18%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of non-additive gene effect and there is a lot of scope for the improvement of this character through selection. High heritability with low genetic advance was also observed by Subbaiah *et al*. (2011).

4.2.6 Panicle length (cm)

The phenotypic variance (2.71) was more or less similar to genotypic variance (1.67) also indicating that least environmental effect for the expression of the character and genetic factor had significant expressivity on the panicle length. GCV (5.48%) and PCV (6.99%) were low for panicle length in the present study (Table 5 and Figure 6).There was a little differences between GCV and PCV on this character. Similar result was found by Padmaja *et al.* (2008). Plant height showed high heritability (61.53%) with low genetic advance (2.09%) and genetic advance in percentage of mean (8.86%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of non-additive gene effect and there is a lot of scope for the improvement of this character through selection. Ketan and Sarkar (2014) reported high heritability with low genetic advance for this traits.

4.2.7 Number of primary branches per panicle

The phenotypic variance (0.58) was more or less similar to genotypic variance (0.36) also indicating that least environmental effect for the expression of the character and genetic factor had significant expressivity on the number of primary branches per panicle. GCV (9.08%) and PCV (7.20%) were low for number of primary branches per panicle in the present study (Table 5 and Figure 6). There was a little differences between GCV and PCV on this character. Similar result was observed by Vange (2008). Number of primary branches per panicle showed high heritability (62.91%) with low genetic advance (0.99%) and genetic advance in percentage of mean (11.76%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that this trait had greater influence of non additive gene action with a big role of non-genetic factors in their expression. Mahto *et al*. (2003) observed high heritability with number of primary branches per panicle.

4.2.8 Number of secondary branches per panicle

The phenotypic variance (31.81) was higher than genotypic variance (25.50) indicating that there was environmental effect for the expression of the number of secondary branches per panicle and genetic factor had low expressivity on the traits. High GCV (21.92%) and PCV (24.48%) (Table 5 and Figure 6) with considerable difference between them indicating that environment had a significant role in the expression of this character. Similar result was found by Padmaja *et al*. (2008). Number of secondary branches per panicle showed high heritability (80.16%) with moderate genetic advance (9.31%) and genetic advance in percentage of mean (40.42%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and selection based on this character could be effective. Mahto *et al*. (2003) observed high heritability with number of secondary branches per panicle.

4.2.9 Total number of spikelet per panicle

The phenotypic variance (532.83) was much higher than genotypic variance (325.54) indicating that there was environmental effect for the expression of the total number of spikelet per panicle and genetic factor had low expressivity on the traits. Moderate GCV (14.54%) and PCV (18.60%) (Table 5 and Figure 6) with considerable difference between them indicating that environment had a significant role in the expression of this character. Total number of spikelet per panicle showed high heritability (61.10%) with high genetic advance (29.05%) and genetic advance in percentage of mean (23.40%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa* which indicating the roles of additive gene action. Therefore, selection could be effective through this character. High heritability coupled with high genetic advance for plant height was observed by Tuwar *et al*. (2013), Nandan *et al*. (2010) and Prajapati *et al.* (2011).

4.2.10 Number of filled grains per panicle

The phenotypic variance (519.85) was much higher than genotypic variance (321.15) indicating that there was environmental effect for the expression of the number of filled grains per panicle and genetic factor had low expressivity on the traits. High GCV (17.69%) and PCV (22.51%) (Table 5 and Figure 6) with considerable difference between them indicating that environment had a significant role in the expression of this character. Similar result was found by Padmaja et al. (2008). Number of filled grains per panicles showed high heritability (61.78%) with high genetic advance (29.02%) and genetic advance in percentage of mean (28.65%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa* which indicating the roles of additive gene action. Therefore, selection could be effective through this character. Nuruzzaman *et al.* (2016), Satheesh kumar *et al. (*2012), Bisne *et al*. (2009) and Babu *et al.* (2012) *were* found high heritability and high genetic advance for number of filled grains per panicle.

4.2.11 Number of unfilled grains per panicle

The phenotypic variance (98.99) was higher than genotypic variance (23.33) indicating that there was environmental effect for the expression of the number of unfilled grains per panicle and genetic factor had low expressivity on the traits. High GCV (20.19%) and PCV (41.60%) (Table 5 and Figure 6) with considerable difference between them indicating that environment had a significant role in the expression of this character. Similar result was found by Padmaja *et al*. (2008).Number of unfilled grains per panicle showed moderate heritability (23.56%) with low genetic advance (4.83%) and genetic advance in percentage of mean (20.19%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of non-additive gene action and selection based on this character will be not effective.

4.2.13 Yield per plant (g)

The phenotypic variance (28.70) was higher than genotypic variance (19.40) indicating least environmental effect for the expression of the yield per plant and genetic factor had low expressivity on the traits. (Satheesh kumar *et al.* 2012) found similar result for yield per plant. High GCV (20.05%) and PCV (24.39%) (Table 5 and Figure 6) with considerable difference between them indicating that environment had a significant role in the expression of this character. Similar findings were reported by Kumar *et al.* (2014) and Anbanandan *et al.* (2009). Yield per plant showed high heritability (67.58%) with moderate genetic advance (7.46%) and genetic advance in percentage of mean (33.95%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and selection based on this character could be effective. Prajapati *et al.* (2011) reported high heritability with moderate genetic advance with yield per plant.

4.2.12 Thousand seed weight (g)

The phenotypic variance (7.78) was slightly higher than genotypic variance (5.27) indicating that environmental effect had a significant role for the expression of the thousand seed weight and genetic factor had low expressivity on the traits. Moderate GCV (11.67%) and PCV (9.61%) (Table 5 and Figure 6) with less difference between them indicating that environment had a significant role in the expression of this character. Thousand seed weight showed high heritability (67.80%) with low genetic advance (3.89%) and genetic advance in percentage of mean (16.30%) (Table 5 and Figure 7) for days to maturity was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and selection based on this character could be effective. High heritability for this trait was also observed by Seyoum *et al.* (2012) and Akhtar *et al*. (2011).

4.2.14 Yield per hectare (t/ ha)

The phenotypic variance (1.58) was more or less similar to genotypic variance (1.15) also indicating that least environmental effect for the expression of the character and genetic factor had significant expressivity on the yield per hectare. High GCV (37.21%) and PCV (43.61%) (Table 5 and Figure 6) with considerable difference between them indicating that environment had a significant role in the expression of this character. Similar result was found by Padmaja *et al*. (2008). Yield per hectare showed high heritability (72.81%) with low genetic advance (1.89%) and genetic advance in percentage of mean (65.41%) (Table 5 and Figure 7) was found in the 11 genotypes of *Oryza sativa*. It indicates that presence of additive gene effect and selection based on this character could be effective.

4.3 Relationship among yield and yield contributing traits

4.3.1 Estimation of correlation co-efficient

Yield is a complex product being influenced by several inter-dependable quantitative characters. When selection pressure is excised for improvement of any characters highly associated with yield and other correlated characters. In our study, both genotypic and phenotypic correlation co-efficient of different characters of 11 genotypes of *Oryza sativa* L. are determined (Table 6 and 7). Most of the characters showed the genotypic correlation coefficients were higher than their respective phenotypic ones. 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). 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 co-efficient were higher than their corresponding genotypic correlation co-efficient 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 flowering

Days to flowering showed significant and positive correlation with days to maturity (G = 0.932, P = 0.919), plant height (G = 0.764, P = 0.722), number of effective tiller per panicle(G = 0.358, phenotypically non significant, 0.0295), panicle length per plant (G = 0.0427, P = 0.356), number of primary branches per panicle (G = 0.775, P =0.604), number of secondary branches per panicle (G=0.588, P=0.55), total number of spikelet per panicle (G = 0.982, P = 0.634) and number of filled grains per panicle (G = 0.926, P = 0.627), number of unfilled grain per panicle (G = 0.616, phenotypically non significant, 0.137), yield per plant (G = 0.977, P = 0.839), thousand seed weight (G = 0.465, phenotypically non significant, 0.317), yield per hectare (G = 0.924, P = 0.872) indicated that if days to flowering increased these characters also increased. It also exhibited non-

significant and positive interaction with total number of tiller per plant (G = 0.021, P = 0.020) (Table 6 and 7). Islam *et al.* (2015), Mahto *et al.* (2003) also revealed that grain yield was found to be positively and significantly correlated with yield.

4.3.2 Days to maturity

Days to maturity showed significant and positive correlation with plant height (G = 0.795, P = 0.730), number of effective tiller per panicle(G = 0.376, phenotypically non significant, 0.323), panicle length per plant (G = 0.501, P = 0.383), number of primary branches per panicle (G = 0.868, P = 0.673), number of secondary branches per panicle (G = 0.709, P = 0.641), total number of spikelet per panicle (G = 0.995, P = 0.661), number of filled grains per panicle (G = 0.983, P = 0.676), number of unfilled grain per panicle (G = 0..487, phenotypically non significant, 0.107), yield per plant (G = 0.927, P = 0.804), thousand seed weight (G = 0.468, P =, 0.345), yield per hectare (G = 0.983, P = 0.892) indicated that if days to maturity increased then these characters also increased. It also exhibited non-significant and positive interaction with total number of tiller per plant (G = 0.071, P = 0.074) (Table 6 and 7). Islam *et al.* (2015), Allam *et al.* (2015), reported positive and significant correlation with yield for this traits.

4.3.3 Plant height (cm)

Plant height showed significant and positive interaction with panicle length per plant (G = 0.890, P = 0.771), number of primary branches per panicle (G = 0.797, P = 0.599), number of secondary branches per panicle (G = 0.8, P = 0.710), total number of spikelet per panicle (G = 0.903, P = 0.649), number of filled grains per panicle (G = 0.767, P = 0.564), number of unfilled grain per panicle (G = 0.8, phenotypically non significant, 0.315), yield per plant (G = 0.754, P = 0.627), thousand seed weight (G = 0.641, P =, 0.484), yield per hectare (G = 0.771, P = 0.657). The results tend to emphasize that if plant height increased then number of unfilled grain per and thousand seed weight also increased. It was significantly

and negatively associated with total number of tiller per plant (G = -0.495, P = -0.429). It had also non-significant negative relation with number of effective tillers per plant (G = -0.169, P = -0.156) (Table 6 and 7).Islam *et al.* (2015); Bhati *et al.* (2015), Ganapati *et al.* (2014), Shabir *et al.*(2013),showed significant and positive interaction of plant height with yield.

4.3.4 Total number of tiller per plant

Number of total tillers per plant showed significant and positive correlation with number of effective tillers (G = 0.952, P = 0.873) indicated that yield per plant can be increased if number of total tillers per plant and number of effective tillers increased. It also exhibited non-significant and positive interaction with number of filled grain per plant (G = 0.083) at genotypic level, yield per plant (G = 0.019, P = 0.03) and yield per hectare (G = 0.024, P = 0.055). Number of total tillers per plant had significant and negative interaction with panicle length (G = -0.665,P = -0.646) and thousand seed weight (G = -0.548, P = -0.476) at both genotypic and phenotypic level. It had also non-significant negative relation with number of primary branches per panicle (G = -0.135, P = -0.193), number of secondary branches per panicle (G = -0.188, P = -0.272), total number of spikelet per panicle (G = -0.028, P = -0.107), number of unfilled grain per panicle (G = -0.325, P = -0.094) at both genotypic and phenotypic level and number of filled grain (P= -0.073 at phenotypic level (Table 6 and 7). Shabir *et al.* (2013), Akinwale *et al.* (2011), Yadav *et al.* (2010), showed significant and positive correlation with yield.

4.3.5 Number of effective tillers per plant

Number of effective tillers per plant showed significant and positive correlation with yield per hectare (G = 0.365, phenotypically positive but non-significant, 0.283) and yield per plant (genotypically positive but non-significant 0.332, P = 0.351) indicated that if number of effective tillers per plant increased then these characters also increased. It also had positive and non-significant correlation with number of primary branches per panicle (G = 0.185, P = 0.089), total number of

spikelet per panicle (G = 0.261, P = 0.079), number of filled grain per panicle (G = 0.338, P = 0.071), number of unfilled grain per panicle (P = 0.039) at phenotypic level. Number of effective tillers per plant had significant and negative interaction with panicle length per plant (G = -0.425, P = -0.432). Negative and non-significant correlation was found with number of secondary branches per panicle (G = -0.60, P = -0.132), number of unfilled grain per panicle (G = -0.093) at genotypic level and thousand seed weight (G = -0.339, P = -0.181) (Table 6 and 7). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Allam *et al.* (2015), Babu *et al.* (2012), Satheesh kumar *et al.* (2012) reported positive and significant correlation of number of effective tillers per plant with yield.

4.3.6 Panicle length (cm)

Panicle length showed significant and positive correlation with number of primary branches per panicle (G = 0.601, P = 0.570), number of secondary branches per panicle (G = 0.740, P = 0.650), total number of spikelet (G = 0.652, P = 0.565), number of filled grain per panicle (G = 0.442, P = 0.502), number of unfilled grain per panicle (G = 1.008, phenotypically non-significant, 0.257), yield per plant (G = 0.403, phenotypically non-significant o.305), thousand seed weight(G = 0.532, P = 0.419) and yield per hectare (G = 0.503, P = 0.367) suggested that yield per hectare can be increased by improving panicle length, number of primary branches per panicle , number of secondary branches per panicle, total number of spikelet, number of filled grain per panicle, and thousand seed weight (Table 6 and 7). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Ullah *et al.* (2011) reported that positive and significant correlation for panicle length was found with yield per hectare. Shabir *et al* (2013) and Yadav *et al.* (2010) showed significant and positive correlation with yield.

Table 6. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of rice

	DF	DM	PH	TNT/P	NET/P	PL/P	NPB/P	NSB/P	TS/P	NFG	NUG	Y/P (dry)	TSW
DM	0.932**												
PH	0.764**	0.795**											
TNT/P	0.021	0.071	-0.495**										
NET/P	0.358*	0.376*	-0.169	0.952**									
PL/P	0.427*	0.501**	0.890**	-0.665**	-0.425*								
NPB/P	0.775**	0.868**	0.797**	-0.135	0.185	0.601**							
NSB/P	0.588**	0.709**	0.800**	-0.188	-0.060	0.740**	0.683**						
TS/P	0.982**	0.995**	0.903**	-0.028	0.261	0.652**	0.903**	0.925**					
NFG	0.926**	0.983**	0.767**	0.083	0.338	0.442**	0.886**	0.902**	0.955**				
NUG	0.616**	0.487**	0.800**	-0.325	-0.093	0.908**	0.318	0.801**	0.332	0.035			
Y/P (dry)	0.977**	0.927**	0.754**	0.019	0.332	0.403*	0.835**	0.468**	0.903**	0.996**	0.404*		
TSW	0.465**	0.468**	0.641**	-0.548**	-0.339	0.532**	0.589**	0.099	0.213	0.155	0.037	0.614**	
Y/ha	0.924**	0.983**	0.771**	0.024	0.365*	0.503**	0.940**	0.653**	0.985**	0.901**	0.475**	0.965**	0.479**

** = Significant at 1%.   * = Significant at 5%.

DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height, TNT/P = Total no of tiller/plant, NET/P = Number of effective tiller/plant, PL/P = Panicle length/plant, NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle, TS/P = Total no of spikelets/panicle, NFG = Number of filled grain of main tiller, NUG = Number of unfilled grain of main tiller, Y/P (Dry) = Yield/plant, TSW = Thousand seed weight and Y/ha = Yield/ha.

Table 7. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of rice

	DF	DM	PH	TNT/P	NET/P	PL/P	NPB/P	NSB/P	TS/P	NFG	NUG	Y/P (dry)	TSW
DM	0.919**												
PH	0.722**	0.730**											
TNT/P	0.020	0.074	-0.429*										
NET/P	0.295	0.323	-0.156	0.873**									
PL/P	0.356*	0.383*	0.771**	-0.646**	-0.432*								
NPB/P	0.604**	0.673**	0.599**	-0.193	0.089	0.570**							
NSB/P	0.550**	0.641**	0.710**	-0.272	-0.132	0.650**	0.523**						
TS/P	0.634**	0.661**	0.649**	-0.107	0.079	0.565**	0.665**	0.682**					
NFG	0.627**	0.676**	0.564**	-0.073	0.071	0.502**	0.689**	0.647**	0.931**				
NUG	0.137	0.107	0.315	-0.094	0.039	0.257	0.063	0.224	0.450**	0.126			
Y/P (dry)	0.839**	0.804**	0.627**	0.030	0.351*	0.305	0.619**	0.416*	0.480**	0.529**	-0.128		
TSW	0.317	0.345*	0.484**	-0.476**	-0.181	0.419*	0.423*	0.121	0.273	0.186	0.256	0.395*	
Y/ha	0.872**	0.892**	0.657**	0.055	0.283	0.367*	0.669**	0.587**	0.535**	0.600**	-0.098	0.844**	0.204

** = Significant at 1%.   * = Significant at 5%.

DF = Days to 50% flowering,, DM = Days to maturity, PH = Plant height, TNT/P = Total no of tiller/plant, NET/P = Number of effective tiller/plant, PL/P = Panicle length/plant, NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle, TS/P = Total no of spikelets/panicle, NFG = Number of filled grain of main tiller, NUG = Number of unfilled grain of main tiller, Y/P (Dry) = Yield/plant, TSW = Thousand seed weight and Y/ha = Yield/ha.

4.3.7 Number of primary branches per panicle

Number of primary branches per panicle showed significant and positive correlation with number of secondary branches per panicle (G = 0.683, P = 0.523), total number of spikelet (G = 0.903 , P = 0.665), number of filled grain per panicle (G = 0.886, P = 0.689),yield per plant (G = 0.835, P = 0.619) thousand seed weight(G = 0.589, P = 0.423) and yield per hectare (G = 0.94, P = 0.669) at both genotypic and phenotypic level indicated that if number of primary branches per panicle increased then theses characters also increased . It also exhibited non-significant and positive interaction with number of unfilled grain per panicle (G = 0.318, P = 0.063) at both genotypic and phenotypic level (Table 6 and 7). Significant positive correlation of this character with yield per hectare was reported by Vange (2008) and Mahto *et al*. (2003).

4.3.8 Number of secondary branches per panicle

Number of secondary branches per panicle showed significant and positive correlation with total number of spikelet (G = 1.025, P = 0.682), number of filled grain per panicle (G = 0.902, P = 0.647), with number of unfilled grain per panicle (G = 0.801) at genotypic level, yield per plant (G = 0.468, P = 416) and yield per hectare (G = 0.653, P = 0.587). 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. Whereas it had the non-significant positive correlation with number of unfilled grain per panicle (P = 0.224) at phenotypic level and thousand seed weight (G = 0.099,P = 0.121) at both genotypic and phenotypic level (Table 6 and 7). Mahto *et al*. (2003) showed positive and significant correlation of yield with number of secondary branches per panicle.

4.3.9 Total number of spikelets per panicle

Total number of spikelet per panicle showed significant and positive correlation with number of filled grain per panicle (G = 0.955, P = 0.931), yield per plant (G =

1.003, P = 0.48) and yield per hectare (G = 1.085, P = 0.535) at both genotypic and phenotypic level and number of unfilled grain per panicle (P = 0.45) at phenotypic level indicated that improvement of yield per plant and yield per hectare can be possible by improving number of filled grain per panicle and total number of spikelet per panicle. But had non-significant positive correlation with number of unfilled grain per panicle (G = 0.332) at genotypic level and thousand seed weight (G = 0.213,P = 0.273) at both genotypic and phenotypic level. Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Total number of spikelet per panicle showed significant and positive correlation with yield per hectare was reported by Allam *et al.* (2015), Akinwale *et al.* (2011) and Yadav *et al.* (2010).

4.3.10 Number of filled grains per panicle

Number of filled grains per panicle showed significant and positive correlation with yield per plant (G = 0.996, P = 0.529) and yield per hectare (G = 1.101, P =0.6) indicated that if number of filled grains per panicle increased then yield per plant and yield per hectare also increased. It also had non-significant positive relation with number of unfilled grains per panicle (G = 0.035, P = 0.126) and thousand seed weight (G = 0.155, P = 0.186) at both genotypic and phenotypic level (Table 6 and 7). Islam *et al.* (2015), Kishore *et al.* (2015), Mahto *et al.* (2003), showed significant and positive correlation with filled grains per panicle.

4.3.11 Number of unfilled grains per panicle

Number of unfilled grains per panicle showed significant and positive correlation with yield per plant (G = 0.404) and yield per hectare (G = 0.475) at genotypic level. This result exposed that yield per plant and yield per hectare can be increased by decreasing the number of unfilled grains per panicle. It also had non-significant positive relation interaction with thousand seed weight (G = 0.037, P =

0.256). It had also non-significant and negative relation with yield per plant (P = -0.128) and yield per hectare (P = -0.098) at phenotypic level (Table 6 and 7).

4.3.12 Yield per plant (g)

Yield per plant had significant and positive correlation with thousand seed weight (G = 0.614, P = 0.395)and yield per hectare (G = 0.965, P = 0.844) indicated that if yield per plant increased then yield per hectare also increased (Table 6 and 7). Babu *et al*. (2012) reported significant and positive correlation of yield per plant with yield.

4.3.13 Thousand seed weight (g)

Thousand seed weight showed significant and positive correlation with yield per hectare (G = 0.479) at genotypic level. It showed non-significant and positive correlation with yield per hectare (P = 0.204) at phenotypic level (Table 6 and 7) indicated that very little contribution of thousand seed weight toward increase in yield per hectare. Significant positive correlation of this characters with yield per hectare was reported by Iftekharuddaula *et al*. (2001), Ganapati *et al.* (2014) and Shabir *et al* (2013) showed significant and positive correlation with yield.

4.4 Estimation of path co-efficient

The correlation coefficient alone is inadequate to interpret the cause and effect relationships among the traits and ultimately with yield. Path analysis technique furnishes a method of partioning the correlation coefficients into direct and indirect effects provide the information on actual contribution of the independent variables on the dependent variable. In the present study, all the thirteen traits were considered as causal variables of yield. Genotypic correlations coefficients of these traits with yield per ha were partitioned into the direct and indirect effects through path coefficient analysis. The results are shown in Table 8.

4.4.1 Days to flowering

Days to flowering had negative direct effect (-0.051) on yield per hectare. Path co-efficient analysis revealed that days to flowering had significant positive correlation with yield per hectare. This trait showed indirect positive effect on yield per hectare through days to maturity (0.309), total number of tiller per plant (0.007),panicle length per plant (0.415), number of primary branches per panicle (0.338), number of filled grains per panicle (1.16), number of unfilled grains per panicle (0.13), yield per plant (1.09). On the hand, it showed indirect negative effect on yield per hectare via plant height (-0.761), number of effective tillers per plant (-0.171), number of secondary branches per panicle (-0.14), total number of spikelet per panicle (-1.24), thousand seed weight (-0.168). Finally it made significant positive correlation with yield per hectare (0.924) (Table 8). Abarshahr *et al*. (2011) reported negative direct effect on grain yield for days to 50% flowering.

4.4.2 Days to maturity

Days to maturity had positive direct effect (0.332) on yield per hectare. It had positive indirect effect on the yield per hectare through total number of tiller per plant (0.024),panicle length per plant (0.487), number of primary branches per panicle (o.378), number of filled grains per panicle (1.23), number of unfilled grains per panicle (0.10), yield per plant (1.03). The indirect negative effect of this trait through days to flowering (-0.048), plant height (-0.792), number of effective tillers per plant (-0.180), number of secondary branch per panicle (-0.17), total number of spikelets per panicle (-1.25), thousand seed weight (-0.169) on yield per hectare. Finally it made significant positive correlation with yield per hectare (0.983) (Table 8). Same result also recorded by Islam *et al.* (2015).

4.4.3 Plant height (cm)

Plant height had positive indirect effect on days to maturity (0.264), number of effective tillers per plant (0.081), panicle length (0.866),number of primary

branches per panicle (0.347), number of filled grains per panicle (0.96), number of unfilled grains per panicle (0.17), yield per plant (0.84), whereas, it had negative indirect effect on days to flowering (-0.039), total number of tiller per plant (-0.166), number of secondary branch per panicle (-0.19), total number of spikelets per panicle (-1.14), thousand seed weight (-0.231). Plant height had negative direct effect (-0.039) on yield per hectare and finally it had significant positive genotypic correlation with yield per hectare (Table 8). Ratna *et al.* (2015), and Abarshahr *et al.* (2011) reported negative direct effect on grain for this traits.

4.4.4 Total number of tillers per plant

Total number of tillers per plant had positive direct (0.336) effect on yield per hectare. It had positive indirect effect on days to maturity (0.024), plant height (0.493), number of secondary branch per panicle (0.04), total number of spikelet per panicle (0.04), number of filled grains per panicle (0.10), yield per plant (0.02), thousand seed weight (0.198), whereas, it had negative indirect effect on days to flowering (-0.001), number of effective tillers per plant (-0.455), panicle length (-0.647), number of primary branches per panicle (-0.059), number of unfilled grains per panicle (-0.07). Finally it had non-significant positive genotypic correlation (0.024) with yield per hectare (Table 8). Selvaraj *et al.* (2011) reported similar result for this traits.

4.4.5 Number of effective tillers per plant

Number of effective tillers per plant had positive indirect effect on yield per hectare through days to maturity (0.125), plant height (0.168), total number of tiller per plant (0.320), number of primary branches per panicle (0.081), number of secondary branches per panicle (0.01), number of filled grains per panicle (0.42), yield per plant (0.37) thousand seed weight (0.122), whereas, it had negative indirect effect on days to flowering (-0.018), panicle length (-0.414), total number of spikelet per panicle (-0.33), number of unfilled grains per panicle (-0.02). It had

negative direct (-0.478) effect on yield per hectare. Finally it had significant positive genotypic correlation (0.365) with yield per hectare (Table 8).

4.4.6 Panicle length (cm)

Panicle length had positive direct effect (0.973) on yield per hectare. It had positive indirect effect through days to maturity (0.166), number of effective tillers per plant (0.203), number of primary branches per panicle (0.262), number of filled grains per panicle (0.55), number of unfilled grains per panicle (0.21) yield per plant (0.45) on yield per hectare. Negative indirect effect on yield per hectare was found through days to flowering (-0.022), plant height (-0.886), total number of tillers per plant (-0.223), number of secondary branches per panicle (-0.17), total number of spikelet per panicle (-0.82), thousand seed weight (-0.192) (Table 8). Its correlation with yield per hectare was positive and significant (0.503) suggested that direct selection of this character may contribute in yield. Ullah *et al.* (2011) reported positive indirect effect for this traits.

4.4.7 Number of primary branches per panicle

Number of primary branches per panicle had positive direct effect (0.436) on yield per hectare. It had positive indirect effect through days to maturity (0.288), panicle length (0.585), number of filled grains per panicle (1.11), number of unfilled grains per panicle (0.07) yield per plant (0.93) on yield per hectare. Negative indirect effect on yield per hectare was found through days to flowering (-0.040), plant height (-0.794), total number of tillers per plant (-0.045), number of effective tillers per plant (-0.088), number of secondary branches per panicle (-0.16), total number of spikelet per panicle (-1.14), thousand seed weight (-0.213) (Table 8).

4.4.8 Number of secondary branches per panicle

Number of secondary branches per panicle had positive indirect effect through days to maturity (0.24), number of effective tillers per plant (0.03), panicle length (0.72), number of primary branches per panicle (0.30),number of filled grains per

panicle (1.13), number of unfilled grains per panicle (0.17) yield per plant (0.52) on yield per hectare. Number of secondary branches per panicle had negative direct effect (-0.23) on yield per hectare. Whereas, it had negative indirect effect on yield per hectare via days to flowering (-0.03), plant height (-0.80), total number of tiller per plant (-0.06),total number of spikelet per panicle (-1.29), thousand seed weight (-0.036).Finally this trait had significant positive genotypic correlation (0.653) with yield per hectare (Table 8).

4.4.9 Total number of spikelet per panicle

Total number of spikelet per panicle had indirect positive effect on yield per hectare via days to maturity (0.33), panicle length (0.63), number of primary branches per panicle (0.39), number of filled grains per panicle (1.20), number of unfilled grains per panicle (0.07), yield per plant (1.12). It had negative direct effect (-1.26) on yield per hectare. This trait had also, indirect negative effect of this trait showed on yield per hectare through days to flowering (-0.05), plant height (-0.90), total number of tiller per plant (-0.01), number of effective tillers per plant (-0.12), number of secondary branch per panicle (-0.24), thousand seed weight (-0.077). Finally this trait had significant positive correlation (1.085) with yield per plant (Table 8).

4.4.10 Number of filled grains per panicle

 Number of filled grains per panicle had positive direct (1.25) effect on yield per hectare. The positive indirect effect through days to maturity (0.33), total number of tillers per plant (0.03), panicle length (0.43), number of primary branches per panicle (0.39), number of unfilled grains per panicle (0.01) and yield per plant (1.11) . Whereas this trait showed negative indirect effect via days to flowering (-0.05), plant height (-0.76), number of effective tillers per plant (-0.16), number of secondary branch per panicle (-0.21), total number of spikelet per panicle (-1.20), thousand seed weight (-0.056). Number of filled grains per panicle had highly

Table 8. Partitioning of genotypic correlations into direct (bold) and indirect effects of different important characters by path analysis of rice

	DF	DM	PH	TNT/P	NET/P	PL/P	NPB/P	NSB/P	TS/P	NFG	NUG	Y/P (dry)	TSW	Genotypic correlation with yield
DF	**-0.051**	0.309	-0.761	0.007	-0.171	0.415	0.338	-0.14	-1.24	1.16	0.13	1.09	-0.168	0.924**
DM	-0.048	**0.332**	-0.792	0.024	-0.180	0.487	0.378	-0.17	-1.25	1.23	0.10	1.03	-0.169	0.983**
PH	-0.039	0.264	**-0.996**	-0.166	0.081	0.866	0.347	-0.19	-1.14	0.96	0.17	0.84	-0.231	0.771**
TNT/P	-0.001	0.024	0.493	**0.336**	-0.455	-0.647	-0.059	0.04	0.04	0.10	-0.07	0.02	0.198	0.024
NET/P	-0.018	0.125	0.168	0.320	**-0.478**	-0.414	0.081	0.01	-0.33	0.42	-0.02	0.37	0.122	0.365*
PL/P	-0.022	0.166	-0.886	-0.223	0.203	**0.973**	0.262	-0.17	-0.82	0.55	0.21	0.45	-0.192	0.503**
NPB/P	-0.040	0.288	-0.794	-0.045	-0.088	0.585	**0.436**	-0.16	-1.14	1.11	0.07	0.93	-0.213	0.940**
NSB/P	-0.03	0.24	-0.80	-0.06	0.03	0.72	0.30	**-0.23**	-1.29	1.13	0.17	0.52	-0.036	0.653**
TS/P	-0.05	0.33	-0.90	-0.01	-0.12	0.63	0.39	-0.24	**-1.26**	1.20	0.07	1.12	-0.077	1.085**
NFG	-0.05	0.33	-0.76	0.03	-0.16	0.43	0.39	-0.21	-1.20	**1.25**	0.01	1.11	-0.056	1.101**
NUG	-0.03	0.16	-0.80	-0.11	0.04	0.98	0.14	-0.19	-0.42	0.04	**0.21**	0.45	-0.013	0.475**
Y/P (dry)	-0.05	0.31	-0.75	0.01	-0.16	0.39	0.36	-0.11	-1.26	1.25	0.08	**1.11**	-0.222	0.965**
TSW	-0.02	0.16	-0.64	-0.18	0.16	0.52	0.26	-0.02	-0.27	0.19	0.01	0.68	**-0.36**	0.479**

Residual effect: 0.10737   ** = Significant at 1%.   * = Significant at 5%.

DF = Days to 50% flowering,, DM = Days to maturity, PH = Plant height, TNT/P = Total no of tiller/plant, NET/P = Number of effective tiller/plant, PL/P = Panicle length/plant, NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle, TS/P = Total no of spikelets/panicle, NFG = Number of filled grain of main tiller, NUG = Number of unfilled grain of main tiller, Y/P (Dry) = Yield/plant, TSW = Thousand seed weight and Y/ha = Yield/ha

significant and positive correlation with yield per plant (1.101) (Table 8) indicated that direct selection of this trait will improve yield per hectare. Hence, selection should be practiced for this trait which had more number of filled grains per panicle in order to improve seed yield. Islam *et al.* (2015) and Satheesh kumar *et al.* (2012) found positive direct effect of filled grains per panicle on yield per hectare.

4.4.11 Number of unfilled grains per panicle

Path coefficient revealed that number of unfilled grains per panicle had positive direct effect (0.21) on yield per hectare. The positive indirect effect on yield per hectare was found via days to maturity (0.16), number of effective tillers per plant (0.04), panicle length (0.98), number of primary branches per panicle (0.14), number of filled grains per panicle (0.04), yield per plant (0.45). It had also negative indirect effect through days to flowering (-0.03), plant height (-0.80), total number of tillers per plant (-0.11), number of secondary branch per panicle (-0.19), total number of spikelet per panicle (-0.42) and thousand seed weight (-0.013). on yield per hectare. Number of unfilled grains per panicle finally made significant positive genotypic correlation (0.475) with yield per hectare.

4.4.12 Yield per plant (g)

Yield per plant had positive direct effect (1.11) on yield per hectare. Path co-efficient analysis revealed that it had significant positive correlation with yield per hectare. This trait showed indirect positive effect on yield per hectare through days to maturity (0.31), total number of tiller per plant (0.01), panicle length per plant (0.39), number of primary branches per panicle (0.36), number of filled grains per panicle (1.25), number of unfilled grains per panicle (0.08). On the hand, it showed indirect negative effect on yield per hectare via days to flowering (-0.05), plant height (-0.75), number of effective tillers per plant (-0.16), number of secondary branches per panicle (-0.11), total number of spikelet per panicle (-1.26), thousand seed weight (-0.222). Finally it made significant positive

correlation with yield per hectare (0.965) (Table 8). Devi *et al.* (2017) and Kishore *et al*. (2015) also found positive direct effect on grain yield per plant.

4.4.13 Thousand seed weight (gm)

Path coefficient revealed that thousand seed weight had negative direct effect (-0.36) on yield per hectare. The positive indirect effect on yield per hectare was found via days to maturity (0.16), number of effective tillers per plant (0.16), panicle length (0.52), number of primary branches per panicle (0.26), number of filled grains per panicle (0.19), number of unfilled grains per panicle (0.01) and yield per plant (0.68). It had also negative indirect effect through days to flowering (-0.02), plant height (-0.64), total number of tillers per plant (-0.18), number of secondary branch per panicle (-0.02) and total number of spikelet per panicle (-0.27) on yield per hectare. Number of unfilled grains per panicle finally made significant positive genotypic correlation (0.479) with yield per hectare. Yield per hectare may be improved through direct selection of thousand seeds weight. Karad *et al*. (2008) was found negative direct effect for this traits.

Chapter V
Summary and Conclusion

The present research work was conducted in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during the period from April 2015 to September 2015. This experiment involved two parents and nine F_5 cross lines of rice and was laid out in a Randomized Complete Block Design (RCBD) with three replications. Data on various yield in attributing characters such as, days to flowering, days to maturity, plant height (cm), total numbers of tillers per plant, number of effective tillers per plant, 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 per panicle, total number of spikelets per panicle, yield per plant (g), thousand seed weight (g), yield per hectare (t) were recorded.

Analysis of variance from F_5 lines revealed that significant variation was observed among all the genotypes studied indicating prevalence of wide range of genetic variability and scope of selection for these traits, except number of unfilled grains per main tiller. In this research work, the maximum days to 50% flowering were found in genotype G9 (BR24 X BRRI dhan29 $F_5S_5P_{10}$) and the minimum was in both genotypes G2 (BR21 X BRRI dhan29 $F_5S_6P_3$(a) and G3 (BR21 X BRRI dhan29 $F_5S_6P_3$(b)). Genotypes exhibited high range from 102.67 to 130.33 days for days to maturity and genotype G5 (BR21 X BRRI dhan29 $F_5S_6P_8$) performed minimum days to maturity, representing earliness and the maximum was in both G1 and G9. Highest plant height was observed in genotype G4 (BR21 X BRRI dhan29 $F_5S_6P_5$) while lowest in genotype G7 (BR21 X BRRI dhan36 $F_5S_1P_9$). Genotype G7 was showed highest significant number of total number of tiller per plant while genotype G5 represented the lowest value of this trait. The most number of effective tiller per plant was exhibited by genotype G7 while genotype

G5 showed the lowest. Genotype G4 represented the longest panicle while shortest was observed by the genotype G7. The genotypes G9 and G6 were produce the highest and lowest number of primary branches per panicle respectively. The highest and lowest number of secondary branches per panicle was exhibited by the genotypes G9 and G11 respectively. Highest total no. of spikelets per panicle was observed by the genotype G9 while G11 showed the lowest no. of spikelets per panicle. The maximum number of filled grains of main tiller was observed in genotype G9 while minimum was observed in genotype G11. The highest yield/plant was observed by the genotype G1 while genotype G5 showed the lowest. The maximum value of thousand seed weight was observed in genotype G11 while minimum value of thousand grain weight was observed in genotype G7. Maximum yield per ha was obtained in genotype G1 while genotype G6 showed the lowest value of this trait.

However, the phenotypic variance and phenotypic co-efficient of variation were higher than the corresponding genotypic variance and genotypic co-efficient of variation for all characters under study. High genotypic co-efficient of variation and phenotypic co-efficient of variation were found for yield per ha, number of unfilled grain of main tiller, number of secondary branches per panicle, yield per plant, number of filled grain of main tiller and total no number of spikelets per panicle. Heritability estimates were high for days to maturity (95.50), days to 50% flowering (93.13), plant height (83.31), number of secondary branches per panicle (80.16), total no of tiller per plant (77.06), yield per ha (72.81), and number of effective tiller per plant (70.62). This indicates that the phenotype is highly correlated with the genotype and that contribution of environmental conditions was relatively low for these traits. Low heritability estimate was observed for number of unfilled grain of main tiller (23.56). This shows that the phenotype is not correlated with the genotype and environmental factors strongly influence this character. The findings indicated that additive gene actions governs the expression

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of traits viz., days to maturity, days to 50% flowering, plant height, number of secondary branches per panicle, total no of tiller per plant, yield per ha, and number of effective tiller per plant, which further suggested that phenotypic selection was appropriate at an early stage. Further, unfilled grain of main tiller is controlled by additive and epistatic genetic components.

High heritability along with high genetic advance in percent of mean was noticed for the traits, days to 50% flowering, plant height, total number of tiller per plant, number of effective tiller per plant, number of secondary branches per panicle, total number of spikelets per plant, number of filled grain of main tiller and yield per ha indicating preponderance of additive gene action in the inheritance of these traits and selection would be effective.

Genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients in most of the associations which might be due to masking or modifying effect of environment. Very close values of genotypic and phenotypic correlations were also observed between some character combinations which might be due to reduction in error (environmental) variance to minor proportions. Yield per ha was positively and significantly correlate with days to 50% flowering (G = 0.924, P = 0.872), days to maturity (G = 0.983, P= 0.892), plant height (G = 0.771, P = 0.657), panicle length per plant (G= 0.503, P= 0.367), number of primary branches per panicle (G = 0.940, P = 0.669), number of secondary branches per panicle (G = 0.653, P = 0.587), total no of spikelets per panicle (G = 0.1.085, P = 0.535), number of filled grain of main tiller (G = 1.101, P = 0.600) and yield/plant (G = 0.965, P = 0.844) at both genotypic and phenotypic levels indicating these traits could be utilize in improvement of seed yield per plant. Correlation coefficients implied that significant negative correlations at both the levels were recorded for plant height with total no of tiller per plant; total no. of tiller per plant with panicle length; and thousand seed weight, number of effective tiller per plant with panicle length.

Genotypic correlations coefficients of these traits with yield per ha were partitioned into the direct and indirect effects through path coefficient analysis. It was revealed that number of filled grain of main tiller (1.25), yield/plant (1.11), panicle length (0.973), number of primary branches per plant (0.436), total number of tillers/plant (0.336), days to maturity (0.332) and number of unfilled grain/panicle (0.21) had direct positive effect on yield per ha, indicating these are the main contributors to yield per ha. Total spikelets per panicle and plant height had direct negative effect on yield/ha. The highest positive indirect effects on yield per ha were obtained by yield per plant (1.25) via number of filled grain per panicle. Again the highest negative indirect effect on yield was obtained by number of secondary branches per panicle via total spikelets per panicle.

The residual effect was 0.10737, indicated that contribution of component characters on yield per hectare was 89.3% by the thirteen characters studied in path analysis.

Sufficient genetic variability was observed among the genotypes for all the traits under study. Hence selection of these characters simultaneously would bring improvement in yield. Among the genotypes studied, G1 and G9 performed statistically similar yield per ha and would be selected as yield yielder with maximum total spikelets per panicle, more filled grains per panicle, more secondary branches per panicle and highest plant height. Genotypes G2 and G5 were the statistically similar for minimum days to maturity and would be selected as early variety. These genotypes can be further tested over years across locations to select for direct release as varieties. Besides, these genotypes can be used in advance generations and in cross-breeding programs to generate trangressive segregants for each traits further selection.

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APPENDICES

Appendix I. Map showing the experimental site under the study
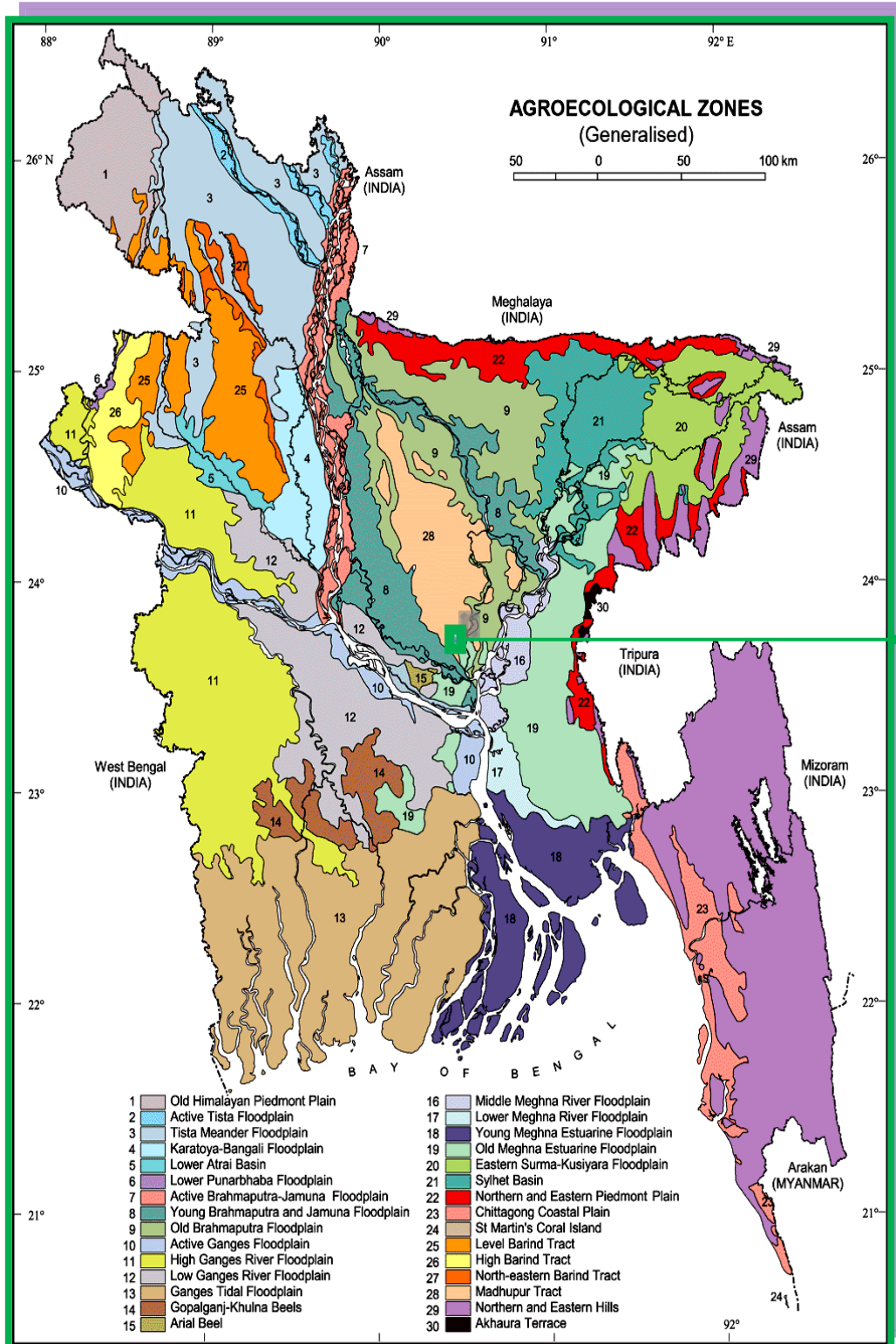
Appendix II: Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site

A. Physical composition of the soil

Soil separates	%	Methods employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1.25 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Appendix III: Meteorological conditions of the experimental site during crop growing period (April, 2015 to September, 2015)

Month	Maximum temperature	Minimum temperature	Average rainfall (mm)
April, 2015	38.0	28.0	5.87
May, 2015	37.5	27.0	6.23
June, 2o15	37.0	27.0	6.45
July, 2015	35.0	25.0	8.77
August, 2015	34.0	25.0	19.9
September,2015	34.5	26.5	7.63

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka – 1212

Appendix IV: Mean performance of 11 genotypes of *Oryza sativa* L. in respect of seven important characters

Genotype	DF	DM	PH	NTT/P	NET/P	PL/P	NPB/P
G1	96.67	130.3	120.3	13.50	12.77	24.26	8.833
G2	70.67	105.0	99.93	13.20	11.34	22.91	8.267
G3	70.67	106.3	93.27	12.23	10.27	24.12	8.467
G4	93.33	125.0	124.7	12.17	11.63	25.25	9.167
G5	75.00	102.7	104.3	10.94	9.787	24.36	7.843d
G6	75.00	108.0	102.9	11.60	9.833	23.57	7.400
G7	75.00	107.0	77.65	18.33	15.39	20.21	7.433
G8	76.67	110.0	105.8	14.00	13.27	24.67	8.367
G9	96.67	130.3	117.2	14.03	13.43	24.66	9.533
G10	90.00	112.0	101.0	12.77	12.13b	22.71	8.400
G11	75.00	110.0	96.83	12.50	11.50	22.53	8.600

DF = Days to 50% flowering,, DM = Days to maturity, PH = Plant height, NTT/P = Number of total tillers/plant, NET/P = Number of effective tiller/plant, PL/P = Panicle length/plant, NPB/P = Number of primary branches/panicle,

G1 = BR21 X BRRI dhan29 F5S6P2, G2 = BR21 X BRRI dhan29 F5S6P3(a), G3 = BR21 XBRRI dhan29 F5S6P3(b), G4 = BR21 X BRRI dhan29 F5S6P5, G5 = BR21 x BRRI dhan29 F5S6P8, G6 = BR21 X BRRI dhan29 F5S6P10, G7 = BR21 X BRRI dhan36 F5S1P9, G8 = BR24 X BRRI dhan28 F5S10P8, G9 = BR24 X BRRI dhan29 F5S5P10, G10 = BRRI dhan 48 and G11= BRRI dhan 55

Appendix V: Mean performance of 11 genotypes of *Oryza sativa* L. in respect of seven important characters

Genotypes	NSB/P	TS/P	NFG/P	NUFG/P	Y/P	TSW	Y/ha
G1	27.70	147.00	126.30	22.99	31.00	26.27	5.000
G2	23.77	120.00	103.70	14.30	19.33	21.23	2.287
G3	23.73	121.90	104.80	17.10	18.67	23.67	2.367
G4	30.67	153.70	120.70	32.97	26.33	21.47	3.427
G5	24.21	117.30	81.08	36.04	17.00	23.00	1.900
G6	21.73	104.70c	85.13	22.92	17.00	23.03	1.807
G7	17.83	107.00	85.40	21.63	18.00	19.67	1.853
G8	19.77	115.80	87.57	29.43	21.33	24.15	2.560
G9	31.17	156.60	136.10	28.60	26.00	22.29	4.887
G10	17.10	123.60	104.80	19.00	26.67	24.60	3.167
G11	15.77	97.93	78.60	18.09	20.33	27.50	2.473

NSB/P = Number of secondary branches per panicle, TS/P = Total number of spikelets per panicle, NFG = Number of filled grain of main tiller, NUG = Number of unfilled grain of main tiller, Y/P = Yield/plant, TSW = Thousand seed weight, Yield/ ha = Yield per hectare.

G1 = BR21 X BRRI dhan29 F5S6P2, G2 = BR21 X BRRI dhan29 F5S6P3(a), G3 = BR21 XBRRI dhan29 F5S6P3(b), G4 = BR21 X BRRI dhan29 F5S6P5, G5 = BR21 x BRRI dhan29 F5S6P8, G6 = BR21 X BRRI dhan29 F5S6P10, G7 = BR21 X BRRI dhan36 F5S1P9, G8 = BR24 X BRRI dhan28 F5S10P8, G9 = BR24 X BRRI dhan29 F5S5P10, G10 = BRRI dhan 48 and G11= BRRI dhan 55