COMPARATIVE TRIAL AND VARIABILITY STUDY IN TEN ADVANCED AUS RICE *(Oryza sativa* L.*)* LINES FOR SHORT DURATION AND HIGHER YIELD

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CERTIFICATE

This is to certify that thesis entitled, ***"Comparative trial and variability study in ten advanced aus rice (Oryza sativa L.) lines for short duration & higher yield"*** *submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE in GENETICS AND PLANT BREEDING,*** *embodies the result of a piece of bona fide research work carried out by* ***KHALEDA PARVIN FAHMIDA****, Registration No.* **10-04036** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

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Place: Dhaka, Bangladesh

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DEDICATED
TO
MY BELOVED PARENTS

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SAU, Dhak

COMPARATIVE TRIAL AND VARIABILITY STUDY IN TEN ADVANCED AUS RICE *(Oryza sativa* L.*)* LINES FOR SHORT DURATION AND HIGHER YIELD

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ABSTRACT

The experiment was conducted with ten genotypes and two check varieties of rice at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period of April 2015 to September 2015 to estimate the comparative trial and to select high yielding and short duration genotypes of rice *(Oryza sativa* L.) and also to find out the genotypes which have potential traits for using in further breeding programs as parent materials. The experiment was conducted using Randomized Complete Block Design with three replications. All the genotypes compared significantly with each other and also with two check varieties for all the studying characters indicated the presence of considerably variations among the genotypes studied. Comparatively phenotypic variances were higher than the genotypic variances and also the PCV values were higher than the respective GCV values for all the characters under study. Highest phenotypic and genotypic variances were showed in plant height (127.32%), total no of spikelet per panicle (803.16%), number of filled grain per panicle (594.19%). On the other hand, the significant positive correlation with seed yield per hectare was found in days to flowering (G= 0.918, P= 0.706), days to maturity (G= 0.835, P= 0.637), plant height (G= 0.628, P= 0.550), number of primary branches per panicle (G= 0.866, P= 0.692), number of secondary branches per panicle (G= 0.834, P= 0.667), total no of spikelet per panicle (G= 0.648, P= 0.465), number of filled grain (G= 0.754, P= 0.552), yield per plant (G= 0.806, P= 0.631). Path co-efficient analysis revealed that number of effective tiller per plant (0.847), panicle length (0.080), number of secondary branches per panicle (0.430), number of filled grain (0.747) and yield per plant (0.858) had the positive direct effect on yield per hectare. The residual effect was found 0.020. This effect indicates that 98% of the variability was accounted for fourteen yield and yield contributing traits in the present studies. Comparing with the check varieties G11(4.49 t) and G12 (3.64 t), the genotype G4 showed higher seed yield per plant (31.47) and yield per hectare (5.28) but duration was long (131 days). On the other hand G3 showed higher seed yield per plant (25.07) and yield per hectare (3.773) and also the duration is short than one check variety G12.

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SOME COMMONLY USED ABBREVIATIONS

FULL WORD	**ABBREVIATION**
Agro-Ecological Zone	AEZ
Agricultural	Agril.
And others	*et al.*
Accessions	ACC
Agronomy	Agron.
Analysis of variance	ANOVA
Bangladesh Agricultural Research Institute	BARI
Bangladesh Rice Research Institute	BRRI
Bangladesh Bureau of Statistics	BBS
Biological	Biol.
Centimeter	Cm
Co-efficient of Variation	CV
Ecology	Ecol.
Etcetera	etc.
Environmental variance	$\delta^2{}_e$
Figure	Fig.
Food and Agricultural Organization	FAO
Genotype	G
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	$\delta^2{}_g$
Gram	G
Genetics and Plant Breeding	GEPB
Heritability in broad sense	h^2b
Journal	J.
Kilogram	Kg
Meter	M
Mean Sum of Square	MSS
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	$\delta^2{}_p$
Randomized Complete Block Design	RCBD
Replication	R
Research	*Res.*
Science	*Sci.*
Sher-e-Bangla Agricultural University	SAU

CHAPTER I

INTRODUCTION

Rice is recognized as the seed of two important grass species like *Oryza sativa* (Asian rice) or *Oryza glaberrima* (African rice). Rice (*Oryza sativa* L.) is a monocotyledonous angiosperm. It belongs to the family Gramineae and the genus *Oryza*. The 2n number of chromosomes of rice is 24. Rice a cereal food crop;it is the most widely consumed staple food for a large part of the world's human population, especially in Asia. It is the agricultural commodity with the third-highest worldwide production, after sugarcane and maize (FAOSTAT, 2012). Since maize is mostly grown for purposes other than human consumption, rice is the most important grain with regard to human nutrition and caloric intake, providing more than one-fifth of the calories consumed worldwide by humans. There are more than 40,000 varieties of rice that grow on every continent except on Antarctica. Over 4,000 years ago, some researchers put on view that rice may have been indigenous to India.

Rice is the most important staple food in Asia. More than 90% of the world's rice is grown and consumed in Asia, where 60% of the world's population lives. Rice accounts for between 35-60% of the caloric intake of three billion Asians (Guyer *et al.*, 1998). Over 150 million hectares of rice are planted annually, covering about 10% of the world's arable land. In 1999/2000, this amounted to some 600 million tons of rice seed, equal to 386 million tons of milled rice. With the world population estimated to increase from 6.2 billion in the year 2000 to about 8.2 billion in the year 2030, the global rice demand will rise to about 765 million tons, or 533 million tons of milled rice (FAO, 2002). For almost three decades since the Green Revolution, the rice yield growth rate was approximately 2.5% per year. During the 1990s, however, this has decreased to only 1.1% (Riveros and Figures, 2000).

Rice is cultivated in Bangladesh throughout the year as Aus, Aman or Boro. Aman (broadcast and transplanted) is generally cultivated in December-January, Boro in March-May, and Aus in July-August cropping seasons. Aus are the pre-monsoon upland rice growing under rainfed conditions. The aus rice is direct or broadcast seeded during March and April after the pre-monsoon shower and harvested between July and August.

Aus are one of the major crops in Bangladesh. It has been contributing to food production in addition to other two rice (aman and boro) crops. The weather condition for aus cultivation was favorable in the growing stage this year. Total area under Aus crop has been estimated at 1.05 million hectares in 2013-2014, (BBS, 2013-2014). Average yield rate of (2013-2014) has been estimated at 2.213 metric tons per hectare which is 8% higher as compared to that of last year (2012-2013) (BBS, 2013-2014). Total Aus production (husked paddy) of 2013-2014 has been estimated at 2.326 million metric tons as compared to 2.158 million metric tons which 7.77 % higher than that is of last (2012-2013) (BBS, 2013-2014).

The Aus rice area and production is decreasing continuously comparing to Boro, which is dominated rice crop in Bangladesh. Boro rice cultivation fully depends on irrigation and the pressure of ground water is increasing day by day and ground water level is going down but Aus rice requires only 5% supplement irrigation and the pressure of ground water is required to be low for Aus than Boro. It is necessary to transfer Boro cultivated area to Aus and also make sure the food security of the country. So if we do forecast the Aus rice area and production then it would help the policy makers to formulate decision in this regard.At the same time the total rice growing area is being continuously declined at about 0.61 per annum due to urbanization and industrialization. So attempts should be made to increase the yield per unit area. A considerable improvement has been done through traditional rice breeding. Traditional rice breeding has made significant progress towards higher yield, improved quality, greater disease resistance and other important characters of agricultural importance in the past and even in future, it will still play an important role. Several high yielding rice varieties were developed through the application of cross. Now the revolutionary changeof climate, affect the yield of rice. So we have badly needed of short duration high yielding variety to avoid bad effect of climate change.

For the improvement of growth, physiological and panicle characters; investigation on their genetic system is vitally important. Studies on character association, combining ability and components of genetic variance will serve the above purpose.Genotypic and phenotypic interrelationships of morphological and physiological characters and their possible influence on yield attributes needs to be analyzed for interpreting the results of breeding works meaningfully.

Therefore, the present study was undertaken with the following objectives:

- To select short duration genotype of Aus rice
- To develop high yielding genotype of Aus rice
- To find out the genotypes which have potential traits for using in further breeding programs as parent materials.

CHAPTER II

RIVIEW OF LITERATURE

Rice is the staple food, of Bangladesh where it constitutes a major part of human diet. It is the order of the day to take better steps for production and quality improvement of our local cultivars. In that respect so many strategies are applied for the enhancement of quality and yield of different rice varieties and cultivars to gain improved production. Due to application of different techniques in breeding process remarkable improvement has been brought in both productivity and quality of rice for using it in human diet. A large number of literatures are available on variability, genetic diversity, correlation and path analysis of yield and yield contributing characters of *Oryza* grown under a particular environment. An attempt has been made here to summarize the findings of this study relevant to the present investigation. The whole review has been divided into following sections, namely-

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

2.1 Genetic Variability, heritability and genetic advance

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

Sinha *et al.* (1985) investigated on gene systems governing yield and its component characters in rice. Analysis was performed, by 2 of B. Griffing’s methods, of data on some botanical characters, yield and various components of yield and some aspects of grain quality from a 6-variety complete diallel cross and a 7- variety half diallel cross. Additive effects were more important than non-additive in every character except height and number of tillers, indicating the suitability of the pedigree method in breeding, though the use of recurrent selection and biparental mating would make it possible to exploit the dominance effects which in some characters were not negligible. The best general combiners for yield and for some components were T141, ASDI and Vijaya, but for protein percentage SLO16 and ADY27 were the best. Vijaya × T141 and Vijaya × ASDI showed high specific combining ability for yield.

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

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

Das *et al*. (l992); evaluated 30 rice genotypes for variability analysis and found that plant height, days to 50% flowering, number of filled grains per panicle, panicle length, 1000-grains weight and days to maturity had high genetic coefficient of variation.

Vivekzuradan and Subramanian (l993) evaluated 28 rice genotypes for the magnitude of genetic divergence using Mahalanobis's D2 statistics. The population was grouped into five clusters.

Plant height and grain yield contributed considerably, accounting for 85% of total divergence. The geographic diversity has not been found related to genetic diversity.

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

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

Pandey and Awasthy (2001), studied genetic variability of 21 genotypes of aromatic rice and reported significant genetic variability for plant height, days to 50% flowering, panicle per hill, panicle length, grains per panicle, grain length and breadth. They concluded that these traits play a major role in the enhancement of production of grain yield and serve as important criteria for screening germplasm to identify the suitable aromatic rice cultivars.

Basher (2002), studied genetic divergence among 36 genotypes by using D2 statistics for 15 characters related to yield and its contributing characters. The genotypes were grouped into six clusters. The results revealed that the harvest index had the highest contribution followed by tillers per plant, panicle length, 1000-grains weight, filled grains per panicle, days to maturity and leaf photosynthetic rate towards genetic divergence.

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

Mishra *et al.* (2003); evaluated 16 rice cultivars and their 72 F1 hybrids for genetic diversity and grouped in twelve clusters using Mahalanobis's D2 statistics. The values revealed that plant height, ear bearing tillers per plant, panicle length, 1000-grain weight, hulling and milling percentage, biological yield, harvest index, kernel length after cooking, gelatinization temperature and grain yield were the main factors for differentiation.

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

Madhavilatha *et al.* (2005) were evaluated Fifty four elite rice genotypes for their variability with regards to grain yield, yield components (plant height, number of effective tillers per plant, panicle length. number of grains per panicle, fertility percentage, days to 50% flowering, days to maturity and harvest index) and quality parameters (hulling recovery, kernel length (L), breadth (B), L/B ratio and elongation ratio, volume expansion ratio and 1000-grains weight). Estimation of heritability and genetic advance were also obtained for the above traits.

Houque and Ahasanul (2013) studied sixty advanced breeding lines including three check varieties of rice were evaluated under field condition during the period from March to December, 2012, at the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh following Randomized Complete Block Design (RCBD) with three replications. The aims were to find out early maturing rice genotypes and the association among thirteen morphophysiological traits including yield along with the diversity among the rice genotypes. The genotypes differed significantly for all the traits viz., days to panicle initiation, days to 50% flowering, days to flowering completion, days to milking stage, days to dough stage, days to maturity, flag leaf area, plant height, effective tiller number per hill, panicle length, number of filled grain per panicle, number of unfilled grain per panicle and yield per plot. Considering all the traits genotype G28 (BAU94026-6-2-4-7-8-6-9-5) was earliest than all other genotypes and highest yielder than the check varieties G55 (BRRI dhan 27) and G56 (BR 26). The phenotypic co-efficient of variation (PCV) were higher than genotypic co-efficient of variation (GCV) for all the traits studied indicating that they all interacted with the environment to some extent. All the studied traits expressed moderate to high heritability estimates ranging from 33.20 to 99.25 percent. High heritability along with high genetic advance was noticed for the traits, number of filled grain per panicle, flag leaf area, plant height and days to maturity. Yield was significantly positively correlated with number of filled grain per panicle and significantly negatively correlated with days to milking stage, days to dough stage, days to maturity, panicle length and number of unfilled grain per panicle. Path analysis suggested that number of filled grains per panicle was related to the yield mostly through the direct positive effect. The selection index revealed that the genotype G16 (BAU7-440-11) possessed the highest selection score and was ranked as the best. Cluster analysis based on D2 values exhibited seven distinct clusters with the range of 3 genotypes in cluster V to 16 in cluster I. Regularly the inter-cluster distances were greater than the intra-cluster distances suggesting wider diversity among the genotypes. Maximum inter cluster distance was observed between cluster III and VII followed by cluster II and VII indicating the possibility to obtain the heterotic progenies, by attempting the crosses among the genotypes of these groups. The results of principal component analysis (PCA) revealed that first three components accounted for more than 80% of total variation. The highest variability was observed in days to 50% flowering, number of filled grain per panicle, number of unfilled grain per panicle, yield per plot, flag leaf area and plant height. Again diversity at molecular level among thirty genotypes, selected based on earliness and morphometric diversity was evaluated through five SSR markers for more precision. Three primers viz., RM147, RM167 and RM215 showed polymorphism. A total of 17 alleles were detected among the 30 rice genotypes with an average of 5.66 alleles per locus. Polymorphism Information Content (PIC) ranged from 0.356 to 0.798 with an average of 0.543. A dendogram based on total microsatellite polymorphism grouped 30 genotypes into four major clusters at 0.39 similarity coefficient differentiating early maturing genotypes from others. The information about the genetic diversity will be very useful for proper identification and selection of appropriate parents for future breeding programs, including gene mapping. The results also showed that microsatellite markers linked to genes or QTLs controlling growth duration properties are suitable tools for marker assisted selection (MAS) to select rice lines with short growth duration.

Humayun and Khaleq (2015) studied to determine some of the morphological characters of local Aus rice germplasm viz. Ausdhan, Lema, Chitri, Ausaloi, Ausgarabinni, Kajli, Gori, Pankhiraj, Kumriaus,Surjomoni and Kalokochi at Bangladesh Agricultural University (BAU), Mymensingh. The morphological characters yield and yield contributing components were significantly different among the tested germplasm. Kajli produced maximum tillers (13 tiller hill-1), flag leaf area (57cm2), effective tillers (11 effective tiller hill-1), straw and grain yield (4 t ha-1). Ausgarabinni produced the highest plant height, panicle length and the highest filled grain panicle-1 but the lowest number of tillerhill-1, number of effective tiller hill-1, straw and grain yield. Ausaloi produced the lowest1000 grain weight (16g) and Pankhiraj yielded the highest harvest index. Among all, the shortest variety was Surjomoni. Kumriaus had the shortest growth duration (87 days) to maturity. The overall results of the field experiment demonstrated that Kajli had the best performance for grain yield.

The study was conducted at the Grain Quality and Nutrition Division, Bangladesh Rice Research Institute, Gazipur, Bangladesh during Aus season 2015-2016. Bangladesh has an agrarian economy in which rice is the dominant crop. Despite pressure from over population, the country has reached self-sufficiency in rice production through Boro rice seasons by using huge amount of ground water. However, ground water irrigation has started to show serious consequences as energy costs are increasing, water levels are declining in the intensive irrigated areas of Bangladesh. So, Aus cultivation should increase in this regard to cope the challenges. In the present study, we have focused to evaluate the physicochemical and cooking properties of some Aus cultivars or landraces which were used to cultivate without irrigation or less irrigation in Bangladesh earlier in Aus season. Due to low yield potential, these cultivars were become outdated. The physicochemical parameters such as appearance, milling outturn (MOT), length (mm), L/B ratio, size and shape; chemical parameters such as Alkali Spreading Value (ASV), Apparent Amylose Content (AAC), protein content and cooking characteristics such as cooking time, Imbibition Ratio (IR), Elongation Ratio (ER) were studied and evaluated for nine (9) traditional cultivars or landraces in comparison with five (5) high yielding varieties (BRRI HYV) for Aus season. The MOT percentage is ranged from 67.4 to 72%. The highest MOT was found in Chakulia (71%). L/B ratio varied from 2.1 to 3.8 mm for varieties. Our data reveals that AAC varied from 21 to 28% and protein content varied from 7.0 to 10.0%. The highest AAC and protein content were found in the local variety of Goria (27.5%) and Bolorum (10.0%) respectively. Both showed intermediate level of ASV score (4.5). Since these traditional rice cultivars had shown superior grain quality parameters for few physicochemical and cooking parameter compare to HYV. So, the acquainted information might be helpful for plant breeders to focus on these examined superior Aus cultivars to select as parental materials for Aus rice breeding program in Bangladesh.

2.2. Correlation coefficient

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

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

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

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

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

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

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

Manuel and Palanisamy (1989) derived correlation coefficients on nine yield components in six cultivars and their F_1 hybrids. Grain yield was significantly and positively correlated with days to flowering, plant height, flag leaf area, panicles/plant, panicle length and grains/panicle.

Sampath *et al.* (1989) generated information on yield correlations which was derived from data on grain yield and 12 related traits in 14 intervarietal hybrids and their parents grown in 1983.Yield was correlaed significantly with 100-grain weight, panicle length and number of grains/panicle in the parents but not the hybrids in which yield was correlated with the number of primary and secondary branches/panicle, number of days to panicle emergence and tiller number.F_1 mean performance was correlated with the mid parental and better parent values, the correlation being less marked with the better parent value, suggesting that the high performance of the F_1's was not due to the better parent alone.

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

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

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

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

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

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

2.3 Path coefficient analysis

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

Iftekharuddaula *et al*. (2001) studied twenty-four modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for grain yield and its component characters. Path analysis revealed that higher number of grains/panicle, bold grains, more panicles/m2 and higher harvest index had positive and higher direct effect on grain yield.

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

Mahto *et al*. (2003); evaluated twenty six early maturing upland rice genotypes for genetic variation, character association and path analysis based on days to 50% flowering. Plant height, number of panicle per plant, panicle length, number of branches per particle.Number of filled grains per panicle, 100.-seed weight and grain yield. The genotypic variance ranged from 5.36 for panicle length to 24.83 for grain yield. The difference between phenotypic and genotypic coefficient of variation was minimum for 1000-grain weight (0.12) and days to 50% flowering (0.13). High values of heritability were observed for 1000-grains weight (98.30%) and days to 50% flowering (97.33%). The number of grains per panicle and panicle length showed a significant difference between phenotypic and genotypic coefficient of variation. The association of high heritability with high genetic advance was observed for 1000-grain weight, days to 50% flowering, grain yield, number of branches per particle and plant height. Grain yield was positively and significantly correlated with days to 50% flowering, number of panicles per plant, number of branches per panicle and number of filled grains per panicle.

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

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

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

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

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

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

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

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

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

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

2.4. Genetic diversity

Soni *et al.* (1999) assessed the genetic divergence of 132 rice genotypes consists of 128 traditional cultivars and four standard genotypes for 18 grain quality traits. The genotypes were grouped into ten clusters. The maximum divergence was found between clusters VI and VII. Ten genotypes were found as promising segregates for grain quality based on mean performance, genetic distance and clustering pattern.

Rather *et al.* (2001) experimented on the genetic divergence of 56 rice cultivars in Jammu and Kashmir of India during the rainy season of 1997 and 1998. Days to 50% flowering, leaf length, leaf breadth, productive tillers per plant, plant height, days to maturity, total grains per panicle, sterile grains per panicle, panicle length, harvest index, grain yield, grain length and breadth ratio, thousand grains weight were showed significant in variation. Geographical distribution was not found significant to genetic divergence. Cultivars of cluster II and IV were found as promising genotypes for future hybridization programs based on the mean performance of plant height, maturity, spikelet fertility, grain yield and inter-cluster distance.

Zafar *et al.* (2004) studied on genetic divergence of 124 landrace genotypes from various parts of Pakistan for seven quantitative and eight qualitative characters using simple statistic. The coefficient of variation was more than 10% for all characters with the exception of grain length. Compared with the modern cultivars, the landrace genotypes showed high range and coefficient of variation for the traits like days to heading, days to maturity but lower values for panicle and grain length. Days to heading was positively correlated with maturity (r = 0.838) and grain length (r = 0.452). Plant height showed positive and significant correlation with panicle length (r = 0.452) indicating the importance of plant height in improving panicle length. Seven genotypes with best performance for individual character were identified. To exploit their genetic potential, these genotypes can beneficially be used in the breeding programs.

Suman *et al.* (2005) evaluated genetic diversity of 114 rice genotypes for 16 metric characters using Mahalanobis's D^2 statistic. The genotypes were grouped into ten clusters. There was revealed no relation between geographical distribution and genetic divergence. The maximum inter-cluster distance was observed between clusters V and X. The most contributing character was harvest index (26.42%) towards divergence followed by seed density (18.35%) and total number of tillers per plant (15.52%). Cluster X had maximum number of spikelet per panicle, panicle length, and filled grains per panicle, plant yield and biological yield. Cluster III exhibited lowest means for plant height, days to 50% flowering, panicle length, 100-grain weight. The genotypes under III and X were suggested as parents for hybridization.

Bose and Pradhan (2005) estimated the nature and the magnitude of genetic divergence in 35 deep water rice genotypes using Mahalanobis's D^2 statistic. The genotypes were grouped into ten clusters showing fair degree of relationship between geographic distribution and genetic divergence. The maximum intra cluster divergence was revealed in cluster IV while the maximum inter cluster distance was revealed between clusters IX and X. All the minimum and maximum cluster values were distributed in relatively distant clusters. The major contributing characters were plant yield, days to 50% flowering, EBT/m^2 and plant height to genetic divergence.

Chandra *et al.* (2007) determined the nature and magnitude of genetic divergence of 57 rice genotypes including 32 local rice germplasm for 14 agro-morphological traits using Mahalanobis's D^2 statistic and Anderson's canonical analysis. The genotypes were grouped into five clusters following Tocher's method. Three clusters were multi-genotypic, while the other two were mono-genotypic. The maximum divergence was found between clusters III and IV (D^2 = 3387.9), followed by clusters III and V (D^2 = 2808.2) and cluster II and III (D^2 = 1908.7). The highest intra-cluster distance was found in cluster I, followed by cluster II. The maximum numbers of genotypes (50) from different origin were fallen in cluster I. The genetic divergence was not related to geographical distribution. The most contributing characters to genetic divergence were found in grain length and breadth ration, 1000-grain weight, grain length, grain yield and biological yield.

Akter *et al.* (2009) estimated genetic divergence of 44 genetically diverged restorers of rice using Mahalanobis's D^2statistic and principal component analysis. The genotypes were grouped into five clusters. The lines chosen from the same ecogeographic region were found scattered in different clusters which indicated that genetic diversity and geographic distribution were not necessarily related. The inter cluster distances were higher than the intra cluster distance reflecting wider genetic diversity among the genotypes of different groups. The maximum inter cluster distance was revealed between clusters II and V followed by clusters I and IV, while the maximum intra cluster was revealed in cluster I indicated that the highly divergent types existed in these clusters. Plant height was found to be the maximum contributors towards the total divergence. The highest mean value was found for the characters grain yield, number of effective tillers/m^2, plant height, days to maturity, number of spikelet per panicle, spikelet fertility, panicle length, panicle weight and 1000-grain weight that could be used for the selection of genetically diverse restorers to develop heterotic hybrid combinations with a promising CMS line.

Rajesh *et al.* (2010) assessed genetic diversity in 29 land races of rice using Mahalanobis's D^2 statistic for eight quantitative characters including grain yield. The genotypes were grouped into five clusters. Geographical distribution was not found related to genetic divergence. The characters days to first flowering and single plant yield contributed maximum towards genetic divergence. The maximum inter-cluster distance was revealed between cluster IV and V. The genotypes in these clusters *Vattan* and *Vellai Chitraikar* (cluster IV) and *Thulasi Munjari* (cluster V) may serve as potential as potential donors for future hybridization program.

Hosan *et al.* (2010) assessed the nature and magnitude of genetic divergence of 20 rice land races collected from different ecological regions of Bangladesh. Based on twelve characters, the genotypes were grouped into five clusters. There was no parallel relationship was found between geographical distribution and genetic divergence. Inter-cluster distances were found higher than intra-cluster distances reflecting wider genetic diversity among the genotypes of different groups. The highest divergence was found among the genotypes under cluster IV as it exhibited highest intra-cluster distance. The maximum inter-cluster distance was found between clusters II and V and between clusters I and III. The characters contributing towards the total divergence were number of filled grains per panicle, number of panicles per plant, biomass index and grain yield. The appropriate selection of high yielders from genotypes having these characters in the genetically distant cluster could be used in the high yielding variety development programs.

De Silva *et al.* (2010) studied on the genetic divergence of 68 rice genotypes, mostly with Indian origin and few with IRRI-Philippines, Pakistan and Japan, using Mahalanobis's D^2 statistic for fourteen traits. The genotypes were grouped into nine clusters. There was no relation of geographical distribution to genetic divergence. The maximum contributing characters towards the genetic divergence were grain yield per plant, number of grains per panicle, plant height and kernel length per breadth (L/B) ratio. Maximum intra cluster distance was found in cluster VII consisting of four rice genotypes having the highest mean performance for number of effective tillers per plant, panicle length, hulling (%), kernel length and kernel L/B ratio. The maximum inter cluster distance was found between cluster V and VII indicating that they were the most divergent clusters.

Vennila *et al.* (2011) studied genetic divergence for different yield and quality traits in 42 rice genotypes from different rice eco-geographical regions of India. The genotypes were found significantly difference for all the characters studied and these genotypes were grouped into twenty three clusters. There was no relationship between geographical distribution and genetic divergence. The maximum inter-cluster distance was found between clusters III and XIII, while the maximum intra-cluster distance was found in clusters XI followed by cluster VI. The characters like number of grains per panicle, plant height, and grain length and grain breadth contributed maximum towards genetic diversity. Therefore, these characters could be given for the selection of genotypes for further crop improvement program.

Latif *et al.* (2011) studied on genetic divergence for blast resistant and susceptible genotypes using 13 morphological characters. The important contributing characters towards genetic divergence were plant height, days to flowering and maturity, panicle length, number of spikelet per panicle, number of filled grains per panicle, number of unfilled grains per panicle, 1000-grain and yield per hill in 14 rice genotypes. The first three principal components accounted for 78.72% of the total variation among resistant and susceptible rice genotypes. The genotypes were grouped into seven clusters according to Mahalanobis'sD^2 statistic and canonical vector analysis.

Yadav *et al.* (2011) assessed the nature and magnitude of genetic divergence of nine rice genotypes. Based on nine characters these genotypes were grouped and arranged in to three non-overlapping clusters by Tocher's method and Mahalanobis's D^2 statistic. There was no definite relationship between genetic divergence and geographical distribution of genotypes. The maximum inter-cluster distance was found between clusters I and III (D = 462.84), clusters II and III (D = 430.04) while highest intra cluster distance was found between III and II. The genotypes from these clusters may be used as potential donors for further hybridization program to develop varieties more tolerance to solidity.

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 April, 2015- September, 2015. The location of the site is 23° 64" N latitude and 90° 45' E longitude with an elevation of 8.3 meter from sea level.

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). Its 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.

3.3 Planting materials used

Twelve rice genotypes were used for the present study. Among twelve rice genotypes, tengenotypes were F5 materials and two genotypes 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.

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

Sl. No.	Designation	Genotypes	Source
1	(G1)	BR 21× BRRI dhan29 $F_5S_7P_5$	SAU,GEPB
2	(G2)	BR 21× BRRI dhan29 $F_5S_6P_3$	
3	(G3)	BR 21× BRRI dhan29 $F_5S_7P_2$	
4	(G4)	BR 21× BRRI dhan29 $F_5S_7P_2$	
5	(G5)	BR 21× BRRI dhan29 $F_5S_6P_{10}$	
6	(G6)	BR 21× BRRI dhan29 $F_5S_7P_1$	
7	(G7)	BR 21× BRRI dhan29 $F_5S_6P_9$	
8	(G8)	BR 21× BRRI dhan29 $F_5S_7P_4$	
9	(G9)	BR 24× BRRI dhan28 $F_5S_{10}P_{10}$	
10	(G10)	BR 24× BR 26 $F_5S_6P_4$	
11	(G11)	BRRI dhan 48 (Check variety)	
12	(G12)	BRRI dhan 55 (Check variety)	

SAU= Sher-e-Bangla Agricultural University
BRRI= Bangladesh Rice Research Institute
GEPB=Genetics and Plant Breeding

3.4 Methods

The following precise methods have been followed to carry out the experiment:

3.4.1 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 toincrease the temperature for facilitating germination. After 72 hours seeds weresprouted properly.

3.4.2 Seedbed preparation and seedling rising

The irrigated land was prepared thoroughly by three times ploughing and cross ploughing followed by laddering. Weeds and stubbles were removed. Twelve separate strips were made and sprouted seeds were sown in 25 Aprilof 2015. The seedlings were raised by maintaining irrigation with regular intervals and protectingfrom birds and insects and infestation of pest and diseases.

3.4.3 Preparation of main land and application of manure and fertilizer

Cowdung was applied to the experimental field and the plot was ploughed thoroughly by two ploughing and cross ploughing followed by harrowing with a tractor drawndisc plough to attain a good puddle. Four days later the final ploughing and cross ploughing were done and weeds and stubbles were removed. The fertilizers Nitrogen, Phosphorous, Potassium, Sulpher and Boron in the form of Urea, TSP, MoP, Gypsum and Borax, respectively were applied. The entire amount of TSP, MoP, Gypsum, Zinc sulphate and Borax all these fertilizers recommended by BRRI were applied during the final preparation of land. Urea was applied in three equal installments.The first 1/3rd(1.693 kg) applied at 4-5 tillering, the second 1/3rd (1.693kg) and last one third at panicle initiation stage. The dose and method of application of fertilizer are shown in (Appendix IV).

3.4.4 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 27m x 15m = 405m^2. Each plot size was 4m x 2.2m and the distance between replication to replication was 1m. The spacing between lines to lines was 25cm. Seeds were sown in lines in the experimental plots on 25 April, 2015.

3.4.5 Transplanting

Thirty days old and healthy seedlings were transplanted to the main field on May 25, 2015followed by proper irrigation. One seedling per hill was transplanted maintaining 25 cm × 25 cm spacing from row to row and plant to plant, respectively. Twelve rice genotypes were distributed in each of the block through randomization process.

3.4.6 Intercultural operations

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

3.4.6.1 Irrigation and drainage

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

3.4.6.2 Gap filling

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

3.4.6.3 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.

3.4.6.4 Top dressing

After basal dose, the remaining doses of urea were top-dressed in 2 equal installments. The fertilizers were applied on both sides of seedlings rows with the soil. Field view of the experiment is presented in Plate 1.

3.4.6.5 Plant protection

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

Plate 1. Field view of the experiment

3.4.7 Crop harvesting

Harvesting was done from 16th August to 8th September, 2015 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 F5 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.

3.4.8 Data collection

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

I. Days to flowering

Difference between the dates of transplanting to the date of 50% flowering of a plot was counted and was recorded when 50% plant of a plot were at the flowering stage.

II. Days to maturity

Maturities of the crops of different combination were recorded considering the symptom such as moisture content of rice, color changing of the plant from greenish to straw colored appearance.

III. Plant height (cm)

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

IV. Number of total tillers per plant

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

V. Number of effective tillers per plant

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

VI. Panicle length (cm)

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

VII. Number of primary branches per panicle

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

VIII. Number of secondary branches per panicle

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

IX. Number of filled grains per panicle

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

X. Number of unfilled grains per panicle

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

XI. Total number of spikelet per panicle

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

XII. Yield per plant (gm)

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

XIII. Thousand seed weight (gm)

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

XIV. Yield per hectare (t/ha)

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

3.4.9 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 MSTATCsoftware program and then phenotypic and genotypic variance was estimated by theformula used by Johnson *et al.* (1955). Heritability and genetic advance weremeasured using the formula given by Singh and Chaudhary (1985) and Allard (1960).Genotypic and phenotypic co-efficient of variation were calculated by the formula ofBurton (1952). Genotypic and phenotypic correlation coefficient was obtained usingthe formula suggested by Miller *et al.* (1958) and Johnson *et al.* (1955); and path coefficientanalysis was done following the method outlined by Dewey and Lu (1959).

3.4.9.1 Estimation of variability

i) Estimation of genotypic and phenotypic variances

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

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

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

ii) 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

δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{x}$ = Population mean

iii) 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

iv) Estimation of genetic advance:

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

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

Where, GA = Genetic advance

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

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

δ_p = Phenotypic standard deviation

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

v) Estimation of genetic advance in percentage of mean

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

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

vi) Estimation of simple correlation co-efficient:

Simple correlation co-efficient (r) was estimated with the following formula (Clarke, 1973; Singh and Chaudhary, 1985).

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

Where, $\sum$ = Summation

x and y are the two variables correlated

N = Number of observation

vii) Path co-efficient analysis:

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

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

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

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

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

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):

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

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

RESULT & 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 tillers/plant, number of effective tillers/plant, panicle length, number of primary branches/panicle, number of secondary branches/panicle, total number of spikelet/panicle, number of filled grain of main tiller, number of unfilled grain of main tiller , dry seed yield per plant (g) , thousand seed weight and yield per hectare (t/ha) . The data were statistically analyzed and thus obtained results are described below under the following heads:

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

4.1 Variability among the twelve genotypes for rice

The analysis of variance (ANOVA) of the data on different yield components and yield of twelve genotypes of *Oryza sativa* are given in Table 2. The mean performance, range and CV (%) over three replications for all the characters of twelve 12 materials of *Oryza sativa* are presented in Table 3, Table4 and Table 5. Phenotypic variance, genotypic variance, phenotypic coefficient of variation and genotypic coefficient of variation for different yield related characters are presented in Table6.

4.1.1. Days to flowering

There were significant variations among the genotypes (204.081) for days to flowering (Table 2). Among 12 genotypes, the lowest (70 days) days to 50% flowering were observed in G5 which is very closed to G1 (71.67 days) , G2 (71.67 days) , G6 (71.67 days) and highest (93.33 days) was observed in G10 (Table 3a).

Whereas the G11 (BRRI dhan 48) and G12 (BRRI dhan 55) were recorded with days to 50% flowering 87.00 days and 80 days respectively. The G1, G2 and G3 were shown lower days to 50% flowering than the two checks varieties.

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

Characters/Variety	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 11	Error (r-1)(g-1) = 22
Days to flowering	16.778	204.081**	6.020
Days to maturity	3.250	269.705**	2.705
Plant height (cm)	50.790	338.910**	21.527
Total no of tiller/plant	2.020	9.181**	1.326
Number of effective tiller/plant	0.086	3.365 **	0.568
Panicle length (cm)	0.803	2.924**	0.726
Number of primary branches/panicle	0.434	1.819**	0.251
Number of secondary branches/panicle	5.517	5.517**	5.650
Total no of spikelets/panicle	289.569	1909.322**	250.082
Number of filled grain per panicle	232.021	1444.664**	168.955
Number of unfilled grain per panicle	23.962	102.576**	22.184
Yield per plant (fresh) (g)	8.812	73.038**	11.806
Yield/plant (dry) (g)	14.763	75.931**	11.732
Thousand seed weight	1.818	4.182**	0.733
Dry weight per square meter	3211.000	23197.848**	6291.485
Yield per hectare	0.029	1.976**	0.322

** Denote Significant at 1% level of probability

Variations in flowering are showing in Plate 2a and Plate 2b.

Phenotypic and genotypic variance for days to flowering was observed as 72.04 and 66.02, 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 (10.96%) and genotypic coefficient of variation (10.49%) (Table 5) 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), Vanga (2008).

4.1.2 Days to maturity

Significant variations were observed among the genotypes (269.705**) for days to maturity (Table 2).The highest days to maturity was taken in G4 (131.7 days) and the minimum days to maturity was taken in G1 G2 (103.7 days) and G3 (103.7 days) among 12 genotypes (Table 3a) (Figure 1). The G1, G2 and G3 were shown lower days to maturity than checks the G11 (BRRI dhan 48) (112 days) and G12 (BRRI dhan 55) (111 days).Variation in days to maturity presented in Plate 3.

The phenotypic and genotypic variance for days to maturity was observed (91.70) and (89.00) respectively with high differences between them, suggested that the expression of the genes controlling this trait is high response to environment. The phenotypic coefficient of variation (8.69%) was less high than genotypic coefficient of variation (8.56%) (Table 5) suggested that environment has least influence on the expression of the genes controlling this trait. Similar result for this trait was also observed by Ketan and Sarkar (2014).

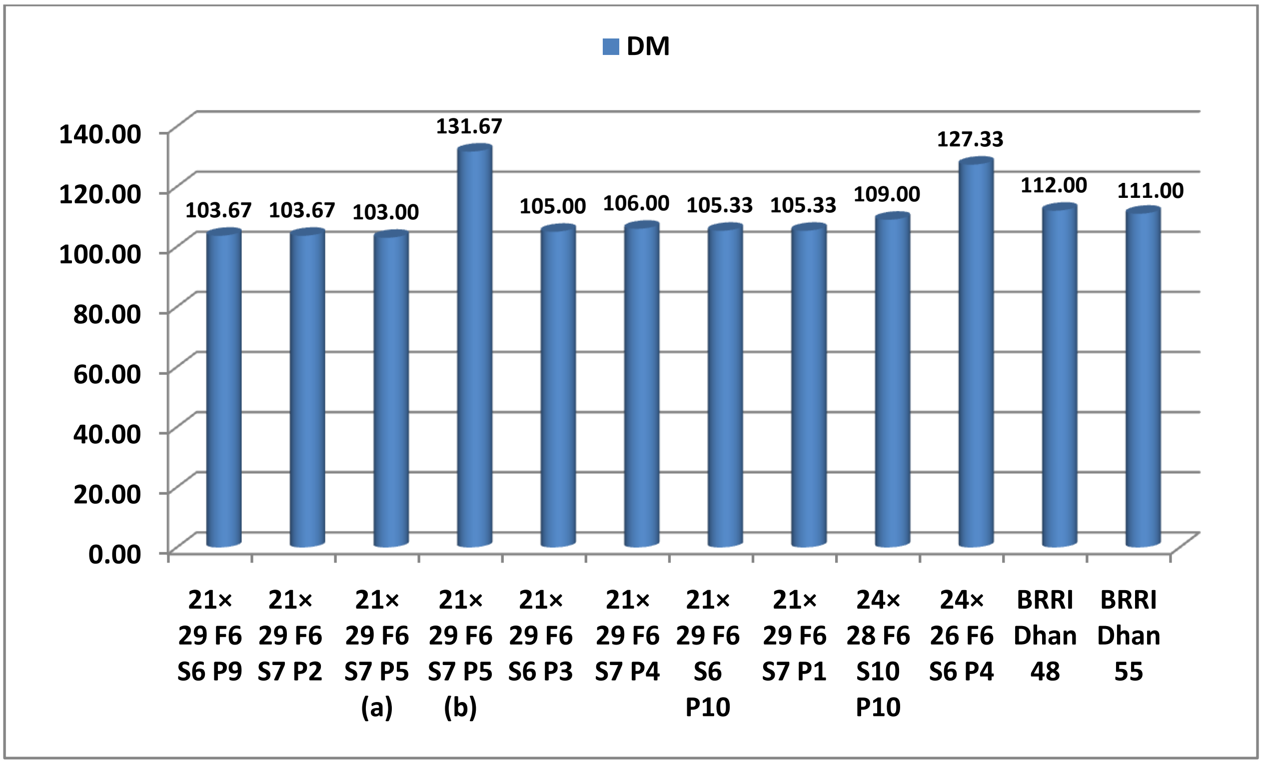

Figure 1: Graphical representation of days to maturity of rice

G1 = 21× 29 F6 S6 P9, G2 = 21× 29 F6 S7 P2, G3 = 21× 29 F6 S7 P5 (a), G4 = 21× 29 F6 S7 P5 (b), G5 = 21× 29 F6 S6 P3, G6 = 21× 29 F6 S7 P4, G7 = 21× 29 F6 S6 P10, G8 = 21× 29 F6 S7 P1, G9 = 24× 28 F6 S10 P10, G10 = 24× 26 F6 S6 P4, G11 = BRRI dhan 48 and G12= BRRI dhan 55.

4.1.3 Plant height (cm)

Significant variations were observed among the genotypes (338.910**) for plant height (Table 2). In this study the highest plant height was observed in G4 (134.6 cm) whereas the minimum plant height was observed in G6 (92.60 cm) (Table 3a). The G6 (92.60 cm) were shown lower plant height than two checks the G11 (BRRI dhan48) (102.9cm) and G12 (BRRI dhan55) (97.77 cm).Variation in plant height is presented in Plate 4.

Table 3a. Mean performance of 12 genotypes of *Oryza sativa* L. in respect of seven important characters

Genotype	DF	DM	PH	NTT/P	NET/P	PL/P	NPB/P
G1	71.67	103.7	107.9	12.53	12.20	25.71	7.233
G2	71.67	103.7	108.0	11.90	11.53	25.56	7.533
G3	73.33	103.0	108.7	12.87	12.17	25.53	7.433
G4	90.67	131.7	134.6	14.47	14.23	26.20	9.800
G5	70.00	105.0	109.2	13.67	12.80	23.80	7.900
G6	71.67	106.0	92.60	15.00	13.42	23.58	7.233
G7	73.33	105.3	101.5	17.73	14.80	25.73	8.167
G8	73.33	105.3	108.2	12.47	11.70	25.44	6.933
G9	73.33	109.0	108.2	14.93	13.23	25.85	8.033
G10	93.33	127.3	119.2	13.70	12.77	26.40	7.933
G11	87.00	112.0	102.9	15.63	14.10	23.95	8.467
G12	80.00	111.0	97.77	16.33	13.97	24.25b	8.600

**Values are statistically identical at 5% level of probability.

DF = Days to flowering, DM = Days to maturity, PH = Plant height (cm), NT = Total no of tiller/plant, NET = Number of effective tiller/plant, PL = Panicle length (cm), NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle.

G1 = 21× 29 F6 S6 P9, G2 = 21× 29 F6 S7 P2, G3 = 21× 29 F6 S7 P5 (a), G4 = 21× 29 F6 S7 P5 (b), G5 = 21× 29 F6 S6 P3, G6 = 21× 29 F6 S7 P4, G7 = 21× 29 F6 S6 P10, G8 = 21× 29 F6 S7 P1, G9 = 24× 28 F6 S10 P10, G10 = 24× 26 F6 S6 P4, G11 = BRRI dhan 48 and G12= BRRI dhan 55.

Table 3b. Mean performance of 12 genotypes of *Oryza sativa* L. in respect of seven important characters

Genotypes	NSB/P	TS/P	NFG/P	NUFG/P	Y/P	TSW	Y/ha
G1	22.75	128.2	103.0	25.50	26.43	22.47	22.20
G2	26.40	122.1	100.1	22.07	25.90	21.40	22.43
G3	24.63	131.6	111.0	23.97	25.07	17.87	21.90
G4	35.27	164.3	141.5	23.40	37.80	31.47	22.30
G5	26.43	127.5	103.1	21.40	27.07	17.53	21.47
G6	21.40	111.2	96.97	19.90	24.40	18.80	21.07
G7	24.03	129.0	119.4	13.90	30.17	24.87	22.08
G8	21.39	129.0	100.9	24.83	26.80	22.00	22.10
G9	24.50	127.8	104.5	19.27	28.33	23.40	22.70
G10	31.20	204.9	170.3	34.67	29.50	22.97	19.70
G11	25.63	147.3	132.9	14.40	39.87	33.40	24.03
G12	24.30	121.6	107.8	14.43	32.40	27.73	24.07

Values with same letter(s) are statistically identical at 5% level of probability.

TS/P = Total no of spikelet/panicle, NFG/P = Number of filled grain per panicle, NUG/P = Number of unfilled grain per panicle, Y/P (F) = yield per plant (fresh) (g), Y/P (D) = Yield/plant (dry) (g), TSW = Thousand seed weight, DW/SM = Dry weight per square meter and Y/ha = Yield per hectare.

G1 = 21× 29 F6 S6 P9, G2 = 21× 29 F6 S7 P2, G3 = 21× 29 F6 S7 P5 (a), G4 = 21× 29 F6 S7 P5 (b), G5 = 21× 29 F6 S6 P3, G6 = 21× 29 F6 S7 P4, G7 = 21× 29 F6 S6 P10, G8 = 21× 29 F6 S7 P1, G9 = 24× 28 F6 S10 P10, G10 = 24× 26 F6 S6 P4, G11 = BRRI dhan 48 and G12= BRRI dhan 55.

Table 4. Range, mean, CV (%) and standard deviation of 12 rice genotypes

Parameters	Range		Mean	CV (%)	SD	SE
	Min	Max				
Days to flowering	70.00	93.33	77.44	3.17	2.45	0.93
Days to maturity	103.00	131.67	110.25	1.49	1.64	0.62
Plant height (cm)	92.60	134.56	108.24	4.29	4.64	1.75
Total no of tiller/plant	11.90	17.73	14.27	8.07	1.15	0.44
Number of effective tiller/plant	11.53	14.80	13.08	5.76	0.75	0.28
Panicle length (cm)	23.58	26.40	25.17	3.39	0.85	0.32
Number of primary branches/panicle	6.93	9.80	7.94	6.31	0.50	0.19
Number of secondary branches/panicle	21.39	35.27	25.66	9.26	2.38	0.90
Total no of spikelets/panicle	111.15	204.93	137.04	11.54	15.81	5.98
Number of filled grain per panicle	96.97	170.27	115.96	11.21	13.00	4.91
Number of unfilled grain per panicle	13.90	34.67	21.48	21.93	4.71	1.78
Yield per plant (fresh) (g)	24.40	39.87	29.48	11.66	3.44	1.30
Yield/plant (dry) (g)	17.53	33.40	23.66	14.48	3.43	1.29
Thousand seed weight	19.70	24.07	22.17	15.45	3.43	1.29
Dry weight per square meter	270.00	528.67	351.83	22.54	79.32	29.98
Yield per hectare	2.63	5.29	3.44	16.50	0.57	0.21

CV (%) = coefficient of variation, SD = standard deviation and SE = standard error

Table 5. Estimation of genetic parameters in ten characters of 12 rice genotypes

Parameters	**σ^2p**	**σ^2g**	**σ^2 e**	**PCV**	**GCV**	**ECV**
Days to flowering	72.04	66.02	6.02	10.96	10.49	3.17
Days to maturity	91.70	89.00	2.70	8.69	8.56	1.49
Plant height (cm)	127.32	105.79	21.53	10.42	9.50	4.29
Total no of tiller/plant	3.94	2.62	1.33	13.92	11.34	8.07
Number of effective tiller/plant	1.50	0.93	0.57	9.37	7.38	5.76
Panicle length (cm)	1.46	0.73	0.73	4.80	3.40	3.39
Number of primary branches/panicle	0.77	0.52	0.25	11.08	9.11	6.31
Number of secondary branches/panicle	19.76	14.11	5.65	17.32	14.64	9.26
Total no of spikelets/panicle	803.16	553.08	250.08	20.68	17.16	11.54
Number of filled grain per panicle	594.19	425.24	168.95	21.02	17.78	11.21
Number of unfilled grain per panicle	48.98	26.80	22.18	32.58	24.10	21.93

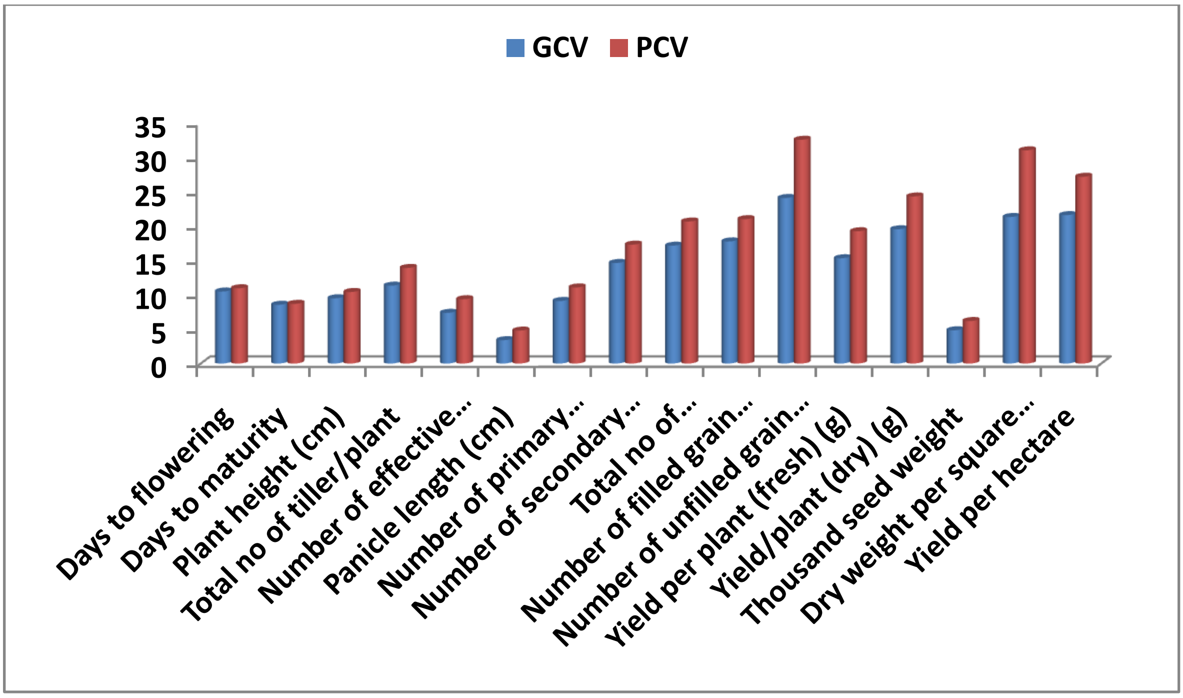

Figure 2. Genotypic and phenotypic variability in rice

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

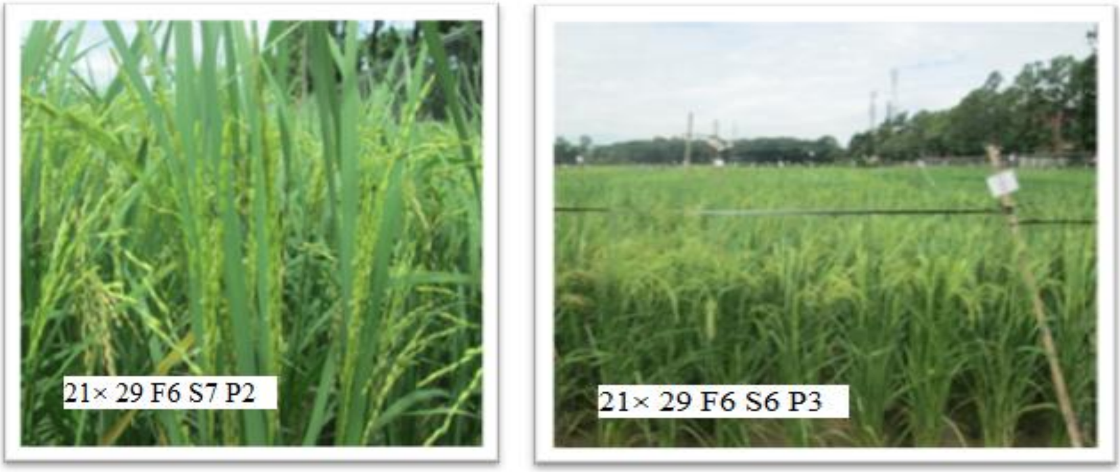

Plate 2b. Photograph showing variation in flowering among different genotypes

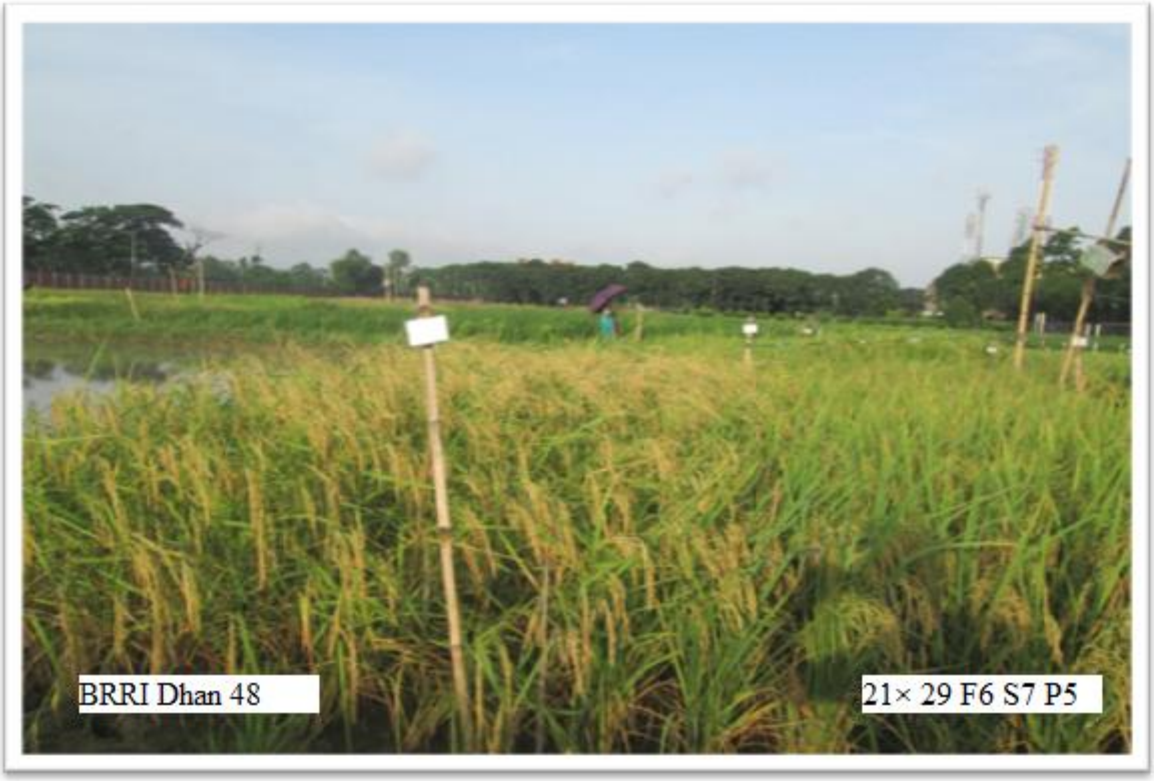

Plate 3. Photograph showing variation in days to maturity in different genotypes

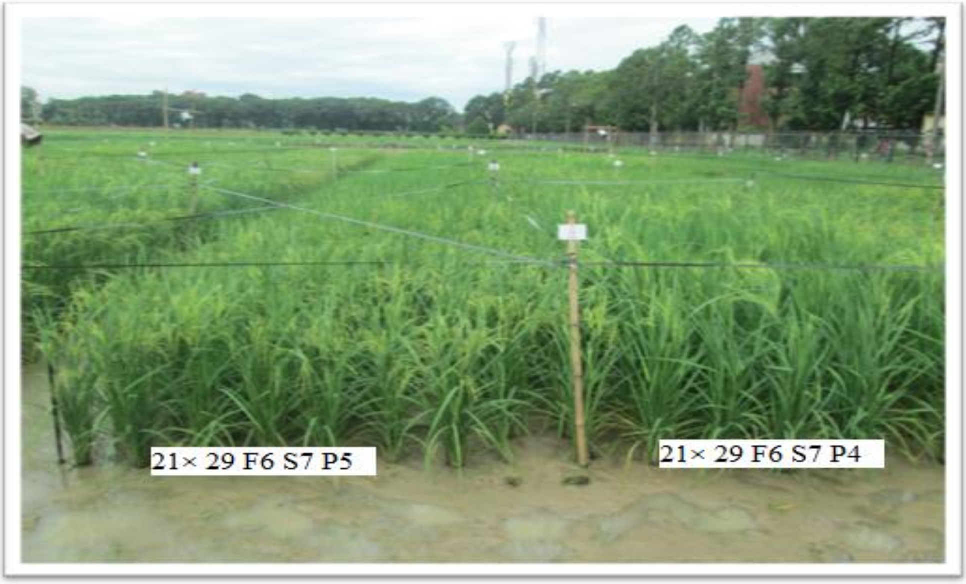

Plate 4. Photograph showing variation in plant height in different gen

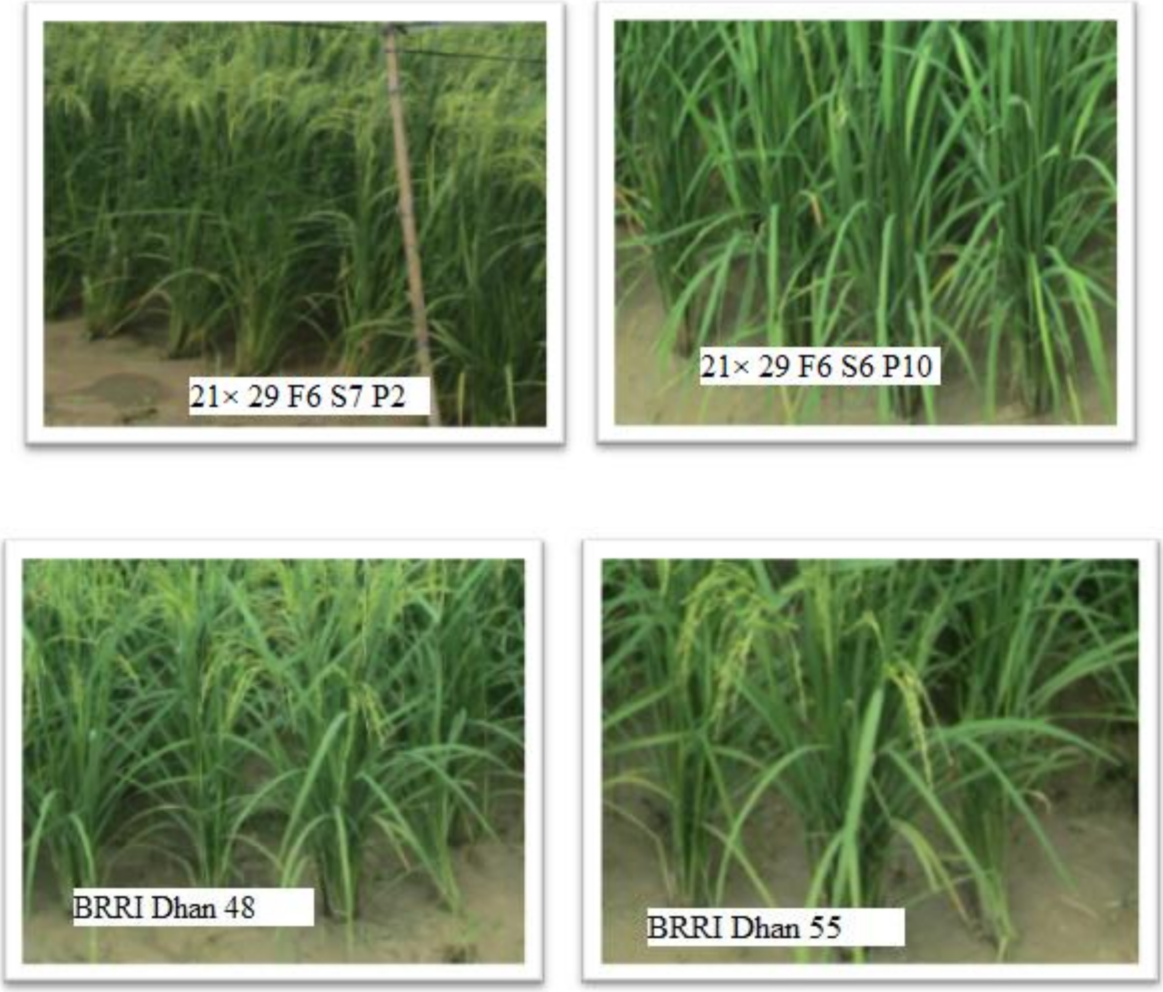

Plate 5. Photograph showing variation in number of total tiller per plant in different genotypes

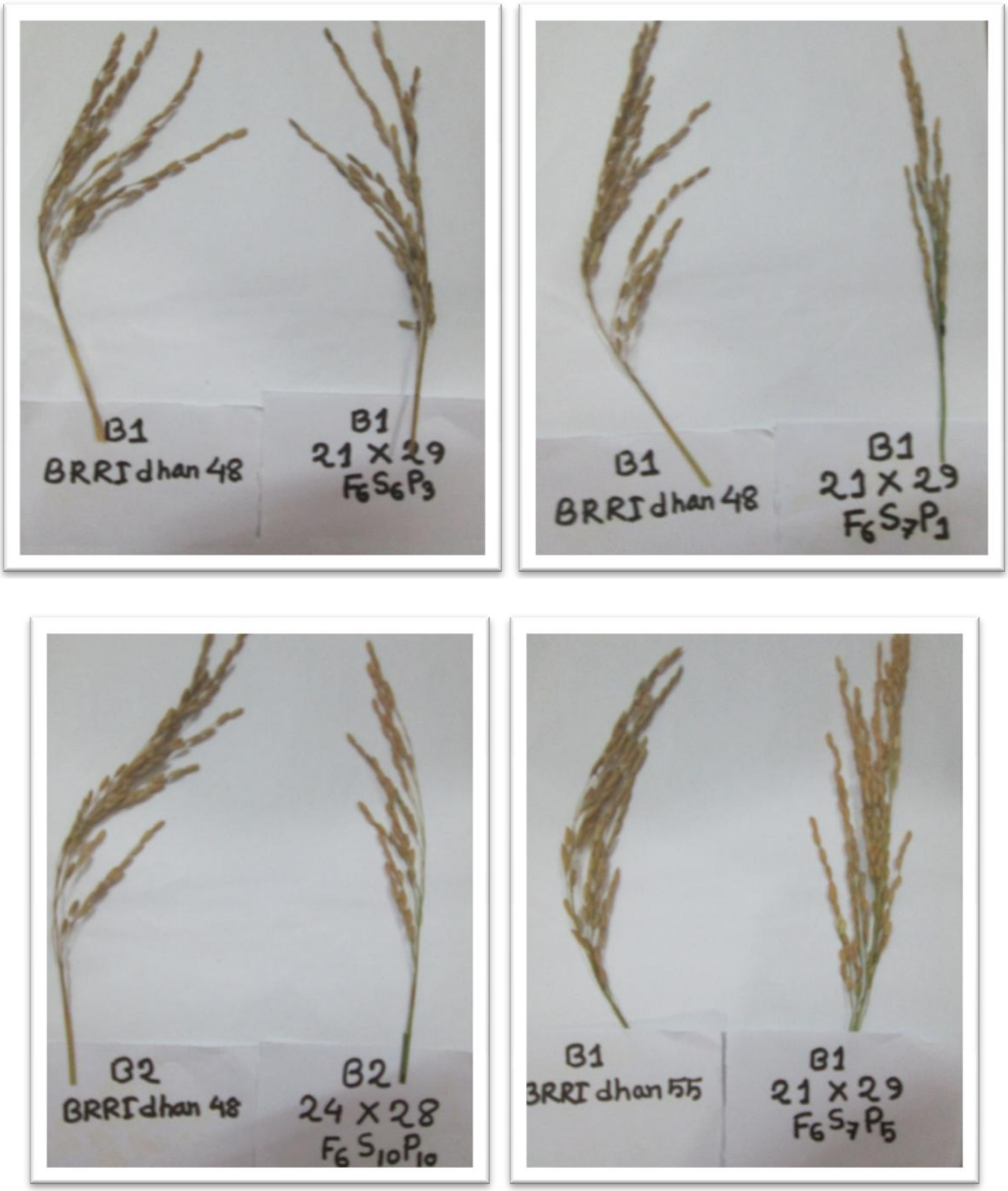

Plate 6. Photograph showing variation in panicle length in different genotypes

Phenotypic variance and genotypic variance were observed as 127.32 and 105.79 respectively. The phenotypic variance appeared to be higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The estimates of PCV (10.42%) and GCV (10.42%) also indicated presence of variability among the genotypes for this trait (Table 5). The highest variation in plant height among 14 rice genotypes was observed by Seyoum *et al*. (2012)

4.1.4 Number of tillers per plant

Significant variations were observed among 12 genotypes (9.181**) at the level of 1% probability for number of total tillers per plant (Table 2). Among the 12 genotypes G7 (17.73) showed the maximum number of total tillers per plant and the minimum one was in G2 (11.90) (Table 3a). The genotypes G7 (17.73) were shown higher number of tiller per plant than two checks the G11 (BRRI dhan 48) (15.63) and G12 (BRRI dhan 55) (16.33).Variation in number of total tillers per plant in Plate 5.

Number of total tillers per plant showed phenotypic variance (3.94) is higher than genotypic variance (2.62) indicating moderate environmental influence on these characters and high difference between PCV (13.92%) and GCV (11.34%) value indicating that this trait is highly influenced by the environment (Table 5). Ghosal *et al.* (2010) reported similar result for this trait.

4.1.5 Number of effective tillers per plant

In present experiment analysis of variance of data in (Table 2) stated that the number of effective tillers per plant showed significant differences among the genotypes (3.365 **). The highest number of effective tillers per plant was recorded in G7 (14.80) whereas the minimum number of effective tillers per plant was recorded in G2 (11.53) (Table 3a). The genotypeG7 (14.80) was shown higher number of effective tiller per plant than two checks the G11 (BRRI dhan48) (14.10) and G12 (BRRI dhan55) (13.97). Phenotypic variance (1.50) was high different from the genotypic variance (0.93) that indicated high environmental effect over the trait. Large difference between PCV (9.37%) and GCV (7.38%) values indicated that less influence of environment on this character (Table 5). Ghosal *et al.* (2010) reported similar result for this trait.

4.1.6 Panicle length (cm)

From ANOVA table (Table 2) significant difference were observed among 12 genotypes (2.924**) at the level of 1% probability for panicle length. Among the 12 genotypes the highest panicle length was observed in G10 (26.40) which are very close to G4 (26.20) whereas the minimum panicle length was observed in G6 (23.58) which is very close to G5 (23.80) (Table 3a). The genotypes G6 (23.58) and G5 (23.80) were shown almost similar panicle length to two checks the G11 (BRRI dhan48) (23.95) and G12 (BRRI dhan55) (24.25). Variations in panicle length are shown in Plate 6.

Panicle length showed less difference between phenotypic variance (1.46) and genotypic variance (0.73) indicating less environmental influence on these character and low difference between PCV (4.80%) and GCV (3.40%) value indicating the apparent variation not only due to genotypes but also due to low influence of environment (Table 5).Low genotypic coefficient of variation than phenotypic coefficient of variation for panicle length was reported by Biswas *et al.* (2000), Kole *et al.* (2008).

4.1.7 Number of primary branches per panicle

The mean square due to genotype from the analysis of variance was found statistically significant at 1% level of probability for number of primary branches per panicle (1.819**) indicating the presence of genotypic differences present among the genotypes (Table 2). From the mean table value it was found that highest number of primary branches per panicle was recorded for G4 (9.80) which are very close to G7 (8.167) and G9 (8.033) while the minimum number of primary branches per panicle was recorded for G8 (6.933) (Table 3a). The genotypeG4 (9.80) was shown higher number of primary branches per panicle than two checks the G11 (BRRI dhan48) (8.467) and G12 (BRRI dhan55) (8.60).

Number of primary branches per panicle showed the low phenotypic variance (0.77) and genotypic variance (0.52) which indicated less environmental influence. The phenotypic coefficient of variability (11.08%) values were recorded for number of primary branches per panicle very close to genotypic coefficient of variability (9.11%) 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 12 genotypes (5.517**) at the level of 1% probability for number of secondary branches per panicle (Table 2). Among 12 genotypes, the highest number of secondary branches per panicle was recorded in G4 (35.27) whereas the minimum number of secondary branches per panicle was observed in G8 (21.39) which are very close to G6 (21.40) (Table 3b). The genotypes G4 (35.27) and G10 (31.20) were found higher number of secondary branches per panicle than two checks the G11 (BRRI dhan 48) (25.63) and G12 (BRRI dhan 55) (24.30).

The value of phenotypic and genotypic variance (19.76) , (14.11) respectively for number of secondary branches per panicle with high difference between them indicating that there were high effect of environment on this character (Table 5). According to table 5, PCV and GCV

(17.32%), (14.64%) respectively 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).

4.1.9 Total number of spikelet per panicle

From the ANOVA table (Table 2), it was found that total number of spikelet per panicle showed significant variations among the genotypes (1909.322**). The total number of spikelet per panicle was maximum in G10 (204.9) and minimum was observed in G6 (111.2d) (Table 3b) among 12 genotypes. The genotypes G10 (204.9) was found higher number of spikelet per panicle than checks the G11 (BRRI dhan 48) (147.3) and G12 (BRRI dhan 55) (121.6).

The phenotypic and genotypic variances for total number of spikelet per panicle were 803.16and 553.08 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 20.68% and 17.16% respectively for total number of spikelet per panicle which indicating that high variation exists among different genotypes (Table 5). 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 recorded by Satish *et al.* (2003).

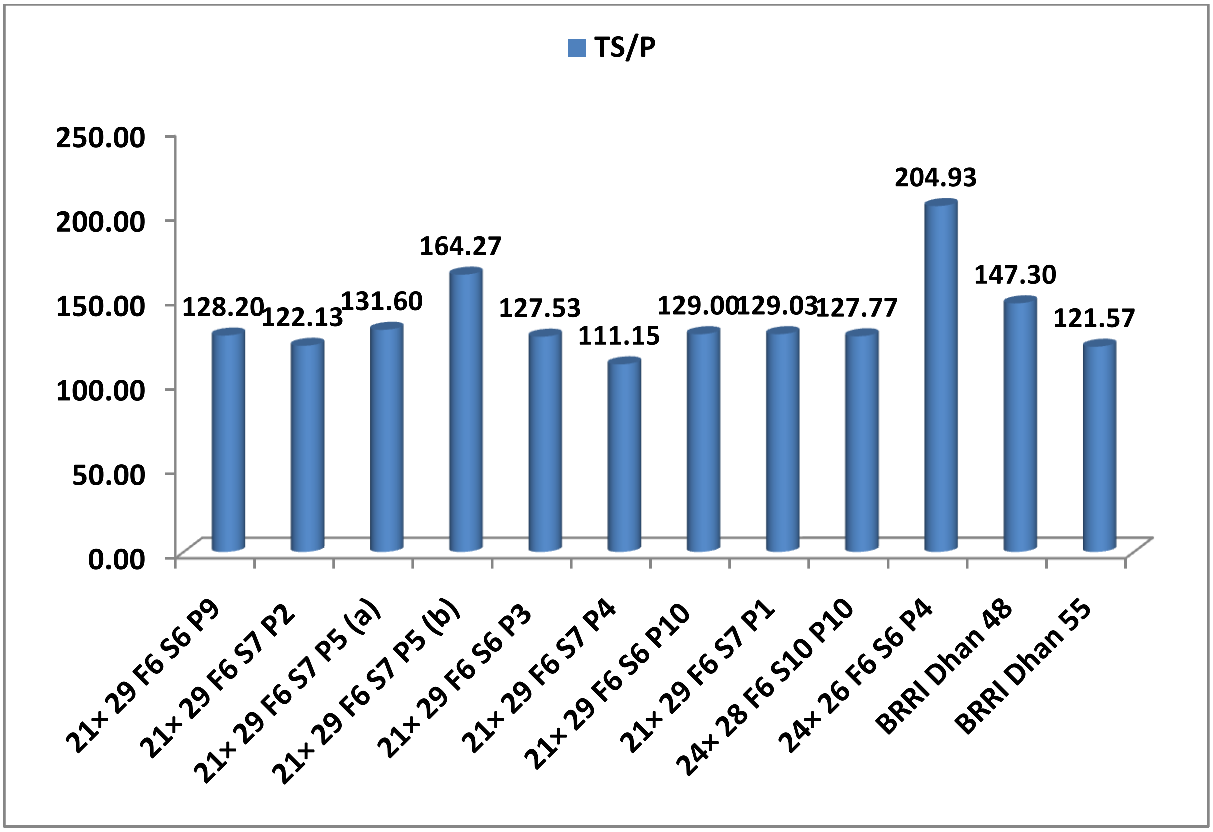

Figure 3. Graphical representation of total spikelet per panicle of rice

4.1.10 Number of filled grains per panicle

The analysis of variance for number of filled grains per panicle showed highly significant difference (1444.664**) among 12 genotypes of *Oryza sativa* used in the present experiment (table 2). In 12 genotypes, the number of filled grains per panicle was recorded highest in G10 (170.3) and minimum was recorded in G6 (96.97) (Table 3b). The genotypes G10 (170.3) was found higher number of spikelet per panicle than checks the G11 (BRRI dhan 48) (132.9) and G12 (BRRI dhan 55) (107.8).

The magnitude of difference between phenotypic and genotypic variances (594.19), (425.24) respectively were higher for number of filled grains per panicle suggested that large environmental influence on this character (Table 5). The high value of phenotypic and genotypic coefficient of variance (21.02%), (17.78%) 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 recorded by Akter *et al*. (2010)

4.1.11 Number of unfilled grains per panicle

From the (Table 2) there were highly significant variations among 12 genotypes (102.576**) for number of unfilled grains per panicle. The G10 showed the highest (34.67) number of unfilled grains per panicle among 12 genotypes whereas the G7 showed the minimum (13.90) number of unfilled grains per panicle (Table 3b). The genotypes G7 (13.90) was found lower number of unfilled grains per panicle than two checks varieties the G11 (BRRI dhan 48) (14.40) and G12 (BRRI dhan 55) (14.43).

The value of phenotypic variance and genotypic variance for number of unfilled grains per panicle were recorded higher (48.98), (26.80) respectively with high difference between them suggested there are highly significant role of environment on the character. The difference between phenotypic and genotypic phenotypic coefficient of variance values (32.58) , (24.10) respectively estimate high for number of unfilled grains per panicle which indicate existence of adequate variation among the genotype (Table 5). The high GCV values of these characters suggest that the possibility of improving these trait through selection. 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 (Table 2), it was found that thousand seed weight showed significant variations among the genotypes (4.182**). Among 12 genotypes, thousand seed weight was found maximum in two checks varieties the G11 (BRRI dhan 48) (24.03) and G12 (BRRI dhan 55) (24.07a) whereas the minimum thousand seed weight was found in G10 (19.70 gm) (Table 3b).

Thousand seed weight showed that phenotypic (1.88) was higher than genotypic (1.15) variance indicating that environment has influence on expression of the character. The values of PCV and GCV were 6.19% and 4.84% indicating that the genotype has considerable variation for this trait (Table 5). Bidhan *et al.* (2001) reported similar result for this trait.

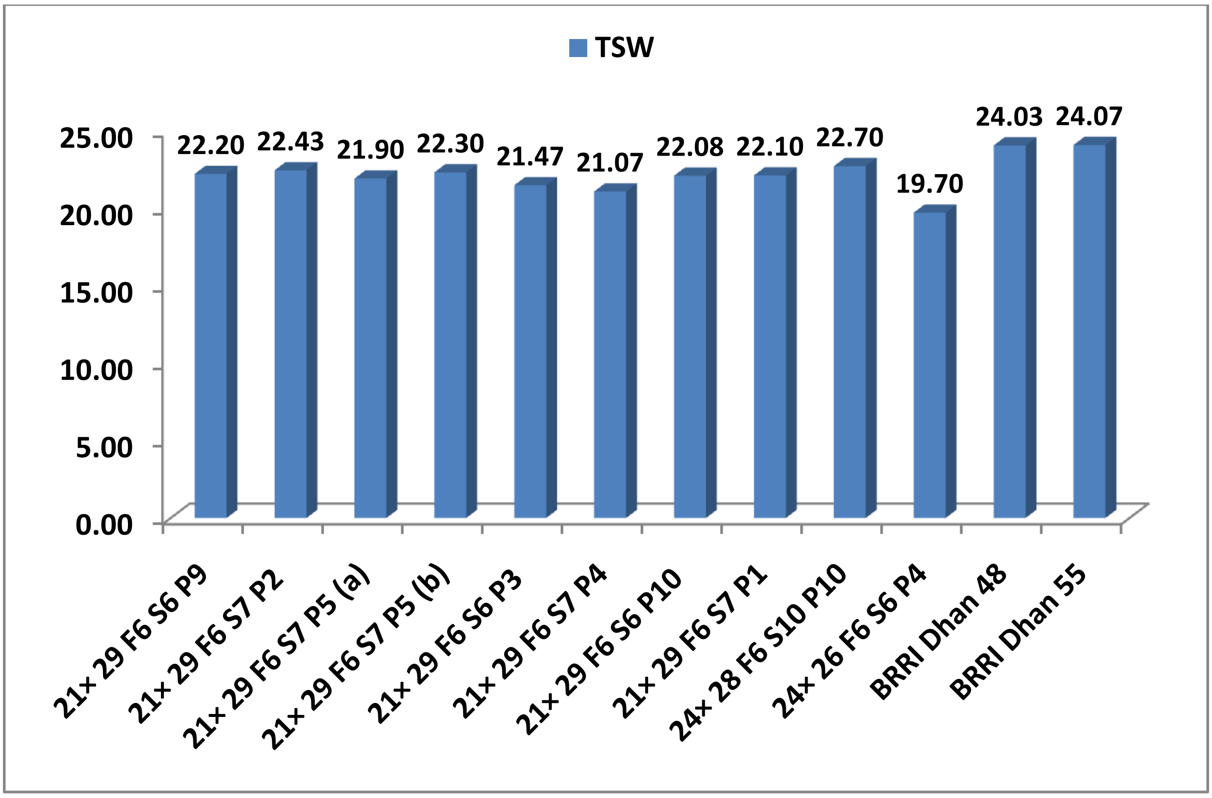

Figure 4. Graphical representation of thousand seed Weight of rice

4.1.13 Yield per plant (gm)

The mean square due to genotype from the analysis of variance was found statistically significant (75.931**)at 1% level of probability for yield per plant indicating the presence of genotypic differences present among the 12 genotypes (Table 2).Yield per plant was recorded highest in G4 (31.47 gm) which is near to the two checks varieties the G11 (BRRI dhan 48) (33.40) and G12 (BRRI dhan 55) (27.73) and the lowest was found in G5 (17.53 g) (Table 3b) (Figure 5).

The phenotypic and genotypic variance for yield per plant (33.13), (21.40) respectively suggested that high influence of environment on the expression of the genes controlling this trait. Same result was also found by Seyoum *et al.* (2012).The values of PCV and GCV were 24.33% and 19.55% indicating that the genotype has considerable variation for this trait (Table 5). Similar result observed by Singh *et al.* (2005).

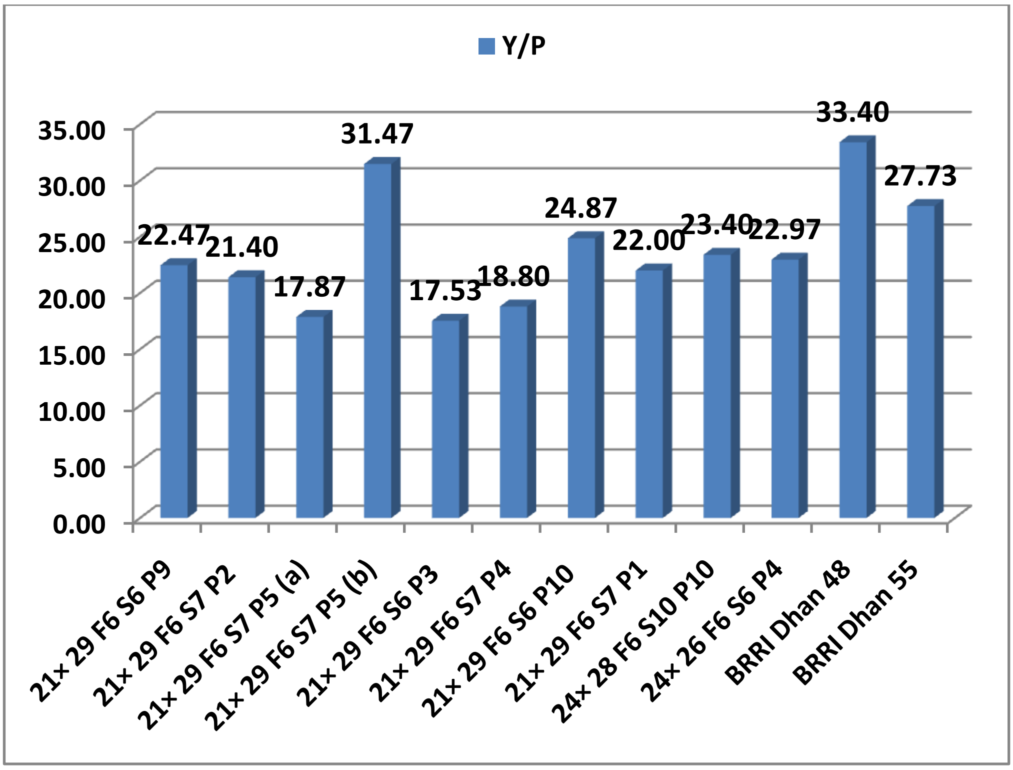

Figure 5. Graphical representation of yield per plant (dry) of rice

4.1.14 Yield per hectare (t/ ha)

In present experiment analysis of variance of data in Table 2 stated that the yield per hectare showed significant differences among the genotypes (1.976**). Among the 12 genotypes G4 showed the maximum (5.287 t/ha) yield per hectare and the minimum one was in G5 (2.633 t/ha) (Table 3b) (Figure 6). The G4 (5.287 t/ha) was found higher yield per hectare than two checks varieties the G11 (BRRI dhan 48) (4.493 t/ha) and G12 (BRRI dhan 55) (3.640 t/ha). Yield per hectare showed phenotypic variance (0.87) is moderately higher than genotypic variance (0.55) indicating moderate environmental influence on this character. The values of PCV and GCV were (27.19%), (21.61%) value indicating that this trait is influenced by the environment (Table 5). Datt *et al.* (2003) reported low value of PCV and GCV for this trait.

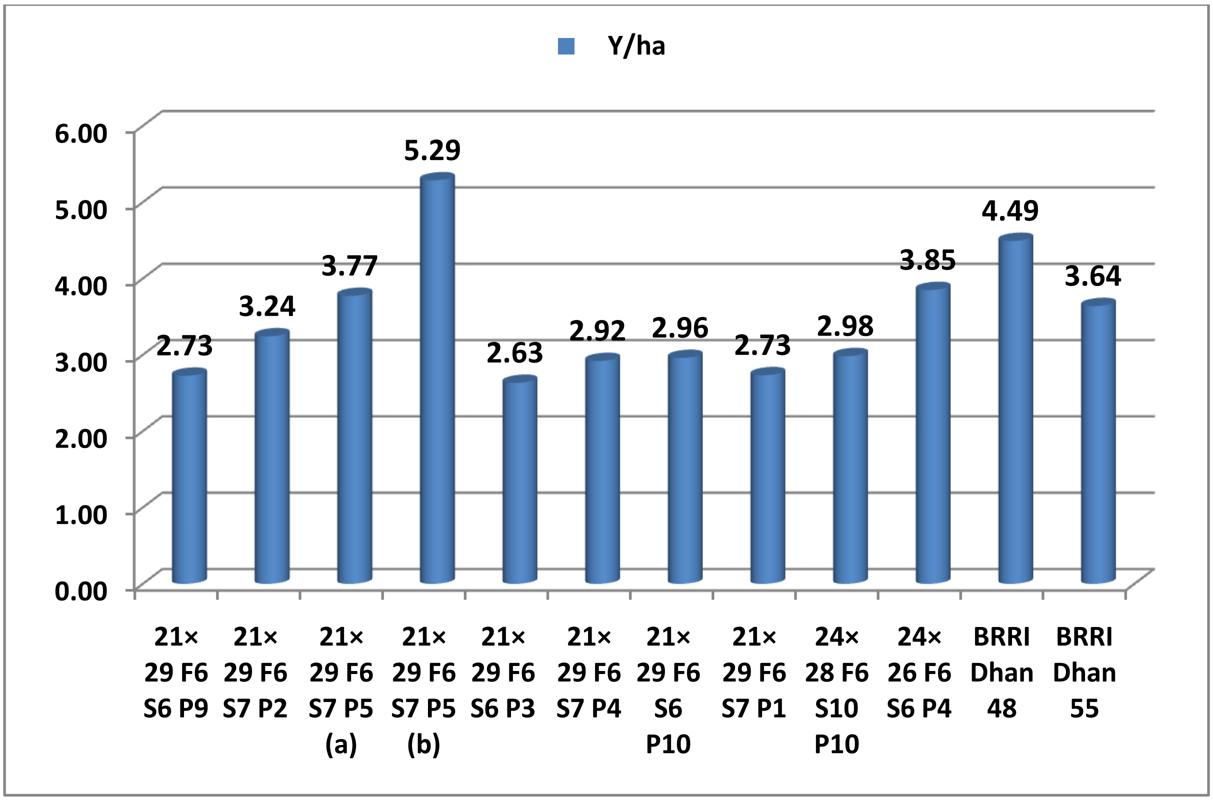

Figure6. Graphical representation of yield per hectare of rice

4.2 Heritability and genetic advance

4.2.1 Days to flowering

High heritability (91.64%) with low genetic advance (16.02) and genetic advance in percentage of mean (20.69%) for days to flowering was found in the 12 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 6). High heritability with low genetic advance was also reported by Chakraborty and Chakraborty (2010).

4.2.2 Days to maturity

Days to maturity showed high heritability (97.05%) coupled with low genetic advance (19.15) and moderate genetic advance in percentage of mean (17.37%) (Table 6). The result showed that due to presence of additive gene effect and medium scope of selection of this trait. High heritability coupled with low genetic advance for this trait was also observed by Akhtar *et al*. (2011).

4.2.3 Plant height (cm)

Plant height of 12 genotypes showed high heritability (83.09%) associated with high genetic advance (19.31) and high genetic advance in percentage of mean of 17.84% (Table 6). This finding revealed that presence of additive gene action and scope of improvement of the character through selection may be rewarding. High heritability in plant height with high genetic advance in percentage of mean was also observed by Sabesan *et al*. (2009).

4.2.4 Number of total tillers per plant

Number of total tillers per plant exhibited high heritability (66.38%) conjunction with low genetic advance (2.72) and genetic advance in percentage of mean (19.03%) (Table 6). These findings revealed that it was indicative of non-additive gene action. Selection for this trait may not be wise. High heritability coupled with low genetic advance was also found by Kishore *et al*. (2008).

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

Parameters	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to flowering	91.64	16.02	20.69
Days to maturity	97.05	19.15	17.37
Plant height (cm)	83.09	19.31	17.84
Total no of tiller/plant	66.38	2.72	19.03
Number of effective tiller/plant	62.13	1.57	11.99
Panicle length (cm)	50.23	1.25	4.97
Number of primary branches/panicle	67.60	1.22	15.42
Number of secondary branches/panicle	71.41	6.54	25.48
Total no of spikelets/panicle	68.86	40.20	29.34
Number of filled grain per panicle	71.57	35.94	30.99
Number of unfilled grain per panicle	54.71	7.89	36.72
Yield per plant (fresh) (g)	63.35	7.41	25.13
Yield/plant (dry) (g)	64.59	7.66	32.37
Thousand seed weight	61.08	1.73	7.79
Dry weight per square meter	47.25	106.30	30.21
Yield per hectare	63.16	1.22	35.37

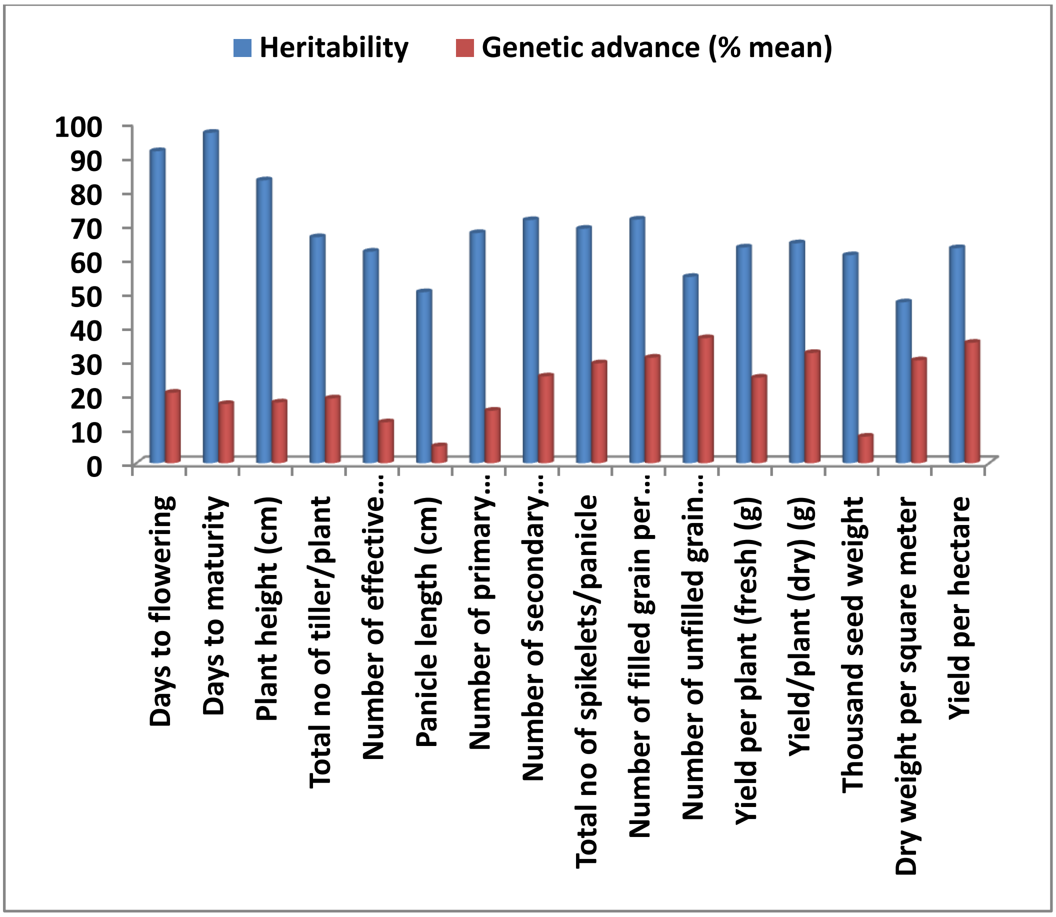

Figure 7. Heritability and genetic advance over mean in rice

4.2.5 Number of effective tillers per plant

High heritability (62.13%) accompanied with low genetic advance (1.57) and genetic advance in percentage of mean (11.99%) was calculated in respect of number of effective tillers per plant (Table 6). These findings discovered the action of non-additive gene effects on the expression of this trait. The high heritability is being exhibited due to high environmental effects. Selection may not be effective in such character. 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 (50.23%) along with low genetic advance (1.25) and genetic advance (4.97%) (Table 6). 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

High heritability (67.60%) along with low genetic advance (1.22) and genetic advance in percentage of mean (15.42%) was calculated in number of primary branches per panicle (Table 6). It is indicated that environmental effect was more than the genotypic effect and due to non-additive gene action; selection for further improvement of the trait might not be wise. Similar results were also found by Biswas *et al.* (2000).

4.2.8 Number of secondary branches per panicle

Number of secondary branches per panicle showed high heritability (71.41%) coupled with low genetic advance (6.54) and genetic advance in percent mean (25.48%) (Table 6), 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 (68.86%) coupled with high genetic advance (40.20) and genetic advance in percentage of mean (29.34%) (Table 6). 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 (71.57%) with high genetic advance (35.94) and high genetic advance in percentage of mean (30.99%) (Table 6). These findings revealed that this trait was controlled by additive gene and selection for this character would be effective. Prasad et al. (2001), 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 (54.71%) accompanied with low genetic advance (7.89) and high genetic advance in percentage of mean (36.72%) (Table 6). 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 of 12 genotypes showed high heritability (61.08%) associated with low genetic advance (1.73) and genetic advance in percentage of mean (7.79%) (Table 6), revealed that thousand seed weight is highly influenced by environmental effects and scope of improvement through selection may not be rewarding.

4.2.13 Yield per plant (gm)

High heritability (64.59%) along with low genetic advance (7.66) and high genetic advance in percentage of mean (32.37%) was calculated in yield per plant (Table 6). It is indicated that presence of additive gene action and selection for further improvement of the trait might be effective. High heritability and high 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 (63.16%) conjunction with low genetic advance (1.22) and genetic advance in percentage of mean (35.37%) (Table6). 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 12 genotypes of *Oryza sativa* L. are determined (Table 7) (table 8). 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 = 0.925, P =0.901), number of secondary branches per panicle (G=0.853, P=0.614), total number of spikelet per panicle (G=0.981, P=0.688) and number of filled grains per panicle (G=0.922) indicated that if days to flowering increased these characters also increased. It also exhibited significant and positive interaction with number of unfilled grains per panicle (G=0.355, P=0.179), yield per plant (G=0.758, P=0.598) and yield per hectare (G=0.918, P=0.706). However, it had significant and positive interaction with number of primary branches per panicle (G= 0.752) at genotypic level and negative interaction with thousand seed weight (G= 0.064, P= -0.031) at both genotypic and phenotypic level. It also showed significant and positive association with plant height (G= 0.632, P=0.482), number of total tillers (G=0.218, P= 0.179), number of effective tillers (G=0.439, P= 0.338), panicle length (G=0.359, P= 0.192) and number of primary branches per panicle (p=0.531) at phenotypic level (Table 7) (table 8). 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=0.941) and total number of spikelet per panicle (G=0.903) at genotypic level suggested that if days to maturity increased the number of secondary branches per panicle and total number of spikelet per panicle also increased . It also exhibited significant and positive interaction with plant height (G=0.782, P=0.686), number of filled grain per panicle (G=0.908, P=0.759), yield per plant (G=0.607, P=0.501), yield per hectare (G=0.835, P=0.673) at both genotypic and phenotypic level and with number of secondary branches per panicle (P=0.775), total number of spikelet per panicle (P=0.730) at phenotypic level. Days to maturity showed significant negative association with thousand seed weight (G=-0.242, P=-0.172) at both genotypic and phenotypic level (Table 7) (table 8). Sadeghi (2011), Akhter *et al.* also revealed that days to maturity had non-significant and positive interaction with yield per hectare.

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

	DF	DM	PH	NT	NET	PL	NPB/P	NSB/P	TS/P	NFG/P	NUG/P	Y/P (F)	Y/P (D)	TSW	DW/SM
DM	0.925**														
PH	0.632**	0.782**													
NT	0.218	0.156	-0.355*												
NET	0.439**	0.418*	-0.034	0.959**											
PL	0.359*	0.469**	0.767**	-0.242	-0.173										
NPB/P	0.752**	0.779**	0.550**	0.551**	0.822**	0.059									
NSB/P	0.853**	0.941**	0.893**	-0.010	0.307	0.441**	0.756**								
TS/P	0.981**	0.903**	0.691**	-0.020	0.181	0.547**	0.346*	0.754**							
NFG/P	0.922**	0.908**	0.601**	0.196	0.396*	0.460**	0.479**	0.755**	0.975**						
NUG/P	0.355*	0.444**	0.586**	-0.730**	-0.620**	0.602**	-0.351*	0.357*	0.642**	0.462**					
Y/P (F)	0.831**	0.672**	0.377*	0.540**	0.720**	-0.079	0.905**	0.578**	0.482**	0.623**	-0.367*				
Y/P (D)	0.758**	0.607**	0.299	0.531**	0.689**	0.111	0.831**	0.437**	0.380*	0.527**	-0.422*	0.903**			
TSW	-0.064	-0.242	-0.281	0.432**	0.351*	-0.289	0.457**	-0.203	-0.478**	-0.332*	-0.914**	0.593**	0.681**		
DW/SM	0.995**	0.985**	0.699**	0.116	0.421*	0.301	0.836**	0.952**	0.903**	0.979**	0.219	0.839**	0.812**	0.061	
Y/ha	0.918**	0.835**	0.628**	0.195	0.474**	0.159	0.866**	0.834**	0.648**	0.754**	0.001	0.829**	0.806**	0.260	0.902**

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

DF = Days to flowering,, DM = Days to maturity, PH = Plant height (cm), NT = Total no of tiller/plant, NET = Number of effective tiller/plant, PL = Panicle length (cm), NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle, TS/P = Total no of spikelets/panicle, NFG/P = Number of filled grain per panicle, NUG/P = Number of unfilled grain per panicle, Y/P (F) = yield per plant (fresh) (g), Y/P (D) = Yield/plant (dry) (g), TSW = Thousand seed weight, DW/SM = Dry weight per square meter and Y/ha = Yield per hectare

Table 8. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of rice

	DF	DM	PH	NT	NET	PL	NPB/P	NSB/P	TS/P	NFG/P	NUG/P	Y/P (F)	Y/P (D)	TSW	DW/SM
DM	0.901**														
PH	0.482**	0.686**													
NT	0.179	0.132	-0.263												
NET	0.338*	0.339*	-0.047	0.906**											
PL	0.192	0.302	0.537**	-0.271	-0.198										
NPB/P	0.531**	0.651**	0.515**	0.437**	0.592**	0.197									
NSB/P	0.614**	0.775**	0.837**	-0.036	0.178	0.447**	0.764**								
TS/P	0.688**	0.730**	0.680**	-0.097	0.016	0.488**	0.452**	0.761**							
NFG/P	0.756**	0.759**	0.591**	0.141	0.250	0.402*	0.577**	0.762**	0.951**						
NUG/P	0.179	0.293	0.530**	-0.652**	-0.570**	0.479**	-0.168	0.384*	0.617**	0.395*					
Y/P (F)	0.622**	0.553**	0.328	0.412*	0.612**	0.044	0.736**	0.498**	0.337*	0.477**	-0.300				
Y/P (D)	0.598**	0.501**	0.247	0.409*	0.557**	0.035	0.660**	0.414*	0.275	0.406*	-0.299	0.890**			
TSW	-0.031	-0.172	-0.244	0.189	0.244	-0.321	0.182	-0.210	-0.400*	-0.322	-0.597**	0.415*	0.495**		
DW/SM	0.712**	0.682**	0.565**	0.168	0.346*	0.238	0.624**	0.649**	0.558**	0.630**	0.129	0.686**	0.545**	0.066	
Y/ha	0.706**	0.673**	0.550**	0.134	0.361*	0.244	0.692**	0.667**	0.465**	0.552**	0.045	0.750**	0.631**	0.187	0.935**

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

DF = Days to flowering,, DM = Days to maturity, PH = Plant height (cm), NT = Total no of tiller/plant, NET = Number of effective tiller/plant, PL = Panicle length (cm), NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle, TS/P = Total no of spikelets/panicle, NFG/P = Number of filled grain per panicle, NUG/P = Number of unfilled grain per panicle, Y/P (F) = yield per plant (fresh) (g), Y/P (D) = Yield/plant (dry) (g), TSW = Thousand seed weight, DW/SM = Dry weight per square meter and Y/ha = Yield per hectare

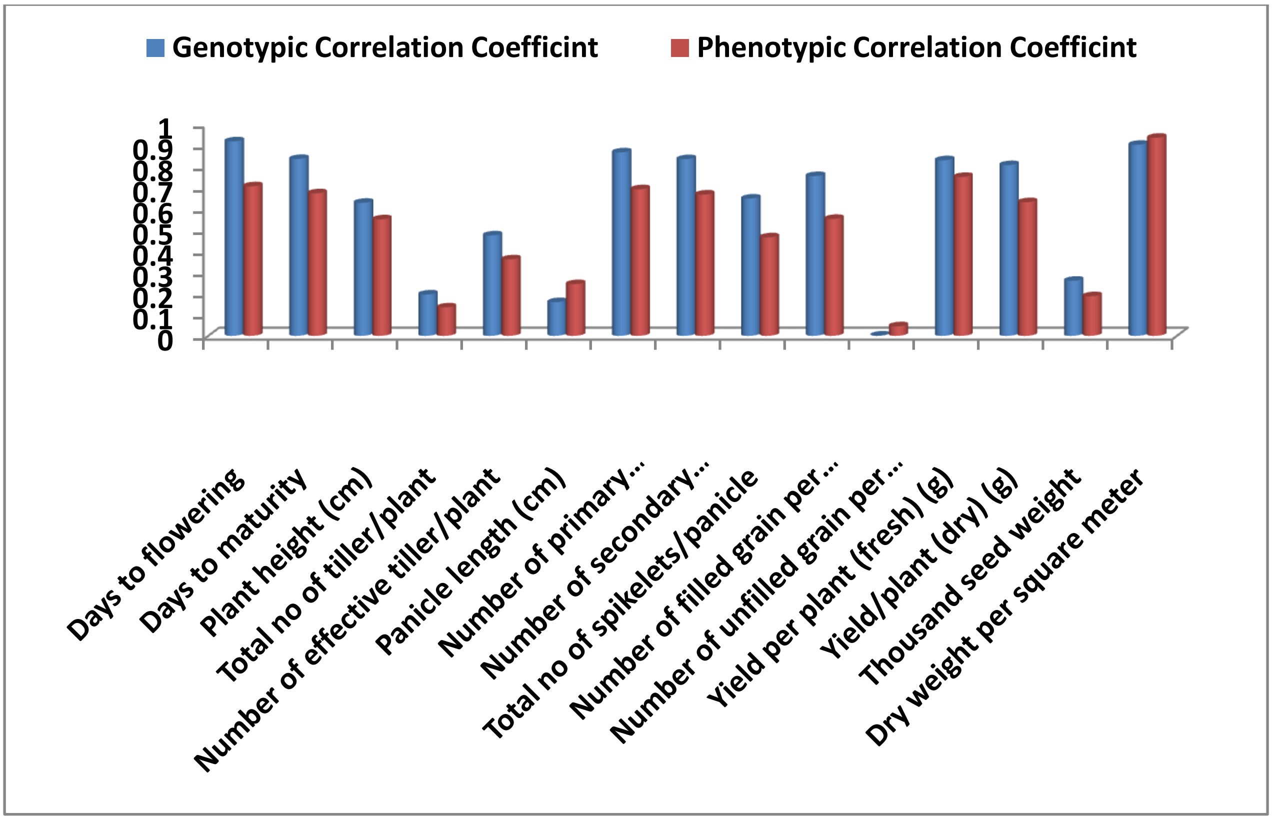

Figure 8. Genotypic and phenotypic correlation coefficient of fifteen characters with seed yield in rice

4.3.3 Plant height (cm)

Plant height showed significant and positive interaction with number of unfilled grain per panicle (G = 0.586, P =0.530), panicle length P (G=0.767, P=0.537) and number of secondary branches per panicle (G =0.893, P =0.837) whereas non-significant and negative interaction with thousand seed weight (G =-0.281, P =-0.244). The results tend to emphasize that if plant height increased the number of unfilled grain per panicle also increased. It was non-significantly and negatively associated with number of total tillers (G=-0.355, P=-0.263), number of effective tillers (G=-0.034, P=-0.047). It had also significant positive relation with number of primary branches per panicle (G=0.550, P=0.515), total number of spikelet per panicle (G= 0.691, P=0.680) and yield per hectare (G= 0.628, P=0.550) (Table 7) (table 8). Prasad *et al*. (2001), Iftekharudduaula *et al*. (2001) also observed that plant height was negative associated with thousand seed weight.

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=0.959, P= 0.906) and yield per plant (G=0.531, P=0.409) indicated that yield per plant can be increased if number of total tillers per plant and number of effective tillers increased. It also exhibited non-significant and positive interaction with number of filled grain per panicle (G= 0.196, P=0.141) and yield per hectare (G=0.195, P=0.134). Number of total tillers per plant had significant and negative interaction with number of unfilled grain per panicle (G=-0.730, P=-0.652). It had also non-significant negative relation with panicle length (G= -0.242, P= -0.271), number of secondary branch per panicle (G=-0.010, P= -0.036), total spikelet per panicle (G=-0.020, P=-0.097), total number of spikelet per panicle (G= -0.020, P=-0.097) at both genotypic and phenotypic level (Table 7) (table 8). 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 number of effective tillers per plant showed significant and positive correlation with number of primary branch per panicle (G=0.822, P= 0.592) and yield per plant (G=0.689, P= 0.557)at both genotypic and phenotypic level but positively significant with yield per hectare at genotypic level (P=0.474) indicated that the traits were governed by same gene and simultaneous improvement would be effective. It also had positive and non-significant correlation with number of secondary branch (G = 0.307, P =0.178) total number of spikelet per panicle (G = 0.181, P =0.016) at both genotypic and phenotypic level. Number of effective tillers per plant had significant and negative interaction with number of unfilled grain per panicle (G = -0.620, P= -0.570) at both genotypic and phenotypic level. Negative and non-significant correlation was found between number of effective tillers per plant and panicle length (G = -0.173, P = -0.198)at both genotypic and phenotypic level (Table 7) (Table 8). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors. Agahi *et al.* (2007) and Babu *et al.* (2012) also found positive and significant correlation of yield with effective tillers per plant at both genotypic and phenotypic level. Selvaraj *et al.* (2011) and Satheeshkumar *et al.* (2012) found positive and significant correlation of yield per hectare with effective tillers per plant at phenotypic level only.

4.3.6 Panicle length (cm)

Panicle length showed significant and positive correlation with number of secondary branches per panicle (G=0.441, P=0.447), total number of spikelet (G= 0.547, P=0.452), suggested that yield per hectare can be increased by improving panicle length, number of secondary branches per panicle, total number of spikelet. It had also non-significant negative relation with thousand seed weight (G= -0.289, P=-0.321) (Table 7) (table 8). 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= 0.756, P= 0.764), number of filled grain per panicle (G=0.479, P= 0.577), yield per hectare (G=0.866, P= 0.692) at both genotypic and phenotypic level, thousand seed weight (G= 0.457) at genotypic level indicated that if number of primary branches per panicle increased then these characters also increased. It also exhibited non-significant and positive interaction with thousand seed weight (P= 0.182) at phenotypic level (Table 7) (table 8). 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= 0.754, P=0.761), number of filled grain per panicle (G=0.755, P= 0.762), yield per hectare (G=0.834, P= 0.667) at both genotypic and phenotypic level and yield per plant (G= 0.437) at genotypic level. This result suggested that yield per plant and yield per hectare can be increased through improvement of total number of spikelet, number of filled grain per panicle. It had significant negative relation with thousand seed weight (G= -0.203, P= -0.210) at both genotypic and phenotypic level (Table 7) (table 8). 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=0.975, P= 0.951), number of unfilled grain per panicle (G=

0.642, P= 0.617) and yield per hectare (G= 0.648, P=0.465) 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= -0.478, P=-0.400) (Table 7) (table 8). 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=0.527, P=0.406) and yield per hectare (G=0.754, P=0.552) 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 thousand seed weight (G= -0.332) at genotypic level and and non-significant negative interaction with thousand seed weight (P= -0.322) at phenotypic level (Table 7) (table 8). 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= -0.422) at genotypic level and thousand seed weight (G=-0.914, P=-0.597) at both genotypic and phenotypic level. This result exposed that yield per plant and thousand seed weight can be increased by decreasing the number of unfilled grains per panicle. It also had non-significant positive relation interaction with yield per hectare (G = 0.001, P = 0.045) (Table 7) (table 8). 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 thousand seed weight (G=0.681, P=0.495), yield per hectare (G= 0.806, P= 0.631) indicated that if yield per plant increased then thousand seed weight and yield per hectare also increased (Table 7) (table 8). 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= 0.260, P=0.187) (Table 7) (table 8) 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 9.

4.4.1 Days to flowering

Days to flowering had negative direct effect (-0.251) on yield per hectare. This trait showed indirect positive effect on thousand seed weight (0.016).Positive direct effect of this character was reported by Abarshahr *et al*. (2011). This trait showed indirect positive effect on yield per hectare through number of effective tillers per plant (0.372), panicle length (0.029), number of secondary branches per panicle (0.367), number of filled grains per panicle (0.763), yield per plant (0.650), and thousand seed weight (0.020). On the hand, it showed indirect negative effect on yield per hectare via days to maturity (-0.014), plant height (-0.239), number of total tiller per plant (-0.254), number of primary branches per panicle (-0.110), total number of spikelet per panicle (-0.846), number of unfilled grain per panicle (-0.109).Finally it made significant and positive correlation with yield per hectare (0.918**) (Table 9).

4.4.2 Days to maturity

Path co-efficient analysis revealed that, days to maturity was positively correlated (0.835**) and had negative direct effect (-0.015) on yield per hectare. It had positive indirect influence on the yield per hectare through number of effective tillers per plant (0.355), panicle length (0.038), number of secondary branches per panicle (0.404), and number of filled grains per panicle (0.678).The indirect negative effect of this trait through days to flowering (-0.232), plant height (-0.296), number of total tiller per plant (-0.182), number of primary branches per panicle (-0.081), total number of spikelet per panicle (-0.596), number of unfilled grain (-0.179) on yield per hectare (Table 9). Same result also recorded by Habib *et al.*(2005), sadeghi (2011).

Table 9. Partitioning of genotypic correlations into direct (bold) and indirect effects of ten important characters by path analysis of rice

	DF	DM	PH	NT	NET	PL	NPB/P	NSB/P	TS/P	NFG/P	NUG/P	Y/P (F)	Y/P (D)	TSW	DW/SM	Genotypic correlation with yield
DF	**-0.251**	-0.014	-0.239	-0.254	0.372	0.029	-0.110	0.367	-0.846	0.763	-0.109	-0.352	0.650	0.020	0.893	0.918**
DM	-0.232	**-0.015**	-0.296	-0.182	0.355	0.038	-0.114	0.404	-0.779	0.678	-0.136	-0.284	0.521	0.075	0.803	0.835**
PH	-0.159	-0.011	**-0.379**	0.414	-0.028	0.061	-0.081	0.383	-0.596	0.449	-0.179	-0.159	0.256	0.087	0.570	0.628**
NT	-0.055	-0.002	0.134	**-1.166**	0.813	-0.019	-0.081	-0.004	0.017	0.146	0.223	-0.229	0.456	-0.133	0.094	0.195
NET	-0.110	-0.006	0.013	-1.118	**0.847**	-0.014	-0.121	0.132	-0.156	0.296	0.190	-0.305	0.591	-0.108	0.344	0.474**
PL	-0.090	-0.007	-0.290	0.282	-0.147	**0.080**	-0.009	0.189	-0.472	0.344	-0.184	0.034	0.095	0.089	0.245	0.159
NPB/P	-0.189	-0.011	-0.208	-0.642	0.697	0.005	**-0.147**	0.325	-0.299	0.358	0.107	-0.383	0.713	-0.141	0.682	0.866**
NSB/P	-0.214	-0.014	-0.338	0.012	0.260	0.035	-0.111	**0.430**	-0.650	0.564	-0.109	-0.245	0.375	0.063	0.777	0.834**
TS/P	-0.246	-0.013	-0.262	0.024	0.153	0.044	-0.051	0.324	**-0.863**	0.728	-0.196	-0.204	0.326	0.148	0.736	0.648**
NFG/P	-0.256	-0.013	-0.228	-0.228	0.335	0.037	-0.070	0.324	-0.841	**0.747**	-0.141	-0.264	0.452	0.102	0.798	0.754**
NUG/P	-0.089	-0.007	-0.222	0.851	-0.525	0.048	0.051	0.153	-0.554	0.345	**-0.306**	0.155	-0.362	0.282	0.179	0.001
Y/P (F)	-0.209	-0.010	-0.143	-0.630	0.610	-0.006	-0.133	0.248	-0.416	0.466	0.112	**-0.423**	0.861	-0.183	0.684	0.829**
Y/P (D)	-0.190	-0.009	-0.113	-0.619	0.584	0.009	-0.122	0.188	-0.328	0.393	0.129	-0.425	**0.858**	-0.210	0.662	0.806**
TSW	0.016	0.004	0.107	-0.504	0.297	-0.023	-0.067	-0.087	0.413	-0.248	0.279	-0.251	0.584	**-0.309**	0.050	0.26
DW/SM	-0.275	-0.014	-0.265	-0.135	0.357	0.024	-0.123	0.409	-0.779	0.731	-0.067	-0.355	0.696	-0.019	**0.815**	0.902**

Residual effect: 0.020 ** = Significant at 1%. * = Significant at 5%.

DF = Days to flowering,, DM = Days to maturity, PH = Plant height (cm), NT = Total no of tiller/plant, NET = Number of effective tiller/plant, PL = Panicle length (cm), NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle, TS/P = Total no of spikelets/panicle, NFG/P = Number of filled grain per panicle, NUG/P = Number of unfilled grain per panicle, Y/P (F) = yield per plant (fresh) (g), Y/P (D) = Yield/plant (dry) (g), TSW = Thousand seed weight, DW/SM = Dry weight per square meter and Y/ha = Yield per hectare

4.4.3 Plant height (cm)

Plant height was positively correlated (0.628**) and had negative direct effect (-0.379) on yield per hectare. It had positive indirect effect on yield per hectare via number of total tillers per plant (0.414), panicle length (0.061), number of secondary branch per panicle (0.383), number of filled grains per panicle (0.449), yield per plant (0.256) and thousand seed weight (0.087).Whereas plant height had indirect influence on yield per hectare through days to flowering (-0.159), days to maturity (-0.011), number of effective tillers per plant (-0.028), number of primary branches per panicle (-0.081), total number of spikelet per panicle (-0.596), number of unfilled grains per panicle (-0.179) (Table 9). 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 (-1.166) effect on yield per hectare. It had positive indirect effect on yield per hectare via plant height (0.134), number of effective tillers per plant (0.813), total number of spikelet per panicle (0.017), number of filled grains per panicle (0.146), and number of unfilled grains per panicle (0.223) and yield per plant (0.456).Whereas, it had negative indirect effect through days to flowering (-0.055), days to maturity (-0.002), panicle length (-0.019), number of primary branches per panicle (-0.081), number of secondary branch per panicle (-0.004), and thousand seed weight (-0.133) on yield per hectare. Number of total tillers per plant finally made non-significant positive genotypic correlation (0.195) with yield per hectare.

4.4.5 Number of effective tillers per plant

The positive direct effect (0.847) 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 plant height (0.013), number of secondary branches per panicle (0.132), number of filled grains per panicle (0.296), number of unfilled grains per panicle (0.190), yield per plant (0.21). The indirect effect of this trait on yield per hectare via days to flowering (-0.110), days to maturity (-0.006), number of total tillers per plant (-1.118), panicle length (-0.014), number of primary branches per panicle (-0.121), total number of spikelet per panicle (-0.156), thousand seed weight (-0.108) was negative. Finally number of effective tillers per plant made significant positive genotypic correlation (0.474**) with yield per hectare (Table 9). 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 (0.080) on yield per hectare. It had positive indirect effect through panicle length (0.282), number of secondary branches per panicle (0.189), number of filled grains per panicle (0.344), yield per plant (0.095), thousand seed weight (0.089) on yield per hectare. Negative indirect effect on yield per hectare was found through days to flowering (-0.090), days to maturity (-0.007), plant height (-0.290), number of effective tillers per plant (-0.147), number of primary branches per panicle (-0.009), total number of spikelet per panicle (-0.472), number of unfilled grains per panicle (-0.184) (Table 9). Its correlation with yield per hectare was positive and non-significant (0.159). 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 negative effect (-0.147) on yield per hectare. It had positive indirect effect on yield per hectare via number of effective tillers per plant (0.697), panicle length (0.005), number of secondary branches per panicle (0.325), number of filled grains per panicle (0.358), number of unfilled grains per panicle (0.107), and yield per plant (0.713).However, number of primary branches per panicle had negative indirect effect on yield per hectare through days to flowering (-0.189), days to maturity (-0.011), plant height (-0.208), number of total tiller per plant (-0.642), total number of spikelet per panicle (-0.299), thousand seed weight (-0.141). The genotypic correlation with yield per hectare was significant and positive (0.866**). 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 (0.430) on yield per hectare. It had positive indirect effect through number of total tiller per plant (0.012), number of effective tillers per plant (0.260), panicle length (0.035), number of filled grains per panicle (0.564), yield per plant (0.375), thousand seed weight (0.063) on yield per hectare., , Whereas, it had negative indirect effect on yield per hectare via days to flowering (-0.214), days to maturity (-0.014),plant height (-0.338)number of primary branches per panicle (-0.111), total number of spikelet per panicle (-0.650), number of unfilled grains per panicle (-0.109). Finally this trait had significant positive genotypic correlation (0.834**) with yield per hectare (Table 9). 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 (-0.863) on yield per hectare. This trait had also indirect positive effect on yield per hectare via number of total tillers per plant (0.024), number of effective tillers per plant (0.153), panicle length (0.044), number of secondary branch per panicle (0.324), number of filled grains per panicle (0.728), yield per plant (0.326), and thousand seed weight (0.148). On the other hand, indirect negative effect of this trait showed on yield per hectare through days to flowering (-0.246), days to maturity (-0.013), plant height (-0.262), number of primary branches per panicle (-0.051), number of unfilled grains per panicle (-0.196). Finally this trait had significant positive correlation (0.648**) with yield per plant (Table 9).

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 (0.747) followed by positive indirect effect through number of effective tillers per plant (0.335), panicle length (0.037), number of secondary branch per panicle (0.324), yield per plant (0.452), and thousand seed weight (0.102). Whereas this trait showed negative indirect effect via days to flowering (-0.256), days to maturity (-0.013), plant height (-0.228), number of total tillers per plant (-0.228), number of primary branches per panicle (-0.070), total number of spikelet per panicle (-0.841), number of unfilled grains per panicle (-0.141), Number of filled grains per panicle had highly significant and positive correlation with yield per plant (0.754**) (Table 9) 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 negative direct effect (-0.306) on yield per hectare. The positive indirect effect on yield per hectare was found via number of total tillers per plant (0.851), panicle length (0.048), number of primary branches per panicle (0.051), number of secondary branch per panicle (0.153), number of filled grains per panicle (0.345), and thousand seed weight (0.282). It had also negative indirect effect through days to flowering (-0.089), days to maturity (-0.007), plant height (-0.222), number of effective tillers per plant (-0.525), total number of spikelet per panicle (-0.554), yield per plant (-0.362) on yield per hectare. Number of unfilled grains per panicle finally made non-significant positive genotypic correlation (0.001) with yield per hectare.

4.4.12 Yield per plant (gm)

The direct effect (0.858) of yield per plant on yield per hectare was positive. The positive indirect effect of this trait on yield per hectare through number of effective tillers per plant (0.584), panicle length (0.009), number of secondary branches per panicle (0.188), number of filled grains per panicle (0.393), number of unfilled grains per panicle (0.129).Whereas, negative indirect effect of this trait was found on yield per hectare via days to flowering (-0.190), days to maturity (-0.009), plant height (-0.113), number of total tillers per plant (-0.619), number of primary branches per panicle (-0.122), total number of spikelet per panicle (-0.328), thousand seed weight (-0.210). The correlation with yield per was positive and non-significant (0.806**) (Table 9). 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 negative direct effect (-0.309) on yield per hectare. It had positive indirect effect on yield per hectare via days to flowering (0.016), days to maturity (0.004), plant height (0.107), number of effective tillers per plant (0.297), total number of spikelet per panicle (0.413), number of unfilled grains per panicle (0.279), and yield per plant (0.584). However, thousand seed weight had negative indirect effect on yield per hectare through number of total tillers per plant (-0.504), panicle length (-0.023), number of primary branches per panicle (-0.067), number of secondary branch per panicle (-0.087), and number of filled grains per panicle (-0.248). , Thousand seeds weight finally made positive genotypic correlation (0.26) 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 V

SUMMARY AND CONCLUSION

This study was undertaken with 12 F_5 aus materials at the Sher-e-Bangla Agricultural University Farm, Bangladesh during April, 2015- September, 2015. 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 12 genotypes of *Oryza sativa* L, it was observed that significant variation existing among all the genotypes used for most of the characters studied. Comparing with two check varieties G11 (BRRI dhan 48) (87.00 days) and G12 (BRRI dhan 55) (80 days) the lowest days to flowering was observed in G5 (21× 29 F6 S6 P3) (70 days) and highest was observed in G10 (24× 26 F6 S6 P4) (93.33 days). The highest days to maturity was taken in G4 (21× 29 F6 S7 P5) (90.67 days) and the minimum days to maturity was taken in G1 (21× 29 F6 S6 P9) (71.67 days), G2 (21× 29 F6 S7 P2) (71.67 days), G3 (21× 29 F6 S7 P5) (73.33 days) which is compared to check varieties G11 (BRRI dhan 48) (112 days) and G12 (BRRI dhan 55) (111 days). Comparing with two check varieties G11 (BRRI dhan 48) (102.9cm) and G12 (BRRI dhan 55) (97.77cm), plant height exhibited highest in G4 (21× 29 F6 S7 P5) (134.6cm) and lowest in G6 (21× 29 F6 S7 P4) (92.60). G7 (21× 29 F6 S6 P10) (17.73) showed the maximum number of total tillers per plant and the minimum one was in G2 (21× 29 F6 S7 P2) (11.90). The highest number of effective tillers per plant was recorded in G7 (21× 29 F6 S6 P10) (14.80) whereas the minimum number of effective tillers per plant was recorded in G2 (21× 29 F6 S7 P2) (11.53). The highest panicle length was observed in G10 (24× 26 F6 S6 P4) (26.40) and the minimum panicle length were observed in G6 (21× 29 F6 S7 P4) (23.58). Highest number of primary branches per panicle was recorded for G4 (21× 29 F6 S7 P5) (9.80) while the minimum number of primary branches per panicle was recorded for G8 (21× 29 F6 S7 P1) (6.933). The highest number of secondary branches per panicle was recorded in G4 (21× 29 F6 S7 P5) (35.27) whereas the minimum number of secondary branches per panicle was observed in G8 (21× 29 F6 S7 P1) (21.39).The total number of spikelet per panicle was maximum in G10 (24× 26 F6 S6 P4) (204.9) and minimum was observed in G6 (21× 29 F6 S7 P4) (111.2). The number of filled grains per panicle was recorded highest in G10 (24× 26 F6 S6 P4) (170.3) and minimum was recorded in G6 (21× 29 F6 S7 P4) (96.97). The G10 (24× 26 F6 S6 P4)(34.67) showed the highest number of unfilled grains per panicle and the G7 (21× 29 F6 S6 P10) (13.67) showed the minimum number of unfilled grains per panicle. Thousand seed weight was found maximum in G12 (BRRI dhan 55) (24.07) whereas the minimum thousand seed weight was found in G10 (24× 26 F6 S6 P4) (19.70). Yield per plant was recorded highest in G11 (BRRI dhan 48) (33.40) and the lowest were found in G5 (21× 29 F6 S6 P3) (17.53). Genotype G4 (21× 29 F6 S7 P5) (5.287) showed the maximum yield per hectare and the minimum one was in G5 (21× 29 F6 S6 P3) 2.633).

The phenotypic variance of 12 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.

However, phenotype coefficients of variation were higher than the corresponding genotypic coefficient of variation for all the characters under study. Number of unfilled grains per panicle, yield per plant, and 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. Days to flowering, days to maturity, 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, thousand seed weight, and yield per hectare 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 days to flowering, days to maturity, plant height, total number of spikelet per panicle, and number of filled grain per panicle indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. High heritability with moderate genetic advance in percent of mean was observed for number of secondary branches per panicle, number of unfilled grains per panicle, 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 number of total tiller, number of effective tiller, number of primary branches per panicle, thousand seed weight 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.

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

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

Results based on Mean Data of F_5 lines, the following conclusions and recommendations may be drawn:

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

Recommendations:

Comparing with the check varieties G11(4.49 t) and G12 (3.64 t), the genotype G4 showed higher seed yield per plant (31.47) and yield per hectare (5.28) but duration was long (131 days). On the other hand G3 showed higher seed yield per plant (25.07) and yield per hectare (3.773) and also the duration is short than one check variety G12.Considering the magnitude of genetic distance, contribution of character towards divergence and agronomic performance,G3 was the best variety which give higher yield in short duration in my experiment.

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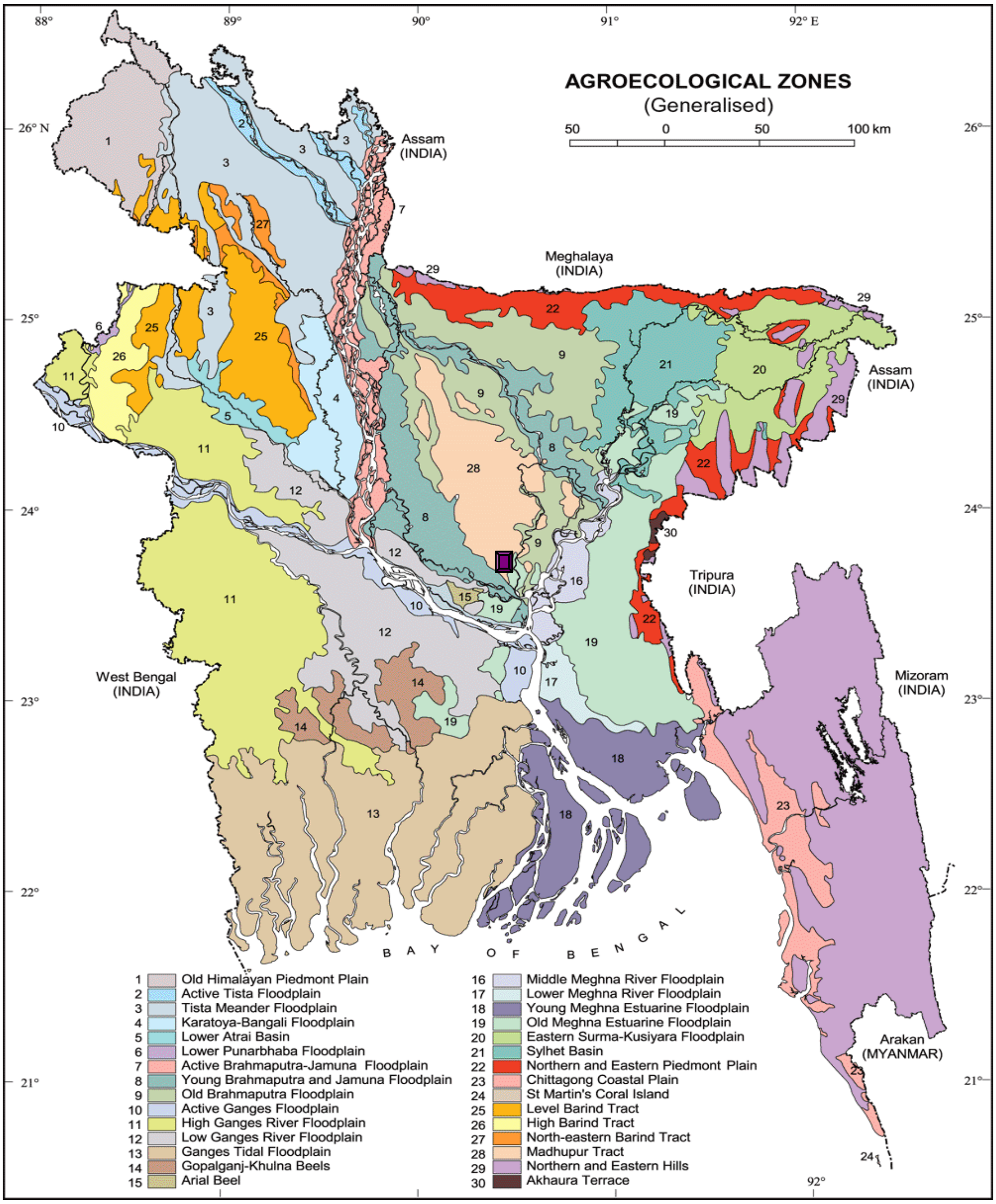
APPENDICES

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

Month	Air temperature (ºc)		Average rainfall (mm)
	Maximum	Minimum	
April	38.0	28.0	5.87
May	37.5	27.0	6.23
June	37.0	27.0	6.45
July, 2011	35.0	25.0	8.77
August, 2011	34.0	25.0	19.9
September, 2011	34.5	26.5	7.63

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

Appendix IV: Mean performance of 12 genotypes of *Oryza sativa* L. in respect of seven important characters

Genotype	DF	DM	PH	NTT/P	NET/P	PL/P	NPB/P
G1	71.67	103.7	107.9	12.53	12.20	25.71	7.233
G2	71.67	103.7	108.0	11.90	11.53	25.56	7.533
G3	73.33	103.0	108.7	12.87	12.17	25.53	7.433
G4	90.67	131.7	134.6	14.47	14.23	26.20	9.800
G5	70.00	105.0	109.2	13.67	12.80	23.80	7.900
G6	71.67	106.0	92.60	15.00	13.42	23.58	7.233
G7	73.33	105.3	101.5	17.73	14.80	25.73	8.167
G8	73.33	105.3	108.2	12.47	11.70	25.44	6.933
G9	73.33	109.0	108.2	14.93	13.23	25.85	8.033
G10	93.33	127.3	119.2	13.70	12.77	26.40	7.933
G11	87.00	112.0	102.9	15.63	14.10	23.95	8.467
G12	80.00	111.0	97.77	16.33	13.97	24.25	8.600

**Values are statistically identical at 5% level of probability.

DF = Days to flowering,, DM = Days to maturity, PH = Plant height (cm), NT = Total no of tiller/plant, NET = Number of effective tiller/plant, PL = Panicle length (cm), NPB/P = Number of primary branches/panicle, NSB/P = Number of secondary branches/panicle.

G1 = 21× 29 F6 S6 P9, G2 = 21× 29 F6 S7 P2, G3 = 21× 29 F6 S7 P5 (a), G4 = 21× 29 F6 S7 P5 (b), G5 = 21× 29 F6 S6 P3, G6 = 21× 29 F6 S7 P4, G7 = 21× 29 F6 S6 P10, G8 = 21× 29 F6 S7 P1, G9 = 24× 28 F6 S10 P10, G10 = 24× 26 F6 S6 P4, G11 = BRRI dhan 48 and G12= BRRI dhan 55.

Appendix V: Mean performance of 12 genotypes of *Oryza sativa* L. in respect of seven important characters

Genotypes	NSB/P	TS/P	NFG/P	NUFG/P	Y/P	TSW	Y/ha
G1	22.75	128.2	103.0	25.50	26.43	22.47	22.20
G2	26.40	122.1	100.1	22.07	25.90	21.40	22.43
G3	24.63	131.6	111.0	23.97	25.07	17.87	21.90
G4	35.27	164.3	141.5	23.40	37.80	31.47	22.30
G5	26.43	127.5	103.1	21.40	27.07	17.53	21.47
G6	21.40	111.2	96.97	19.90	24.40	18.80	21.07
G7	24.03	129.0	119.4	13.90	30.17	24.87	22.08
G8	21.39	129.0	100.9	24.83	26.80	22.00	22.10
G9	24.50	127.8	104.5	19.27	28.33	23.40	22.70
G10	31.20	204.9	170.3	34.67	29.50	22.97	19.70
G11	25.63	147.3	132.9	14.40	39.87	33.40	24.03
G12	24.30	121.6	107.8	14.43	32.40	27.73	24.07

**Values are statistically identical at 5% level of probability.

TS/P = Total no of spikelet/panicle, NFG/P = Number of filled grain per panicle, NUG/P = Number of unfilled grain per panicle, Y/P (F) = yield per plant (fresh) (g), Y/P (D) = Yield/plant (dry) (g), TSW = Thousand seed weight, DW/SM = Dry weight per square meter and Y/ha = Yield per hectare.

G1 = 21× 29 F6 S6 P9, G2 = 21× 29 F6 S7 P2, G3 = 21× 29 F6 S7 P5 (a), G4 = 21× 29 F6 S7 P5 (b), G5 = 21× 29 F6 S6 P3, G6 = 21× 29 F6 S7 P4, G7 = 21× 29 F6 S6 P10, G8 = 21× 29 F6 S7 P1, G9 = 24× 28 F6 S10 P10, G10 = 24× 26 F6 S6 P4, G11 = BRRI dhan 48 and G12= BRRI dhan 55.