SELECTION OF SHORT DURATION HIGH YIELDING AUS MATERIALS IN F_4 GENERATION OF RICE (*Oryza sativa* L.) THROUGH AUS-AUS CROSS

BY

RAFIQUL ISLAM

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Approved by:

Prof. Dr. Md. Shahidur Rashid Bhuiyan
Supervisor

Hossai

Prof. Dr. Md. Sarowar Hossain
Co-supervisor

Prof. Dr. Mohammed Ali
Chairman
Examination Committee

Dr. Md. Shahidur Rashid Bhuiyan
Professor
Department of Genetics and Plant Breeding
Sher-e-Bangla Agricultural University
Sher-e-Bangla Nagar, Dhaka-1207,
E-mail: msbhuiyan@yahoo.com
Cell No. : +88-01552467945

CERTIFICATE

This is to certify that the thesis entitled "*SELECTION OF SHORT DURATION HIGH YIELDING AUS MATERIALS IN* F_4 *GENERATION* of *RICE* (*Oryza sativa L.*) *THROUGH AUS-AUS CROSS, Sher-e-Bangla Agricultural University (SAU), Dhaka in partial fulfillment of the requirements for the degree of MASTER OF SCIENCE (MS) IN SEED TECHNOLOGY, embodies the results of a piece of bonafide research work carried out by* ***RAFIQUL ISLAM, Registration no. 07-02342*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2014
Place: Dhaka, Bangladesh

Prof. Dr. Md. Shahidur Rashid Bhuiyan
Supervisor

Dedicated To

My
Respectable
Parents

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SELECTION OF SHORT DURATION HIGH YIELDING AUS MATERIALS IN F_4 GENERATION OF RICE (*Oryza sativa* L.) THROUGH AUS-AUS CROSS

ABSTRACT

BY

RAFIQUL ISLAM

The present study involved fifteen F_4 populations of rice (*Oryza sativa* L.) with three check varieties to select short duration and high yielding Aus varieties. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications in the experimental farm of Sher-e-Bangla Agricultural University (SAU), Dhaka during April 2014 to July 2014. Variability, correlation and path coefficient were analyzed mainly on the basis of days to maturity, yield/plant and yield(t/ha) but other eleven characters also studied as these traits directly or indirectly contribute on yield. The lowest days to maturity (96.33 days) was observed in G4 (BR 21×BR 24, F_4, S_2P_3) following as G3 (BR 21×BR 24, F_4, S_2P_2) (97 days) and G2 (BR 21×BR 24, F_4, S_2P_1) (97.67 days). The highest yield among F_4 populations was recorded in G8 (BR 24×BR 26, F_4, S_5P_1) (5.7 ton/ha) following by G3 (BR 21×BR 24, F_4, S_2P_2) (4.57 ton/ha) and G4 (BR 21×BR 24, F_4, S_2P_3) (4.37 ton/ha). The characters were observed and concluded that the phenotypic variances were higher than the genotypic variances. Phenotypic coefficient of variation (PCV) was also higher than the genotypic coefficient of variation (GCV) for all the characters studied. High heritability with high genetic advance in percent of mean was found for total number of tiller/plant, total number of effective tiller/plant, number of secondary branches/ panicle, total number of spikelet/ panicle, number of filled grain/ panicle, yield/ plant, yield(t/ ha) and moderate heritability with high genetic advance found in days to maturity. The significant positive correlation with yield/ hectare were found in days to 80% maturity, number of secondary branches/ panicle, total number of spikelet/panicle, number of filled grain/ panicle and yield/plant. Path co-efficient analysis revealed that days to 80% maturity, number of secondary branches/panicle, total number of spikelet/panicle, number of filled grain/ panicle and yield/ plant had the positive significant direct effect on yield(t/ ha) and as these parameters were also good for variability, heritability and correlation so, they may be used for further crop improvement practices. By comparing check varieties with segregating populations some better genotypes as G2, G3, G4, G8 and some individual plants from different populations were selected as early maturity and high yielding Aus rice (*Oryza sativa* L) for future trial.

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LIST OF ABBREVIATED TERMS

Abbreviation	Full word
%	Percent
°C	Degree Celsius
@	At the rate
σ^2p	Phenotypic variance
σ^2g	Genotypic variance
σ^2e	Environmental variance
h^2 b	Heritability in broad sense
AEZ	Agro-Ecological Zone
Agric.	Agriculture
Agril.	Agricultural
Agron.	Agronomy
ANOVA	Analysis of variance
BARI	Bangladesh Agricultural Research Institute
BBS	Bangladesh Bureau of Statistics
BD	Bangladesh
BES	Bangladesh Economic Survey
Biol.	Biological
BINA	Bangladesh Institute of Nuclear Agriculture
BR	Bangladesh Rice
Breed.	Breeding
BRRI	Bangladesh Rice Research Institute
cm	Centi-meter
CV%	Percentage of Coefficient of Variation
Df	Degrees of Freedom
DF	Days to flowering
DM	Days to maturity
DMRT	Duncan's Multiple Range Test
E	East
EC	Emulsified Concentrate
Ecol.	Ecology
ECV	Environmental co-efficient of variation
Env.	Environment
et al.	And others

(Continued...)

Abbreviation	**Full word**
etc.	Etcetera
F_1	The first generation of a cross between two dissimilar homozygous parents
F_4	The fourth generation of a cross between two dissimilar homozygous parents
F_5	The fifth generation of a cross between two dissimilar homozygous parents
FAO	Food and Agricultural Organization
FGP	Filling spikelet percentage
g	Gram
G	Genotype
GA	Genetic Advance
GAPM	Genetic advance as percentage of mean
GCV	Genotypic coefficient of variation
GDP	Gross Domestic Product
Genet.	Genetics
GW	Spikelet weight
HI	Harvest Index
IARI	Indian Agricultural Research Institute
J.	Journal
K	Potassium
Kg	Kilogram
m	Meter
M_3	Third generation of mutant lines
MS	Mean sum of square
MP	Murate of Potash
MOA	Ministry of Agriculture
m^2	Square meter
N	Nitrogen
N	North
n	Number of Chromosome
NET	Number of effective tiller per plant
NFG	Number of filled grain per panicle

(***Continued…***)

Abbreviation	**Full word**
NSB	Number of secondary branches per panicle
NTT	Number of total tiller per plant
NUFG	Number of unfilled grain per panicle
P	Phosphorous
PCV	Phenotypic coefficient of variation
PH	Plant Height
pH	Negative logarithm of Hydrogen ion
PL	Panicle length
RCBD	Randomized Complete Block Design
Res.	Research
RIL	Recombinant inbreed lines
S	Sulfur
SAU	Sher-e-Bangla Agricultural University
Sci .	Science
TNSP	Total number of spikelet per panicle
TSP	Triple Super Phosphate
TGW	1000- spikelet weight
TSW	*1000* seed weight
Y	Yield ton per hectare
YP	Yield per plant

Chapter I

Introduction

Chapter I

INTRODUCTION

Rice (*Oryza sativa* L.) is main food crop for south and South East Asia specially for Bangladesh and grown all over the world. It has 24 species, of which 22 are wild and two *viz*., *Oryza sativa* and *Oryza glaberrima* are cultivated (Ray, 1985). *Oryza sativa* L.was originated from South and Southeast Asia. *Oryza glaberrima* was domesticated in South and Southeast Asia around the world. Rice is generally considered a semi aquatic annual plant belongs to the family Gramineae (synonym-Poaceae) having chromosome no. 2n=24 under the order Cyperales and class Monocotyledon (Hooker, 1979).Indian subcontinent is the ancestral home *Oryza sativa* L. It has three major sub-species- *indica*, *japonica* and *javanica* (Purseglove, 1985). The rice cultivars grown in Bangladesh belong to sub species indica (Alim, 1982).

Rice is not only use for food but also linked with custom and culture of Bangladeshi peoplante. Rice constitutes about 92% of the total food grain produced in Bangladesh annually. It provides 75% calory and 55% protein in the average dietary of the Bangladeshi peoplante (Bhuiyan *et al.* 2002). Rice is rich in carbohydrate. The protein content is about 8.5 percent. The thiamin and riboflavin contents are 0.27 and 0.12 micrograms per 100g respectively.

Bangladesh is the fourth position in rice production in the world. Nearly 47.5% of our emplantoyments are engaged in rice sector. The contribution of rice to GDP is 13.09%. Total production of grain crops in Bangladesh in 2012-2013 fiscal year is 372.66 lac metric ton, where as Aus, Aman and Boro rice contribute 21.58, 128.97, 187.78 lac metric ton respectively, (BBS, 2014). At present, the occupied land of Aus rice is 2602 thousand acre and Aman rice is 13863 thousand acres as well as Boro rice is 12763 thousand acre (BBS, 2014).

Now the world is facing negatively for food security because total cultivable area is decreasing day by day due to high population pressure.

In case of Bangladesh included rapid growth (1.36%) of population and diminishing rice production area are influencing on reduced rice yields to feed the peoplante. In this circumstance, there is no alternative rather than restoring development and adoption of yield enhancing technologies such as explantoitation of genotype vigor (Rothschild, 2007). In general, increased panicle number, number of spikelet per panicle and percent filled grains per panicle being of secondary and tertiary importance (Jones and Synder, 1987). Therefore, information about the yield contributing traits is very important to the plant breeders for the development of improved varieties/ lines of rice with increased yield. This study was undertaken to find out and establish high yielding short duration populations through study of genetic variability, genetic advance and relationship between yield and its components.

On the top of that, rice is grown as Aus, Aman and Boro crops in three overlapping season. Aus rice is one of the major crops in Bangladesh. The sowing period and weather condition are favorable for this season. The rainfall also helpful for Aus production which reduces irrigation cost as a result total cost of production is reduced. Every year, the production rate is decreasing with the decreased total Aus crop area due to crop competition with some profitable vegetables. Therefore short duration variety of rice will be promising practice for our farmers and it will suit with crop competition. It can be minimized by using improved Aus varieties. Inter-varietal crosses and evaluation of generations need to be performed to select high yielding short duration populations for using them in generating Aus rice varieties. This research will facilitate to develop high yielding short duration Aus rice variety. So, following are the main objectives of this study.

- To study the variability in the F_4 segregating populations
- To know the interrelationship of yield contributing characters and their direct and indirect effect on yield
- To selection of short duration and high yielding populations of Aus rice

Chapter II

Review of Literature

Chapter II

REVIEW LITERATURE

Rice has wide adaptability to different environmental conditions, as it is evident from its worldwide distribution. Yield of rice variety is determined by the morphological parameters such as 50% flowering, days to 80% maturity, plant height (cm), total no. of tiller/plant, no. of effective tiller/plant, panicle length(cm)/plant, no. of primary branches/ plant, no of secondary branches/ plant, total no. of spikelet /panicle, no. of filled grain of main tiller, , no. of unfilled grain of main tiller, yield/plant(g), 1000 seed weight (g) and yield (ton/hectare). The identification of suitable combinations of genotypes in comparison to the best parent varieties for yield and some important yield contributing characters are essential tool for a successful assessment. The present study has aimed to assess the performance of genotypes as compared to the check varieties. The available information most relevant to the present study has been reviewed here under the following sub-headings:

2.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

A study was conducted by Yadav (1992) on 11 plant characters in 16 rice genotypes and revealed that heritability estimate was high for days to 50% flowering and for yield/plant.

Abarshahr *et al.* (2011) estimated genetic variability and relationships among some agronomic traits of 30 varieties of rice under two irrigation regimes. There were significant differences among the varieties for all traits. Broad sense heritability varied from 0.05 for brown grain width to 0.99 for plant height and number of spikelets for panicle under optimum irrigation and from 0.1 for brown grain with to 0.99 for plant height. The lowest and highest phenotypic coefficient of variation (PCV) under optimum irrigation regime was observed to panicle fertility percentage and paddy yield and genotypic coefficient of variation (GCV) was related to brown grain width and plant height, respectively, while under drought stress condition, days to 50% flowering had the lowest PCV and GCV and paddy yield and plant height had the highest PCV and GCV.

According to Bihari *et al*. (2004) who conducted an experiment with seventeen aromatic rice genotypes observed the days to 50% flowering and test weight were highly heritable traits.

Akhtar *et al.*(2011) studied on the variance and heritability for yield contributing characters in ten rice genotypes. The heritability was found to be high for number of grains per panicle, days to maturity, plant height and paddy yield while lower for number of tillers per plant.

Akhter *et al.*(2010) estimated the genetic variability, character association and path analysis of 52 exotic rice genotypes for reproductive traits. There was found significant genetic variability among genotypes. The highest genotypic variance and phenotypic variance were found for pollen sterility and filled grains per panicle. High heritability and genetic advance were recorded for pollen sterility. This study suggested that selection could be based on filled grains per panicle only according to genetic parameters, association and path analysis.

Ananthi *et al.* (2006) studied genotypic and phenotypic coefficient of variation, heritability, expected genetic advance (GA) and genetic advance as percent of mean for grain yield and its contributing characters. Relatively high PCV and heritability estimates were recorded for 1000- grain weight

Ashvani and Vinod (2007a) studied the genetic parameters of variability and heriatbility of different characters in 32 genotypes of rice, grown in Ghaziabad, Uttar Pradesh, India, in Kharif 1992. The heritability estimates were highest for days to 50% flowering.

Ashwani and Panwar (2007a) carried out Path analysis in 22 genotypes of rice, grown in Hardwar, Uttaranchal, India, during kharif 1990-91. Data were recorded on days to 50% flowering. Days to 50% flowering had the highest positive direct effect on grain yield. Thus greater emphasis should be given for selection of these characters.

Awasthi and Pandey (2000) observed significant genetic variability among 21 aromatic low land rice genotypes for days to 50% flowering.

Awatshi and Sharma (1996) recorded considerable genetic variability for plant height in 15 of high quality aromatic *Oryza sativa* L. genotypes.

Bai *et al.* (1992) reported that grain yield per plant positively correlated with numbers of positively tillers and number of grains per/plant

Bansal *et al.* (1998) studied heterosis and combining ability in an 11-parent diallel involving 8 scented (Dawg, Bindi, N750, Basmati 1A, Basmati 372, Karnal Local, Basmati 1 and Basmati 405) and 3 non-scented (Pusa 44-33, IET8585 and TNI) rice (*O. Sativa*) stocks. The estimates of general combining ability (GCA) and specific combining ability indicated predominance of non- additive gene effects for panicle length.

Bansal *et al.* (1999) studied heterosis and combining ability effects in an 11-parent diallel cross involving 8 scented (Dawg, Bindi, N750, Basmati 1A, Basmati 372, Karnal Local, Basmati 1 and Basmati 405) and 3 non-scented (Pusa 44-33, IET8585 and TNI) rice (*O. Sativa*) stocks. The estimates of general combining ability (GCA) and specific combining ability indicated predominance of non- additive gene effects for 1000-grain weight.

Bhave *et al.* (2002) stated 32 rice genotypes derived from two CMS lines (JR 580256 A and JR 62829 A) and 16 local restorers (RTN 73, KJT 1, KJT 4, RTN 711, RTN 24, RTN 1, PNL 1, PNL 2, KiT 3, PLANTG 1, KJT2, RTN 3, KiT 147 and RTN 68) were evaluated for heterosis, heterobeltiosis and yield advantages in percent heterosis, heterobeltiosis and yield advantages in percent productive number per plant range from -26.10 to 124.32%, -44.79 to 90.80% and 58.50 to 80.43% respectively.

Bidhan *et al.* (2001) studied the genetic variability, heritability, and genetic advance for yield and yield components in 25 medium duration rice genotypes West Bengal, India, during kharif 1996-97. Observations were recorded for 1000- grain weight and 1000- grain weight exhibited less environmental effect and high heritability couplanted with moderate to high genetic advance.

Bisne *et al.* (2009) estimated the genetic parameters for yield and its correspondent characters in rice from a trial with four CMS lines, eight testers and thirty two hybrids for thirteen characters related to yield. High genotypic and phenotypic coefficients of variations were found in harvest index, total number of filled spikelets per panicle, 100-grain weight and spikelet fertility percentage. High heritability couplanted with high genetic advance was exhibited by harvest index, total number of chaffy spikelets per panicle, grain yield per plant, total number of filled spikelets per panicle and spikelet fertility percentage and selection may be effective for these characters.

Biswas *et al.* (2000) observed higher genotypic and phenotypic variance (GCV and PCV) for plant height, filled grains per panicle and 1000-grain weight of 30 advanced breeding lines of rice. Lower GCV and PCV were found for number of panicles per hill and panicle length. High broad sense heritability was found for 1000-grain weight followed by panicle length. Moderate heritability was found for grains per panicle, plant height, number of panicle per hill, number of primary branches and yield per plant.

BRRI (1997) conducted an experiment with rice and observed that weight of 1000-grains of Halio, Tilochachari, Nizershail and Latishail were 26.5, 27.7 and 25.2 respectively.

Chakraborty and Chakraborty (2010) assessed the genetic variability, correlation and coheritability of 47 bold grained rice genotypes with two locally recommended high yielding check varieties namely Ranjit and Monohar Sali of Barak Valley, Assam for eight morpho-physiological characters. Very small difference between genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) was observed for the characters like days to 50% flowering. Wide difference between GCV and PCV was observed for the characters like plant height, effective branch tillers per hill, panicle length, sterility percentage and yield per plant. There was high heritability associated with high genetic advance was found in the characters grain yield per hill and sterility percentage. High heritability with moderate genetic advance was observed for the characters effective branch tillers per hill. High heritability with low genetic advance was observed for the character days to 50% flowering.

Chakraborty and Hazarika (1994) reported a very small difference between phenotypic and genotypic coefficient of variation, high heritability along with moderate genetic advance for panicle length.

Chakrabothi and Hazarika (1994) observed least difference indicating non-additive gene action.

Chand *et al.* (2004) studied nineteen genotypes of aman paddy [rice] (Oryza *sativa*) emanating from different sources different sources were evaluated for grain yield and their components during kharif. Heritability and genetic advance as percentage of mean were high for 1000- grain weight

Chaubey and Singh (1994) worked with 20 rice varieties and reported high genotypic coefficient of variation, heritability and genetic advance for yield per plant. Thirty rice genotypes were evaluated for variability by Das *et al.* (1992). The highest GCV was found in grain per plant. High heritability with high genetic advance in percent of mean was also found in grain yield per plant.

Chaudhury and Das (1998) estimated genetic variability in 11 deep water rice varieties for yield and yield related characters like effective tillers plant^{-1}. They found a large difference between genotypic and phenotypic co-efficient of variation for effective tillers plant^{-1}.

Chaudhury and Das (1998) worked out estimates of variability, heritability and genetic advance in 11 deep water rice varieties for yield and its yield attributing characters. High genotypic co-efficient of variation was also observed for grains per panicle. High heritability with high genetic advance was found for grains per panicle.

Chauhan *et al.* (1993) showed wide of range of variation among the genotypes studied. High estimated genetic advance associated with high heritability estimates was recorded to 1000- grain weight, indicating additive gene action and liability to phenotypic selection.

Chen and Hong (2008) did genetic analysis on plant height in hybrid rice Shanyou 63 and found that plant height was mainly governed by major genes.

Chen-Liang *et al.* (2000) showed that the cross between Peiai 64s and the new plant type lines had strong heterosis for filled grains per plant, number of spikes per plant and grain weight per plant, but heterosis for spike fertility was low. Xiao *et al.* (1996) indicated that heterosis in F1 hybrids for spikelets/panicle showed a positive and significant correlation with genetic distance in indica x indica but not in indica x japonica crosses. Choi (1985) reported that grain yield was positively correlated with spikelet numbers/panicle.

Chuhan *et al.* (1993) estimated high heritability in broad sense couplanted with high genetic advance in rice.

Das *et al.* (1992) evaluates for thirty rice genotypes for variability and genetic association. The highest genotypic coefficient of variation (GCV) was found for grain yield per plant followed by fertile spikelet per panicle, total spikelet per panicle and fertile tillers per plant. High heritability was observed for all the characteristics except total spikelet per panicle. High broad sense heritability with high genetic advance in percent of means (GAPM) was found in plant height, fertile tillers per plant, fertile spikelet per panicle, 1000-grain weight, days to 50% flowering, days to maturity and grain yield per plant.

Debi *et al*. (1997) studied 29 irrigated rice genotypes and found high GCV, h^2b and genetic advance as percentage of mean (GAPM) for number of panicle plant^{-1}.
Diaj *et al.* (2000) noted wide variation in panicle length, panicle type, grain panicle^{-1} and panicle weight and secondary branches panicle^{-1}.

Fang and Wu (2001) suggested that the expression of several QTLs associated with plant height could be induced by low Nitrogen stress.
Genetic variability was determined for 7 quantitative characters in 13 diverse genotypes of uplantand rice by Paul and Sarmath (1997). Heritability estimates for all characters including grain yield were above 90%. Genetic grain was low yield per hectare.

Gomez and Kalamain (2003) reported high heritability couplanted with high genetic advance for biological yield Plant^{-1}, Plant height and no. f panicle, indicating that these characters can be considered during selection for drought tolerance.

Guimara (2002) indicate that the plants with cooperatively large panicles tend to have high number of filled grains. However, most of the cases a positive correlation were observed between number of panicle/ plant and panicle length.

Guo *et al.* (2002) studied the genetic relationships between rice yield and its components using correlation and path analyses involving a set of 241recombinant inbreed lines (RIL) population of Shanyou 63, Data were recorded for 1000- grain weight (TGW) and it showed tremendous transgressive variation.

Haque *et al.* (1991) reported negative association of 1000 grain weight and yield per plant in traditional varieties.

Hegde and Patil (2000) studied the genetic divergence in 40 genotypes of rainfed rice using Mahalanobis D^2 statistic. The cultivars fell into 7 clusters. The highest contributing characters to D^2 values were 1000-grain weight.

Hemareddy *et al,* (1994) studied genetic variability for grain yield and its component traits in 81 genotypes of rice and found that phenotypic coefficient of variation (PCV) was higher than the genetic coefficient of variation (GCV) for all traits studied indicating the interaction of traits with the environment. Days to flowering had the highest heritability (98.61%).

Hemareddy *et al.* (1994) studied genetic variability for grain yield and its component traits in 81 genotypes of rice and found that phenotypic coefficients of variation were higher than the genetic coefficient of variation for all traits studied indication the interaction of traits with environment. Days to 50% flowering had the highest heritability (98.61).

Honarnejad (1995) observed low heritability days to 50% flowering 15 F_1 hybrids and from a diallel cross. Low variation, high heritability with moderate genetic advance was reported by Chakraborty and Hazarika (1994) in 36 rice genotypes. But Das *et al.* (1992) evaluated 360 rice genotypes for variability. High heritability couplanted with genetic advance in percent of mean found for days to 50% flowering.

Honarnejad and Tarang (2001) evaluated seven local and alien rice cultivars for yield and yield contributing traits. They observed only 39% low sense heritability for tillers plant^{-1}.

Honarnejad and Tarang (2001) evaluated seven local and alien rice cultivars for traits grain yield other contributing characters. They observed narrow sense heritability 46% for grain yield.

Hossain and Haque (2003) determined the variability of 56 rice genotypes. High genotypic coefficient of variation (GCV) was found for number of panicles per hill (16.06) followed by grains per panicle (15.74), yield per plant (15.65), plant height (12.23) and 1000-grain weight (10.74). Lower GCV was found for days to maturity (5.64). The differences between phenotypic coefficient of variation and genotypic coefficient of variation were very low indicating less influence of environment on these characters. High heritability with high genetic advance in percentage of mean was found for yield per plant, number of filled grains per panicle, days to maturity and plant height. Low heritability with low genetic advance was found for number of panicles per hill, and number of primary branches per panicle.

Hu-WenHe *et al.* (2002) conducted an experiment to study the relationship between yield and yield components of different rice populations, a decreased the 1000- grain weight. Path coefficient analysis showed the number of grains per panicle as the highest yield determinant followed by 1000-grain weight.

Iftekharuddaula *et al.* (2001) recorded high genotypic and phenotypic coefficient of variations (GCV and PCV) for number of filled grains per panicle and spikelet sterility in twenty four modern rice genotypes. Lower GCV and PCV were found for days to maturity and harvest index. Moderate value of heritability was found for number of panicles per hill.

In a genetic study on yield and its component of 52 late duration rice genotypes, Sawant *et al.* (1994) observed high genotypic and phenotypic coefficient of variation for ear bearings tillers plant^{-1}.In a study of genetic variability and heritability of 8 yield components in 28 cultivars, Loknathan *et al.* (1991) found expected genetic advance as high as 68.4% for plant height.

Ingale *et al.* (2007) conducted an experiment Effect of seedling age on 50% flowering of parental lines of Sahyadri rice hybrid. The experiment was formulated to assess the effect of seedling age at transplanting on 50% flowering of A, B, and R lines of Sahyadri rice hybrid. The 50% flowering was delayed in both younger and older aged seedlings than the recommended age of seedling (25 days old) at transplanting by approximately half the number of days by which the seedlings are younger and older than the recommended age.

Jiang *et al.* (2000) observed the importance of number of tillers/plant influencing yield. Productive tillers/hill showed significant positive correlations with correlations with grain yield (Reddy and Kumar, 1996).

Jiang *et al.* (2002) evaluated twenty four genetically diverse elite breeding lines and reported those days to 50% flowering showed high heritability couplanted with high genetic advance indication additive gene effects con A few crosses showed heterobeltiosis for days to 50% flowering.

Kamal *et al.* (1998) performed an experiment to assess the yield of nine modern varieties (MV) and six improved varieties (LIV). They observed that modern variety BR11 gave the highest grain yield followed by BR10, BR23, Binasail and BR24.

Karim *et al.* (2007) studied on variability and genetic parameter analysis of 41 aromatic rice genotypes. The phenotypic variance was higher than the corresponding genotypic variance for the characters. These differences were in case of number of panicles per hill, number of primary branches, number of filled grains per panicle, spikelet sterility (%) and grain yield per hill indicating greater influence on environment for expression of these characters. 1000-grain weight and days to maturity showed least difference between phenotypic and genotypic variance, which indicated additive gene action for expression of the characters. High genotypic coefficient of variation (GCV) value was revealed for 1000-grain weight followed by spikelet sterility (%), grain yield per hill and number of filled grains per panicle, whereas days to maturity showed very low GCV.

Kishore *et al*. (2007) conducted an experiment during kharif 2004 in Hyderabad Andhra Pradesh, India with 70 rice genotypes, including aromatic and non-aromatic lines. Observations were recorded on days to 50% flowering. Path coefficient analysis revealed that days to 50% flowering showed positive direct effects on grain yield.
Kumar (2001) carried out an experiment with 42 genotypes derived from seven crosses of rice and reported that phenotypic coefficient of variation was comparatively higher than the corresponding genotypic coefficient of variation for panicle length.

Kumar *et al.* (1994) evaluated 9 genotypes of rice for 10 characters and found high genotypic coefficient of variation, high heritability and moderate genetic advance for plant height, indicating the predominance of additive gene effects controlling the character.

Kumar *et al.* (2001) evaluated 42 genotypes derived from seven crosses and found comparatively higher phenotypic coefficient of variation than the corresponding genotypic coefficient of variation for days to 50% flowering.

Kumar *et al.* (2001) evaluated 42 genotypes derived from seven crosses and found comparatively higher phenotypic coefficient of variation than the corresponding genotypic coefficient of variation for 100-grain weight.

Kumari *et al*. (2003) reported that plant height shoed high heritability couplanted with modern genetic advances.

Kumer *et al*. (2001) carried out an experiment with 42 genotypes derived from seven crosses of rice and reported that phenotypic coefficient of variation was comparatively higher than the corresponding genotypic coefficient of variation form number of panicle plant^{-1}.

Li and Yuan (1998) reported the parental genotype divergence had a relatively low impact on heterosis for panicle number and 1000 grain weight. Plant height, panicle per plant, grain per panicle and 1000 grain weight increase the yield in modern varieties (Saha Ray *et al.* 1993).

Li *et al.* (1991) worked on 9 rice cultivars and estimated that genetic coefficient of variation was high for yield per plant but they got moderate heritability and moderate genetic advance.

Liu *et al.* (2001) analyzed three CMS lines of Japonica rice crossed with 18 restorers and heterosis of 8 agronomic characters in the 54 F1 lines was. Grain yield per plant and seed-bearing tillers per plant of the F1s showed considerable positive heterobeltiosis and competitiveness while panicle length, 1000-grain weight and seed set demonstrated a negative heterobeltiosis and some yield advantages in percent in terms of grain yield per plant and 216A showed the highest average yield of F1 grain, followed by 16A and 552A.

Mahto *et al*. (2003) evaluated 26 early maturing rice genotypes and found significant differences between phenotypic and genotypic coefficient of variation for panicle length.

Mahto *et al*. (2003) evaluated twenty six early maturing rice genotypes and found that the difference between phenotypic and genotypic coefficient of variation was minimum for days to 50% flowering (13) high values for heritability (97.33) and high genetic advance.

Manual and Prasad (1993) observed little differences between phenotypic and genotypic coefficient of variation indicating less environmental influences. They reported low value of genotypic coefficient of variation, high heritability and low genetic advance for panicle length.

Mishra and Verma (2002) evaluated 16 rice parental cultivars and 72 F_1 progenies and found higher phenotypic co-efficient of variation (PCV) than the genotypic coefficient of variation (GCV) for grain yield/plant. They also found that high heritability couplanted with high genetic advance for yield/plant.

Nayak *et al.* (2001) studied the genotypic and phenotypic correlations and path analysis in 10 quantitative traits of 200 scented rice genotypes, including 1 scented rice control. Path coefficient analysis revealed that 1000-grain weight contributed to the grain yield of the plant.

Neerja and Sharma (2002) conducted an experiment on non-aromatic rice (cvs. IR8, Jaya, PR103, 106, 108, 111, 114,115 and PR 116) and found that the highest 1000 kernel weight of husked rice, brown rice and milked rice was recorded for PR113. BRRI (1997) reported that weight of 1000- grains of Halio, Tilockachari, Nizershail and Latisail were 26.5, 27.2, 25.2 and 25 g. respectively.

Nuruzzaman *et al.* (2000) conducted an experiment to fix out the relationship between the tillering ability and morphological characters among 14 rice varieties. They observed that tiller number varied widely among the varieties and the number of tillers plant-1 at the maximum tillering stage ranged between 14.3 and 39.5 in 1995 and 12.2 and 34.6 in 1996. Among all the varieties, IR-36 followed by Suweon 258 produced the highest maximum tiller number and Dawn produced the lowest tiller number.

Panday and Awasthi (2002) observed genetic variability in 21 genotypes of aromatic rice and significant genetic variability was observed for all the yield contributing traits including plant height.

Pandey and Awasthi (2001) observed genetic variability for the character panicle length among the genotypes that plantayed a major role in the enhancement of production of grain yield.

Pandey and Awasthi (2002) studied 21 genotypes of aromatic rice for yield contributing traits and observed significant genetic variability for 100-grain weight. They also concluded that 100-grain weight and grain yield per plant plantay a major role in the enhancement of production of grain yield.

Pandey and Awasthi (2002) studied genetic variability in 21 genotypes of aromatic rice for yield contributing traits, significant genetic variability was observed for days to 50% flowering.

Pandey and Awasthi (2002) studied genetic variability in 21 genotypes of aromatic rice for yield contributing traits. Significant genetic variability was observed among the 21 genotypes for the entire yield for contributing traits. They concluded that traits plant height, days to 50% flowering effective tillers per plant, panicle length, number of grains per panicle, test weight and grain yield per plant plantay a major role in the enhancement of production of grain yield.

Pandey *et al.* (2010) studied on the genetic variability among forty rice genotypes for yield and yield contributing components. High significant difference was found for all the characters for the presence of substantial genetic variability. The maximum genotypic and phenotypic coefficient of variability was found for harvest index, grain yield per hill, plant height and biological yield per hill. High heritability couplanted with high genetic advance was found for plant height and number of spikelet per panicle.

Patil and Sarawgi (2005) evaluated 128 aromatic rice accessions and estimate genetic variation and correlation for 7 traits and found that number of ear-bearing tiller hill^{-1} had high genotypic and phenotypic coefficient of variation. High heritability couplanted with high genetic advance was also estimated for this character.

Patil and Sarawgi (2005) studied genetic variability in traditional aromatic rice accessions and found that the genetic and phenotypic coefficients of variation were high for 100- grain weight.

Patil *et al.* (2003) evaluated 128 traditional aromatic rice genotypes and found high heritability (>70%) in broad sense for all the characters expected panicle length (54.9).

Patil *et al.* (2003) evaluated 128 traditional aromatic rice genotypes and found high heritability for 100-grain weight associated with yield/hectare.

Patil *et al.* (2003) investigated the heterosis in 7 thermosensitive genic male sterile rice lines(TGMS) and 12 non-TGMS lines was investigated through 84 crosses in the kharif season of 1998-99 in Coimbatore, Tamil Nadu, India. The magnitude of relative heterosis, heterobeltiosis and yield advantages in percent were investigated, and compared with those of the control (genotypes CORH 2 and ADTRH 1). The crosses TGMS 15 x ADT 36, Pei 64S x ADT 36, TGMS 18 x White Ponni, TGMS 18 x ADT 36, IR 68945-4-33-14 x ADT 36 and IR 68948-12-3-7 x C 20 showed high heterosis for early flowering.

Peng *et al.* (2009) studied the developmental genetics of plant height from two groups of three-line indica hybrid rice at two environmental conditions based on the NCII design, using the additive- dominant developmental genetics models and the statistic methods. The results showed that the rice genotypes and environmental conditions could both affect plant height, and the effects of environment on plant height decreased gradually with plant development. At most developmental stages, conditional heterosis over the mid parent (HMP) was positively significant. All above results suggest that HMP and HBP have some new expressions in all developmental periods and the levels and directions are quite different.

Prasad *et al.* (2001) observed that days to flowering are negatively correlated with plant height. Grain yield is negatively correlated with plant height (Amirthadevarathinam, 1983).

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. 1000-grain weight, number of effective tillers per plant, number of fertile grains per panicle and yield per plant showed high genotypic coefficient of variation and high heritability along with high genetic advance in percentage of mean, pointed out their importance for achieving genetic gain through selection.

Rajesh and Singh (2000) reported that in hybrid, yield wad primarily influenced by effective tillers per plant and fertile grains per panicle, whereas in check varieties it was panicle length, maturity and effective tillers par plant. Number of effective tillers per plant and fertile grains per panicle remained constant and common in explantaining heterosis for yield of most of the hybrids. The heterosis for grain yield was due to the significant heterosis for the number of spikelet's/panicle, test weight and total dry matter accumulation (Patnaik *et al.* 1990)

Sabesan *et al.* (2009b) studied on genetic variability of forty four rice genotypes of diverse origin. The phenotypic coefficients of variation (PCV) values were slightly greater than genotypic coefficient of variation (GCV), indicating little influence of environment in character association. High values of heritability along with genetic advance were observed for grain yield per plant, grain per panicle, panicle length and plant height.

Sadeghi (2011) studied on the nature and magnitude of variation for yield and yield contributing characters in 49 rice varieties. Broad sense heritability ranged from 69.21% for plant height to 99.53% for grain width.

Sangeeta-Mahitkar *et al.* (2000) conducted an experiment during the kharif season of 1998 in Akola, Maharashtra, India to investigate the correlation between the growth and yield contributing characters, and crop yield of uplantand rice, A positive and significant correlation was observed between grain yield and 1000- grain weight.

Sanjeev (2005) conducted an experiment on 19 mutant derived from 2 Basmati rice cultivars for genetic analysis based on 17 characters and found that plant height had higher heritability.

Sanjeev (2005) conducted an experiment with 19 mutant lines (M_3) derived from pusa Basmati and Taraori Basmati and observed higher heritability for days to flowering compared to other characters.

Sanjeev (2005) studied 19 mutant lines and found that number of panicle bearing tillers plant^{-1} in Taro Basmati had high genetic advance.

Sankar *et al.* (2006) conducted an experiment with 34 rice genotypes and high heritability as well as genetic advance was obtained for productive tillers plant^{-1}.

Sanker *et al.* (2006) studied on variability and correlation in 34 rice genotypes. High heritability and genetic advance were obtained for days to 50% flowering, plant height. Positive and significant correlations were reported with days to 50% flowering and productive tillers per plant.

Sanker *et al.* (2006) studied on variability and correlation in 34 rice genotypes. High heritability and genetic advance were obtained for productive tillers per plant, panicle length. Positive and significant correlations with productive tillers per plant, panicle length and hence these traits can be taken as indices for improving yield of rice.

Sarma anfd Bhuiyan (2004) studied genetic variation and divergence in 58 aus rice genotypes and observed highest broad- sense heritability for plant height.

Satyanarayana *et al.* (2005) studied variability, correlation and path coefficient analysis for 66 restorer lines in rice and observed high heritability, heritability and genetic advance for days to 50% flowering.

Satyanarayana *et al.* (2005) studied variability, correlation and path coefficient analysis for 66 restorer lines in rice and observed low heritability in number of effective tillers plant^{-1}.

Satyanarayana *et al.* (2005) studied variability, correlation and path coefficient analysis for 66 restorer lines in rice and observed low heritability for panicle length.

Satyavathi *et al.* (2001) evaluated 15 rice varieties and found moderate to high co-efficient of variation for plant height.

Satynarayana *et al.* (2005) studied variability, correlation and path coefficient analysis for 66 restorer lines in rice and observed high variability, heritability and genetic advance for plant height.

Sawant and Patil (1995) evaluated 75 genotypes of rice and found high coefficient of variation for grain yield per plant. High value of heritability couplanted with high expected genetic advance was observed for grain yield per plant.

Seyoum *et al.* (2012) studied on the genetic variability, heritability of fourteen rice genotypes for grain yield and yield contributing characters. Highly significant (P<0.01) variations were found for days to 50% flowering, days to 85% maturity, plant height, panicle length, spikelets per panicle and 1000-grains weight. Significant difference (P<0.05) were found for panicles per plant, grains per panicle, total spikelet fertility and grain yield. Relatively high genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found for days to 50% flowering, plant height, grains per panicle, spikelet per panicle, 1000-grain weight and grain yield. High heritability was found for plant height (97.17%), followed by 50% flowering (90.16%), 1000-grains weight (83.17%), days to 85% maturity (82.45%), panicle length (79.25%) and spikelet per panicle (60.25%).

Shanthi and Singh (2001) found significant variation among the genotypes for all characters studied. Panicle length exhibited low variation between phenotypic and genotypic coefficient of variations.

Shanthi and Singh (2001) observed that plant height exhibited low variation between phenotypic and genotypic coefficient of variation. High heritability couplanted with high genetic advance was observed in plant height, which governed largely through the additive effect of genes.

Shanthi and Singh (2001) studied 16 M6 generation of induced along with non-mutant Mashiur for variation in yield and component and found significant variation among the genotypes for all characters studied. Heritability in the broad sense was high (more than 80%) for all characters except grain yield per plant (78.99%).

Shanti and Singh (2008) observed plant height exhibited low variation between phenotypic and genotypic co-efficient of variations, high heritability couplanted with high genetic advance was recorded in plant height, which governed largely through the additive effect of genes.

Sharma *et al.* (2006) evaluated 39 uplantand rice genotypes for the estimation of genetic variability. The significant mean sum square indicated strong variability for days to 50% flowering. Though days to 50% flowering had high heritability (92.8%), it had low GCV.

Shashidhar *et al.* (2005) reported positive association grain yield with plant height, number of productive tillers hill^{-1}, dry matter plant^{-1} and harvest index at phenotypic and genotypic level.

Shrama and Haloi (2004) studied genetic variation and divergence in 58 aus rice and found the highest genotypic as well as phenotypic coefficient of variation for number of effective tillers plant^{-1}.

Siddique *et al.* (2002) studied some rice varieties included JPS, SWAT-1, SWAT-11, DILROSH-97, PARC-3, IETI- 13711, IRRI-4, GOMAL-6, GHOMAL-7. The data were recorded on number tillers hill^{-1} plant height, number panicles plant^{-1}, 1000-grain weight, sterility percentage, straw yield, biological and grain yield and harvest index. The analysis of data reveled that statistically significant differences were register for all the parameters studied except number of tiller plant^{-1} and number panicles plant^{-1}.

Singh and Chaudhury (1996) estimated genetic variability, heritability and genetic advance for 12 characters in 100 genotypes of rice. Phenotypic coefficients of variation (PCV) were higher than genotypes coefficient of variation (GCV) for most of the character. But high GCV was observed for grains per panicle. High heritability and high genetic advance estimated for grains per panicle.

Singh and Chaudhury (1996) estimated genetic variability, heritability and genetic advance for 12 characters in 100 genotypes of rice. 1000 grain weight showed high value of genotypic coefficient of variation (GCV) than phenotypic coefficients of variation (PCV), while low heritability for 1000 grain weight was reported by Honarnejad (1995).

Singh *et al.* (2002) showed that approximately 38-50% of the hybrids exhibited significant and positive heterobeltiosis and standard heterosis for grain yield per plant. Heterosis for grain yield was mainly due to heterosis for 1000-grain weight.

Singh *et al*. (2006) conducted an experiment with 32 genotypes of rice and found high heritability and high genetic advance for plant height, indicating the predominance of additive gene action for this trait.

Singh *et al*. (2006) conducted an experiment with 37 rice genotypes and reported that there were highly significant differences among the genotypes for plant height and the estimates of phenotypic coefficient of variation and genotypic coefficient of variation were of the same magnitude for the character but high heritability was recorded for the character.

Singh *et al*. (2006) conducted an experiment with 37 rice genotypes and reported that they were highly significant differences among the genotypes for number of effective tiller plant^{-1} and the estimates of phenotypic coefficient of variation and genotypic coefficient of variation were of the same magnitude for the character. High heritability was recorded for the character.

Singh *et al.* (2006) evaluated thirty two genotypes of rice for seven traits to estimate genetic variability and interrelationship among them. There was found a wide range variation for all the characters. Highest genotypic and phenotypic coefficients of variations were recorded for grain yield. High heritability and high genetic advance for height suggested the predominance of additive gene action for this trait.

Singh *et al.*(2011) evaluated eighty one rice (*Oryza sativa* L.) genotypes during *kharif, 2010*, for 13 quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. The genotypes were significantly different for all the characters except flag leaf width. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found for number of spikelet per panicle followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that these traits would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as percent of mean was recorded for number of spikelet per panicle with high value of heritability.

Sitaramaiah *et al.* (1998) showed negative and significant standard heterosis for 1000 grain weight because the check had bold grains. .

Subbaiah *et al.* (2011) studied on the extent of variability and genetic parameters with 16 check varieties and 48 hybrids for nine yield and yield related components and twenty five quality characters. The magnitude of difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was relatively low for all the traits. There was less environmental effect. High GCV and PCV were found for harvest index, total number of productive tillers per plant in check varieties and for total number of productive tillers per plant, number of grains per panicle in hybrids. High heritability couplanted with high genetic advance as percent of mean were recorded for harvest index, total number of productive tillers per plant, number of grains per panicle and grain yield per plant in case of check varieties and total number of productive tillers per plant, number of grains per panicle and harvest index in case of hybrids indicating the additive gene effects in the genetic control of these traits and can be improved by simplante selection in the present breeding material.

Tang *et al.* (2007) studied the agronomic traits and heterosis of javanica varieties and the indicaljavanica genotypes of rice in Changsha, Hunan, China, Javanica rice exhibited long panicles, big grains, less panicle per plant, a long growth duration and high plant height in Changsha. The hybrid of (Pei'ai RNT 711, RNT 24, RNT 1, PNL 2, PLANTG 1, RTN 2, KJT 2, RNT 3, KJT 147 and RNT 68) were evaluated for heterosis, heterobeltiosis and yield advantages in percent. Heterosis, heterobeltiosis and yield advantages in percent for productive tiller number per plant ranged from -26.10 to 124.32%, -44.79% to 90.80% and 58.50% to 80.43% respectively.

Tripathi *et al.* (1999) estimated genetic variability, heritability and genetic advance for yield components in 20 deep water rice genotypes. Plant height showed high genotypic and phenotypic variation.A high heritability of 93.1% was observed for plant height in some rice genotypes by Kaw *et al.* (1999). Similar findings were also reported by Ashvani *et al.* (1997).

Ullah, *et al.* (2011) estimated the genetic variability, interrelationship and cause effect analysis of ten traditional fine birion rice cultivars for morpho-physiological traits.

There was found significant variation for all the characters. The higher genotypic coefficient of variation (GCV) was found for grains per panicle followed by grain yield per plant, 1000-grain weight and panicles per plant. High heritability was observed for all the tested characters except harvest index. High heritability with high genetic advance in percentage of means was found for grains per panicle, grain yield per plant and 1000-grain weight indicating role of additive gene action.

Vange (2008) evaluated the performance and genetic diversity of some uplantand rice accessions. Genotypic coefficient of variation (GCV) was generally lower than phenotypic coefficient of variation (PCV). Days to 50% heading, days to maturity, panicle length, number of branch per panicle, number of seeds per panicle, grain weight per panicle and seed yield showed very low differences between their PVC and GCV values. Also these traits had high estimate for heritability and genetic advance.

Vijayakumar *et al,* (1997) found that hybrids out yielded than their check varieties when their days to 50%mflowering were similar or more than their respective restorers. They concluded that superior hybrids could be early by comparing their tiller number, plant height and days to 50% flowering with those of their respective restorers.

Wang *et al.* (2007) the effects of panicle type and source-sink relation on the variation in grain weight (GW) and quality within a panicle were investigated using four japonica (*Oryza sativa* L.) varieties differing in grain density and two source-sink adjusting treatments. There were significantly differences in GW and filling grain percentage (FGP) among superior and inferior grains for compact- panicle varieties (Xiushui 994 and Xiushui 63), while not for loose-panicle ones (Xiushui 11 and Chunjiang 15).

Won *et al.* (2000) studied to estimate the general and specific combining ability for direct sowing in a flooded paddy field. The effect of GCA was significant for 10000-grain weight, which indicated the importance of the additive effects of the genes for the traits.

Yadav (2000) studied 15 genotypes and found that genetic variability, heritability and genetic advance was not appreciable for number of panicle plant^{-1}.

Yang *et al.* (2001) studied the grain and yield components of two rice cultivars (JND3 and JND13). They observed JND3 exhibited a higher tillering capacity than JND13. Zahid *et al.* (2005) studied 14 genotypes of basmati rice and observe high heritability couplante with high genetic advance for plant height and 1000- grain weight. He also reported that plant height has negative correlation with yield. In addition he observed the positive relationship of plant high with grain quality.

Zahid *et al.* (2006) studied phenotypic and genotypic variances, co-efficient of variation, genetic advance, heritability, correlation coefficient and path analysis for yield and yield components and found that plant height had high heritability couplanted with high genetic advance.

2.2 CORRELATION AMONG DIFFERENT CHARACTERS

Agahi *et al.* (2007) studied on correlation and path analysis of grain yield and sixteen yield related traits to evaluate the interrelationships between first and second order yield related traits of 25 lines of rice. The grain yield was significantly correlated with days to heading (r_p=0.403**, r_g=0.525**), total tillers (r_p=0.585**, r_g=0.524**), number of productive tillers (r_p=0.604**, r_g=0.570**), days to maturity (r_p=0.296*, r_g=0.424**), number of grains per panicle (r_p=0.349*, r_g=0.339*) and plant height (r_p=-0.220^{ns}, r_g=-0.300). The study suggested that grain yield could be improved by selecting the cultivars for higher number of productive tillers and higher number of grains per panicle while 100 grain weight and flag leaf width, grain length and grain width were the co-partners in grain yield gain.

Akhtar *et al.* (2011) studied on the genotypic and phenotypic correlation for yield contributing characters in ten rice genotypes. Paddy yield had strong genetic correlation with number of grains per panicle, days to maturity and 1000-grain weight. Paddy yield had significant positive correlation with number of grains per panicle and 100-grain weight.

Akhter *et al.* (2010) estimated the genetic variability, character association and path analysis of 52 exotic rice genotypes for reproductive traits. Filled grains per panicle, days to 50% flowering and pollen sterility of different genotypes had a high degree of significant positive association with grain yield per hill. Filled grains per panicle could be the only selection criteria.

Biswas *et al.* (2000) experiment with 30 advanced breeding lines of rice and found significant positive correlation for yield per plant with panicle length, number of panicles per hill and filled grains per panicle. Negative correlation was found for yield per plant with plant height and 1000-grain weight. Significant negative correlation was found for filled grains per panicle with plant height, 1000-grain weight in genotypic level and insignificant negative correlation in phenotypic level. Panicle length showed significant positive correlation with plant height and filled grains per panicle.

Chakraborty and Chakraborty (2010) assessed the genetic variability, correlation and coheritability of 47 bold grained rice genotypes with two locally recommended high yielding check varieties for eight morpho-physiological characters. This indicates a strong inherent association among grain yield per plant and other morpho-physiological characters. The characters sterility percentage, effective branch tiller per hill and panicle length showed significant positive genotypic correlation with grain yield per hill. Sterility percentage, effective branch tiller per hill and panicle length had high coheritability with grain yield suggesting that selection for these characters would improve grain yield.

Chakraborty *et al.* (2010) studied on the genotypic and phenotypic correlation along with coheritability between two characters of 29 genotypes of boro rice. Correlation analysis revealed significant positive genotypic correlation of yield per plant with plant height (0.21), panicles per plant (0.53), panicle length (0.53), effective grains per panicle (0.57) and harvest index (0.86). The study suggested that five component characters, namely harvest index, effective grains per plant, panicle length, panicles per plant and plant height influenced the yield of boro rice. A genotype with higher magnitude of these component characters could be either selected from the existing genotypes or evolved by breeding program for genetic improvement of yield in boro rice.

Hossain and Haque (2003) showed the plant height as significant positive correlation with panicle length, grains per panicle and yield per plant both at genotypic and phenotypic level. Positive correlation was found for grains per panicle and 1000-grains weight with yield per plant at both the levels.

Iftekharuddaula *et al.* (2001) revealed positively significant correlation for grain yield with days to maturity, number of filled grains per panicle, 1000-grain weight and harvest index both at genotypic and phenotypic level. Negatively significant correlation was found for grain yield with plant height and spikelet sterility. Positive significant correlation for plant height with days to maturity, number of filled grains per panicle and 1000-grain weight, while negatively significant with number of panicles per hill and harvest index.

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. Correlation coefficient study revealed high positive correlation of grain yield with effective tillers per plant, fertile grains per panicle and 1000-grain weight. A significant negative correlation was obtained between grain yield and plant height.

Sabesan *et al.* (2009) studied on genetic variability and correlation of forty four rice genotypes of diverse origin. Significant association with plant height and productive tillers per plant at both genotypic and phenotypic levels. The 100-grain weight was positively significantly correlated with plant height, grains per panicle and grain breadth.

Sadeghi (2011) studied on correlation for yield and yield contributing characters in 49 rice varieties. Grain yield was found to be positively and significantly correlated with grains per panicle, days to maturity, panicle weight, the number of productive tillers, days to flowering, plant height, panicle length, flag leaf width and flag leaf length indicating the importance of these characters for yield improvement in this population

Sadeghi (2011) studied on path coefficient for yield and yield contributing characters in 49 rice varieties. Phenotypic path analysis revealed that the number of productive tillers had the highest positive direct effect followed by days to maturity, grains per panicle and 1000-grain weight on grain yield.

Seyoum *et al.* (2012) studied on 14 rice genotypes for correlation coefficient of grain yield and yield contributing characters. Grains per panicle had maximum positive direct effect and highly significant (r = 0.906**) genotypic correlation coefficient with grain yield.

Singh *et al.* (2006) evaluated thirty two genotypes of rice for seven traits to estimate genetic variability and interrelationship among them. Genotypic and phenotypic correlation coefficients indicated that biological yield per plantot and harvest index were significantly and positively associated with grain yield. It is suggested that selection for these two traits might be helpful in enhancing the grain yield.

Ullah *et al.* (2011) estimated the genetic variability, interrelationship and cause effect analysis of ten traditional fine birion rice cultivars for morpho-physiological traits. Genotypic correlations were higher than the phenotypic correlations in most cases.

Vange (2008) analysed the genotypic correlation analysis of yield with other traits revealed that yield had a significantly positive correlation with flag leaf area, number of tillers, number of panicles, panicle weight, panicle length, number of branches per panicle, number of seeds per panicle and seed weight per panicle, grain length and 1000 seed weight. The direct and indirect effect of the rice traits on yield was assessed.

2.3 PATH CO-EEFICIENT ANALYSIS

Abarshahr *et al.* (2011) estimated genetic variability and relationships among some agronomic traits of 30 varieties of rice under two irrigation regimes. Path analysis for paddy yield indicated that the number of spikelet panicle and flag leaf length had positive direct effects and days to complantete maturity and plant height had negative direct effects on paddy yield under optimum irrigation condition, while flag leaf width and number of filled grains per panicle had positive direct effects and days to 50% flowering had negative direct effect on paddy yield under drought stress condition.

Agahi *et al.* (2007) studied on correlation and path analysis of grain yield and sixteen yield related traits to evaluate the interrelationships between first and second order yield related traits of 25 lines of rice. Genotypic and phenotypic path coefficient analysis revealed that the number of productive tillers had the highest positive direct effect on grain yield (P_p=1.034, P_g=1.196). The second and third traits were the number of grain per panicle (P_p=0.665, P_g=0.813) and 100-grain weight (P_p=0.440, P_g=0.425) respectively

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.

Das *et al.* (1992) evaluated thirty rice genotypes for variability and genetic association. Path coefficient analysis revealed that adequate fertile spikelets per panicle, heavy grains, fertile tillers per plant and days to maturity had higher direct effects on yield per plant.

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

Chapter III

Materials and Methods

Chapter III

MATERIALS AND METHODS

The details of different populations used and methodology followed during the experimental period are described in this chapter as follows:

3.1 Experimental site

The experiment was conducted at the experimental field (plantot no: 30) of Sher-E-Bangla Agricultural University, Dhaka-1207 from April 2014 to July 2014. Geographically the experimental field is located at 8.4 metre above the mean sea level (Anon., 1989). The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.2 Soil and Climate

The experimental site was medium high land belonging of Old Madhupur Tract (AEZ-28) (UNDP, 1988) and the soil series was Tejgaon (FAO, 1988). The soil of the experimental plantot was clay loam in texture having pH around 6.5 and organic carbon content is 0.84%.

The experimental site was under the subtropical climate. It is characterized by three distinct seasons, winter season from November to February and the pre-monsoon or hot season from March to April and the monsoon period from May to October (Edris *et. al.* 1979). Details of the metrological data of air temperature, relative humidity, rainfall and sunshine hour at the time of experiment was collected from the Weather Station of Bangladesh, Sher-e-Bangla Nagar, Dhaka and has been presented in Appendix IV.

3.4 Design and Layout

The experiment was laid out in Randomized Complantete Block Design (RCBD) with three replantications. The total experimental area was divided into three blocks. The layout of the experiment was prepared for distributing the genotype.

3.5 Collection of Seed

The experimental seeds (F_4) were collected from germplantasm center of Sher-E-Bangla Agricultural University (SAU).

3.3 Planting Materials

Eighteen (18) populations of F_4 generation including three check varieties (BR 21, BR 24, BR 26) were used as experimental materials.

Table 1. Populations used for the experiment

Gentypes	Populations	Source
G1	BR 26	BRRI
G2	BR 21×BR 24, F_4, S_2P_1	SAU
G3	BR 21×BR 24, F_4, S_2P_2	SAU
G4	BR 21×BR 24, F_4, S_2P_3	SAU
G5	BR 21	BRRI
G6	BR 21×BR 26, F_4, S_6P_7	SAU
G7	BR 24×BR 26, F_4, S_5P_4	SAU
G8	BR 24×BR 26, F_4, S_5P_1	SAU
G9	BR 24×BR 26, F_4, S_5P_1	SAU
G10	BR 21×BR 26, F_4, S_6P_6	SAU
G11	BR 24	BRRI
G12	BR 21×BR 26, F_4, S_6P_2	SAU
G13	BR 21×BR 26, F_4, S_6P_8	SAU
G14	BR 21×BR 26, F_4, S_6P_3	SAU
G15	BR 21×BR 26, F_4, S_6P_1	SAU
G16	BR 21×BR 26, F_4, S_6P_4	SAU
G17	BR 24×BR 26, F_4, S_5P_6	SAU
G18	BR 21×BR 26, F_4, S_6P_9	SAU

3.6 Seedling Raising

The seed bed was prepared well by puddling the wetland with repeated plantoghing following by laddering. The seeds were soaked for 24 hours and then kept in a gunny bag in dark condition. After sprouting, the seeds were sown in the previously wet seed bed on April, 2014. Proper care was taken so that there was no infestation of pest and diseases and no damage by birds.

3.7Land Preparation for Tranplanting

The experimental field was first opened by a tractor on November and two plantoghing were performed. After a few days the land was further plantoghed and cross plantoghed with power tiller followed by laddering to get a good tilth condition. Weeds and stubble were removed from the field prior to tranplanting of seedlings. The boundaries around the individual plantot were made firmenough to vontrol water and fertilizer movement between plantots.

3.8 Fertilizers and Manure applantication

The fertilizers N, P, K, S and B were applantied in the form of Urea, TSP, MP, Gypsum and Borax respectively. The entire amount of TSP, MP, Gypsum, Zinc Sulphate and Borax were applantied during final preparation of the field. Urea was applantied in three equal installments during plantoughing, vegetative stage and before flowering. The dose and method of applantication of fertilizer are shown in Table 1.

Table 1. Dose and method of applantication of fertilizers in rice field

Fertilizers	Dose(kg/ha)	Applantication (%)		
		Basal	1st installment	2nd installment
Urea	127	33.33	33.33	33.33
TSP	52	100	--	--
MP	60	100	--	--
Gypsum	0	100	--	--
Borax	0	100	--	--

Source: BRRI (2012)

3.9 Transplanting

The check varieties first transplanted randomly in each block. Then experimental genotypes were tranplanted randomly to the remaining plantots. Each entry was grown as single seedling per hill in the rows on May 06, 2014 with a spacing of 20 cm between rows and 20 cm between plants.

3.10 After Care

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

3.10.1 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 discourge late tillering. The field was finally dried out 15 days before harvesting.

3.10.2 Gap filling

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

3.10.3 Weeding

Weddings were done to keep the plantots 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.

3.10.4 Top dressing:

The remaining doses of urea were top-dressed in two equal installments. The fertilizers were applantied on both sides of seedlings rows with the soil.

3.10.5 Plant Protection

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

3.11 Harvesting, Threshing and Cleaning

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

3.12 Data Recording

Data were recorded on the following characters

3.12.1Days to 50% flowering

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

10.12.2 Days to maturity

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

3.12.3 Plant height (cm)

The height of plant was recorded in centimeter (cm) at the time of harvesting. Data were recorded as the average of 10 plants selected at random from the inner rows of each plantot after harvest.

3.12.4 Panicle length (cm)

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

3.12.5 Effective tillers per hill

The total number of effective tiller per hill was counted as the number of panicle bearing hill per plant. Data on the effective tiller per hill were counted from 10 selected hills and average value was recorded.

3.12.6 Number of spikelet per panicle

The total number of filled spikelet was collected randomly from 10 selected of a plantot and then average number of filled spikelet per panicle was recorded.

3.12.7 Filled grains per panicle

The total numbers of filled grain was collected randomly from selected 10 plants of a plantot on the basis of grain in the spikelet and then average numbers of filled grain per panicle was recorded.

3.12.8 Number of unfilled grains per panicle

The total number of unfilled spikelet's was collected randomly from selected 10 plants on the basis of grains in the spikelets.

Grain yield per plant (g)

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

3.12.9 1000 seed weight (g)

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

3.12.10 Grain yield per hectare (ton)

Grains obtained from each unit plantot were sun dried and weighted carefully and converted to t h^{-1}

3.13 Statistical analysis

The data obtained for different characters were statistically analyzed to observe the significant differences among the treatment combination.The significance of the difference among the treatments means was estimated by the least significant difference (LSD) test at 5% level of probably (Gomez and Gomez, 1984).

3.13.1 Estimation of variability

Genotypic and phenotypic coefficient of variation and heritability were estimated by using the following formula-

i) **Estimation of components of variance from individual environment**

ii) Genotypic and phenotypic variances were estimated with the help of the following formula suggested by Johnson *et al.* (1995). The genotypic variance (σ^2_g)was estimated by

Subtracting error mean square (σ^2_e) from the genotypic mean square and dividing it by the number of replantication (r). This is given by the following formula-

Genotypic variance (σ^2_g) $= \frac{MS_V - MS_E}{r}$

Where,

MS_V = genotypic mean square

MS_E = error mean square

r = number of replantication

The phenotypic variance ($\sigma^2{}_p$), was derived by adding genotypic variances with the error variance, as given by the following formula-

Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_e^2$

Where,

σ_p^2= phenotypic variance

σ_g^2 = genotypic variance

σ_e^2 = error variance

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

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

Genotypic coefficient of variance (%) = $\frac{\sigma_g}{\bar{x}} \times 100$

Where,

σ_g = genotypic standard deviation

$\bar{x}$ = population mean

Phenotypic coefficient of variance (%)= $\frac{\sigma_{ph}}{\bar{x}} \times 100$

Where,

σ_{ph}= phenotypic standard deviation

$\bar{x}$ = population mean

iii) Estimation of heritability

Heritability in broad sense was estimated following the formula as suggested by Johnson *et al.* (1955):

Heritability (%) = $\frac{\sigma_g^2}{\sigma_p^2} \times 100$

Where,

σ_g^2 = genotypic variance

σ_p^2 = 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): $GA = \frac{\sigma_g^2}{\sigma_{ph}^2} \times K.\sigma_p$

Where,

GA = Genetic Advance

σ_g^2 = genotypic variance

σ_p^2= phenotypic variance

σ_p = phenotypic standard deviation

K = Selection differential which is equal to 2.64 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):

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

Where,

$\bar{x}$= population mean

3.13.2 Estimation of Correlation

Simplante correlation was estimated with the following formula (Singh and Chaudhury, 1985):

$$r = \frac{\sum xy - \frac{\sum x.\sum y}{N}}{\left[\left\{\sum x^2 - \frac{(\sum x)^2}{N}\right\}\left\{\sum y^2 - \frac{(\sum y)^2}{N}\right\}\right]^{\frac{1}{2}}}$$

Where,

$\sum$ = Summation

x and y are the two variables

N= Number of observations

3. 13. 3 Path co-efficient analysis

Path co-efficient analysis was done according to the procedure emplantoyed by Dewey and Lu (1959) also quoted in Singh and Chaudhury (1985), using simplante correlation values. In path analysis, correlation co-efficient is partitioned into direct and indirect of independent variables on the dependable variable.

In order to estimate direct and indirect effect of the correlated characters, say x_1, x_2, x_3 yield y, a set of simultaneous equations (three equations in this examplante) is required to be formulated as given below:

$ryx_1 = Pyx_1 + Pyx_2rx_1x_2 + Pyx_3rx_1x_3$

$ryx_2 = Pyx_1rx_1x_2 + Pyx_2 + Pyx_3rx_2x_3$

$ryx_3 = Pyx_1rx_1x_3 + Pyx_2rx_2x_3 + Pyx_3$

Where, r's denotes simplante correlation co-efficient and P's denote path co-efficient (unknown). P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x_1 and y is thus partitioned as follows:

Pyx_1 = the direct effect of x_1 on y

$Pyx_1rx_1x_2$ = the indirect effect of x_1 via x_2 on y

$Pyx_1rx_1x_3$ = the indirect effect of x_1 via x_3 on y

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

$P^2RY = 1 - \sum Piy.\, riy$

Where,

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

Piy = Direct effect of the character on yield

riy = Correlation of the character with yield

3.14 Statistical packaged used

The various statistical packages were used for data analysis and these are MS Excel 2007 (Microsoft) MSTATC for windows.

Chapter IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

The present study was conducted with a view to determine the variability among 15 F_4 rice populations and three check varieties of *Oryza sativa* L. 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 80% maturity, plant height (cm), total no. of tiller/plant, no. of effective tiller/plant, panicle length (cm)/plant, no. of primary branches/ plant, no of secondary branches/ plant, total no. of spikelet /panicle, no. of filled grain of main tiller, no. of unfilled grain of main tiller, yield/plant(g) dry, 1000 seed weight (g) and yield (ton/hectare), The data were statistically analyzed and thus obtained results are described below under the following heads:

4.1.1 Variability among 15 F_4 populations and the three check varieties of rice for yield related traits

The analysis of variance (ANOVA) of the data on different yield components and yield of rice are given in Table 2 and the mean values over three replantications for characters of all lines are presented in Table 3 and Table 4. Genotypic, phenotypic and environmental variance and genotypic, phenotypic and environmental coefficients of variation are presented in Table 5. Among the genotypes almost all characters showed highly significant variation indicating wide scope for selection for these characters i.e. the data revealed substantial variability and thus high possibility of improvement in most of the traits. The variability in the present study indicated the potentiality of the populations generated through inter-varietal crosses i.e., advanced lines for selecting desirable lines for releasing new varieties. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding of the pattern of variations.

4.1.2.1 Days to 50% flowering

The analysis of variance (ANOVA) showed significant difference among all the genotypes (67.33**) for days to 50% flowering. The highest as in G15 (BR 21×BR 26, F_4, S_6P_1) (89.67 days) and the lowest was observed in G3 (BR 21×BR 24, F_4, S_2P_2) (74.67 days) Among the check varieties the days to 50% flowering was observed in 80.67 days in BR 26, 78.33 days in BR21 and 80.0 days in BR24(Table3).

Table 2. Analysis of variance (ANOVA) for yield and its related characters in 15 F_4 rice populations and 3 check varieties

Sl.No.	Characters	Mean sum of squares (MSS)		
		Replantication	Genotypes	Error
	d.f	2	17	34
1	50%flowering	442.67	67.33**	1.97
2	80%maturity	527.85	98.14**	1.87
3	Plant Height (cm)	654.42	129.47**	10.67
4	Total no. of tiller/ plant	75.88	9.49**	0.80
5	No. of effective tiller/ plant	74.12	9.63**	0.88
6	Panicle length (cm)/plant	127.90	6.83**	0.40
7	No. of primary branches/panicle	36.37852	2.15*	0.231264
8	No. of secondary branches/ panicle	273.0822	52.74**	1.593987
9	Total no. of spikelet/ panicle	301.97	44.60**	1.43
10	No. of filled grain of main tiller	3506.401	960.35**	38.11487
11	No. of unfilled grain of main tiller	27.70	77.90**	21.06
12	Yield/ Plant (gm)	669.82	34.92**	2.11
13	1000 seed weight (gm)	139.19	6.27**	0.34
14	Yield (ton/ hectare)	442.67	67.33**	1.97

* = Significant at 5% level of probability, ** = Significant at 1% level of probability

Table3. Mean performance of yield and yield contributing characters of 15 F_4 rice populations and 3 check varieties

Genotypes	50%flowering (days)	80%maturity (days)	Plant height (cm)	Total no. of tiller/ plant	No. of effective tiller/ plant	Panicle length (cm)/plant	No. of primary branches/panicle
G_1	80.67	104.70	114.80	16.20	15.47	24.90	9.87
G_2	76.67	97.67	125.20	16.10	15.30	22.93	9.13
G_3	74.67	97.00	129.30	12.27	11.33	21.83	9.43
G_4	78.67	96.33	130.80	11.47	10.67	21.90	9.20
G_5	78.33	105.30	124.90	14.67	13.80	23.79	9.23
G_6	81.00	103.30	130.10	15.37	13.93	22.94	10.10
G_7	85.33	105.70	145.30	13.93	13.17	26.97	11.27
G_8	82.00	106.00	142.10	10.50	9.77	24.25	11.30
G_9	85.00	106.30	145.50	12.37	11.00	27.15	12.03
G_{10}	88.33	111.00	135.40	13.13	12.03	23.80	10.43
G_{11}	80.00	103.00	117.70	15.00	14.00	25.67	9.47
G_{12}	80.33	105.30	129.80	14.03	13.10	23.75	9.73
G_{13}	87.67	110.00	129.50	15.07	13.50	24.96	11.13
G_{14}	88.67	109.70	130.60	12.47	11.65	24.49	10.60
G_{15}	89.67	112.70	131.70	14.73	13.83	24.33	10.50
G_{16}	85.00	110.30	139.20	10.70	9.73	22.30	10.10
G_{17}	85.33	108.70	138.50	11.73	10.23	24.93	10.57
G_{18}	84.67	109.30	133.40	13.77	12.90	24.67	11.07
Maximum	89.67	112.70	145.50	16.20	15.47	27.15	12.03
Minimum	74.67	96.33	114.80	10.50	9.73	21.83	9.13
Mean	82.78	105.47	131.79	13.51	12.50	24.17	10.24
CV (%)	1.82	1.34	2.47	6.59	7.48	2.62	4.67

CV=coefficient of variance

Table 3 (cont'd)

Genotypes	No. of secondary branches/ panicle	Total no. of spikelet/ panicle	No. of filled grains of main tiller	No. of unfilled grains of main tiller	Yield/ Plant (g)	1000 seed weight (g)	Yield (ton/ hectare)
G_1	24.57	136.80	124.10	12.70	28.60	20.67	5.56
G_2	18.37	111.10	92.90	18.23	21.12	19.33	3.95
G_3	19.73	113.80	99.43	14.33	19.89	19.33	4.57
G_4	24.50	118.20	98.80	19.43	21.98	21.00	4.37
G_5	29.00	150.40	131.80	18.60	27.01	18.33	4.22
G_6	26.40	127.00	118.90	8.10	21.18	20.33	3.63
G_7	30.90	179.70	152.40	27.33	26.24	19.67	5.14
G_8	30.63	158.50	133.90	24.67	21.97	21.33	5.70
G_9	36.83	186.80	161.10	25.73	26.87	17.67	4.49
G_{10}	29.83	140.90	121.10	19.80	23.70	21.33	4.10
G_{11}	29.27	152.30	124.80	27.50	29.03	18.67	3.83
G_{12}	26.03	140.00	120.60	19.33	18.13	17.33	4.29
G_{13}	28.37	133.40	116.40	16.93	26.18	22.00	3.56
G_{14}	27.90	126.00	110.20	15.77	24.43	20.33	3.81
G_{15}	26.57	136.00	111.70	24.33	24.77	21.67	3.80
G_{16}	27.20	120.90	101.90	19.07	14.69	20.00	2.44
G_{17}	30.23	148.70	130.10	18.60	20.67	20.33	3.02
G_{18}	29.87	150.90	132.00	18.90	26.97	22.33	3.79
Maximum	36.83	186.80	161.10	27.50	29.03	22.33	5.70
Minimum	18.37	111.10	92.90	8.10	14.69	17.33	2.44
Mean	27.43	140.03	120.60	19.44	23.32	19.96	4.15
CV (%)	4.58	3.76	5.09	23.64	5.08	2.91	9.38

CV=coefficient of variance

G3 (BR 21×BR 24, F_4, S_2P_2) was early flowering than check varieties. G4(BR 21×BR 24, F_4, S_2P_3) was statistically similar as G3.Phenotypic and genotypic variance for days to 50% flowering was observed as 23.76 and 21.79, respectively with moderate differences between them, suggested less influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (5.88%) was higher than the genotypic coefficient of variation (5.63%), which reaveled that environment had less effect but gene had great role on the expression of this trait. So selection could be allowed. Highly significant was also reported by Seyoum *et al.* (2012).

4.1.2.2 Days to 80% maturity

The highest days to 80% maturity was observed in G15 (BR 21×BR 26, F_4, S_6P_1) (112.70days) and the minimum days (96.33) to maturity was observed in G4 (BR 21×BR 24, F_4, S_2P_3) (Table 3). Among the check varieties the days to 80% maturity was observed in 104.70 days in BR26, 105.30 days in BR21, and 103 days in BR24 (Table 3). G4 (BR 21×BR 24, F_4, S_2P_3) following G3 (BR 21×BR 24, F_4, S_2P_2) that matured early than that of three check varieties. Phenotypic and genotypic variance for days to maturity was observed 33.96 and 32.09, respectively with less difference between them, suggested low influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (5.53 %) was higher than the genotypic coefficient of variation (5.38 %) (Table 3), which suggested that environment had lest role on the expression of this trait so, no problem for selection. Similar result was reported by Iftekharuddaula *et al.* (2001).

4.1.2.3 Plant height (cm)

The analysis of variance showed highly significant difference among all the genotypes (129.47**) studied for Plant height at 1% level of probability (Table 2). Highly significant variation for this character was also reported by seyoum *et al.* (2012) The highest plant height was found in G9 (BR 24×BR 26, F_4, S_5P_1) (145.50 cm) and G1 (BR 26) was the shortest plant (101.00 cm) (Table 2). G3 (BR 21×BR 24, F_4, S_2P_2) and G4 (BR 21×BR 24, F_4, S_2P_3) were moderate plant height 129.30cm, 130.80cm respectively.

Plantate 1. Days to 50% flowering time variation in F_4 populations of rice (*Oryza sativa* L.)

Plantate 2. Days to Flowering time variation in F_4 populations of rice (*Oryza sativa* L.)

Plantate 3. Days to maturity time variation in F_4 populations of rice (*Oryza sativa* L.)

Plantate 4. Days to 80% maturity time variation in F_4 populations of rice (*Oryza sativa* L.)

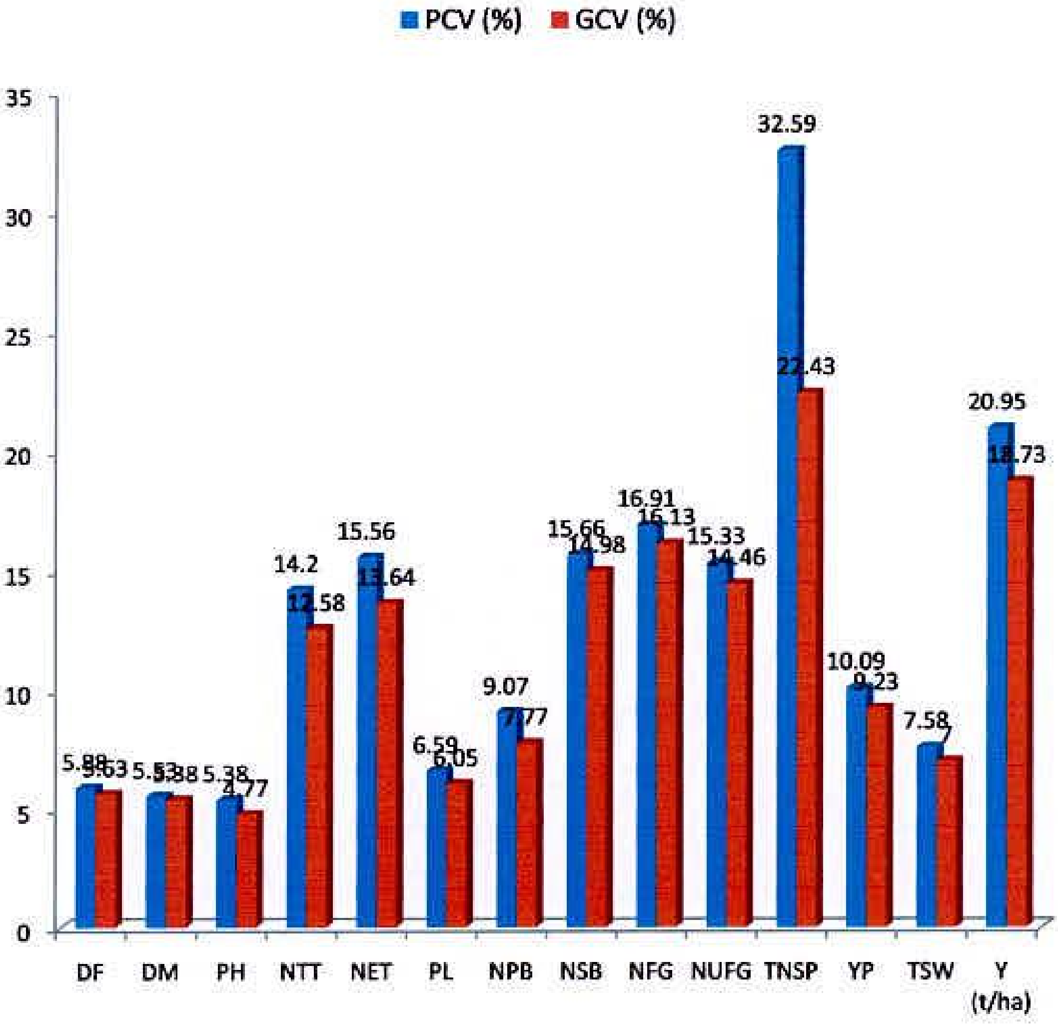


Figure 1. Genotypic and phenotypic coefficient of variation in *Oryza sativa* L.

The phenotypic variance (50.27) was moderately higher than the genotypic variance (39.60). The moderate difference indicated that the environmental factors had moderate influence on plant height traits of these genotypes. The phenotypic and genotypic co-efficient of variations were 5.38% and 4.77% respectively, (Table 3) which indicated that the genotypes had relatively moderate and environment had low influence on this character expression. Hossain and Haque (2003) also reported similar result for PCV and GCV.

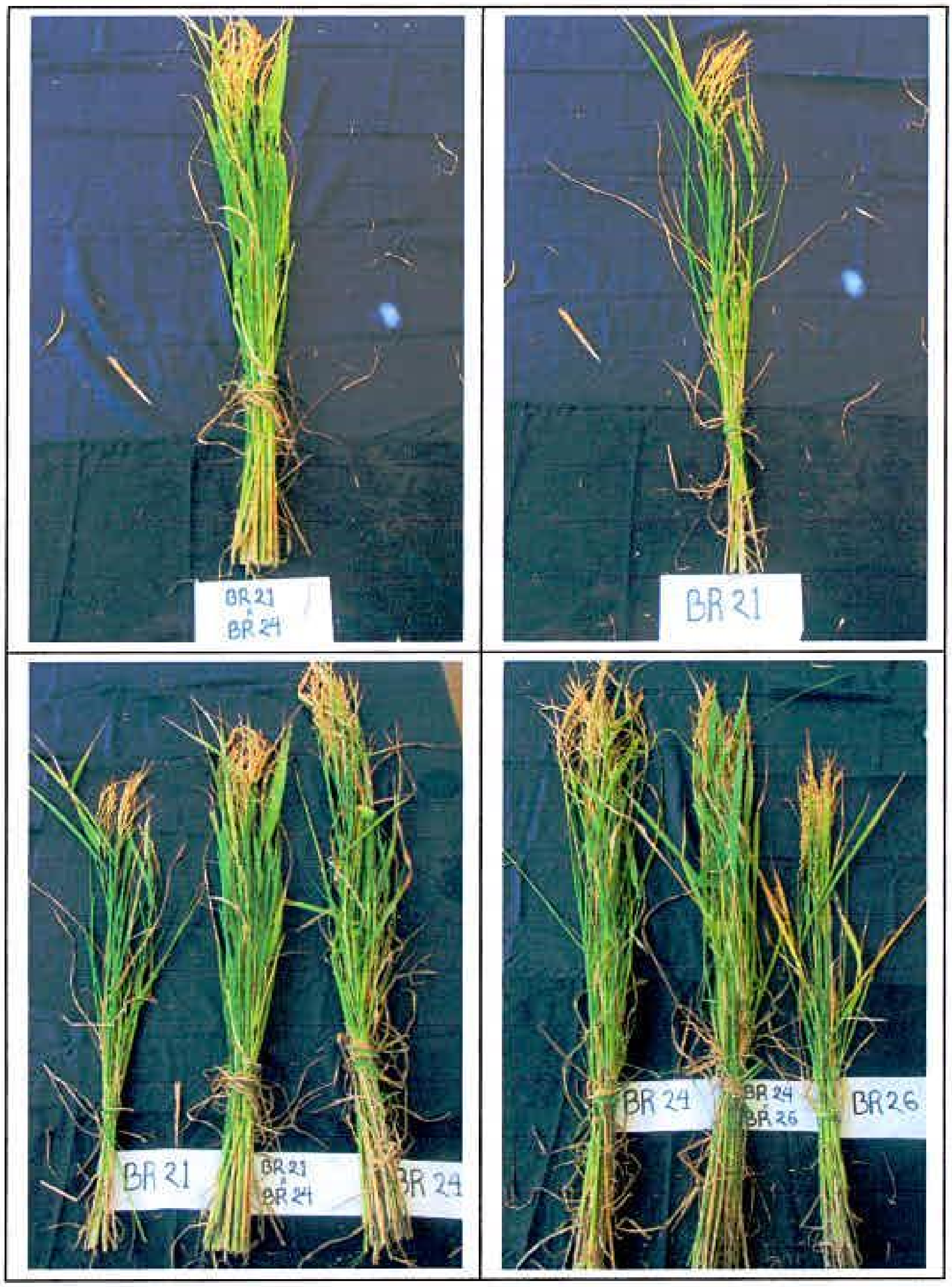
4.1.2.4 Total Number of tillers per plant

From the ANOVA given in Table 2, it was observed that number of tiller per plant showed highly significant differences (9.49) among the genotypes at the level of 1% probability. G1 (BR 26) showed the highest number of tiller per plant (16.20) following G2 (BR 21×BR 24, F_4, S_2P_1), while the lowest number of tillers per plant (10.50) in G8 (BR 24×BR 26, F_4, S_5P_1) which was significantly different with all the other genotypes (Table 2). Other two check varieties showed tiller per plant G5 (14.67), G11 (15) respectively. The genotype G3 (BR 21×BR 24, F_4, S_2P_2), G4 (BR 21×BR 24, F_4, S_2P_3), G7 (BR 24×BR 26, F_4, S_5P_4) and G12 (BR 21×BR 26, F_4, S_6P_2) showed moderate tillers performance.

The phenotypic variance of number of tiller per plant (3.69) was higher than genotypic variance of tiller per plant (2.90). This high difference between phenotypic variance and genotypic variance indicated that environmental had less influence on number of tiller per plant. Values of PCV and GCV were 14.20% and 12.58% respectively. The difference between PCV and GCV was low which indicated that the genetic variation existed among the genotypes and environment had low influence on this character expression. So there was available scope of selection for further trial.

4.1.2.5 Number of effective tiller per plant

It was observed that number of effective tillers per plant showed highly significant differences (9.63**) among the genotypes (Table 2). So there was no impediment for selection. Genotype G1 (BR 26) showed the highest number of tillers per plant (15.47)



Plantate 5. Difference showing plant height, effective tiller/plant and yield/plant of rice (*Oryza sativa* L.).

following G2 (BR 21×BR 24, F_4, S_2P_1) while the lowest number of tillers per plant (9.73) in G16 (BR 21×BR 26, F_4, S_6P_4) which was significantly different with all the other genotypes (Table 3). The genotype G3 (BR 21×BR 24 F_4, S_2P_2), G4 (BR 21×BR 24, F_4, S_2P_3), G7 (BR 24×BR 26, F_4, S_5P_4) and G12 (BR 21×BR 26, F_4, S_6P_2) showed effective tillers performance that not so bad.

The phenotypic variance of number of tillers per plant (3.79) was higher than genotypic variance of tillers per plant (2.92). This difference between phenotypic variance and genotypic variance indicated that environmental influence (0.88) had present on number of tillers per plant but less. Values of PCV and GCV were 15.56% and 13.64% respectively. The difference between PCV and GCV was moderate (7.48%) which indicated that the genetic variation was mild among the genotypic variation and environment had medium influence on this character expression. So there was an opportunity for selection. Similar result for GCV was also reported by Li *et al.* (1991).

4.1.2.6 Panicle length (cm)

Panicle length showed the high significant variations (6.838*) among the genotype at 1% level of probability (Table 2). Similar result was also reported by Seyoum *et al.* (2012) Table 2 showed that G9 (BR 24×BR 26, F_4, S_5P_1) produced the longest panicle (27.15 cm) which was significantly different with all the genotypes and the shortest panicle in G3 (BR 24×BR 26, F_4, S_5P_1) (21.83 cm) (Table 3). It will not be wise to consideration this trait in case of selection for further trial. The phenotypic and genotypic variance of panicle length were 2.55 and 2.14 respectively. With low difference between them indicated that environment had negligible influence on panicle length. for various traits and found that Low difference between PCV (6.59%) and GCV (6.05%) indicated that the genetic variability is less for panicle length and environment had low influence on this character expression. This low environmental influence made hope for further selection. The longest panicle (31.84 cm) was recorded in AL-42(II), while the shortest panicle (26.35 cm) in S-5. Tahir *et al.* (2002) studied genetic variability panicle

Table 4. Estimation of genetic parameters for yield related traits of 15 F_4 rice populations and three check varieties.

Parameters	σ^2p	σ^2g	σ^2e	PCV (%)	GCV (%)	ECV (%)
Days to flowering	23.76	21.79	1.97	5.88	5.63	1.69
Days to maturity	33.96	32.09	1.87	5.53	5.38	1.30
Plant Height (cm)	50.27	39.60	10.67	5.38	4.77	2.48
Total no. of tillers/ plant	3.69	2.90	0.80	14.20	12.58	6.59
No. of effective tillers/ plant	3.79	2.92	0.88	15.56	13.64	7.48
Panicle length (cm)	2.55	2.14	0.40	6.59	6.05	2.62
No. of primary branches/panicle	0.87	0.64	0.23	9.07	7.77	4.67
No. of secondary branches/ panicle	18.64	17.05	1.59	15.66	14.98	4.58
No. of filled grains /panicle	15.82	14.39	1.43	16.91	16.13	5.08
No. of unfilled grains of /panicle	345.53	307.41	38.11	15.33	14.46	5.09
Total no. of spikelets/ panicle	40.01	18.95	21.06	32.59	22.43	23.64
Yield/ Plant (g)	13.05	10.94	2.11	10.09	9.23	4.05
1000 seed weight (g)	2.32	1.97	0.34	7.58	7.00	2.91
Yield (ton/ hectare)	0.75	0.60	0.15	20.95	18.73	9.37

σ^2p = Phenotypic variance, σ^2g = Genotypic variance and σ^2e = Environmental variance, GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation and ECV = Environmental Coefficient of Variation length under the genetic control and could be use in the selection of a desirable trait. Padmavathi *et al.* (1996) reported that the plants with large panicles tend to have a high number of fertile grains.

4.1.2.7 Number of primary branches per panicle

It was calculated the significant variations (2.15*) among the genotype (Table 2) for number of primary branches/panicle. Among the 18 F_4 populations the highest number of primary branches/panicle was observed in G9 (BR 24×BR 26, F_4, S_5P_1) (12.03) whereas the minimum number of primary branches/plant was observed in G2 (BR 21×BR 24, F_4, S_2P_1) (9.13) (Table 3). No. of primary branches per plant were observed in three check varieties 9.87 in BR26, 9.23 in BR21 and 9.47 in BR24 respectively, (Table 2). G3 (BR 21×BR 24, F_4, S_2P_2) (9.13), G4 (BR 21×BR 24, F_4, S_2P_3) (9.20), G7 (BR 24×BR 26, F_4, S_5P_4) and G12 (BR 21×BR 26, F_4, S_6P_2), which were statistically similar as check varieties .Number of primary branches per panicle showed little differences between phenotypic variance (1.9) and genotypic variance (0.11) indicating low environmental influence on this character and low difference between PCV % (o.87 %) and GCV % (o.64 %) value indicating the apparent variation not only due to genotypes but also due to the influence of environment (Table 4) so selection may be possible following this character. It interpreted for further selection. Karim *et al.* (2007) found higher differences between GCV and PCV for this trait.

4.1.2.8 Number of secondary branches per panicle

it can be concluded from ANOVA that the number of secondary branches/panicle showed the highly significant variation (52.74**) among the genotypes (Table 2). Among 18 F_4 population the highest number of secondary branches/panicle was observed in G9 (BR 24×BR 26, F_4, S_5P_1) (36.83) whereas the minimum number of secondary branches/plant was observed in G2 (BR 21×BR 24, F_4, S_2P_1) (18.37) (Table 3). No. of primary branches per plant depicted in three check varieties 24.57 in BR26, 29.00 in BR21 and 29.27 in BR24 (Table 2). G3 (BR 21×BR 24, F_4, S_2P_2) (19.73), G4 (BR 21×BR 24, F_4, S_2P_3) (24.50), G7 (BR 24×BR 26, F_4, S_5P_4) (30.90) and G12 (BR 21×BR 26, F_4, S_6P_2) (26.03) which were comparable with check varieties. Number of primary branches per panicle showed little differences between phenotypic variance (18.64) and genotypic variance (17.05) indicating low environmental(1.59) influence on these character and relatively difference between PCV% (15.66 %) and GCV% (14.98 %) value indicating the apparent variation not only due to genotypes but also due to the influence of environment (4.59%) (Table 3). No doubt, selection will be rewarded for this trait.

4.1.2.9 Total number of spikelets per panicle

Findings from the ANOVA (Table 2), number of spikelet/panicle showed the highly significant variations (44.60**) among the genotype. The number of spikelets per panicle was observed highest in G9 (BR 24×BR 26, F_4, S_5P_1) (186.80) .Whereas the minimum number of spikelet per panicle was observed in G2 (BR 21×BR 24, F_4, S_2P_1) (111.10) (Table 3). Number of spikelet/panicle were observed in three check varieties, these were 136.80 in BR26, 150.40 in BR21 and 152.30 in BR24 respectively, (Table 2). G7 (BR 24×BR 26, F_4, S_5P_4) (179.70) and G12 (BR 21×BR 26, F_4, S_6P_2) (140.00) which considered like check varieties. Number of spikelet per plant showed highest phenotypic variance (15.82) with genotypic variance (14.39) and low environmental influence. The difference between the PCV% (16.91 %) and GCV% (16.13 %) indicated existence of less environmental influence among the genotypes (Table 3). So selection could be considered by this variable.

4.1.2.10 Number of filled grain of main tiller

Significant differences (960.35**) among the genotypes were calculated for number of filled grain of the tillers. The highest number of filled grain was observed in G9 (BR 24×BR 26, F_4, S_5P_1) (161.10) and in G2 (BR 21×BR 24, F_4, S_2P_1) (92.90). The number of filled grains of the tillers were observed in three check varieties , these were 124.10 in BR26, 118.90 in BR21 and 120.60 in BR24 (Table 3). Number of filled grain found in G7 (BR 24×BR 26, F_4, S_5P_4) (152.40) and G12 (BR 21×BR 26, F_4, S_6P_2) (120.60) were higher than check varieties. The phenotypic and genotypic variances for this trait were 345.53 and 307.41 respectively. The phenotypic variance appeared to be very high than the genotypic variance suggested very much influence of environment (38.11) on the expression of the genes controlling this trait. The highest phenotypic and genotypic variance was also reported by Akhter *et al.* (2010). The value of PCV and GCV were 15.33% and 14.46% respectively for number of filled grains of the tiller which indicating moderate environmental effect (5.09%) exists among different genotypes.

4.1.2.11 Number of unfilled grain of the tillers

There were significant difference (77.90**) among the genotypes recorded for number of unfilled grain of the tillers (Table2). It was observed highest number unfilled grains in genotype G11 (BR 24) (27.50). The minimum number of unfilled grains of the tillers was observed in G6 (BR 21×BR 26, F_4, S_6P_7) (8.10). number of filled grain of main tiller was observed in three check varieties such as 12.70 in BR26, 8.10 in BR21 and 19.33 in BR24 (Table 3).Among them G3 (BR 21×BR 24, F_4, S_2P_2) (14.33), G4 (BR 21×BR 24, F_4,S_2P_3) (19.43), G7 (BR 24×BR 26, F_4, S_5P_4) (27.33) and G12 (BR 21×BR 26, F_4, S_6P_2) (19.33) respectively which were more than check varieties. The phenotypic and genotypic variances for this trait were 40.01 and 18.95 respectively. The phenotypic variance appeared to be very high than the genotypic variance suggested very much influence of environment (21.06) on the expression of the genes controlling this trait. The value of PCV and GCV were 32.59% and 22.43% respectively for number of unfilled grain of main tiller which indicating moderate environmental effect (23.64%) exists among different genotypes. Wide difference between GCV and PCV was reported by Chakraborty and Chakraborty (2010). High GCV and PCV were reported by Iftekharuddaula *et al.* (2001).

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4.1.2.12 Yield per plant (g)

Seed yield per plant showed highly significant mean sum of squares (34.92**) due to different genotypes that suggested considerable range of variation for this trait.

Yield per plant was found maximum in G11 (BR 24) (29.03 g) when it was minimum in G16 (BR 21×BR 26, F_4, S_6P_4) (14.69g). Yield per plant was observed in three check varieties, these were 28.60g in BR26, 21.18g in BR21 and 18.13g in BR24 (Table 2). G3 (BR 21×BR 24, F_4, S_2P_2) (19.89), G4 (BR 21×BR 24, F_4, S_2P_3) (21.98), G7 (BR

24×BR 26, F_4, S_5P_4) (26.24) and G12 (BR 21×BR 26, F_4, S_6P_2) (18.13) showed significant similar to parent. So, larger scope present for selection on this parameter.

The phenotypic variances and genotypic variances for this trait were 13.05 and 10.94respectively. The values are close to each other indicated moderate environmental influences on this trait. The values of PCV and GCV were 10.09% and 9.23% indicating that the genotype has minimum environmental variation for this trait. High PCV and GCV were reported for this character by Seyoum *et al.* (2012).

4.1.2.13 Thousand seed weight (g)

The highly significant differences were observed among the genotypes for thousand seed weight (6.27**). Similler result was observed by Seyoum *et al.* (2012).Thousand seed weight was found maximum in G18 (BR 21×BR 26, F_4, S_6P_9) (22.33g) which is nearly similar as G13 (BR 21×BR 26, F_4, S_6P_8) (22.0) whereas the minimum thousand seed weight was found in G12 (BR 21×BR 26, F_4, S_6P_2) (17.33g). Significant thousand seed weight found in G3 (BR 21×BR 24, F_4, S_2P_2) (19.33 g), G4 (BR 21×BR 24, F_4,S_2P_3) (21.00 g), G7 (BR 24×BR 26, F_4, S_5P_4) (19.67 g) which were comparable to check varieties G1 (BR 26) (20.67 g), G5 (BR 21) (18.33) and G11 (BR 24) (18.67). The phenotypic variance (2.32) and genotypic variance (1.97) with little differences indicating that they were low responsive to environmental factors. The lower phenotypic coefficient of variation (7.58%) and genotypic coefficient of variation (7.00%) were close to each other. There had less difference between phenotypic and genotypic co-efficient of variation, indicating environmental influence on this character was less. High GCV was reported by Prasad *et al.* (2001), Ullah *et al.* (2011).

4.1.2.14 Total yield per hectare (ton)

Yield is the most outstanding character for all the research work and objectives are dependent on yield. From the ANOVA given in Table 2, yield per hectare was showed the highly significant variation (67.338**) among the genotype .

The highest amount of yield per hectare was observed in G8 (BR 24×BR 26, F_4, S_5P_1) (5.70 ton), whereas the minimum yield per hectare was in G16 (BR 21×BR 26, F_4, S_6P_4) (2.44 ton) (Table 3). The yield per hectare of three check varieties were 5.56 ton in G1 (BR26), 3.36 ton in G5 (BR21) and 4.29 ton in G11(BR24) (Table 3). More or less similar yield were depicted in G3 (BR 21×BR 24, F_4, S_2P_2) (19.89 ton), G4 (BR 21×BR 24, F_4, S_2P_3) (21.98 ton), G7 (BR 24×BR 26, F_4, S_5P_4) (26.24 ton) G8 (BR 24×BR 26, F_4, S_5P_1) (5.70 ton),G9 (BR 24×BR 26, F_4, S_5P_1) (4.49ton) and G12 (BR 21×BR 26, F_4, S_6P_2) (4.29 ton). The phenotypic variance (0.75) appeared to be moderate higher than the genotypic variance (0.60), suggested less influence of environment on the expression of this trait. The phenotypic co-efficient of variation (20.95 %) had higher than the genotypic co-efficient of variation (18.73 %) Which suggested that environment had a little bit role (9.37%) on the expression of this trait (Table 4).

4.2 Heritability and genetic advance

4.2.1 Days to 50% flowering

Days to 50% flowering exhibited high heritability (91.71%), low genetic advance (9.21) with moderate genetic advance in percent of mean (11.11) which revealed that the character was governed by additive gene action and high heritability indicates that this character is least influenced by the environmental effect. So selection may be considered basis of this character. High heritability and low genetic advance was reported by Chakraborty and Chakraborty (2010).

4.2.2 Days to 80% maturity

Days to 80% maturity showed high heritability (94.49%) with moderate genetic advance (11.34) and genetic advance in percentage of mean (10.77%) indicated that this trait was controlled by additive gene action and selection for such trait might be rewarding. Li *et al.* (1991), akhtar *et al.* (2011) reported same result.

4.2.3 Plant height (cm)

The magnitude of heritability of this trait was high heritability (78.77%) with moderate genetic advance (11.50) and low genetic advance in percent of mean (8.72%). These findings were the indication of non-additive gene action and selection for such trait not be effective. Additive gene action for this character was reported by Das *et al.* (1992).

4.2.4 Total number of tillers per plant

Number of tiller per plant exhibited high heritability (78.45%) with low genetic advance (3.11) and high genetic advance in percentage of mean (22.95). These results revealed the possibility of predominance of additive gene action in the inheritance of this trait. There was both environmental and genotypic influence on the character. This trait possessed high variation, it is high potential for effective selection for further genetic improvement of this character. High heritability with moderate genetic advance was observed by Chakraborty and Chakraborty (2010). High heritability and high genetic advance on this character was also found by Subbaiah *et al.* (2011).

4.2.5 Number of effective tiller per plant

Number of effective tiller per plant exhibited high heritability (76.88%) with low genetic advance (3.01) and high genetic advance in percentage of mean (24.64). These results revealed the possibility of predominance of additive gene action in the inheritance of this trait. There was both environmental and genotypic influence on the character. This trait possessed high variation, it is high potential for effective selection for further genetic improvement of this character. Satheeshkumar *et al.* (2012) also found high heritability with high genetic advance in percent of mean for the character effective tillers per plant.

4.2.6 Panicle length (cm)

Panicle length showed high heritability (84.18%) with very low genetic advance (2.77) and moderate genetic advance in percent of mean (11.43) that indicated that environmental effect was more than the genotypic effect and due to additive gene action, selection for further improvement of the trait might be rewarding.

4.2.7 No .of primary branches per panicle

Number of primary branches per panicle exhibited high heritability (73.44%) and very low genetic advance (1.41) and moderate genetic advance in percent of mean (13.72) that determined the presence of additive gene effect on the character and for this reason, improvement through selection might be wise. Moderate heritability was reported by Biswas *et al.* (2001).

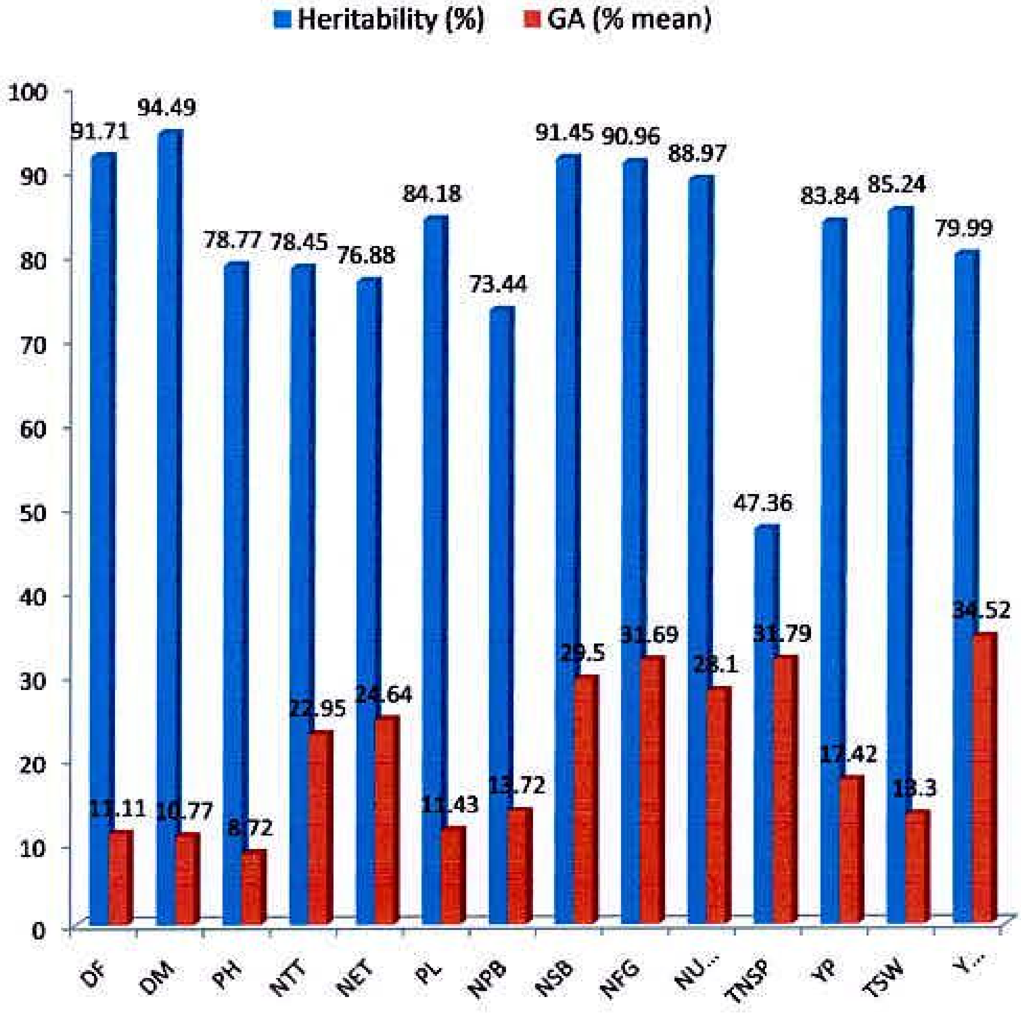

Figure 2. Heritability and genetic advance over mean in *Oryza sativa* L.

4.2.8 Number of secondary branches per panicle

Number of secondary branches per plant exhibited high heritability (91.45%) with low genetic advance (8.13) and moderate genetic advance in percentage of mean (29.50%). These findings discovered that the action of additive gene involved on the expression of this character as well as a scope of improvement through selection must be rewarding.

4.2.9 Number of spikelet per panicle

Number of spikelet per panicle showed high heritability (90.96%) with low genetic advance (7.45) and high genetic advance in percent of mean (31.69%). The character was governed by additive genes and selection for this trait may be rewarding.

4.2.10 Number of filled grain of main tiller

Number of filled grain of main tiller showed high heritability (88.97%) with high genetic advance (34.07) and high genetic advance in percent of mean (28.10%). The character was governed by additive genes and selection for this trait must be rewarding. High heritability with high genetic advance was also reported by bisne *et al.* (2009).

4.2.11 Number of unfilled grain of main tiller

Number of unfilled grain of main tiller showed moderate heritability (47.36%) with moderate genetic advance (6.17) and high genetic advance in percent of mean (31.69%). The character was governed by additive genes and selection for this trait may be rewarding.

4.2.12 Yield per plant

High heritability (83.84%) couplanted with low genetic advance (6.24) with moderate genetic advance in percent of mean (17.42%) indicated that additive gene effect was there .so rewarding for selection was considered. High heritability with high genetic advance was reported by Chakraborty and Chakraborty (2010).

4.2.13 Thousand seed weight (g)

The magnitude heritability of this trait was high heritability (85.24%) and low genetic advance (2.67) and moderate genetic advance in percent of mean (13.30%). These result indicated additive genes involvement in the expression of the trait and there is a scope of improvement by direct selection. Similar result was revealed by Ullah *et al.* (2011).

4.2.14 Yield per hectare (ton)

High heritability (79.99%) couplanted with low genetic advance (1.43) and high genetic advance in percent of mean (34.52) was recorded in respect of yield/hectare. These findings revealed that it was predominated by additive genes and the environmental influence was low on the trait and selection for this trait might be rewarding for farther improvement. High heritability couplanted with high genetic advance in percent of mean was recorded by Sabesan *et al.* (2009).

4.3 Correlation co-efficient

Yield is a complantex product being influenced by several quantitative traits. Some of these traits are highly associated with seed yield. The analysis of the relationship among those traits and their association with seed yield is very much essential to establish selection criteria. Breeders always look for genetic variation among traits to select desirable type. It is evident that in most of the cases, the genotypic correlation co-efficient were higher association between the characters studied and suppressive effect of theenvironment modified the phenotypic expression of these characters by reducing than the corresponding phenotypic correlation co-efficient. This indicated a strong inherent phenotypic correlation values. In few cases, however, phenotypic correlation co-efficient were same or higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act on the same direction and finally maximize their expression at phenotypic level.

4.3.1 Days to 50% flowering

Days to 50% flowering showed highly significant and positive correlation with days to maturity (G = 0.911, P = 0.866) indicated that yield could be improved by using this character. Similar result was reported by Sadeghi (2011).It also exhibited insignificant and positive interaction with plant height for phenotype (P=0.320) but significant for genotype (G=0.348). Insignificant and positive for total no. of tiller/plant (G= 0.052, P=0.055) and highly significant for number of effective tiller per plant for genotyp (G=0.826) insignificant for phenotype (P=0.091) but both are positive interaction.

Table 5. Estimation of heritability and genetic advance of 15 F_4 populations with three check varieties of rice

Parameters	Heritability	Genetic advance (5%)	Genetic advance (% mean)
Days to 50%flowering	91.71	9.21	11.11
Days to 80%maturity	94.49	11.34	10.77
Plant Height (cm)	78.77	11.50	8.72
Total no. of tiller/ plant	78.45	3.11	22.95
No. of effective tiller/ plant	76.88	3.08	24.64
Panicle length (cm)	84.18	2.77	11.43
No. of primary branches/panicle	73.44	1.41	13.72
No. of secondary branch/ panicle	91.45	8.13	29.50
No. of filled grain /panicle	90.96	7.45	31.69
No. of unfilled grain/panicle	88.97	34.07	28.10
Total no. of spikelet/ panicle	47.36	6.17	31.79
Yield/ Plant (g)	83.84	6.24	17.42
1000 seed weight (g)	85.24	2.67	13.30
Yield (ton/ hectare)	79.99	1.43	34.52

Table 6. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different Genotypes of *Oryza sativa* L.

	DM	PH	NTT	NET	PLANT	NPB	NSB	NFG	NUG	TNSP	YP	TSW	Y (t/ha)
DF	0.9118**	0.348*	0.052	0.826**	-0.393*	-0.754**	-0.603**	-0.446**	0.305	-0.267	-0.271	-0.580**	-0.470**
DM		0.330	0.308	0.236	0.424*	0.637**	0.610**	0.337*	0.340*	-0.210	-0.124	0.347*	0.369*
PH			-0.699**	-0.421*	0.269	-0.663**	-0.760**	-0.507**	0.474**	-0.204	-0.393*	0.068	-0.063
NTT				0.855**	-0.203	0.295	0.608**	-0.089	-0.031	-0.380*	-0.531**	-0.074	-0.084
NET					-0.177	0.372*	-0.350*	0.111	-0.052	0.219	0.495**	-0.083	0.271
PLANT						0.777**	0.742**	0.752**	-0.901**	0.702**	0.726**	-0.154	0.306
NPB							0.806**	0.727**	-0.663**	0.422*	0.259	-0.282	-0.123
NSB								0.870**	-0.855**	0.606**	0.388*	-0.038	0.427**
NFG									-0.971**	0.271	0.519**	-0.241	0.375*
NUFG										0.635**	0.541**	0.232	0.402*
TNSP											-0.296	-0.200	-0.297
YP												0.116	0.414*
TSW													0.159

** Correlation is significant at the 0.01 and * for 0.05 level, respectively.

DF = Days to 50% flowering, DM = Days to 80% maturity, PH= Plant height, NTT = Number of total tiller per plant, NET=Number of effective tiller per plant, PLANT= Panicle length, NPB= Number of primary branches per panicle, NSB= Number of Secondary branches per panicle, NFG = Number of filled grain per panicle, NUFG= Number of unfilled grain per panicle, TNSP= Number of total spikelet per panicle, , YP= Yield per plant (gram) ,TSW= Weight of thousand seed (gram), Y(t/ha) = Yield (ton per hectare).

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

	DM	PH	NTT	NET	PLANT	NPB	NSB	NFG	NUFG	TNSP	YP	TSW	Y (t/ha)
DF	0.866**	0.320	0.055	0.747**	-0.326	-0.641**	-0.567**	-0.423*	0.280	-0.201	-0.266	-0.515**	-0.425*
DM		0.317	0.269	0.190	0.401*	0.573**	0.570**	0.324	0.325	-0.165	-0.133	0.331	0.341*
PH			-0.632**	-0.367*	0.255	-0.565**	-0.696**	-0.475**	0.435**	-0.162	-0.333*	0.045	-0.050
NTT				0.825**	-0.167	0.264	0.522**	-0.079	-0.030	-0.252	-0.467**	-0.066	-0.103
NET					-0.133	0.291	-0.342*	0.093	-0.067	0.193	0.448**	-0.090	0.180
PLANT						0.614**	0.662**	0.677**	-0.817**	0.469**	0.631**	-0.139	0.218
NPB							0.730**	0.673**	-0.546**	0.318	0.245	-0.245	-0.084
NSB								0.844**	-0.778**	0.456**	0.383*	-0.039	0.375*
NFG									-0.873**	0.231	0.507**	-0.228	0.342*
NUFG										0.363*	0.498**	0.208	0.333*
TNSP											-0.255	-0.168	-0.173
YP												0.107	0.380*
TSW													0.131

**,Correlation is significant at the 0.01 and* for 0.05 level, respectively.

DF = Days to 50% flowering, DM = Days to 80% maturity, PH= Plant height, NTT = Number of total tiller per plant, NET=Number of effective tiller per plant, PLANT= Panicle length, NPB= Number of primary branches per panicle, NSB= Number of Secondary branches per panicle, NFG = Number of filled grain per panicle, NUFG= Number of unfilled grain per panicle, TNSP= Number of total spikelet per panicle, YP= Yield per plant (gram) ,TSW= Weight of thousand seed (gram) ,Y (t/ha) = Yield (ton per hectare).

However, it had significant and negative interaction with panicle length for genotype (G = -0.393) insignificant and negative for phenotypic (P = -0.326), primary branch and secondary branch both had highly significant negative interaction (G=-0.754, P=-0.641) and (G=-0.603, P=-0.567) respectively. Total no. of spikelet/panicle had highly significant for genotype and significant for phenotype but negative interaction (G=-0.446, P=-0.423), number of filled grain had insignificant and positive interaction (G=0.305, P=0.280), unfilled grain had insignificant and negative relation (G= -0267, P=0.201), thousand seed weight had significant but negative interaction (G= -0.580, P= -0.515) and seed yield per plant (G= -0.271, P= -0.266), yield per hectare had also highly and negative interaction(G=-0.470, P=-0.425), (Table 6 and table 7). Non-significant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.3.2 Days to 80% maturity

Days to maturity showed highly significant and positive correlation with panicle length (G=0.424, P=0.401), primary branch (G=o.637, P=0.573), secondary branch (G=0.610, P=0.570) and significant positive interaction with filled grain (G=0.474, P=0.325), thousand seed weight (G= 0.347, P= 0.331), yield per hectare (G= 0.369, P= 0.341) indicated that yield could be improved by using this character ,insignificant and positive interaction with plant height, spikelet/panicle. Positive significant correlation of this character with grain yield was observed by Akhtar *et al.* (2011).Insignificant association of these traits indicated that the association among these traits was largely influenced by environmental factors.

4.3.3 Plant height (cm)

Plant height showed highly significant and negative interaction with total no. of tiller/plant (G=-0.699, P=-0.632) number of primary branches (G=-0.663, P=-0.565), number of secondary branches (G=-0.760, P=-0.696), spikelet/panicle (G= -0.507, P=-0.475). It showed significant and negative correlation with effective tiller (G=-0.421, P=-0.367), yield/plant (G=-0.393, P=-0.333). It implantied that if plant height increases the above traits will decrease and vice versa. So there is a great scope to selection for above traits. Same result was reported by Prasad *et al.* (2001), Iftekharudduala *et al.* (2001). Insignificant negative relation with unfilled grain (G=-0.204, P=-0.162), yield/hectare (G=-0.063, P=-0.050) positive interaction with panicle length (G=0.269, P=0.255), thousand seed weight (G= 0.068, P= 0.045). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. It also exhibited significant and negative interaction with yield per plant (P=-0.418).

4.3.4 Total number of tillers per plant

Tiller per plant showed highly significant and positive correlation with effective tiller (P=0.825, G=0.855), secondary branch (G=0.608, P=0.522) and negative for yield per plant (G=-0.531, P=-0.467). It indicated that these above traits could be used for improvement of the varieties .Insignificant and negative correlation with panicle length (G= -0.203, P= -0.167), spikelet/panicle (G=-0.089, P=-0.079), filled grain (G=-0.031, P=-0.030), 1000 seed weight (G=-0.074, P=-0.066) and yield/hectare (G=-0.084, P=-0.103). It also showed insignificant and positive correlation with primary branch/panicle (G=0.295, P=0.264). The higher phenotypic correlation of the trait to yield per hectare indicated that the positive correlation between them was not only for genes but also for the favorable influence of environment.

4.3.5 Total number of effective tillers per plant

Effective tiller per plant showed highly significant and positive correlation with yield/plant (G=0.495, P=0.448) indicated that yield could be improved by using this character. Same result was reported by Agahi *et al.* (2007). Insignificant and negative correlation with panicle length (G= -0.177, P= -0.133) filled grain(G=-0.052, P=-0.067), 1000 seed weight (G=-0.083, P=-0.090) and positive relation with spikelet/panicle (G=0.111, P=0.093), yield/hectare (G=0.271, P=0.180), unfilled grain (G=0.219, P=0.193) also showed significant and negative correlation with secondary branch/panicle (G=-0.350, P=-0.342). The higher phenotypic correlation of the trait to yield per hectare indicated that the positive correlation between them was not only for genes but also for the favorable influence of environment.

4.3.6 Panicle length (cm)

Panicle length showed highly significant and positive interaction with number of primary branches (G=0.777, P=0.614), number of secondary branches (G=0.742, P=0.662), spikelet/panicle (G= 0.752, P=0.677), unfilled grain (G=0.702, P=0.469), yield/plant (G=0.726, P=0.631). It indicated that these above traits could be used for improvement of the varieties. Negative for filled grain (G=-0.901, P=-0.817). Insignificant and negative correlation with 1000 seed weight (G=-0.154, P=-0.139) and positive relation with yield/hectare (G=0.306, P=0.218). Highly significant positive correlation of panicle length with grain yield was found by ullah *et al.* (2011).The higher phenotypic correlation of the trait to yield per hectare indicated that the positive correlation between them was not only for genes but also for the favorable influence of environment, (Table 6 and table 7).

4.3.7 Number of primary branches per panicle

Number of primary branches per panicle showed positive and highly significant interaction with number of secondary branch (G = 0.806, P = 0.730), spikelet/panicle (G= 0.727, P=0.673). It indicated that if primary branches per plant increase the number of secondary branch, spikelet/panicle will increase. It implantied that yield could be improved by using these characters but negative relation was found in filled grain (G=-0.663, P=-0.546), significant positive interaction in unfilled grain (G=0.422, P=0.318 These suggesting if number of primary branches increases then yield per plant also increases. Similar conclusion revealed by vange (2008). It had insignificant and positive correlation with number of yield per plant (G = 0.259, P = 0245) and negative for thousand seed weight (G = -0.282, P = -0.245). However, it had insignificant and negative interaction was found in seed yield per hectare (G = -0.123, P = -0.084) (Table 6 and table 7). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.3.8 Number of secondary branches per plant

Number of secondary branch highly significant and positive interaction with spikelet/panicle (G= 0.870, P=0.844), unfilled grain (G=0.606, P=0.456), yield/hectare

(G=0.427, P=0.375). It implantied that yield could be improved by using these characters and negative for filled grain (G=-0.901, P=-0.817), significant and positive relation with yield/plant (G=0.388, P=0.383). Insignificant and negative correlation with 1000 seed weight (G=-0.038, P=-0.039) (Table 6 and table 7). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors.

4.3.9 Number of spikelets per panicle

Number of spikelet per panicle showed highly significant and positive interaction with yield/plant (G=0.519, P=0.507) and highly significant negative for filled grain (G=-0.971, P=-0.873). Significant and positive relation yield/hectare (G=0.375, P=0.342). It implantied that yield could be improved by using these above characters. Insignificant and negative correlation with 1000 seed weight (G=-0.241, P=-0.228) and positive for unfilled grain (G=0.271, P=0.131), (Table 6 and table 7). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. It also implantied that these variables are independent in case of insignificant for yield.

4.3.10 Number of filled grains of main tiller

Number of filled grain of main tiller showed highly significant and positive interaction with yield/plant (G=0.541, P=0.498), yield/hectare (G=0.402, P=0.333). It implantied that yield could be improved by using this above character. Same result also recorded by Vange (2009), Chakraborty *et al.* (2010) and highly significant negative relation for) . Significant and negative relation for unfilled grain (G=0.635, P=0.363). Insignificant and positive correlation with 1000 seed weight (G=0.232, P=0.208)), (Table 6 and table 7). Insignificant association of these traits indicated that the association between these traits is largely influenced by environmental factors. It also implanties that these variables are independent in case of insignificant for yield.

4.3.11 Number of unfilled grains of main tiller

Number of unfilled grain of main tiller showed insignificant and negative interaction for yield/plant (G=-0.296, P=-0.255), yield/hectare (G=-0.297, P=-0.173). It implantied that these two variable with association with unfilled grain had least role on yield. Insignificant and negative correlation with 1000 seed weight (G=-0.200, P=-0.168)) also observed, (Table 5 and table 6). Iftekharuddaula *et al.* (2001) reported significant negative correlation for yield with unfilled grain.

4.3.12 Yield per plant

Yield per plant showed significant and positive interaction with yield/hectare (G=0.414, P=380). It implantied that yield/hectare was increased for increasing yield per plant. Insignificant and positive correlation with 1000 seed weight (G=116, P=0.107), (Table 6 and table 7). Insignificance relation indicated that these two variables are independent for yield/hectare.

4.3.13 **Thousand seed weight (g)**

Thousand seed weight showed positive insignificant correlation with yield per hectare (G=0.159, P=0.131) (Table 5 and table 6). It indicated that thousand seed weight had least influence on yield/hectare. Positive significant correlation was reported by Vange (2008), das *et al.* (1992), Iftekharuddaula *et al.* (2001).

4.4 Path Co-efficient analysis

Correlation co-efficient determines association of characters that might not provide an exact picture of the relative importance of direct and indirect influence of each yield components on seed yield of the plant. A clear picture of the inter-relationship between seed yield and others yield contributing characters, direct and indirect effects of them can be worked out by using path analysis at phenotypic level which also measures the relative importance of each component on yield/hectare. Yield is considered as a resultant (dependent) variable. The data were recorded on different characters such as days to 50% flowering, days to 80% maturity, plant height (cm), total no. of tiller/plant, no. of effective tiller/plant, panicle length (cm)/plant, no. of primary branches/ panicle, no of secondary branches/ plant, total no. of spikelet /panicle, no. of filled grain of main tiller, , no. of unfilled grain of main tiller, yield/plant(g)dry, 1000 seed weight (g) and yield (ton/hectare), (independent) variable. Estimation of direct and indirect effect of path co-efficient analysis for *Oryza sativa* L. is presented in Table 7

4.4.1 Days to 50% flowering

Path co-efficient analysis revealed that, days to 50% flowering had highly negative direct effect (-0.368) with highly significant negative correlation on yield/hectare (-0.47) (Table8). Abarshahr *et al.* (2011) also reported negative direct effect of days to 50% flowering on yield/plant. Selvaraj *et al.* (2011) and Rangare *et al.* (2012) also reported positive direct effect of days to 50% flowering on yield/plant. This trait indicated that yield would not be improved through direct selection. The indirect effect of this character on yield/hectare (-0.47) via 80% maturity (0.248), effective tiller/plant, number of primary branches/panicle (0.701), filled grain (0.290), yield/plant (0.194) were positive. These traits could not be effective for indirect selection. It had negative indirect effect on plant height (-0.244), total no. of tiller/plant (-0.031), panicle length (cm)/plant (-0.340), number of secondary branches per plant (-0.210), total no. of spikelet /panicle (-0.420), no. of unfilled grain of main tiller (-0.188), thousand seed weight (-0.372). (Table7). Indirect selection may not be wise via these traits.

4.4.2 Days to 80% maturity

Path co-efficient analysis revealed that, days to 80% maturity had positive direct moderate effect (0.272) with significant positive correlation on yield per hectare (0.369). So, selection based on this character would be effective. Sadeghi (2011) reported high positive direct effect on yield. The indirect effect of this character on yield/hectare (0.369) via effective tiller/plant (0.074), number of secondary branches per panicle (0.213), panicle length(cm)/plant (0.367), filled grain (0.324), yield/plant (0.089), total no. of spikelet /panicle (0.318), 1000 seed weight (0.222) were positive . These traits could be effective for indirect selection. It had negative indirect effect

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

	DF	DM	PH	NTT	NET	PLANT	NPB	NSB	NFG	NUFG	TNSP	YP	TSW	Genotypic correlation with yield (t/ha)
DF	**-0.368**	0.248	-0.244	-0.031	0.259	-0.340	0.701	-0.210	-0.420	0.290	-0.188	0.194	-0.372	**-0.470****
DM	-0.335	**0.272**	-0.232	-0.185	0.074	0.367	-0.591	0.213	0.318	0.324	-0.148	0.089	0.222	**0.369***
PH	-0.244	0.090	**-0.701**	0.420	-0.132	0.233	0.616	-0.265	-0.477	0.451	-0.144	0.281	0.043	**-0.063**
NTT	-0.053	0.096	0.491	**-0.601**	0.268	-0.176	-0.274	0.212	-0.084	-0.030	-0.268	0.380	-0.047	**-0.084**
NET	-0.089	0.040	0.420	0.409	**0.314**	-0.153	-0.345	-0.122	0.105	-0.050	0.154	-0.354	-0.053	**0.271**
PLANT	0.187	0.116	-0.189	0.122	-0.055	**0.866**	-0.722	0.259	0.708	-0.856	0.494	-0.519	-0.099	**0.306**
NPB	0.277	0.225	0.541	-0.177	0.117	-0.442	**-0.929**	0.281	0.684	-0.630	0.297	-0.185	-0.181	**-0.123**
NSB	-0.222	0.166	0.412	-0.192	-0.110	0.642	-0.748	**0.349**	0.819	-0.813	0.427	-0.278	-0.025	**0.427****
NFG	-0.254	0.132	0.355	0.053	0.035	0.744	-0.675	0.303	**0.941**	-0.923	0.191	-0.371	-0.155	**0.375***
NUFG	-0.340	0.093	-0.332	0.029	-0.053	-0.680	0.413	-0.316	-0.853	**0.951**	0.447	0.387	-0.149	**0.402***
TNSP	0.098	-0.057	0.143	0.177	0.069	-0.587	-0.392	0.211	0.255	-0.037	**0.704**	-0.212	-0.128	**-0.297**
YP	0.063	-0.034	0.223	-0.315	0.164	0.628	-0.241	0.135	-0.388	0.604	0.209	**-0.715**	0.075	**0.414***
TSW	0.213	0.094	-0.047	0.044	-0.026	-0.122	0.262	-0.013	-0.227	-0.435	-0.141	-0.083	**0.642**	**0.159**
Residual effect	0.183													

Diagonally **bold figures** indicate the direct effect

**, * Correlation is significant at the 0.01 and 0.05 level, respectively.

DF = Days to 50% flowering, DM = Days to 80% maturity, PH= Plant height, NTT = Number of total tiller per plant, NET=Number of effective tiller per plant, PLANT= Panicle length, NPB= Number of primary branches per panicle, NSB= Number of Secondary branches per panicle, NFS = Number of filled grain per panicle, NUFS= Number of unfilled grain per panicle, TNSP= Number of total spikelet per panicle, , YP= Yield per plant (gram) ,TSW= Weight of thousand seed (gram), Y= Yield (ton per hectare on 50% flowering (-0.335), plant height (-0.232), total no. of tiller/plant (-0.185), panicle number of primary branches per plant (-0.591), no. of unfilled grain of main tiller (-0.148). (Table 8). Indirect selection may not be wise via these traits.

4.4.3 Plant height (cm)

Plant height showed negative direct effect (-0.701) with negligible insignificant negative correlation on yield/hectare (-0.063) (Table 8). Same result was also recorded by Abarshahr *et al.* (2011).therefore selection based on this character would not be effective. Positive indirect effects through days to 80% maturity (0.090), number of primary branches/plant (0.616) panicle length (cm)/plant (0.233), filled grain (0.451), yield/plant (0.281), no. of thousand seed weight (0.043). These traits could be effective for indirect selection. On the other hand, it had negative indirect effect on days to 50% flowering (-0.244), number of secondary branches per plant (-0.265), no. of unfilled grain of main tiller (-0.144) total no. of spikelet /panicle (-0.477), (Table7).

4.4.4 Total number of tillers per plant

Tiller per plant showed highly negative direct effect (-0.601) with negligible insignificant negative correlation on yield/hectare (-0.063) (Table 8). Therefore selection based on this character would not be effective. Positive indirect effects through days to 80% maturity (0.096), number of secondary branches/plant (0.212) yield/plant (0.281), plant height (0.491) and effective tiller/panicle (0.268). These traits could be effective for indirect selection. On the other hand, it had negative indirect effect on days to 50% flowering (-0.053), number of primary branches per plant (-0.274), panicle length (cm)/plant (-0.176), filled grain (-0.030), no. of unfilled grain of main tiller (-0.268), total no. of spikelet /panicle (-0.084) and no. of thousand seed weight (-0.047), (Table7).

4.4.5 Total number of effective tillers per plant

Effective tiller per plant showed highly positive direct effect (0.314) with insignificant positive correlation on yield per hectare. So selection based on this character would not be wise. Effective tiller per plant showed positive direct effect with significant positive correlation on yield per hectare was revealed by Sadeghi (2011).positive indirect effects through days to 80% maturity (0.040), plant height (0.420) total tiller/panicle (0.409) no. of unfilled grain of main tiller (0.154) total no. of spikelet /panicle (0.105) for indirect selection these variable may be considered. On the other hand, the indirect effect via days to 50% flowering (-0.089), number of primary branches per plant (-0.345), number of secondary branches/plant (-0.122) panicle length (cm)/plant (-0.153), filled grain (-0.050), yield/plant (-0.354), no. of thousand seed weight (-0.053) were negative, (Table 8).

4.4.6 Panicle length (cm)

Panicle length had direct positive high effect (0.866) with insignificant positive correlation on yield per hectare. So selection based on this character must not be rewarded. Chakraborty *et al.* (2010) found direct positive small effect with insignificant negative correlation on yield per hectare .On the other hand, length of panicle had positive indirect effect on days to 50% flowering (0.187) on days to 80% maturity (0.116), total no of tiller (0.122) number of secondary branches per plant (0.259), no. of unfilled grain of main tiller (0.494), total no. of spikelet /panicle (0.708). This trait had negative indirect effect plant height (-0.189), number of primary branches/plant (-0.722), yield/plant (-0.519), effective tiller/panicle (-0.055), thousand seed weight (-0.-0.099), (Table 8).

4.4.7 Number of primary branches per panicle

Path analysis showed that number of primary branches/panicle had negative direct effect (-0.929) with negligible insignificant negative correlation on yield/hectare (-0.123). Therefore selection based on this character would not be effective. This trait had positive indirect effect on days to 50% flowering (0.277), on days to 80% maturity (0.225), effective tiller/panicle (0.177) plant height (0.541), number of secondary branches per plant (0.281), no. of unfilled grain of main tiller(0.297), total no. of spikelet /panicle(0.684) . This trait had negative indirect total no of tiller (-0.177), yield/plant (-0.185), thousand seed weight (-0.181), (Table 8).

4.4.8 Number of secondary branches per plant

Path co-efficient analysis revealed that number of secondary branches per plant had positive direct effect (0.349) with highest significant positive correlation on yield per hectare (0.427) .Therefore, selection based on this character must be effective. This trait indicated that it can be improved through direct selection. The indirect effect of this character on yield/hectare (0.427) via days to 80% maturity (0.166), plant height (0.412), panicle length (0.642), no. of unfilled grain of main tiller (0.427), total no. of spikelet /panicle (0.819) were positive and could be selected indirectly. This trait had negative indirect effect on days to 50% flowering (-0.222), effective tiller/panicle (-0.110) total no of tiller (-0.192), yield/plant (-0.278), thousand seed weight (-0.025) (Table8). Indirect selection may not be wise via these traits.

4.4.9 Number of spikelets per panicle

Number of spikelet per panicle showed highly direct positive effect (0.941) with third highest significant positive correlation on yield per hectare (0.375).This trait indicated that it can be improved through direct selection. It had a true relationship between them. The indirect effect of this character on yield/hectare (0.375) via days to 80% maturity (0.132), plant height (0.355), effective tiller/panicle (0.035) total no of tiller (0.053), panicle length (0.744), no. of unfilled grain of main tiller (0.191) were positive and could be selected indirectly. This trait had negative indirect effect on days to 50% flowering (-0.254), number of primary branches per plant (-0.675), yield/plant (-0.371), thousand seed weight (0.155). (Table 8). Indirect selection may be fault via these traits.

4.4.10 Number of filled grains of main tiller

Number of filled grain of main tiller showed highly direct inverse effect (0.951) with significant negative correlation on yield per hectare (-0.402). This trait indicated that it must be improved via direct selection to reduce undesirable indirect traits. This trait had positive indirect effect on days to 80% maturity (0.093), no. of unfilled grain of main tiller (0.447), total no of tiller (0.029), primary branch/panicle (0.413) yield/plant (0.387). This trait had negative indirect effect on days to 50% flowering (-0.340), effective tiller/panicle (-0.053), plant height (-0.332), panicle length (-0.680), total no. of spikelet /panicle (-0.853) thousand seed weight (-0.149). (Table7). Positive direct effect was reported for number of filled grain per panicle by Agahi *et al.* (2007), Prasad *et al.* (2001).

4.4.11 Number of unfilled grains of main tiller

Number of unfilled grain of main tiller showed highly direct positive effect (0.704) with insignificant positive correlation on yield/hectare (0.297). This trait indicated that it may not be wise via direct selection. This trait had positive indirect effect on days to 50% flowering (0.098), effective tiller/panicle (0.069) plant height (0.143) total no of tiller (0.177), secondary branch/panicle (0.211), total no. of spikelet /panicle (0.255). This trait had negative indirect effect on days to 80% maturity (-0.057), panicle length (-0.587 thousand seed weight (-0.128). yield/plant (0.212). (Table8). Indirect selection may not be wise via these traits.

4.4.12 Yield per plant (g)

Yield per plant showed highly negative direct inverse effect (-0.715) on positive significant yield per hectare (0.414). This trait determined that it may be improved via direct selection to reduce undesirable indirect traits. This trait had positive indirect effect on days to 50% flowering (0.063), no. of unfilled grain of main tiller (0.209), total no of tiller (0.177), secondary branch/panicle (0.135) effective tiller/panicle (0.164) plant height (-0.223), panicle length (628) thousand seed weight (0.075). (Table8). Agahi *et al.* (2007) also found positive direct effect of thousand grains weight on yield per plant.

.This trait had negative indirect effect on days to 80% maturity (-0.034), total no of tiller (-0.315), primary branch/panicle (-0.241), total no. of spikelet /panicle (-0.388) . (Table8). Indirect selection would despair via this parameter.

4.4.13 Thousand seed weight (g)

Thousand seed weight had positive direct effect (0.642) on insignificant positive yield per hectare (0.159) it is a true association between the variables but direct selection may be prudent. Positive indirect effect through days to 50% flowering (0.213), days to 80% maturity (0.094), number of primary branches/plant (0.262), total no of tiller (0.044) were assured for indirect selection but less effective .This trait had negative indirect effect on total no. of spikelet /panicle (-0.227) secondary branch/panicle (-0.013) effective tiller/plant (-0.026) plant height (-0.047), panicle length (-0.122), no. of unfilled grain of main tiller (-0.141), yield/plant (-0.083). This trait showed positive significant correlation with yield per plant therefore yield/plant will be increased through direct selection, (Table 8). Siddikee (2006) reported that thousand seed weight had the highest positive direct effect on seed yield per plant.

In plant breeding, it is very difficult to have complantete knowledge of all component traits of yield. The residual effect permits precise explantanation about the pattern of interaction of other possible components of yield which was not included in the study on the dependent variables. The residual effect was 0.183, indicated that contribution of component characters on yield per hectare was 81.7% by the eighteen characters studied in path analysis, the rest 18.3% was the contribution of other factors which were not included in the study on the dependent variable and some for samplanting error.

The correlation and path co-efficient studies revealed that days to maturity, number of secondary branches per panicle, number of filled grains per panicle and yield per plant are the most important yield component. Recent research had also emphasized on the importance of these characters.

4.5 Selection

By comparing check varieties with segregating populations some better genotypes and individual plants from different populations were selected for future trial which are presented in Table 9 and Table 10.

4.5.1 Selection of promising genotypes

Promising genotypes were selected mainly on the basis of days to maturity and yield/hectare. The lowest days to maturity (96.33 days) was observed in G4 (BR 21×BR 24, F_4, S_2P_3) following by G3 (BR 21×BR 24, F_4, S_2P_2) (97 days) and G2 (BR 21×BR 24, F_4, S_2P_1) (97.67 days). They had short duration than 3 check varieties as G1 (BR 26) (104.70 days), G5 (BR 21) (105.30 days) and G11 (BR 24) (103.00 days). (Table 9. Figure2. Plantate 3, 4).

The highest yield/hectare was observed in G8 (BR 24×BR 26, F_4, S_5P_1) (5.70 ton) which was higher than 3 check varieties. The genotypes G3 (BR 21×BR 24, F_4, S_2P_2) (4.57 ton) and G4 (BR 21×BR 24, F_4, S_2P_3) (4.37 ton) had higher yield than check varieties G5 (BR 21) (4.22 ton) and G11 (BR 24) (3.83 ton) and finer grain than 3

Table 9. Comparing selected F_5 populations for further trial with check varieties

G	POPULATIONS	DM	YH (ton)
G4	BR 21×BR 24, F_4, S_2P_3	96.33	4.37
G3	BR 21×BR 24, F_4, S_2P_2	97.00	4.57
G2	BR 21×BR 24, F_4, S_2P_1	97.67	3.95
G8	BR 24×BR 26, F_4, S_5P_1	106.00	5.70
G11	BR 24	103.00	3.83
G1	BR 26	104.70	5.56
G5	BR 21	105.30	4.22

G=genotype, DM= days to maturity, YH=yield per hectare check varieties. The genotype G2 (BR 21×BR 24, F_4, S_2P_1) (3.95 ton) had higher yield than check variety G11 (BR 24) (3.83 ton) and also finer grain than 3 check varieties. (Table 9. Figure 7. Plantate 5).

So, considering days to maturity and yield/hectare of segregating populations with check varieties the G2, G3, G4, G8 genotypes were selected.

4.5.2 Selection of individual plants

The highest yield/plant was observed 63.3 (g) in plant number 8, replantication number 2, under genotype G7. Besides plant no.9,6,8 (RN. 1,2,3) under genotype G2 which yield/plant 38 (g), 31.6 (g), 32.7 (g) respectively, Plant no. 4, 8, 10 (RN. 1,2,2) under genotype G3 which yield/plant 39.3 (g) ,39.8 (g), 32.7 (g) respectively and Plant no. 5,4 (RN. 1,2,2) under genotype G4 which yield/plant 35.9 (g), 31.2 (g) respectively had higher yield/plant than check varieties G1(BR 26) 28.60 (g), G5 (BR21) 27.01 (g) and G11 (BR 24) 29.03 (g) respectively. (Table 10. Figure 5. Plantate 5).

Selected all plants had days to maturity 93 (days) to 94 (days) under genotypes G2, G3, G4 and days to maturity 101 (days) to 102 (days) under genotypes G7, G8, G12 that were lower days to maturity than 3 check varieties as G1 104.70 (days), G5 105.30 (days) and G11 103.00 (days). (Table 10. Figure 2. Plantate 3, 4).

So, considering days to maturity and yield/plant comparing with check varieties the plant number 9, 6, 8 under genotype G2; the plant number 4, 8, 10 under genotype G3; the plant number 5, 4 under genotype G4; the plant number8, 1, 4, 8, 9, 1, 7 under genotype G7; the plant number 6, 3 under genotype G8 and the plant number 6 under genotype G12 were selected.

Table 10. Comparing selected F_5 plants for further trial with check varieties

G	RN	PN	YP(g)	DM
G2	1	9	38	93
	2	6	31.6	93
	3	8	32.7	94
G3	1	4	29.3	93
	2	8	29.3	93
	2	10	39.8	93
G4	1	5	35.9	94
	3	4	31.2	94
G7	1	8	34	101
	2	1	41.1	101
	2	4	53.6	102
	2	8	63.3	102
	2	9	32.3	101
	3	1	35	102
	3	7	41.4	102
G8	1	6	31.5	102
	2	3	52.6	102
G12	1	6	29.4	101
G1	-	-	28.60	104.70
G5	-	-	27.01	105.30
G11	-	-	29.03	103.00

G=genotype, RN=replantication number, PN=plant number, YP= yield per plant, DM= days to maturity,

Chapter V

Summary and Conclusion

Chapter-V
SUMMARY

The research work was conducted in the experimental farm area of Sher-e-Bangla Agricultural University (SAU), Dhaka-1207, during April 2014 to July 2014. This experiment was undertaken with 15 F_4 rice populations and 3 check varieties of *Oryza sativa* L. It was laid out in a Randomized Complantete Block Design (RCBD) with three replantications. Data on various yield attributing characters such as, days to flowering, days to maturity, plant height (cm), number of total tillers per plant, number of effective tillers per plant, panicle length (cm), number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, number of unfilled grains per panicle, total number of spikelet per panicle, yield per plant (gm), 1000 seed weight (gm), yield (ton/ ha) were recorded.

From variability analysis of F_4 progenies, it was observed that significant variation exist among all the genotypes used for most of the characters studied. In this study out of 18 populations G15 (BR 21×BR 26, F_4, S_6P_1) (89.67 days) took the longest period for days to flowering and G3 (BR 21×BR 24, F_4, S_2P_2) (74.67 days) took minimum days for flowering. The highest number of days to maturity was recorded in G15 (BR 21×BR 26, F_4, S_6P_1) (112.70days) and minimum days to maturity recorded in G4 (BR 21×BR 24, F_4, S_2P_3) (96.33days). The highest plant height was recorded in G9 (BR 24×BR 26, F_4, S_5P_1) (145.50 cm) and G1 (BR 26) was the shortest plant (101.00 cm). The highest number of tillers per plant was recorded in G1 (BR 26) showed the highest number of tiller per plant (16.20) and the minimum number of tillers per plant was recorded (10.50) in G8 (BR 24×BR 26, F_4, S_5P_1). The highest number of effective tillers per plant was recorded in G1 (BR 26) (15.47) and the minimum number of effective tillers per plant was recorded in G16 (BR 21×BR 26, F_4, S_6P_4). The highest number of panicle length was recorded in G9 (BR 24×BR 26, F_4, S_5P_1) and the minimum panicle length was recorded in G3 (BR 24×BR 26, F_4, S_5P_1) (21.83 cm). The highest number of primary branches per panicle was recorded in G9 (BR 24×BR 26, F_4, S_5P_1) (12.03) and the minimum number of primary branches per panicle was recorded in G2 (BR 21×BR 24, F_4, S_2P_1) (9.13). The highest number of secondary branches per panicle was recorded in G9 (BR 24×BR 26, F_4, S_5P_1) (36.83) and the minimum number of secondary branches per panicle was recorded in G2 (BR

21×BR 24, F_4, S_2P_1) (18.37). The highest number filled grains per panicle was recorded in G9 (BR 24×BR 26, F_4, S_5P_1) (161.10) and the minimum number of filled grains per panicle was recorded in G2 (BR 21×BR 24, F_4, S_2P_1) (92.90). The highest number unfilled grains of per panicle was recorded in G11 (BR 24) (27.50) and the minimum number of unfilled grains per panicle was recorded in G6 (BR 21×BR 26, F_4, S_6P_7) (8.10). The highest number of spikelet per panicle was recorded in G9 (BR 24×BR 26, F_4, S_5P_1) (186.80) and the minimum number of spikelet per panicle was recorded in G2 (BR 21×BR 24, F_4, S_2P_1) (111.10). The highest number of yield per plant was recorded in G11 (BR 24) (29.03 g) and the minimum number of yield per plant was recorded in G16 (BR 21×BR 26, F_4, S_6P_4) (14.69g). The highest number of 1000-seed weight was recorded in G18 (BR 21×BR 26, F_4, S_6P_9) (22.33g) and the minimum number of 1000-seed weight was recorded in G12 (BR 21×BR 26, F_4, S_6P_2) (17.33 g).The highest number of yield was recorded in G8 (BR 24×BR 26, F_4, S_5P_1) (5.70 ton) and the minimum number of yield was recorded in G16 (BR 21×BR 26, F_4, S_6P_4) (2.44 ton).

The phenotypic variance and phenotype coefficient of variation were higher than the corresponding genotypic variance and genotypic coefficient of variation for all the characters under study.

Number of filled grains per panicle and number of unfilled grains per panicle showed higher influence of environment for the expression of phenotypic variance and genotypic variance.

On the other hand, 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, total number of spikelet per panicle, 1000-seed weight, yield per hector showed least difference phenotypic and genotypic variance suggesting additive gene action for the expression of the characters.

Maturity exhibits the highest value of heritability (94.49%) while number of unfilled grains per panicle exhibits the lowest value of heritability (47.36%). High heritability with high genetic advance in percent of mean was observed for number of tillers per plant, effective tillers per plant, number of secondary branches per panicle, number of filled grains per panicle, number of unfilled grains per panicle, total number of spikelet per panicle, indicating that these traits had under additive gene control and selection for genetic improvement for these traits would be effective except number of unfilled grains per panicle.

High heritability with moderate genetic advance were observed for days to flowering ,days to maturity , panicle length, number of primary branches per panicle, yield per plant and 1000-seed weight, yield per hector indicating medium possibility of selecting genotypes. High heritability with low genetic advance in percent of mean was observed for plant height, indicating that non-additive gene effects were involved for the expression of this character and selection for such trait might not be rewarding but there would be possibility for future selection.

Correlation coefficients were generally higher than that of corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters and it indicated that environmental effects were suppressed by gene contribution.

In few cases, phenotypic correlation co-efficient were higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level.

The significant positive correlation with seed yield per hector were found in days to maturity (G = 0.911, P = 0.866), number of secondary branches per panicle (G=0.427, P=0.375) total number of spikelet per panicle (G=0.375, P=0.342) and yield per plant (G=0.414, P=380). In addition, there were non-significant positive correlation with yield per hector was also found in number of effective tillers per plant (G=0.271, P=0.180), panicle length (G=0.306, P=0.218) and 1000 seed weight (G=0.159, P=0.131). The significant negative correlation with seed yield per hector was for 50% flowering (G=-0.271, P= -0.266). The insignificant negative correlation with seed yield per hector were for plant height (G=-0.063, P=-0.050), number of total tillers per plant (G=-0.084, P=-0.103), number of primary branches per panicle (G = -0.123, P = -0.084) and no. of unfilled grain (G=-0.297, P=-0.173)

Path co-efficient analysis revealed that, days to maturity, number of effective tillers per plant, panicle length, number of secondary branches per panicle, total number of spikelet per panicle, number of unfilled grains per panicle, and 1000-seed weight had the positive direct effect on yield per plant. Whereas, days to flowering, plant height, number of total tillers per plant, number of primary branches per panicle had the negative direct effect on yield per plant but yield per plant had negative direct effect on yield per hectare.

The genotypic correlation of days to maturity, number of secondary branches per panicle, number of filled grains per panicle, total number of spikelet per panicle was positive and considerably higher in magnitude. It is mainly due to high positive direct effect and positive indirect effects of others characters and selection would be effective for this trait.

As days to 80% maturity, number of secondary branches/panicle, total number of spikelet/panicle, number of filled grain/ panicle and yield/ plant commonly showed good performance for variability, heritability, correlation and Path co-efficient on yield/hectare. So, they may be used for further crop improvement practices

Therefore, considering maturity, yield/plant, yield/hectare and their variability, correlation and path coefficient analysis, the genotypes G2 (BR 21×BR 24, F_4, S_2P_1), G3 (BR 21×BR 24, F_4, S_2P_2), G4 (BR 21×BR 24, F_4, S_2P_3) and G8 (BR 24×BR 26, F_4, S_5P_1) might be suggested as early maturity and high yielding Aus populations for future trial. Specially plant number 9, 6, 8 under genotype G2; the plant number 4, 8, 10 under genotype G3; the plant number 5, 4 under genotype G4; the plant number8, 1, 4, 8, 9, 1, 7 under genotype G7; the plant number 6, 3 under genotype G8 and the plant number 6 under genotype G12 must be rewarded for selection.

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Appendices

APPENDICES

Appendix I: 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 emplantoyed
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 emplantoyed
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 II. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from April, 2014 to July, 2014

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)
	Maximum	Minimum		
March,2014	31.50	23.30	40	0.04
April,2014	35.80	23.20	45	1.58
May,2014	35	24.20	58	2.63
June,2014	30.30	21.80	71.08	2.89
July,2014	33.45	25.50	65.43	4.55

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