# VARIABILITY AND INTERRELATIONSHIPS OF YIELD AND YIELD CONTRIBUTING TRAITS IN $F_5$ POPULATION OF BORO RICE (*Oryza sativa* L.)

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# VARIABILITY AND INTERRELATIONSHIPS OF YIELD AND YIELD CONTRIBUTING TRAITS IN $F_5$ POPULATION OF BORO RICE (*Oryza sativa* L.)

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# CERTIFICATE

*This is to certify that thesis entitled, "VARIABILITY AND INTERRELATIONSHIPS OF YIELD AND YIELD CONTRIBUTING TRAITS IN $F_5$ POPULATION OF BORO 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 MD.GOLAM ROBBANI, Registration No. 08-02755 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.*

**Dated: December, 2014**
**Place: Dhaka, Bangladesh**

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Prof. Dr. Md. Shahidur Rashid Bhuiyan

**Supervisor**

*DEDICATED*

*TO*

*MY BELOVED PARENTS*

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## ABSTRACT

The experiment was conducted with 29 genotypes of rice at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period of December, 2013 to May, 2014 to estimate the variability and interrelationship between yield and yield contributing characters and their direct and indirect effect on yield. The experiment was laid out in Randomized Complete Block Design with three replications. All the genotypes varied significantly from each other for all the studied characters which indicate the presence of considerable variations among the genotypes. The PCV values were higher than the respective GCV values for all the characters under study. Plant height, total spikelet per panicle, number of filled grains per panicle and number of unfilled grains per panicle showed high genotypic and phenotypic coefficient of variation. These characters also showed high heritability coupled with high genetic advance and very high genetic advance in percentage of mean which is normally more helpful in predicting the genetic gain under selection. Correlation co-efficient analysis revealed that yield per hectare had significant positive association with panicle length, number of secondary branches per panicle, total number of spikelet per panicle, number of filled grains per panicle and yield per plant. Path coefficient analysis revealed that number of filled grains per panicle showed the highest positive direct effect on yield per hectare followed by panicle length, number of secondary branches per panicle and yield per plant. Considering variability, heritability, genetic advance, correlation co-efficient and path analysis, number of filled grain per panicle showed high heritability, genetic advance, high significant positive correlation and the highest positive direct effect on yield per hectare.

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**December, 2014**

**The Author**

**SAU, Dhaka**

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# LIST OF ABREVIATIONS

| **Abbreviation** | **Full Name** |
|---|---|
| % | Percent |
| $^oC$ | Degree Celsius |
| $\sigma^2$ p | Phenotypic variance |
| $\sigma^2$ g | Genotypic variance |
| $h^2$ b | Heritability in broad sense |
| AEZ | Agro-Ecological Zone |
| Agril. | Agricultural |
| ANOVA | Analysis of variance |
| BARI | Bangladesh Agricultural Research Institute |
| BBS | Bangladesh Bureau of Statistics |
| BD | Bangladesh |
| Cm | Centimeter |
| CV% | Percentage of Coefficient of Variation |
| Df | Degrees of Freedom |
| *et al.* | And others |
| etc. | Etcetera |
| $F_5$ | The third generation of a cross between two dissimilar homozygous parents |
| FAO | Food and Agricultural Organization |
| gm | Gram |
| G | Genotype |
| GA | Genetic Advance |
| GCV | Genotypic coefficient of variation |
| Ha | Hactare |
| J. | Journal |
| Kg | Kilogram |
| M | Meter |
| MSS | Mean sum of square |
| MP | Murate Potash |
| MOA | Ministry of Agriculture |
| $m^2$ | Square meter |
| PCV | Phenotypic coefficient of variation |
| RCBD | Randomized Complete Block Design |
| SAU | Sher-e-Bangla Agricultural University |
| T | Ton |
| TSP | Triple Super Phosphate |

# CHAPTER I

# INTRODUCTION

Rice is a self pollinated cereal crop belonging to genus *Oryza* of family Gramineae under the order Cyperales and class Monocotyledon having chromosome number 2n = 24 (Hooker, 1979). The genus *Oryza* has twenty three wild and two cultivated species viz., *Oryza sativa* and *Oryza glaberrima* (Brar and Khush, 2003) .

Rice is a major food crop, ranking second to wheat among the most cultivated cereals in the world (Abodlereza *et al*., 2009). It is the staple food crop of more than half of the world's population (Anonymous, 2009). Rice provides 21% energy and 15% of per capita protein of global human (Maclean *et al*., 2002). The world dedicated 162.3 million hectares in 2012 for rice cultivation and the total production were about 738.1 million tons (Anonymous, 2012). By 2030, the world must have to produce 60% more rice than it produce in 1995 to meet the demands (Virmani *et al*., 1997).

More than 90% of the world's rice is produced and consumed in Asia (Chopra, 2001). Bangladesh is the fourth largest producer of rice in the world with production of 33.8 million tons in 2012 (Anonymous, 2012). It is the staple food in Bangladesh, and grown in a wide range of environments ranging from the hilly areas like Chittagong Hill Tracts, Sylhet and Garo Hills, with little moisture, to situations where the water is 3-4 m deep (Alim, 1982). It occupies 74.77% total cropped areas and it alone constitutes 90% of the total food grain produced annually in the country (Anonymous, 2009). Bangladesh needs 2.7% increases in rice production per year due to increasing population (Alam *et al*., 2004).

Grain yield, being a quantitative trait is a complex character of any crop. Various morphological and physiological plant characters contribute to yield. These yield contributing components are interrelated with each other showing a complex chain of relationship and also highly influenced by the environmental conditions (Prasad *et al*., 2001). Measurement of correlation coefficient helps to identify the relative contribution of component characters toward yield (Panse, 1992). Path coefficient analysis partitions the genetic correlation between yield and its component traits into direct and indirect effects and hence has effectively been used in identifying useful traits as selection criteria to improve grain yield in rice (Mustafa and Elsheikh, 2007; Kole *et al*., 2008; Akinwale *et al*., 2011; Sadeghi, 2011).

Rice is grown in Bangladesh under diverse ecosystem of irrigated, rain fed and deep water conditions in three distinct seasons namely Aus, Aman, and Boro (Rashid, 1994). Among Aus, Aman and Boro seasons, boro occupied the highest area coverage. Moreover, there is lack of short duration boro rice variety in our country. So we have to give more attention for the improvement of boro rice varieties to increase rice production in order to satisfy our population's need of food.

The presence and magnitude of genetic variability in a gene pool is the pre-requisite of a breeding programme. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability, and genetic advance are necessary to start an efficient breeding programme (Mishra *et al*., 1988). Knowledge of heritability is essential for selection based improvement, as it indicates the extent of transmissibility of a character into future generations (Sabesan *et al*., 2009). Genetic advance provides a information on expected genetic gain resulting from selection of superior individuals (Satheeshkumar and Saravanan, 2012). High heritability estimates along with high genetic advance are more helpful in predicting the gain under selection than heritability estimates alone (Thomas and Lal, 2012).

Therefore the present study was undertaken with the following objectives:

1. To study the genetic variability among 29 $F_5$ of rice populations and

2. To study the interrelationship between yield and yield contributing characters and their direct and indirect effect on yield

# CHAPTER II

# REVIEW OF LITERATURE

## 2.1 Variability, heritability and genetic advance

Ketan and Sarkara (2014) to observed significant variability for nineteen quantitative characters in an experiment conducted with 26 indigenous aman rice cultivars. The magnitude of PCV was observed 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.

Sarwar (2013) conducted with 42 genotypes of rice to estimate the genetic variability, correlation, path and diversity among the genotypes. Analysis revealed that total tillers per plant, effective tillers per plant, filled grains per panicle, unfilled grains per panicle and yield per plant showed high heritability along with high genetic advance as percentage of mean were normally more helpful in predicting the genetic gain under selection.

Tuwar *et al*. (2013) studied with 29 genotypes of rice from diverse locations to estimate the genetic components of variability. Analysis revealed that plant height exhibited high estimates of GCV and PCV proceeded by number of tillers and grain weight per panicle. 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 high genetic variability and transmissibility. 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 expression and would respond to selection effectively as they are least influenced by environment.

Babu *et al.* (2012) carried out an experiment to study the genetic parameters for yield, quality and nutritional characters in 21 rice hybrids. Analysis of variance revealed significant differences for all the traits under study. The Characters namely, 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.

Satheesh kumar *et al.* (2012) estimated variability, heritability, genetic advance in 53 genotypes of rice for 15 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. High heritability was 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, spikelet fertility, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel L/B ratio and grain yield per plant. 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.

Seyoum *et al.* (2012) conducted a field experiments using 14 rice genotypes 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.

Akinwale *et al.* (2011) evaluated 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 $m^2$ 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.

Selvaraj *et al.* (2011) studied variability, correlation and path coefficient on 21 rice genotypes for grain yield and other yield attributes. Analysis of variance revealed considerable variability among the genotypes for all the characters. The phenotypic correlation coefficient (PCV) values were slightly greater than genotypic correlation coefficient (GCV), revealing negligible influence of environment in character expression. 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) conducted experiment with 38 genotypes to study the nature and magnitude of variability, heritability and genetic advance of 12 quantitative traits. 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.

Akhtar *et al*. (2011) carried out an experiment to study variability and heritability of yield contributing traits in ten rice genotypes. Analysis of variance revealed significant differences among the genotypes for all the traits. The 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.

Singh *et al*. (2011) evaluated 81 rice genotypes during kharif 2010 for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flag leaf width. Among all the traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that this this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as percent of mean was recorded for number of spikelets per panicle with high value of heritability.

Abarshahr *et. al.* (2011) conducted an experiment with 30 varieties of rice under two irrigation regimes in order to estimate genetic variability and relationships among some agronomic traits of rice. Broad-sense heritability varied from 0.05 for brown grain width to 0.99 for plant height and number of spikelet for panicle under optimum irrigation and from 0.1 for brown grain width to 0.99 for plant height. Evaluation of phenotypic and genotypic coefficient of variations (CV) showed that the lowest and highest phenotypic CV under optimum irrigation regime was observed to panicle fertility percentage and paddy yield and genotypic CV was related to brown grain width and plant height, respectively, while under drought stress condition, days to 50% flowering had the lowest phenotypic and genotypic CV and paddy yield and plant height had the highest phenotypic and genotypic CV. Furthermore, the lowest and highest expected genetic advance using selection intensity of 10% (i =1.75) were evaluated for brown grain width and plant height under optimum irrigation regime, respectively.

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. He found broad sense heritability range from 69.21% (plant height) to 99.53% (grain width).

Ullah *et al.* (2011) found higher genotypic coefficient of variations for grains per panicle followed by grain yield perplant, 1000-grain weight and panicles per plant in an experiment conducted with 10 traditional fine Biron rice. 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.

Singh *et al.* (2011) evaluated eighty one rice (*Oryza sativa* L.) genotypes during kharif 2010 for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flag leaf width. Among all the traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by harvest index, grain yield per hill and number of panicles per hill. The highest broad sense heritability was found for biological yield per hill, which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as percent of mean was recorded for number of spikelets per panicle with high value of heritability.

Subbaiah *et al*. (2011) studied the extent of variability and genetic parameters of 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 low genetic advance as percent of mean were recorded for harvest index, total number of productive tillers per plant, number of grains per panicle ratio and grain yield per plant in case of parents and for total number of productive tillers per plant, number of grains per panicle and harvest index in case of hybrids.

Nandan *et al*. (2010) did an experiment to evaluate thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. They found 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.

Chakraborty and Chakraborty (2010) assessed the genetic variability, correlation and coheritability 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. Wide difference between GCV and PCV was observed for the characters like plant height, effective branch tillers per hill, panicle length, sterility percentage and yield per plant. 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 observed for the characters effective branch tillers per hill. High heritability with low genetic advance was observed for the character days to 50% flowering.

Nandeshwar *et al*. (2010) evaluated twenty five $F_2$ progenies derived from the crosses involving HYV and quality rices during kharif 2005. High GCV and PCV were observed for grain yield plant $^{-1}$, panicle number plant $^{-1}$ and panicle weight. High heritability was observed against all the characters studied excepting panicle weight, grain number panicle $^{-1}$ and grain breadth. Grain yield plant$^{-1}$ showed maximum genetic advance as percentage of mean followed by panicle number plant $^{-1}$, plant height and panicle weight, respectively.

Ghosal *et al*. (2010) evaluated eighteen advanced breeding lines for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Boro season, 2009. All the tested characters showed significant variation. Effective tillers/m$^2$ and spikelet sterility (%) had high genotypic variance, high heritability, high genetic advance and high genotypic coefficient of variation. Effective tillers/m$^2$, panicle length (cm), thousand grain weight (g) and growth duration (days) showed significant positive association with grain yield.

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 high heritability coupled with high to moderate genetic advance as % of mean was observed on plant height, seed yield per plant, biological yield, harvest index, test weight and number of spikelets per panicle suggesting preponderance of additive gene action in the expression of these characters.

Jayasudha and Sharma (2010) carried out an experiment on 47 rice genotypes revealed that a high genotypic and phenotypic coefficient of variation was observed for grain yield per plant, harvest index, pollen fertility (%) and spikelet fertility (%). Characters like pollen fertility (%), spikelet fertility (%), days to 50% flowering and grain yield per plant showed high value of heritability coupled with high genetic advance.

Anbanandan *et al.* (2009) studied four crosses of $F_2$ generation were advanced to $F_3$ and $F_4$ 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 $F_3$ and $F_4$ generations for almost all the economic characters studied including yield. This cross also recorded increased performance from $F_3$ to $F_4$ 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 $F_3$ and $F_4$ 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 $F_3$ and $F_4$ 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.

Bisne *et al*. (2009) conducted an experiment on 44 rice genotype in Raipur, Chhattisgarh in *kharif* 2005 for 13 characters. Low, moderate, and high genotypic and phenotypic coefficient of variations were observed. High genotypic and phenotypic coefficient of variations were expressed by harvest index, total number of filled spikelets per panicle, 100-grain weight and spikelet fertility percentage. 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.

Vange (2008) conducted 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 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.

Karad and Pol (2008) observed a wide range of variability in yield and yield contributing characters. The PCV was slightly higher than GCV 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.

Kole *et al*. (2008) studied variability for twelve morphological characters were studied on 18 morphologically distinct mutants in M4 generation along with their two mother genotypes (IET 14142 and IET 14143), which were developed from Tulaipanja, an aromatic non-basmati rice cultivar of West Bengal. Genotypic and phenotypic coefficients of variation were high for flag leaf angle and panicle number; moderate for grain number per panicle, straw weight, harvest index and grain yield per plant; and low for days to flower, plant height, panicle length, spikelet number, spikelet fertility (%) and test weight. High heritability accompanied by high to moderate genetic advance for flag leaf angle, panicle number, grain number, straw weight and grain yield indicated the predominance of additive gene action for the expression of these characters.

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 $F_2$ and $F_3$ segregating populations of six crosses of rice for six yield and yield component characters. The $F_2$ populations of the cross $P_1$ $P_3$ 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 $F_3$ population of the cross $P_2$ $P_1$ 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.

A study conducted by Singh *et al.* (2006) to estimate genetic variability and correlation studies in rice during kharif in Khudwani, Anantnag district, Jammu and Kashmir. Thirty-two genotypes were evaluated for days to 50% heading, days to maturity, plant height, panicles per plant, biological yield, grain yield and harvest index. A wide range of variation was recorded for all traits. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability and high genetic advance were recorded for plant height, indicating the predominance of additive gene action for this trait. Genotypic and phenotypic correlation studies indicated that biological yield per plant and harvest index were significantly and positively correlated with yield. Thus, selection for these two traits might be helpful in enhancing rice grain yield.

Observed (Elayaraja *et al.*, 2005) high heritability associated with moderate to high genetic advance as a percent of mean for number of productive tillers, panicle length, number of grains per panicle, 100 grain weight and grain yield per plant in $M_2$ generation.

Satish *et al.* (2003) genetic variability, heritability and genetic advance were studied in 200 scented rice genotypes including one non-scented check, Ratna for grain yield and its nine attributing characters. High GCV and PCV values spikelets/panicle, number of grains/ panicle and grain yield/plant. High heritability along with high genetic advance was observed for number of spikelets/panicle, number of grains/panicle, grain yield/plant followed by other characters. Emphasis should be given on these characters while selecting scented rice varieties to improve grain yield.

Nayak *et al.*, (2001) observed by () genetic variability for grain yield and nine yield contributing characters in 200 scented rice genotypes in Cuttack, Orissa. They obtained high estimates of genotypic and phenotypic coefficients of variation for number of spikelets per panicle, number of panicles per plant, number of grains per panicle and grain yield per plant. Further they also observed high heritability and high genetic advance for number of spikelets per panicle, number of grains per panicle and grain yield per plant.

Singh *et al.* (2002) evaluated 52 genotypes of low land rice for 15 characters and reported high genotypic and phenotypic variances for grain yield per plant, panicle weight, number of grains per panicle and number of branches per panicle, medium for panicle length, 1000-seed weight and low for panicle length and milling percent. They also found that heritability in broad sense ranged from 3.61% for number of effective tillers per plant to 99.55% for grain length. High heritability with high genetic advance was recorded for number of grains per panicle followed by panicle weight and grain yield per plant.

Genetic variability heritability and expected genetic advance were estimated for length of grain, breadth of grain, L/B ratio, kernel elongation, gel consistency, amylase content and gelatinization in rice. The experimental material included 150 rice germplasm categorized into three groups. *i.e*. long slender, medium slender and short slender. Maximum variability was recorded for test weight in long slender and medium slender groups and for amylase content in medium and short slender groups. Water updake, volume expansion ratio, kernel elongation and gel consistency appeared to be the useful traits in all the groups because high heritability and high genetic gain were recorded for these characters (Yadav *et al.,* 2002).

Bidhan *et al.,* (2001) evaluated 25 medium duration genotypes for eight traits and observed high phenotypic and genotypic variances for grain yield, followed by number of filled grains per panicle. They recorded heritability which ranged from 50% (grain yield per hill) to 90% (grain breadth). Genetic advance as percent of mean was highest for number of filled grains per panicle (70.34), followed by grain yield (68.72). Number of filled grains per panicle, 1000-grain weight, grain length and breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance.

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 coefficient

Ganapati *et al*. (2014) evaluated twenty five rice genotypes for yield and yield contributing characters to observe their associations during Amon season, 2010. Tiller per hill, plant height and thousand grain weights showed significant positive association with grain yield.

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.

Satheeshkumar *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.

Rangare *et al.* (2012) evaluated forty exotic and Indian rice germplasm including one local check for their efficiency with respect to eleven yield and yield contributing characters from Kharif 2009 under normal conditions. Associated studies have indicated that for an improvement in grain yield the intensive selection should be positive for biological yield per plant, number of fertile tillers per plant, number of spikelets per panicle, test weight, panicle length and days to maturity as these traits showed significantly strong positive association with grain yield, but days to 50% flowering, days to initial flowering, harvest index and plant height through had positively non significant association with grain 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.

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.

Selvaraj *et al.* (2011) studied variability, correlation and path coefficient on 21 rice genotypes for grain yield and other yield attributes. Result of correlation analysis revealed that characters like plant height, number of tillers/plant, number of productive tillers/plant, panicle length, filled grains per panicle and test weight had significant positive association with grain yield.

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. Grain yield was found to be positively and significantly correlated with grains per panicle, days to maturity, panicle weight, number of productive tillers, days to flowering, plant height, panicle length indicating the importance of these characters for yield improvement in this population.

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.

Nandeshwar *et al*. (2010) evaluated twenty five $F_2$ progenies derived from the crosses involving HYV and quality rices during kharif 2005. Grain yield plant $^{-1}$ possessed significant positive correlation with panicle number plant $^{-1}$, panicle weight and grain number panicle $^{-1}$ while it had significant negative correlation with plant height.

Nandan *et al*. (2010) made an experiment to evaluate thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. The correlation studies revealed strong positive association of yield with days to 50 % flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility.

Ghosal *et al*. (2010) evaluated eighteen advanced breeding lines for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Boro season, 2009. Effective tillers/m$^2$, panicle length (cm), thousand grain weight (g) and growth duration (days) showed significant positive correlation with grain yield.

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.

In a genetic study conducted by Jayasudha *et al.* (2010) the results indicated that spikelet fertility (%) and harvest index showed positive and significant correlation with seed yield per plant both at genotypic and phenotypic levels.

Wattoo *et al.* (2010) conducted an experiment in order to determine the associations among yield components and their direct and indirect influence on grain yield of rice. For this purpose, 30 genotypes collected from different sources were tested. The phenotypic correlations among the yield traits were estimated. Grain yield was significantly correlated with its component characters; number of productive tillers per plant, number of grains per panicle and flag leaf area.

Sabesan *et al*. (2009) evaluated fifty four rice varieties of diverse origin for correlation analysis under coastal saline low lands. The 100 grain weight was positively significantly correlated with plant height, grains per panicle and grain breadth.

Kole *et al*. (2008) studied correlation for twelve morphological characters were studied on 18 morphologically distinct mutants in M4 generation along with their two mother genotypes (IET 14142 and IET 14143), which were developed from Tulaipanja, an aromatic non-basmati rice cultivar of West Bengal. Grain yield was found to be positively and significantly correlated with plant height, panicle number per plant, straw weight and harvest index at both genotypic and phenotypic levels indicating the importance of these characters for yield improvement in this population.

Karad and Pol (2008) observed a wide range of variability in yield and yield contributing characters. The grain yield was positively correlated with almost all the characters except 1000-grain weight at both genotypic and phenotypic levels. Genotypic correlation estimates were higher than phenotypic correlation with grain yield plot$^{-1}$.

Twenty modern Boro rice varieties were evaluated with a view to find variability and genetic association for grain yield and yield components characters by Rokonuzzaman *et al.* (2008). The experiment was conducted at BRRI farm during the Boro season of 2004. Genotypic and Phenotypic correlation among these characters were computed. Both genotypic and phenotypic correlation coefficients were significant between plant height and number of effective tillers per plant followed by panicle length. There was a positive significant correlation between yield and number of effective tillers per plant followed by percent filled grain per panicle.

Vange (2008) conducted 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.

Mustafa *et al.* (2007) evaluated fourteen rice (*Oryza sativa* L.) genotypes at the Gezira Research Station Farm (GRSF), Sudan for correlation coefficient between yield and yield components among phenotypic markers and polygenic trait analysis. Phenotypic correlations between grain yield and number of filled grain panicle$^{-1}$, number of panicle m$^{-2}$ and 1000 grain weight were 0.52, 0.36 and 0.27, respectively. These results suggested that improvement in yield could be attained by selecting rice plants for higher number of filled grain panicle$^{-1}$, number of panicle m$^{-2}$, and 1000 grain weight.

Agahi *et al.* (2007) conducted an experiment to investigate correlation coefficient of grain yield and sixteen yield-related traits among 25 lines. The results showed that grain yield was significantly correlated with days to heading, total tillers, number of productive tillers, days to maturity, number of grain per panicle, flag leaf length, flag leaf width 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. 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 coefficient analysis

Ganapati *et al.* (2014) evaluated twenty five genotypes of rice for yield and yield contributing characters to observe their direct and indirect effect on yield during Aman season, 2010. From the results of path analysis it was evident that direct positive effects contributed by tiller per hill, number of filled grain per panicle and thousand grain weight were high indicating that among the component traits, these four characters contributed maximum for grain yield in rice.

Satheesh kumar *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.

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

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.

In order to estimate genetic variability and relationships among some agronomic traits of rice an experiment were conducted with 30 varieties of rice under two irrigation regimes by Abarshahr *et al*. (2011). Path analysis for paddy yield indicated that the number of spikelet per panicle and flag leaf length had positive direct effects and days to complete maturity and plant height had negative direct effects on paddy yield under optimum irrigation condition, while flag leaf width and number 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.

Hairmansis *et al.* (2011) evaluated agronomic characters and grain yield of nine advanced rice breeding lines and two rice varieties in a series of experiments in tidal swamp areas, Karang Agung Ulu Village, Banyuasin, South Sumatra, for four cropping seasons in dry season (DS) 2005, wet season (WS) 2005/2006, DS 2006, and DS 2007. Result from path analysis revealed that the following characters had positive direct effect on grain yield, i.e. number of productive tillers per hill ($p = 0.356$), number of filled grains per panicle ($p = 0.544$), and spikelet fertility ($p = 0.215$). Plant height had negative direct effect ($p = -0.332$) on grain yield, while maturity, number of spikelets per panicle, and 1000-grain weight showed negligible effect on rice grain yield.

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.

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) evaluated eighteen advanced breeding lines for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Boro season, 2009. Path coefficient analysis revealed that effective tillers/m$^2$, thousand grain weight (g) and growth duration (days) had higher direct effects on yield (t/ha).

Yadav *et al.* (2010) carried out a field experiment was to establish the extent of association between yield and yield components and others characters in rice. They found that the path coefficient at genotypic level revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of spikelets per panicle, plant height and test weight had direct positive effect on seed yield per hill, indicating these are the main contributors to yield.

Nandeshwar *et al*. (2010) evaluated twenty five $F_2$ progenies derived from the crosses involving HYV and quality rices during kharif 2005. Panicle number plant $^{-1}$ imparted maximum direct effect on grain yield followed by grain number panicle $^{-1}$, 1000 grain weight and panicle length in this regard.

Nandan *et al*. (2010) made an experiment to evaluate thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. The result of path analysis indicated that the number of grains per panicle had maximum direct effect on grain yield per plant followed by kernel length after cooking (KLAC), days to 50 % flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking (KBAC ).

Studies on genetic variability, character association and path-coefficient analysis were conducted on forty seven (47) rice genotypes by Jayasudha *et al.* (2010). Results of path-coefficient analysis revealed that productive tillers per plant had the highest positive direct effect on grain yield followed by harvest index, spikelet fertility (%), pollen fertility (%) and plant height.

Wattoo *et al.* (2010) conducted an experiment in order to determine the associations among yield components and their direct and indirect influence on grain yield of rice. For this purpose, 30 genotypes collected from different sources were tested. Path analysis revealed that days to maturity had the highest direct effect (0.751) on grain yield per plant. In addition, the yield components had positive direct effect on grain yield except the days to heading (-0.834). The order of yield components was the number of productive tillers per plant, flag leaf area and 1000 grain weight.

Rokonuzzaman *et al.* (2008) evaluated twenty modern Boro rice varieties with a view to find variability and genetic association for grain yield and yield components characters. The experiment was conducted at BRRI farm during the Boro season of 2004. Path coefficient showed that number of effective tiller per plant and plant height are the characters that contribute largely to grain yield.

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

Karad *et al*. (2008) observed a wide range of variability in yield and yield contributing characters. Path coefficient analysis revealed that length of panicle had the highest positive direct effect followed by number of panicles, number of tillers plant$^{-1}$ and number of mature panicles whereas the characters plant height, number of immature panicles and 1000 grain weight had the negative direct effect via indirect effect on grain yield plot$^{-1}$.

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

Iftekharuddaula *et al*. (2001) studied twenty-four modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for grain yield and its component characters. Path analysis revealed that higher number of grains/panicle, bold grains, more panicles/m$^2$ 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 details of the materials and methods employed have been presented below:

## 3.1 Experimental site and experimental period

The present research work was carried out in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during December, 2013- May, 2014. The location of the site is 23° 74' N latitude and 90° 35' E longitude with an elevation of 8.2 meter from sea level (Appendix I).

## 3.2 Climate and soil

The experimental site was situated in the sub-tropical zone. The soil of the experimental site lies in Agroecological region of “Madhupur Tract” (AEZ No. 28). It’s top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 6.1 and organic carbon content is 0.82%. The record of air temperature, humidity, rainfall and sunshine (hr) during the period of experiment were noted from the SAU Weather Station, Sher-e-Bangla nagar Dhaka-1207 (Appendix II and III).

## 3.3 Planting materials

Twenty nine rice genotypes were used for the present study. Among twenty nine rice genotypes, twenty seven genotypes were $F_5$ materials and two were check materials. The physically healthy seeds of these genotypes were obtained from the Department of Genetics and Plant Breeding (SAU), Dhaka. The name and origin of these genotypes are presented in Table 1.

## 3.4 Germination of seed

Seed of all collected 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.

**Table 1. List of the genotypes used in the experiment with their origin and source**

| Sl. No. | Genotypes | Origin of genotypes | Source |
|---|---|---|---|
| 1 | G1 | BR 21 × BR 26 $F_5$ S6 P1 P6 | |
| 2 | G2 | BR 21 × BR 26 $F_5$ S6 P3 P1 | |
| 3 | G3 | BR 21 × BR 26 $F_5$ S6 P9 P7 | SAU |
| 4 | G4 | BR 21 × BRRI Dhan 28 $F_5$ S5 P2 P1 | |
| 5 | G5 | BR 21 × BRRI Dhan 28 $F_5$ S5 P4 P1 | |
| 6 | G6 | BR 21 × BRRI Dhan 28 $F_5$ S5 P4 P2 | |
| 7 | G7 | BR 21 × BRRI Dhan 28 $F_5$ S5 P6 P3 | |
| 8 | G8 | BR 21 × BRRI Dhan 28 $F_5$ S5 P7 P6 | |
| 9 | G9 | BR 21 × BRRI Dhan 29 $F_5$ S6 P1 P1 | |
| 10 | G10 | BR 21 × BRRI Dhan 29 $F_5$ S6 P2 P4 | |
| 11 | G11 | BR 21 × BRRI Dhan 29 $F_5$ S6 P6 P2 | |
| 12 | G12 | BR 21 × BRRI Dhan 36 $F_5$ S1 P4 P1 | |
| 13 | G 13 | BR 24 × BR 26 $F_5$ S5 P1 P3 | |
| 14 | G 14 | BR 24 × BR 26 $F_5$ S5 P3 P2 | |
| 15 | G 15 | BR 24 × BR 26 $F_5$ S5 P4 P4 | |
| 16 | G 16 | BR 24 × BRRI Dhan 36 $F_5$ S8 P1 P1 | |
| 17 | G 17 | BR 26 × BRRI Dhan 28 $F_5$ S1 P7 P2 | |
| 18 | G 18 | BR 26 × BRRI Dhan 28 $F_5$ S1 P9 P3 | |
| 19 | G 19 | BR 26 × BRRI Dhan 28 $F_5$ S1 P9 P4 | |
| 20 | G 20 | BR 26 × BRRI Dhan 29 $F_5$ S6 P3 P1 | |
| 21 | G 21 | BR 26 × BRRI Dhan 29 $F_5$ S6 P3 P2 | |
| 22 | G 22 | BRRI Dhan 28 × BRRI Dhan 29 $F_5$ S2 P2 P1 | |
| 23 | G 23 | BRRI Dhan 28 × BRRI Dhan 29 $F_5$ S2 P3 P3 | |
| 24 | G 24 | BRRI Dhan 28 × BRRI Dhan 29 $F_5$ S2 P4 P3 | |
| 25 | G 25 | BRRI Dhan 29 × BRRI Dhan 36 $F_5$ S5 P2 P4 | |
| 26 | G 26 | BRRI Dhan 29 × BRRI Dhan 36 $F_5$ S5 P2 P7 | |
| 27 | G 27 | BRRI Dhan 29 × BRRI Dhan 36 $F_5$ S5 P3 P1 | |
| 28 | G 28 | BRRI Dhan 29 | BRRI |
| 29 | G 29 | BRRI Dhan 28 | |

### 3.5 Seedbed preparation and rising seedling

The irrigated land was prepared thoroughly by three times ploughing and cross ploughing followed by laddering. Weeds and stubbles were removed. Twenty nine separate strips were made and sprouted seeds were sown on 5 December of 2013. The seedlings were raised by maintaining irrigation with regular intervals and protecting from birds and insects and infestation of pest and diseases.

### 3.6 Preparation of main land and application of manure and fertilizer

Cow dung was applied to the experimental field and the plot was ploughed thoroughly by two ploughing and cross ploughing followed by harrowing with a tractor drawn disc plough to attain a good puddle. Four days later the final ploughing and cross ploughing were done and weeds and stubbles were removed. First split of urea and full portion of all other fertilizers recommended by BRRI were added to the main land before final ploughing. Urea, TSP, MP, Gypsum and Zinc Sulphate were applied at the rate 261.45, 97.11, 119.52, 112.05, and 11.205 kg/ha, respectively. The second, third and fourth splits of urea was applied at 15, 30 and 45 days after transplanting (DAT), respectively (BRRI, 2014).

### 3.7 Experimental design and layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The total area of the experiment was 30 m×12.2 m = 366 $m^2$. The experimental field was divided into three blocks, representing three replications. Each replication size was 30m×3.4m, and the distance between replication was 50 cm.

### 3.8 Transplanting

Thirty days old and healthy seedlings were transplanted to the main field on January 6, 2014 followed by proper irrigation. One seedling per hill was transplanted by maintaining 25 cm × 20 cm spacing from row to row and plant to plant, respectively. Twenty nine rice genotypes were distributed in each of the replication through randomization process.

### 3.9 Intercultural operations

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

### 3.9.1 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.

### 3.9.2 Gap filling

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

### 3.9.3 Weeding

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

### 3.9.4 Top dressing

After basal dose, the remaining doses of urea were top-dressed in two equal installments. The fertilizers were applied on both sides of seedlings rows with the soil. Field view of the experiment is presented in Plate 1.

### 3.9.5 Plant Protection

Furadan 5G @1g per square meter were applied at active tillering stage and panicle initiation stage for controlling the stem borer and later on other insecticides were applied as and when necessary.

### 3.10 Crop harvesting

Harvesting was done from 25th April to 6th May, 2014 depending 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.

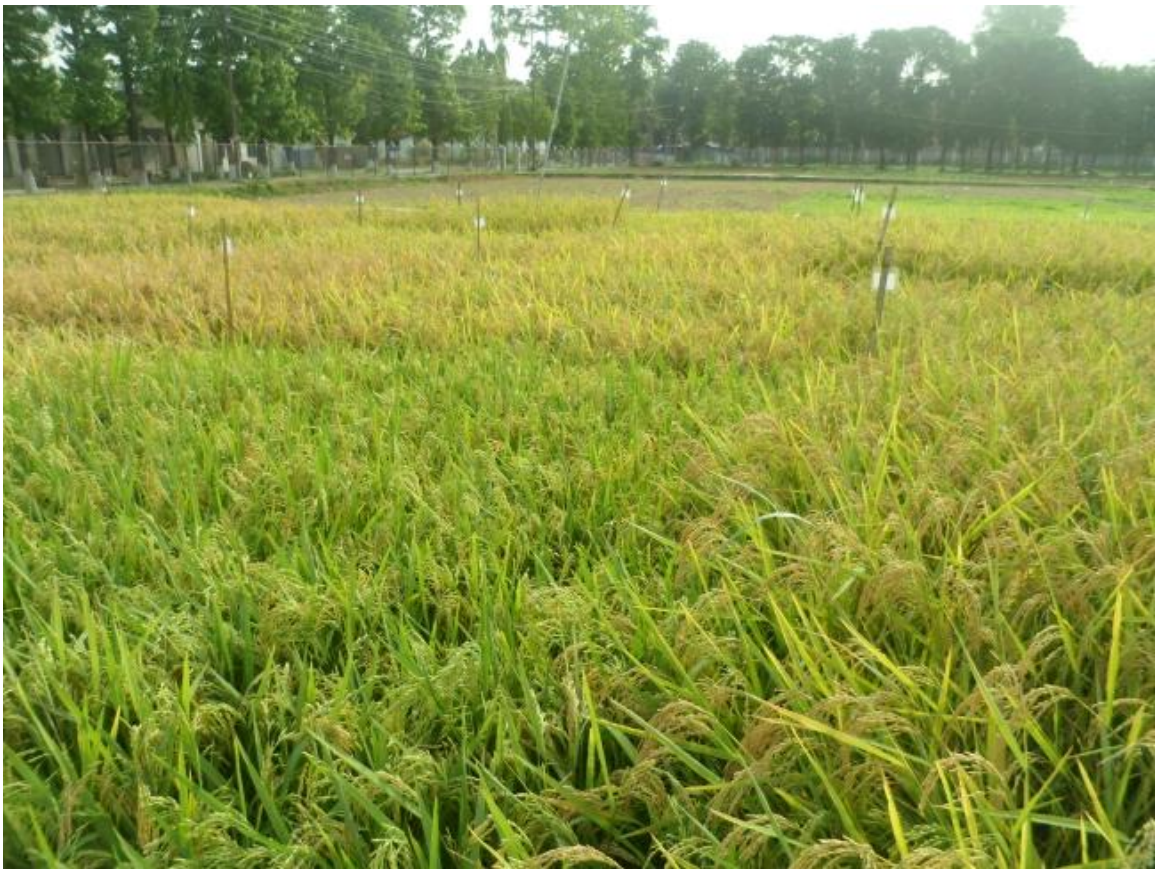

**Plate 1. Field view of the experiment**

### 3.11 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-

#### 3.11.1 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.

#### 3.11.2 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.

#### 3.11.3 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.

#### 3.11.4 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.

#### 3.11.5 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.

#### 3.11.6 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.

#### 3.11.7 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.

### 3.11.8 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.

### 3.11.9 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.

### 3.11.10 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.

### 3.11.11 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.

### 3.11.12 Yield per plant (gm)

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

### 3.11.13 Thousand seed weight (gm)

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

### 3.11.14 Yield per hectare (t/ha)

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

## 3.12 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 a software based 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).

### 3.12.1 Estimation of variability

### 3.12.1.1 Estimation of genotypic and phenotypic variance

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

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

Where, MSG = Mean sum of square for genotypes
MSE = Mean sum of square for error and
r = Number of replication

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

Where, $\delta^2 g$ = Genotypic variance,
$\delta^2 e$ = Environmental variance = Mean square of error

### 3.12.1.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the following formula (Burton, 1952).

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

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

Where, GCV = Genotypic co-efficient of variation
PCV = Phenotypic co-efficient of variation
$\delta_g$ = Genotypic standard deviation
$\delta_p$ = Phenotypic standard deviation
$\bar{x}$ = Population mean

### 3.12.1.3 Estimation of heritability

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

$$h^2{}_b(\%) = \frac{\delta^2{}_g}{\delta^2{}_p} \times 100$$

Where, $h^2{}_b$ = Heritability in broad sense

$\delta^2{}_g$ = Genotypic variance

$\delta^2{}_p$ = Phenotypic variance

### 3.12.1.4 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).

$$GA = \frac{\delta^2{}_g}{\delta^2{}_p} \,.\, K \,.\, \delta_p$$

Where, GA = Genetic advance

$\delta^2{}_g$ = Genotypic variance

$\delta^2{}_p$ = Phenotypic variance

$\delta_p$ = Phenotypic standard deviation

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

### 3.12.1.5 Estimation of genetic advance in percentage of mean

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

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

### 3.12.2 Estimation of simple correlation co-efficient

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

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

### 3.4.10.3 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 Chaudhary (1985) using simple correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect effects of independent variables on the dependent variable.

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

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

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

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

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

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

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

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

Riy = Correlation of the character with yield.

# CHAPTER IV

# RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among twenty nine $F_5$ materials of *Oryza sativa* genotypes and also to study the correlation and path co-efficient for seed yield and different yield contributing characters. The data were recorded on different characters such as days to 50% flowering, days to maturity, plant height (cm), number of total tillers per plant, number of effective tillers per plant, panicle length, number of primary branches per panicle, number of secondary branches per panicle, total number of spikelet per panicle, number of filled grains per panicle, number of unfilled grains per panicle, yield per plant (gm) , thousand seed weight (gm) and yield per hectare (t/ha) . The data were statistically analyzed and thus obtained results are described below under the following heads:

## 4.1 Variability among the twenty nine genotypes of rice for yield and related traits

The analysis of variance (ANOVA) of the data on different yield components and yield of twenty nine genotypes of *Oryza sativa* are given in Table 2. The mean performance, range and CV (%) over three replications for all the characters of 29 O*ryza sativa* genotypes are presented in Table 3a and Table 3b. Phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters are presented in Table 4.

### 4.1.1. Days to flowering

There were significant variations among the genotypes (25.61**) for days to flowering (Table 2 and Plate 2, 3). Among 29 genotypes, the lowest (118 days) days to 50% flowering were observed in G7 which is very closed to G4 (118.3 days) , G12 (118.3 days) and the highest (129 days) was observed in G28 (Table 3a). Whereas the G28 (BRRI Dhan29) and G29 (BRRI Dhan28) were recorded with days to 50% flowering 122.00 days and 121.58 days, respectively. The genotypes G7, G4 and G12 were taken less number of days to 50% flowering than the checks varieties.

Phenotypic and genotypic variance for days to flowering was observed as 10.38 and 7.62, respectively with less difference between them, suggested less influence of environment on the expression of the genes controlling this trait. The less difference between phenotypic coefficient of variation (5.56%) and genotypic coefficient of variation (4.76%) (Table 4) suggested that days to 50% flowering is least influenced by environment. Less difference between PCV and GCV was also observed by Chakraborty and Chakraborty (2010), Vange (2008) in rice.

### 4.1.2 Days to maturity

Significant variations were observed among the genotypes (48.28**)for days to maturity (Table 2). The highest days to maturity was taken in G28 (155.30 days) and the minimum days to maturity was taken in G19 (141.3 days), G29 (141.3 days) and G10 (141.7 days) among 29 genotypes (Table 3a). The genotypes G19, G29 and G10 were shown lower days to maturity than the checks G28 (BRRI Dhan29) (155.30 days) but similar to G29 (BRRI Dhan28) (141.30 days). Variation among different genotypes for days to maturity presented in Plate 4.

The phenotypic and genotypic variance for days to maturity was observed (21.28) and (13.5) respectively with high differences between them, suggested that the environment had significant role in the expression of trait . The phenotypic coefficient of variation (7.96%) was higher than genotypic coefficient of variation (6.34%) (Table 4) suggested that environment has high influence on the expression of the genes controlling this trait. Similar result for this trait was also observed by Ketan and Sarkar (2014) in aman rice.

### 4.1.3 Plant height (cm)

The highest plant height was observed in G20 (128.80 cm) where as the minimum plant height was observed in G25 (83.12 cm) which is near to G23 (84.82 cm) (Table 3a). The genotypes G25 (83.12 cm), G23 (84.82 cm) and G22 (87.53 cm) were shown lower plant height than two checks G28 (BRRI Dhan29) (93.14 cm) and G29 (BRRI Dhan28) (96.59 cm).Variation in plant height is presented in Plate 5.

Phenotypic variance and genotypic variance were observed as 148.48 and 112.35 respectively. The phenotypic variance appeared to be higher than the genotypic

## Table 2. Analysis of variances for fourteen important characters of 29 genotypes of *Oryza sativa* L.

| Source of variation | df | Mean sum of squares (MSS) | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | characters | | | | | | | | | | | | | |
| | | DF | DM | PH (cm) | NTT | NET | LP (cm) | NPBP | NSBP | TSP | NFG/P | NUFGP | Y/P (gm) | TSW (gm) | Y/H (t/ha) |
| Replication | 2 | 3.8 | 10.48 | 16.65 | 16.17 | 13.36 | 0.11 | 0.02 | 6.73 | 502.34 | 557.95 | 159.65 | 3.62 | 2.06 | 0.16 |
| Genotype | 28 | 25.61** | 48.28** | 373.18** | 11.27** | 10.41** | 2.78** | 2.84** | 32.54** | 1683.43** | 2392.05** | 901.57** | 136.68** | 10.04** | 5.93** |
| Error | 56 | 2.75 | 7.78 | 36.12 | 2.37 | 2.17 | 0.781 | 0.72 | 8.33 | 351.37 | 305.72 | 74.379 | 31.27 | 2.74 | 1.3 |
| CV% | | 1.37 | 1.91 | 5.73 | 10.7 | 10.84 | 3.76 | 8.65 | 9.73 | 11.06 | 12.1 | 34.08 | 16.27 | 6.85 | 16.84 |

** = significant at the 0.01 level. * = significant at the 0.05 level

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

**Table 3a. Mean performance of 29 genotypes of *Oryza sativa* L. in respect of seven important characters**

| Genotype | DF | DM | PH (cm) | NTT | NET | LP (cm) | NPBP |
|---|---|---|---|---|---|---|---|
| G1 | 124.00 | 151.30 | 107.00 | 13.73 | 12.40 | 21.39 | 8.73 |
| G2 | 123.00 | 150.30 | 109.70 | 13.30 | 12.57 | 23.32 | 8.17 |
| G3 | 127.00 | 152.70 | 111.80 | 14.57 | 13.63 | 21.95 | 8.10 |
| G4 | 118.30 | 144.30 | 124.50 | 13.80 | 12.73 | 24.49 | 11.97 |
| G5 | 119.70 | 143.70 | 112.60 | 12.53 | 12.13 | 23.44 | 8.77 |
| G6 | 119.30 | 142.00 | 111.60 | 14.57 | 13.70 | 24.11 | 10.57 |
| G7 | 118.00 | 145.30 | 118.50 | 12.43 | 11.33 | 24.03 | 9.00 |
| G8 | 120.70 | 150.00 | 114.90 | 15.27 | 14.60 | 24.62 | 10.03 |
| G9 | 119.00 | 144.00 | 104.80 | 13.17 | 12.77 | 22.89 | 9.90 |
| G10 | 119.00 | 141.70 | 92.02 | 17.63 | 16.13 | 22.28 | 9.77 |
| G11 | 119.30 | 142.70 | 101.90 | 11.73 | 11.60 | 23.87 | 11.47 |
| G12 | 118.30 | 143.00 | 100.50 | 16.00 | 14.80 | 22.75 | 10.63 |
| G13 | 125.70 | 151.00 | 111.70 | 12.67 | 11.60 | 21.39 | 9.73 |
| G14 | 126.70 | 152.30 | 115.30 | 12.63 | 12.13 | 24.44 | 10.37 |
| G15 | 126.30 | 149.00 | 108.90 | 13.63 | 12.70 | 23.88 | 9.50 |
| G16 | 120.00 | 143.00 | 108.10 | 9.20 | 9.00 | 23.75 | 11.87 |
| G17 | 121.00 | 143.00 | 109.80 | 15.73 | 15.83 | 24.76 | 9.60 |
| G18 | 120.30 | 143.70 | 105.90 | 16.17 | 15.67 | 23.94 | 9.03 |
| G19 | 121.00 | 141.30 | 93.71 | 16.47 | 15.87 | 23.81 | 10.19 |
| G20 | 119.70 | 147.30 | 128.80 | 12.73 | 11.67 | 22.61 | 9.30 |
| G21 | 119.00 | 143.70 | 108.10 | 14.47 | 13.43 | 23.87 | 9.23 |
| G22 | 121.00 | 144.00 | 87.53 | 16.87 | 16.20 | 24.06 | 10.60 |
| G23 | 123.30 | 144.00 | 84.82 | 13.43 | 12.77 | 23.36 | 9.97 |
| G24 | 121.70 | 149.30 | 104.30 | 14.53 | 14.27 | 23.83 | 10.20 |
| G25 | 121.00 | 145.70 | 83.12 | 18.23 | 17.20 | 21.88 | 9.10 |
| G26 | 121.70 | 150.70 | 94.34 | 14.37 | 13.53 | 23.70 | 11.07 |
| G27 | 120.70 | 147.30 | 99.47 | 15.00 | 14.23 | 23.26 | 9.43 |
| G28 | 129.00 | 155.30 | 93.14 | 14.07 | 13.93 | 24.19 | 9.83 |
| G29 | 122.00 | 141.30 | 96.59 | 16.77 | 15.93 | 24.80 | 9.23 |
| Mean | 121.58 | 146.31 | 104.95 | 14.33 | 13.60 | 23.47 | 9.84 |
| Max | 129.00 | 155.30 | 128.80 | 18.23 | 17.20 | 24.80 | 11.97 |
| Min | 118.00 | 141.30 | 83.12 | 9.20 | 9.00 | 21.39 | 8.10 |
| LSD | 2.716 | 4.562 | 2.519 | 2.519 | 2.411 | 1.445 | 1.392 |
| CV% | 1.37 | 1.91 | 5.73 | 10.7 | 10.84 | 3.76 | 8.65 |

DF = days to flowering, DM = days to maturity, PH = plant height, NTT = number of total tillers per plant, NET = number of effective tillers per plant, LP = Length of panicle, NPBP = number of primary branches per panicle

**Table 3b. Mean performance of 29 genotypes of *Oryza sativa* L. in respect of seven important characters**

| Genotype | NSBP | TSP | NFG/P | NUFG/P | Y/P (gm) | TSW (gm) | Y/H (t/ha) |
|---|---|---|---|---|---|---|---|
| G1 | 31.43 | 153.00 | 102.50 | 64.47 | 19.00 | 21.76 | 3.91 |
| G2 | 27.47 | 144.80 | 115.60 | 29.50 | 27.93 | 22.50 | 5.52 |
| G3 | 24.77 | 151.50 | 103.50 | 47.97 | 27.87 | 22.48 | 5.48 |
| G4 | 31.10 | 187.30 | 98.53 | 89.90 | 31.80 | 26.40 | 6.17 |
| G5 | 28.37 | 159.60 | 130.50 | 29.17 | 30.80 | 25.81 | 6.38 |
| G6 | 28.70 | 164.60 | 136.30 | 31.63 | 35.53 | 28.07 | 7.42 |
| G7 | 27.03 | 131.30 | 97.90 | 35.07 | 23.27 | 27.24 | 4.70 |
| G8 | 33.43 | 166.90 | 153.70 | 13.17 | 48.20 | 25.84 | 10.19 |
| G9 | 31.13 | 197.20 | 183.70 | 13.57 | 35.73 | 23.36 | 7.01 |
| G10 | 25.83 | 154.90 | 142.20 | 12.67 | 36.47 | 21.41 | 6.81 |
| G11 | 30.47 | 183.80 | 173.50 | 10.40 | 38.20 | 27.58 | 7.52 |
| G12 | 25.40 | 139.60 | 115.20 | 24.43 | 29.87 | 25.24 | 5.59 |
| G13 | 27.43 | 161.60 | 132.00 | 22.57 | 34.33 | 23.48 | 6.78 |
| G14 | 37.53 | 238.10 | 199.00 | 36.80 | 36.40 | 21.08 | 7.21 |
| G15 | 32.03 | 185.10 | 164.20 | 24.93 | 35.43 | 24.71 | 7.20 |
| G16 | 31.03 | 201.70 | 182.30 | 19.43 | 28.77 | 22.85 | 6.45 |
| G17 | 28.83 | 177.60 | 162.90 | 14.67 | 37.20 | 23.78 | 7.53 |
| G18 | 27.13 | 163.70 | 149.60 | 14.03 | 38.53 | 23.17 | 7.67 |
| G19 | 32.43 | 165.80 | 149.00 | 16.80 | 31.93 | 22.97 | 6.01 |
| G20 | 28.50 | 146.80 | 122.30 | 25.40 | 22.13 | 24.37 | 4.45 |
| G21 | 30.33 | 156.80 | 141.50 | 15.33 | 31.20 | 24.80 | 6.34 |
| G22 | 28.53 | 153.40 | 136.60 | 16.47 | 37.90 | 24.92 | 5.59 |
| G23 | 31.50 | 186.30 | 164.70 | 21.67 | 32.53 | 23.60 | 6.41 |
| G24 | 26.77 | 150.70 | 141.90 | 8.70 | 43.33 | 26.37 | 9.23 |
| G25 | 24.80 | 156.10 | 135.30 | 17.87 | 38.47 | 23.33 | 6.38 |
| G26 | 30.77 | 186.40 | 175.00 | 11.37 | 37.40 | 23.93 | 8.16 |
| G27 | 29.27 | 160.80 | 130.00 | 30.77 | 38.20 | 22.99 | 7.79 |
| G28 | 38.67 | 216.70 | 194.00 | 19.67 | 47.27 | 22.40 | 9.13 |
| G29 | 30.23 | 172.70 | 158.00 | 15.57 | 41.33 | 24.29 | 7.66 |
| Mean | 29.69 | 169.48 | 144.53 | 25.31 | 34.38 | 24.16 | 6.78 |
| Max | 38.67 | 238.10 | 199.00 | 89.90 | 48.20 | 28.07 | 10.19 |
| Min | 24.77 | 131.30 | 97.90 | 8.70 | 19.00 | 21.08 | 3.91 |
| LSD | 4.722 | 30.66 | 28.6 | 14.11 | 9.147 | 2.708 | 1.868 |
| CV% | 9.73 | 11.06 | 12.1 | 34.08 | 16.27 | 6.85 | 16.84 |

NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUFGP = number of filled grains per panicle, Y/P = yield per plant, TSW = thousand seed weight, Y/H = yield per hectare

**Table 4. Estimates of genetic parameters in fourteen important characters of 29 genotypes in *Oryza sativa* L .**

| **Characters** | **$\sigma^2$P** | **$\sigma^2$g** | **PCV (%)** | **GCV(%)** |
|---|---|---|---|---|
| DF | 10.38 | 7.62 | 5.56 | 4.76 |
| DM | 21.28 | 13.5 | 7.96 | 6.34 |
| PH | 148.48 | 112.35 | 21.03 | 18.29 |
| NTT | 5.34 | 2.97 | 3.99 | 2.97 |
| NET | 4.92 | 2.75 | 3.83 | 2.86 |
| LP | 1.45 | 0.67 | 2.08 | 1.41 |
| NPBP | 1.43 | 0.71 | 2.07 | 1.45 |
| NSBP | 16.41 | 8.07 | 6.99 | 4.9 |
| TSP | 795.4 | 444.02 | 48.68 | 36.37 |
| NFG/P | 1001.17 | 695.44 | 54.61 | 45.51 |
| NUFGP | 350.11 | 275.73 | 32.29 | 28.66 |
| Y/P | 66.41 | 35.14 | 14.07 | 10.23 |
| TSW | 5.17 | 2.43 | 3.93 | 2.69 |
| Y/H | 2.85 | 1.54 | 2.91 | 2.14 |

$\sigma^2$p = Phenotypic variance, $\sigma^2$g = Genotypic variance, DF = days to flowering, DM = days to maturity, PH = plant height, NTT = number of total tillers per plant, NET = number of effective tillers per plant, LP = panicle length, NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUFGP = number of filled grains per panicle, Y/P = yield per plant, TSW = thousand seed weight, Y/H = yield per hectare

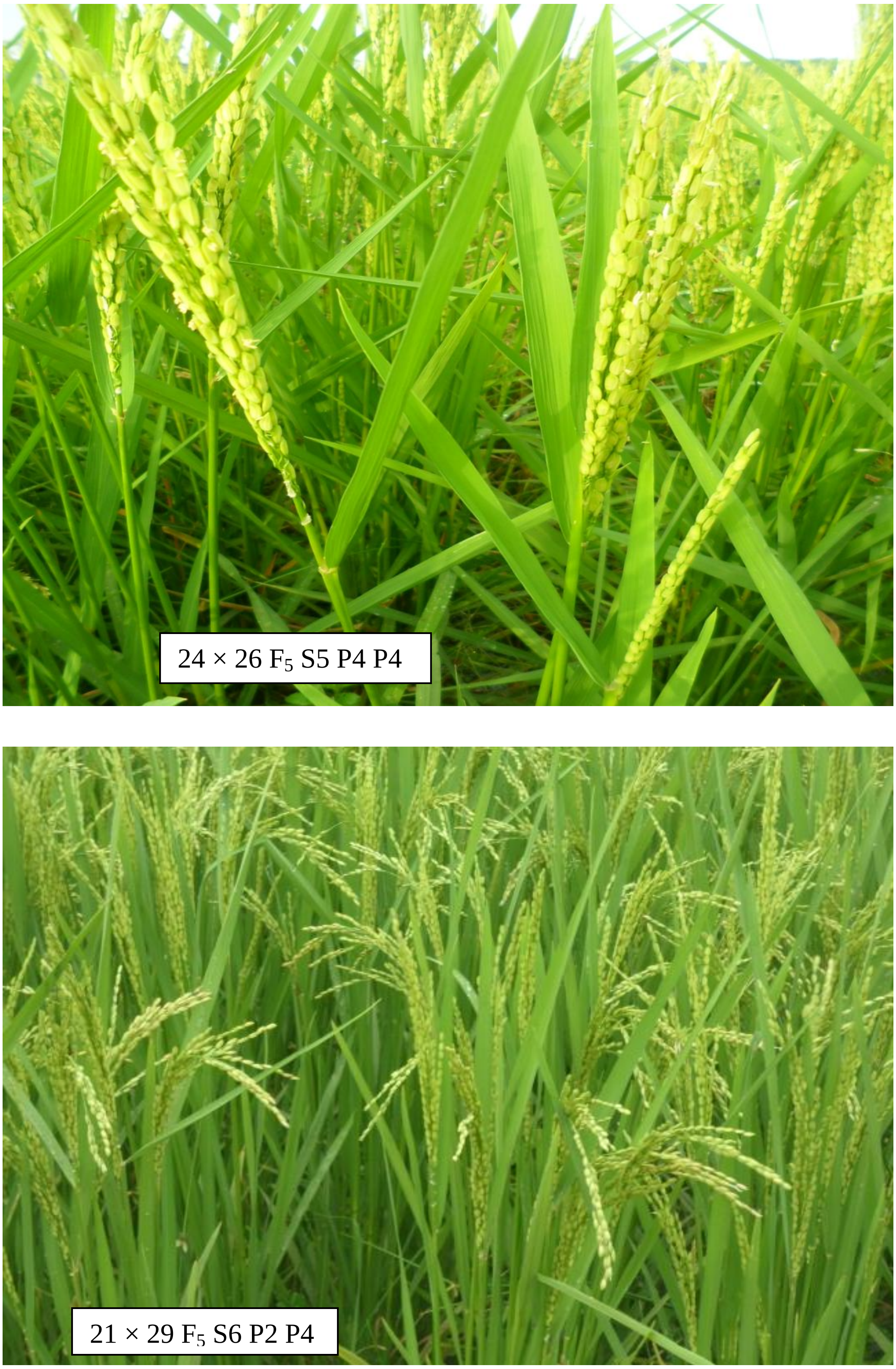

**Plate 2. Photograph showing variation in flowering among different genotypes**

**Plate 3. Photograph showing variation in flowering among different genotypes**

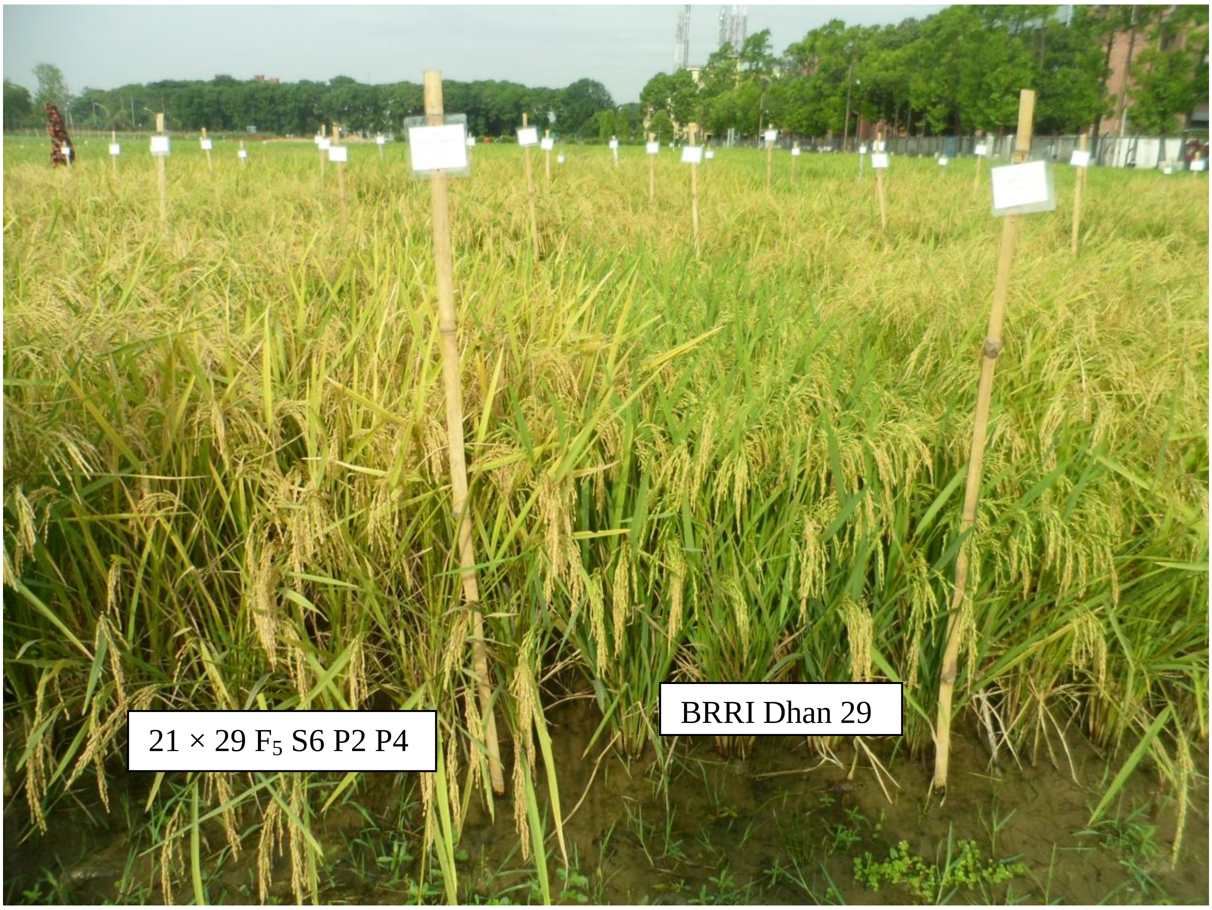

**Plate 4. Photograph to understand differences among genotypes for days to maturity.**

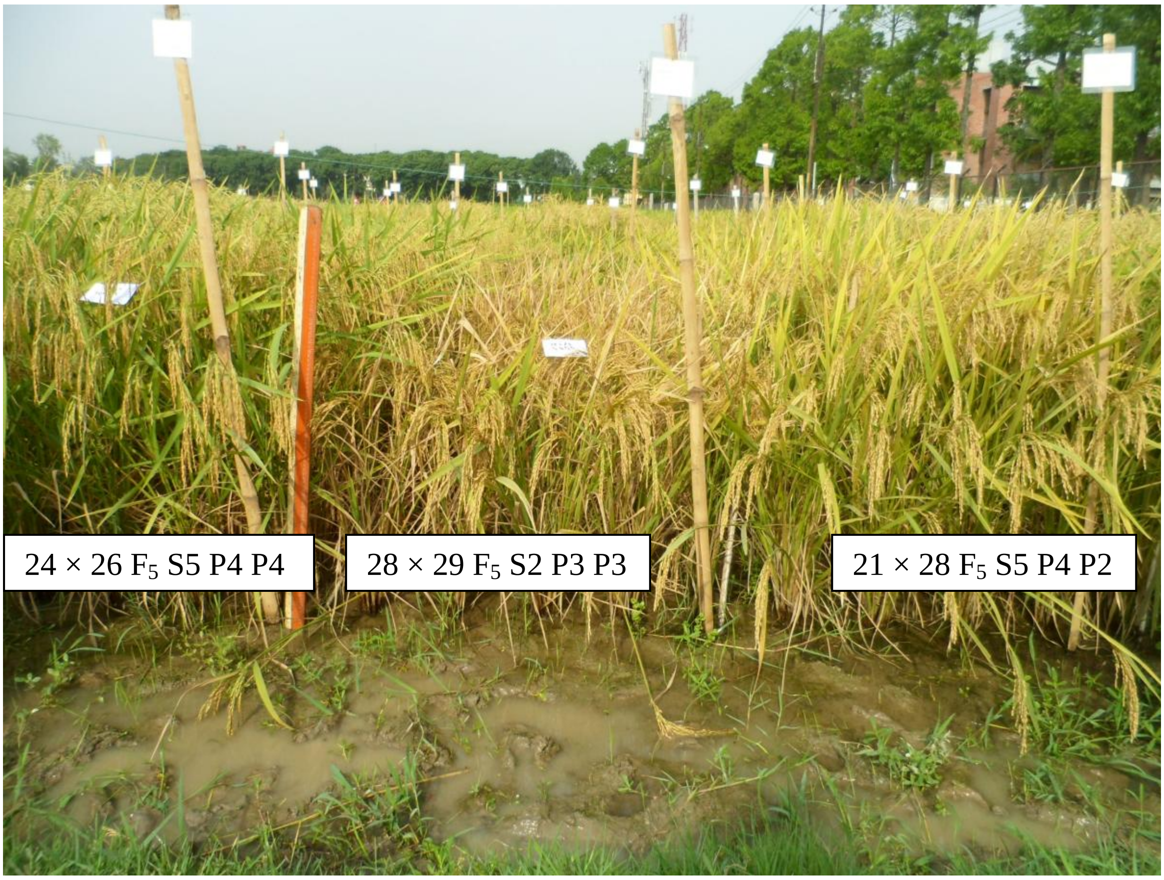

**Plate 5. Photograph to understand differences among genotypes for plant height.**

variance suggested higher influence of environment on the expression of the genes controlling this trait.The estimates of PCV (21.03%) and GCV (18.29%) also indicated presence of variability among the genotypes for this trait (Table 4). The highest variation in plant height among 14 upland rice genotypes was observed by Seyoum *et al*. (2012).

### 4.1.4 Number of total tillers per plant

Significant variations were observed among 29 genotypes (11.27**) for number of total tillers per plant (Table 2). Among 29 genotypes, G25 (18.23) showed the maximum number of total tillers per plant and the minimum by G16 (9.20) (Table 3a). The genotypes G10 (17.63) and G25 (18.23) were produced higher number of tillers per plant than the checks G28 (BRRI Dhan29) (14.07) and G29 (BRRI Dhan28) (16.77). Variation in number of total tillers per plant are presented in Plate 6.Number of total tillers per plant showed phenotypic variance (5.34) is higher than genotypic variance (2.97) indicating moderate environmental influence on these characteres and high difference between PCV (3.99%) and GCV (2.97%) value indicating that this trait is highly influenced by the environment (Table 4). Ghosal *et al.* (2010) reported similar result for this trait in irrigated rice.

### 4.1.5 Number of effective tillers per plant

Analysis of variance (Table 2) revealed significant differences among the genotypes (10.41**) for number of effective tillers per plant. The highest number of effective tillers per plant was recorded in G25 (17.20) whereas the minimum number of effective tillers per plant was recorded in G16 (9.00) (Table 3a). The genotypes G10 (16.13) and G25 (17.20) produced higher number of effective tiller per plant than two checks G28 (BRRI Dhan29) (13.93) and G29 (BRRI Dhan28) (15.93). Phenotypic variance (4.92) was high different from the genotypic variance (2.75) that indicated high environmental effect over the trait. Large difference between PCV (3.83%) and GCV (2.86%) values indicated that less influence of environment on this character (Table 4). Ghosal *et al.* (2010) reported similar result for this trait in rice.

BRRI Dhan 29

21 × 28 $F_5$ S5 P4 P2

26 × 28 $F_5$ S1 P9 P3

21 × 29 $F_5$ S6 P1 P1

**Plate 6. Photograph showing variation in number of total number of tillers per plant in different genotypes.**

### 4.1.6 Panicle length (cm)

From ANOVA table (Table 2) significant difference were observed among 20 genotypes (2.78**) for panicle length. Among the 29 genotypes the highest panicle length was observed in G29 (24.80) which is very close to G17 (24.76) and the lowest panicle length was observed in G1 (21.39) and G13 (21.39) (Table 3a). The genotypes G4 (24.49), G6 (24.11), G8 (24.62), G14 (24.44), G17 (24.76) and G22 (24.06) produced almost similar panicle length with two checks G28 (24.19) and G29 (24.80). Variations of panicle length in different genotypes are presented in Plate 7. Panicle length showed less difference between phenotypic variance (1.45) and genotypic variance (0.67) indicating less environmental influence on these character and low difference between PCV (2.08%) and GCV (1.41%) value indicating the apparent variation due to genotypes with little low influence of environment (Table 4). Low phenotypic coefficient of variation than genotypic coefficient of variation for panicle length was reported by Biswas *et al.* (2000), Kole *et al.* (2008) in rice.

### 4.1.7 Number of primary branches per panicle

The mean square due to genotype from the analysis of variance was found statistically significant for number of primary branches per panicle (2.84**) indicating the presence of genotypic differences among the genotypes (Table 2 ). From the mean table value it was found that the highest number of primary branches per panicle was recorded in G4 (11.94) which is very close to G16 (11.87) while the minimum number of primary branches per panicle was recorded in G3 (8.10) (Table 3a). The genotypes G4 (24.49), G11 (11.47), G16 (11.87) and G26 (11.07) were produced higher number of primary branches per panicle than two checks G28 (9.83) and G29 (9.23). Number of primary branches per panicle showed the low phenotypic variance (1.43) and genotypic variance (0.71) which indicated less environmental influence. The phenotypic coefficient of variability (2.07) values were recorded for number of primary branches per panicle very close to genotypic coefficient of variability (1.45) which indicated a less extent of the environment influences on the character. Elayaraja *et al.* (2005) found similar result.

### 4.1.8 Number of secondary branches per panicle

Significant variations were observed among 29 genotypes (32.54**) for number of

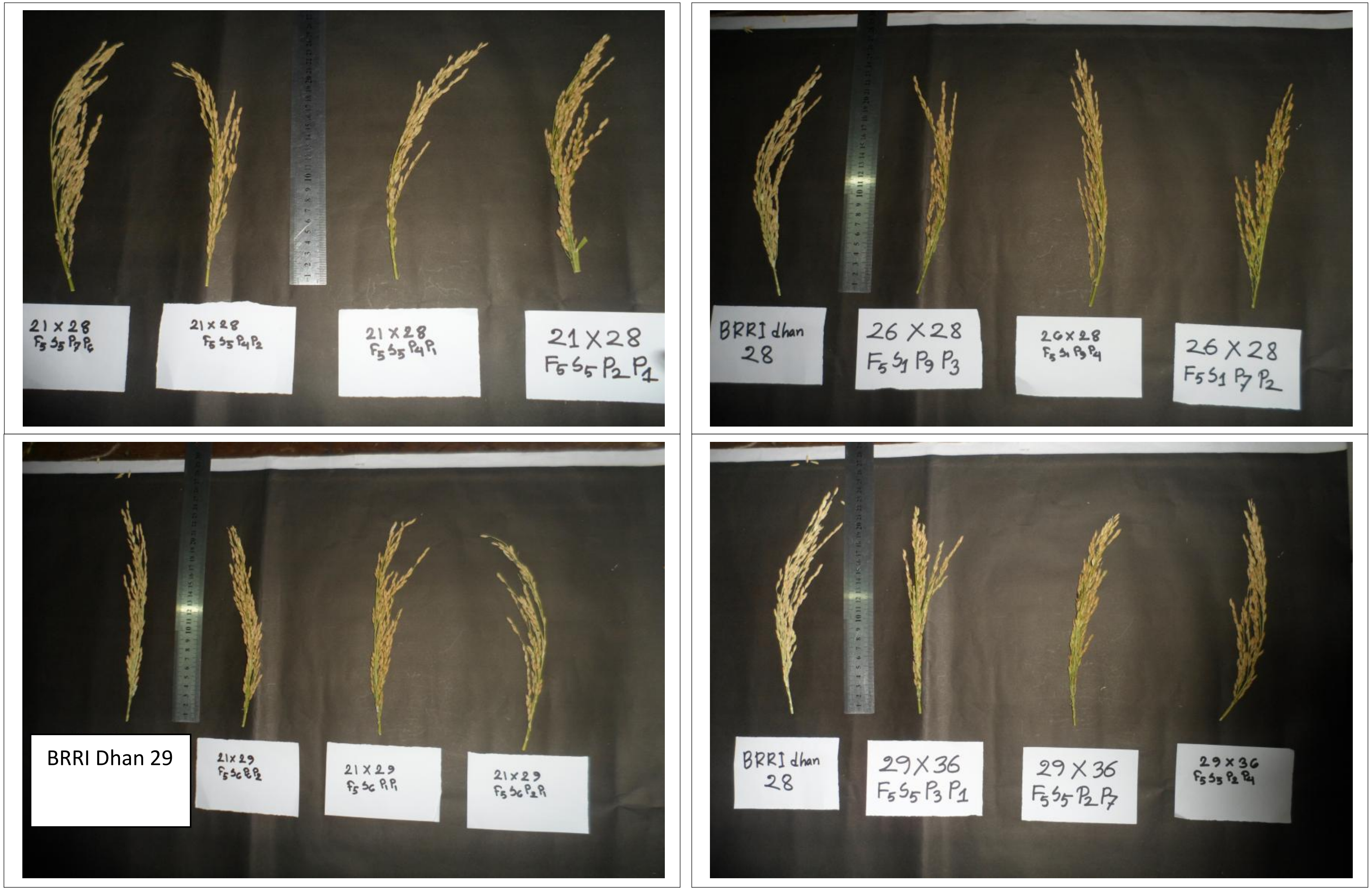

**Plate 7. Photograph showing variation in panicle length in different genotypes**

secondary branches per panicle (Table 2). Among 29 genotypes, the highest number of secondary branches per panicle was recorded in G28 (38.67) where as the minimum number of secondary branches per panicle was observed in G3 (24.77) which are very close to G25 (24.80) (Table 3b). The genotypes G14 (37.53) was found similar number of secondary branches per panicle to the checks G28 (38.67).

The value of phenotypic and genotypic variance (16.41) and (8.07), respectively for number of secondary branches per panicle with high difference between them indicates high effect of environment on this character (Table 4). According to Table 4, PCV (6.99%) and GCV (4.9%) for number of secondary branches per panicle which indicate that sufficient variation exist among genotypes for this trait. Low PCV, GCV for this trait was also recorded by Kumar *et al*. (2007) in segregating generation of rice.

### 4.1.9 Total number of spikelet per panicle

From the ANOVA (Table 2), it was found that total number of spikelet per panicle showed significant variations among the genotypes (1683.43**). The total number of spikelet per panicle was maximum in G14 (238.1) and minimum was observed in G7 (131.3) (Table 3b) among 29 genotypes. The genotypes G14 (238.10) was found higher number of spikelet per panicle than the checks G28 (216.70).

The phenotypic and genotypic variances for total number of spikelet per panicle were 795.4 and 444.02, respectively. The phenotypic variance was higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 48.68% and 36.37 % respectively for total number of spikelet per panicle which indicating that high variation exists among different genotypes (Table 4). The high GCV values of this characters suggest that the possibility of improving this trait through selection. High genotypic, phenotypic variance and high GCV, PCV for this trait was also reported by Satish *et al.* (2003).

### 4.1.10 Number of filled grains per panicle

The analysis of variance for number of filled grains per panicle showed highly significant difference (2392.05**) among 29 genotypes of *Oryza sativa* used in the present experiment (Table 2). In 29 genotypes, the number of filled grains per panicle was recorded highest in G14 (199) and minimum was recorded in G7 (97.9) (Table 3b) (Figure 1). The genotypes G14 (199) was found higher number of filled grains per panicle than checks the G28 (BRRI Dhan29) (194.00).

The magnitude of difference between phenotypic (1001.17) and genotypic variances (695.44) were higher for number of filled grains per panicle suggested that large environmental influence on this character (Table 4). The high value of phenotypic (54.61) and genotypic coefficient of variance (45.51) respectively for this character indicated that the existence of high variation among the population with possibility of high potential for the selection. High genotypic, phenotypic variance and high GCV, PCV for this trait was also reported by Akter (2010)

### 4.1.11 Number of unfilled grains per panicle

Highly significant variation (901.57**) among 29 genotypes (901.57**) for number of unfilled grains per panicle (Table 2). The G4 showed the highest (89.90) number of unfilled grains per panicle among 29 genotypes where as the G24 showed the minimum (8.70) number of unfilled grains per panicle (Table 3b). The genotypes G14 (10.40) and G24 (8.70) was found to produce lower number of unfilled grains per panicle than two check varieties G28 (19.67) and G29 (15.57).

The high value of phenotypic (350.11) and genotypic (275.73) variance for number of unfilled grains per panicle with high difference between them suggests significant role of environment on the character. The difference between phenotypic (32.29) and genotypic (28.66) coefficient of variances were high for number of unfilled grains per panicle which indicates the existence of adequate variation among the genotype (Table 4). The high GCV values of this character suggests the possibility of improvement of this trait through selection . The highest phenotypic variance, genotypic variance and phenotypic coefficient of variance, genotypic coefficient of variance were also observed by Iftekharudduaula *et al.* (2001).

### 4.1.12 Thousand seed weight (gm)

From the ANOVA (Table 2), it was found that thousand seed weight showed significant variations among the genotypes (10.04**). Thousand seed weight was found maximum in G6 (28.07 gm) where as the minimum thousand seed weight was found in G14 (21.08 gm) (Table 3b). Higher thousand seed weight was found in the genotypes G4 (26.40), G5 (25.81), G6 (28.07), G7 (27.24), G8 (27.58), G11 (27.58) and G24 (26.37) than two check varieties the G28 (22.40) and G29.

The phenotypic variance (5.17) was higher than genotypic variance (2.43) indicating that environment has influence on expression of this character. The values of PCV and GCV were 3.93% and 2.69% indicating that the genotype has considerable variation for this trait (Table 4). Bidhan *et al.* (2001) reported similar result for this trait.

### 4.1.13 Yield per plant (gm)

The mean square due to genotype was found significant (136.68**) at for yield per plant indicating the presence of genotypic differences present among 29 genotypes (Table 2 ). The highest yield per plant was recorded in G8 (48.20 gm) and the lowest was found in G1 (19.00g) (Table 3b) (Figure 2). The genotypes G8 (48.20 gm) gave higher yield per plant than two check varieties G28 (47.27) and G29 (41.33).

The phenotypic (66.41) and genotypic (35.14) variance for yield per plant suggests that high influence of environment on the expression of the genes controlling this trait. Same result was also found by Seyoum *et at.* (2012). The values of PCV and GCV were 14.07% and 10.23%, respectively which indicates that the genotype has considerable variation for this trait (Table 4). Similar result observed by Singh *et al.* (2005).

### 4.1.14 Yield per hectare (t/ ha)

Table 2 revealed that the yield per hectare showed significant differences among the genotypes (5.93**). Among 29 genotypes G8 showed the maximum (10.19 t/ha) yield per hectare and the minimum by in G1 (3.91 t/ha) (Table 3b, (Figure 3). The genotypes G8 (10.19 t/ha) and G24 (9.23 t/ha) had found higher yield per hectare than two check varieties G28 (9.13 t/ha) and G29 (7.66 t/ha) but G8 (8.18 t/ha) showed higher yield per hectare than check variety G29 (7.66 t/ha). Yield per hectare showed phenotypic variance (2.85) is moderately higher than genotypic variance (1.54) indicating moderate environmental influence on this character. The value of PCV (2.91%) and GCV (2.14%) indicates that this trait is influenced by the

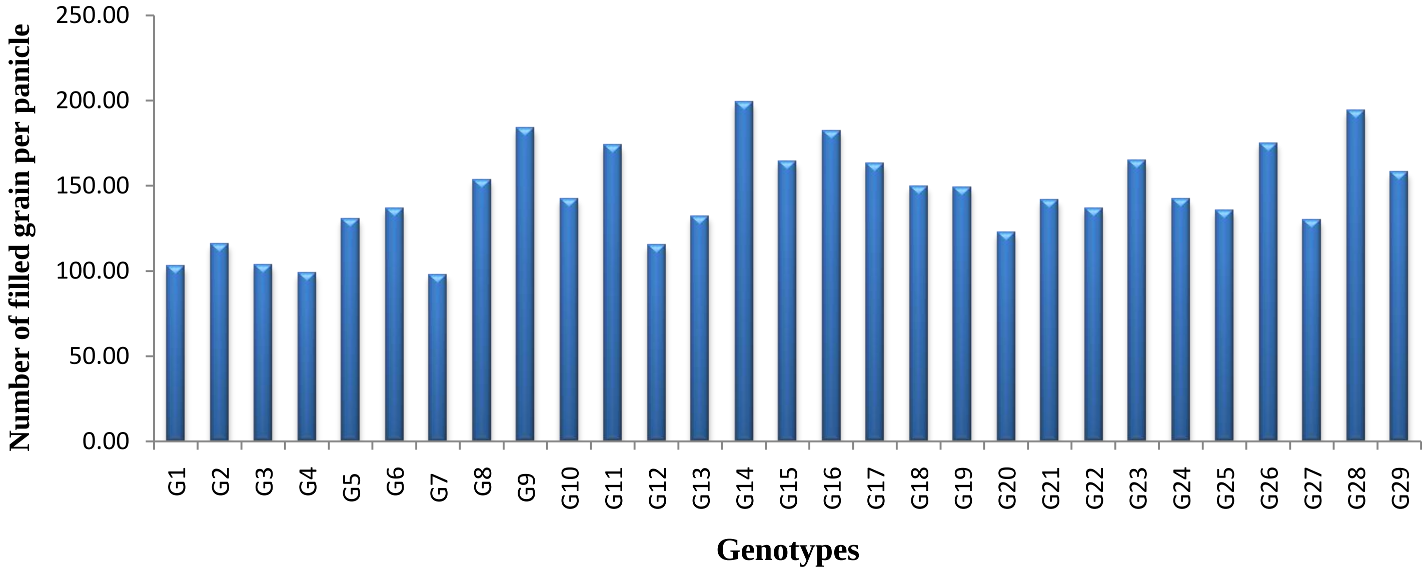

**Figure 1. Variation in mean performance of 29 genotypes for of number of filled grains per panicle.**

environment (Table 7). Datt *et al.* (2003) reported low value of PCV and GCV for this trait.

## 4.2 Heritability and genetic advance

### 4.2.1 Days to flowering

High heritability (73.43%) with low genetic advance (4.87) and genetic advance in percentage of mean (8.41%) for days to flowering was found in the 29 genotypes of *Oryza sativa***.** It indicates that presence of non-additive gene effect and this character is highly influenced by environmental effects and selection would be ineffective (Table 5). High heritability (72.03) with low genetic advance (8.54) was also reported by Chakraborty and Chakraborty (2010) in bold grain rice.

### 4.2.2 Days to maturity

Days to maturity showed high heritability (63.44%) coupled with low genetic advance (6.03) and moderate genetic advance in percentage of mean (10.41%) (Table 5). The result showed that due to presence of additive gene effect and medium scope of selection of this trait. High heritability (64.34) coupled with low genetic advance (3.29) for this trait was also observed by Akhtar *et al*. (2011) in fine grain rice.

### 4.2.3 Plant height (cm)

Plant height of 29 genotypes showed high heritability (75.67%) associated with high genetic advance (18.99) and high genetic advance in percentage of mean of 32.78% (Table 5). This finding revealed that presence of additive gene action and scope of improvement of the character through selection may be rewarding. High heritability in plant height with high genetic advance in percentage of mean was also observed by Sabesan *et al*. (2009) .

### 4.2.4 Number of total tillers per plant

Number of total tillers per plant exhibited high heritability (55.57 %) conjunction with low genetic advance (2.64) and genetic advance in percentage of mean (4.57%) (Table 5). These findings revealed that it was indicative of non-additive gene action.

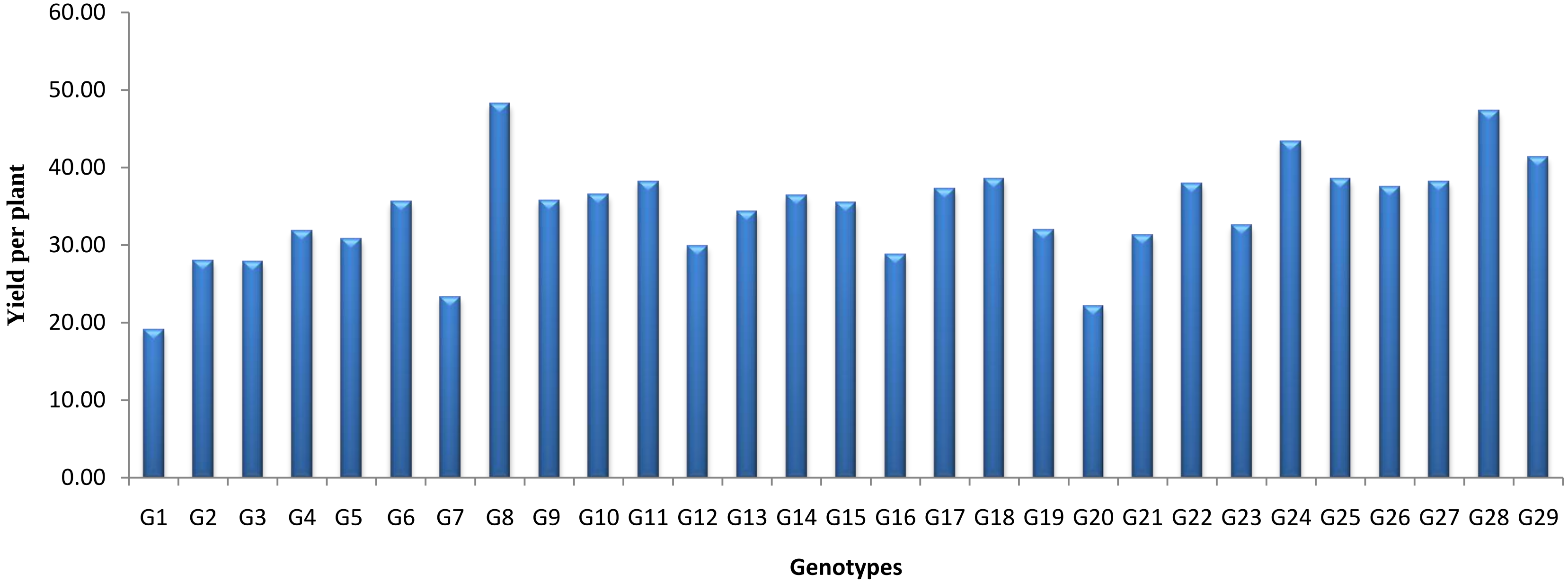

**Figure 2. Variation in mean performance of 29 genotypes for yield per plant (gm).**

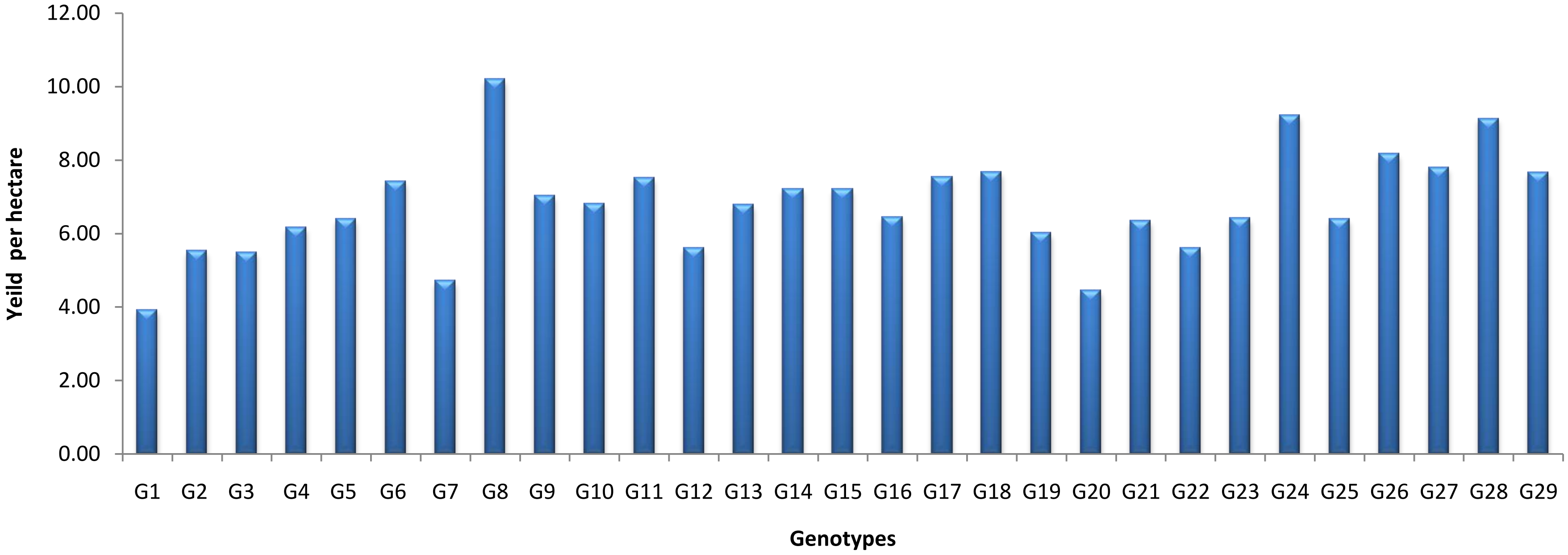

**Figure 3. Variation in mean performance of 29 genotypes for yield per hectare (ton)**

**Table 5. Estimates of heritability, genetic advance and genetic advance in percent mean 14 important characters**

| Characters | Heritability (%) | Genetic advance | Genetic advance (%) mean |
|---|---|---|---|
| DF | 73.43 | 4.87 | 8.41 |
| DM | 63.44 | 6.03 | 10.41 |
| PH | 75.67 | 18.99 | 32.78 |
| NTT | 55.57 | 2.64 | 4.57 |
| NET | 55.84 | 2.55 | 4.4 |
| LP | 46.13 | 1.14 | 1.97 |
| NPBP | 49.45 | 1.22 | 2.1 |
| NSBP | 49.2 | 4.1 | 7.08 |
| TSP | 55.82 | 32.43 | 55.98 |
| NFG/P | 69.46 | 45.28 | 78.14 |
| NUFGP | 78.76 | 30.36 | 52.39 |
| Y/P | 47.03 | 2.2 | 3.8 |
| TSW | 52.91 | 8.88 | 15.33 |
| Y/H | 54.18 | 1.88 | 3.25 |

DF = days to flowering, DM = days to maturity, PH = plant height (cm), NTT = number of total tillers per plant, NET = number of effective tillers per plant, LP = panicle length (cm), NPBP = number of primary branches per panicle, NSBP = number of secondary branches per panicle, TSP = total number of spikelet per panicle, NFG/P = number of filled grains per panicle, NUFGP = number of filled grains per panicle, Y/P = yield per plant (gm), TSW = thousand seed weight (gm), Y/H = yield per hectare (ton)

Selection for this trait may not be wise. High heritability coupled with low genetic advance was also found by Kishore *et al*. (2008).

### 4.2.5 Number of effective tillers per plant

High heritability (55.84%) accompanied with low genetic advance (2.55) and genetic advance in percentage of mean (4.4%) was calculated in respect of number of effective tillers per plant (Table 5). These findings discovered the action of non-additive gene effects on the expression of this trait. The high heritability is being exhibited due to high environmental effects. Selection may not be effective in such character. High heritability with low genetic advance was also reported by Chakraborty and Chakraborty (2010).

### 4.2.6 Panicle length (cm)

Panicle length exhibited moderate heritability (46.13%) along with low genetic advance (1.14) and genetic advance (1.97%) (Table 5). These results revealed the presence of additive gene. Selection for this trait may not be effective. Sarma *et al.* (1996) also found moderate heritability with low genetic advance.

### 4.2.7 Number of primary branches per panicle

Moderate heritability (49.45%) along with low genetic advance (1.22) and genetic advance in percentage of mean (2.10%) was calculated in number of primary branches per panicle (Table 5). It is indicated that environmental effect was more than the genotypical effect and due to non-additive gene action, selection for further improvement of the trait might not be wise. Similar results were also found by Biswas *et al.* (2000).

### 4.2.8 Number of secondary branches per panicle

Number of secondary branches per panicle showed moderate heritability (49.20%)

coupled with low genetic advance (4.10) and genetic advance in percent mean (7.08%) (Table 5) which indicating the roles of non-additive gene action and selection of this trait will be not effective. Karthikeyan *et al*. (2009) found similar result.

### 4.2.9 Total number of spikelet per panicle

Total number of spikelet per panicle showed high heritability (55.82%) coupled with high genetic advance (32.43) and genetic advance in percentage of mean (55.98%) (Table 5). These finding exposed the predominance of additive genes for controlling total number of spikelet per panicle. Thus, selection based on this character will be rewarding for improvement. High heritability with high genetic advance in percentage of mean was also observed by Sabesan *et al*. (2009) .

### 4.2.10 Number of filled grains per panicle

The magnitude of heritability in broad sense of number of filled grains per panicle was high (69.46%) with high genetic advance (45.28) and high genetic advance in percentage of mean (78.14%) (Table 5). These findings revealed that this trait was controlled by additive gene and selection for this character would be effective. Prasad *et al.* (2001), Singh *et al.* (2011) and Tuwar *et al.* (2013) also found high heritability coupled with high genetic advance as percent of mean for the trait filled grains per panicle**.**

### 4.2.11 Number of unfilled grains per panicle

Seed yield per plant showed high heritability (78.76%) accompanied with high genetic advance (30.36) and high genetic advance in percentage of mean (52.39%) (Table 5). These finding revealed that the additive gene effect on the expression of this character and selection for this character would be effective. Sarwar (2013) found similar result for this trait.

### 4.2.12 Thousand seed weight (gm)

Thousand seed weight showed high heritability (52.91%) associated with low genetic advance (8.88) and genetic advance in percentage of mean (15.33%) (Table 5). Results revealed that thousand seed weight is highly influenced by environmental effects and scope of improvement through selection may not be rewarding.

### 4.2.13 Yield per plant (gm)

Moderate heritability (47.03%) along with low genetic advance (2.2) and moderate genetic advance in percentage of mean (3.8%) was calculated in yield per plant (Table 5). It is indicated that presence of non-additive gene action and selection for further improvement of the trait might not be effective. High heritability and low genetic advance in percentage of mean were also found by Subbaiah *et al*. (2011).

### 4.2.14 Yield per hectare (t/ ha)

Yield per hectare exhibited high heritability (54.18%) conjunction with low genetic advance (1.88 ) and genetic advance in percentage of mean (3.25%) (Table 5). These findings revealed that it was indicative of non-additive gene action. Selection for this trait might not be wise.

## 4.3 Correlation coefficient

Yield is an important economic character which is influenced by several interdependable quantitative characters. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeder for making improvement through selection vis-à-vis provide a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu 1959). In our study, both genotypic and phenotypic correlation co-efficient of different characters of 29 genotypes of *Oryza sativa* L. are determined (Table 6 and table 7). Most of the characters showed the genotypic correlation coefficients were higher than their respective phenotypic ones. These values indicated that these traits were strongly associated genetically and the phenotypic expression of these traits was less influenced by the environment. In few cases, phenotypic correlation 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 = 0.85, P =0.66), number of secondary branches per panicle (G=0.51, P=0.33), total number of spikelet per panicle (G=0.48, P=0.33) and number of filled grains per panicle (G=0.31) indicated that if days to flowering increased these characters also increased. It also exhibited non-significant and positive interaction with number of unfilled grains per panicle (G=0.09, P=0.09), yield per plant (G=0.17, P=0.17) and yield per hectare (G=0.22, P=0.07). However, it had significant and negative interaction with number of secondary branches per panicle (G= -0.32) at genotypic level and thousand seed weight (G= -0.64, P= -0.38) at both genotypic and phenotypic level. It also showed non-significant and negative association with plant height (G= -0.12, P=-0.11), number of total tillers (G=-0.07, P= -0.13), number of effective tillers (G=-0.06, P= -0.09), panicle length (G=-0.21, P= -0.08) and number of secondary branches per panicle (p=-0.25 ) at phenotypic level (Table 6) (table 7). Sadeghi (2011) also revealed that days to flowering had positive interaction with yield per hectare.

### 4.3.2 Days to maturity

Days to maturity showed significant and positive correlation with number of secondary branches per panicle (G=0.44) and total number of spikelet per panicle (G=0.27) at genotypic level suggested that if days to maturity increased then number of secondary branches per panicle and total number of spikelet per panicle also increased . It also exhibited non-significant and positive interaction with plant height (G=0.2, P=0.15), number of filled grain per panicle (G=0.09, P=0.03), number of unfilled grain per panicle (G=0.21, P=0.22), yield per plant (G=0.1, P=0.04) , yield per hectare (G=0.21, P=0.09) at both genotypic and phenotypic level and with number of secondary branches per panicle (P=0.21), total number of spikelet per panicle (P=0.13) at phenotypic level. Days to maturity showed significant negative association with number of total tillers (G= -0.27), number of effective tillers (G= -0.29), panicle length (G=-0.34), number of primary branches per panicle (G=-0.30) only at phenotypic level and thousand seed weight (G=-0.38, P=-0.33) at both genotypic and phenotypic level. It also exhibited non-significant and negative interaction with number of total tillers (P=-0.16), number of effective tillers (P=-

0.17), panicle length (P=-0.12) and number of primary branches per panicle (P=-0.25) at phenotypic level (Table 6) (table 7). Sadeghi (2011), Akhter *et al.* also revealed that days to maturity had non-significant and positive interaction with yield per hectare.

### 4.3.3 Plant height (cm)

Plant height showed significant and positive interaction with number of unfilled grain per panicle (G = 0.51, P =0.42), and thousand seed weight (G =0.92, P =0.63) whereas non-significant positive interaction with panicle length P (G=0.05, P=0.17) and number of secondary branches per panicle (G =0.04, P =0.1). 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 number of total tillers (G=-0.56, P=-0.48), number of effective tillers (G=-0.60, P=-0.52), number of filled grain per panicle (G= -0.37, P=-0.27) and yield per plant (G= -0.48, P=-0.30). It had also non-significant negative relation with number of primary branches per panicle (G=-0.06, P=-0.05), total number of spikelet per panicle (G= -0.09, P=-0.03) and yield per hectare (G= -0.25, P=-0.11) (Table 6) (table 7). Prasad *et al*. (2001), Iftekharudduaula *et al*. (2001) also observed that plant height was negative associated with yield per hectare.

### 4.3.4 Number of total tillers per plant

Number of total tillers per plant showed significant and positive correlation with number of effective tillers (G=0.99, P= 0.96) and yield per plant (G=0.40, P=0.36) 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 panicle le (G= 0.04, P=0.1) and yield per hectare (G=0.09, P=0.2). Number of total tillers per plant had significant and negative interaction with number of primary branches per panicle (G=-0.37), total number of spikelet per panicle (G=-0.45) at genotypic level and number of secondary branches per panicle (G=-0.34, P=-0.28) at both genotypic and phenotypic level. It had also non-significant negative

## Table 6. Genotypic correlation coefficients among different pairs of yield and yield contributing characters of 29 genotypes of *Oryza sativa* L.

| **Characters** | **DM** | **PH** | **NTT** | **NET** | **LP** | **NPBP** | **NSBP** | **TSP** | **NFG/P** | **NUFGP** | **Y/PD** | **TSW** | **Y/H** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DF** | 0.85** | -0.12 | -0.07 | -0.06 | -0.21 | -0.32* | 0.51** | 0.48** | 0.31* | 0.09 | 0.17 | -0.64** | 0.22 |
| **DM** | | 0.2 | -0.27* | -0.29* | -0.34** | -0.30* | 0.44** | 0.27* | 0.09 | 0.21 | 0.1 | -0.38** | 0.21 |
| **PH** | | | -0.56** | -0.60** | 0.05 | -0.06 | 0.04 | -0.09 | -0.37** | 0.51** | -0.48** | 0.92** | -0.25 |
| **NT** | | | | 0.99** | 0.04 | -0.37** | -0.34** | -0.45** | -0.21 | -0.24 | 0.40** | -0.16 | 0.09 |
| **NET** | | | | | 0.15 | -0.31* | -0.28* | -0.34** | 0.08 | -0.34** | 0.51** | -0.16 | 0.23 |
| **LP** | | | | | | 0.46** | 0.43** | 0.44** | 0.46** | -0.17 | 0.52** | 0.47** | 0.57** |
| **NPBP** | | | | | | | 0.32* | 0.49** | 0.38** | 0.02 | 0.26 | 0.43** | 0.29* |
| **NSBP** | | | | | | | | 0.92** | 0.71** | 0.05 | 0.34** | -0.30* | 0.43** |
| **TSP** | | | | | | | | | 0.82** | -0.05 | 0.41** | -0.39** | 0.50** |
| **NFG/P** | | | | | | | | | | -0.61** | 0.63** | -0.33** | 0.68** |
| **NUFG/P** | | | | | | | | | | | -0.57** | 0.04 | -0.52** |
| **Y/P** | | | | | | | | | | | | 0.12 | 0.68** |
| **TSW** | | | | | | | | | | | | | 0.19 |

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

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

**Table 7. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters of 29 genotypes of *Oryza sativa* L.**

| Characters | DM | PH | NTT | NET | LP | NPBP | NSBP | TSP | NFG/P | NUFGP | Y/PD | TSW | Y/H |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DF** | 0.66** | -0.11 | -0.13 | -0.09 | -0.08 | -0.25 | 0.33** | 0.33** | 0.24 | 0.09 | 0.17 | -0.38** | 0.07 |
| **DM** | | 0.15 | -0.16 | -0.17 | -0.12 | -0.25 | 0.21 | 0.13 | 0.03 | 0.22 | 0.04 | -0.33** | 0.09 |
| **PH** | | | -0.48** | -0.52** | 0.17 | -0.05 | 0.1 | -0.03 | -0.27* | 0.42** | -0.30* | 0.63** | -0.11 |
| **NTT** | | | | 0.96** | 0.1 | -0.09 | -0.28* | -0.21 | -0.1 | -0.16 | 0.36** | -0.1 | 0.2 |
| **NET** | | | | | 0.02 | -0.07 | -0.2 | -0.13 | 0.02 | -0.24 | 0.46** | -0.08 | 0.28* |
| **LP** | | | | | | 0.30* | 0.51** | 0.34** | 0.36** | -0.13 | 0.41** | 0.31* | 0.43** |
| **NPBP** | | | | | | | 0.30* | 0.44** | 0.37** | 0.03 | 0.24 | 0.22 | 0.26 |
| **NSBP** | | | | | | | | 0.68** | 0.58** | 0.06 | 0.26 | -0.09 | 0.30* |
| **TSP** | | | | | | | | | 0.82** | -0.04 | 0.36** | -0.28* | 0.36** |
| **NFG/P** | | | | | | | | | | -0.51** | 0.52** | -0.13 | 0.52** |
| **NUFGP** | | | | | | | | | | | -0.43** | 0.05 | -0.41** |
| **Y/P** | | | | | | | | | | | | 0.05 | 0.66** |
| **TSW** | | | | | | | | | | | | | 0.08 |

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

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

relation with number of filled grain per panicle (G= -0.21, P= -0.1), number of unfilled grain per panicle (G=-0.24, P= -0.16) , thousand seed weigh (G=-0.16, P=-0.1) at both genotypic and phenotypic level and number of primary branches per panicle (P= -0.09), total number of spikelet per panicle (P= -0.21) at phenotypic level (Table 6) (table 7). Agahi *et al*. (2007), Selvaraj *et al*. (2011) and Ganapati *et al*. (2014) also reported positive correlation of yield per hectare with number of total tillers per plant at both genotypic and phenotypic level.

### 4.3.5 Number of effective tillers per plant

The correlation between number of effective tillers per plant and yield per plant was significant and positive at both genotypic (G = 0.51) and phenotypic level (P = 0.46) but positively significant with yield per hectare at phenotypic level (P=0.28) indicated that the traits were governed by same gene and simultaneous improvement would be effective. It also had positive and non-significant correlation with panicle length (G = 0.15, P =0.02) number of filled grain per panicle (G =0.08, P = 0.02) and yield per hectare (G =0.23) at genotypic level. Number of effective tillers per plant had significant and negative interaction with number of primary branches per panicle (G = -0.31), number of secondary branches per panicle (G = -0.28), total number of spikelet per panicle (G = -0.34) and number of unfilled grain per panicle (G = -0.34) at genotypic level. Negative and non-significant correlation was found between number of effective tillers per plant and number of primary branches per panicle (P= -0.07), number of secondary branches per panicle (P=-0.2), total number of spikelet per panicle (P=-0.13), number of unfilled grain per panicle (P=-0.24) at phenotypic level and thousand seed weight (G=-0.16, P=-0.08) (Table 6) (table 7). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Agahi *et al.* (2007) and Babu *et al.* (2012) also found positive and significant correlation of yield with effective tillers per plant at both genotypic and phenotypic level. Selvaraj *et al*. (2011) and Satheesh kumar *et al.* (2012) found positive and significant correlation of yield per hectare with effective tillers per plant at phenotypic level only.

### 4.3.6 Panicle length (cm)

Panicle length showed significant and positive correlation with number of primary branches per panicle (G=0.46, P=0.30), number of secondary branches per panicle (G=0.43, P=0.51), total number of spikelet (G= 0.44, P=0.34), number of filled grain per panicle (G= 0.46, P=0.36), yield per plant (G= 0.52, P=0.41), thousand seed weight(G=0.47, P=0.31) and yield per hectare (G=0.57, P=0.43) 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, yield per and thousand seed weight. It had also non-significant negative relation with number of unfilled grain per panicle (G= -0.17, P=-0.13) (Table 6) (table 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.

### 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= 0.32, P= 0.30), total number of spikelet (G=0.49 , P=0.44 ), number of filled grain per panicle (G=0.38, P= 0.37) at both genotypic and phenotypic level, thousand seed weight (G= 0.43) and yield per hectare (G= 0.29) at genotypic 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=0.02, P=0.03), yield per plant (G=0.26, P= 0.24) and thousand seed weight (P= 0.22), yield per hectare (P=0.26) at phenotypic level (Table 6) (table 7). Significant positive correlation of this character with yield per hectare was reported by Vange (2008).

### 4.3.8 Number of secondary branches per panicle

The significant and positive correlation was found between number of secondary branches per panicle and total number of spikelet (G= 0.92, P=0.68), number of filled grain per panicle (G=0.71, P= 0.58), yield per plant (G=0.34) at genotypic level and yield per hectare (G=0.43, P= 0.30). 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 (G=0.05, P=0.06) and yield per plant (P= 0.26) at phenotypic level. It had significant negative relation with thousand seed weight (G= -0.30) but non-significant at phenotypic level (P= -0.09) (Table 6) (table 7). Mustafa *et al.* (2007) found that this significant and positive correlation with yield per hectare.

### 4.3.9 Total number of spikelet per panicle

Total number of spikelet per panicle showed significant and positive correlation with number of filled grain per panicle (G=0.82, P= 0.82), yield per plant (G= 0.41, P= 0.36) and yield per hectare (G= 0.50, P=0.36) 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 it had significant negative relation with thousand seed weight (G= -0.39, P=-0.28) whereas non- significant negative relation number of unfilled grain per panicle (G= -0.05, P=-0.04) (Table 6) (table 7). 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 Mishra and Verma (1988).

### 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=0.63, P=0.52) and yield per hectare (G=0.68, P=0.52) indicated that if number of filled grains per panicle increased then yield per plant and yield per hectare also increased. It also had significant negative relation with number of unfilled grains per panicle (G= -0.61, P= -0.51) and thousand seed weight (G= -0.33) at genotypic level and non-significant negative interaction with thousand seed weight (p= -0.13) at phenotypic level (Table 6) (table 7). Habib *et al*. (2005) found similar result.

### 4.3.11 Number of unfilled grains per panicle

Number of unfilled grains per panicle showed significant and negative correlation with yield per plant (G= -0.57, P=-0.43) and yield per hectare (G=-0.52, P=-0.41). 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 = 0.04, P = 0.05) (Table 6) (table 7). Same result for this trait was reported by Iftekharudduaula *et al.* (2001).

### 4.3.12 Yield per plant (gm)

The significant and positive correlation was found between yield per plant and yield per hectare (G= 0.68, P= 0.66) indicated that if yield per plant increased then yield per hectare also increased. But it had non-significant positive relation with thousand seed weight (G=0.12, P=0.05) (Table 6) (table 7). Nayak *et al* (2001) found same result for this trait.

### 4.3.13 Thousand seed weight (gm)

Thousand seed weight showed non-significant and positive correlation with yield per hectare (G= 0.19, P=0.08) (Table 6) (table 7) indicated that very little contribution of thousand seed weight toward increase in yield per hectare.

## 4.4 Path Co-efficient analysis

Path coefficient analysis splits the correlation coefficient into direct and indirect effects. It reveals whether the association of the traits with yield is due to their direct effect or is a consequence of their indirect effect via other traits. Path coefficient analysis was done with days to 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 of per panicle, total number of spikelet per panicle, yield per plant (gm), thousand seed weight. Estimation of direct and indirect effect of path co-efficient analysis for *Oryza sativa* is presented in Table 8.

### 4.4.1 Days to flowering

Days to flowering had positive direct effect (0.05) on yield per hectare. Positive direct effect of this character was reported by Abarshahr *et al*. (2011) This trait showed indirect positive effect on yield per hectare through plant height (1.04), number of total tillers per plant (0.19), number of secondary branches per panicle (0.55), number of filled grains per panicle (0.18), number of unfilled grains per panicle (0.01), yield per plant (0.07). On the hand, it showed indirect negative effect on yield per hectare via days to maturity (-0.22), number of effective tillers per plant (-0.12), panicle length (-0.11), number of primary branches per panicle (-0.13), total number of spikelet per panicle (-1.13), thousand seed weight (-0.10). Finally it made non-significant positive correlation with yield per hectare (0.22) (Table 8).

### 4.4.2 Days to maturity

Path co-efficient analysis revealed that, days to maturity was positively correlated (0.21) and had negative direct effect (-0.26) on yield per hectare. It had positive indirect influence on the yield per hectare through days to flowering (0.89), number of total tillers per plant (0.74), number of primary branches per panicle (0.47), number of filled grains per panicle (0.05), number of unfilled grains per panicle (0.02), yield per plant (0.04). The indirect negative effect of this trait through plant height (-0.07), number of effective tillers per plant (-0.61), panicle length (-0.18), number of primary branches per panicle (-0.12), total number of spikelet per panicle (-0.65), and thousand seed weight (-0.06) on yield per hectare (Table 8). Same result also recorded by Habib *et al.*(2005), sadeghi (2011).

### 4.4.3 Plant height (cm)

Plant height had negative direct (-0.33) effect on yield per hectare. It had positive indirect effect on yield per hectare via number of total tillers per plant (1.53), panicle length (0.03), total number of spikelet per panicle (0.21), number of unfilled grains per panicle (0.05) and thousand seed weight (0.15). Whereas plant height had indirect influence on yield per hectare through days to flowering (-0.12), days to maturity (-0.05), number of effective tillers per plant (-1.27), number of

**Table 8. Path coefficient analysis showing direct and indirect effects of different characters on yield per hectare of *Oryza sativa* L.**

| | **DF** | **DM** | **PH** | **NT** | **NET** | **LP** | **NPB/P** | **NSB/P** | **TS/P** | **NFG/P** | **NFUG/P** | **Y/p** | **TSW** | Y/H |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DF** | **0.05** | -0.22 | 1.04 | 0.19 | -0.12 | -0.11 | -0.13 | 0.55 | -1.13 | 0.18 | 0.01 | 0.07 | -0.10 | 0.22 |
| **DM** | 0.89 | **-0.26** | -0.07 | 0.74 | -0.61 | -0.18 | -0.12 | 0.47 | -0.65 | 0.05 | 0.02 | 0.04 | -0.06 | 0.21 |
| **PH** | -0.12 | -0.05 | **-0.33** | 1.53 | -1.27 | 0.03 | -0.03 | -0.04 | 0.21 | -0.21 | 0.05 | -0.20 | 0.15 | -0.25 |
| **NT** | -0.07 | 0.07 | 0.19 | **-0.72** | 2.10 | 0.02 | -0.15 | -0.36 | 1.07 | -0.12 | -2.02 | 0.17 | -0.03 | 0.09 |
| **NET** | -0.06 | 0.07 | 0.20 | -2.70 | **0.11** | 2.08 | -0.13 | -0.30 | 0.81 | -0.04 | -0.03 | 0.21 | -0.03 | 0.23 |
| **LP** | -0.22 | 0.09 | -0.02 | -0.12 | 0.31 | **0.52** | 0.19 | 0.46 | -1.06 | 0.26 | -0.02 | 0.22 | 0.08 | 0.57** |
| **NPB/P** | -0.34 | 0.08 | 0.02 | 1.01 | -0.66 | 0.24 | **0.42** | 0.35 | -1.18 | 0.22 | 0.00 | 0.11 | 0.07 | 0.29* |
| **NSB/P** | 0.54 | -0.11 | 0.01 | 0.92 | -0.60 | 0.22 | 0.13 | **0.06** | -2.20 | 0.40 | 1.00 | 0.14 | -0.05 | 0.43** |
| **TS/P** | 0.50 | -2.07 | 0.03 | 1.22 | -0.72 | 0.23 | 0.20 | 0.98 | **-0.38** | 0.47 | 0.00 | 0.17 | -0.06 | 0.50** |
| **NFG/P** | 0.33 | -0.02 | 0.12 | 0.58 | -0.17 | 0.24 | 0.16 | 0.75 | -1.96 | **0.57** | -0.05 | 0.26 | -0.05 | 0.68** |
| **NUFG/P** | 0.09 | -0.05 | -0.17 | 0.65 | -0.71 | -0.09 | -0.01 | 0.06 | 0.11 | 0.28 | **0.09** | -0.24 | 0.01 | -0.52** |
| **Y/p** | 0.18 | -0.03 | 0.16 | -1.08 | 1.08 | 0.27 | 0.11 | 0.36 | -0.99 | -0.34 | -0.05 | **0.42** | 0.02 | 0.68** |
| **TSW** | -0.67 | 0.10 | -0.30 | 0.43 | -0.34 | 0.24 | 0.18 | -0.32 | 0.93 | 0.36 | 0.00 | 0.05 | **0.16** | 0.19 |

Bold faces are direct effect.

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

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

primary branches per panicle (-0.03), number of secondary branch per panicle (-0.04), number of filled grains per panicle (-0.21), yield per plant (-0.20). It made a negative correlation (-0.25) with yield per hectare (Table 8). Same result also recorded by Abarshahr *et al.* (2011).

### 4.4.4 Number of total tillers per plant

Number of total tillers per plant had negative direct (-0.72) effect on yield per hectare. It had positive indirect effect on yield per hectare via days to maturity (0.07), plant height (0.19), number of effective tillers per plant (2.10), panicle length (0.02), total number of spikelet per panicle (1.07), and yield per plant p (0.17). Whereas, it had negative indirect effect through days to flowering (-0.07), number of primary branches per panicle (-0.15), number of secondary branch per panicle (-0.36), number of filled grains per panicle (-0.12) , number of unfilled grains per panicle (-2.02) and thousand seed weight (-0.03) on yield per hectare. Number of total tillers per plant finally made non-significant positive genotypic correlation (0.09) with yield per hectare.

### 4.4.5 Number of effective tillers per plant

The positive direct effect (0.11) of number of effective tillers per plant was found on yield per hectare. Number of effective tillers per plant had positive indirect effect on yield per hectare through days to maturity (0.07), plant height (0.20), panicle length (2.08), total number of spikelet per panicle (0.81), yield per plant (0.21). The indirect effect of this trait on yield per hectare via days to flowering (-0.06), number of total tillers per plant (-2.70), number of primary branches per panicle (-0.13), number of secondary branches per panicle (-0.30), number of filled grains per panicle (-0.04), number of unfilled grains per panicle (-0.03), thousand seed weight (-0.03) was negative. Finally number of effective tillers per plant made non-significant positive genotypic correlation (0.23) with yield per hectare (Table 8). Rokonuzzaman *et al.* (2008), Agahi *et al.* (2007), Sadeghi (2011) found similar findings for this character.

### 4.4.6 Panicle length (cm)

Panicle length had positive direct effect (0.52) on yield per hectare. It had positive indirect effect through days to maturity (0.09), number of effective tillers per plant (0.31), number of primary branches per panicle (0.19), number of secondary branches per panicle (0.46), number of filled grains per panicle (0.26), yield per plant (0.22), thousand seed weight (0.08) on yield per hectare. Negative indirect effect on yield per hectare was found through days to flowering (-0.22), plant height (-0.02), number of total tillers per plant (-0.12), total number of spikelet per panicle (-1.06), number of unfilled grains per panicle (-0.02) (Table 8). Its correlation with yield per hectare was positive and highly significant (0.57) suggested that direct selection of this character may contribute in yield. Selvaraj *et al.* (2011) found positive and significant correlation of this trait with yield per hectare.

### 4.4.7 Number of primary branches per panicle

Path analysis revealed that, number of primary branches per panicle had direct positive effect (0.42) on yield per hectare. It had positive indirect effect on yield per hectare via days to maturity (0.08), plant height (0.02), number of total tiller per plant (1.01), panicle length (0.24), number of secondary branches per panicle (0.35), number of filled grains per panicle (0.22) , yield per plant (0.11), thousand seed weight (0.07). However, number of primary branches per panicle had negative indirect effect on yield per hectare through days to flowering (-0.34), number of effective tillers per plant (-0.66), total number of spikelet per panicle (-1.18). The genotypic correlation with yield per hectare was significant and positive (0.29). This result exposed that yield per hectare will be increased by direct selection of number of primary branches per panicle. Selvaraj *et al.* (2011) also found positive and significant correlation of this trait with yield per hectare. Chakraborty *et al*. (2001) found similar finding.

### 4.4.8 Number of secondary branches per panicle

Number of secondary branches per panicle had positive direct effect (0.06) on yield per hectare. It had positive indirect effect through days to flowering (0.54), plant height (0.01), number of total tiller per plant (0.92), panicle length (0.22), number of primary branches per panicle (0.13), number of filled grains per panicle (0.40), number of unfilled grains per panicle (1.00), yield per plant (0.14) on yield per hectare. Whereas, it had negative indirect effect on yield per hectare via days to maturity (-0.11), number of effective tillers per plant (-0.60), total number of spikelet per panicle (-2.20), thousand seed weight (-0.05). Finally this trait had significant positive genotypic correlation (0.43) with yield per hectare (Table 8). Hence, selection should be practiced for this trait which had more number of secondary branches per panicle in order to improve seed yield. Chakraborty *et al.* (2001) found similar finding.

### 4.4.9 Total number of spikelet per panicle

Total number of spikelet per panicle had direct negative effect (-0.38) on yield per hectare. This trait had also indirect positive effect on yield per hectare via days to flowering (0.50), plant height (0.03), number of total tillers per plant (1.22), panicle length (0.23), number of primary branches per panicle (0.20), number of secondary branch per panicle (0.98), number of filled grains per panicle (0.47), yield per plant (0.17) . On the other hand, indirect negative effect of this trait showed on yield per hectare through days to maturity (-2.07), number of effective tillers per plant (-0.72), thousand seed weight (-0.06). Finally this trait had significant positive correlation (0.50) with yield per plant (Table 8).

### 4.4.10 Number of filled grains per panicle

Path co-efficient analysis revealed that number of filled grains per panicle exhibited positive direct effect on yield per hectare (0.57) followed by positive indirect effect through days to flowering (0.33), plant height (0.12), number of total tillers per plant (0.58), panicle length (0.24), number of primary branches per panicle (0.16), number of secondary branch per panicle (0.75), and yield per plant (0.26) . Whereas this trait showed negative indirect effect via days to maturity (-0.02), number of effective tillers per plant (-0.17), total number of spikelet per panicle (-1.96), number of unfilled grains per panicle (-0.05), thousand seed weight (-0.05). Number of filled grains per panicle had highly significant and positive correlation with yield per plant (0.68) (Table 8) indicated that direct selection of this trait will improve yield per hectare. Abarshahar *et al.* (2011), Hairmanis *et al.* (2011), Selvaraj *et al.* (2011), Satheeshkumar *et al* (2012) also found positive direct effect of filled grains per panicle on yield per hectare.

### 4.4.11 Number of unfilled grains per panicle

Number of unfilled grains per panicle had positive direct effect (0.09) on yield per hectare. The positive indirect effect on yield per hectare was found via days to flowering (0.09), number of total tillers per plant (0.65), number of secondary branch per panicle (0.06), total number of spikelet per panicle (0.11), number of filled grains per panicle (0.28), and thousand seed weight (0.01). It had also negative indirect effect through days to maturity (-0.05), plant height (-0.17), number of effective tillers per plant (-0.71), panicle length (-0.09), number of primary branches per panicle (-0.01), yield per plant (-0.24) on yield per hectare. Number of unfilled grains per panicle finally made significant negative genotypic correlation (-0.52) with yield per hectare.

### 4.4.12 Yield per plant (gm)

The direct effect (0.42) of siliqua length on yield per hectare was positive. The indirect effect of this trait on yield per hectare through days to flowering (0.18) , plant height (0.16), number of effective tillers per plant (1.08), panicle length (0.27), number of primary branches per panicle (0.11),  number of secondary branches per panicle (0.36), thousand seed weight (0.02).Whereas, negative indirect effect of this trait was found on yield per hectare via days to maturity (-0.03), number of total tillers per plant (-1.08), total number of spikelet per panicle (-0.99), number of filled grains per panicle (-0.34), number of unfilled grains per panicle (-0.05).The correlation with yield per was positive and non-significant (0.68) (Table 8). This result indicated that selection based on this character would have greater chance for improving yield per hectare. Agahi *et al.* (2007) also found positive direct effect of this trait on yield per hectare.

### 4.4.13 Thousand seed weight (gm)

Thousand seed weight had positive direct effect (0.16) on yield per hectare. It had positive indirect effect on yield per hectare via days to maturity (0.10) , number of total tillers per plant (0.43), panicle length (0.24), number of primary branches per panicle (0.18), total number of spikelet per panicle (0.93), number of filled grains per panicle (0.36), yield per plant  (0.05) . However, thousand seed weight had negative indirect effect on yield per hectare through days to flowering (-0.67), plant height (-0.30) , number of effective tillers per plant (-0.34), number of secondary branch per panicle (-0.32) . Thousand seeds weight finally made positive genotypic correlation (0.19) with yield per hectare. Yield per hectare may be improved through direct selection of thousand seeds weight. Agahi *et al.* (2007) also found positive direct effect of thousand grains weight on yield per hectare.

# CHAPTER IV

# SUMMARY AND CONCLUSION

The present study was undertaken with 29 genotypes of *Oryza sativa* L. at the Sher-e-Bangla Agricultural University Farm, Bangladesh during December, 2013- May,2014. Seedlings were transplanted in the main field in Randomized Complete Block Design (RCBD) with three replications. Data on various yield attributing characters such as, days to flowering, days to maturity, 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 of per panicle, total number of spikelet per panicle, yield per plant (gm), thousand seed weight and yield per hectare were recorded.

From variability analysis of 29 genotypes of *Oryza sativa* L, it was observed that significant variation existing among all the genotypes used for most of the characters studied. The lowest days to flowering was observed in G7 (21× 28 $F_5$ S5 P6 P3) and highest was observed in G28 (BRRI Dhan29). The highest days to maturity was taken in G28 (BRRI Dhan29) and the minimum days to maturity was taken in G19 (26 × 28 $F_5$ S1 P9 P4), G29 (BRRI Dhan28) and G10 (21× 29 $F_5$ S6 P2 P4). Plant height exhibited highest in G20 (26 × 29 $F_5$ S6 P3 P1) and lowest in G25 (29×36 $F_5$ S5 P2 P4). G25 (29×36 $F_5$ S5 P2 P4) showed the maximum number of total tillers per plant and the minimum one was in G16 (24 × 36 $F_5$ S8 P1 P1). The highest number of effective tillers per plant was recorded in G25 (29×36 $F_5$ S5 P2 P4) whereas the minimum number of effective tillers per plant was recorded in G16 (24 × 36 $F_5$ S8 P1 P1). The highest panicle length was observed in G29 (BRRI Dhan28) and the minimum panicle length was observed in G1 (21× 26 $F_5$ S6 P1 P6) and G13 (24 × 26 $F_5$ S5 P1 P3). Highest number of primary branches per panicle was recorded for G4 (21× 28 $F_5$ S5 P2 P1) while the minimum number of primary branches per panicle was recorded for G3 (21× 26 $F_5$ S6 P9 P7). The highest number of secondary branches per panicle was recorded in G28 (BRRI Dhan29) where as the minimum number of secondary branches per panicle was observed in G3 (21× 26 $F_5$ S6 P9 P7). The total number of spikelet per panicle was maximum in G14 (24 × 26 $F_5$ S5 P3 P2) and minimum was observed in G7 (21× 28 $F_5$ S5 P6 P3). The number of filled grains per panicle was recorded highest in G14 (24 × 26 $F_5$ S5 P3 P2) and minimum was recorded in G7 (21× 28 $F_5$ S5 P6 P3). The G4 (21× 28 $F_5$ S5 P2 P1) showed the highest number of unfilled grains per panicle and the G24 (28×29 $F_5$ S2 P4 P3) showed the minimum number of unfilled grains per panicle. Thousand seed weight was found maximum in G6 (21× 28 $F_5$ S5 P4 P2) where as the minimum thousand seed weight was found in G14 (24 × 26 $F_5$ S5 P3 P2). Yield per plant was recorded highest in G8 (21× 28 $F_5$S5 P7 P6) and the lowest was found in G1 (21× 26 $F_5$ S6 P1 P6). Genotype G8 (21× 28 $F_5$S5 P7 P6) showed the maximum yield per hectare and the minimum one was in G1 (21× 26 $F_5$ S6 P1 P6).

The phenotypic variance of 29 genotypes was considerably higher than the genotypic variance for all the characters studied. days to flowering , panicle length, number of primary branches per panicle, showed minimum difference between genotypic and phenotypic variance which indicated low environmental influence on these characters. days to maturity, plant height, number of total tillers per plant, number of effective tillers per plant, number of secondary branches per panicle, total number of spikelet per panicle, number of filled grains per panicle, number of unfilled grains per panicle, thousand seed weight, yield per plant, yield per hectare showed much difference between genotypic and phenotypic variance suggested that high environmental influence on expression of these characters.

Plant height, number of total tillers per plant, number of secondary branches per panicle, total number of spikelet per panicle, number of filled grains per panicle, number of unfilled grains per panicle, thousand seed weight, yield per plant, yield per hectare showed high difference between genotypic and phenotypic coefficient of variation indicated that high influence of environment on the expression of these characters. Plant height, Total number of spikelet per panicle, number of filled grain per panicle, number of unfilled grain per panicle, exhibited highest value of genotypic variance and genotypic phenotypic coefficient of variation. Days to flowering, number of effective tillers per plant, panicle length, number of primary branches per panicle exhibited low difference genotypic and phenotypic coefficient of variation implies that low influence of environment and additive gene action on the expression of these characters.

High heritability with high genetic advance and genetic advance in percent of mean was observed for plant height, total number of spikelet per panicle, number of filled grain per panicle and number of unfilled grain per panicle indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. High heritability with moderate genetic advance in percent of mean was observed for days to maturity and yield per plant indicating medium possibility of selecting genotypes. High heritability with low genetic advance and genetic advance in percent of mean was recorded for days to flowering, number of total tiller, number of effective tiller and Yield per hectare indicating that non-additive gene effects were involved for the expression of these characters and selection for such traits might not be rewarding.

Study on correlation revealed that yield per hectare had significant positive association with panicle length, number of secondary branches per panicle, total number of spikelet per panicle, number of filled grain per panicle, yield per plant at both genotypic and phenotypic level and number of primary branch per panicle at genotypic level, number of effective tiller at phenotypic level. In addition, there were non-significant positive correlation with seed yield per hectare was also found in days to flowering, days to maturity, number of total tillers per plant, thousand seed weight.

Path co-efficient analysis exposed that days to days to flowering, number of effective tillers per plant, panicle length, number of primary branches per panicle , number of secondary branches per panicle, number of filled grain per panicle, number of unfilled grain per panicle, yield per plant and thousand seed weight had the positive direct effect on yield per hectare. Among these characters panicle length, number of filled grain per panicle, yield per plant showed high direct effect and highly significant correlation with yield per hectare. Days to maturity, plant height, number of total tillers per plant and total number of spikelet per panicle had the negative direct effect on yield per hectare.

A parameter which had high range of genetic variability, high heritability, high genetic advance, high genetic advance percent in mean, highest degree of positive and significant correlation and highest direct positive effect on yield per hectare would be very effective and excellent tool for improving yield potential. Such parameter in this study was number of filled grain per panicle which could raise the yield potential up to 78.14% followed by yield per plant. It is concluded that selection of plants on the basis of higher number of filled grain per panicle would raise the potential of yield per hectare from 15.33% to 78.14%.

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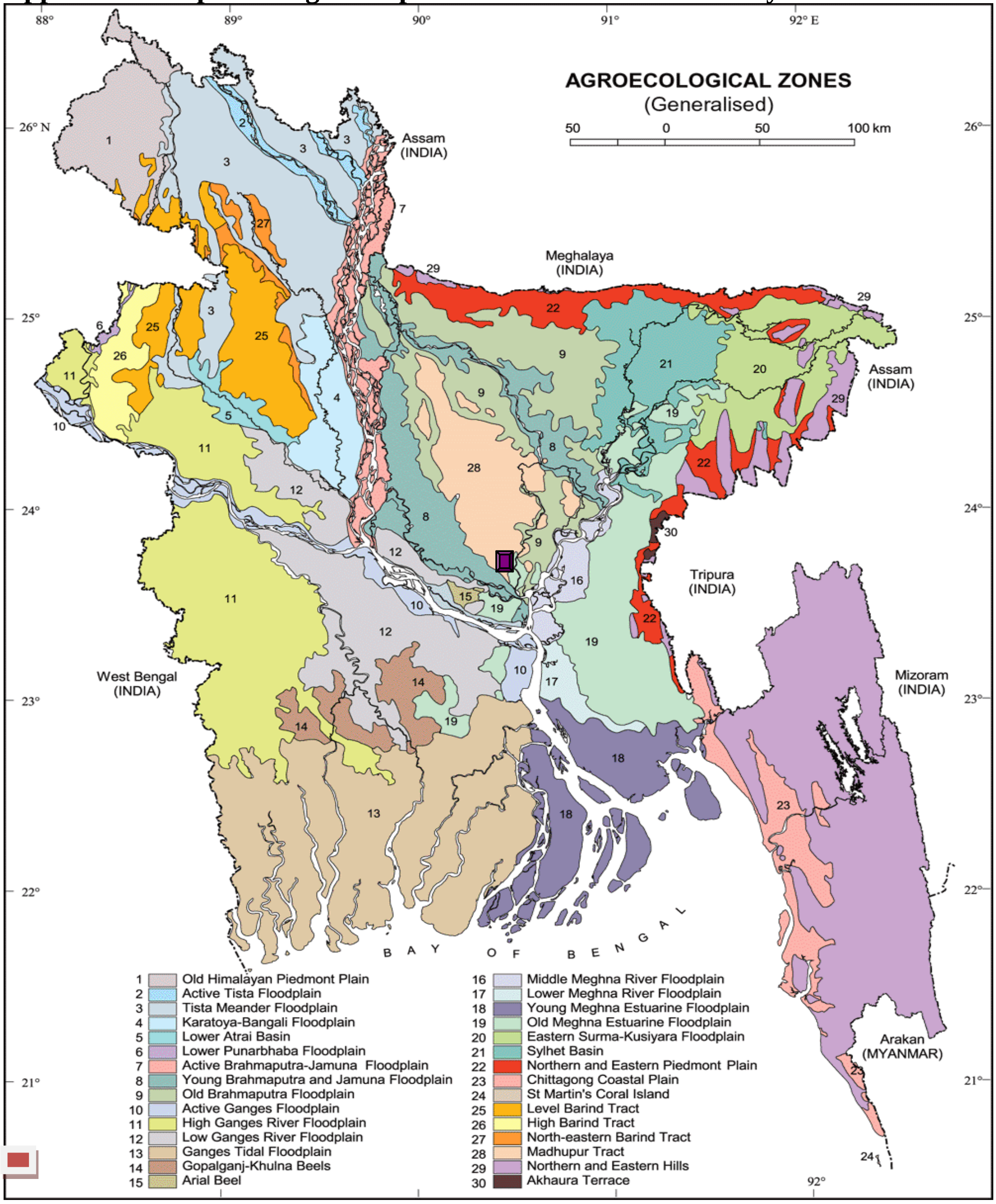
# APPENDICES

## Appendix I. Map showing the experimental site under the study



The experimental site under 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 (1:2.5 soil to water) | 5.55 | Jackson, 1958 |
| **10** | CEC | 11.23 | Chapman, 1965 |

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

## Appendix III. Monthly average Temperature, Relative Humidity and Total Rainfall and sunshine of the experimental site during the period from November, 2013 to May, 2014

| Month | Air temperature (°c) | | Relative humidity (%) | Rainfall (mm) (total) |
|---|---|---|---|---|
| | Maximum | Minimum | | |
| November, 2013 | 28.10 | 6.88 | 58.18 | 1.56 |
| December, 2013 | 25.36 | 5.21 | 54.30 | 0.63 |
| January, 2014 | 21.17 | 15.46 | 64.02 | 0.00 |
| February, 2014 | 24.30 | 19.12 | 53.07 | 2.34 |
| March, 2014 | 29.78 | 22.37 | 48.66 | 0.12 |
| April, 2014 | 29.80 | 23.40 | 47.76 | 5.90 |

Source: Weather station, Sher-e-Bangla Agricultural University, Dhaka – 1207

# VARIABILITY AND INTERRELATIONSHIPS OF YIELD AND YIELD CONTRIBUTING TRAITS IN $F_5$ POPULATION OF BORO RICE (*Oryza sativa* L.)

**BY**

**MD. GOLAM ROBBANI**

## ABSTRACT

The experiment was conducted with 29 genotypes of rice at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period of December, 2013 to May, 2014 to estimate the variability and interrelationship between yield and yield contributing characters and their direct and indirect effect on yield. The experiment was laid out in Randomized Complete Block Design with three replications. All the genotypes varied significantly from each other for all the studied characters which indicate the presence of considerable variations among the genotypes. The PCV values were higher than the respective GCV values for all the characters under study. Plant height, total spikelet per panicle, number of filled grains per panicle and number of unfilled grains per panicle showed high genotypic and phenotypic coefficient of variation. These characters also showed high heritability coupled with high genetic advance and very high genetic advance in percentage of mean which is normally more helpful in predicting the genetic gain under selection. Correlation co-efficient analysis revealed that yield per hectare had significant positive association with panicle length, number of secondary branches per panicle, total number of spikelet per panicle, number of filled grains per panicle and yield per plant. Path coefficient analysis revealed that number of filled grains per panicle showed the highest positive direct effect on yield per hectare followed by panicle length, number of secondary branches per panicle and yield per plant. Considering variability, heritability, genetic advance, correlation co-efficient and path analysis, number of filled grain per panicle showed high heritability, genetic advance, high significant positive correlation and the highest positive direct effect on yield per hectare.

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***December, 2014***

***The Author***

***SAU, Dhaka***

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# LIST OF ABREVIATIONS

| **Abbreviation** | **Full Name** |
|---|---|
| % | Percent |
| ºC | Degree Celsius |
| $\sigma^2$ p | Phenotypic variance |
| $\sigma^2$ g | Genotypic variance |
| $h^2$ b | Heritability in broad sense |
| AEZ | Agro-Ecological Zone |
| Agril. | Agricultural |
| ANOVA | Analysis of variance |
| BARI | Bangladesh Agricultural Research Institute |
| BBS | Bangladesh Bureau of Statistics |
| BD | Bangladesh |
| Cm | Centimeter |
| CV% | Percentage of Coefficient of Variation |
| Df | Degrees of Freedom |
| *et al.* | And others |
| etc. | Etcetera |
| $F_5$ | The third generation of a cross between two dissimilar homozygous parents |
| FAO | Food and Agricultural Organization |
| gm | Gram |
| G | Genotype |
| GA | Genetic Advance |
| GCV | Genotypic coefficient of variation |
| Ha | Hactare |
| J. | Journal |
| Kg | Kilogram |
| M | Meter |
| MSS | Mean sum of square |
| MP | Murate Potash |
| MOA | Ministry of Agriculture |
| $m^2$ | Square meter |
| PCV | Phenotypic coefficient of variation |
| RCBD | Randomized Complete Block Design |
| SAU | Sher-e-Bangla Agricultural University |
| T | Ton |
| TSP | Triple Super Phosphate |