CORRELATION, PATH ANALYSIS AND GENETIC DIVERSITY IN AMAN RICE (*Oryza sativa* L.)

BY

GOLAM SARWAR

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Approved by:

Hossain

(Dr. Md. Sarowar Hossain)
Professor
Dept. of GEPB, SAU
Supervisor

Harun-Ur-Rashid

(Md. Harun-Ur-Rashid)
Assistant Professor
Dept. of GEPB, SAU
Co-supervisor

Hossain

(Dr. Md. Sarowar Hossain)
Chairman
Examination Committee

Dr. Md. SAROWAR HOSSAIN
Professor
Dept. of Genetics and Plant Breeding
Sher-e Bangla Agricultural University
Dhaka-1207, Bangladesh
E-mail: sarowar2001@rediffmail.com, Cell phone: 01552499169

CERTIFICATE

*This is to certify that the thesis entitled, "**CORRELATION , PATH ANALYSIS AND GENETIC DIVERSITY IN AMAN RICE (Oryza sativa L).**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **GOLAM SARWAR**, Registration No. 08-03106 under my supervision and my guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: December, 2013
Dhaka, Bangladesh

(Professor. Dr. Md. Sarowar Hossain)
Supervisor

DEDICATED TO

MY

BELOVED PARENTS

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Place: SAU, Dhaka, Bangladesh

The author

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By

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ABSTRACT

The experiment was conducted with forty two genotypes of rice at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during the period of July-December, 2013 to estimate the genetic variability, correlation, path and diversity among the genotypes. The experiment was conducted using Randomized Complete Block Design with three replications. All the genotypes varied significantly with each other for all the studied characters indicated the presence of considerably variations among the genotypes studied. The PCV values were higher than the respective GCV values for all the characters under study except unfilled grains per panicle indicating that the characters were less influenced by the environment. Total tillers per plant, effective tillers per plant, filled grains per panicle, unfilled grains per panicle and yield per plant showed high heritability along with high genetic advance as percentage of mean were normally more helpful in predicting the genetic gain under selection. From the correlation and path analysis it was revealed that total tillers per plant, effective tillers per plant and days to maturity showed significantly positive genotypic correlation with yield as well as employed positive direct effect on yield suggesting that the selection for these traits would helpful for the improvement of yield per plant. As PCA, D^2 and clusters analysis the genotypes were grouped into five different clusters. Clusters IV had the maximum fourteen and cluster III had the minimum three genotypes. The highest inter-cluster distance was observed between II and III and the lowest was observed between IV and V. The highest and lowest intra-cluster distance was observed in III and IV respectively. Genotypes included in cluster V were important for total tillers per plant, effective tillers per plant, days to 50% flowering and thousand grains weight, cluster III were important for filled grains per panicle and unfilled grains per panicle, cluster IV were for plant height and yield per plant. Considering the diversity pattern and other agronomic performances, the genotypes Special from AL-29, AL-36, PP-4B(i), AL-17(iii)B, AL-17(iii), AL-17(ii)A, Special from-129, Special from 17(iv), AL-44(i), AL-17, Special from AL-36(D), PP-48, IR-25B, Special from AL-33, IR-25B (Tall), P-5B (ii) might be considered better parents for the future efficient hybridization programme.

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SYMBOLS AND ABBREVIATION

ABBREVIATION	ELABORATION
%	Percent
@	At the rate of
√	Square root
°C	Degree Celcious
AEZ	Agro-Ecological Zone
AL	Advanced Line
ANOVA	Analysis of variance
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
CV	Coefficient of variation
DAT	Days after transplanting
No.	Number
df	Degree of freedom
ECV	Environmental coefficient of variation
EMS	Error mean square
et al.	And others
etc.	Etecetera
F_1	First filial generation
Fig.	Food and Agriculture Organization
g	Gram
GA	Genetic advance
GAPM	Genetic advance in percentage of mean
GCV	Genotypic coefficients of variation
GMS	Genotypic mean suare
h^2_b	Heritability
ha	Hetare
i.e.	That is
IRRI	International Rice Research Institute
J.	Journal
K	Selection differential

SYMBOLS AND ABBREVIATION (cont.)

ABBREVIATION	ELABORATION
L:B	Length: Breadth
m	Meter
m^2	Square meter
mm	Millimeter
MOP	Muriate of potash
No.	Number
PCV	Phenotypic coefficients of variation
r	Number of replication
RCBD	Randomized Complete Block Design
Res.	Research
SAU	Sher-e-Bangla Agricultural University
TSP	Triple Superphosphate

CHAPTER I

INTRODUCTION

Rice is a cereal crop belonging to genus *Oryza* of family Poaceae. The genus *Oryza* has twenty two wild and two cultivated species viz., *Oryza sativa* and *Oryza glaberrima*. All the germplasms found in Asia, America and Europe belong to *Oryza sativa*, while those in West Africa belong to *Oryza glaberrima*. *Oryza sativa* is a cultivated diploid species having 24 chromosomes of AA genome.

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

More than 90% of the world's rice is produced and consumed in Asia (Chopra, 2001). Bangladesh is the fourth largest producer of rice in the world with production of 33.8 million tons in 2012 (Anonymous, 2012). It occupies 74.77% total cropped areas and it alone constitutes 90% of the total food grain produced annually in the country (Anonymous, 2009). Bangladesh needs 2.7% increases in rice production per year due to increasing population (Alam *et al.*, 2004).

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

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

Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations (Thomas and Lal, 2012). Hybridization programme involving genetically diverse parents belonging to different clusters would provide an opportunity for bringing together gene constellations of diverse nature, promising hybrid derivatives resulted probably due to complementary interaction of divergent genes in parents (Ovung *et al.*, 2012).

Rice is grown in Bangladesh under diverse ecosystem of irrigated, rain fed and deep water conditions in three distinct seasons namely Aus, Aman, and Boro (Rashid, 1994). Among Aus, Aman and Boro seasons, Aman occupied the highest area coverage (34% of gross cropped area) (Anonymous, 2009). Moreover, there is lack of well developed Aman rice variety in our country. So we have to give more attention for the improvement of Aman rice varieties to increase rice production in order to satisfy our population's need of food.

Therefore the present study was undertaken with the following objectives:

1. To study the genetic variability among different Aman rice genotypes;
2. To study the interrelationship between yield and yield contributing characters and their direct and indirect effect on yield; and

3. To assess the genetic diversity among the Aman rice genotypes for identifying the genetically divergent parents to utilize them in the future hybridization programme.

CHAPTER II

REVIEW OF LITERATURE

2.1 Genetic variability

Iftekharuddaula *et al.* (2001) studied twenty-four modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for grain yield and its component characters. All the characters tested were showed significant variation among the varieties. The highest genetic variability was obtained in spikelets/panicle and grains/panicle. High heritability together with high genetic advance in percentage of mean was observed in plant height, 1000-grain weight, grains/panicle and spikelets/panicle.

Bisne *et al.* (2009) conducted an experiment on 44 rice genotype in Raipur, Chhattisgarh in *kharif* 2005 for 13 characters. Low, moderate, and high genotypic and phenotypic coefficient of variations were observed. High genotypic and phenotypic coefficient of variations were expressed by harvest index, total number of filled spikelets per panicle, 100-grain weight and spikelet fertility percentage. High heritability coupled with high genetic advance was exhibited by harvest index, total number of chaffy spikelets per panicle, grain yield per plant, total number of filled spikelets per panicle and spikelet fertility percentage and selection may be effective for these characters.

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

Anbanandan *et al.* (2009) studied four crosses of F_2 generation were advanced to F_3 and F_4 generations to study variability, heritability and genetic advance of four crosses of rice genotypes. Among the four crosses studied, cross 1 exhibited superior *per* se performance in both F_3 and F_4 generations for almost all the economic characters studied including yield. This cross also recorded increased performance from F_3 to F_4 generations. This indicated the improvement of the genotypes as the generation progresses. High PCV and GCV values were observed for grain yield per plant for cross 1 followed by cross 2 in both F_3 and F_4 generations. Also cross 1 and cross 2 recorded high heritability and genetic advance for the characters *viz,* number of productive tillers per plant, 1000 grain weight and grain yield per plant in both F_3 and F_4 generations. This indicated that these characters are controlled by additive gene action. Hence the expected progress under selection could be obtained in the early generation itself. Genetic improvement for quantitative traits can be achieved through a clear understanding of the nature and amount of variability present in the genetic stocks and the extent to which the desirable traits are heritable. Therefore, information on the genetic parameters such as coefficient of variation, heritability, genetic advance and the influence of environment on the expression of these characters will help the breeder to evolve suitable cultivars within a short time.

Bharadwaj *et al.* (2007) conducted an experiment in which heritability and genetic advance were studied in three New Plant Type (NPT) based crosses of rice for thirteen characters in two environments of normal and high dose of nitrogen. Significant genetic variability was observed between the two filial generations and their parents of three crosses of rice for all the characters under study. High heritability estimates coupled with high genetic advance as percent of mean was seen in all the crosses for days to fifty percent flowering, days to maturity, plant height, panicle length, L : B ratio and 1000 grain weight, while high heritability with moderate genetic advance was seen in average grain length and grain breadth. Spikelets per panicle and filled grains per panicle had moderate heritability and high genetic advance. Productive tillers per plant, spikelet sterility and grain yield per plant showed low to moderate heritability coupled with low to moderate genetic advance as per cent mean.

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

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

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

Seyoum *et al.* (2012) conducted a field experiments using fourteen rice genotypes during the main rainy seasons of 2009 and 2010 at three rainfed upland locations of

Southwest Ethiopia to estimate the genetic variability, heritability of grain yield and yield contributing traits in upland rice. Days to 50% flowering, plant height, grains per panicle, spikelets per panicle, thousand grains weight and grain yield showed relatively high GCV and PCV estimates. High heritability was obtained for plant height (92.17%), followed by 50% flowering (90.16%), thousand grains weight (83.17%), days to 85% maturity (82.45%), panicle length (79.25%) and spikelet per panicle (60.25%) which indicates high heritable portion of variation. High to medium estimates of heritability and genetic advance were obtained for plant height, days to 50% flowering, panicles per plant, spikelets per panicle, grains per panicle and thousand grains weight, indicating the roles of additive gene action and a good scope of selection using their phenotypic performance.

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

Yadav *et al.* (2010) carried out a field experiment was to establish the extent of association between yield and yield components and others characters in rice. They found high heritability coupled with high to moderate genetic advance as % of mean was observed on plant height, seed yield per plant, biological yield, harvest index, test weight and number of spikelets per panicle suggesting preponderance of additive gene action in the expression of these characters.

Vange (2009) conducted a field experiments in 2005 in the Experimental Farm Station of the University of Agriculture, Makurdi, Nigeria to evaluate the performance and genetic diversity of some upland rice accessions. Genotypic coefficient of variability (GCV) was generally lower than phenotypic coefficient of variability (PCV). Days to 50% heading, days to maturity, flag leaf area, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle, grain weight/panicle and seed yield showed very low differences between their PVC and GCV values. Also these traits had high estimates for heritability and genetic advance.

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

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

Sadeghi (2011) used 49 rice varieties (*Oryza sativa* L.) in an experiment to determine variability, heritability and correlation between yield and yield components for 2 years. He found broad sense heritability range from 69.21% (plant height) to 99.53% (grain width).

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

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

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

Akinwale *et al.* (2011) evaluated twenty rice genotypes in the International Institute of Tropical Agriculture, Ibadan, Nigeria during 2008/2009 cropping season. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the traits studied, indicating considerable influence of the environment on the expression of the traits. High to medium broad sense heritability estimates observed on days to heading, days to maturity, plant height, grain yield and number of grains per panicle, panicle weight, number of panicles per m^2 and panicle length. The low broad sense heritability observed for the number of tillers per plant and 1000 grain weight is indicative of the influence of the environment on these traits. Low heritability of these traits indicates the ineffectiveness of direct selection for these traits. High to medium heritability and genetic advance were recorded for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant.

Selvaraj *et al.* (2011) studied variability, correlation and path coefficient on 21 rice genotypes for grain yield and other yield attributes. Analysis of variance revealed considerable variability among the genotypes for all the characters. The phenotypic correlation coefficient (PCV) values were slightly greater than genotypic correlation coefficient (GCV), revealing negligible influence of environment in character expression. High heritability coupled with high genetic advance and high GCV were observed for number of tillers/plant followed by number of productive tillers per plant, plant height and grain yield / plant.

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

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

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

Satheeshkumar *et al.* (2012) estimated variability, heritability, genetic advance in fifty three genotypes of rice for fifteen characters. The highest genotypic and phenotypic coefficient of variation was found for number of productive tillers per plant, grain L/B ratio and grain yield per plant. High heritability was observed for the characters, days to first flower, plant height, number of productive tillers per plant, panicle length, filled grains per panicle, total number of grains, spikelet fertility, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel L/B ratio and grain yield per plant. High genetic advance as percent of mean were observed for the characters, days to first flower, plant height, number of productive tillers per plant, panicle length, filled grains per panicle, total number of grains, hundred grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel L/B ratio and grain yield per plant. Hence, the study suggested the selection based on these traits could be more effective in rice.

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

Rahman *et al.* (2012) carried out an experiment with twenty one genotypes of rice in T. Aman season 2008 at Sonagazi Regional station of BRRI. Analysis of variance revealed significant differences among the genotypes for all the traits. Flag leaf area, LAI at flowering, CGR at flowering, RGR at flowering, NAR at flowering and harvest index exhibited that they were controlled by additive gene action and selection for the improvement of these traits would be rewarding. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation. The highest genotypic variance was noticed for growth duration and the highest phenotypic variance was found for CGR at flowering. Genotypic coefficient of variation and phenotypic coefficient of variation highest for NAR at flowering (41.21 and 45.75, respectively) followed by CGR at flowering and lowest for panicle exertion rate (3.75 and 4.05, respectively). Growth duration showed the highest heritability (98.97) followed by days to flowering (98.00) and flag leaf area (92.29). The highest genetic advance was found for NAR at flowering and the lowest for panicle exertion rate.

Tuwar *et al.* (2013) studied with twenty nine genotypes of rice from diverse locations to estimate the genetic components of variability. Analysis revealed that plant height exhibited high estimates of GCV and PCV proceeded by number of tillers and grain weight per panicle. Heritability was higher for days to 50% flowering followed by days to maturity, plant height and panicle length which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. High heritability coupled with high genetic advance as percent of mean was recorded for number of spikelets and number of grains per panicle and grain weight per panicle. These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment.

2.2 Correlation coefficient

Iftekharuddaula *et al.* (2001) studied twenty-four modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for grain yield and its component characters. Genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients in most of the traits. Days to flowering, days to maturity, grains/panicle, 1000-grain weight and harvest index showed significant positive correlation with grain yield.

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

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

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

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

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

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

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

Yadav *et al.* (2010) carried out a field experiment was to establish the extent of association between yield and yield components and others characters in rice. They found that the correlation coefficient between seed yield per plant and other quantitative attributing to yield showed that grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicle per plant, panicle length, number of spikelet's per panicle and test weight at both genotypic and phenotypic levels.

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

Vange (2009) conducted a field experiments in 2005 in the Experimental Farm Station of the University of Agriculture, Makurdi, Nigeria to evaluate the performance and genetic diversity of some upland rice accessions. Genotypic correlation analysis of yield with other traits revealed that yield had a significantly positive correlation with flag leaf area, number of tillers, number of panicles, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle and seed weigh/panicle, grain length and 1000 seed weight.

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

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

Sadeghi (2011) used 49 rice varieties (*Oryza sativa* L.) in an experiment to determine variability, heritability and correlation between yield and yield components for 2 years. Grain yield was found to be positively and significantly correlated with grains per panicle, days to maturity, panicle weight, number of productive tillers, days to flowering, plant height, panicle length indicating the importance of these characters for yield improvement in this population.

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

Karad *et al.* (2008) observed a wide range of variability in yield and yield contributing characters. The grain yield was positively correlated with almost all the characters except 1000-grain weight at both genotypic and phenotypic levels.

Genotypic correlation estimates were higher than phenotypic correlation with grain yield plot^{-1}.

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

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

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

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

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

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

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

2.3 Path coefficient

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

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

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

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

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

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

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

Ghosal *et al.* (2010) evaluated eighteen advanced breeding lines for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Boro season, 2009. Path coefficient analysis revealed that effective tillers/m^2, thousand grain weight (g) and growth duration (days) had higher direct effects on yield (t/ha).

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

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

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

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

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

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

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

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

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

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

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

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

2.4 Genetic diversity

Islam *et al.*, (2004) studied genetic diversity of 62 genotypes of irrigated rice originating from BRRI, IRRI and China through Mahalanobis D^2 statistic. They grouped the 62 genotypes into five clusters. The cluster II and IV contained the highest number of genotypes (16) and cluster contained lowest (7). The highest infra cluster distance was noticed for cluster III. The highest inter cluster distance was observed between cluster I and cluster IV, followed by cluster I and cluster V, cluster I and cluster III, cluster III and cluster IV and the lowest between cluster IV and cluster V. The highest cluster mean for yield and other three yield contributing characters were obtained from cluster I, Six highest and two second highest means for yield contributing characters were found in cluster III but the lowest mean for yield. Therefore more emphasis should be given on cluster I for selecting genotypes as parents for crossing with the genotypes of cluster III, which may produce new recombinents with desired traits.

Balram *et al.* (2004) stated that the estimation of D^2 resulted in grouping the germplasm into 6 clusters. Maximum genotypes are in the cluster III followed ay cluster II through the survey was conducted in geographically small area, existence of six clusters among these shows that they are not genetically related. Among the characters studied, days to 50% flowering and test weight with 35.8% and 33.0%, respectively contributed maximum to the total divergence. Panicle length exhibited least contribution of 0.47% to the divergence. The cluster mean for each character indicated that days to 50% flowering was maximum in cluster VI, plant height in cluster II, panicle length in cluster I, productive tillers per plant in cluster V, grain/panicle in cluster IV, test weight in cluster I and grain yield in cluster VI. It would be logical to effect cross among the genotypes belonging to different clusters and selection within cluster with maximum inter-cluster distance to improve the rice grain yield.

Deepak *et al.*, (2006) conducted a genetic divergence study to estimate the nature and magnitude of diversity in 50 aromatic rice accessions including five scented improved varieties. The D^2 analysis indicated the presence of appreciable amount of genetic diversity in the material. The genotypes were grouped into 7 clusters. The cluster VI had the highest mean for grain yield per plant and for biological yield per plant. Inter cluster distance was recorded highest between cluster III and cluster IV. The least distance was recorded in between cluster I and cluster V. The conclusion drawn by the cluster analysis is that in the studied population high variability was observed between the genotypes in different clusters for different characters.

Devi *et al.*, (2006) studied genetic diversity in fifty-four rice cultivars collected from various locations in India. The analysis of variance revealed highly significant variation for plant height, panicle length, and flag leaf length, number of tillers per hill, number of seeds per panicle, number of days to 50% flowering, number and yield per plot. The genotypes were grouped into 9 clusters. Cluster VI recorded high mean values for plant height (140.33 cm), flag leaf length (48.11 cm) and flag leaf width (2.10 cm). Plant height contributed the most to genetic divergence (40.16%), followed by flag leaf width (20.12%), yield per plant (15.79%).

Mundhe *et al.,* (2006) conducted an experiment to assess genetic diversity of 39 midlate rice genotypes from India and IRRI, Manila, Philippines. Based on D^2 values, the genotypes were grouped into 7 clusters. Intra cluster distance was maximum in cluster III followed by cluster II and cluster I. Inter-cluster distance was maximum between cluster V and VII followed by cluster III and V, and cluster II and V. The genotypes from cluster I had better average for plant height, number of spikelets per panicle, number of filled spikelets per panicle, 1000 grain weight, yield per plant, kernel breadth and protein content, while cluster V had better average for number of tillers per plant, number of fertile tillers per plant, days to 50% flowering, yield per plant.

Ravinder *et al.,* (2006) assessed genetic divergence in 50 unscented rice genotypes for yield and its different component traits in under normal and late sown situations. The genotypes were grouped in 3 and 4 clusters in normal and late-sown conditions, respectively. There was no relationship between clustering pattern and geographical distribution. Based on the high cluster mean and wide genetic distance, hybridization between superior genotypes of clusters Individuals (IR 36, Palman 579, BR 827, HKR 117, HKR 126, HKR 86-105, IR 64 and RP 2151-21-22) and cluster III (Govind and NDR 84) had been advocated to achieve high heterosis and high yielding segregants.

Chandra *et al.,* (2007) assessed the nature and magnitude of genetic divergence among the fifty seven upland rice genotypes including 32 local rice germplasm based on 14 agro-morphological traits. On the basis of D^2 values, the 57 genotypes were grouped into five clusters. The most divergent clusters were III and IV (D^2=3387.9) followed by III and V (D^2=2808.2) and clusters II and III (D^2=1908.7). The clustering pattern of the genotypes were quite at random indicating that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were 1000-grain weight, grain yield and biological yield.

Sandhyakishore *et al.*, (2007) evaluated the genetic divergence for yield attributing traits in 70 rice genotypes. The analysis of variance revealed significant differences among the genotypes for each character. The genotypes were grouped into nine different clusters. The mode distribution of genotypes from differenteco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related.

Kumar *et al.*, (2008) studied 30 genetically diverse genotypes of rice to estimate the genetic divergence for 12 quantitative characters using Mahalanobis D^2 statistics. These genotypes were grouped into eight clusters. The clustering pattern of genotypes did not follow the geographic origin. The inter-cluster distance was highest between clusters V and VI. This indicated that the genotypes included in these clusters had broad spectrum of genetic diversity and could be used in hybridization programme and are likely to exhibit high heterosis and possibility of throwing transgressive segregants in subsequent generations.

Ahmad et al. (2010) carried out an experiment during kharif- 2005 to study the genetic divergence in sixteen genotypes of rice. Mahalonabis's D^2 statistic analysis revealed considerable amount of diversity in the material. Sixteen genotypes were grouped into six heterogeneous clusters. Among these clusters, clusters B and cluster C had maximum number of genotypes (five each). The maximum average inter-cluster distance was recorded between cluster C and cluster F. Hence the selected material could be further utilized for future breeding programme.

Thomas *et al.* (2012) evaluated sixty nine genotypes of rice to know the extent of genetic divergence with respect to thirteen yield attributing characters viz. days to 50% flowering, plant height, number of tillers per hill, panicle length, flag leaf length, flag leaf width, number of spikelets per panicle, days to maturity, biological yield, test weight, harvest index and grain yield per hill. On the basis of D^2 values the genotypes were grouped into nine clusters. Cluster I, V and VIII was the largest containing the 12 genotypes followed by cluster III with 9 genotypes. The composition of cluster indicated non existence of correspondence between genetic diversity and geographical distribution. The highest inter cluster distance was observed between cluster II and VII therefore genotypes from cluster II and VII may be used in hybridization programme to achieve desired segregants with high yield. Traits like spikelets per panicle, plant height and biological yield were the major contributors to genetic divergence.

Ovung *et al.* (2012) estimated the nature and magnitude of genetic divergence in seventy rice genotypes using Mahalanobis D^2 statistics by considering 13 quantitative characters. Mahalanobis D^2 analysis revealed considerable amount of diversity in the material. The genotypes were grouped into nine clusters. Cluster I and cluster III constituted maximum number of genotypes (12 each). The genotypes falling in cluster VII (2907) had the maximum divergence, which was closely followed by cluster V (2027) and cluster I (1762). The inter cluster distance was maximum between cluster VI and VII (18054) followed by cluster III and IX (12520), suggesting that the genotypes constituted in these clusters may be used as parents for future hybridization programme. Traits like spikelets per panicle; plant height and biological yield were the major contributors to genetic divergence.

Sohrabi *et al.* (2012) carried out an experiment in experimental field of University Putra, Malaysia with fifty accessions of upland rice to study the genetic diversity. Fifty accessions of upland rice were clustered into six groups based on twelve quantitative traits. Group A composed of only one member and groups B, C, and D contained 14, 20, and 23 members. Principal component analysis indicated diversity among 50 accessions of upland rice by a few eigen vectors. The first four principal components indicated 76.4% of total variations which PC1 showed 36.4% of the variation PC2, PC3, and PC4 explained 17.9%, 12.8%, and 9.6% of total variation, respectively.

Chakrovorty *et al.* (2013) carried out an field experiment with fifty one landraces of rice to study the the genetic diversity considering eighteen agro-morphological traits. Principal component analysis revealed that six quantitative characters viz., leaf length, culm number, culm diameter, number of grains per panicle, grain length/breadth ratio and grain length significantly influenced the variation in these cultivars. Cluster analysis permitted the separation of landraces into ten major clusters from diverse geographical location, suggesting environmental adaptation of the landraces.

CHAPTER III

MATERIALS AND METHODS

The details of the materials and methods employed have been presented below:

3.1 Experimental site and experimental period

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

3.2 Climate and Soil

The experimental site was situated in the sub-tropical zone. The soil of the experimental site lies in Agroecological region of "Madhupur Tract" (AEZ No. 28). It's top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 6.1 and organic carbon content is 0.82%. The record of air temperature, humidity, rainfall and sunshine (hr) during the period of experiment were noted from the SAU Weather Station, Sher-e-Bangla nagar Dhaka-1205 (Appendix 2).

3.3 Materials

Forty two rice genotypes (lines) were used for the present study. The genetically pure and physically healthy seeds of these genotypes were obtained from the Department of Genetics and Plant Breeding (SAU), Dhaka. The name and origin of these genotypes are presented in Table 1.

3.4 Land preparation

The experimental plot was prepared by ploughing with proper tiller. The weeds and other unwanted plant materials were removed from the field during the land preparation. Proper laddering was done to bring the soil at proper tilth condition.

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

Sl. No.	Genotypes	Source
1	G1: AL-17 (iii) B	SAU
2	G2: AL-17 (iii)	
3	G3: AL-42	
4	G4: From IR-25B (Yellow)	
5	G5: From IR-25B	
6	G6: Special (Early)	
7	G7: Richer	
8	G8: AL-35	
9	G9: Special-130	
10	G10: IR-25B (Dwarf)	
11	G11: AL-36(C)	
12	G12: Special from AL-36(D)	
13	G13: P-5B (i)	
14	G14: Hira	
15	G15: AL-17(iii) (Tall)	
16	G16: Aloron	
17	G17: IR-25B (Tall)	
18	G18: AL-36(iii)	
19	G19: Special from AL-33	
20	G20: Special from AL-29 (Basmoti type)	
21	G21:S-1 (Basmoti type)	
22	G22: S-2 (Basmoti type)	
23	G23: S-5 (Basmoti type)	
24	G24: AL-33(ii) (Basmoti type)	
25	G25: AL-36 (Basmoti type)	
26	G26: AL-42(ii) (Basmoti-Yellow type)	
27	G27: AL-44(i) (Basmoti-Yellow type)	
28	G28: AL-17(ii) A	
29	G29: AL-47	
30	G30: PP-48	
31	G31: PP-4B(i)	
32	G32: Special from-129	
33	G33: P-5B (ii)	
34	G34: AL-36	
35	G35: Special stigma color	
36	G36: IR-25B	
37	G37: Special from-17(iv)	
38	G38: Special from S-2	
39	G39: Special from AL-33	
40	G40: AL-44(i)	
41	G41: AL-17	
42	G42: AL-104	

3.5 Experimental design and layout

A Randomized Complete Block Design (RCBD) was used in the experiment with three replications. The field was divided into three blocks, the blocks were subdivided into 42 plots. Genotypes were randomly assigned into 42 plots in each block. The plot size was 2m × 1m. Block to block and plot to plot distance were 1 m and .5 m respectively.

3.6 Sowing and Transplanting

The seeds were sown on 22 July 2013 and 1 seedling per hill was transplanted to the main plot on 24 August 2013. Plant to plant and row to row distance were maintained at 20 cm and 25 cm respectively.

3.7 Fertilizer Application

Urea, TSP, MP, Gypsum @ 180, 55, 80, 60 kg/ha respectively were used in the experiment. Total TSP, MP and Gypsum were applied in final land preparation. Total urea was applied in three installments, at 15 days after transplanting (DAT), 35 DAT and 55 DAT respectively.

3.8 Intercultural operation and after care

Necessary intercultural operation was taken during cropping period for proper growth and development of the plants. Weeding, during first two top dressing of urea, was done to break the soil crust, to keep the plots free from weed and to incorporate the urea fertilizer into the soil for reducing the loss of urea through denitrification. Irrigation with regular interval was given to maintain 5-7 cm water up to hard dough stage of rice.

3.9 Plant protection measures

Proper control measures were taken against rice stem borer during tillering and heading stage of rice. Furadan 5G @ 1 g per square meter were applied at active tillering stage and panicle initiation stage of rice for controlling the stem borer. Lani rate and malathion were applied to protect from rat and rice bug respectively.

3.10 Irrigation

2-3 cm of water level was maintained at the time of transplanting. 5 cm depth of water was given at the time of maximum tillering stage. Then field was irrigated as and when required up to physiological maturity.

3.11 Harvesting

Harvesting was started when 80% of the plant population of each plot reached maturity.

3.12 Collection of data

Data were recorded on individual plant basis from 10 randomly selected plants. The following data were collected from field and in the laboratory after harvest.

1. **Days to 50% flowering (days):** It was recorded as days from sowing to 50% flowering of the plants of each plot.
2. **Days to maturity (days):** It was recorded as days on plant basis from sowing time to about 80% of the plants were ready for harvesting.
3. **Plant height (cm):** The plant height (cm) was taken from 10 randomly selected plants of each plot. The length of the main culm (cm) from the ground level to the tip of its panicle was measured and the average was taken.
4. **Total tillers per plant (No.):** Total tiller number per plant was counted in all the plants under study.
5. **Effective tillers per plant (No.):** The total numbers of the tillers bearing panicle were counted from each of the sample hills.
6. **Panicle length (cm):** It was recorded as the distance (cm) from the last node of the rachis to the tip of the main panicle of each sample plant and the average was taken.

7. **Fertile grains per panicle (No.):** The total number of fertile grains was counted from the main panicle of each sample plant and the average was taken.

8. **Unfertile grains per panicle (No.):** The total number of sterile grains was counted from the main panicle of each sample plant and the average was taken.

9. **1000 grain weight (gm):** One thousand clean sun dried grains were weighted randomly from the sample plant after which the weight (g) average was taken.

10. **Yield per plant (g):** Total grain weight (g) of sample plant of each plot was taken after cleaning and sun drying the samples to a measure level of 12% and the average was taken.

3.13 Statistical analysis

Analysis of variances was done for all the characters under study using the mean value (Singh and Chaudhary, 1985). Mean, range, co-efficient of variation (CV), correlation and path coefficient was estimated using MSTAT computer programme. Multivariate analysis viz., Principal Component Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT programme.

3.13.1 Computation of Variance Component

i. Estimation of genotypic and phenotypic variance

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

$$\text{Genotypic variance } (\sigma^2 g) = \frac{GMS - EMS}{r}$$

Where,

GMS = Genotypic mean square

EMS = Error mean square

r = Number of replication

Plate 1. Close view of the experimental field

Plate 2. Collection of data at the experimental field

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

Genotypic and phenotypic co-efficient of variation were estimated according to Burton (1952) and Singh and Chaudhary (1985).

Genotypic coefficients of variation (GCV) = $\frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$ = Population mean

Phenotypic coefficients of variation (PCV) = $\frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$

Where,

$\sigma^2 p$ = Phenotypic variance and $\bar{x}$ = Population mean

iii. Estimation of heritability

Heritability was estimated in broad sense by the formula suggested by Johnson *et al.* (1955) and Hanson *et al.* (1960).

Heritability (h^2_b) = $\frac{\sigma^2 g}{\sigma^2 p} x100$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

iv. Estimation of genetic advance

Estimation of genetic advance was done following formula given by Johnson *et al.* (1955) and Allard (1960).

Genetic advance (GA) = h^2_b. K. σ_p

Where,

h^2_b = Heritability

K = Selection differential, the value of which is 2.06 at 5% selection intensity; and

σ_p = Phenotypic standard deviation.

v. Estimation of genetic advance in percent of mean, GA (%)

Genetic advance in percent of mean was calculated by the formula of Comstock and Robinson (1952) as follows:

Genetic advance in percentage of mean, GA (%) = $\frac{GA}{\bar{x}} x100$

Where,

GA = Genetic advance; and $\bar{x}$ = Population mean

vi. Estimation of correlation coefficients

The genotypic and phenotypic correlation coefficients between yield and different yield contributing characters were estimated as:

Genotypic correlation = $\frac{Cov(g)1.2}{\sqrt{\sigma^2(g)1.\sigma^2(g)2}}$

Where,

$Cov_{g\,(xy)}$ = Genotypic covariance between the variables X and Y

$\sigma^2_{(g)1}$ = Genotypic variance of the variable X_1

$\sigma^2_{(g)2}$ = Genotypic variance of the variable X_2

Similarly, phenotypic correlation $r_{p(xy)}$ = $\frac{Cov(ph)1.2}{\sqrt{\sigma^2(ph)1.\sigma^2(ph)2}}$

Where,

$Cov_{ph(xy)}$ = phenotypic covariance between the variables X and Y

$\sigma^2_{(ph)1}$ = phenotypic variance of the variable X_1

$\sigma^2_{(ph)2}$ = phenotypic variance of the variable X_2

vii. Estimation of Path coefficients

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using genotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on grain yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3………………..and 10 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$$r_{1.y} = P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y} + r_{1.9} P_{9.y} + r_{1.10} P_{10.y}$$

$$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y} + r_{2.9} P_{9.y} + r_{2.10} P_{10.y}$$

$$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y} + r_{3.9} P_{9.y} + r_{3.10} P_{10.y}$$

$$r_{4.y} = r_{1.4} P_{1.y} + r_{2.4} P_{2.y} + r_{3.4} P_{3.y} + P_{4.y} + r4_{1.5} P_{5.y} + r_{4.6} P_{6.y} + r_{4.7} P_{7.y} + r_{4.8} P_{8.y} + r_{4.9} P_{9.y} + r_{4.10} P_{10.y}$$

$$r_{5.y} = r_{1.5} P_{1.y} + r_{2.5} P_{2.y} + r_{3.5} P_{3.y} + r_{4.5} P_{4.y} + P_{5.y} + r_{5.6} P_{6.y} + r_{5.7} P_{7.y} + r_{5.8} P_{8.y} + r_{5.9} P_{9.y} + r_{5.10} P_{10.y}$$

$$r_{6.y} = r_{1.6} P_{1.y} + r_{2.6} P_{2.y} + r_{3.6} P_{3.y} + r_{4.6} P_{4.y} + r_{5.6} P_{5.y} + P_{6.y} + r_{6.7} P_{7.y} + r_{6.8} P_{8.y} + r_{6.9} P_{9.y} + r_{6.10} P_{10.y}$$

$$r_{7.y} = r_{1.7} P1.y + r_{2.7} P_{2.y} + r_{3.7} P_{3.y} + r_{4.7} P_{4.y} + r_{5.7} P_{5.y} + r_{6.7} P_{6.y} + P_{7.y} + r_{7.8} P_{8.y} + r_{7.9} P_{9.y} + r_{7.10} P_{10.y}$$

$$r_{8.y} = r_{1.8} P_{1.y} + r_{2.8} P_{2.y} + r_{3.8} P_{3.y} + r_{4.8} P_{4.y} + r_{5.8} P_{5.y} + r_{6.8} P_{6.y} + r_{7.8} P_{7.y} + P_{8.y} + r_{8.9} P_{9.y} + r_{8.10} P_{10.y}$$

$$r_{9.y} = r_{1.9} P_{1.y} + r_{2.9} P_{2.y} + r_{3.9} P_{3.y} + r_{4.9} P_{4.y} + r_{5.9} P_{5.y} + r_{6.9} P_{6.y} + r_{7.9} P_{7.y} + r_{8.9} P_{8.y} + P_{9.y} + r_{9.10} P_{10.y}$$

$$r_{10.y} = r_{1.10} P_{1.y} + r_{2.10} P_{2.y} + r_{3.10} P_{3.y} + r_{4.10} P_{4.y} + r_{5.10} P_{5.y} + r_{6.10} P_{6.y} + r_{7.10} P_{7.y} + r_{8.10} P_{8.y} + r_{9.10} P_{9.y} + P_{10.y}$$

Where,

r_{1y} = Genotypic correlation coefficients between y and 1 th character (y= Grain yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,..........,10)

1 = Plant height
2 = Total tillers/plant
3 = Effective tillers/plant
4 = Days to 50% flowering
5 = Panicle length
6 = Filled grains/panicle
7 = Unfilled grains/panicle
8 = Days to maturity
9 = 1000 grain weight
10 = Yield/plant

Total correlation, say between 1 and y i. e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y
$r_{1.2} P_{2.y}$ = indirect effect of 1 via 2 on y
$r_{1.3} P_{3.y}$ = indirect effect of 1 via 3 on y
$r_{1.4} P_{4.y}$ = indirect effect of 1 via 4 on y
$r_{1.5} P_{5.y}$ = indirect effect of 1 via 5 on y
$r_{1.6} P_{6.y}$ = indirect effect of 1 via 6 on y
$r_{1.7} P_{7.y}$ = indirect effect of 1 via 7 on y
$r_{1.8} P_{8.y}$ = indirect effect of 1 via 8 on y
$r_{1.9} P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10}\,P_{10.y}$ = indirect effect of 1 via 10 on y

Where,

$P_{1.y}, P_{2.y}, P_{3.y}$ …………….. $P_{10.y}$ = Path coefficient of the independent variables 1, 2, 3,…………..,10 on the dependent variable y, respectively.

$r_{1.y}, r_{2.y}, r_{3.y}$, …………., $r_{10.y}$ = Correlation coefficient of 1, 2, 3, ………., 10 with y, respectively.

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

$$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots + r_{10.y}P_{10.y})$$

Where,

$$P^2_{RY} = R^2$$

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

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y

3.13.2 Analysis of Genetic Divergence

Genetic divergence among the genotypes was assessed by Mahalanobis's (1936) generalized distance (D^2) statistic and its auxiliary analyses. Selection of parents in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are efficient method of evaluating genetic diversity.

i. Principal Component Analysis (PCA)

Principal component analysis, one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from the sum of squares and product matrix for the characters. Therefore, principal components were computed from the correlation matrix and genotype scores obtained from the first components (which has the property of accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jager *et al.*, 1983). Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

ii. Clustering

To divide the genotypes of the study into some number of mutually exclusive groups clustering was done using non-hierarchical classification. Starting from some initial classification of the genotypes from one group to another so long as such transfers improve the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swapping two genotypes of different classes, and so on.

iii. Canonical Vector Analysis (CAV)

Using canonical vector analysis a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Thus, in this analyses a series of orthogonal transformations sequentially maximizing the ratio of the among groups to the within group variations.

iv. Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury (1985). For each combination the mean deviation, i.e. Y^1_i-Y^2_i with i=1, 2 ... p was estimated and the D^2 was calculated as sum of the squares of these deviations, i.e.1 (Y^1_i - Y^2_i). The D^2 values were estimated for all possible pairs of combinations between genotypes.

v. Calculation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula suggested by Singh and Chaudhary (1985).

$$\text{Average intra- cluster } D^2 = \frac{\sum D^2_i}{N}$$

Where,

$\sum D^2_i$ = Sum of distances between all possible combinations (n) of genotypes included in a cluster

N = Number of all possible combinations between the populations in a cluster

vi. Calculation of average inter-cluster distances

Average inter-cluster distances were calculated by the formula suggested by Singh and Chaudhary (1985)

$$\text{Average intra- cluster } D^2 = \frac{\sum D^2_{ij}}{n_i \times n_j}$$

Where,

$\sum D^2_{ij}$ = Sum of distances between all possible combinations of the populations in cluter I and j

n_i = Number of populations in cluster i

n_j = Number of populations in cluster j

CHAPTER IV

RESULTS AND DISCUSSION

Genetic variability among traits is important for breeding and in selecting desirable types. Heritability of a trait is important in determining its response to selection. Character association derived by correlation coefficient, forms the basis for selecting desirable plant, aiding in evaluation of relative influence of various component characters on yield. Path coefficient analysis discerns correlation into direct and indirect effects. Diversity is the function of parent selection and also heterosis. The availability of transgressive segregants in a breeding programme depends upon the divergence of parents. Thus, the accurate information on the nature and degree of diversity of the parents is the prerequisite of an effective breeding programme. The data on plant height , total tillers per plant, effective tillers per plant, days to 50 percent flowering, panicle length, filled grains per panicle, unfilled grains per panicle, days to maturity, thousand grains weight, yield per plant were recorded. Genetic diversity was analyzed using GENSTAT software programme.

4.1 Genetic parameters

The analysis of variance indicated the existence of highly significant variability for all the characters studied. The mean sum of square, mean, range, variance components, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in Table 2 and Table 4.

4.1.1 Plant height (cm)

The grand mean of plant height recorded was 102.40 cm. It was ranged from 88 cm to 116.44 cm (Table 2). The maximum plant height (116.44 cm) was recorded by G1 and the lowest (61.00cm) was recorded by G3 (Table 3). The PCV and GCV were 7.98 and 7.27 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character showed high heritability (83.17) coupled with low genetic advance in percent of mean (13.66) which indicated non additive gene action for expression of this character.

4.1.2 Total tillers per plant

The grand mean of total tillers per plant recorded was 20.32. It was ranged from 12.78 to 30.56 (Table 2). The maximum total tillers per plant (30.56) was recorded by the G30 and the lowest total tillers per plant (12.78) was recorded by G27 (Table 3). The PCV and GCV were 22.96 and 19.39 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character The character showed high heritability (71.3) with high genetic advance in percent of mean (33.71) which indicated the governance of additive gene action for expression of this character. Therefore selection could be effective through this character.

4.1.3 Effective tillers per plant

The grand mean of effective tillers per plant recorded was 18.88. It was ranged from 11.11 to 28.00 (Table 2). The maximum effective tillers per plant (28.00) were recorded by the G30 and the lowest (11.11) were recorded by G3 (Table 3). The PCV and GCV were 23.86 and 20.27 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character also showed high heritability (72.15) with high genetic advance in percent of mean (35.49) which indicated the governance of additive gene action for expression of this character. Therefore selection could be effective through 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.

4.1.4 Days to 50% flowering

The grand mean of days to 50% flowering recorded was 101.48. It was ranged from 92.00 to 108.00 (Table 2). The maximum days to 50% flowering (108.00) was recorded by the G35 and the lowest (92.00) was in G41 (Table 3). The PCV and GCV were 3.72 and 3.61 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character showed high heritability (93.64) coupled with low genetic advance in percent of mean (7.19) which indicated non additive gene action for expression of the character.

Table 2. Estimation of genetic parameters in ten characters of 42 genotypes in rice

Parameters	Range	Mean	MS	CV (%)	σ^2 p	σ^2g	σ^2 e
PH	88.00-116.44	102.40	177.70**	3.27	66.72	55.49	11.23
TTP	12.78-30.56	20.32	52.80**	12.30	21.77	15.52	6.25
ETP	11.11-28.00	18.88	49.56**	12.59	20.29	14.64	5.65
DFF	92.00-108.00	101.48	41.09**	0.94	14.31	13.4	0.91
PL	22.08-30.39	25.90	12.20**	4.90	5.14	3.53	1.61
FG	87.67-208.89	148.28	1915.94**	11.33	826.67	544.64	282.03
UFG	7.89-45.78	19.35	166.42**	22.00	67.57	49.43	18.14
DM	126.00-138.00	133.28	34.36**	0.74	12.11	11.13	0.98
TGW	20.36-30.45	24.32	17.77**	6.10	7.4	5.19	2.21
YPP	13.83-52.61	38.25	279.45**	15.41	116.32	81.57	34.75

PH = Plant height (cm), TTP = Total tillers per plant, ETP = Effective tillers per plant, DFF = Days to 50% flowering, PL = Panicle length (cm), FG = Filled grains per panicle, UFG = Unfilled grains per panicle, DM = Days to maturity, TGW = Thousand grain Weight (g), YPP = Yield per plant (g), MS = mean square, CV (%) = Coefficient of variation, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance

Table 4. Estimation of genetic parameters in ten characters of 42 genotypes in rice

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
PH	7.98	7.27	3.27	83.17	13.99	13.67
TTP	22.96	19.39	12.3	71.3	6.85	33.72
ETP	23.86	20.27	12.59	72.15	6.7	35.49
DFF	3.73	3.61	0.94	93.64	7.3	7.19
PL	8.75	7.25	4.9	68.68	3.21	12.4
FG	19.39	15.74	11.33	65.88	39.02	26.31
UFG	42.48	36.33	22.01	73.15	12.39	64.03
DM	2.61	2.5	0.74	91.91	6.59	4.94
TGW	11.19	9.37	6.11	70.14	3.93	16.16
YPP	28.2	23.61	15.41	70.13	15.58	40.73

PH = Plant height (cm), TTP = Total tillers per plant, ETP = Effective tillers per plant, DFF = Days to 50% flowering, PL = Panicle length (cm), FG = Filled grains per panicle, UFG = Unfilled grains per panicle, DM = Days to maturity, TGW = Thousand grain weight (g), YPP = Yield per plant, PCV = Phenotypic co-efficient of variation, GCV = Genotypic co-efficient of variation, ECV = Environmental co-efficient of variation

4.1.5 Panicle length

The grand mean of panicle length recorded was 25.90 cm. It was ranged from 22.08 cm to 30.39 cm (Table 2). The maximum panicle length (30.39 cm) was recorded by the G13 and the lowest was recorded by G29 (22.08 cm) (Table 3). The PCV and GCV were 8.75 and 7.25 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character also showed high heritability (68.68) with low genetic advance in percent of mean (12.4) which indicated non additive gene action for expression of this character.

4.1.6 Filled grains per panicle

The grand mean of filled grains per panicle recorded was 148.28. It was ranged from 87.67 to 208.89 (Table 2). The maximum filled grains per panicle (208.89) was recorded by the G31 and the lowest (87.67) was recorded by G14 (Table 3). The PCV and GCV were 19.39 and 15.74 percent respectively (Table 4). There was lower difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character also showed high heritability (65.88) with high genetic advance in percent of mean (26.31) which indicated the governance of additive gene action. Therefore selection could be effective through this character. Prasad *et al.* (2001), Singh *et al.* (2011) and Tuwar *et al.* (2013) also found high heritability coupled with high genetic advance as percent of mean for the trait filled grains per panicle.

4.1.7 Unfilled grains per panicle

The grand mean of unfilled grains per panicle recorded was 19.35. It was ranged from 7.89 to 45.78 (Table 2). The maximum unfilled grains per panicle (45.78) was recorded by the G20 and the lowest (7.89) was recorded by G36 (Table 3). The PCV and GCV were 42.48 and 36.33 percent respectively (Table 4). There was considerable difference between the phenotypic and genotypic co-efficient of variation indicating significant environmental influence in the expression of this character. The character also showed high heritability (73.15) with high genetic advance in percent of mean (64.03) which indicated that additive genes are said to control the traits and also highlights the usefulness of plant selection based on phenotypic performance.

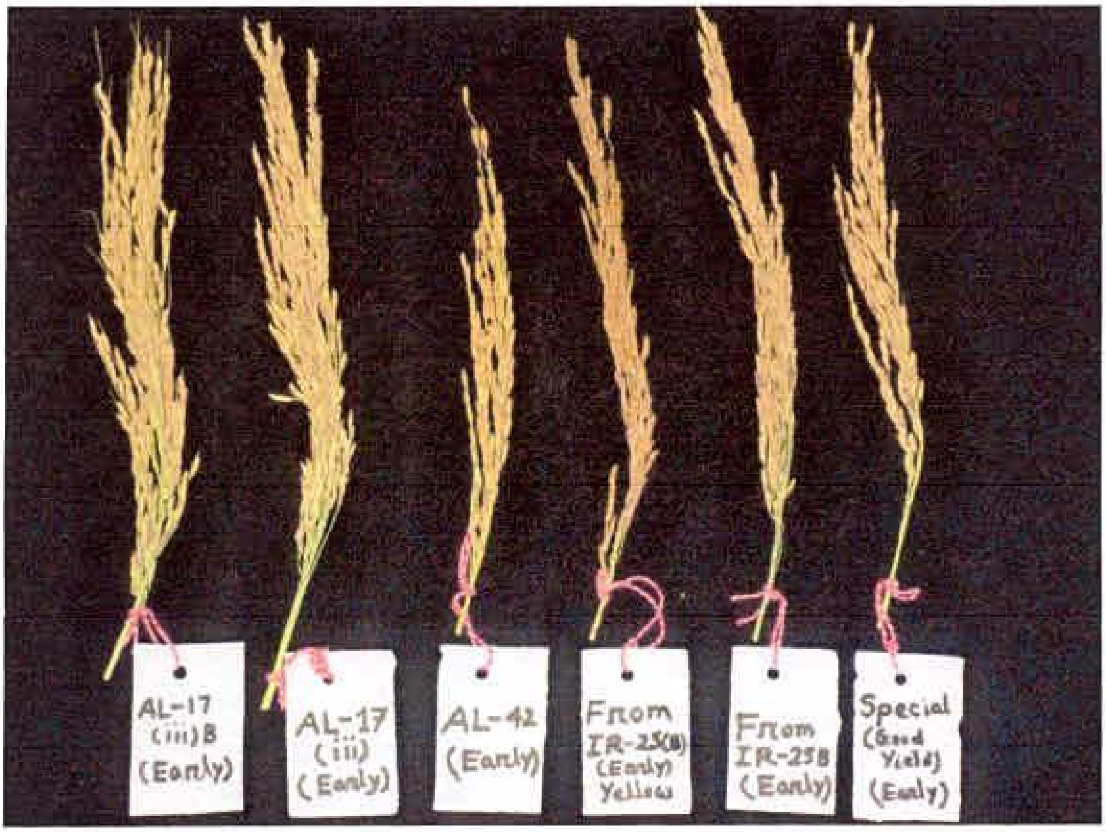

Plate 3. Some panicle appearance of different rice genotypes

Plate 4. Some grain appearance of different rice genotype

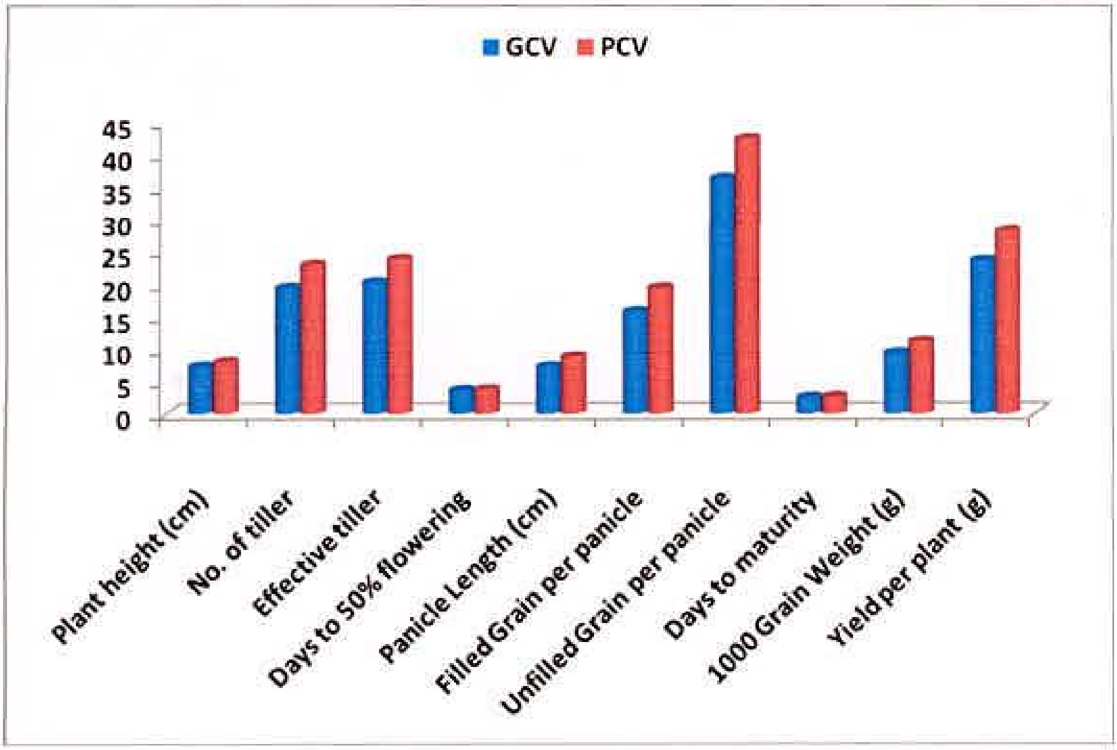

Figure 1. Genotypic and phenotypic variability in rice genotypes

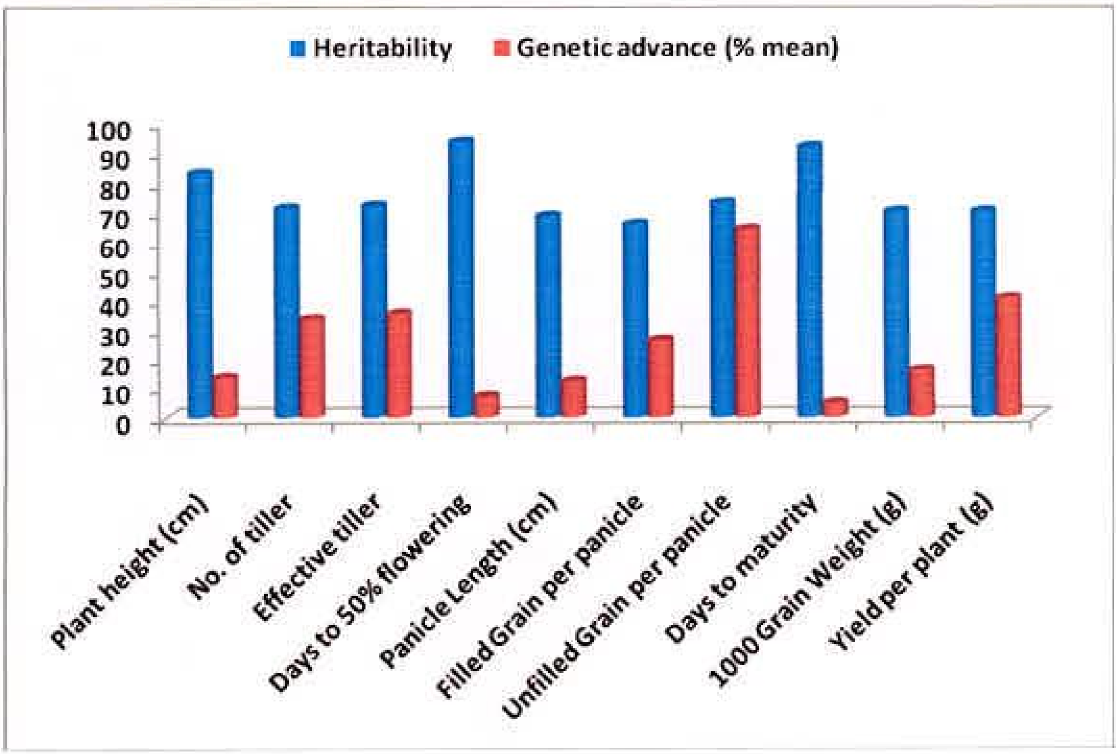

Figure 2. Heritability and genetic advance over mean in rice genotypes

4.1.8 Days to maturity

The grand mean of days to maturity recorded was 133.38. It was ranged from 126.00 to 138.00 (Table 2). The maximum days to maturity (138.00) was recorded by G37 and the lowest (126) was in G6 (Table 3). The PCV and GCV were 2.61 and 2.50 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character also showed high heritability (91.91) with low genetic advance in percent of mean (4.94) which indicated the non additive gene action for expression of the character.

4.1.9 Thousand grain weight

The grand mean of thousand grain weight recorded was 24.32. It was ranged from 20.36 to 30.45 (Table 2). The maximum thousand grain weight (30.45) was recorded by the G22 and the lowest thousand grain weight (20.36) was recorded by G29 (Table 3). The PCV and GCV were 11.19 and 9.37 percent respectively (Table 4). There was little difference between the phenotypic and genotypic co-efficient of variation indicating little environmental influence in the expression of this character. The character showed high heritability (70.14) with low genetic advance in percent of mean (16.16) which is indicative of non-additive (dominant/epistatic) control for expression of this character.

4.1.10 Yield per plant

The grand mean of yield per plant recorded was 38.25 g. It was ranged from 13.83 g to 52.61 g (Table 2). The maximum yield per plant (52.61 g) was recorded by the G30 and the lowest (13.83 g) was recorded by G24 (Table 3). The PCV and GCV were 28.20 and 23.61 percent respectively (Table 4). There was lower difference between the phenotypic and genotypic co-efficient of variation indicating lower environmental influence in the expression of this character. The character also showed high heritability (70.13) with high genetic advance in percent of mean (40.73) which indicated the governance of additive gene action for expression of this character. Therefore selection could be effective through the character.

4.2 Correlation study

The correlation co-efficient between yield and yield contributing characters in rice are presented in Table 5. Correlation analysis among yield and its contributing character revealed that the genotypic correlation in most cases were higher than their phenotypic correlation coefficients indicating the association is largely due to genetic reason. In some cases phenotypic correlation coefficients were higher than genotypic correlation indicating suppressing effect of the environment which modified the expression of the characters at phenotypic level.

Plant height was positively and significantly correlated with panicle length at both genotypic and phenotypic level. It was positively and significantly correlated with filled grains per panicle at the genotypic level only. It was negatively and significantly correlated with total tillers per plant and effective tillers/plant at the genotypic level. Days to 50% flowering, unfilled grains/panicle, 1000 grain weight and yield per plant was positively and non-significantly correlated with plant height at both genotypic and phenotypic level.

Total tillers per plant showed positive and significant correlation with effective tillers/plant and yield per plant at both genotypic and phenotypic level. This indicates relative utility of total tillers per plant for selection with respect to yield per plant. Total tillers per plant showed negative and significant association with panicle length and thousand grains weight at genotypic level only. Filled grains/panicle, unfilled grains per panicle, days to 50% flowering and days to maturity was positively and non significantly correlated with total tillers per plant at both genotypic and phenotypic level. Total tillers per plant showed non-significant negative association with filled grains per panicle at both genotypic and phenotypic level. Agahi *et al*. (2007), Selvaraj *et al.* (2011) and Ganapati *et al.* (2014) also reported positive and significant correlation of yield with total tillers/plant at both genotypic and phenotypic level.

Table 5. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of rice

Parameters		TTP	ETP	DFF	PL	FG	UFG	DM	TGW	YPP
PH	rg	-0.357*	-0.316*	0.067	0.373*	0.309*	0.068	-0.018	0.131	0.111
	rp	-0.215	-0.198	0.045	0.359*	0.285	0.101	-0.047	0.123	0.167
TTP	rg		0.501**	0.257	-0.312*	-0.119	0.009	0.271	-0.313*	0.416**
	rp		0.499**	0.204	-0.177	-0.097	-0.013	0.223	-0.259	0.458**
ETP	rg			0.449**	-0.261	-0.030	-0.026	0.276	-0.265	0.461**
	rp			0.376*	-0.142	-0.034	-0.049	0.236	-0.230	0.499**
DFF	rg				-0.111	-0.161	0.048	0.277	-0.162	0.262
	rp				-0.098	-0.141	0.019	0.261	-0.138	0.208
PL	rg					0.483**	0.222	-0.019	0.309*	-0.025
	rp					0.419**	0.247	-0.033	0.218	0.078
FG	rg						0.385**	0.017	-0.012	0.205
	rp						0.318*	0.013	-0.006	0.173
UFG	rg							0.050	-0.026	-0.340*
	rp							0.031	-0.015	-0.309*
DM	rg								0.085	0.360*
	rp								0.066	0.281
TGW	rg									0.187
	rp									0.137

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

PH = Plant height (cm), TTP = Total tillers per plant, ET = Effective tillers per plant, DF = Days to 50% flowering, PL = Panicle length (cm), FG = Filled grains per panicle, UFG = Unfilled grains per panicle, DM = Days to maturity, TGW = Thousand grain weight (g), YPP = Yield per plant (g)

Effective tillers per plant showed positive and significant correlation with days to 50% flowering and yield per plant at both genotypic and phenotypic level. This indicates relative utility of effective tillers per plant for selection with respect to yield per plant. It showed positive and non significant association with days to maturity at both genotypic and phenotypic levels. Effective tillers/plant was negatively and non significantly correlated with panicle length, filled grains/panicle, unfilled grains/panicle and thousand grain weight at both genotypic and phenotypic level. Agahi *et al.*, (2007) and Babu *et al.* (2012) also found positive and significant correlation of yield with effective tillers/plant at both genotypic and phenotypic level and Selvaraj *et al.* (2011) and Satheeshkumar *et al.* (2012) found positive and significant correlation of yield with effective tillers/plant at genotypic level only.

Days to 50% flowering showed positive and non significant correlation with unfilled grain, days to maturity and yield per plant at both genotypic and phenotypic level. It was negatively and non-significantly associated with panicle length, filled grains per panicle and thousand grains weight at both genotypic and phenotypic level.

Panicle length showed significant and positive association with filled grains per panicle at both genotypic and phenotypic level whereas it was positively and significantly associated with thousand grains weight at genotypic level only. It showed non-significant positive association with unfilled grains per panicle at both genotypic and phenotypic level. It showed non significant negative association with yield per plant at genotypic level whereas non significantly and positively correlated with yield per plant at phenotypic level.

Filled grains per panicle showed significant positive association with unfilled grains per panicle at both genotypic and phenotypic level. It showed positive and non-significant association with days to maturity and yield per plant at both genotypic and phenotypic level. It was negatively and non-significantly correlated with thousand grain weight at both genotypic and phenotypic level.

Unfilled grains per panicle showed negative and significant association with yield per plant at both genotypic and phenotypic level. It showed positive and non-significant association with days to maturity and days to 50% flowering at both genotypic and phenotypic level whereas it showed negative and non-significant association with 1000 grain weight at both genotypic and phenotypic level.

Days to maturity showed positive and significant association with yield per plant at genotypic level only. This indicates relative utility of days to maturity for selection with respect to yield per plant. It showed positive and non-significant association with 1000 grains weight at both genotypic and phenotypic level. Agahi *et al.*, (2007) reported positive and significant correlation of days to maturity with yield at both genotypic and phenotypic level.

Thousand grain weight showed non-significant positive association with yield per plant at both genotypic and phenotypic level.

Pleiotropy or linkage relations among genes controlling the traits are some of the reasons of genetic trait correlations. Directions and rates of short term evolution are effected by genetic trait correlations (Falconer, 1989; Roff, 1997; Lynch & Walsh, 1998). Much of dissimilarity phenotypic and genetic correlation estimates seems to be due to imprecise estimates of genetic correlations. In many situations, phenotypic correlations are likely to be fair estimates of their genetic counterparts (Cheverud, 1988). Genetic correlations between morphological traits are more often positive than correlation between other traits (Roff, 1996 & 1997). Competition between processes for a resource may result in negative correlations (Atchley, 1987).

4.3 Path coefficient analysis

Plant height employed positive direct effect on yield/plant (0.243) as well as positive indirect effect via filled grains per panicle, days to 50% flowering and thousand grain weight. It also showed negative indirect effect of total tillers per plant, effective tillers per plant, panicle length, unfilled grains per panicle and days to maturity. Kole *et al.* (2008), Yadav *et al.* (2010) and Selvaraj *et al.* (2011) also found positive direct effect of plant height on yield per plant. But Hairmansis *et al.* (2011) found negative direct effect of plant height on yield per plant.

Total tillers per plant employed positive direct effect on yield/plant (0.440) and exhibited significant positive correlation with yield per plant at both genotypic and phenotypic level, indicating true relationship between these traits. This may indicate that the direct selection for total tillers per plant would likely be effective in increasing yield per plant. Total tillers per plant employed positive indirect effect via panicle length, effective tillers per plant, days to maturity and days to 50% flowering. But it showed negative indirect effect of plant height, filled grains per panicle and unfilled grains per panicle and thousand grains weight. Karad *et al.* (2008), Yadav *et al.* (2010), Selvaraj *et al.* (2011) and Ganapati *et al.* (2014) also found positive direct effect of total tillers/plant on yield/plant.

Effective tillers per plant employed positive direct effect on yield/plant (0.318) and exhibited significant positive correlation with yield per plant at both genotypic and phenotypic level, indicating true relationship between these traits. This might indicate that the direct selection for effective tillers per plant would likely be effective in increasing yield per plant. Effective tillers per plant employed indirect positive effect via total tillers per plant, panicle length, unfilled grains per panicle, days to maturity and days to 50% flowering. On the other hand it showed negative indirect effect of plant height, filled grains per panicle and thousand grains weight. Satheeshkumar *et al.* (2012) also found positive direct effect of effective tillers per plant on yield per plant. But Agahi *et al.* (2007), Hairmansis *et al.* (2011) and Selveraj *et al.* (2011) found negative direct effect of effective tillers per plant on yield per plant.

Days to 50% flowering employed positive direct effect on yield/plant (0.113) as well as positive indirect effect via plant height, total tillers per plant, effective tillers/plant, panicle length and days to maturity. It also showed negative indirect effect of filled grains per panicle, unfilled grains per panicle and thousand grains weight. Selvaraj *et al.* (2011) and Rangare *et al.* (2012) also reported positive direct effecs of days to 50% flowering on yield/plant. But Abarshahr *et al.* (2011) also reported negative direct effect of days to 50% flowering on yield/plant.

Panicle length employed negative direct effect on yield/plant (-0.122) as well as indirect positive effect via total tillers per plant, unfilled grains per panicle, effective tillers per plant, days to 50% flowering and days to maturity. It also showed positive indirect effect of plant height, filled grains per panicle and thousand grains weight. But Yadav *et al.* (2010) and Selvaraj *et al.* (2011) found direct positive effect of panicle length on yield per plant.

Table 6. Path coefficient analysis showing direct and indirect effects of different characters on yield of rice genotypes

Characters	Direct (Bold) and Indirect effect									Genotypic correlation with yield
	PH	TTP	ETP	DF	PL	FG	UFG	DM	TGW	
PH	**0.243**	-0.157	-0.100	0.008	-0.046	0.144	-0.034	-0.002	0.055	0.111
TTP	-0.087	**0.440**	0.159	0.029	0.038	-0.056	-0.005	0.029	-0.131	0.416**
ETP	-0.077	0.220	**0.318**	0.051	0.032	-0.014	0.013	0.029	-0.111	0.461**
DFF	0.016	0.113	0.143	**0.113**	0.014	-0.075	-0.024	0.029	-0.067	0.262
PL	0.091	-0.137	-0.083	-0.013	**-0.122**	0.225	-0.112	-0.002	0.129	-0.025
FG	0.075	-0.053	-0.009	-0.018	-0.059	**0.466**	-0.195	0.002	-0.005	0.205
UFG	0.016	0.004	-0.008	0.005	-0.027	0.180	**-0.505**	0.005	-0.011	-0.340*
DM	-0.005	0.119	0.088	0.031	0.002	0.008	-0.025	**0.106**	0.035	0.360*
TGW	0.032	-0.138	-0.084	-0.018	-0.038	-0.005	0.013	0.009	**0.417**	0.187

** = Significant at 1% and * = Significant at 5%

Residual effect: 0.47

PH = Plant height (cm), TTP = Total tillers per plant, ETP= Effective tillers, DFF= Days to 50% flowering, PL= Panicle length (cm), FG=Filled grains per panicle, UFG = Unfilled grains per panicle, DM = Days to maturity, TGW = Thousand grain weight (g), YPP = Yield per plant (g)

Filled grains per panicle employed positive direct effect on yield/plant (0.466) as well as indirect positive effect via plant height and days to maturity. It also showed negative indirect effect of effective tillers per plant, days to 50% flowering, total tillers per plant, panicle length, unfilled grains per panicle and thousand grain weight. Abarshahar *et al.* (2011), Hairmanis *et al.* (2011), Selvaraj *et al.* (2011), Satheeshkumar *et al.* (2012) also found positive direct effect of filled grains per panicle on yield/plant.

Unfilled grains/panicle employed negative direct effect on yield/plant (-0.505) as well as indirect negative effect via, panicle length, effective tillers per plant and thousand grain weight. It also showed positive indirect effect of plant height, total tillers per plant, days to 50% flowering, filled grains per panicle and days to maturity.

Days to maturity employed direct positive effect on yield/plant (0.106) and exhibited significant positive correlation with yield per plant at genotypic level only, indicating true relationship between these traits. This may indicate that the direct selection for days to maturity would likely be effective in increasing yield per plant. Days to maturity employed indirect positive effect via total tillers/plant, panicle length, filled grains per panicle, effective tillers per plant, days to 50% flowering and thousand grain weight. It also showed negative indirect effect of plant height and unfilled grains per panicle.

Thousand grain weight employed direct positive effect on yield/plant (0.417) but exhibited non significant positive association with yield per plant at both genotypic and phenotypic level. It may be due to higher indirect negative effect of total tillers per plant (-0.138) and effective tillers per plant (-0.084). Thousand grain weight showed indirect positive effect via plant height, unfilled grains per panicle and days to maturity. It also showed negative indirect effect of days to 50% flowering, total tillers per plant, effective tillers/plant, panicle length and filled grains per panicle. Agahi *et al.* (2007) also found positive direct effect of thousand grains weight on yield per plant.

4.4 Genetic Diversity

4.4.1 Principal component analysis

The principal Components analysis yielded eigen values of each principal component axes of coordination of genotypes in which the first axes totally accounting for the variation among the genotypes, whereas four of these eigen values above unity accounted for 74.19%. The first three principal axes accounted for 62.50 % of the total variation among the 10 characters describing in 42 rice genotypes (Table 7). Based on principal component axis I and II, a two dimensional chart (Z1 –Z2) of the genotypes are presented in Figure 3. The scatter diagram (Figure 3) represented that apparently there were mainly five clusters and the genotypes were distantly located from each other.

4.4.2 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional (Z_1-Z_2) scatter diagram was constructed, using component score 1 as X-axis and component score 2 as Y-axis, which is presented in figure 5. The positions of the genotypes in the scatter diagram were random, which indicated the considerable diversity among the genotypes included in the cluster. Some distantly located genotypes of different clusters were the genotypes number G31, G20, G25, G15, G37, G40, G36, G30, G28, G1, G32, G41, G12, G39, G33, G17.

Table 7. Eigen values and yield percent contribution of 10 characters of 42 rice genotypes

Characters	**Eigen values**	**Percent variation**	**Cumulative % of Percent variation**
Plant height (cm)	3.053	30.53	30.53
Total tillers per plant	1.900	19.00	49.53
Effective tillers per plant	1.297	12.97	62.50
Days to 50% flowering	1.169	11.69	74.19
Panicle Length (cm)	0.895	8.95	83.14
Filled Grains per panicle	0.645	6.45	89.59
Unfilled Grains per panicle	0.506	5.06	94.65
Days to maturity	0.291	2.91	97.56
1000 grain weight (g)	0.227	2.27	99.83
Yield per plant (g)	0.016	0.17	100.00

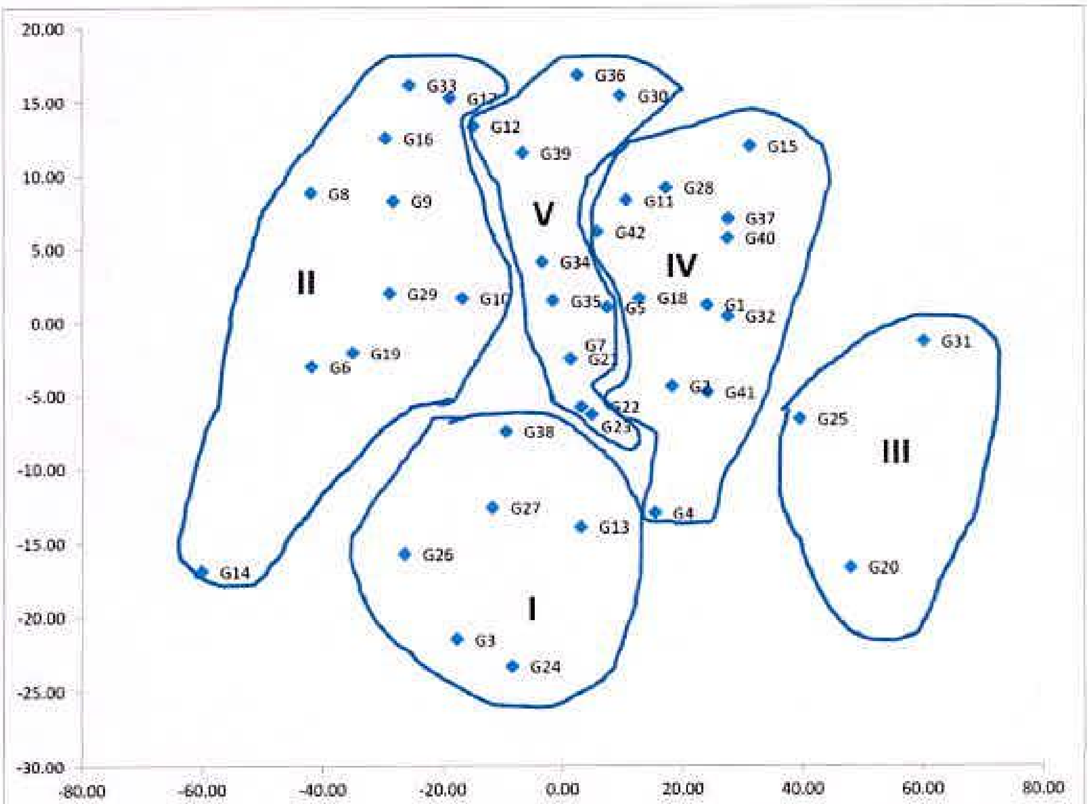

Figure 3. Scatter diagram of forty two rice genotypes based on their principal component scores

4.4.3 Non-hierarchical clustering

By using these inter-genotypic distances intra-cluster genotypic distances were calculated (Table 10) as suggested by Singh and Chowdhary (1985). On the basis of D^2 values, the 42 genotypes were grouped into five highly divergent clusters (Table 8).The clusters divergence was proved by the high inter- cluster and low intra clusters D^2 values. Cluster IV was the largest and consisted fourteen genotypes followed by cluster II with ten genotypes, clusters V, I and III had 9, 6 and 3 genotypes respectively. The grouping pattern did not show any relationship between genetic divergence and geographical diversity which has been a point of debate in the past. A perusal of the Table 8 clearly showed the genotypes usually did not cluster according to geographical distributions. One of the possible reasons may be the fact that it is very difficult to establish the actual location of origin of a genotype. The free and frequent exchange of genetic material among the crop improvement programmes in the country makes it difficult to maintain the real identify of the genotypes. Moreover, breeding progenies incorporate genes from varied sources, thus losing the basic geographical identity of the genotype. The absence of relationship between genetic diversity and geographical distance indicates that forces others than geographical origin, such as exchange of genetic stocks, genetic drift, spontaneous variation, natural and artificial selection are responsible for genetic diversity, It may also be possible that causes for clustering pattern were much influenced by environment and (genotype x environment) interaction resulting in differential gene expression. Another possibility may be that estimates might not have been sufficient to account for the variability caused some other traits of physiological or biochemical nature which might have important in depicting the total genetic diversity in the population.

The cluster mean of 42 genotypes (Table 9) showed that the mean value of clusters varied in magnitude for all the ten characters. Genotypes in cluster I showed maximum performance for panicle length (27.14). Cluster II showed maximum performance for days to maturity (134.13). Cluster III recorded highest mean performance for filled grain per panicle (197.11) and unfilled grains per panicle (31.70). Cluster IV showed maximum performance for plant height (108.15) and yield per plant (41.99). Cluster V showed maximum performance for total tillers per plant (22.90), effective tillers per plant (21.83), days to 50% flowering (103.11) and thousand grain weight (24.93).

Table 8. Distribution of 42 rice genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	3, 13, 24, 26, 27, 38	6	AL-42, P-5B (i), AL-33(ii), AL-42(ii), AL-44(i), Special from S-2
II	6, 8, 9, 10, 14, 16, 17, 19, 29, 33	10	Special (Early), AL-35, Special-130, IR-25B (Dwarf), Hira, Aloron, IR-25B (Tall), Special from AL-33, AL-47, P-5B (ii)
III	20, 25, 31	3	Special from AL-29, AL-36, PP-4B(i)
IV	1, 2, 4, 5, 11, 15, 18, 22, 28, 32, 37, 40, 41, 42	14	AL-17(iii)B, AL-17(iii), From IR-25B (Yellow), From IR-25B, AL-36 (C), AL-17(iii) (Tall), AL-36(iii), S-2, AL-17(ii) A, Special from-129, Special from-17(iv), AL-44 (i), AL-17, AL-104
V	7, 12, 21, 23, 30, 34, 35, 36, 39	9	Richer, Special from AL-36(D), S-1, S-5, PP-48, AL-36, Special stigma color, IR-25B, Special from AL-33

Table 9. Cluster mean values of 10 different characters of 42 genotypes

Characters	I	II	III	IV	V
Plant height (cm)	99.67	100.37	102.37	108.15	97.56
Total tillers per plant	16.46	22.12	19.52	19.20	22.90
Effective tillers per plant	15.07	20.10	18.74	17.77	21.83
Days to 50% flowering	98.50	102.57	100.67	101.12	103.11
Panicle length (cm)	27.14	24.42	27.03	26.49	25.42
Filled grains per panicle	137.57	115.76	197.11	165.63	148.28
Unfilled grains per panicle	20.73	16.41	31.70	21.31	14.54
Days to maturity	130.56	134.13	134.11	133.19	134.00
Thousand grain weight (g)	24.24	23.71	23.62	24.55	24.93
Yield per plant (g)	23.02	40.13	35.58	41.99	41.38

4.4.4 Canonical Variate Analysis (CVA)

Canonical Variate Analysis was performed to compute the inter-cluster Mahalanobis's values. Statistical distances represent the index of genetic diversity among the clusters. The divergence within the cluster (intra- cluster distance) indicates the divergence among falling in the same cluster. On the other hand, inter cluster divergence suggest the distance (divergence) between the genotypes of different clusters. The intra and inter clusters D^2 values among 42 genotypes presented in Table 10 revealed that cluster IV showed minimum intra cluster D^2 value (0.01) distance followed by cluster II (0.105), whereas, maximum intra cluster D^2 value (0.81) was shown by cluster IIII followed by cluster I (0.10) indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. Minimum inter cluster D^2 value was observed between the clusters IV and V (3.82) indicated close relationship among the genotypes included in these clusters. Maximum inter – clusters D^2 value was observed between the clusters II and III (10.94) indicated that the genotypes belongings to these groups were genetically most divergent and the genotypes included in these clusters can be used as a parent in hybridization programme to get higher heterotic hybrids from the segregant population (Mehta and Asati, 2008). Several authors also reported profound diversity in the germplasm of rice by assessing genetic divergence on the basis of quantitative traits following Mahalanobis D^2 statistics (Ovung *et al.* 2012, Thomas *et al* 2012 and Chakrovorty *et al.* 2013). Average inter and intra- cluster distance revealed that, in general inter- cluster distance were much higher than those of intra- cluster distances, suggesting homogenous and heterogeneous nature of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Ovung *et al.* (2012).

Results obtained from different multivariate techniques from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one.

Table 10. Intra (Bold) and inter cluster distances (D^2) for 42 rice genotypes

Cluster	I	II	III	IV	V
I	**0.10**	4.66	8.54	5.47	4.15
II		**0.03**	10.94	6.61	4.56
III			**0.81**	4.80	7.37
IV				**0.01**	3.82
V					**0.04**

The clustering pattern of the genotypes revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. This indicated that geographic diversity was not related to genetic diversity that might be due to continuous exchange of genetic materials among the countries of the world. Same results have been reported by Murty and Anand (1966); Anand and Rawat (1984) in brown mustard; Patel *et al.* (1989) in sunflower; Verma (1970) in groundnut and soybean. It had been observed that geographic diversity was not always related to genetic diversity and therefore, it was not adequate as an index of genetic diversity. Murty and Arunchalam (1966) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance. Furthermore, there was a free exchange of seed material among different region, as a consequence, the characters constellation that might be associated with particular region in nature, lose their individually under human interference, and however, in some cases effect of geographic origin influenced clustering that was why geographic distribution was not the sole criterion of genetic diversity.

The free clustering of the genotypes suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favor constancy of the associated characters would thus indiscriminate clustering. This would be suggested that it was not necessary to choose diverse parents for diverse geographic regions for hybridization.

4.4.5 Contribution of characters towards divergence of the cultivars

The character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al.*, 1991). The PCA revealed that in vector I (Z1) the important characters responsible for genetic divergence in the major axis of differentiation were plant height, panicle length, filled grains per panicle, unfilled grains per panicle, days to maturity and yield per plant (Table 11). In vector II (Z2) that was the second axis of differentiation, plant height, total tillers per plant, effective tillers per plant, days to 50% flowering, days to maturity and yield per plant were important. The role of plant height, days to maturity and yield per plant in both the vectors were positive across two axes indicating the important components of genetic divergence in those materials.

Table 11. Relative contributions of the ten characters of 42 rice genotypes to the total divergence

Characters	Vector-1	Vector-2
Plant height (cm)	0.09867	0.02898
Total tillers per plant	-0.01777	0.20832
Effective tillers per plant	-0.00486	0.21611
Days to 50% flowering	-0.02063	0.11111
Panicle length (cm)	0.03660	-0.02108
Filled grains per panicle	0.98511	-0.02257
Unfilled grains per panicle	0.10797	-0.37279
Days to maturity	0.00299	0.10897
Thousand grain weight (g)	-0.00053	-0.02131
Yield per plant (g)	0.07778	0.86282

4.4.6 Comparison of different multivariate techniques

The clustering pattern of D^2 analysis through non-hierarchical clustering had taken care of simultaneous variation in all the characters under study. However, the distribution of genotypes in different clusters of the D^2 analysis had followed more or less similar trend of the Z1 and Z2 vector of the principal component analysis. The $D^2$and principal component analysis was found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the principal component analysis provided the information regarding the contribution of characters towards divergence of rice.

4.4.7 Selection of cultivars for future hybridization

Genotypically distant parents were able to produce higher heterosis (Falconer, 1960; Moll *et al.*, 1962; Ramanujam *et al.*, 1974; Chauhan and Singh, 1982; Arunachalam *et al.*, 1981; Ghaderi *et al.*, 1984; Mian and Bhal, 1989). Beside this, Arunachalam *et al.* (1981) reported in groundnut that the higher heterosis for yield and its components could be obtained from the crosses between the intermediate divergent parents than extreme ones. Mian and Bahl (1989) also reported the same in chick pea that medium divergent genotypes showed higher heterosis in crosses for different yield contributing characters. Srivastava and Arunachalam (1977) reported in triticale that very high or very low parental divergent failed result in heterosis.

Considering this idea and other agronomic performances, the genotypes Special from AL-29, AL-36, PP-4B(i) from cluster III; AL-17(iii)B, AL-17(iii), AL-17(ii)A, Special from-129, Special from 17(iv), AL-44(i) and AL-17 from cluster IV; Special from AL-36(D), PP-48, IR-25B, Special from AL-33 from cluster V; IR-25B (Tall) and P-5B(ii) from cluster II might be considered better parents for efficient hybridization programme.

CHAPTER V

SUMMARY AND CONCLUSION

The present study was conducted in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during July-December, 2013. This experiment involved forty two genotypes of rice and was laid out in a Randomized Complete Block Design (RCBD) with three replications.

The forty two (42) genotypes were used to determine variation, heritability, genetic advance and genetic advance in percentage of mean, genetic diversity, character associations and direct and indirect effect of different traits on yield. All the genotypes varied significantly for all the studied characters indicated the presence of considerably variations among the genotypes. The PCV values were slightly higher than the respective GCV values for all the characters except unfilled grains per panicle indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of the traits. High heritability with high genetic advance as percentage of mean was found for the characters total tillers per plant, effective tillers per plant, filled grains per panicle, unfilled grains per panicle and yield per plant which indicated the governance of additive gene action for the expression of these characters. Therefore selection could be effective for these characters. High heritability coupled with low genetic advance as percentage of mean was found for the characters plant height, days to 50% flowering, panicle length, days to maturity and thousand grain weight. It revealed that there is non additive gene action for expression of these characters. Correlation analysis revealed that significant and positive correlation of total tillers per plant and effective tillers per plant with yield per plant at both genotypic and phenotypic level whereas significant and positive correlation of days to maturity with yield per plant at genotypic level only. This indicates the relative utility of these traits for selection with respect to yield per plant. On the other hand it revealed significant and negative association of unfilled grains per panicle with yield per plant at both genotypic and phenotypic level. From the result of path analysis it was evident that direct positive effect was contributed by filled grains per panicle, total tillers per plant, thousand grain weight, effective tillers per plant, plant height, days to 50% flowering and days to maturity. From the correlation and path analysis it was revealed that total tillers per plant, effective tillers per plant and days to maturity showed significantly positive genotypic correlation with yield as well as employed positive direct effect on yield per plant and this suggested that the selection for total tillers per plant, effective tillers per plant and days to maturity would likely the best parameter for improvement in yield per plant. Significant difference among the clusters was observed through multivariate analysis, clusters analysis and canonical variate analysis. As PCA, D^2 and clusters analysis the genotypes were grouped into five different clusters. Clusters IV had the maximum fourteen and cluster III had the minimum three genotypes. The highest inter-cluster distance was observed between II and III and the lowest was in between IV and V. The highest and lowest intra-cluster distance was observed in III and IV respectively. Genotypes included in cluster V were important for total tillers per plant, effective tillers per plant, days to 50% flowering and thousand grains weight whereas filled grains per panicle and unfilled grains per panicle were remarkable feature for cluster III. Plant height and yield per plant was remarkable feature for cluster IV. Genotypes in cluster I and cluster II showed maximum performance for panicle length and days to maturity respectively. Considering this idea and other agronomic performances, the genotypes Special from AL-29, AL-36, PP-4B(i), AL-17(iii)B, AL-17(iii), AL-17(ii)A, Special from-129, Special from 17(iv), AL-44(i), AL-17, Special from AL-36(D), PP-48, IR-25B, Special from AL-33, IR-25B (Tall), P-5B (ii) might be considered as better parents for future efficient hybridization programme.

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APPENDICES

Appendix I: Meteorological conditions of the experimental site during crop growing period (July, 2013 to December, 2013)

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm)	Sunshine (hr)
	Maximum	Minimum			
July, 2013	31.75	16.14	71.42	2.39	2.70
August, 2013	31.02	15.27	74.41	2.73	5.11
September, 2013	31.46	14.82	73.20	2.10	4.15
October, 2013	30.18	14.85	67.82	1.40	7.48
November, 2013	28.10	9.88	58.18	0.52	7.85
December, 2013	25.36	6.89	54.3	0.02	6.85

Source: SAU weather station, Sher-e-Bangla nagar, Dhaka-1205.

Appendix II: Analysis of variance of ten important characters in respect of forty two genotypes of rice

Source of variation	Degrees of freedom	Plant height	Total tillers per plant	Effective tillers per plant	Days to 50% flowering	Panicle length	Filled grains per panicle	Unfilled grains per panicle	Days to maturity	Thousand grains weight	Yield per plant
Replication	2	41.54	9.68	9.90	9.06	1.94	59.82	19.26	11.08	1.97	185.73
Genotypes	41	177.70**	52.80**	49.56**	41.09**	12.20**	1915.94**	166.42**	34.36**	17.77**	279.45**
Error	82	11.22	6.25	5.65	0.91	1.61	282.03	18.13	0.98	2.20	34.75
Co-efficient of variation		3.27	12.30	12.59	0.94	4.90	11.33	22.00	0.74	6.10	15.41

** Significant at 1% level of probability

Appendix III: Principal component score for forty two rice genotypes

Genotypes	Z_1	Z_2
1	27.56	0.41
2	18.30	-4.40
3	-17.58	-21.49
4	15.48	-12.99
5	7.51	1.03
6	-41.69	-2.99
7	1.40	-2.49
8	-41.86	8.85
9	-28.13	8.29
10	-16.55	1.66
11	10.63	8.34
12	-14.79	13.35
13	3.13	-13.97
14	-60.00	-16.87
15	31.26	12.00
16	-29.39	12.55
17	-18.67	15.29
18	12.89	1.65
19	-34.85	-2.07
20	47.97	-16.70
21	1.48	-2.48
22	4.96	-6.31
23	3.20	-5.82
24	-8.35	-23.34
25	39.64	-6.62
26	-26.24	-15.76
27	-11.60	-12.63
28	17.24	9.17
29	-28.65	2.02
30	9.68	15.43
31	60.32	-1.31
32	24.11	1.19
33	-25.43	16.16
34	-3.25	4.15
35	-1.48	1.51
36	2.60	16.84
37	27.55	7.08
38	-9.36	-7.46
39	-6.57	11.56
40	27.52	5.75
41	24.20	-4.79
42	5.79	6.20