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

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CERTIFICATE

This is to certify that thesis entitled, "**GENETIC DIVERSITY, CORRELATION AND PATH ANALYSIS IN RICE (Oryza sativa L.)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **SHYAMA PRASHAD CHAKMA**, Registration No. 05-1838 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2010
Place: Dhaka, Bangladesh

(Homayra Huq)
Assistant Professor
Supervisor

I dedicate this thesis to

His Holiness Most Venerable Sadhanananda Mahathero

Late Priyong Boda Chakma

and my beloved parents for their constant support and unconditional love.

I love you all dearly.

LIST OF ABREVIATIONS

Full Word	Abbreviation	Full Word	Abbreviation
Acre	A	Gross Domestic Product	GDP
Agro-ecological Zone	AEZ	Haploid Chromosome Number	n
Analysis of Variance	ANOVA	Harvest Index	HI
and others (*at elli*)	*et al.*	Hectare	ha
Bangladesh Agricultural Research Institute	BARI	High Yielding Variety	HYV
Bangladesh Bureau of Statistics	BBS	Journal	J
Bangladesh Rice Research Institute	BRRI	Kilogram	kg
Centimetre	cm	Mean sum of Square	MS
Chittagong Hill Tracts	CHT	Meter	m
Coefficient of variation	CV	Millimetre	mm
Continued	Cont'd	Modern Variety	MV
Days after sowing	DAS	Month	mo
Days after transplanting	DAT	Muriate of Potash	MP
Degree Celsius (Centigrade)	°C	Mean Sum of Square	MSS
Degree of freedom	df	Phenotypic coefficient of variation	PCV
Diploid Chromosome Number	2n	Randomized Complete Block Design	RCBD
Environmental coefficient of variation	ECV	Relative humidity	RH
Food and Agricultural Organization	FAO	Sher-e-Bangla Agricultural University	SAU
Genetic advance over percent of mean	GAPM	Square meter	m^2
Genetic advance	GA	Standard deviation	SD
Genotype	G	Standard error	SE
Genotypic coefficient of variation	GCV	Triple Super Phosphate	TSP
Gram	g	Year	yr

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May all living beings in this world live in peace and harmony and may all be free from pain and sufferings.

December, 2010 *The Author*

SAU, Dhaka

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

BY

SHYAMA PRASHAD CHAKMA

ABSTRACT

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka under the agro-ecological zone of Modhupur Tract (AEZ-28) during January to June of 2011. The experiment was intended to estimate the nature and magnitude of genetic variability, correlation, path coefficient and genetic diversity of 39 rice genotypes collected from Bangladesh Rice Research Institute, Lal Teer Seed Ltd. and Chittagong Hill Tracts. All the characters tested showed significant variations among the genotypes. High genotypic coefficient of variation was observed for grain yield and number of unfilled grains per panicle. High heritability coupled with high genetic advance in percent of mean was observed in grain yield, harvest index, 1000-grains weight, unfilled grains per panicle, secondary branches number and plant height indicating additive gene control on the expression of these characters and that selection based on these characters might be effective. The significant positive correlations were recorded for number of effective tillers per plant, 1000-grains weight and harvest index with grain yield at both genotypic and phenotypic levels indicating that the improvement of these characters would lead to increase in grain yield. The highest positive direct effect on grain yield for harvest index followed by number of filled grains indicated that the direct selection based on these characters would be effective for yield improvement. The genotypes were grouped into six clusters. Cluster I consisted of the highest 11 genotypes from different origin, whereas cluster IV consisted of the lowest three genotypes. The genotypes of Chittagong Hill Tracts were distributed in different clusters indicated that the geographical distribution was not related to genetic diversity. The highest inter genotypic distance was observed between *Tharak dhan* and BRRI dhan 45 and the lowest between BRRI dhan 33 and BRRI dhan 50. The highest inter cluster distance was observed between cluster II and III and the highest intra cluster distance for cluster IV. *Cluster III* had the highest mean values for grain yield, harvest index, 1000-grains weight and number of effective tillers and cluster V for number of primary branches and cluster VI for number of filled grains that had significant positive correlation with grain yield. Considering all the data analyses, the genotypes BRRI dhan 36, Gold, BRRI dhan 28, Dowel, BRRI dhan 45, BRRI dhan 50 and Indian Pajam could be selected for hybridization program.

Chapter I

Introduction

CHAPTER I

INTRODUCTION

Rice is a self pollinated cereal crop belonging to the family Gramineae (synonym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number 2n=24 (Hooker, 1979). The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild species and two, *Oyza sativa* and *Oryza glaberrima* are cultivated (Brar and Khush, 2003).

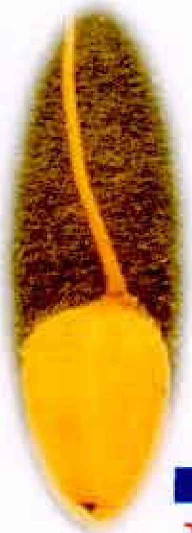
Rice (*Oryza sativa* L.) is the staple food in Bangladesh, and grown in a wide range of environments ranging from the upland areas like Chittagong Hill Tracts, Sylhet and Garo Hills, with little moisture, to situations where the water is 3-4 m deep (Alim, 1982). Rice is the second largest produced cereal in the world in 158.3 million hectare area with annual production of about 685.24 million metric tons (Anonymous, 2011) and also the staple food for over one third of the world's population (Poehlman and Sleper, 1995) and more than 90% to 95% of rice is produced and consumed in Asia (Virmani, 1996). Bangladesh is ranked as fourth in rice production with annual production of 47.72 million metric ton in the world (Anonymous, 2011). By 2030, the world must have to produce 60% more rice than it produced in 1995 to meet the demands (Virmani *et al.*, 1997). In Bangladesh there is about 79.77% area under modern varieties (MV) in 2009 (BBS, 2010). It is the major source of calorie (75%) and protein (55%) in the average daily diet of the people and shares 95% of the cereal consumption (Bhuiyan *et al.*, 2002). About 55 rice HYVs have been released from BRRI from 1970-2011 and those are suitable for different ecosystem (BRRI, 2011). Bangladesh has a good source of indigenous rice cultivars with two million hectares coverage, while the HYV and hybrids occupy eight million hectares and 1 million hectares respectively (Talukder, 2011). The yield potential of HYVs of rice is wandering around 6-7 ton/ha that needs to be increased to tackle the forthcoming situation (Biswas *et. al.*, 2000).

A plant breeding program consists of building up a gene pool of variable germplasm, selection of individuals from the gene pool and utilization of selected individual to evolve a superior variety (Kempthorne, 1957). The available variability in a population can be partitioned into heritable and non-heritable parts using genetic parameters like variability, heterosis and genetic advance (Miller *et al.*, 1958). Yield components are directly related to the genotypes and the environments of cultivation (Uddin *et al.*, 2010). The evaluation of phenotypic diversity usually reveals important traits of interest to plant breeders (Singh, 1989). The improvement of yield and yield contributing characters are under polygenic control that are influenced by environment and determined by the magnitude and nature of their genetic variability (Singh *et al.*, 2000). The improvement of superior rice genotypes and any traits depend on the genetic variability, interrelationship and path coefficient analysis (Krishnaveni *et al.*, 2006). The determination of genotypic and phenotypic correlation between yield and its component characters is essential for yield improvement through selection programs (Ismail *et al.*, 2001, and Kumar and Sukla, 2002). Yield components have influence on ultimate yield both directly and indirectly (Tukey, 1954). Path coefficient analysis provides an effective means of partitioning the correlation coefficients into direct and indirect effects of the component characters on yield on the basis of which crop improvement programs can be logically devised (Kozak *et al.*, 2007). Therefore, correlation in combination with path coefficient analysis will be an important tool to find out the association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959).

Knowledge of genetic diversity among existing cultivars of any crop is essential for long term success of breeding program and maximizes the exploitation of the germplasm resources (Belaj *et al.,* 2002). Hybridization is one of the major tools for the improvement of a crop that needs the analysis of genetic diversity for the selection of parents (Singh, 1983). Moreover, evaluation of genetic diversity is important for the source genes of particular traits within the available germplasm (Roy and Panwar, 1993). Multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of several characters and assess relative contribution of different components to the total divergence both at intra- and inter-cluster levels (Bhatt, 1973; Jatasra and Parada, 1978; Ghaderi *et al.,* 1984; Naidu and Satanarayana, 1991 and Zahan *et al.* 2008).

Considering the above ideas and facts the present investigation was conducted with the following objectives:

a) To study the variability among the available genotypes,
b) To assess the correlation coefficients among the characters towards grain yields of the genotypes,
c) To find out the direct and indirect effect of component characters on grain yield with the help of path coefficient analysis, and
d) To assess the genetic diversity among the rice genotypes.



Chapter II

Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Review of literature on the genetic diversity, correlation and path analysis in rice has been presented in the following headings:

2.1. Variability

2.2. Correlation

2.3. Path coefficient analysis

2.4. Genetic diversity

2.1. Variability

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

Ullah, *et al.* (2011) estimated the genetic variability, interrelationship and cause effect analysis of ten traditional fine birion rice cultivars for morpho-physiological traits. There was found significant variation for all the characters. The higher genotypic coefficient of variation (GCV) was found for grains per panicle followed by grain yield per plant, 1000-grain weight and panicles per plant. High heritability was observed for all the tested characters except harvest index. High heritability with high genetic advance in percentage of means was found for grains per panicle, grain yield per plant and 1000-grain weight indicating role of additive gene action.

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

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

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

Akinwale *et al.* (2011) estimated the phenotypic and genotypic coefficients of variation, broad sense heritability, genetic gain and correlations in rice (*Oryza sativa* L.). There was found significant difference for all the traits studied. Genotypic coefficient of variation was lower than the corresponding phenotypic coefficients in all the traits studied, indicating considerable influence of the environment on the expression of the traits.

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

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

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

Pandey and Anurag (2010) observed significant genetic variability among twenty two indigenous rice genotypes for yield and quality contributing traits. There was found sufficient amount of variability in the study materials and scope of selection. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for various characters. However the difference between GCV and PCV was low for most of the characters studied indicating less degree of environmental influence on manifestation of these characters. High heritability coupled with high genctic advance were recorded for number of spikelet per panicle indicated the major role of additive gene action in the inheritance of these characters and characters could be improved by selection in segregating generation and could serve as an effective selection parameter during breeding programme for crop improvement.

Iwo and Obok (2010) studied on the performance and genetic variability of five upland rice genotypes. The genetic variability estimates revealed low values of genotypic coefficient of variability (GCV) and corresponding high values of phenotypic coefficient of variability (PCV) for all the characters investigated with exception of plant height. High heritability (h^2) and high genetic advance (GA) were observed for number of tillers and productive tillers. Number of days to 50% flowering, number of grains per panicle and grain yield had high heritability (h^2) values with corresponding low genetic advance (GA). These two characteristics were considered as selection indices for further improvement.

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

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

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

Khan *et al.* (2009) estimated genetic variability of rice genotypes for grain yield components in rice. Analysis of variance indicated highly significant differences among 25 genotypes for all morphological traits and six genotypes used for the grain quality studies also showed significant differences among grain quality traits except volume expansion ratio and grain elongation ratio. Broad sense heritability estimates were higher for morphological traits ranging from 67.37 to 98.24.

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

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

Padmaja *et al.* (2008) studied on the genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for eleven characters in 150 genotypes including five check varieties of rice. There was found significant differences for all characters except leaf width and 100-seed weight among the genotypes. Genotypic and phenotypic coefficient of variations were found high for all the characters except days to 50% flowering and panicle length, which had moderate genetic advance along with high heritability indicating the involvement of additive type gene action in controlling these characters.

Kole *et al.* (2008) studied on variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice of 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 panicle number, moderate for grain number per panicle, 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 panicle number, grain number and grain yield indicated the predominance of additive gene action for the expression of these characters. The study suggested that selection favouring higher panicle number per plant, test weight and medium plant height with a reasonable balance for moderate grain number would help to achieve higher grain yield in this population of aromatic rice.

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

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

Habib *et al.* (2005) evaluated 10 local birion rice varieties to find 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 filled grains per panicle. High heritability associated with high genetic advance was observed in filled grains per panicle, 1000-grain weight, harvest index and grain yield.

Nayak *et al.* (2004) studied on genetic variability of 28 scented genotypes along with one non-scented check Ratna over four environments for yield and yield attributes. The genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV) and genetic advance were high for number of grains per panicle and harvest index in all the four environments as well as in pooled analysis.

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

Prasad *et al.* (2001) studied genetic variability and selection criteria of eight fine rice genotypes for some yield contributing characters through correlation and path analysis. 1000-grain weight, number of effective tillers per plant, number of fertile grains per panicle and yield per plant showed high genotypic coefficient of variation and high heritability along with high genetic advance in percentage of mean, pointed out their importance for achieving genetic gain through selection.

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

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

Ali *et al.* (2000) studied on genetic variability and broad sense heritability in F_2 population of *Oryza sativa* L. and found significant for all characters evaluated except for number of tillers per plant and panicle length. The maximum heritability was found for plant height, 100-seed weight, number of tillers per plant, spikelet density and panicle length. The maximum genetic gain relative to the mean was expected for number of tillers per plant, plant height and spikelet density. Expected relative genetic advance was the function of heritability and coefficient of genotypic variability, latter being more important.

Yousuf *et al.* (1994) estimated variability of 32 rice genotypes for yield and yield contributing characters. High genotypic and phenotypic coefficient of variation was found for 1000-grain weight (274.53 and 594.44, respectively) and grain yield per plant (129.53 and 165.71). High broad sense heritability was found for grain yield per plant (78.17) and days to maturity (77.54). Maximum genetic advance was found for grain yield per plant (19.81%) and 1000-grain weight (8.30%). High heritability with moderate genetic advance in percentage of mean was found for panicle length.

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

Li *et al.* (1991) estimated the variability of nine rice genotypes for yield components. Higher genotypic coefficient of variation (GCV) was found for number of panicles per hill (8.45%) followed by grain weight per plant (7.79%). Lower GCV was found for plant height (2.87%) and spikelet fertility (3.22). High heritability was found for days to maturity (97.25%) followed by 1000-grain weight (78.04%) and the lowest for spikelets per panicle (31.28%).

Sardana *et al.* (1989) found high variability for number of panicles per hill among the yield and yield contributing characters of rice. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for days to maturity, plant height and panicle length.

Singh and Yunus (1988) found high phenotypic and genotypic coefficient of variation (PCV and GCV) for grain yield and harvest index in rice. Lower PGV and GCV were found for plant height. High heritability was found for plant height (82.14%). High genetic advance was found for biological yield (18.24).

De and Suriya (1988) evaluated 30 lowland rice genotypes. There was found less variation among 1000-grain weight. Genetic coefficient of variation (GCV) ranged from 6.2 for 1000-grain weight to 34.5 for sterility percentage. The highest heritability was found for sterility percentage followed by number of panicles per hill, yield per plant and 1000-grain weight. Higher genetic advance in percent of mean was found for sterility percentage, yield per plant, and number of panicles per hill. But high heritability with very low genetic advance in percent of mean was found for 1000-grain weight.

Balakakrishna *et al.* (1973) studied variability of 32 rice genotypes. High variability was found for number of filled grains per panicle and plant height followed by panicle weight, number of panicles per hill and grain yield per hill. The genotypic variance was high for number of filled grains per panicle and plant height. The genotypic coefficient of variability varied from 1.02% for panicle length to 25.30% for number of panicles per hill. High heritability coupled with high genetic advance was found for plant height, number of panicles per hill and number of spikelet per panicle.

2.2. Correlation

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

Bhadru *et al.* (2011) studied on the direct and indirect influence on grain yield in 68 hybrids, 21 parents and four checks. Significant positive association was found for plant height, panicle length, productive tillers per plant, productivity per day and filled grains per panicle with grain yield per plant, direct positive effect and indirect association themselves at both genotypic and phenotypic levels.

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

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

Golam *et al.* (2011) evaluated a total of 53 rice genotypes including 12 globally popular aromatic rice cultivars and 39 advance breeding lines for yield and yield contributing characters in Malaysian tropical environment. Two local varieties MRQ 50 and MRQ 72 were used as check varieties. Correlation analysis revealed that the number of fertile tillers (r=0.69), grain per panicle (r=0.86) and fertile grain per panicle (r=0.65) had the positive contribution to grain yield.

Akinwale *et al.* (2011) estimated the phenotypic and genotypic coefficients of variation, broad sense heritability, genetic gain and correlations in rice (*Oryza sativa* L.). 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 result suggested that these traits can be used for grain yield selection.

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

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

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

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

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

Khan *et al.* (2009) estimated the correlation for grain yield components in rice using 25 genotypes. Correlation analysis indicated that plant height had positive and significant association with all the morphological traits at genotypic level. Grain yield per plant was correlated positively and significantly with plant height, panicle length, flag leaf area and number of grains per panicle at genotypic level. Genotypic correlation of plant height with number of tillers per plant was positive. Number of grains per panicle had positive correlation with grain yield per plant. The grain quality studies revealed better performance of Basmati-385 with higher values for volume expansion, water absorption, elongation ratio and score for aroma.

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

Rokonuzzaman *et al.* (2008) evaluated the variability and genetic association for grain yield component characters of twenty Boro rice varieties. 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.

Kole *et al.* (2008) studied on variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice of 18 morphologically distinct mutants in M4 generation along with their two mother genotypes. 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 improvement in this population.

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

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

Habib *et al.* (2005) evaluated 10 local birion rice varieties to find out variability and genetic association for grain yield and its component characters. Genotypic correlation coefficient was higher than the corresponding phenotypic correlation coefficient in the most of the cases. Plant height, days to maturity and filled grains per panicle showed significant positive correlation with grain yield.

Nayak *et al.* (2004) studied on correlation over four environments for yield and yield attributes in 28 scented genotypes along with one non-scented check Ratna. Significant positive correlation was observed for number of grains per panicle and harvest index with grain yield in all the four environments and pooled data.

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

Prasad *et al.* (2001) studied genetic variability and selection criteria of eight fine rice genotypes for some yield contributing characters through correlation and path analysis. Correlation coefficient study revealed high positive correlation of grain yield with effective tillers per plant, fertile grains per panicle and 1000-grain weight. A significant negative correlation was obtained between grain yield and plant height.

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

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

Cheema *et al.* (1998) experimented on four commercial varieties of basmati rice. Highly significant correlation was found between yield per plant with number of spikelet per panicle, number of primary branches per panicle and panicle length, and number of spikelets per panicle with panicle length and number of primary branches per panicle.

Das *et al.* (1992) evaluates for thirty rice genotypes for variability and genetic association. Genotypic correlations were higher than the phenotypic correlation. Fertile spikelets per panicle, 1000-grain weight, days to 50% flowering and days to maturity showed highly significant positive correlation with grain yield per plant both at genotypic and phenotypic levels.

Yousuf *et al.* (1994) found significant positive correlation for grain yield per plant with panicle length (0.404), days to maturity (0.50) and 1000-grain weight (0.61). Negative correlation was found for yield with number of primary branches and sterility percent.

Mahajan *et al.* (1993) studied on correlation in yield contributing characters of 37 rice genotypes of upland rice. Positively significant correlation was found for grain yield with straw yield per plant and filled grains per panicle.

Mirza (1992) studied on correlation and path analysis of yield and yield component of rice. Positive correlation was found in plant height with panicle length and 1000-grain weight. Grain yield was positively correlated with 1000-grain weight and number of grains per panicle.

Kumar (1992) studied on character association of yield component of rice. Positive significant association was found between tiller number and panicle length. Negative association was found between plant height and panicle length.

De and Suriya (1988) evaluated 30 lowland rice genotypes. There was found significant positive correlation of grain yield with number of panicles per hill and plant height at both genotypic and phenotypic level. Significant negative correlation was found for plant height with sterility percentage at both genotypic and phenotypic level.

Balakakrishna *et al.* (1973) studied on correlation for yield and yield contributing characters of 32 rice genotypes. Highly significant, positive phenotypic and genotypic correlations were found between yield and number of panicles per hill, 1000-grain weight and plant height. Significant negative phenotypic and phenotypic correlations were found for 1000-grain weight with number of panicles per hill and number of filled grains per panicle.

2.3. Path coefficient analysis

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

Abarshahr *et al.* (2011) estimated genetic variability and relationships among some agronomic traits of 30 varieties of rice under two irrigation regimes. Path analysis for paddy yield indicated that the number of spikelet panicle and flag leaf length had positive direct effects and days to 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.

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

Khan *et al.* (2009) analysed the path coefficient of 25 rice genotypes indicating highest direct effect of number of grains per panicle on grain yield per plant.

Kole *et al.* (2008) studied on variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice of 18 morphologically distinct mutants in M4 generation along with their two mother genotypes. The result of genotypic path analysis revealed that panicle number had the highest positive direct effect followed by grain number, test weight.

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

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

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

Nayak *et al.* (2004) studied on path analysis over four environments for yield and yield attributes in 28 scented genotypes along with one non-scented check Ratna. The path analysis revealed the importance of number of grains per panicle and harvest index for the improvement of grain yield in scented rice.

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

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

2.4. Genetic diversity

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

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

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

Baradhan and Thangavel (2011) studied on the nature and magnitude of genetic diversity among 45 genotypes of rice using Mahalanobis's D^2 statistic. The genotypes were grouped into six clusters. The highest genotypes (13) were fallen in cluster III followed by cluster I (9). The maximum divergence (8.04) was found in cluster I closely followed by cluster II (8.03) and cluster V (8.03). The inter cluster distance ranged from 7.58 to 13.20 as exhibited between clusters III and V and clusters II and VI, respectively. In this study, parental lines were selected from cluster VI for grain yield, number of productive tillers per hill, panicle length and plant height and cluster I for number of grains per panicle exhibited high mean values. It was suggested that varietal improvement through hybridization, should be done among the genotypes more of divergent clusters.

Anandan *et al.* (2011) assessed genetic diversity of 44 salt tolerant rice genotypes from different geographical regions using Mahalanobis's D^2 and principal component analysis (PCA). The genotypes were grouped into twelve distinct clusters. Clusters I was the largest containing 19 genotypes, followed by cluster II with nine genotypes. Meanwhile clusters III, IV, VI, VII, IX, and XII were mono-genotypic. The maximum inter-cluster distance was exhibited between clusters IX and X (144.91), followed by clusters II and X (131.87), as well as clusters VII and X (126.27). The maximum divergence of total divergence was found in case of number of grains per panicle (42.71%), followed by grain yield per plot (29.81%). The PCA revealed that axes 1 and 2 accounted for 82.88% and 11.14% of the variance, respectively. The highest contributing variable was the number of grains per panicle in PC1 and the plant height in PC2. The genotypes from different locations were grouped in different clusters, whereas the genotypes of same location were grouped in the same cluster. There was no contribution of the geographical diversity to genetic diversity. The inter-clusters showing maximum distances could be used to produce heterotic combinations and wide variability in segregating generation for many beneficial traits in hybridization program.

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

Pandey and Anurag (2010) assessed the nature and magnitude of genetic divergence of 40 genotypes of rice for twelve yield and yield component using Mahalanobis's D^2 statistic. The genotypes were grouped into seven clusters. Cluster VI contained the maximum number of genotypes followed by cluster III with nine genotypes. There was no relation of geographical distribution to genetic diversity. Plant height, biological yield and test weight showed considerable contribution, accounting for 86.16%, to total divergence. The highest inter cluster distance was found between clusters II and VII therefore the genotypes from cluster II (Triguna, MAUB-15, Pant dhan-6) having desired mean values for characters like days to 50% flowering, panicle length and harvest index, were more divergent from the genotypes of cluster VII (Sonachur and Mala) having desired mean values for plant height, flag leaf width, spikelets per panicle, biological yield and test weight, may be used in hybridization programme to achieve desired segregants with higher yield.

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

Ganta and Jyothula (2010) studied on genetic divergence among 25 genotypes of rice from different geographic origin considering 12 quantitative characters. Analysis of variability revealed the presence of considerable amount of variability among the genotypes for all the twelve quantitative characters. The multivariate analysis following Mahalanobis's D^2 statistic, revealed considerable genetic diversity in the material and led to their grouping into six clusters. The three characters, *viz.*, plant height, biological yield and flag leaf width appeared as the major source of divergence. On the basis of genetic distance, cluster meansvand performance a crossing programme involving diverse genotypes like RNR 196, SKL-61-14-15-10, BGL-11694 was suggested to obtain superior segregants for yield improvement.

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

Ahmed *et al.* (2010) experimented with 36 accessions of traditional (local) Boro rice germplasms from three different groups (twenty accessions as Kaliboro, twelve as Jagliboro and four as Tepiboro) during Boro season in 2004 at BRRI farm to identify the duplicates with the help of morpho-agronomic characters. The genotypes were grouped into six clusters. The maximum numbers of genotypes, ten genotypes, were grouped cluster I. The clusters III, IV, V, VI and II contained 6,7,5,7 and 1 genotypes, respectively. The canonical variant analysis showed in general that the important characters for the differentiation in the descending order of importance were grain length, days to 50% flowering, grains per panicle, grain yield per hill, panicle length, flag leaf area, plant height, seedling height, 1000-grain weight, panicle per hill, harvest index, and tillers per hill, but the similar name group accessions are not duplicate mainly due to dissimilarity of grain length, days to 50% flowering, grains per panicle and grain yield per hill characters. It was apparent from the result that the same name group accessions were quite different from each other.

Shahidullah *et al.* (2009) studied on the genetic divergence of 40 rice genotypes composed of 32 local aromatic, five exotic aromatic and three non-aromatic rice varieties. The genotypes were grouped into six clusters using multivariate analysis. The inter-cluster D^2 was maximum (26.53) between cluster I and IV followed by 21.28 between clusters I and V. Minimum D^2 value was found 5.90 between clusters II and III. Majority of the local aromatic rice varieties with smaller kernels were included in the cluster I. The cluster III contains Elai, Sawati and Sugandha-1 with long slender kernel and very good appearance. These varieties could be used in breeding programme for improvement of germplasm in cluster I.

Sabesan *et al.* (2009a) evaluated genetic diversity among 26 genotypes of rice from four states of South Eastern Region of India using Mahalanobis's D^2 statistic.

The genotypes were grouped into thirteen cluster based on 12 morphological and quality characters. The highest seven genotypes were grouped into cluster I, followed by cluster IV with four genotypes, while clusters IV, VII, VIII, X, XI, XII and XIII were mono genotypic. Some clusters contained genotypes from different state and genotypes from same state were grouped into different clusters. There was no contribution of geographical distribution to genetic divergence. The maximum intra cluster distance (D = 100.90) was found in cluster I. The maximum inter cluster distance (D^2 = 8235.56) was found between clusters II and III. Clusters VI, III, and XII showed high values for most of the characters. Cluster XII showed the highest value for grain yield per plant and lowest mean value for days to first flower. The maximum contributing characters to total diversity was number of grains per panicle (42.71%) followed by days to first flower (25.62%). Hybridization among genotypes AUR 4, Amamalai mutant ponmani, Karnol sona, Jeeraga samba, AUR 7 and PY 5 from clusters III, II, XII and IX which had maximum inter-cluster distances and desirable values for days to first flower, number of grains per panicle, kernel length, kernel breadth, 1000-grains weight and grain yield per plant was likely to produce heterotic combinations and wide variability was segregating generations.

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

Singh *et al.* (2008) studied on genetic diversity of 56 'new plant type' lines including four improved cultivars using Mahalanobis's D^2 statistic under shallow lowland ecosystem. The genotypes were grouped into eleven clusters showing fair degree of relationship between geographic distribution and genetic divergence. The maximum number of genotypes (23) were grouped into cluster I, followed by clusters IV, VII and IX with 12, 10 and 4 genotypes respectively, while clusters II, III, V, VII, X, and XI were monogenotypic. The highest intra-cluster distance was found in cluster IX, followed by clusters IV and VII. The highest inter-cluster distance was found between clusters VII and XI, followed by that between clusters VI and XI. The most contributing character towards the total genetic divergence was maturity, while the other contributing characters were spikelet per panicle, grain filling, panicle number/m^2, panicle length, and harvest index. The member of clusters VIII, V, IV, X, VI, and I could be further evaluated, as these clusters were observed to possess high cluster mean for grain yield.

Rashid *et al.* (2007) observed the deviations by Metroglyph method regarding the number of clusters formed. Metroglyph scatter diagram provided the possibility of eleven clusters of rice genotypes. Cluster I and II possessed the highest index scores I.e., 66 and 56 respectively on morphological basis. On the basis of this clustering, it can be interpreted that mutants between cluster I and cluster II would be expected to give better types after hybridization.

Kumar (2007) worked on genetic diversity among 71 red rice genotypes using Mahalanobis's D^2 statistic and grouped into ten distinct clusters based on genetic distances. The maximum genotypes, twenty genotypes, were grouped into cluster X, while clusters I, II, III, IV and IX contained two genotypes each. There was no parallelism between genetic diversity and geographical distribution. The most significantly contributing characters to genetic divergence were plant height, panicle length and grain yield. The maximum inter cluster distance (38.09) was found between clusters II and V.

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

Bisht *et al.* (2007) evaluated the pattern of genetic diversity of 13 landraces of paddy using multivariate analysis of Mahalanobis's D^2 statistic. The landraces were grouped into seven distinct clusters. Clusters V and VII contained three genotypes each, while clusters I, IV and VI were monogenotypic and clusters II and III contained two genotypes each.

Singh *et al.* (2006) investigated genetic divergence of 52 traditional lowland rice genotypes from five states of North Eastern Region of India using Mahalanobis's D^2 statistic for 15 agro-morphological characters. The genotypes were grouped into six clusters. The maximum 26 genotypes were grouped in cluster I, while cluster VI was mono-genotypic. There was no relationship found between geographical distribution and genetic divergence. Clusters II, III and IV showed high values for most of the characters. Plant height, followed by leaf angle and leaf area, highly contributed (32.43%) to the formation of clusters. Clusters II, IV and V, which had maximum inter-cluster distances as high values of plant height, days to 50% flowering, panicle length, grain yield per plant and milling percent, may be used for initiating a hybridization programme.

Naik *et al.* (2006) studied on the genetic divergence of fifty aromatic rice genotypes to estimate the nature and magnitude of diversity using D^2 statistic. The genotypes were grouped into seven 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 IV. The least distance was found in between clusters I and V. The genotypes Taraori Basmati, Jaigundhi, Krishnabhog, Samuderphool, Sansari, Amtma Shital, Bhataphool, Ghodapunchi, Tulsimala, Dunerphool, Loktimachii and Elaychi can be used as potential donors for future hybridization programme to develop scented rice variety with good grain yield and quality traits.

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

Madhavilatha *et al.* (2005) evaluated genetic diversity of 54 elite germplasm lines using Mahalanobis's D^2 statistic. The genotypes were grouped into nine clusters. There was revealed no relation between geographical distribution and genetic diversity. The maximum inter-cluster distance was found between clusters IV and VIII. The maximum intra-cluster distance was found in cluster V. A perusal of the results on cluster means revealed greater yield, number of grains per panicle, panicle length, plant height and days to 50% flowering for cluster IV, indicating the desirability of genotypes from the cluster for improvement of grain yield and the above yield components. Further, plant height and days to 50% flowering, together accounted for 82.04% of the total genetic divergence, indicating their importance in the choice of parents for hybridization programmes.

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

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

Iftekharuddaula *et al.* (2002) studied on the genetic divergence, correlation and path coefficient analysis among 19 genotypes of irrigated rice for grain yield and yield contributing characters. The genotypes were grouped into five clusters. The inter-cluster distances were higher than the intra-cluster distance indicating wider genetic diversity among the genotypes of different clusters. The intra cluster distances were lower in all the cases reflecting homogeneity of the genotypes within each of the clusters. Cluster II showed high genetic divergence from other clusters. The genotypes of cluster II could be hybridized with the genotypes of any other clusters for producing transgressive segregants. There was no relationship between geographical distribution and genetic divergence. Harvest index, panicle length and 1000-grain weight showed significant positive correlation with grain yield. Highest direct effect on grain yield was exhibited by spikelets per panicle followed by plant height, harvest index, 1000-grain weight and panicle length, respectively. Grains per panicle, spikelets per panicle, flag leaf area, 1000-grain weight and plant height had highest contribution towards divergence, respectively. The most important characters were plant height, spikelets per panicle, grains per panicle, 1000-grain weight, flag leaf area and grain yield that would offer a good scope for the improvement of irrigated rice through rational selection.

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

Hegde and Patil (2000) experimented on the genetic divergence of 40 genotypes of rainfed rice using Mahalanobis's D^2 statistic and found seven clusters. Cluster I, II, III and IV consisted of 18, 14, 3 and 2 genotypes, respectively, while cluster V, VI and VII were solitary clusters. The maximum divergence was found between the cluster V and VII and the highest contributing character to D^2 values were spikelet number per panicle, photosynthetic rate and thousand grain weight. Based on genetic distance, mean performance and clustering pattern, hybridization of

Pankaj with CTH-3 or Kanthimori or Chachakki bilakki, and CTH-3 with Kanthimori or Jolagabatta or Dodabatta was suggested to be appropriate in breeding.

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

Singh *et al.* (1999) studied on the genetic divergence of 42 rice genotypes for 11 quantitative traits using multivariate analysis. The analysis showed considerable genetic divergence. The genotypes were grouped into four clusters. Geographical distribution was not significant to genetic diversity. 90.6% of the total divergence was related to harvest index, total number of grains per panicle, number of fertile grains per panicle and stand ability.

Bansal *et al.* (1999) experimented on the genetic divergence of 34 rice genotypes for ten economic traits collected from seven different countries using D^2 statistic. The genotypes were grouped into fifteen clusters and their distributions into clusters were not related to geographical distribution. Intervarietal crosses were identified on the basis of the mean performance, genetic distance and clustering pattern that may be promising in creating wider variability for early maturity, dwarf and high yielding segregants.

Sarawgi *et al.* (1998) measured the genetic divergence of 132 genotypes consisting of 128 traditional cultivars and four standard genotypes for 18 grain qualities using D^2 statistic. The genotypes were grouped into ten clusters and the maximum was found in cluster VIII. Bakal-B and Jondhera dhan of cluster VI, Gondha Jhul of cluster VIII, poorva and IR-36 of cluster VII, Kranchi, X-12, Moti Bakiya and Assam Chudi of cluster V and Kranti of cluster X were found as the promising varieties based on the cluster means and cluster distance.

Morais *et al.* (1998) evaluated the genetic divergence of 10 parent lines of the irrigated rice population CNA-IRAT 4 using Mahalanobis's D2 statistic and multivariate analysis for ten selected traits. The experiment was conducted in randomized block design with four replications in Goianira, GO.Canonical variate analysis and cluster analysis using Tocher's agglomerative method and hierarchical method (nearest neighbour) were used. The maximum diversity was found between Nanicao and CNA4840. The most similar genotypes were CNA3848 and CNA3887. Variability was found in plant height, days to flowering and grain weight, while the least divergence was found for grain size and number of spikelets.

Mokate *et al.* (1998) experimented on genetic divergence of 25 rice genotypes. The genotypes were distributed into five clusters based on yield component data. The maximum inter-cluster divergence was found in between cluster B and C (63.04%) followed by C and D (51.90%) and cluster B and E (48.30%). The genotypes under these clusters were found promising for the differences in the means for important yield contributing characters for future hybridization program.

Sardana *et al.* (1997) estimated the nature of genetic divergence of 82 local rice varieties of Tripura using D^2 statistic based on 15 agro-morphological characters and varieties were grouped into eighteen clusters while cluster I was the largest containing 15 genotypes. The genetic diversity was found due genetic drift, selection in peculiar topography and diverse agro-climatic condition of Tripura. Numbers of grains per panicle, leaf area, grain weight per panicle, effective tillers per plant and grain yield per plant were the major contributing character to cluster VIII.

Rahman *et al.* (1997) determined the nature and magnitude of genetic divergence of 52 lowland rice cultivars under 40-50 cm water depth that were grouped into eight clusters. The geographical diversity was not found. The highest mean values of spikelet per panicle and grain yield per plant were found in cluster V while the highest value for ear bearing tillers per plant and panicle length were found in cluster VI.

Kumari and Rangasamy (1997) determined the genetic divergence of 62 early rice genotypes from 16 countries and from CIAT, IITA and IRRI using Mahalanobis's D^2 Statistic. These genotypes were grouped into six clusters for eight important yield contributing characters. Cluster I contained 85% of the total genotypes, while cluster II, III, IV and V consisted of only two genotypes each and cluster VI contained only one genotype. Geographical distribution was not significant to genetic divergence. The maximum diversity was found in case of grain yield per plant, panicle exertion and plant height. The result suggested that distantly placed clusters to be used as parents to obtain highly heterotic combinations.

Singh *et al.* (1996) estimated the nature and magnitude of genetic divergence of 40 genotypes of scented and fine rice using Mahalanobis's D^2 statistic for ten important yield contributing characters. The genotypes were grouped into six clusters. The maximum diversity was found in case of grain yield that was 40.6% of total divergence, followed by plant height (16.5%). The maximum inter-cluster distance was found in between cluster II and V that were suggested for inclusion in a hybridization program as promising segregants.

Sawant *et al.* (1995) experimented on the genetic divergence of 75 genotypes of rice grown in Kharif season in 1991. The genotypes were grouped into ten clusters based on eight yield contributing characters. The result suggested that geographical distribution was not significant to genetic divergence. The maximum diversity was found between clusters IX and X (66.58), followed by clusters VI IX (62.59) and clusters IV and X (56.52). The positive and significant correction with grain yield was found in case of ear bearing tillers per plant, thousand grain weight, panicle length and number of grains per panicle. While direct correlation with yields was found in case of number of grains per panicle, thousand grain weight and plant height.

Mishra *et al.* (1994) studied on the genetic divergence of 37 genotypes of rice for seven quantitative characters using multivariate analysis. The genotypes were grouped into five clusters. Cluster I was the largest for containing 31 genotypes, while cluster II contained three genotypes and the others each contained single genotype. The most contributing characters were number of fertile grains per panicle, number of sterile grains per panicle and plant height to the Mahalanobis's D^2 values. The UPR 485-10-1-1, Basmati 370 and Kamod were found as promising for breeding program based on cluster distance.

Chauhan and Chauhan (1994) assessed genetic divergence of 44 breeding lines and two improved cultivars of rice under rainfed upland conditions using D^2 statistic and found twelve clusters. The most contributing character (43.3%) was thousand grains weight to the total genetic divergence followed by 50% flowering, panicle weight and spikelet per panicle.

Vivekananda and Subramanian (1993) investigated genetic divergence of 28 rainfed rice genotypes using Mahalanobis's D^2 statistic grouping them into five clusters and found plant height and grain yield responsible for 85% of total divergence but not the geographical diversity.

Mahapatra *et al.* (1993) determined the genetic diversity of 34 mutant lines of an upland rice cultivar Kalakeri that are derived treating with physical and chemical mutagenesis along with the parents and five upland standard using Mahalanobis's D^2 statistic, canonical analysis and numerical taxonomic approach. The study suggested the promising varieties with desirable characters to be cultivated in upland and the most promising varieties were selected on the basis of the statistical distance and cluster mean values.

Mall and Maurya (1992) examined the genetic divergence of 50 breeding lines of rice and 10 cultivars including parents and standard varieties using D^2 statistic. The maximum divergence was found in plant height (39.04%) followed by test weight and days to 50% flowering.

Ibrahim *et al.* (1992) experimented on the genetic divergence of upland rice population that are morphologically different over different environment using Mahalanobis's D^2 analysis and considerable genetic diversity among genotypes was found that were fall into three constellation in D^2.

Dem *et al.* (1992) explained the genetic divergence of 28 early maturing genotypes of rice for 12 quantitative characters grown under direct seeded and transplanted conditions during Rabi season. The genotypes were grouped into five and six clusters under direct seeded and transplanted conditions, respectively. Geographical distribution was not found significant to genetic divergence. RP670-6-36-14 was suggested as promising parental line, while RAU4045-2A was suggested as promising genotype for varietal improvement program.

Sinha *et al.* (1991) examined genetic divergence of 30 traditional upland rice varieties for ten agro-morphological characters from nine states of India using Mahalanobis's D^2 statistic. The varieties were grouped into six clusters. The maximum numbers of genotypes from different states except Punjab were fall under cluster I (66.6%) while clusters IV, V and VI contained single genotype. Varieties from Northeastern region showed the maximum diversity, and were fall into all clusters except cluster V. There was not found of any parallelism between geographic and genetic diversity. The most contributing characters to total genetic divergence were number of secondary branches per panicle, yield per fertile grains per panicle. These characters could be used in selection of promising parents from distantly placed clusters to obtain high heterotic combinations.

Rangel *et al.* (1991) evaluated genetic divergence of 72 local rice cultivars, adapted to lowland conditions, using multivariate procedures. The cultivars were grouped into four clusters based on clustering procedure proposed by Tocher was applied to Mahalanobis's generalized distances. Measures of divergence permitted the recognition of two special groups within the set of 13, namely, group 1, with cultivars 49, 6, 35, 34, 38 and 13; group 2, with cultivars 59, 41, 37, 23, 3, 21 and 30. These grouped seemed to be adequate for inter crossing in a factorial mating design (group 1 × group 2). Alternatively, cultivars of these groups could be used for inter crossing with introduced elite lines, already improved in terms of plant architecture.

Selvakumar *et al.* (1989) experimented on genetic diversity on 40 genotypes of rice for four yield contributing characters using D^2 statistic. The genotypes were grouped into eleven clusters. The genotypes that fall into the same cluster were related by pedigree. Gadakasala was found as promising parent for breeding program for cold tolerance that fall under cluster XI. There was no correlation between geographical distribution and genetic diversity.

Wu and Huang (1988) grouped 35 slender grained and high quality rice varieties from Southern China into six clusters based on clustering analysis of quantitative characters where he found high genetic divergence between group I and group VI and between group II and VI.

De *et al.* (1988) experimented on genetic divergence of 75 strains comprising indica, japonica, ponlai and javanica rice using D^2 statistic. The strains were grouped into thirteen clusters. Two characters, *viz.*, 100-grain weight and number of grains per panicle, were the highest contribution to D^2 values. Six clusters consisting of 14 strains (10 in ARC, 2 in javanica and 2 in ponlal) was supposed as important for use as base material for varietal improvement programme on the basis of their grater inter cluster distances and higher cluster mean values to the aforementioned two characters.

Kotaiah *et al.* (1987) studied on divergence by grouping 36 long duration rice genotypes into ten and eight clusters using D^2 statistic and metroglyph analysis, respectively, where he found that days to 50 % flowering and 1000-grain weight were the main contributors to total divergence and also recommended the metroglyph analysis for preliminary grouping before using D^2 analysis.

Singh *et al* (1986) determined genetic divergence of 50 cultivars of lowland rice for 15 yield contributing characters using D^2 statistic. The genotypes were grouped into ten clusters. Two-third of the total genotypes were fallen under clusters I, II and III. The geographical distribution was not significant to genetic diversity. The most contributing characters to genetic divergence were plant height, test weight, panicle length and number of spikelets. The more diverse clusters were statistically larger in distances. The genetically diverse cultivars with high yield potential and having specific unit of interest could be used in inter crossing program. Cultivars Anandi, Adamchini, Bhatafool, Kanakjiri and Motibadam of cluster IV; Dehradoon and Kesar of cluster V; Lawangchur of cluster VIII; and Jilhore of cluster X were found genetically diverse with high yield potential.

Julfiquar *et al.* (1985) investigated the divergence among 67 restorers and 33 maintainers that were developed from 68 crosses at IRRI and grouped them into different clusters that were found as significant to be used in breeding programs to produce heterotic F_1 hybrids.

Kanwal *et al.* (1983) studied on the genetic divergence of 100 rice strains using Mahalanobis's D^2 statistic and canonical analysis. Panicle weight, days of maturity, height and grain size were found significant to genetic divergence. Nine characters, which were not correlated with geographical diversity, were used to group the strains.

Mahajan *et al.* (1981) experimented on the genetic diversity (D^2 statistic) for 11 yield related characters of 60 cultures developed from 14 crosses of 23 parents and grouped into eighteen clusters that are mostly came from the same cross. The geographical diversity was associated to genetic diversity to some extent and seven cultures were identified for genetic diversity, high yield component and multiple resistances that would be favourable for future rice breeding programs.

Vairavan *et al.* (1973) studied on the nature of genetic divergence of 190 rice genotypes from North-East India along with four standard varieties, three of which were indica and one japonica. The genotypes were preliminarily grouped by canonical analysis and resultant 42 groups were further classified using D^2 statistic. The final grouping resulted nine divergent clusters. Height followed by leaf area was found to be important for primary and 100-grain weight, followed by amylase content for secondary differentiation. Geographical distance was not found to be related to genetic divergence. The study suggested that *Oryza sativa* contained innumerable but divergent forms, its classification into definite varietal groups on an arbitrary basis such as isolation barrier, sexual affinity or geographical distribution would be far from reality.

Bhaumik (1971) experimented to screen better types among 10 strains with the help of the D^2 statistic. The strains were grouped into four clusters. The maximum numbers of genotypes (6) were fallen in cluster B, while cluster A contained two genotypes and clusters C and D were mono genotypic. The constituents of cluster A were expected to be transgressive segregantes. The inter clusters distance was maximum between clusters A and D, while minimum in between clusters B and C. The best strains were grouped in clusters D, followed by B, C and A.

Chapter III

Materials and Methods

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MATERIALS AND METHODS

3.1. Field experiment and observations

3.1. 1. Experimental site

The experiment was conducted at the experimental field under the Department of Genetics and Plant Breeding of Sher-e-Bangladesh Agricultural University (SAU), Dhaka-1207, Bangladesh, during January to June in 2011. The experiment site was typically rice growing lowland. The location of the experimental site was at 23°77′N latitude and 90°33′E longitudes with elevation of 9 m from sea level.

3.1.2. Soil and climate of the experimental site

The soil of the experimental site was deep red brown, clay loam with pH of 6.00-6.63 and belonged to "*Nodda*" cultivated series of Madhupur Tract in Agro Ecological Zone (AEZ) 28 (Appendix I and Appendix III). The experimental site was characterized by heavy rainfall during June to September and scantly rainfall during rest of the year. The climate of this area was subtropical (Appendix II).

3.1.3. Experimental materials

The experimental materials of the study comprised of 39 rice genotypes. The seeds were collected from Genetic Resource Centre (GRC) of Bangladesh Rice Research Institute (BRRI), Lal Teer Seed Ltd. and Chittagong Hill Tracts. The details of these genotypes are given in Table 1.

Table 1. List of thirty nine rice genotypes along with their sources

Sl. No.	Indicating Symbols	Variety Name	Source
1	G1	Sada Kabarak	Chittagong Hill Tracts
2	G2	Kala kabarak	Chittagong Hill Tracts
3	G3	Kamrang dhan	Chittagong Hill Tracts
4	G4	Badeye dhan	Chittagong Hill Tracts
5	G5	Sada gelon	Chittagong Hill Tracts
6	G6	Jumma Bini (longer grain)	Chittagong Hill Tracts
7	G7	Jumma Bini (Shorter grain)	Chittagong Hill Tracts
8	G8	Kabarak Dhan	Chittagong Hill Tracts
9	G9	Ameiye Dhan	Chittagong Hill Tracts
10	G10	Tharak Dhan	Chittagong Hill Tracts
11	G11	Paijam (Indian)	Chittagong Hill Tracts
12	G12	Jumma Kabarak	Chittagong Hill Tracts
13	G13	Gold	Lal Teer Seed Ltd.
14	G14	Tia	Lal Teer Seed Ltd.
15	G15	Dowel	Lal Teer Seed Ltd.
16	G16	Moyna	Lal Teer Seed Ltd.
17	G17	BR-3 (Biplob)	GRC, BRRI
18	G18	BR-10 (Pragati)	GRC, BRRI
19	G19	BR-11 (Mukta)	GRC, BRRI
20	G20	BR-22 (Kiran)	GRC, BRRI
21	G21	BR-24 (Rahmat)	GRC, BRRI
22	G22	BR-25 (Naya Pajam)	GRC, BRRI
23	G23	BR-26 (Shraboni)	GRC, BRRI
24	G24	BRRI Dhan-27	GRC, BRRI
25	G25	BRRI Dhan-28	GRC, BRRI
26	G26	BRRI Dhan-29	GRC, BRRI
27	G27	BRRI Dhan-30	GRC, BRRI
28	G28	BRRI Dhan-31	GRC, BRRI
29	G29	BRRI Dhan-32	GRC, BRRI
30	G30	BRRI Dhan-33	GRC, BRRI
31	G31	BRRI Dhan-36	GRC, BRRI
32	G32	BRRI Dhan-39	GRC, BRRI
33	G33	BRRI Dhan-40	GRC, BRRI
34	G34	BRRI Dhan-42	GRC, BRRI
35	G35	BRRI Dhan-44	GRC, BRRI
36	G36	BRRI Dhan-45	GRC, BRRI
37	G37	BRRI Dhan-48	GRC, BRRI
38	G38	BRRI Dhan-49	GRC, BRRI
39	G39	BRRI Dhan-50	GRC, BRRI

BRRI = Bangladesh Rice Research Institute, GRC = Genetic Resource Centre

3.1.4. Design and layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The experimental field was divided into three blocks, representing three replications. Two seedlings per hill were transplanted maintaining 25 cm × 20 cm spacing from row to row and plant to plant, respectively. Thirty nine rice genotypes were distributed in each of the block through randomization process.

3.1.5. Germination of seeds

Seeds were soaked separately for 48 hours in a water container using cloth bags. Then the seed bags were kept inside the straw heap to increase the temperature for facilitating germination.

3.1.6. Preparation of seedbed, seeds sowing and seedlings raising

The irrigated land was prepared thoroughly by three times ploughing and cross ploughing followed by laddering. Weeds and stubbles were removed. Thirty nine separate strips were made and sprouted seeds were sown in 25th January of 2011. The seedlings were raised by maintaining irrigation with regular intervals and protecting from birds and insects.

3.1.7. Preparation of main land

Cow dung was applied to the experimental field and the plot was ploughed thoroughly by two ploughing and cross ploughing followed by harrowing with a tractor drawn disc plough to attain a good puddle. Four days later the final ploughing and cross ploughing were done and weeds and stubbles were removed. First split of urea and full portion of all other fertilizers recommended by BRRI were added to the main land before final ploughing. Urea, TSP, MP and Gypsum were applied at 150, 100, 70 and 60 kg/ha, respectively. The second, third and fourth splits of urea was applied at 15, 30 and 45 days after transplanting (DAT), respectively (BRRI, 2008).

3.1.8. Transplanting of seedlings

Thirty five days old and healthy seedlings were transplanted to the main field in 1st March of 2011 at 25cm × 20cm spacing from row to row and plant to plant, respectively, followed by proper irrigation.

3.1.9. Intercultural operations and plant protection

All the necessary intercultural operations were taken during cropping period for better growth and development of the plants. Necessary gap filling was done within 7 DAT. Weeding were done before the first two top dressings of urea fertilizers. Irrigation was given to maintain 5-7 cm water to hard dough stage of rice in regular intervals. Crop was protected from different harmful insects and diseases through insecticides and fungicides application in proper doses recommended by BRRI (BRRI, 2008). Rats and birds were also controlled in proper ways.

3.1.10. Harvest and post harvest operations

The crops were harvested separately only after attaining maturity and threshed, cleaned and dried in proper ways avoiding any kind of mixtures within the varieties.

3.1.11. Collection of data

All the data were taken at proper stages during the growing, harvest and post harvest periods. Data were collected on plant height at maturity (PH), number of effective tillers (NET), length of panicles (LP), days to 80% flowering (DF), number of primary branches (NPB), number of secondary branches (NSB), days to maturity (DM), number of unfilled grains (NUG), number of filled grains (NFG), 1000-grain weight (TGW), harvest index (HI) and grain yield per ten plants (GYPTP). Data were taken from 10 hills of each genotype.

a) Plant height at maturity (cm) : Average length of the plants from base to the terminal spikelet including awn in centimetre.

b) Number of effective tillers : Average number of tillers bearing panicles per hill.

c) Length of panicle (cm) : Average length of panicles in centimetre from base of the panicles to the top of the terminal spikelet including awn.

d) Days to 80% flowering (DAS) : The days required for 80% flowering after sowing.

e) Number of primary branches per panicle : Average number of primary branches per panicle

f) Number of secondary branches per panicle : Average number of secondary branches per panicle

g) Days to maturity (DAS) : The days required to attain maturity for harvesting after sowing.

h) Number of unfilled grains per panicle : Average number of unfilled grains per panicle

i) Number of filled grains per panicle : Average number of fully developed grains per panicle.

j) 1000-grain weight (gm) : Weight of well dried and cleaned 1000-grains in gram.

k) Harvest index (HI) : Ratio of economic yield to biological yield. It was estimated from the following formula,

$$\text{HI} = \frac{\text{Dry weight of grains (g) of 10 hills}}{\{\text{Dry weight of grains (g)} + \text{dry weight of straw (g)}\}\text{ of 10 hills}}$$

l) Grain yield per ten plants (g/ten plants) : The weight of grains in gram per ten plants.

3.2. Statistical analysis of data

The data was statistically analysed as mentioned bellow:

3.2.1. Analysis of variance (ANOVA)

The analysis of variance (ANOVA) for all characters was carried out individually.

The structure of ANOVA

Source of variation	d.f.	M.S.S.	EMSS	F-Ratio
Replication (r)	r-1	M_1		M_1/M_3
Genotypes (g)	g-1	M_2	$\sigma_e^2+r\,\sigma_g^2$	M_2/M_3
Error (e)	(r-1)(g-1)	M_3	σ_e^2	

Where,

r = Number of replications

g = Number of genotypes

d.f. = degree of freedom

M.S.S.=Mean sum of square

EMSS = Expected values of M.S.S.

3.2.2. Estimation of genetic parameters

The genetic parameters for the characters under study were estimated as followings:

3.2.2.1. Estimation of variance components

The phenotypic and genotypic variances were estimated according to the following formula given by Lush (1940) and Chaudhary and Prasad (1968).

$$\text{Genotypic variance } (\sigma_g^2) = \frac{MSS_G - MSS_E}{r} = \frac{M_2 - M_3}{r}$$

Phenotypic variance $(\sigma_p^2) = \sigma_g^2 + MSS_E = \frac{M_2 - M_3}{r} + M_3$

Where, MSS_G = MSS for genotypes

MSS_E = MSS for error = σ_e^2

3.2.2.2. Estimation of genotypic and phenotypic coefficient of variation

The genotypic and phenotypic coefficient of variation were estimated using the formula given by Burton and Devane (1953).

1. Phenotypic coefficient of variation (PCV) = $\frac{\sigma_p}{\overline{X}} \times 100$
2. Genotypic coefficient of variation (GCV) = $\frac{\sigma_g}{\overline{X}} \times 100$

Where,

σ_p = Phenotypic standard deviation

σ_g = Genotypic standard deviation

$\overline{X}$ = Grand mean

GCV and PCV values were categorized as followings by Sivasubramanian and Menon (1973):

1-10% : Low

11-20% : Moderate

$\geq$ 21% : High

3.2.2.3. Heritability in broad sense

Heritability in broad sense (h^2) was estimated (defined by Lush, 1949) by using the following formula suggested by Johnson *et al.* (1955) and Hanson *et al.*, (1956).

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The heritability percentage was categorized as followings given by Robinson *et al.* (1949):

0-30% : Low

31-60% : Moderate

$\geq$ 61% : High

3.2.2.4. Genetic advance

The genetic advance (GA) was estimated according to the formula suggested by Lush (1949) and Johnson *et al.* (1955).

$$GA = i\,\sigma_p h^2$$

Where,

i = 2.06 when top 5% individuals are selected

3.2.2.5. Genetic advance as percentage of mean

Genetic advance as percentage of mean (GAPM) was estimated according to the following formula given by Comstock and Robinson (1952).

$$GAPM = \frac{GA}{\overline{X}} \times 100$$

Genetic advance as percent of mean was categorized according to the followings used by Johnson *et al.* (1955).

0-10% : Low

11-20% : Moderate

$\geq$ 21% : High

3.2.3. Correlation coefficient

The correlation coefficients were for all possible combinations using the formula suggested by Miller *et al.* (1958), Hanson *et al.* (1956), Johnson *et al.* (1955), Weber and Moorty (1952).

$$r_p = \frac{Cov_p\,(xy)}{\sqrt{\{\sigma^2_P(x).\sigma^2_p(y)\}}}$$

$$r_g = \frac{Cov_g\,(xy)}{\sqrt{\{\sigma^2_g(x).\sigma^2_g(y)\}}}$$

Where,

r_p = Phenotypic correlation

r_g = Genotypic correlation

$Cov_p(xy)$ = Phenotypic covariance between the characters 'X' and 'Y'

$Cov_g(xy)$ = Genotypic covariance between the characters 'X' and 'Y'

$\sigma^2_p(x)$ = Phenotypic variance for character 'X'

$\sigma^2_p(y)$ = Phenotypic variance for character 'Y'

$\sigma^2_g(x)$ = Genotypic variance for character 'X'

$\sigma^2_g(y)$ = Genotypic variance for character 'Y'

Test of significance for both genotypic and phenotypic correlation was carried out with (n-2) degrees of freedom by referring to the table given by Snedecor and Cochraw (1961).

3.2.4. Path coefficient analysis

Direct and indirect effects of different characters (independent variables) on the grain yield (dependent variable) were estimated using correlation coefficient of these characters as suggested by Wright (1921 and 1923) and elaborated by Dewey and Lu (1959). The path coefficients were obtained by solving the simultaneous equations that express the basic relationship between correlations and path coefficients. The equations were as follows:

$r_1y = P_1y + r_{12}P_2y + r_{13}P_3y + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{1\,11}P_{11}y$

$r_2y = r_{21}P_1y + P_2y + r_{23}P_3y + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{2\,11}P_{11}y$

$r_3y = r_{31}P_1y + r_{32}P_2y + P_3y + \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{3\,11}P_{11}y$

$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$

$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$

$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$

$r_{11}y = r_{11\,1}P_1y + r_{11\,2}P_2y + r_{11\,3}P_3y + \ldots\ldots\ldots\ldots\ldots + r_{11\,10}P_{11}y + P_{11}y$

Where, r_1y to $r_{11}y$ denote the correlation coefficient between independent characters 1 to 11 and dependent character y, r_{11} to $r_{11\,10}$ denote the correlation coefficients between all possible combinations of independent characters. P_1y to $P_{11}y$ denote the direct effects of characters 1 to 11 on character y. Residual effect (R) was estimated with the help of direct effects and simple correlation coefficients. Path diagram was also drawn using the direct and indirect effects of different independent characters on the yield. The values of direct or indirect effects were categorized using the scales of path coefficients in rice that was suggested by Lenka and Mishra (1973).

0.00 to 0.09 : Negligible
0.10 to 0.19 : Low
0.20 to 0.29 : Moderate
0.30 to 0.99 : High
$\geq$ 1.00 : Very high

3.2.5. Genetic diversity analysis

Genetic diversity in respect of thirteen different morphological traits of 39 rice genotypes was analyzed using the GENSTAT 5.13 software program (Copyright 1987, Lawes Agricultural Trust, Rothamasted Experimental Stastion, UK). Mean data for each character was subjected to multivariate analysis *viz.* principal component analysis (PCA), principal coordinate analysis (PCO), canonical vector analysis (CVA) and cluster analysis (CLSA) (Mahalanobis, 1936; Digby *et al.*, 1989; Jager *et al.*, 1983). More than one multivariate required to represent the results more clearly as found in many researches (Juned *et al.*, 1988; Ariyo, 1987; Patil *et al.*, 1987, Dani and Murthy, 1985 and Balasch *et al.* 1984). Genetic diversity was studied following the Mahalanobis's generalized distance (D^2) method extended by Rao (1952) and principal component analysis was according to Jager *et al.*, (1983). The following multivariate techniques were used using the mean data of each character to analyse the genetic diversity.

3.2.5.1. Principal components analysis

Principal components analysis (PCA) is a method of data reduction and was estimated to identify the patterns in data and to express the data in such a way to highlight their similarities and differences. The principal components were estimated using eigen values and vectors calculated from the correlation matrix and genotype scores obtained from first components that had the property to account for maximum variance. The succeeding components with latent roots greater than the unity (Jager *et al.*, 1983). The principal components analysis assumed that each original measure was collected without measurement error. The latent vectors from the first two principal components were used in the discussion of the contribution of the different morphological characters.

3.2.5.2. Non hierarchical cluster analysis

Non hierarchical cluster analysis was prepared for large number of data to be analysed and it also allowed moving from one cluster to another. The data sets of thirty nine rice genotypes were divided into some number of mutually exclusive clusters using non-hierarchical classification. The optimum values of chosen criterion were derived using algorithm. The criterion values were improved by transferring the units from one group to another or by swapping with units from other groups starting from an initial classification.

3.2.5.3. Principal coordinate analysis

Principal coordinate analysis (PCO) was used to find out any symmetric distance matrix in the manner of Gower (1966). It was equivalent to PCA but it is used to calculate inter unit distance. It was the simplest use of factorial analysis.

3.2.5.4. Canonical variate analysis

Canonical variate analysis (CVA) was complementary to D^2-statistic that was a sort of multivariate analysis where canonical vector and roots responding different axes of differentiation and the amount of variation accounted for by each of such axes, respectively and derived. Linear combination of original variability could be found out using CVA and gave the function of the original variables that can be used to discriminate between the groups. It gave a series of orthogonal transformation that sequentially maximize the ratio of among groups to within group variation.

3.2.5.5. Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters followed by Rao (1952), and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes using the following formuls:

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} (Y_i^j - Y_j^k)^2 \qquad j \neq k$$

Where,
Y = Uncorrelated variable (character) which varies from i = 1................ to x

x = Number of characters

Superscript j and k to Y = A pair of any two genotypes.

3.2.5.6. Computation of average intra-cluster distances

All possible D^2 values within the members of a cluster from PCO were used to calculate the average intra cluster distance for each cluster using the following formula:

$$\text{Intra cluster distance} = \sum D^2/n$$

Where,

D^2 was the sum of distances between all possible combinations (n) of the genotypes included in a cluster. The square root of the D^2 values represented the distance (D) within cluster.

3.2.5.7. Computation of average inter-cluster distances

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

$$\text{Inter cluster distances} = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}$ = The sum of distances between all possible combinations of the populations in cluster i and j

n_i = number of population in cluster i

n_j = number of population in cluster j

3.2.5.8. Cluster diagram

Using the values of intra and inter cluster distances ($D = \sqrt{D^2}$), a cluster diagram was drawn according to Singh and Chaudhury (1985) that gave a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.2.5.9. Selection of genotypes for further hybridization program

The parents for hybridization program was selected based on the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance having maximum heterosis and wide genetic variability. According to Singh and Chaudhury (1985), the following points should be considered during selection of genotypes for further hybridization program:

a) Choice of cluster from which genotypes are selected for use as parents,

b) Selection of particular genotypes from the selected clusters,

c) Relative contribution of the characters to the total divergence, and

d) Other important characters of the genotypes performance.

Chapter IV

Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

A field experiment consisted of 39 rice genotypes was laid out in a randomized complete block design (RCBD) with all recommended agronomic practices during January to June of 2011. This chapter comprises the presentation and discussion of the findings obtained from the study. The results of the present investigation are presented under the following headings.

4.1. Genetic variability, heritability and genetic advance

4.2. Correlation coefficient

4.3. Path analysis

4.4. Genetic diversity

4.1. Genetic variability, heritability and genetic advance

The analysis of variance for 12 characters was carried out to partition the total variance due to genotypes and other sources. All the thirty nine genotypes were significantly different for all yield and yield contributing characters (Table 2). The extent of variation among the genotypes in respect of yield and yield contributing characters were studied. The ranges, mean values, mean sum of square (MS_G), phenotypic variance (σ^2_p), genotypic variance (σ^2_g), environmental variance (σ^2_e), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), Environmental coefficient of variation (ECV), heritability (h^2_b), genetic advance (GA) at 5% selection intensity, genetic advance (GA) as percent of mean and coefficient of variation (CV) for characters studied have been presented in Table 2. The PCV was higher than all the corresponding GCV for all the characters indicating the interactions of all the characters with environment to some extent. PCV range

Table 2. Estimation of genetic parameters in thirteen characters of 39 genotypes in rice

Parameters	Range	Mean	MS$_G$	σ^2 p	σ^2g	σ^2 e
Plant height (cm)	**78.93-136.60**	101.45	495.10**	174.02	160.55	13.47
Effective tiller per plant	**8.27-12.47**	10.92	3.35**	1.52	0.92	0.61
Days to 80% flowering (DAS)	**85.33-123.33**	105.31	303.85**	108.90	97.48	11.41
Panicle Length (cm)	**22.11-29.33**	25.38	12.13**	5.40	3.37	2.03
Primary branches per panicle	**8.33-13.44**	10.38	5.49**	2.95	1.27	1.67
Secondary branches per panicle	**17.34-39.44**	25.35	74.26**	39.08	17.59	21.49
Unfilled grains per panicle	**8.89-42.45**	22.09	160.85**	106.85	27.00	79.84
Filled grains per panicle	**109.11-166.78**	136.17	160.85**	255.23	157.05	98.18
1000 seed weight (g)	**17.67-31.00**	24.46	41.47**	17.80	11.84	5.96
Days to maturity (DAS)	**114.00-150.67**	133.65	41.47**	144.17	140.51	3.66
Harvest index	**0.34-0.61**	0.47	0.01**	0.01	0.01	0.00
Grain yield per plant	**132.64-365.48**	243.20	12,217.77**	4522.95	3450.27	1072.68

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

MS$_G$ = Genotypic mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance and σ^2 e = Environmental variance.

Table 2. Cont'd

Parameters	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)	CV (%)
Plant height (cm)	13.00	12.49	3.62	92.26	25.07	24.71	3.62
Effective tiller per plant	11.29	8.76	7.12	60.20	1.53	14.01	7.12
Days to 80% flowering (DAS)	9.91	9.37	3.21	89.52	19.24	18.27	3.21
Panicle Length (cm)	9.15	7.23	5.61	62.38	2.99	11.76	5.61
Primary branches per panicle	16.54	10.87	12.47	43.17	1.53	14.71	12.47
Secondary branches per panicle	24.65	16.54	18.28	45.02	5.80	22.87	18.28
Unfilled grains per panicle	46.77	23.51	40.43	25.27	5.38	24.36	40.43
Filled grains per panicle	11.73	9.20	7.28	61.53	20.25	14.87	7.28
1000 seed weight (g)	17.24	14.06	9.98	66.52	5.78	23.63	9.98
Days to maturity (DAS)	8.98	8.87	1.43	97.46	24.11	18.04	1.43
Harvest index	15.62	15.34	2.95	96.43	0.15	31.30	2.95
Grain yield per ten plants	27.65	24.15	13.47	76.28	105.68	43.46	13.47

PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, ECV: Environmental coefficient of variation and CV%: Coefficient of variation.

from 9.91% for panicle length to 46.77% for unfilled grains per panicle. Performances of the genotypes for each character are described below.

4.1.1. Plant height (cm)

In the present study, plant height showed the highly significant mean sum of square for genotypes indicating a wide range of variation among the genotypes for plant height (Table 2). Highly significant variation for this character was also reported by Seyoum *et al.* (2012). The mean plant height was 101.45 cm with a range of 78.93 cm to 136.60 cm. Variation in plant height is presented in figure 1. The phenotypic and genotypic variances for this character were very high (174.02 and 160.55, respectively). Similar result was also reported by Balakakrishna *et al.* (1973). The environmental variance was also high (13.47) as the phenotypic variance was higher than the genotypic variance indicating influence of environment on the expression of the genes controlling this character (Table 2). Same result was also observed by Chakraborty and Chakraborty (2010). The PCV and GCV values were moderate (13% and 12.49%, respectively) with little difference indicating least influence of environment on this characters (Table 2). Hossain and Haque (2003) also reported similar result for GCV. The heritability estimation for this character was high (92.2%) with high genetic advance (25.07) and high genetic advance in percent of mean (24.71) indicating apparent variation for genotypes, predominance of additive gene action in the expression this trait which may help in phenotypic selection (Table 2). Similar findings were reported by Balakakrishna *et al.* (1973), Das *et al.* (1992), Hossain and Haque (2003), Singh *et al.* (2006), Sabesan *et al.* (2009) and Pandey *et al.* (2010). Therefore, this character is potential to be used for achieving genetic gain through selection. This result confirmed the findings of Prasad *et al.* (2001).

Figure 1. Showing variation in plant height and flowering in different genotypes

4.1.2. Number of effective tillers per plant

Number of effective tillers per plant showed a highly significant mean sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of number of effective tillers per plant was 10.92 with a range from 8.27 to 12.47. The phenotypic and genotypic variances for this character were 1.52 and 0.92, respectively. The phenotypic variance was higher than genotypic variance indicating influence of environment on the expression of this character. The PCV (11.29%) was greater than GCV (8.76%) indicating influence of environment on this character, whereas moderate values were for PVC but low for the GCV (Table 2). Similar result for GCV was also reported by Li *et al.* (1991) and Biswas *et al.* (2000). The environmental variation was found 60.20%. The heritability estimation of this character was high (60.20) with very low genetic advance (1.53) and moderate genetic advance in percent of mean (14.01) indicating non-additive gene effects and that expression might be influenced by non-genetic factors (Table 2). High heritability with high genetic advance over percent of mean was obtained by Subbaiah *et al.* (2011). High heritability with moderate genetic advance was observed by Chakraborty and Chakraborty (2010). Therefore, this character could be used in genetic gain through selection.

4.1.3. Days to 80% flowering (DAS)

Days to 80% flowering showed a highly significant mean sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). Highly significant variation for this character was also reported by Seyoum *et al.* (2012). The mean of this character was 105.31 with a range from 85.33 to 123.33. Variation in flowering is presented in Figure 1. The phenotypic and genotypic variances for this character were 108.90 and 97.48, respectively, where former was higher than later indicating influence of environment on expression of this trait. The PCV (9.91%) slightly differed from GCV (9.37%) indicating minor influence of environment and additive gene action on this character and both with lower values (Table 2). Less difference between GCV and PCV was also reported by Chakraborty and Chakraborty (2010), Vange (2008). Low PCV and GCV were also reported by Kole *et al.* (2008) and Abarshahr *et al.* (2011). The environmental coefficient of variation was 89.52%. The heritability estimation showed high heritability (89.52) with moderate genetic advance (19.24) and moderate genetic advance in percent of mean (18.27) indicating the presence of additive and non-additive gene effect on the control of this character (Table 2). High heritability with low genetic advance was also reported by Chakraborty and Chakraborty (2010). High heritability with high genetic advance was reported by Vange (2008). Therefore, this character also could be used to achieve genetic gain through selection.

4.1.4. Panicle length (cm)

Panicle length showed a highly significant mean sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). Highly significant variation was also reported by Seyoum *et al.* (2012). The mean of this character was 25.38 with a range from 22.11 cm to 29.33 cm. Panicles from different genotypes are presented in Figure 2 and Figure 3 showing variation. The phenotypic and genotypic variances for this character were 5.40 and 3.37, respectively, whereas the former was higher than later indicating influence of environment on expression of this character. The PCV (9.15%) was moderately differed from GCV (7.23%) indicating the moderate influence of environment on this

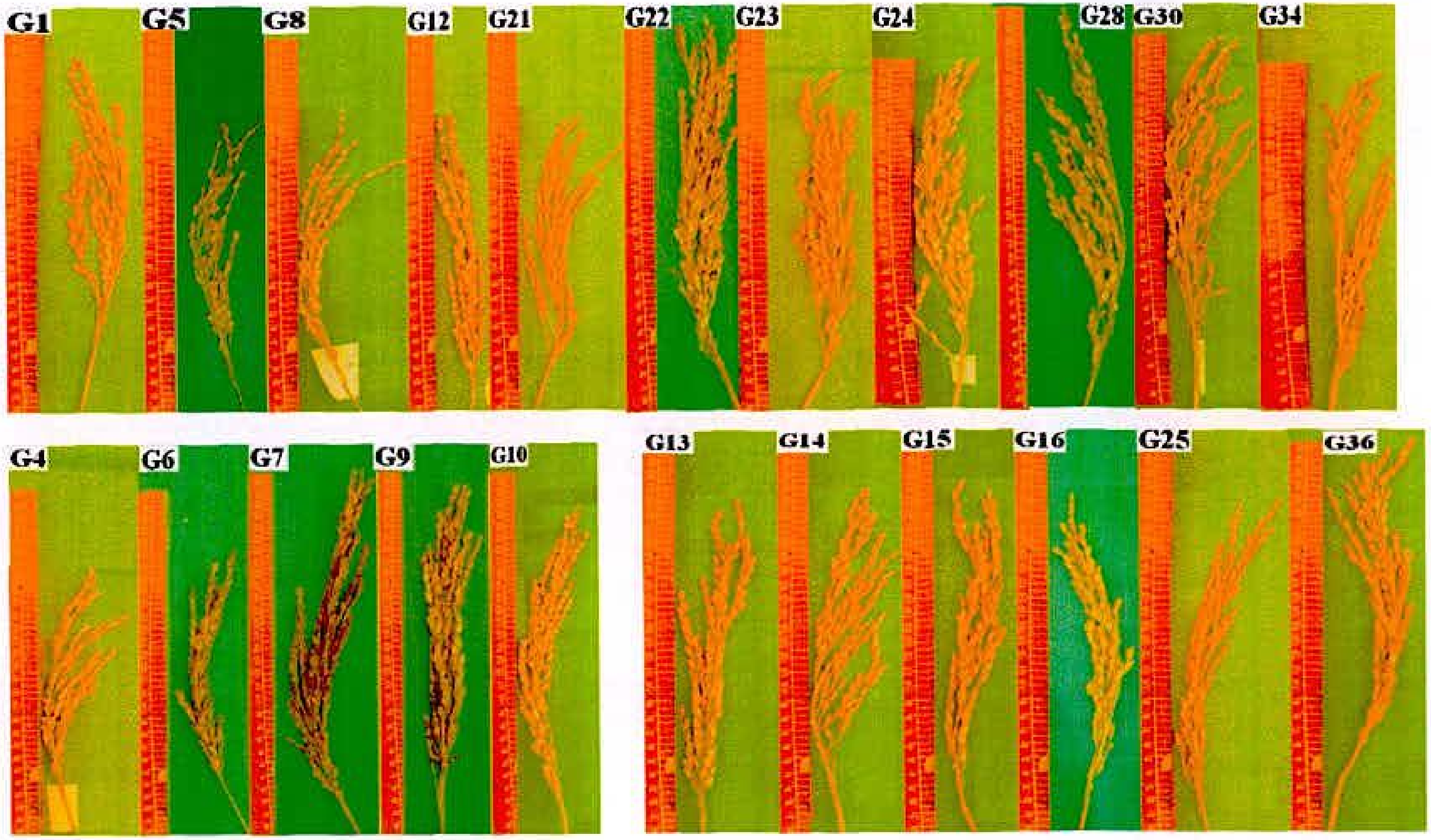


Figure 2. Panicles of different genotypes from cluster I (top), cluster II (bottom left) and cluster III (bottom right)

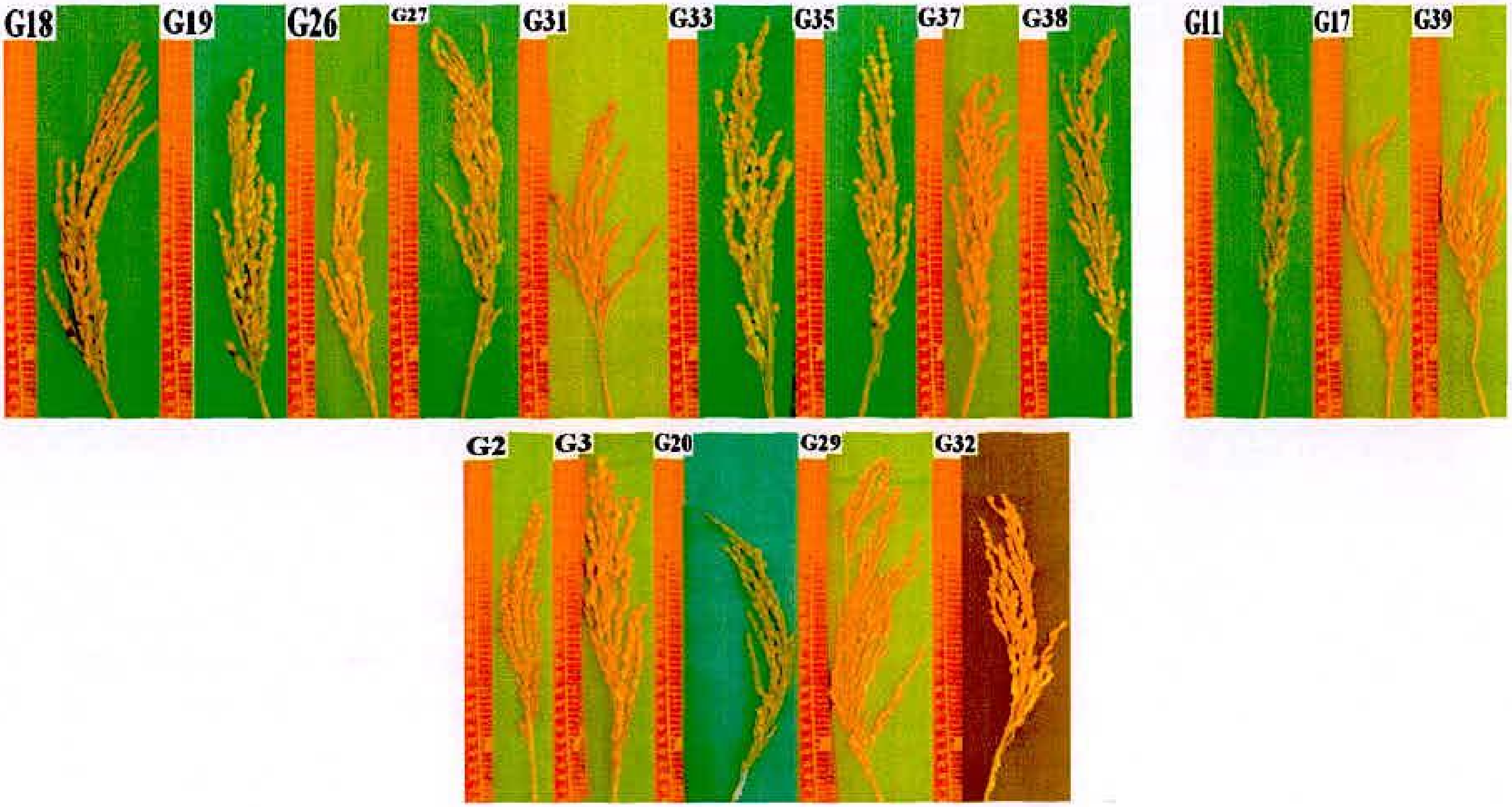


Figure 3. Panicles of different genotypes from cluster V (top left), cluster IV (top right) and cluster VI (bottom)

character and both with lower values (Table 2). Lower GCV and PCV values were also reported by Biswas *et al.* (2000), Kole *et al.* (2008) and Vange (2008). The environmental coefficient of variability was 62.38%. This character showed low heritability estimation (5.61) with low genetic advance (2.99) and moderate genetic advance in percent of mean (11.76) (Table 2). Therefore, this character is considered to be of no use in achieving genetic gain through selection.

4.1.5. Number of primary branches per panicle

Number of primary branches per panicle showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 10.38 with a range from 8.33 to 13.44. The phenotypic and genotypic variances for this character were 2.95 and 1.27, respectively, whereas the former was slightly higher than the later indicating minor influence of environment on expression of this character. The PCV (16.54%) was greater than the GCV (10.87%) indicating the influence of environment on this characters and both with moderate values. The environmental coefficient of variation was 12.47%. This character showed moderate heritability estimates (43.17) with genetic advance of 1.53 and moderate genetic advance in percent of mean (14.71) (Table 2). Moderate heritability was also reported by Biswas *et al.* (2000). Therefore this character would have least potentiality to achieve genetic gain through selection.

4.1.6. Number of secondary branches per panicle

Secondary branches number showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 25.35 with a range from 17.34 to 39.44. The phenotypic and genotypic variances for this character were 39.08 and 17.59, respectively, whereas the former was higher than the later indicating the influence of environment on the expression of this character. The PCV (24.65%) was higher than the GCV (16.54%) indicating the influence of environment on this character, whereas the PCV with higher value but moderate for the GCV. The third highest PCV and GCV were found in this character. The environmental coefficient of variation was 18.28%. This character showed moderate heritability estimation (45.02) with genetic advance 5.80 and high genetic advance in percent of mean (22.87) (Table 2). Therefore, this character could be used in selection for genetic gain.

4.1.7. Number of unfilled grains per panicle

Unfilled grains per panicle showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 22.09 with a very highly variable range from 8.89 to 42.45. The phenotypic and genotypic variances for this character were 106.85 and 27.00, respectively, whereas the former was very high than the later indicating great influence of environment on the expression of this character. The PCV (46.77) was very high than the GCV (23.51) indicating a great influence of environment on this character and both showed higher values (Table 2). High GCV was also indicated by De and Suriya (1988). The highest PCV and second highest GCV were found in this character. High GCV and PCV were observed by Iftekharuddaula *et al.* (2001). Wide difference between GCV and PCV was reported by Chakraborty and Chakraborty (2010). The environmental coefficient of variation was 40.4%. This character showed low heritability estimation (25.27) with genetic advance (5.38) and high genetic advance in percent of mean (24.36) (Table 2). Therefore, this character could not or could have little importance in selection for genetic gain.

4.1.8. Number of filled grains per panicle

Filled grains per panicle showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 136.17 with a range from 109.11 to 166.78. Grains from different genotypes are presented in Figure 4 and Figure 5 showing variation. The phenotypic and genotypic variances for this character were 255.23 and 157.05, respectively, whereas the former was greatly higher than the later indicating great influence of environment on this character (Table 2). The highest genotypic variance and phenotypic variance was also reported by Akhter *et al.* (2010), Balakakrishna *et al.* (1973). The PCV (11.73%) was slightly higher than the GCV (9.20%) indicating influence of environment on this character, whereas the PCV showed moderate values but low for the GCV. The environmental coefficient of variation was 7.28%. This character showed high heritability estimation (61.53) with genetic advance 20.25 and moderate genetic advance in percent of mean (14.87) indicating the importance of additive and non-additive gene effect on the control of this character (Table 2). High heritability with high genetic advance was also reported by Bisne *et al.* (2009), Hossain and Haque (2003), Habib *et al.* (2005), Prasad *et al.* (2001). High heritability with high genetic advance over percent of mean was reported by Ullah, *et al.* (2011). Therefore, this character could be used in genetic gain through selection.

Figure 4. Grains of different genotypes from cluster I (top), cluster III (bottom left) and cluster II (bottom right)

Figure 5. Grains of different genotypes from cluster V (top), cluster IV (bottom left) and cluster VI (bottom right)

4.1.9. 1000-grain weight (g)

1000-grain weight showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). Highly significant of variation for this character was also showed by Seyoum *et al.* (2012). The mean of this character was 24.46 gm with a range from 17.67gm to 31.00 gm. The phenotypic and genotypic variances for this character were 17.80 and 11.84, respectively, the former was higher than the later indicating the influence of environment on this character. Both the PCV (17.024%) and GCV (14.06%) had moderate value indicating the influence of environment on this character, whereas ECV (9.98) had lower value (Table 2). High genotypic coefficient of variation was reported by Prasad *et al.* (2001), Hossain and Haque (2003), Ullah, *et al.* (2011), Seyoum *et al.* (2012). This character showed high heritability estimation (66.52) with genetic advance 5.78 and high genetic advance in percent of mean (23.63) indicating role of additive gene action in the expression of this character (Table 2). Same result was also observed by Habib *et al.* (2005), Ullah, *et al.* (2011), Das *et al.* (1992), De and Suriya (1988). Therefore, this character could be used to achieve genetic gain through selection.

4.1.10. Days to maturity (DAS)

Days to 80% maturity showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 133.65 days after sowing (DAS) with a range from 114.00 DAS to 150.67 DAS. The phenotypic and genotypic variances for this character were 144.17 and 140.51 respectively, the former was slightly higher than the later indicating minor influence of environment on this character. Both PCV (8.98%) and GCV (8.87%) had low values with very low ECV

(1.43%). Slight difference was observed between PCV and GCV indicating negligible influence on this character with almost only additive gene action (Table 2). Lower GCV and PCV were also reported by Iftekharuddaula *et al.* (2001), Hossain and Haque (2003). Lower difference between GCV and PCV indicating less influence of environment on these characters was also found by Vange (2008), Hossain and Haque (2003). This character showed very high heritability estimation (97.46) with high genetic advance 24.11 and moderate genetic advance in percent of mean (18.04) suggesting the importance of additive and non-additive gene effects on the control of this character (Table 2). Same result was also reported by Das *et al.* (1992), Akhtar *et al.* (2011), Li *et al.* (1991), Hossain and Haque (2003).

4.1.11. Harvest index

Harvest index showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 0.47 with a range from 0.34 to 0.61. Both the phenotypic and genotypic variances for this character were 0.01 indicating no environmental influence on this character. Both PCV (15.62%) and GCV (15.34%) had moderate values with very low ECV (2.95%) (Table 2). Slight difference in between PCV and GCV indicating negligible influence of environment on this character Moderate GCV and PCV were also reported by Kole *et al.* (2008). The heritability estimation for this character was very high (96.43) with very low genetic advance 0.15 and high genetic advance in percent of mean (31.30) indicating presence of both additive and non-additive gene action that may be expressed consistently in segregating generations and might be very helpful in breeding programs (Table 2).

4.1.12. Grain yield per ten plants (g/ten plants)

Grain yield per ten plants showed a highly significant sum of square for genotypes indicating a wide range of variation among the genotypes for this character (Table 2). The mean of this character was 243.20 gm with a range from 132.64 gm to 365.48 gm. The phenotypic and genotypic variances for this character were 4522.95 and 3450.27, respectively, the former is higher than the later indicating the influence of environment on this character. Both the PCV (27.65%) and GCV (24.15%) were high with moderate ECV (13.47%) indicating the influence of environment on this character (Table 2). Same result was also found by Seyoum *et al.* (2012), Sing and Yunus (1988), Yousuf *et al.* (1994). The highest GCV and second highest PCV were found in this character. The highest PCV and GCV were also reported by Pandey *et al.* (2010), Singh *et al.* (2006), Das *et al.* (1992). The heritability estimation for this character was high (76.28) with very high genetic advance 105.68 and high genetic advance in percent of mean (43.46) indicating the presence of additive and non-additive gene action and could be helpful to achieve genetic gain through selection (Table 2). High heritability with high genetic advance was also reported by Chakraborty and Chakraborty (2010), Habib *et al.* (2005), Bisne *et al.* (2009), Subbaiah *et al.* (2011), Prasad *et al.* (2001), Yousuf *et al.* (1994). High heritability with high genetic advance in percentage of means was reported by Ullah, *et al.* (2011), Das *et al.* (1992), Sabesan *et al.* (2009).

4.2. Correlation coefficient

The genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes in rice are presented in Table 3. Generally the genotypic correlation co-efficient is higher than the phenotypic correlation coefficient indicating a fairly strong inherent relationship among the characters. Lower value of phenotypic correlation coefficient indicates less influence of environment on the character. Yield is directly or indirectly influenced by several correlated quantitative characters that make difficult for the selection of yield. For the breeding or crop improvement programs, yield should be selected on the base of yield considering the direct or indirect effect of the yield contributing characters.

4.2.1. Plant height (cm)

At both genotypic and phenotypic levels, plant height showed highly significant negative correlation with grain yield per ten plants (Table 3). Same result was reported by Prasad *et al.* (2001), Iftekharuddaula *et al.* (2001). This indicated the yield could be improved by dwarfing the plant. Number of secondary branches showed significant positive correlation with this character only at genotypic level indicating number of secondary branches was dependent on plant height. This character showed highly significant negative correlation with harvest index and number of effective tillers per ten plants and insignificant negative correlation with 1000-grains weight, whereas insignificant positive correlation with days to flowering, panicle length, primary branches per panicle, filled grains per panicle, and days to maturity at both genotypic and phenotypic level (Table 3). Significant correlation of this character with number of effective tillers was also reported by Rokonuzzaman *et al.* (2008).

4.2.2. Number of effective tillers per plant

Number of effective tillers per plant showed highly significant positive correlation with grain yield per ten plants and harvest index at both genotypic and phenotypic levels (Table 3). Same result for grain yield also reposted by Akinwale *et al.* (2011), Golam *et al.* (2011), Chakraborty *et al.* (2010), Chakraborty and

Table 3. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters 39 rice genotypes

Characters		ETPP	DF	PL	PBP	SBP	UGPP	FGPP	TGW	DM	HI	GY
PH	r_g	-0.408**	0.074	0.136	0.102	0.218*	0.022	0.167	-0.176	0.134	-0.756**	-0.560**
	r_p	-0.299**	0.069	0.092	0.054	0.003	-0.054	0.168	-0.170	0.132	-0.720**	-0.537**
ETPP	r_g		0.047	-0.051	-0.250*	-0.283*	0.163	-0.059	0.152	0.006	0.501**	0.441**
	r_p		0.068	-0.027	-0.118	-0.185*	0.030	-0.032	0.035	0.001	0.375**	0.327**
DF	r_g			0.778**	0.591**	0.399**	0.503**	0.060	-0.247*	0.896**	-0.128	-0.138
	r_p			0.594**	0.399**	0.217*	0.239*	-0.002	-0.168	0.854**	-0.116	-0.125
PL	r_g				0.545**	-0.076	0.403**	0.114	-0.292**	0.669**	-0.009	-0.014
	r_p				0.400**	0.040	0.369**	0.004	-0.069	0.542**	-0.013	-0.013
PBP	r_g					0.006	0.230*	0.243*	-0.045	0.413**	-0.020	0.032
	r_p					0.146	0.168	0.135	0.180	0.309**	-0.016	0.020
SBP	r_g						-0.011	-0.169	-0.469**	0.340**	-0.523**	-0.557**
	r_p						0.078	0.002	-0.196*	0.241*	-0.364**	-0.390**
UGPP	r_g							-0.296**	-0.768**	0.421**	-0.305**	-0.526**
	r_p							-0.202*	-0.223*	0.212*	-0.192*	-0.278**
FGPP	r_g								0.195*	-0.036	0.102	0.345**
	r_p								0.122	-0.038	0.084	0.272*
TGW	r_g									-0.300**	0.495**	0.537**
	r_p									-0.230*	0.405**	0.442**
DM	r_g										-0.229*	-0.173
	r_p										-0.222*	-0.172
HI	r_g											0.833**
	r_p											0.833**

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

PH: Plant height (cm), ETPP: Effective tiller per plant, DF: Days to 80% flowering (DAS), PL: Panicle Length (cm), PBP: Primary branches per panicle, SBP: Secondary branches per panicle, UGPP: Unfilled grains per panicle, FGPP: Filled grains per panicle, TGW: 1000 grains weight (g), DM: Days to maturity (DAS), HI: Harvest index and GY: Grain yield per ten plants

Chakraborty (2010), Khan *et al.* (2009), Vange (2008), Rokonuzzaman *et al.* (2008), Kole *et al.* (2008), Agahi *et al.* (2007) and Prasad *et al.* (2001). This indicated the yield could be improved by increasing the number of effective tillers. Number of primary branches per panicle showed significant negative correlation with this character only at genotypic level indicating number of primary branches was dependent on number of effective tillers negatively. This character showed significant negative correlation with secondary branches per panicle and insignificant negative correlation with panicle length, filled grains per panicle, whereas insignificant positive correlation with days to flowering, unfilled grains per panicle, 1000-grain weight and days to maturity at both genotypic and phenotypic level (Table 3).

4.2.3. Days to 80% flowering (DAS)

Days to 80% flowering showed insignificant negative correlation with grain yield per ten plants and harvest index at both genotypic and phenotypic levels. This indicated the yield could not be improved by using this character (Table 3). Significant positive correlation of this character with grain yield was reported by Sadeghi (2011), Akhter *et al.* (2010). 1000-grain weight showed significant negative correlation with this character only at genotypic level indicating 1000-grains weight was dependent on flowering negatively. This character showed significant positive correlation with panicle length, primary branches per panicle, secondary branches per panicle, number of unfilled grains per panicle and days to maturity at both genotypic and phenotypic level (Table 3).

4.2.4. Panicle length (cm)

Panicle length showed insignificant negative correlation with grain yield per ten plants and harvest index at both genotypic and phenotypic levels (Table 3). This indicated the yield could not be improved by using this character. Highly significant positive correlation of this character with grain yield was found by Ullah *et al.* (2011), Sadeghi (2011), Chakraborty and Chakraborty (2010), Khan *et al.* (2009). This character showed significant positive correlation with number of primary branches per panicle, number of unfilled grains per panicle and days to maturity, whereas there was insignificant positive correlation with number of filled grains per panicle at both genotypic and phenotypic levels (Table 3).

4.2.5. Number of primary branches per panicle

Primary branches per panicle showed insignificant positive correlation with grain yield per ten plants and number of secondary branches per panicle at both genotypic and phenotypic levels (Table 3). This indicated the yield could not be improved by using this character. Significant positive correlation of this character with yield was reported by Vange (2008). Significant negative correlation was reported by Yousuf *et al.* (1994. Number of unfilled grains and number of filled grains per panicle showed significant positive correlation with this character only at genotypic level indicating the former characters were dependent on primary branches per panicle positively. This character showed significant positive correlation with days to maturity but insignificant positive correlation with secondary branches per panicle at both genotypic and phenotypic levels (Table 3).

4.2.6. Number of secondary branches per panicle

Secondary branches per panicle showed significant negative correlation with grain yield per ten plants, harvest index and 1000-grains weight at both genotypic and phenotypic levels (Table 3). This indicated the yield could be improved by using this character. This character showed significant positive correlation with days to maturity at both genotypic and phenotypic levels (Table 3).

4.2.7. Number of unfilled grains per panicle

Number of unfilled grains per panicle showed significant negative correlation with grain yield per ten plants, harvest index, 1000-grain weight and number of filled grains per panicle at both genotypic and phenotypic levels (Table 3). Same result for grain yield was also reported by Iftekharuddaula *et al.* (2001). This character could be used in the improvement of yield.

4.2.8. Number of filled grains per panicle

Number of filled grains per panicle showed significant positive correlation with grain yield per ten plants at both genotypic and phenotypic levels (Table 3). Same result also recorded by Vange (2008), Khan *et al.* (2009), Habib *et al.* (2005), Agahi *et al.* (2007), Chakraborty *et al.* (2010), Akhter *et al.* (2010), Prasad *et al.* (2001), Bhadru *et al.* (2010), Mahajan *et al.* (1993), Biswas *et al.* (2000), Ullah *et al.* (2011). This indicated the yield could be improved by using this character. 1000-grains weight showed significant positive correlation with this character only at genotypic level indicating 1000-grains weight was dependent on number of filled grains per panicle. This character showed insignificant negative correlation with days to maturity at both genotypic and phenotypic levels (Table 3).

4.2.9. 1000-grains weight (g)

1000-grains weight showed significant positive correlation with grain yield per ten plants and harvest index at both genotypic and phenotypic levels (Table 3). Same result for grain yield also reported by Vange (2008), Das *et al.* (1992), Akhtar *et al.* (2011), Balakakrishna *et al.* (1973), Mirza (1992), Yousuf *et al.* (1994), Iftekharuddaula *et al.* (2001). This indicated the yield could be improved by using this character. This character showed significant negative correlation with days to maturity at both genotypic and phenotypic levels (Table 3).

4.2.10. Days to maturity (DAS)

Days to maturity showed insignificant negative correlation with grain yield per ten plants but significant negative correlation with harvest index (Table 3). This indicated the yield could not be used in the improvement of yield. Positive significant correlation of this character with grain yield was observed by Sadeghi (2011), Akhtar *et al.* (2011).

4.2.11. Harvest index

Harvest index showed significant positive correlation with grain yield per ten plants at both genotypic and genotypic levels (Table 3). Same result also reported by Kole *et al.* (2008), Chakraborty *et al.* (2010), Singh *et al.* (2006), Nayak *et al.* (2004), Iftekharuddaula *et al.* (2001), Ullah *et al.* (2011). This indicated that the yield could be increased by improving harvest index.

4.3. Path coefficient analysis

In this experiment grain, the grain yield was the resultant variable, whereas the plant height, number of effective tillers per plant, days to 80% flowering, panicle length, number of primary branches per panicle, number of secondary branches per panicle, number of unfilled grains per panicle, number of filled grains per panicle, 1000-grains weight, days to maturity and harvest index were causal (independent) variables. The relationship between resultant and causal variables has been presented with path diagram in Figure 6. The residual effect (0.485) indicated that about 50% of the variability in yield per ten plants was contributed by the twelve characters studied in path analysis. This high residual effect towards yield in the present study might be due to many reasons such as other characters which were not studied, environmental factors and sampling errors (Sengupta and Karatia, 1971). Path coefficient analysis showing direct and indirect effects of different characters on yield of rice has been presented in Table 4.

4.3.1. Plant height (cm)

Plant height showed small negative direct effect (-0.020) on grain yield with highly significant negative Pearson correlation (Table 4). Same result was also recorded by Abarshahr *et al.* (2011). This direct effect was moderate. Therefore, selection based on this character would not be effective. The positive indirect effect of this character on yield via panicle length (0.003), number of primary branches per panicle (0.002), number of filled grains per panicle (0.022) and days to maturity (0.024) were negligible in magnitude. The negative indirect effect via number of effective tiller per plant (-0.016), days to 80% flowering (-0.008), number of secondary branches per panicle (-0.016), number of unfilled grains per panicle

Table 4. Path coefficient analysis showing direct and indirect effects of different characters on yield of rice

Characters	Direct effect	Indirect effects											Pearson correlation with yield
		PH	ETPP	DF	PL	PBP	SBP	UGPP	FGPP	TGW	DM	HI	
PH	-0.020	-	-0.016	-0.008	0.003	0.002	-0.016	-0.001	0.022	-0.015	0.024	-0.505	-0.532**
ETPP	0.058	0.006	-	-0.012	-0.001	-0.005	0.021	-0.004	-0.007	0.009	0.000	0.268	0.335**
DF	-0.192	-0.001	0.003	-	0.019	0.017	-0.025	-0.016	0.004	-0.015	0.167	-0.083	-0.114
PL	0.033	-0.002	-0.001	-0.112	-	0.017	-0.004	-0.032	-0.001	-0.007	0.106	-0.009	-0.009
PBP	0.044	-0.001	-0.007	-0.076	0.013	-	-0.017	-0.013	0.022	0.016	0.060	-0.010	0.042
SBP	-0.108	-0.003	-0.011	-0.045	0.001	0.007	-	-0.001	0.005	-0.018	0.048	-0.256	-0.376**
UGPP	-0.088	0.000	0.003	-0.035	0.012	0.006	-0.002	-	-0.043	-0.019	0.036	-0.127	-0.256**
FGPP	0.172	-0.003	-0.002	-0.004	0.000	0.006	-0.003	0.022	-	0.012	-0.005	0.056	0.242**
TGW	0.093	0.003	0.006	0.032	-0.002	0.007	0.021	0.018	0.022	-	-0.045	0.287	0.447**
DM	0.196	-0.002	0.000	-0.164	0.018	0.013	-0.026	-0.016	-0.004	-0.021	-	-0.159	-0.157
HI	0.715	0.014	0.022	0.022	0.000	-0.001	0.039	0.016	0.014	0.037	-0.044	-	0.833**

Residual effect: 0.485, ** Correlation is significant at the 0.01 level. * Correlation is significant at the 0.05 level.

PH: Plant height (cm), ETPP: Tiller number per plant, DF: Days to flowering (DAS), PL: Panicle Length (cm), PBP: Primary branches per panicle, SBP: Secondary branches per panicle, UGPP: Unfilled grains per panicle, FGPP: Filled grains per panicle, TGW: 1000 grains weight (g), DM: Days to maturity (DAS), HI: Harvest index and GY: Grain yield per ten plants

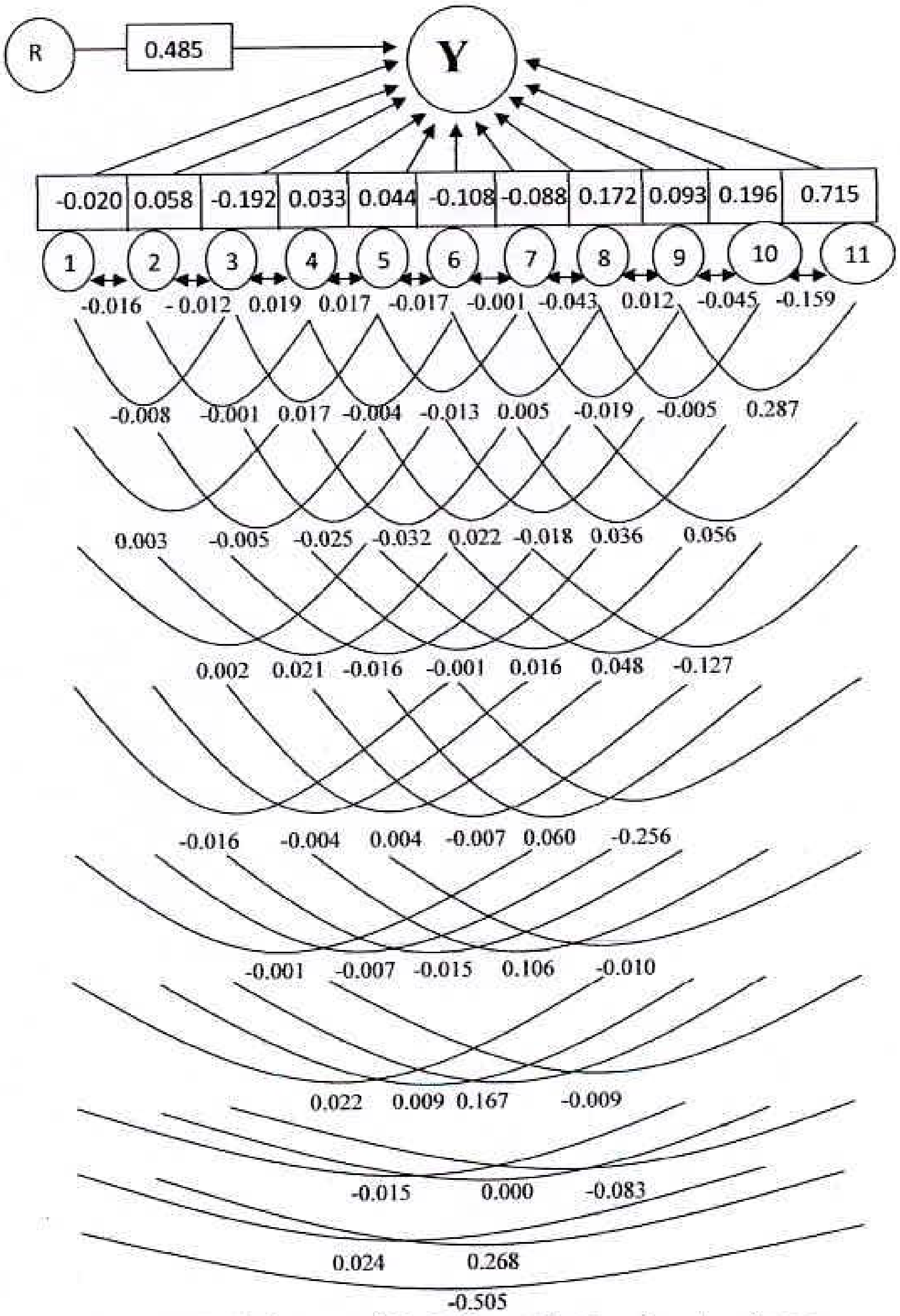


Figure 6. Path diagram of 11 yield contributing characters in rice

Y=Grain yield per ten plants, R=Residual effect, 1=Plant height, 2=Number of effective tillers per plant, 3=Days to 80% flowering, 4=Panicle length, 5=Number of primary branches per panicle, 6=Number of secondary branches per panicle, 7=Number of unfilled grains per panicle, 8=Number of filled grains per panicle, 9=1000-grains weight, 10=Days to maturity, 11=Harvest index

(-0.001), 1000-grains weight (-0.015) were also negligible in magnitude and harvest index (-0.505) was high in magnitude (Table 4).

4.3.2. Number of effective tillers per plant

The number of effective tillers per plant showed positive direct effect (0.058) on grain yield with highly significant positive Pearson correlation (Table 4). Same result also reported by Rokonuzzaman *et al.* (2008), Agahi *et al.* (2007), Sadeghi (2011). This direct effect was negligible. Therefore, selection based on this character would be effective for little bit. The indirect effect of this character via number of secondary branches per panicle (0.021), 1000-grain weight (0.009) and harvest index (0.268) were positive, where the former two were negligible and the rest was moderate. There was no indirect effect this character on grain yield via days to maturity (0.000). The indirect effect of this character on grain yield via days to 80% flowering (-0.012), panicle length (-0.001), number of primary branches per panicle (-0.005), number of unfilled grains per panicle (-0.004) and number of filled grains per panicle (-0.007) were negative and negligible in magnitude (Table 4).

4.3.3. Days to 80% flowering (DAS)

The direct effect of days to 80% flowering on grain yield per ten plants was negative (-0.192) and had insignificant negative Pearson correlation (Table 4). This direct effect was in lower category. Positive direct effect was reported by Abarshahr *et al.* (2011). Therefore, selection based on this character would not be effective. The indirect effect of this character on grain yield per ten plants via panicle length (0.019), number of primary branches per panicle (0.017), number of filled grains per panicle (0.004) and days to maturity were positive but very low in magnitude excluding later one. The indirect negative effect of this character on grain yield per ten plants via number of secondary branches per panicle (-0.025), number of unfilled grains per panicle (-0.016), 1000-grain weight (-0.015) and harvest index (-0.083) were negative and very low in magnitude (Table 4).

4.3.4. Panicle length (cm)

Panicle length showed small direct positive effect (0.033) on grain yield per ten plants and insignificant negative Pearson correlation (Table 4). Same result was also suggested by Chakraborty *et al.* (2010). This direct effect was negligible. Therefore, selection based on this character would be effective for little bit. The indirect effect of this character on grain yield via number of primary branches per panicle (0.017) and days to maturity (0.106) were positive and the former was negligible in magnitude and the rest was also low in magnitude. The indirect effect of this character on grain yield via number of secondary branches per panicle (-0.004), number of unfilled grains per panicle (-0.032), number of filled grains per panicle (-0.001), 1000-grains weight (-0.007) and harvest index (-0.009) were negative and negligible in magnitude (Table 4).

4.3.5. Number of primary branches per panicle

Number of primary branches per panicle showed small direct positive effect (0.044) and insignificant positive Pearson correlation (Table 4). This direct effect was negligible. Therefore, selection based on this character would be effective for little bit. The indirect effect of this character on grain yield per ten plants via number of filled grains per panicle (0.022), 1000-grain weight (0.016) and days to maturity was positive but negligible in magnitude. The indirect effect of this character on grain yield via number of secondary branches per panicle (-0.017), number of unfilled grains per panicle (-0.013) and harvest index (-0.010) were negative and negligible in magnitude (Table 4).

4.3.6. Number of secondary branches per panicle

Number of secondary branches per panicle showed negative direct effect (-0.108) on grain yield per ten plants and significant negative correlation. This direct effect was in lower category (Table 4). Therefore, selection based on this character would not be effective. The indirect effect of this character on grain yield via number of filled grains per panicle (0.005) and days to maturity (0.048) were positive and negligible in magnitude. The indirect of this character on grain yield via number of unfilled grains per panicle (-0.001), 1000-grains weight (-0.018) and harvest index (-0.256) were negative where the former two was negligible in magnitude and the rest was moderate (Table 4).

4.3.7. Number of unfilled grains per panicle

The negative direct effect (-0.088) was found in case of number of unfilled grains per panicle on grain yield and this character had highly significant negative Pearson correlation (Table 4). This direct effect was negligible. Therefore, selection based on this character would not be effective. The indirect effect of this character on grain yield via days to maturity (0.036) was positive and negligible. The indirect effect of this character on grain yield via number of filled grains per panicle (-0.043), number 1000-grains weight (-0.019) and harvest index (-0.127) were negative and the former two were negligible whereas the rest one also in lower category (Table 4).

4.3.8. Number of filled grains per panicle

The third highest positive direct effect (0.172) was estimated for number of filled grains per panicle on grain yield per ten plants and this character had highly significant positive Pearson correlation (Table 4). This direct effect was in lower category. Therefore, selection based on this character would be effective for little bit. Same result also reported by Khan *et al.* (2009), Agahi *et al.* (2007), Kole *et al.*

(2008), Prasad *et al.* (2001), Sadeghi (2011). The indirect effect of this character on grain yield via 1000-grains weight (0.012) and harvest index (0.056) were positive and small in magnitude. The indirect effect of this character on grain yield via days to maturity (-0.005) were negative and negligible in magnitude (Table 4).

4.3.9. 1000-grains weight (g)

1000-grains weight showed positive direct effect (0.093) on grain yield per ten plants and this character had very highly significant positive Pearson correlation (Table 4). This direct effect was negligible. Same result was also reported by Habib *et al.* (2005), Agahi *et al.* (2007), Kole *et al.* (2008), Chakraborty *et al.* (2010), Sadeghi (2011). Therefore, selection based on this character would be effective for little bit. The indirect effect of this character on grain yield via harvest index (0.287) and via days to maturity (-0.045) were moderately positive and negligible negative, respectively (Table 4).

4.3.10. Days to maturity (DAS)

Days to maturity showed the second highest positive direct effect (0.196) on grain yield per ten plants and had insignificant negative Pearson correlation (Table 4). Same result also recorded by Habib *et al.* (2005), Sadeghi (2011). This direct effect was in lower category. Therefore, selection based on this character would be effective for little bit. The indirect effect of this character on grain yield via harvest index (-0.159) was negative and in lower category (Table 4).

4.3.11. Harvest index

Harvest index showed the highest positive direct effect (0.715) on grain yield per ten plants and had highly significant positive Pearson correlation (Table 4). Same result was also recorded by Chakraborty *et al.* (2010). This was categorized in higher category. Therefore, selection based on this character would be the most effective.

4.4. Genetic diversity

Genetic diversity assessment between and within groups or clusters is very important for the proper selection of parents for the better search of heterosis (Murthy and Arunachalam, 1966). The results of genetic diversity analysis are discussed in followings.

4.4.1. Principal component analysis

The principal component analysis (PCA) provided eigen values and percent of variation in respect 12 component characters in 39 rice genotypes (Table 5). The result showed that only the first three principal components jointly accounted for 65.79% of the total variation among the genotypes, while these three exhibited eigen values above unity. The first two principal axes accounted for 52.76% of the total variation among the 12 characters of the total genotypes. Genetic diversity analysis using PCA were also followed by Anandan *et al.* (2011), Latif *et al.* (2011), Anandan *et al.* (2011).

4.4.2. Construction of scatter diagram

A two dimensional scatter diagram (Z_1-Z_2) was constructed using component 1 as X-axis and component 2 as Y-axis based on the values of principal component scores 1 and 2 obtained from the principal component analysis. The distribution of genotypes in scattered diagram (Figure 7) was apparently distributed into six clusters, which revealed that there exists considerable diversity among the genotypes. The scatter diagram of 39 rice genotypes revealed that the genotype G36 (BRRI dhan 45) was most distantly located from G10 (Tharak dhan), followed by G7 (Jumma Bini-shorter grain), G4 (Badeye dhan) and G9 (Ameiye dhan) indicating that these genotypes were more diverged than the others.

Table 5. Eigen values and percent of variation in respect of 12 characters in 39 rice genotypes

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
1	3.7732	31.44	31.44
2	2.5580	21.32	52.76
3	1.5635	13.03	65.79
4	0.9523	7.94	73.73
5	0.8738	7.28	81.01
6	0.7403	6.17	87.18
7	0.5872	4.89	92.07
8	0.3144	2.62	94.69
9	0.2965	2.47	97.16
10	0.1542	1.28	98.44
11	0.1117	0.93	99.37
12	0.0750	0.63	100.00

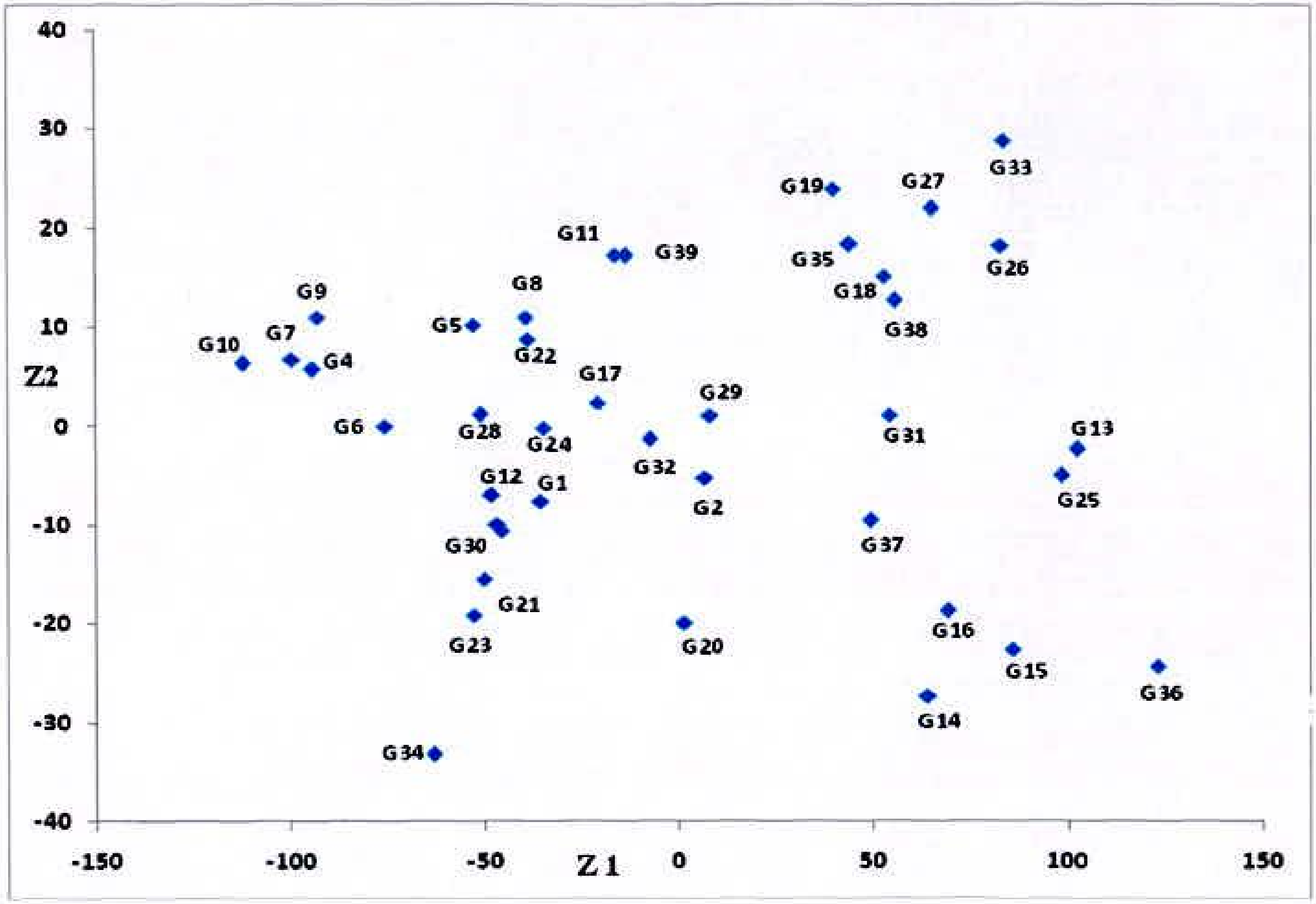


Figure 7. Scatter diagram of 39 rice genotypes based on their principal component scores

4.4.3. Principal coordinate analysis

Inter genotypic distance was obtained from principal coordinate analysis (PCO) on auxiliary of principal component analysis for all possible combinations between pairs of genotypes. The ten highest and ten lowest genotypic distances among 39 rice genotypes are presented in Table 6. The highest inter genotype distance was found between genotypes G10 (Tharak dhan) and G36 (BRRI dhan45) (237.406) followed by distances between G7 (Jumma Bini-shorter grain) and G36 (BRRI dhan 45) (224.811). The most distantly genotypes were between cluster II and cluster III. The difference between the highest and lowest inter genotypic distance indicated the presence of variability among the genotypes.

The lowest inter genotypic distance was found between G30 (BRRI dhan 33) and G39 (BRRI dhan 50) (1.234) followed by genotypes between G8 (Kabarak dhan) and G22 (BR25) (2.241), G3 (Kamarang dhan) and G11 (Indian Pajam) (2.432) and G12 (Jumma Kabarak) and G30 (BRRI dhan 33) (3.230). The magnitude of the intra cluster distances was not always proportional to the number of genotypes in the clusters (Table 6). The cluster I was consisted of 11 genotypes (Table 8) but its intra cluster distance was not necessarily the highest (Table 7). The highest intra cluster distance was estimated for cluster IV (0.589) consisted of 3 genotypes followed by cluster VI (0.143) with 5 genotypes, cluster II (0.139) with 5 genotypes, cluster III (0.065) with 6 genotypes, cluster V (0.026) with 9 genotypes and cluster I (0.023) with highest number of genotypes (11).

Table 6. Ten highest and ten lowest inter genotypic distance among the 39 rice genotypes

Highest distance				Lowest distance			
Sl. No.	Genotype		Distance	Sl. No.	Genotype		Distance
01	G10	G36	237.406	01	G30	G39	1.234
02	G7	G36	224.811	02	G8	G22	2.241
03	G4	G36	219.431	03	G3	G11	2.432
04	G9	G36	218.957	04	G12	G30	3.230
05	G10	G13	214.954	05	G18	G38	3.750
06	G10	G25	211.047	06	G12	G39	4.255
07	G7	G13	202.222	07	G21	G23	4.539
08	G10	G15	200.211	08	G13	G25	4.870
09	G6	G36	199.847	09	G4	G7	5.387
10	G7	G25	198.329	10	G4	G9	5.452

4.4.4. Canonical variate analysis

The canonical variant analysis (CVA) was carried out to obtain the cluster distances (Mahalanobis's D^2 values). The values of the inter cluster distance (D^2) are presented in Table 7. Inter cluster distances represented the distances among the clusters and indicated the index of genetic diversity among them. The inter cluster distance was larger than the intra cluster distances that suggested the wider genetic diversity among the genotypes of different clusters.

The inter cluster distance was maximum between cluster II and cluster III (15.842) indicating more diversity among the genotypes of this two clusters followed by the distance between cluster II and cluster V (11.914), cluster I and cluster III (11.680), cluster III and cluster IV (10.996), cluster I and cluster V (8.659), cluster IV and cluster VI (8.439), cluster II and cluster IV (7.973), cluster II and cluster VI (7.947), cluster IV and cluster V (6.970), cluster III and cluster V (6.375), cluster I and cluster IV (5.953), cluster V and cluster VI (5.696), cluster IV and cluster VI (5.500), cluster I and cluster II (4.833), cluster I and cluster VI (3.614) (Table 6). The maximum inter cluster distance indicated that the genotypes of cluster II were far away from the genotypes of cluster III. Similarly, the higher inter cluster values between clusters II and V, I and III, III and IV, I and V, IV and VI, II and IV, II and VI, IV and V, III and V, I and IV, V and VI, IV and VI, I and II, I and VI indicated that the genotypes belonging to each pair of cluster were far diverse from each other (Figure 8). The lowest inter cluster distance was found between cluster I and cluster VI (3.614) indicating the genotypes this two clusters were genetically closed to each other. The higher the inter cluster distance and intra cluster distance, the higher the variability among genotypes between and within clusters, respectively. On the other hand, the lower the inter cluster distances and intra cluster distances, the lower the

Table 7. Intra cluster distances (Bold) and inter cluster distances (D^2) for 39 genotypes

Cluster	I	II	III	IV	V	VI
I	**0.023**	4.833	11.680	5.953	8.659	3.614
II		**0.139**	15.842	7.973	11.914	7.947
III			**0.065**	10.996	6.375	8.439
IV				**0.589**	6.970	5.500
V					**0.026**	5.696
VI						**0.143**

variability among the genotypes between and within the clusters, respectively. The relationships were also reflected in the scatter diagram (Figure 7). The cluster mean of 12 characters of 39 rice genotypes are presented in Table 10. There was existence of differences for almost all of the characters.

The genotypes belonging to the distant clusters could be used in hybridization programs for obtaining a wide spectrum of variation among the segregates. Similar report was also suggested by Yadav *et al.* (2011), Vennila *et al.* (2011), Baradhan and Thangavel (2011). These results of this study confirmed the clustering pattern of the genotypes according to principal component analysis. It is expected that the crosses between the genotypes of clusters II and III, clusters II and V, clusters I and III, clusters III and IV would exhibit high heterosis and produce new combination with desirable traits. The genotypes of distant cluster could be used for further hybridization programs.

4.4.5. Non-hierarchical clustering

Thirty nine rice genotypes were grouped into six different clusters based on non-hierarchical clustering using co-variance matrix. Distributions of genotypes into different clusters are presented in Table 9. The maximum number of genotypes were grouped in cluster I containing 11 genotypes, followed by cluster V, cluster III, cluster II/cluster VI and cluster IV containing 9, 6, 5 and 3 genotypes, respectively. The minimum numbers of genotypes were grouped in cluster IV containing 3 genotypes. The genotypes collected from Chittagong Hill Tracts (CHT) were distributed in all clusters except cluster V. Whereas the genotypes collected from BRRI were distributed in all the clusters except cluster II. All the four genotypes collected from Lal Teer Seed Ltd. along with BRRI Dhan 28 and BRRI Dhan 45 were grouped in

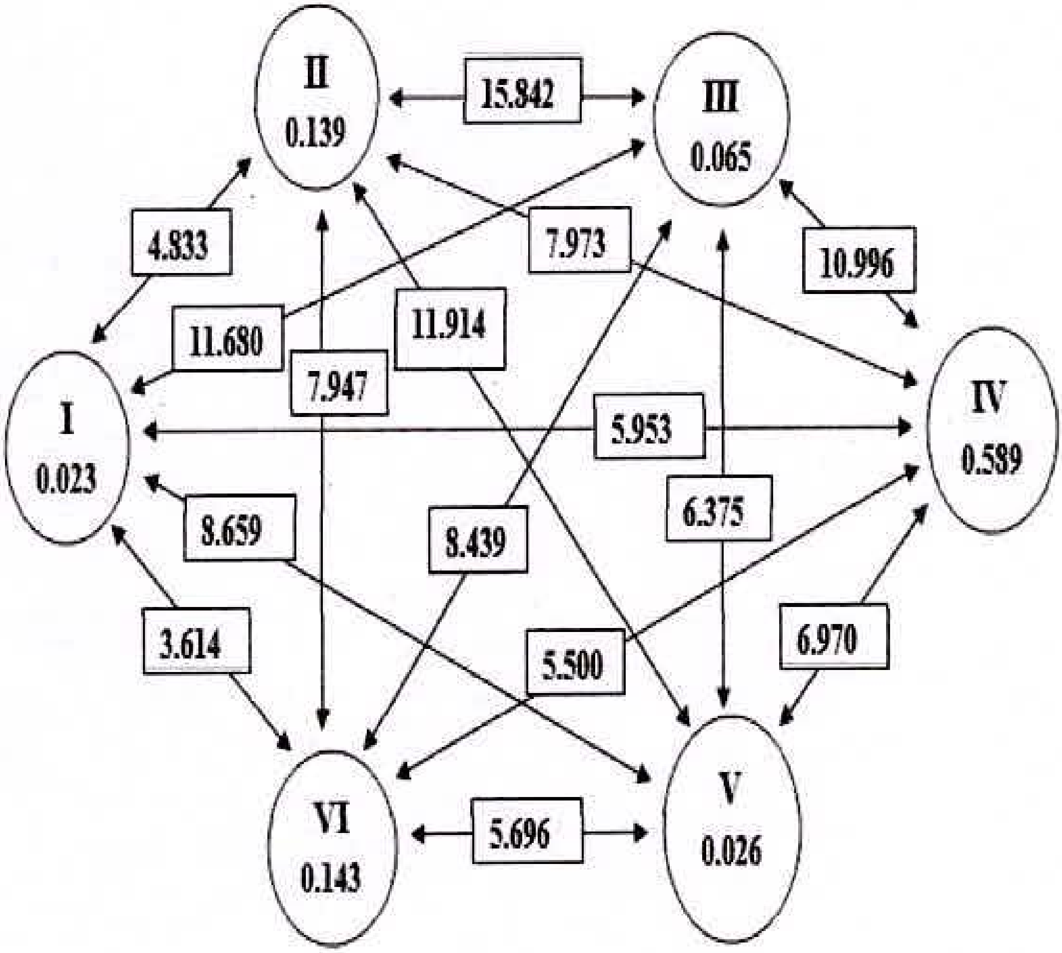


Figure 8. Diagram showing intra and inter clusters distances of 39 rice genotypes

cluster III that were resulted maximum yield in this study (Table 9). The clustering pattern suggests that the genotypes collected from same locations (hilly area) can also be grouped into different clusters. This shows that geographic diversity was not related to genetic diversity of these materials. Similar result was also reported by Yadav *et al.* (2011), Anandan *et al.* (2011), Rajesh *et al.* (2010), Hosan *et al.* (2010), De Silva *et al.* (2010), Sabesan *et al.* (2009), Akter *et al.* (2009), Kumar (2007), Chandra *et al.* (2007), Singh *et al.* (2006), Suman *et al.* (2005), Singh *et al.* (1999), Sinha *et al.* (1991), Kanwal *et al.* (1983).

4.4.6. Characterization of individual cluster

Intra cluster mean values of 12 different characters of 39 rice genotypes are presented in Table 8. The maximum intra cluster mean for plant height was found in cluster II (114.10) followed by cluster I (110.41) and cluster VI (106.88), whereas the lowest intra cluster mean was found in cluster IV (81.51) followed by cluster V (92.44) and cluster III (93.42). The maximum intra cluster mean for number of effective tillers per hill was observed in cluster III (11.57) followed by cluster V (11.44) and cluster IV (10.98), whereas the lowest was found in cluster VI (10.36) followed by cluster II (10.50) and cluster (10.64). The maximum intra cluster mean for panicle length was shown in cluster V (26.72) followed by cluster II (25.82) and cluster VI (25.32), whereas the lowest was in cluster III (23.77) followed by cluster I (25.06) and cluster IV (25.26). The maximum intra cluster mean for days to80% flowering was observed in cluster V (113.58) followed by cluster IV (110.78) and cluster II (109.47), whereas the minimum was observed in cluster III (91.78) followed by cluster I (102.88) and cluster VI (104.60). The highest intra cluster mean

Table 8. Distribution of genotypes in different clusters

Cluster No.	No. of Genotypes	Members	Varieties
I	G1, G5, G8, G12, G21, G22, G23, G24, G28, G30, G34	11	Sada Kabarak, Sada Gelon, Kabarak, Jumma Kabarak, BR-24, BR-25, BR-26, BRRI Dhan 27, BRRI Dhan 31, BRRI Dhan 33, BRRI Dhan 42
II	G4, G6, G7, G9, G10	5	Badeye, Jumma Bini (longer grain), Jumma Bini (shorter grain), Ameiye, Tharak
III	G13, G14, G15, G16, G25, G36	6	Gold, Tia, Dowel, Moyna, BRRI Dhan 28, BRRI Dhan 45
IV	G11, G17, G39	3	Paijam (Indian), BR-3, BRRI Dhan 50
V	G18, G19, G26, G27, G31, G33, G35, G37, G38	9	BR 10, BR 11, BRRI Dhan 29, BRRI Dhan 30, BRRI Dhan 36, BRRI Dhan 40, BRRI Dhan 44, BRRI Dhan 48, BRRI Dhan 49
VI	G2, G3, G20, G29, G32	5	Kala Kabarak, Kamrang, BR 22, BRRI Dhan 32, BRRI Dhan 39

for number of primary branches was observed in cluster V (11.71) followed by cluster II (10.62) and cluster VI (10.31), whereas the minimum was observed in cluster III (9.03) followed by cluster IV (9.52) and cluster I (10.18). The maximum intra cluster mean for number of secondary branches was found in cluster II (29.80) followed by cluster I (26.79) and cluster VI (25.09), whereas the minimum was in cluster III (20.24) followed by cluster IV (24.26) and cluster V (25.06). The highest intra cluster mean for number of unfilled grains was observed in cluster IV (30.82) followed by cluster II (27.31) and cluster I (22.17), whereas the minimum was in cluster III (17.39) followed by cluster VI (18.02) and cluster V (21.62). The maximum intra cluster mean was found in cluster VI (142.22) followed by cluster V (141.80) and cluster III (135.22), whereas the minimum was found in cluster IV (120.44) followed by cluster II (126.96) and cluster I (134.39). The maximum intra cluster mean for 1000-grains weight was observed in cluster III (27.69) followed by cluster VI (25.87) and cluster V (24.77), whereas the lowest was in cluster II (19.73) followed by cluster IV (22.89) and cluster I (24.40). The maximum intra cluster mean for days to maturity was shown in cluster II (143.07) followed by cluster V (142.19) and cluster IV (140.67), whereas the minimum was in cluster III (119.50) followed by cluster I (129.82) and cluster VI (130.13). The highest intra cluster mean for harvest index was observed in cluster III (0.55) followed by cluster V (0.53) and cluster IV (0.51), whereas the lowest was observed in cluster II (0.35) followed by cluster I (0.44) and cluster VI (0.46). The maximum intra cluster mean for grain yield per ten plants was observed in cluster III (332.75) followed by cluster V (301.72) and cluster VI (242.30), whereas the minimum was in cluster II (150.39) followed by

Table 9. Intra cluster mean values (the highest with bold and the lowest with italic bold) of 12 different characters of 39 genotypes

Characters	I	II	III	IV	V	VI
Plant height (cm)	110.41	**114.10**	93.42	***81.51***	92.44	106.88
Effective tiller number per hill	10.64	10.50	**11.57**	10.98	11.44	***10.36***
Panicle length (cm)	25.06	25.82	***23.77***	25.26	**26.72**	25.32
Days to flowering (DAS)	102.88	109.47	***91.78***	110.78	**113.58**	104.60
Primary branches number	10.18	10.62	***9.03***	9.52	**11.71**	10.31
Secondary branches number	26.79	**29.80**	***20.24***	24.26	25.06	25.09
Days to maturity (DAS)	129.82	**143.07**	***119.50***	140.67	142.19	130.13
Number of unfilled grains per panicle	22.17	27.31	***17.39***	**30.82**	21.62	18.02
Number of filled grains per panicle	134.39	126.96	135.22	***120.44***	141.80	**142.22**
1000 grains weight (g)	24.40	19.73	**27.69**	22.89	24.77	25.87
Harvest index	0.44	0.35	**0.55**	0.51	0.53	0.46
Grain yield per plant	197.34	150.39	**332.75**	215.23	301.72	242.30

cluster I (197.34) and cluster IV (215.23). The highest intra cluster mean for respected characters were shown in bold and the lowest intra cluster mean for respect characters were shown in italic in Table 9. The cluster III had ranked first for the maximum times (4 times) followed by clusters III and V (3 times each), cluster IV and VI (once each), whereas cluster I had no first ranking. However, the cluster III again had ranked in first for the maximum times (6 times) followed by cluster II (3 times), cluster IV (2 times) and cluster VI (once), whereas there was no first ranking of cluster I and cluster V for minimum value.

4.4.7. Contribution of characters towards divergence

The relative contributions of twelve different characters of thirty nine rice genotypes towards the total divergence are presented in Table 10. The result of the canonical variant analysis (CVA) revealed that in both the vectors number of unfilled grains per panicle, 1000-grain weight and grain yield per ten plants had positive values, whereas number of effective tillers per plant, days to 80% flowering, number of primary branches per panicle, number of filled grains per panicle and days to maturity had negative values. The positive values in both the vectors revealed the most important whereas the negative values in both the vectors indicated the least important of these characters towards the divergence among thirty nine rice genotypes. In the vector (Z_1), the all other characters, excluding those were showing positive values in both vectors, showed negative values indicating that these characters showed less importance towards the genetic divergence. In the vector (Z_2), the other important characters towards the genetic divergence were plant height, panicle length, number of secondary branches per panicle and harvest index. Therefore the most importance should be given on number of unfilled grains per panicle, 1000-grain weight and grain yield per ten plants.

Table 10. Relative contributions of the twelve characters of 39 varieties to the total divergence

Characters	Vector-1	Vector-2
plant height (cm)	-0.0297	0.1247
Tiller number per plant	-0.1531	-0.0932
Days to flowering	-0.0003	-0.0363
Panicle Length (cm)	-0.0069	0.1609
Primary branches number	-0.2114	-0.6256
Secondary branches number	-0.0103	0.0717
Unfilled grains per panicle	0.0498	0.0327
Filled grains per panicle	-0.0341	-0.1004
1000 seed weight (g)	0.0363	0.1541
Days to maturity	-0.0150	-0.0185
Harvest index	-4.4883	1.3369
Grain yield per ten plants	0.0823	0.0089

4.4.8. Relation between geographic origin and genetic divergence

Clustering pattern of thirty nine rice genotypes showed that the genotypes from same geographical region did not include consistently in the same cluster. From the Table 8, the cluster I was consisted of 11 genotypes including four genotypes from Chittagong Hill Tracts (CHT) and rest from BRRI. Clusters I, II, IV and VI were found to include genotypes from CHT. Therefore there was no effect of the geographical origin in the genetic divergence. Same result was also reported by Yadav *et al.* (2011). The present result and information suggest that geographical diversity can not be used as a criterion for predicting the genetic diversity.

4.4.9. Comparison of result based on different multivariate techniques

Result obtained from different multivariate techniques were super imposed in Figure 9. Similr results were obtained from all the multivariate techniques. Each of the technique confirmed the results of the others and supplementary to each other. The clustering pattern of D^2 analysis obtained from non-hierarchical clustering using all the characters under study simultaneously that followed more or less similar trend of the principal component analysis (PCA). Therefore, the clustering could be done using either PCA or D^2 analysis as supplementary to each other. Whereas the canonical variant analysis (CVA) was dependent on the characters responsible for genetic divergence.

4.4.10. Selection of characters for future improvement

The parents for hybridization program should be selected based on the magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance having maximum heterosis and wide genetic variability. A higher heterosis could be

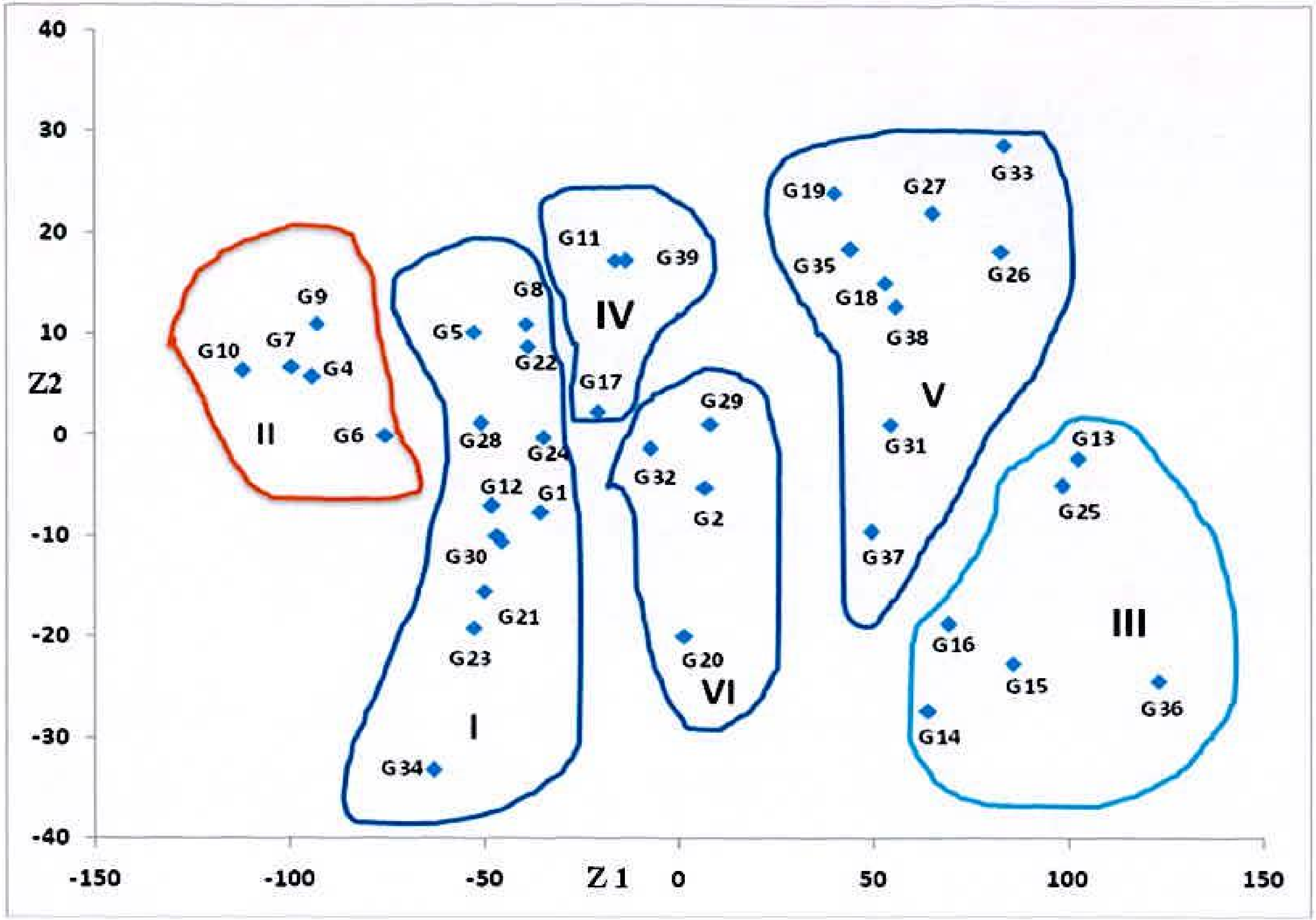


Figure 9. Scatter diagram of 39 rice genotypes based on PCA scores superimposed with clustering from D^2 analysis

produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.,* 1962, Ramanujan *et al.,* 1974 and Ghaderi *et al.,* 1984). Therefore crosses between clusters II and III, II and V, I and III, III and IV would give high manifestation of heterosis as well as wide spectrum of genetic variation in F_2 generation. Genotypes included in cluster III was important for number of effective tillers per hill, earliness, number of unfilled grains per panicle, 1000-grains weight, harvest index and grain yield. The cluster VI genotypes were important for number of filled grains per panicle. As the plant height, number of secondary branches were significantly negatively correlated with grain yield, cluster II was important for dwarfness and number of secondary branches. Considering thesignificant to grain yield, variability, cluster distance, inter genotypic distance, cluster mean and other agronomic performances, genotypes G36 (BRRI dhan 45), G13 (Gold), G25 (BRRI dhan 28) and G15 (Tia), G39 (BRRI dhan 50), G10 (Tharak dhan), G7 (Jumma bini-shorter grain), G4 (Badeye dhan), G9 (Ameiye dhan), may be selected from different clusters for hybridization program. The most distantly genotypes were between cluster II and cluster III. The most important cluster was cluster III (Table 10).

The important characters reported by some researchers were plant height (Latif *et al.,* 2011; Madhavilatha *et al.*, 2005; Singh *et al*, 1986), panicle length (Latif *et al.*, 2011; Singh *et al*, 1986), number of filled grains per panicle (Latif *et al.,* 2011; Sabesan *et al.*, 2009; Madhavilatha *et al.*, 2005), number of unfilled grains per panicle (Latif *et al.,* 2011), 1000-grains weigth (Latif *et al.,* 2011; Sabesan *et al.*, 2009), grain yield (Baradhan and Thangavel, 2011, Sabesan *et al.*, 2009; Chandra *et al.*, 2007; Madhavilatha *et al.*, 2005) number of effective tillers (Baradhan and Thangavel, 2011; Ahmed *et al.*, 2010), harvest index (Ahmed *et al.*, 2010), days to maturity (Kanwal *et al.*, 1983).

Table 11. Promising genotypes selected from diverse cluster

Sl. No.	Cluster	Desirable characters and mean values in parenthesis	Significant correlation with grain yield
1	III	Grain yield (332.75 g/ten plants), Harvest Index (55%), 1000-grains weight (27.69 g), Number of effective tillers (11.57)	Positive, Significant
		Number of secondary branches per panicle (20.24)	Negative, Significant
		Days to maturity (119.50 DAS), Days to flowering (91.78 DAS), Panicle length (23.77 cm)	Negative, insignificant
2	IV	Plant height (81.51 cm)	Negative, Significant
3	V	Primary branches per panicle (11.71 cm)	Positive, insignificant
4	VI	Filled grains per panicle (142.22)	Positive, Significant

Table 12. Finally selected genotypes against important traits

Sl. No.	Selection traits	Genotypes	Clustered from	Cluster mean values	Heritability, Genetic advance in percent of mean
1	Grain yield	G36 (BRRI dhan 45), G13 (Gold), G25 (BRRI dhan 28), G15 (Dowel)	III	332.75	High, High
2	Harvest index	G36 (BRRI dhan 45), G13 (Gold)	III	55%	High, High
3	1000-grains weight	G15 (Dowel), G13 (Gold), G36 (BRRI dhan 45)	III	27.69	High, High
4	Number of effective tillers	G13 (Gold), G15 (Dowel)	III	11.57	High, Moderate
5	Plant height	G39 (BRRI dhan 50), G11 (Indian Pajam)	IV	81.51	High, High
6	Secondary branches	G36 (BRRI dhan 45), G15 (Dowel)	III	20.24	Moderate, High

Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was undertaken to evaluate a set of genotypes for variability in morphological characters, extent of character association and genetic diversity. The material for this study comprised of 39 rice genotypes. The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University during January to June in 2011. The experiment was laid out in randomized complete block design (RCBD) with three replications. Data were recorded on plant height (cm), number of effective tillers, days to 80% flowering (DAS), panicle length (cm), number of primary branches per panicle, number of secondary branches per panicle, number of unfilled grains per panicle, number of filled grains per panicle, 1000-gains weight (g), days to maturity (DAS), harvest index and grain yield per ten plants (g/ten plants).

The highest mean value was observed for gain yield per ten plants (243.20 g/ten plant) and the highest range was also observed for the same character (132.64-365.48 g/ten plant). The significant variation was found for all the characters tested. The phenotypic variance was more or less greater than genotypic variance for all the characters under study but the harvest index showed balance. The higher differences for these two variances were observed for number of secondary branches per panicle, number of unfilled grains per panicle, number of filled grains per panicle and grain yield per ten plants indicating greater influence of environment for expression of these characters and the least difference were observed for plant height, number of effective tillers per plant, number days to 80% flowering, panicle length, number of primary branches per panicle, 1000-grain weight and days to maturity. In case of harvest index, there was no difference between phenotypic and genotypic variance.

The highest genotypic coefficient of variation was found for grain yield per ten plants (24.15 g) followed by number of unfilled grains per panicle (23.51), number of secondary branches per panicle (16.54), harvest index (15.34) and 1000-grains weight (14.06 g). The highest heritability was observed for days to maturity (97.46) followed by harvest index (96.43), plant height (92.26) and days to 80% flowering (89.52). The highest genetic advance in percent of mean was found for grain yield per ten plants (43.46) followed by harvest index (31.30), plant height (24.71), number of unfilled grains per panicle (24.36) and 1000-grains weight (23.63). High heritability with high genetic advance in percent of mean was recorded for grain yield per ten plants, harvest index, plant height and 1000-grains weight. The days to maturity, days to 80% flowering, 1000-grains weight, panicle length, number of filled grains per panicle and number of effective tillers per plant showed high heritability with moderate genetic advance in percent of mean. The significant positive correlations were recorded for number of effective tillers per plant, 1000-grains weight and harvest index with grain yield, whereas the significant negative correlations were observed for plant height, number of secondary branches per panicle and number of unfilled grains per panicle at both genotypic and phenotypic levels. The highest positive direct effect on grain yield was found for harvest index (0.715) followed by days to maturity (0.196) and number of filled grains per panicle (0.172) and the highest negative direct effect on grain yield was found for days to 80% flowering (-0.192) followed by number of secondary branches per panicle (-0.108) and number of unfilled grains per panicle (-0.088).

Multivariate analysis was performed through Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis and Canonical Variate Analysis (CVA). The PCA showed 65.79% variation against first three eigen values. Based on the PCA, D^2 and cluster analysis, thirty nine genotypes were grouped into six different clusters. Based on the PCO analysis, the highest inter genotypic distance (237.406) was observed between genotypes G10 (Tharak dhan) and G36 (BRRI dhan 45) followed by distance (224.811) between G7 (Jumma Bini-shorter grain) and G36 (BRRI dhan 45). The lowest inter genotype distance (1.234) was recorded between genotypes G30 (BRRI dhan 33) and G39 (BRRI dhan 50) followed by distance (2.241) between G8 (Kabarak dhan) and G22 (BR25). The intra cluster distances varied from 0.023 (cluster I) to 0.139 (cluster II). The highest intra cluster distance was estimated for cluster IV (0.589) consisted of 3 genotypes followed by cluster VI (0.143) with 5 genotypes, cluster II (0.139) with 5 genotypes, cluster III (0.065) with 6 genotypes, cluster V (0.026) with 9 genotypes and cluster I (0.023) with highest number of genotypes (11). The highest inter cluster distance was observe between cluster II and cluster III (15.842) followed by cluster V and cluster III (11.914), whereas distance was minimum between cluster I and cluster VI (3.614) followed by cluster I and cluster II (4.833). Cluster II showed the highest intra cluster mean values for plant height (114.10 cm), panicle length (25.82 cm), number of secondary branches per panicle (29.80) and number of filled grains per panicle (143.07). Cluster III showed the highest intra cluster mean values for number of effective tillers per plant (11.57), 1000-grains weight (27.69 g), harvest index (0.55) and grain yield per ten plants (332.75). Cluster V showed the highest intra cluster means for days to 80% flowering (113.58 DAS) and number of primary branches per panicle (11.71). Cluster VI showed the highest intra cluster mean for days to maturity (142.22 DAS). Cluster III showed the lowest intra cluster means for the maximum six characters *viz.* days to 80% flowering (91.78 DAS), panicle length (23.77 cm), primary branches per panicle (9.03), secondary branches per panicle (20.24), number of unfilled grains per panicle (17.39) and number of filled grains per panicle (119.50). Cluster IV showed lowest intra cluster means for plant height (81.51 cm) and days to maturity (120.44 DAS). Cluster II showed the lowest intra cluster means for 1000-grains weight (19.73 g), grain yield per ten plants (150.39 g) and harvest index (0.35). Cluster VI showed the lowest intra cluster mean for number of effective tillers per ten plants (10.36). The values of vector I and vector II obtained from CVA revealed that number of unfilled grains per panicle, 1000-grains weight and grain yield per ten plants had positive values for both the vectors.

Considering the degree of variability, heritability, genetic advance in percent of mean, correlation with grain yield, path analysis, magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and performance, the genotypes G36 (BRRI dhan 45), G13 (Gold), G25 (BRRI dhan 28), G15 (Dowel) from cluster III for grain yield; G36 (BRRI dhan 45) and G13 (Gold) from cluster III for harvest index; G15 (Dowel), G13 (Gold) and G36 (BRRI dhan 45) from cluster III for 1000-grains weight; G13 (Gold) and G15 (Dowel) from cluster III for number of effective tillers; G39 (BRRI dhan 50) and G11 (Indian Pajam) from cluster IV for dwarfness; and G36 (BRRI dhan 45) and G15 (Dowel) from cluster III for less number of secondary branches per panicle could be selected for hybridization program.

References

REFERENCES

Abarshahr, M., Rabiei, B. and Lahigi, H. S. (2011). Genetic variability, correlation and path analysis in rice under optimum and stress irrigation regimes. *Nat. Sci. Biol.* **3**(4): 134-142.

Agahi, K., Fotokian, M. H. and Farshadfar, E. (2007). Correlation and path analysis for some yield related traits in rice genotypes (*Oryza sativa* L.). *Asian J. Pl. Sci.* **6**(3): 513-517.

Ahmed, M. S., Akter, K., Khalequzzaman, M., Rashid, E. S. M. H. and Bashar, M. K. (2010). Diversity analysis in boro rice (*Oryza sativa* L.) accessions. *Bangladesh J. Agric. Res*. **35**(1): 29-36.

Akhtar, N., Nazir, M. F., Rabnawaz, A., Mahmood, T., Safdar, M. E., Asif, M. and Rehman, A. (2011). Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *J. Anim. Pl. Sci.* **21**(4): 660-664.

Akhter, T., Ivy, N. A., Rasul, M. G. and Mian, M. A. K. (2010). Variability and character association of reproductive traits in exotic rice germplasm. *Bangladesh J. Pl. Breed.* **23**(1): 39-44.

Akinwale, M. G., Gregorio, G., Nwilene, F., Akinyele, B. O., Ogunbayo, S. A. and Odiyi, A. C. (2011). Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African J. Pl. Sci.* **5**(3): 207-212.

Akter, A., Hasan, M. J., Paul, A. K., Motalib, M. M. and Hossain, M. K. (2009). Selection of parent for improvement of restorer line in rice (*Oryza sativa* L.). *SAARC J. Agri.* **7**(2) : 43-50.

Ali, S. S., Jafri, S. J. H., Khan, T. Z., Mahmood, A. and Butt, M. A. (2000) Heritability of yield and yield components of rice. *Pakistan J. Agric. Res.* **16**(2): 89-91.

Alim, A. (1982). Bangladesh Rice. pp: 35-39.

Anandan, A., Eswaran, R. and Prakash, M. (2011). Diversity in rice genotypes under salt affected soil based on multivariate analysis. *Pertanika J. Trop. Agric. Sci.* **34**(1): 33-40.

Anonymous, 2011. Food and Agricultural Organisation of the United Nations. Production: FAOSTAT. Available: http://faostat.fao.org/site/567/defaults.aspx #ancor

Ariyo, O. J. (1987). Multivariate analysis and choice of parents for hybridization in Okra. *Theor. Appl. Genet.* **74** : 361-363.

Balakrishna, M. J., Chaudhary, D., Ratho, S. N. and Mishra, R. N. (1973). Variability and correlation studies in upland rice. *Oryza.* **10**(1): 15-21.

Balasch, S., Nuez, F., Palomares, G. and Cuartero, J. (1984). Multivariate analysis applied to tomato hybrid production. *Theor. Appl. Genet.* **69** : 39-45.

Bansal, U. K., Sani, R. G., Rani, N. S. and Kaur, A. (1999). Genetic divergence in quality rice. *Oryza*. **36**(1) : 20-23.

Baradhan, G. and Thangavel, P. (2011). D^2 analysis in rice (*Oryza sativa* L.). *Pl. Arch.* **11**(1) : 373-375.

BBS (Bangladesh Bureau of Statistics. (2010). Statistical year book of Bangladesh. Ministry of Planning, Govt. of the People's Republic of Bangladesh.

Belaj, A., Satovic, Z., Rallo, L. and Trujillo, I. (2002). Genetic diversity and relationship in olive germplasm collection as determined by RAPD. *Theor. Appl. Genet.* **105**(4): 638-644.

Bhadru, D., Reddy, D. L. and Ramesha, M. S. (2011). Correlation and path analysis of yield and yield components in hybrid rice and their parental lines. *Elect. J. Pl. Breed.* **2**(1): 112-116.

Bhaumik, P. K., Sinha, M. K. and Banerjee, S. P. (1971). Genetic divergence among rice strains. *Theor. Appl. Genet.* **41**(1) : 31-35.

Bhuiyan, N. I., Paul, N. R. and Jabber, M. A. (2002). Feeding the extra millions by 2025: challenges for rice research and extension in Bangladesh, Proceedings of the Workshop on Modern Rice Cultivation in Bangladesh, 29-31 January. pp. 4-23.

Binse, P., Sarawgi, A. K. and Verulkar, S. B. (2009). Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh J. Agric. Res.* **34**(2): 175-179.

Bisht, V., singh, B., Rao, K. S., Maikhuri, R. K. and Nautiyal, A. R. (2007). Genetic divergence of paddy landraces in Nanakosi micro-watershed of Uttarakhand Himalaya. *J. Trop. Agric.* **45**(1-2): 48-50.

Biswas, P. S, Prasad, B. and Dewan, S. B. A. (2000). Variability, character association and path analysis in rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet.* **13**(1):19-27.

Bose, L. K. and Pradhan, S. K. (2005). Genetic divergence in deep water rice genotypes. *J. Central European Agric.* **6**(4) : 635-640.

Brar, D. S. and Khush, G. S. (2003). Utilization of wild species of genus *Oryza* in rice improvement. In: J. S. Nanda, S. D. Sharma (eds.), *Monograph on Genus Oryza*, pp. 283-309.

BRRI (2011). Adhunik Dhaner Chash, Bangladesh Rice Research Institute, Gazipur-1701, Bangladesh.

BRRI (2008). Adhunik Dhaner *Chash*, 14th Ed., Bangladesh Rice Research Institute, Gazipur-1701, Bangladesh.

Burton, G. N. and Devane, E. M. (1952). Estimating heritability in tall fescue (*Festuca arundianacea* L.) from replicated clonal material. *Agron. J.* **45** : 478-481.

Chakraborty, R. and Chakraborty, S. (2010). Genetic variability and correlation of some morphometric traits with grain yield in bold grained rice (*Oryza sativa* L.) gene pool of Barak valley. *Aerican. Eurasia J. Sustain. Agric.* **4**(1): 26-29.

Chakraborty, S., Das, P. K., Guha, B., Sarmah, K. K. and Barman, B. (2010). Quantitative genetic analysis for yield and yield components in boro rice (*Oryza sativa* L.). *Nat. Sci. Biol.* **2**(1): 117-120.

Chandra, R., Pradhan, S. K., Singh, S., Bose, L. K. and Singh, O. N. (2007). Multivariate analysis in upland rice genotypes. *World J. Agric. Sci.* **3**(3): 295-300.

Chaudhary, L. B. and Prasad, B. (1968). Genetic variation and heritability of quantitative characters in India mustard (*Brassica juncea*). *Indian J. Agric. Sci.* **35** : 172-195.

Chauhan, J. S. and Chauhan, V. S. (1994). Hybrid performance for panicle exsertion and flag leaf angle in rice. *Oryza*. **30**: 352-354.

Cheema, A. A., Yousuf, A., Awan, M. A. and Tahir, G. R. (1998). Path analysis of yield components of some mutants of basmati rice. *Tropic. Agric. Res. Ext.* **8**: 14-18.

Comstock, R. E. and Robinson, H. F. (1952). Genetic parameters, their estimation and significance. *Proceeding 6th Intercroping Grassland Congress.* **1** : 284-291.

Dani, R. G. and Murthy, B. R. (1985). Genetic divergence and biology of adaptation in *Cicer arietiman.* Theor. Appl. Genet. **69** : 383-392.

Das, R. K., Islam, M. A., Howlader, M., Ibrahim, S. M., Ahmed, H. U. and Miah, N. M. (1992). Variability and genetic association in upland rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet.* **5**(1-2): 51-56.

De Silva, P. S., Malik, B. P. S. and Battan, K. R. (2010). Genetic divergence analysis using yield and selected traits in rice (*Oryza sativa* L.). Extended summery, proc. 3rd Int. Rice Congress, Nov. 8-12, Hanoi, Vietnam.

De, R. N. and Suriya Rao, A. V. (1988). Genetic variability and correlation studies in rice under semi deep waterlogged situation. *Oryza.* **25**: 360-340.

De, R. N., Seetharaman, R., Sinha, M. K. and Banerjee, S. P. (1988). Genetic divergence in rice. *Indian J. Genet. Pl. Breed.* **48**(2) : 189-194.

Dem, J., Reddy, N., Rao, A. V. S. and Mohanty, K. K. (1992). Genetic divergence in early rice under two situations. *Indian J. Genet. Pl. Breed.* **52**(3): 225-229.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path coefficient analysis of components of crested wheat grass production. *Agron. J.* **52** : 515-518.

Digby, P., Galway, N. and Lane, P. (1989). GENSTAT 5: A Second Course. Oxford Science Publications, Oxford. pp. 103-108.

Falconer, D. S. (1960). Introduction to Quantiatative Genetics. The Ronald Press, New York.

Ganta, D. and Jyothula, D. P. B. (2010). Genetic divergence studies in rice. *Int. J. Agric. Sci.* **6**(1) : 189-192.

Golam, F., Yin, Y. H., Masitah, A., Afnierna, N., Majid, N. A., Khalid, N. and Osman, M. (2011). Analysis of aroma and yield components of aromatic rice in Malaysian tropical environment. *Australian J. Crop Sci.* **5**(11): 1318-1325.

Habib, S. H., Bashar, M. K., Khalequzzaman, M., Ahmed, M. S. and Rashid, E. S. M. H. (2005). Genetic analysis and morpho-physiological selection criteria for traditional birion Bangladesh rice germplasms. *J. Biol. Sci.* **5**(3): 315-318.

Hanson, C. H., Robinson, H. R. and Comstock, R. S. (1956). Biometrical studies of yield in segregating population of Korean lespedeza. *Agron. J.* **48** : 268-272.

Hedge, S. G. and Patil, C. S. (2000). Genetic divergence in rainfed rice. *Karnataka J. Agric. Sci.* **13**(3): 549-553.

Hooker, J.D. (1979). The Flora of British India. Vol. 2L. Reeve. Co. Kent, England. pp. 25.

Hosan, S. M., Sultana, N., Iftekharudduala, K. M., Ahmed, M. N. U. and Mia, S. (2010). Genetic divergence in landraces of Bangladesh rice (*Oryza sativa* L.). *The Agriculturists* **8**(2): 28-34.

Hossain, M. A. and Haque. M. E. (2003). Genetic variability and path analysis in rice genotypes. *Bangladesh J. Pl. Breed. Genet.* **16**(1): 33-37.

Ibrahim, S. M., Ramalingam, A. and Subramnian, M. (1992). Multivariate analysis of genetic divergence over different environments in upland rice. *Oryza*. **29**: 137-138.

Iftekharuddaula, K. M., Akter, K., Hassan, M. S., Fatema, K. and Badshah, A. (2002). Genetic divergence, character association and selection criteria in irrigated rice. *J. Biol. Sci*. **2**(4) : 243-246.

Iftekharuddaula, K. M., Badshah, M. A., Hassan, M. S., Bashar, M. K. and Akter, K. (2001). Genetic variability, character association and path analysis of yield components in irrigated rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet.* **14**(2):43-49.

Ismail, A.A., Khalifa, M. A. and Hamam, K. A. (2001). Genetic studies on some yield traits of durum wheat. *Asian J. Agric. Sci.,* **32**: 103-120.

Iwo, G. A. and Obok, E. E. (2010). Agronomic performance and estimate of genetic variability of upland rice genotypes on acid soil of Cross River State. *Global J. Agric. Sci.* **9**(1) : 1-7.

Jager, M. I., Garethojies, D. and Griffiths, E. (1983). Components of partial resistance of wheat seedling of *Septoria nodorum. Euphytica.* **32** : 575-584.

Johnson, H. W., Robinson, H.F. and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybeans. *Agron. J.* **47**: 314-318.

Julfiquar, A. W., Virmani, S. S., Kabir, K. A. and Molla, A. P. (1985). Differential heterosis in some growth physiological characters of indica/japonica and japonica/japonica crosses of rice. *Progress. Agric.* **5**(2) : 671-678.

Junned, S. A., Jackson, M. T. and Catty, J. P. (1988). Diversity in the wild potato species chaeoenese Btt. *Euphytica.* **37**(2) : 149-156.

Kanwal, K. S., Singh, R. M., Singh, J. and Singh, R. B. (1983) Divergence gene pools in rice improvement. *Theor. Appl. Genet.* **65** : 263-267.

Karim, D., Sarkar, U., Siddique, M. N., Miah, M. A. K. and Hasnat, M. Z. (2007). Variability and genetic parameter analysis in aromatic rice. *Int. J. Sustain. Crop Prod.* **2**(5): 15-18.

Kempthorne, O. (1957). An Introduction to Genetical Statistics. John Wiley and Sons. Inc., New York. pp. 545.

Khan, A. S., Imran, M. and Ashfaq, M. (2009). Estimation of genetic variability and correlation for grain yield components in rice (*Oryza sativa* L.). *American Eurasia J. Agric. Environ. Sci.* **6**(5): 585-590.

Kole, P. C., Chakraborty, N. R. and Bhat, J. S. (2008). Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-basmati rice. *Trop. Agric. Res. Ext.* **11**: 60-64.

Kotaiah, K. C., Rao, C. P., Reddy, J. R. and Reddy, M. V. (1987). Comparison of Mahalanobis's D^2 and metroglyph analysis in long duration genotypes of rice. *Indian J. Genet.* **47** : 55-60.

Kozak, M., Singh, K. P., Verma, M. R. and Hore, D. K. (2007). Causal mechanism for determination of grain yield and milling quality of lowland rice. *Field Crops Res.*, **102**: 178-184.

Krishnaveni, B., Shobharani, N. and Ramprasad, A. S. (2006). Genetic parameters for quality characteristics in aromatic rice. *Oryza*, **43**: 234-237.

Kumar, B. M. D. (2007). Genetic divergence in red rice. *Karnataka J. Agric. Sci.* **21**(3): 346-348.

Kumar, C. R. (1992). Variability and character association studies in upland rice. *Oryza.* **29**: 11-13.

Kumar, P. and Shukla, R. S. (2002). Genetic analysis for yield and its attributed traits in bread wheat under various situation. *JNKVV Res. J.*, **36**: 95-97.

Kumari, R. U. and Rangasamy, P. (1997). Studies on genetic diversity in international early rice genotypes. *Annals Agric. Res.* **18**(1): 29-33.

Latif, M. A., Rahman, M. M., Kabir, M. S., Ali, M.A., Islam, M. T. and Rafii, M. Y. (2011). Genetic diversity analyzed by quantitative traits among rice (*Oryza sativa* L.) genotypes resistant to blast disease. *African J. Micro. Res.* **5**(25) : 4483-4391.

Lenka, D. and Mishra, B. (1973). Path coefficient analysis of yieldbin rice varieties. *Indian J. Agric. Sci.* **43** : 376-379.

Li, Q. L., Guo, G. Z. and Jiang, G. (1991). Study on high yield breeding and genetic analysis of yield components of main rice cultivars in Jilin, China. *Hereditas-Beijing.* **13**: 3-6.

Lush, J. L. (1940). Intra-sire correlation and regression of offspring on dams as method of estimating heritability of characters. In: *Proceedings of American Society of Animal Protection,* **33** : 293-301.

Madhavilatha, L., Shekhar, M. R., Suneetha, Y. and Srinivas, T. (2005). Studies on genetic divergence and isozyme variability in rice (*Oryza sativa* L.). *Res. On Crops*. **6**(3): 520-526.

Mahajan, C. R., Pati, P. A., Mehetre, S. S. and Hajare, D. N. (1993). Relationship of yield contributing characters to the grain yield in upland rice. *Ann. Pl. Physiol.* 7(2): 266-269.

Mahajan, R. K., Rao, J. R., Sharma, Y. R. S. and Ghosh, A. (1981). Genetic divergence in rice. *Crop Improv.* **8** : 85-89.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Nat. Inst. Sci. India,* **2** : 49-55.

Mahapatra, K. C., Mishra, H.P., Mishra, P. K. and Acharya, B. (1993). Genetic diversity in mutant of upland rice. *Oryza*. **30**: 100-105.

Mall, C. N. and Maurya, D. M. (1992). Genetic diversity in breeding lines of two crosses in rainfed lowland rice. *Oryza*. **29**: 89-91.

Miller, P. J., Williams, J. C., Robinson, H. F. and Comstock, R. E. (1958). Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. *Agron. J.* **50** : 126-131.

Mirza, P. J., Faiz, F. A., Abdul, M. A. and Majid, A. (1992). Correlation studies and path analysis of yield and yield components in rice. *Sarhad J. Agric.* **8**(6): 647-653.

Mishra, S. B., Singh, U. K. and Sahu, S. P. (1994). Studies on genetic divergence in fine land races of rice in North Bihar. *Ann. Agric. Res.* **15**(2): 217-221.

Mokate, A. S., Mehetre, S. S., Bendale, V. W. and Birari, S. P. (1998). Genetic divergence in rice. *Adv. Pl. Sci.* **11**(2): 189-192.

Moll, R. H, Salhuana, W. S. and Robinson, H. F. (1962). Heterosis and genetic diversity in variety crosses of maize. *Crop Sci.* **2** : 197-198.

Morais, O. P., Silvia, J.C., Cruz, C. D., Regazzi, A. I., Neves, P. C. F. and Morals, O. P. (1998). Genetic divergence among the irrigated rice population CAN-IRAT 4. *Pesquisa Agropecuaria Brasileira.* **33**(8): 1339-1348.

Naik, D., Sao, A., Sarawgi, A. K. and Singh, P. (2006). Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) accessions of Central India. *Asian J. Pl. Sci.* **5**(2): 197-200.

Nayak, A. R., Chaudhury, D. and Reddy, J. N. (2004). Studies on variability and characters association in scented rice over environments. *Indian J. Agric. Res.* **38**(4): 250-255.

Padmaja, D., Radhika, K., Rao, L. V. S. and Padma, V. (2008). Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). *J. Pl. Genet. Res.* **21**(1): 196-198.

Pandey, P. and Anurag, P. J. (2010). Depiction of genetic divergence in rice (*Oryza sativa* L.). *Int. J. Biof. Soc.* **2**(3): 285-291.

Pandey, P. and Anurag, P. J. (2010). Estimation of genetic parameters in indigenous rice. *Int. J. Bioflux Soc..* **2**(1): 79-84.

Pandey, P., Anurag, P. J. and Rangare, N. R. (2010). Genetic parameters for yield and associated characters in rice. *Ann. Pl. Soil Res.* **12**(1): 59-61.

Patil, F. B., Thombre, M. B. and Sindde, W. M. (1987). Genetic divergence in onion. *J. Maharastra Agric. Univ.* **12**(2) : 252-253.

Poehlman, J. M. and Sleper, D. A. (1995). Breeding Field Crops. Panima Publishing Corporation, New Delhi, India. pp. 278.

Prasad, B., Patwary, A. K. and Biswas, P. S. (2001). Genetic variability and selection criteria in fine rice (*Oryza sativa*L.). *Pakistan J. Biol. Sci.* **4**(10): 1188-1190.

Rahman, M., Acharya, B., Shukla, S. N. and Pande, K. (1997). Genetic divergence in lowland rice germplasm. *Oryza.* **34**(3) : 209-212.

Rajesh, T., Paramasivam, K. and Thirumeni, S. (2010). Genetic divergence in land races of rice. *Elect. J. Pl. Breed.* **1**(2) : 199-204.

Ramanujam, S., Tiwari, A. S. and Mehra, R. B. (1974). Genetic divergence and hybrid performance in mung bean. *Theor. Appl. Genet.* **45**: 211-214.

Rangel, P. H. N., Cruz, C. D., Vencovsky, R. and Ferreira, R. P. (1991). Selection of local lowland rice cultivars based on multivariate genetic divergence. *Rev. Brasil Genet*. **14**(2): 437-453.

Rao, C. R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons, New York.

Rashid, M., Cheema, A. A. and Ashraf, M. (2007). Clustering of basmati rice mutants by metroglyph analysis. *Pakistan J. Bot.* **39**(6) : 2043-2049.

Rather, A. G., Zargar, M. A. and Sheikh, F. A. (2001). Genetic divergence in rice (*Oryza sativa* L.) under temperate conditions. *Indian J. Agric. Sci.* **71**(5): 344-345.

Robinson, H. F., Comstock, R. E. and Harvey, P. H. (1949). Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J.* **48** : 282-287.

Rokonuzzaman, M., Zahangir, M. S., Hussain, I. and Hossain, S. (2008). Genotypic variability of the components and their effects on the rice yield: correlation and path analysis study. *Italian J. Agron.* **3**(2): 131-134.

Roy, A. and Panwar, D. V. S. (1993). Genetic divergence in rice. *Oryza,* **30**: 197-201.

Sabesan, T., Saravanak, K. and Anandan, A. (2009a). Genetic divergence analysis for certain yield and quality traits in rice (*Oryza sativa* L.) grown in irrigated saline low land of Annamalinagar, South India. *J. Central European Agric.* **10**: 405-410.

Sabesan, T., Suresh, R. and Saravana, K. (2009b). Genetic variability and correlation for yield and grain quality characters of rice grown in coastal saline low land of Tamilnadu. *Elect. J. Pl. Breed.* **1**: 56-59.

Sadegi, S. M. (2011). Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in landrace rice varieties. *World Appl. Sci. J.* **13**(5): 1229-1233.

Sarawgi, A. K., Rastogi, N. K. and Soni, D. K. (1998). Genetic diversity for grain quality parameters in traditional rice (*Oryza sativa* L.) accessions from Madhya Pradesh, India. *Trop. Agric. Res. Ext.* **1**(2): 103-106.

Sardana, S., Borthakur, D. N. and Lakhanpal, T. N. (1997). Genetic divergence in rice germplasm of Tripura. *Oryza.* **34**(3) : 201-208.

Sardana, S., Sasikumar, B. and Modak, D. (1989). Variability and path analysis in fixed cultures in rice. *Oryza.* **26**: 250-251.

Sawant, D. S., Patil, S. L., Jadhav, B. B. and Bhave, S. G. (1995). Genetic divergence, character association and path analysis in rice. *J. Maharasthra Agric. Univ.* **20**(3): 412-414.

Selvakumar, K. S., Soundrapandian, G. and Amirthadevarathinam, A. (1989). Genetic divergence for yield and yield components in cold tolerant rice. *Madras Agric. J.* **76**(12): 688-694.

Sengupta, K. and Karatia, A. S. (1971). Path co-efficient analysis for some characters in soybean. *Indian J. Genet.* **31** : 290-295.

Seyoum, M., Alamerew, S. and Bantte, K. (2012). Genetic variability, heritability, correlation and path analysis for yield and yield contributing traits in upland rice (*Oryza sativa* L.). *J. Pl. Sci.* (*http://scialert.net/abstract/?doi=jps.0000. 40013.40013*).

Shahidullah, S. M., Hanafi, M. M., Ashrafuzzaman, M., Islam, M. R. and Khair, A. (2009). Genetic diversity in grain quality and nutrition of aromatic rice. *African J. Biotech.* **8**(7) : 1238-1246.

Singh SP (1989). Pattern of variation in cultivated dry bean. *Ann. Rep. Bean improv. Coop.* **31**: 180 – 182.

Singh, A. K., Singh, S. B. and Singh, S. M. (1996). Genetic divergence in scented and fine genotypes of rice (*Oryza sativa* L.). *Ann. Agric. Res.* **17**(2) : 163-166.

Singh, P. (1983). Studies on genetic variability and diversity of rice. *Madras Agric. J.* **70**(7): 436-440.

Singh, P. K., Mishra, M. N., Hore, D. K. and Verma, M. R. (2006). Genetic divergence in lowland rice of north eastern region of India. *Comm. Biomet. Crop Sci.* **1**(1) : 35-40.

Singh, R. K. and Chaudhury, B. D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci.,* **12** (2): 151-156.

Singh, R.K., Gautam, P. L., Saxena, S. and Singh, S. (2000). Scented Rice Germplasm: Consevation, Evaluation and Utilization. In: Aromatic Rices, Singh, R.K., U.S. Singh and G.S. Khush (Eds.). Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi, pp: 107-133.

Singh, S. and Yunus, M. (1988). Genetic variability of some quantitative characters in rice (*Oryza sativa* L.). *Indian J. Agric. Res.* **22**(4): 193-196.

Singh, S. K., Singh, C. M. and Lal, G. M. (2011). Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Res. Pl. Biol.* 1(4): 73-76.

Singh, S. K., Singh, R. S., Maurya, D. M. and Verma, O. P. (1986). Genetic divergence among lowland rice cultivars. *Indian J. Genet.* **47**(1): 11-14.

Singh, S. P., Singhara, G. S., Parray, G. A. and Bhat, G. N. (2006). Genetic variability and character association studies in rice (*Oryza sativa* L.). *Agric. Sci. Digest.* **26**(3): 212-214.

Singh, S., Pradhan, S. K. and Virk, P. (2008). Genetic divergence in new plant type rice under shallow lowland ecosystem. *SABRAO J. Bred. Genet.* **40**(1) : 1-8.

Singh, U. K., Mishra, S. B. and Thakur, R. (1999). Genetic divergence in boro rice. *Oryza*. **36**(1): 76-77.

Sinha, P. K., Chauhan, V. S., Prasad, K. and Chauhan, J. S. (1991). Genetic divergence in indigenous upland rice varieties. *Indian J. Genet*. **51**(1): 47-50.

Sivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agric. J.* **60**: 1139.

Snedecor, G. W. and Cochran, W. G. (1961). Statistical Methods. *Oxford and IBH Publishing Company*, New Delhi, pp. 593.

Soni, D. K., Sarawgi, A. K. and Rastogi, N. K. (1999). Genetic divergence in traditional rice accessions of Madhya Pradesh, India. *Oryza*. **36**(2): 118-120.

Subbaiah, P. V., Sekhar, M. D., Reddy, K. H. P. and Reddy, N. P. E. (2011). Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). *Int. J. Appl. Biol. Pharm. Tech.* **2**(3):603-608.

Suman, A., Shankar, V, G., Rao, L. V. S. and Sreedhar, N. (2005). Analysis of genetic divergence in rice (*Oryza sativa* L.) germplasm. *Res. On Crops*. **6**(3): 487-491.

Talukder, M. M. H. 2011. Governance crisis in production and distribution of hybrid seeds and its impact on market behavior and trust deficit among farmers of Bangladesh. Proceedings of the SAARC Seed Congress & Fair, Dhaka, Bangladesh. pp: 48-57.

Tukey, J. W. (1954). Causation, segregation and path analysis of causal path. *Biometrics*, **15**: 236-258.

Uddin, M. J., Ahmed, S., Hasan, M. M. and Hasan, M. M. (2010). Effect of spacing on morphology and yield response of different T. Aman rice cultivars under coastal high land ecosystem. *Ind. J. Agric. Res.* **44**(4) : 251-258.

Ullah, M. Z., Bashar, M. K., Bhuiyan, M. S. R., Khalequzzaman, M. and Hasan, M. J. (2011). Interrelationship and cause-effect analysis among morpho-physiological traits in birion rice of Bangladesh. *Int. J. Pl. Breed. Genet.* **5**: 246-254.

Vairavan, S., Siddiq, E. A., Arunachalam, V. and Swaminathan, M. S. (1973). A study on the nature of genetic divergence in rice from Assam and North East Himalayas. *Theor. Appl. Genet.* **43**(5) : 213-221.

Vange, T. (2008). Biometrical studies on genetic diversity of some upland rice (*Oryza sativa* L.) accessions. *Nat. Sci.* **6**(4): 36-41.

Vennila, S., Anbuselvam, Y. and Palaniraja, K. (2011). Genetic divergence analysis using yield and quality traits in rice (*Oryza sativa* L.). *Int. J. Recent Scientific Res*. **2**(7) : 237-239.

Virmani, S. S. (1996). Hybrid Rice. *Adv. Agron.* **57**: 379.

Virmani, S. S., Viraktamath, B. C., Casal, C. L., Taledo, R. S., Lopez, M. T. and Manalo, J. O. (1997). Hybrid rice breeding manual. International Rice Research Institute, Manila, Philippines. pp. 1-15.

Vivekananda, P. and Subramnian, S. (1993). Genetic divergence in rainfed rice. *Oryza*. **30**: 60-62.

Weber, C. R. and Moorthy, B. R. (1952). Heritability and variability of oil content and agronomic characteristics in the F_2 generation of Soybean crosses. *Agron. J.* **44** : 202-209.

Wright, S. (1921). Correlation and causation. *J. Agric. Res.* **20** : 557-587.

Wright, S. (1923). Theory of pathcoefficient. *Genetics.* **8** : 239-255.

Wu, S. Z. and Huang, C. W. (1988). Studies on varietal characterization in cultivars of *Oryza sativa* L. VI application of genetic variation in quantitative characters among high quality rice breeding. *Acta Agron. Sinica.* **14**: 202-207.

Yadav, V. K., Singh, Y., Soni, S. K. and Yadav, A. K. (2011). Genetic divergence analysis in salt tolerance rice (*Oryza sativa* L.) genotypes. *Pl. Arch.* **11**(2) : 593-595.

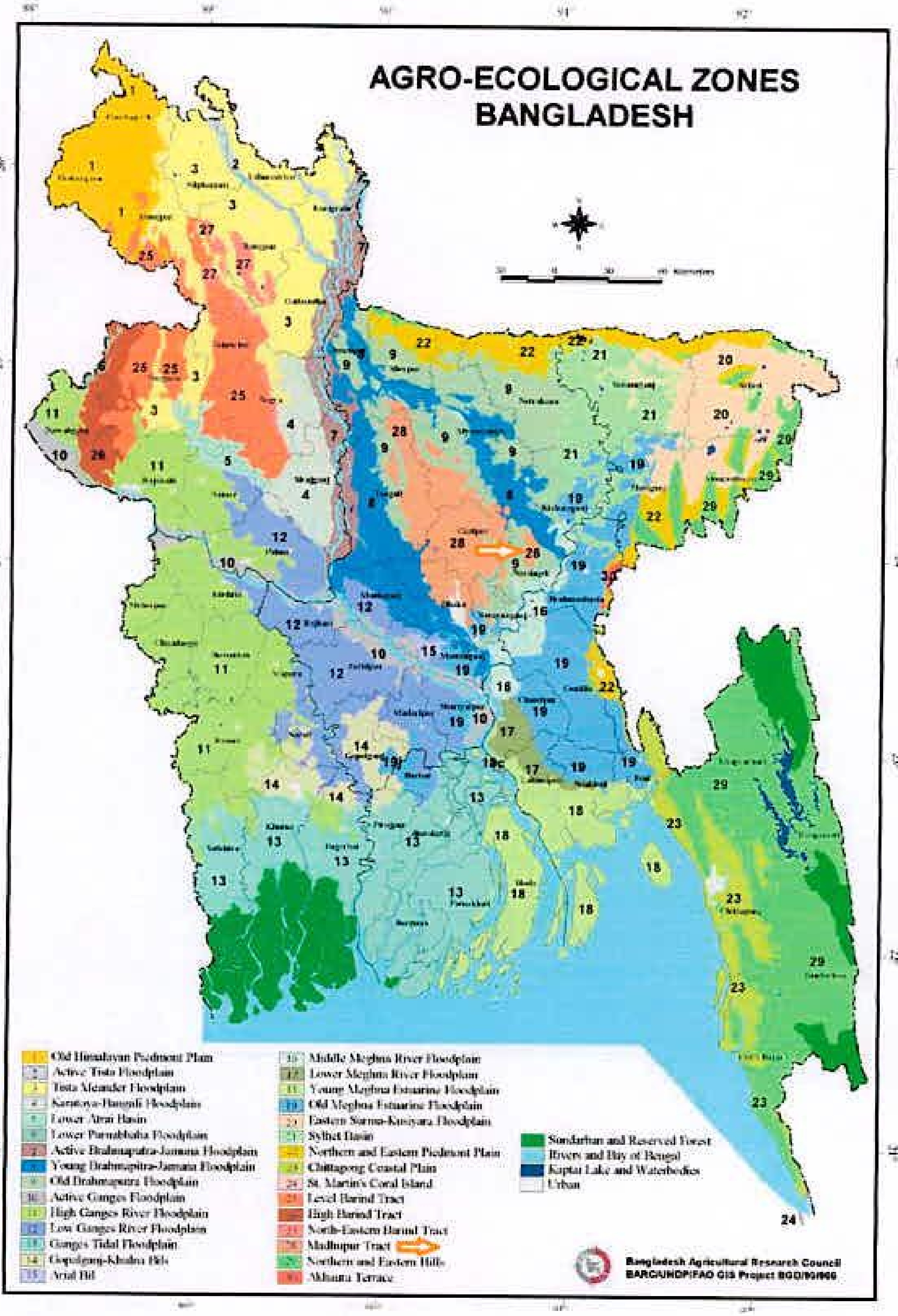
Yousuf, M. A., Sarker, R. A., Kabir, K. M. and Islam, M. H. (1994). Estimates of genetic parameters, characters association and path analysis in different rice genotypes. *Bangladesh J. Pl. Breed. Genet.* **7**(2): 49-52.

Zafar, N., Aziz, S. and Masood, S. (2004). Phenotypic divergence for agro-morphological traits among landrace genotypes of rice (*Oryza sativa* L.) from Pakistan. *Int. J. Agric. Biol.* **6**(2): 335-339.

Zahan, M. I., Bhuiyan, M. S. R. and Hossain, M. S. (2008). Genetic divergence in Oleiferous *Brassica* species. *J. Sher-e-Bangla Agric. Univ.* **2**(1): 1-6.

Appendices

Appendix I. Map showing the experimental site under study



Appendix II. Monthly average records of air temperature, precipitation, relative humidity, wind speed, bright sunshine hour per day and dew point during the period from January to June, 2011

Month	Year	Average temperature (°C)	Average high temperature (°C)	Average low temperature (°C)	Average precipitation (mm)	Average morning relative humidity (%)	Average evening relative humidity (%)	Average dew point (°C)	Average wind speed (km/h)	Average bright sunshine hours/day
January	2011	19	24	14	……	90	47	13	4	8.7
February	2011	22	26	17	20	86	39	13	4	9.1
March	2011	26	30	22	50	87	41	17	8	8.8
April	2011	28	31	25	110	88	53	22	9	8.9
May	2011	28	31	26	260	91	64	23	8	8.2
June	2011	28	31	27	350	93	76	8	6	4.9

Source: Bangladesh Meteorological Department (Climate & Weather Division), Agargaon, Dhaka

Appendix III. Physical characteristics and chemical composition of soil of the experimental plot

Soil characteristics	Analytical results
Agroecological Zone	Madhupur Tract
pH	6.00-6.63
Organic matter	0.84
Total N (%)	0.46
Available phosphorous	21 ppm
Exchangeable K	0.41 meq/100g soil

Source: Soil Resource and Development Institute (SRDI), Dhaka