CHARACTER ASSOCIATION AND PATH ANALYSIS OF T. AMAN RICE VARIETIES (*Oryza sativa* L.)

BY

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CERTIFICATE

*This is to certify that thesis entitled, "**CHARACTER ASSOCIATION AND PATH ANALYSIS OF T. AMAN RICE VARIETIES (Oryza sativa L.)**" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **MD. ROMEL BISWASH, Registration No. 06-02108** 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, 2013
Place: Dhaka, Bangladesh

(Prof. Dr. Naheed Zeba)
Supervisor


DEDICATED
TO
MY BELOVED PARENTS

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SAU, Dhaka

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ABSTRACT

A field experiment was conducted during June 2012 to December 2012 to study the character association and path analysis of 15 T. Aman rice varieties (*Oryza sativa* L.) in randomized block design with three replications. Analysis of variance for each trait showed significant differences among the varieties. Phenotypic coefficient of variation (PCV) was also close to genotypic coefficients of variation (GCV) for all the characters indicating maximum environmental influence on the expression of these characters. High heritability associated with high genetic advance in percent of mean was observed for plant height and thousand seed weight which indicated that selection for these characters would be effective. Rice yield per plant had highest significant positive correlation with Primary branches per panicle (G = 0.709 and P = 0.520) which indicating that, if primary branches per panicle increase, grain yield per plant increase. Path coefficient analysis revealed that grain yield and filled grains per panicle had the highest positive direct effect on seed. Hence, thrust has to be given for these characters in future breeding programme to improve the yield in rice. Multivariate analysis based on 10 agronomic characters indicated that the 15 varieties were grouped into four distant clusters. The inter cluster distance was maximum between cluster II and cluster IV. The highest intra-cluster distance was found in cluster IV. From the results it can be concluded that the following varieties *viz.*, G8 (BRRI dhan40), G10 (BRRI dhan44), G11 (BRRI dhan46), G12 (BRRI dhan49) and G15 (BINA dhan7) may be suggested for future hybridization program.

TABLE OF CONTENTS

TABLE OF CONTENTS (Cont'd.)

TABLE OF CONTENTS (Cont'd.)

TABLE OF CONTENTS (Cont'd.)

LIST OF TABLES

TABLE OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LIST OF ABBREVIATED TERMS

ABBREVIATED	FULL WORD
FY	Fiscal Year
AEZ	Agro-ecological Zone
BBS	Bangladesh Bureau of Statistics
DAE	Department of Agricultural Extension
MoA	Ministry of Agricultural
GCV	Genotypic Co-efficient of Variation
PCV	Phenotypic Co-efficient of Variation
A.D	After the Death.
B.C	Before Christ
IRRI	International Rice Research Institute
BRRI	Bangladesh Rice Research Institute
RAPD	Random Amplified Polymorphic DNA
CMS	Cytoplasmic Male Sterility
FAO	Food and Agricultural Organization
INGER	International Network on Genetic Evaluation in Rice
RCBD	Randomized Complete Block Design
GPA	Global Plan of Action
ECV	Environmental Co-efficient of Variation
GIS	Geographic Information Systems
cm	Centimeter
σ^2_g	Genotypic variance
σ^2_p	Phenotypic variance
PCA	Principal Component analysis
p	Principal Coordinate Analysis
CA	Cluster Analysis
CVA	Canonical Vector Analysis
GAPM	Genetic Advance in Percent of Mean
Res.	Research
g	Gram
BINA	Bangladesh Institute of Nuclear Agricultural
et al.	And others
etc	Etcetera
Kg	Kilogram
J.	Journal

Chapter I

INTRODUCTION

Rice is the world's largest food crop, providing the caloric need of millions of people daily (Vaughan *et al.*, 2003). There are two distinct types of cultivated rice, *Oryza sativa* or Asian rice and *Oryza glaberrima or* African rice. The genus *Oryza* contains 21 wild relatives of the domesticated rice. The genus is divided into four species complexes such as: *O. sativa, O. officialis, O. ridelyi* and *O. granulata* species complexes. All members of the *Oryza* genus have $n = 12$ chromosomes and while interspecific crossing is possible within each complex, it is difficult to recover fertile offspring from crosses across complexes. *Oryza sativa* is distributed globally with a high concentration in Asia. Large scale food shortage was experienced in Bangladesh and in several neighboring countries in Asia during late 50s and early 60s (Vaughan *et al.*, 2003). The current global population of 6.4 billion is expected to reach 7.5 billion by 2020 and 9.0 billion by 2050 (Viraktamath, 2007). Most of this population increase will occur in developing countries of Asia and Africa, where rice is the staple food. Globally, rice is cultivated now on 154 million hectares with annual production of around, 600 million tones and average productivity of 3.9 tons/ha (Viraktamath, 2007). More than 90% of the rice is produced and consumed in Asian countries. The other continents in which rice is grown are Africa (7.78% of the global area), South America (6.4%) and North America (1.4%) (Viraktamath, 2007).

The production of rice in Bangladesh of over 155 million people was around 33.8 million tones. The production of Aman which constitutes 40 per cent of the total rice production (BBS: 2012-13). Aman is one of the main crops in Bangladesh. At present it is the second largest crop in the country in respect of the volume of production. Aman is a nature based crop. Total area under aman crop has been estimated at 5.61 million hectares in 2012-13 (BBS: 2012-13). Total aman production of 2012-2013 has been estimated at 12.897 million metric tons as compared to 12.798 million metric tons in 2011-12 which is 0.77 percent higher than that of last year (BBS: 2012-13).

Rice production has more than doubled over the last three decades or so, but the yield of MV rice have declined or stagnated at a lower level. The demand for rice will continue to increase and cannot be met from the present levels of yield and area under MV rice. Achieving higher yield through increased cropping intensity and varietal development of MV rice are the most logical ways of raising the total production at national level. Attention should be focused not only on irrigated but also on rainfed areas. Increasing supply of quality seeds and application of improved management practices (crop, soil, water, fertilizer, and pests)) at farm level should be introduced to accelerate rice production. A 2-3 percent increase in rice production per annum has to be attained over the next few decades to feed the growing population. A technological break through in varietal development having higher yield potential, particularly for irrigated ecosystem, is a must for sustaining rice production in the long term.

Genetic diversity in the available gene pool is the foundation of all plant improvement programs. It is source of variation, which is raw material for the improvement work. This genetic diversity is essential to decrease crop vulnerability to abiotic and biotic stress, ensure long-term selection grain in genetic improvement and promote rational use of genetic resource (Lin and Yaun, 1993). Genetic divergence is one of the criteria of parent selection for exploiting heterosis. The availability of transgressive segregate in any breeding program depends upon the divergence of involving parents. Precise information on the nature and degree of genetic divergence of the parents is the perquisite of an effective breeding program. Knowledge of genetic diversity among plant populations and its quantative assessment usually helps a breeder in choosing breeding programs as selection of parents on the basis of divergence. Inclusion of more diverse parents in hybridization is supposed to increase the chance of obtaining maximum heterosis and gives board spectrum of variability in segregating generations. Genetically distant parents usually able to produce higher heterosis. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Devi *et al.*, 2006). IRRI seeks to understand rice genetic diversity and uncover new genes and traits in rice that will help rice producers face challenges brought about by climate change, pests and diseases, and other unfavorable conditions. Although the vast catalogue of more than 40,000 rice genes has been mapped (Devi *et al.*,

2006). As a result of recent advances in biotechnology, most of their functions remain largely unknown. Thousands of undiscovered genes may have the potential to benefit rice productivity and quality.

Genetic diversity can be evaluated with morphological traits, seed protein, isozymes and DNA markers. Conventionally, it is estimated by the D^2 analysis metroglyph and principal component analysis using morphological traits. The D^2 technique is based on multivariate analysis developed by Mahalanobis (1936) had been found to be a potent tool in quantifying the degree of divergence in germplasm. This analysis provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generation.

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

1. To determine the pattern of variability exist in the T. Aman rice genotypes for different traits,
2. To assess the magnitude of diversity and classify them under different groups based on genetic divergence,
3. To identify the contribution of character to genetic diversity and
4. To identify divergent genotypes for hybridization program expecting to provide superior segregates.

Chapter II

REVIEW OF LITERATURE

2.1 Genetic Divergence

The expression "divergence in character" was used by Darwin (1859) for the variation in genera and species. Another term "morphism" was used by Huxley (1955) for genetic diversity implying "genetic polymorphism" which means the coexistence of distant genetic forms in population. Early workers regarded the geographical isolation as a reasonable index of genetic diversity (Vavilov, 1926).

The varieties, which come from different localities are usually presumed to diverse and are utilized in hybridization programme. However, several workers in different crop species have emphasized that there is no parallelism in geographical distribution and genetic diversity (Murthy and Anand, 1966 ; Maurya and Singh, 1977 and De *et al.*, 1992) advocating that varieties with the same geographical origin could have undergone changes under selection pressure. Thus, the estimation of variation within the germplasm divergence study in the form of classification into different homogenous groups is an important practice. Multivariate analysis based on Mahalanobis-D^2 statistics and canonical variant analysis has been considered as an important tool in quantifying the genetic divergence in different crops (Rao, 1952).

A number of scientists (Griffing and Lindstrom, 1954; Mall *et al.*, 1962; Arunachalam, 1981) have emphasized the importance of genetic diversity in plant breeding for obtaining broad spectrum of desirable variability in segregating generations. Some of the earlier reports on genetic diversity in rice have been reviewed below:

Multivariate analysis of data on 13 yield components in 25 breeding lines grown in shallow and intermediate depth water showed 6 and 7 clusters, respectively (Pradhan and Roy, 1990). The composition of the clusters differed under the 2 regimes due to pronounced genotype – environment interactions.

The estimation of genetic divergence for grain yield and 9 yield-related traits in 99 diverse genotypes grouped these genotypes into 16 clusters and showed that genetic divergence was controlled mainly by panicles/plant, grains/panicle, grain yield/plant, spikelet's/panicle. The results indicated a significant divergence for the traits measured. (Roy and Ponwar, 1993)

The assessment of seventeen diversified genotypes of upland rice was raised during 1989 and 1990 into 5 clusters on the basis of D^2 analysis of data on 11 characters (Sharma and Hore, 1993). Inter - and Intra-cluster distances are given and their use in the selection of parents for breeding programmes is mentioned.

The estimation of genetic diversity among thirty-nine rice genotypes grouped them into 8 clusters. The distribution of highest and lowest mean values in distant clusters indicated the importance of traits contributing to the divergence (days to 50% flowering, days to maturity, secondary branches per panicle and spikelets per panicle). (Sharma and Richaria, 1995)

Rice was grown in 75 genotypes in kharif, 1991, on the basis of data on 8 yield components into 10 clusters. Clustering pattern revealed that geographic diversity is not a reasonable index of genetic diversity (Sawant *et al.*,1996).

The assessment of nature and magnitude of genetic divergence in 40 genotypes was scented and fined using Mahalanobis D^2-statistic for 10 characters. The genotypes were grouped into six clusters. Grain yield contributed 40.6% and plant height contributed 16.5% to genetic divergence (Singh *et al.*,1996).

The genetic divergence was estimated by using Mahalanobis's D^2 statistics in 62 early rice genotypes obtained from sixteen countries. Based on eight important yield contributing characters, these genotypes were grouped into six clusters. They found that there was no relationship between geographical distribution and genetic diversity. Characters like grain yield per plant, panicle exertion and plant height made largest contribution to total divergence (Kumari and Rangasamy, 1997).

An experiment was conducted during the rainy season of 1991-1994 to study genetic diversity in 10 genotypes of aromatic rice (*Oryza sativa* L.). Pooled data on 9 quantitative characters, *viz.* 50% flowering, plant height, tillers/hill, panicles/hill, panicle length, grain/panicle, chaffs/panicle, 100-grain weight and grain yield, were analyzed for 4 environments and 4 clusters of genotypes were formed on the basis of D^2 statistics (Mishra and Dash, 1997) .

Fifth rice genotypes were used for 10 yield components in low and upland environments in cluster analysis into 18 and 17 clusters under low and upland conditions, respectively. Genotypes were found independent of their geographic origin (Hanamaratti *et al.,* 1998).

Twenty-five genotypes of rice (*Oryza sativa* L.) were used into five clusters on the basis of yield components data. The maximum inter cluster divergence was observed between cluster B and components (63.04); followed by components and D (51.90) and cluster B and E (48.30) indicating that these groups of genotypes were highly divergent from each other. The genotypes in above clusters revealed substantial differences in the means for important yield contributing characters, suggesting that the genotypes belonging to these clusters forms ideal pairs for planning a hybridization programme (Mokate *et al.* 1998).

Genetic divergence among 85 indigenous glutinous rice varieties from Assam was estimated by using D^2 analysis. The genotypes were grouped into 12 clusters based on 13 agronomic characters. Tillers number, panicles per hill, grains per panicle, grain fertility and grain yield accounted for the major portion of divergence (Ahmad and Borah, 1999).

Genetic diversity in 34 rice stocks collected from seven countries which were grouped into 15 clusters, was assessed by using D^2 analysis for 10 economic traits. The pattern of distribution of genotypes within various clusters was independent of geographical distribution (Bansal *et al.,*1999).

Genetic diversity among 52 indigenous and exotic genotypes of rice was assessed by using Mahalanobis D^2 statistics in *kharif* 1996 under 2 sowing dates and 2 nitrogen fertilizer levels (Kandhola and Panwar, 1999). Based on 16 agro-morphological and quality characters, these genotypes were grouped into 11 clusters. Cluster 1 with 26 genotypes was largest, while clusters VII, VIII, IX, X and XI were mono-genotypic.

There was no association between genetic and geographic diversity. The maximum inter-cluster distance was observed between genotypes of clusters V and IX (18984.4). It was concluded that hybridization among genotypes drawn from widely divergent clusters with high yield potential were likely to produce heterotic combinations and wide variability in segregating generation (Kandhola and Panwar, 1999).

The assessment of 50 genotypes were grown in iron-toxic soil at Barapani in Meghalaya during rainy seasons of 1992 and 1993 and evaluated for 12 yield-related and morphological traits. On the basis of D^2 analysis of the data collected, the 50 genotypes were grouped into 6 clusters. The characters contributing most total divergence were days to 50% flowering, plant height, primary branches per panicle and 100-seed weight (27.9, 24.7, 16.4 and 10.4, respectively). Genetic diversity was not correlated with geographical diversity (Pandey *et al.,* 1999).

Genetic divergence was assessed in 42 genotypes of boro rice. Multivariate analysis revealed considerable genetic diversity in the material and led to their grouping in four clusters. Harvest index, total number of grains per panicle, number of fertile grains per panicle and stability accounted 90.6% of the total divergence (Singh *et al.*, 1999).

Genetic divergence in 40 genotypes of rainfed rice was assessed by using D^2 statistics. The cultivars fell into 7 clusters. The highest contributing characters to D^2 values were spikelet number per panicle, photosynthetic rate, and 1000-grain weight (Hegde and Patil, 2000).

Fifty six rice cultivars for 12 characters were grouped into six clusters in genetic divergence (Rather *et al.*, 2001). The grouping of cultivars from various regions into the same cluster indicated that the geographical distribution did not necessarily suggest genetic divergence.

An experiment was conducted to assess genetic divergence for yield and its components in 17 induced mutants (induced by gamma rays, EMS and their combinations) including one non-mutant mother variety of Mahsuri rice, for six qualitative characters (plant height, number of tillers/plant, panicle length, number of grains/panicle, 1000-seed

weight, and grain yield/plant). The genotypes differed significantly for six characters considered collectively and were grouped into four clusters.

Genetic diversity was assessed for 28 yield and morphological traits in 100 aromatic rice genotypes at Hyderabad, Andhra Pradesh. It was observed that the pattern of distribution of genotypes within various clusters was random and independent of geographical isolation (Arun *et al.*, 2002).

The association analysis of seed and seedling characters with adult plant characters, genetic divergence with hybrid performance and genetic distance with hybrid performance helps for prediction of hybrid performance at early stages of crop growth and can become a very good tool in the hands of breeders. Genetic divergence showed significant positive association with mean performance of hybrid for tillers/plant and productive tillers/plant while genetic distance showed significant negative association with plant height, panicle length and grain/panicle (Bhave *et al.*, 2002).

Genetic diversity was assessed in 54 genotypes for 19 morphological and quality traits. The analysis of variance indicated that the genotypes differed for almost all the traits under study. The genotypes were grouped into five clusters (Chaudhary and Sarawgi., 2002).

The D^2 statistics was applied to group 36 genotypes of low land rice grown in Cuttack. Significant varietal differences were observed for all 13 characters studied. The genotypes were grouped into 12 clusters. Among the different characters, 1000-grain weight, grain length, number of grains per panicle and plant height played a major role in the formation of clusters. The diversity was not related to geographic diversity (Reddy *et al.*, 2002).

Genetic diversity was worked out among 33 rice cultivar planted in Madurai, Tamil Nadu and the genotypes were grouped into 10 clusters by using Mahalanobis D^2 statistics based on genetic distance. Among the eight different characters, the trait days to 50% flowering contributed maximum towords genetic diversity (51.89%), followed by plant height (22.92%) and panicle length (9.47%) (Babu *et al.*, 2003).

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The assessment of genetic divergence in forty-five elite rainfed upland rice cultivars showed that the D^2 values among the genotypes were ranged from 1.69 (between CR 544-1-1 and CR 544-1-6) to 257.8 (between CR 636-7 and Sattari). Based on divergence, 45 genotypes were grouped into eleven clusters. The average intra-cluster distance indicated the divergence among the genotypes of the same cluster (Chauhan and Singh., 2003).

The worked out of genetic divergence for yield and yield components showed that the clustering pattern based on genetic diversity did not correlate with the grouping of cultivars based on growing conditions. The cultivars were categorized into clusters II and IV, which exhibited the greatest inter-cluster distance and superiority for most of the traits, may be used for the development of superior genotypes (Manna *et al.*, 2003).

The nature and magnitude of the genetic diversity for 20 quantitative and qualitative characters were determined for 16 rice cultivars and their 72 F_1 hybrids. The genotypes were grouped in 12 clusters based on the relative magnitude of multivariate D^2 values. Based on the cluster means, plant height, flag leaf width, ear bearing tillers per plant, 100 seed weight, panicle length, biological yield, harvest index. Analysis of variance indicated highly significant differences for the most of the characters studied (Mishra *et al.*, 2003).

To determine the degree and nature of genetic divergence,a set of 61 Elite Basmati rice genotypes were collected from different parts of India and abroad and grouped them into 4 clusters. Plant height contributed maximum to the genetic divergence (52.24%), followed by days to 50% flowering (22.56%) and grain yield per plant (8.63%) (Shiv and Moni., 2003).

To assess the genetic variation, 17 mutants and their respective parents (from Indonesia, Malaysia, Korea, India, Vietnam, Thailand, Philippines, Bangladesh, Pakistan, China and IRRI) were evaluated in Faisalabad, Pakistani, during 2002-2003. Deviations observed by metroglyph method regarding the number of clusters formed, number of genotypes in the cluster, and super imposition of the genotypes within the cluster indicated the possibility of genetic improvement for yield and yield components. Metroglyph scatter diagram

classified the genotypes into 11 groups. Based on this grouping, hybridization between group-Individuals and group-II was expected to yield superior rice cultivars (Cheema *et al.*, 2004).

An experiment was conducted to assess genetic divergence in fifty land race collections of rice. The genotypes were grouped in 10 clusters. Days to 50% flowering, grain yield per plant, grain length, kernel breadth and 100-kernel weight were identified as potential characters that can be used as parameters while selecting diversified parents in the hybridization programme for yield and quality improvement (Das *et al.*, 2004),

The nature and magnitude of genetic divergence among 200 genotypes of scented rice including one non-scented check was studied by using Mahalanobis D19 ^{2} statistics for 10 quantitative characters. On the basis of D^2 values, the genotypes were grouped into 10 clusters. Grain length and days to 50% flowering played important role in the formation of clusters. Among the different characters, panicle length contributed minimum (0.7%) to total divergence (Nayak *et al.*, 2004).

To evaluate the 60 rice cultivars for their organoleptic qualities, divergence of sample was measured by Mahalanobis D^2 statistics and clustering was done by Tocher's method. For rice, the cultivars formed 6 clusters, while for the parboiled samples, 10 clusters could be recognized. Results of the D^2 analysis revealed that among the 60 rice cultivars, as much as 35 were homogenous with respect to quality attributes such as appearance, colour, flavour, texture and taste for the preparation of boiled rice either in the row of parboiled forms (Nandini *et al.*, 2004).

An experiment was conducted to assess thirty-five aman rice cultivars for 10 traits (number of panicles per plant, panicle length, number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, number of unfilled grains per panicle, 1000-grain weight, panicle weight, grain yield per plant and sterility) over 2 environments. The assessment showed the cultivars were grouped into 5 clusters and the greatest genetic divergence was observed between clusters II and IV. As clusters II (Nagra, Khayersali, CRM-30 and Langulmutha) and IV (Randhunipagal) showed the greatest divergence and higher mean values for characters contributing to

genetic divergence, the cultivars from both clusters may be used in hybridization programmes to obtain good recombinants (Roy *et al.*, 2004).

The principal component analysis as well as cluster analysis was performed on 53 somatic lines from regenerated plants of early maturing restorer rice line 402. The 53 somatic lines might be divided into 6 groups. There were larger variation for shelled seed length, shelled seed length/width, brown rice rate, milled rice rate, head rice rate, number of spikelets per panicle, grain weight per plant, effective panicles per plant and plant height among 21 quantitative characters studied. There were significant differences among the quantitative characters in various groups of somatic lines. The first and sixth group of somatic lines, which had better comprehensive characters, may be employed as key crossing lines in breeding programme (Xie *et al.*, 2004).

A field experiment was conducted to determine the genetic divergence of 21 Indian aromatic rice genotypes. The genotypes were grouped into 6 clusters for different characters. The inter-cluster distance was observed to be highest between clusters II and III, indicating that the genotypes of these 2 clusters were genetically more diverse. The number of grains per panicle, grain yield per plant, days to 50% flowering, leaf length and leaf width showed high percent contribution towards total genetic divergence (Awasthi *et al.*, 2005).

The assessment of genetic divergence using Mahalanobis D^2 statistics was carried out on 41 high yielding and local genotypes of rice (Oryza sativa). The genotypes were grouped into six clusters. Cluster IV showed the maximum genetic distance from cluster VI followed by its distance from cluster V. The desirable yield and quality characteristics were distributed mainly in clusters III and IV and cluster V. The genotypes included in clusters III and IV may be used as parents in hybridization programme to improve yield (Bhutia *et al.*, 2005).

A field experiment was conducted to assess the nature and magnitude of genetic divergence among 35 deep water rice genotypes from India by using Mahalanobis D^2 statistics. The genotypes were grouped into 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Traits such as plant

yield, days to 50% flowering, and plant height were the major contributors to genetic divergence (Bose and Pradhan., 2005).

The assessment of genetic divergence using Mahalanobis D^2 statistics was carried out on 19 genotypes of Aman rice for 12 characters. Based on D^2 values, the genotypes were grouped into six clusters. Cluster Individuals was the largest with eight genotypes followed by cluster II with four genotypes. Intra-cluster IV. The maximum inter-cluster distance was found diversity between these groups. The major part of total divergence was imported by single trait *i.e.* 1000-grain weight and panicle length, grain length and plant height were also very important in this regard (Chand *et al.*, 2005).

The assessment of genetic divergence analysis was carried out on 26 genotypes of rice for 20 characters. The genotypes were grouped in 8 clusters. Comparison of cluster means revealed that cluster VIII gave exceptionally high values for 7 characters followed by cluster VII. The maximum inter-cluster D^2 value was obtained between cluster III and VI and III and VIII. It is suggested that for developing better cultivar, the genotypes of cluster III could be utilized in hybridization programme with the genotypes of cluster VI and VIII (Chaturvedi and Maurya., 2005).

An experiment was conducted on 30 extra-early rice genotypes on genetic diversity. Analysis of variance showed a significant difference among the genotypes for all the observed characteristics indicating high genetic variability among the genotypes. Cluster I had the highest number of genotypes. The highest inter-cluster distance was observed between cluster I and III followed by cluster II in direct sown condition. Under transplanted condition, cluster II showed the highest inter-cluster distance with cluster V followed by cluster II and IV. Plant height and days to flowering contributed to genetic diversity in transplanted conditions (Kandamoorthy and Govindarasu., 2005).

The genetic diversity was estimated in 38 elite basmati rice genotypes for 12 characters. The genotypes were grouped into ten clusters. Cluster means indicated that none of the clusters was superior with respect to all the characters studied. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Therefore

hybridization between genotypes of different clusters for development of superior genotypes is suggested in the present study (Pradhan *and* Mani, 2005).

A study was conducted to assess the genetic diversity among 100 genotypes of rice germplasm. Among the characters studied, days to 50% flowering, flag leaf length, flag leaf width, plant height and panicle length were the major components contributing to the total genetic diversity. The rest of the characteristics showed low contribution towards the total divergence (Patil *et al.,* 2005).

An experiment was conducted to assess the nature and magnitude of genetic divergence among 34 genotypes for 8 characters by using Mahalanobis D^2 statistics. The genotypes were grouped into 7 clusters. Days to 50% flowering, single plant yield and grains per panicle were the major characters contributing towards divergence (Sankar *et al.,* 2005).

To evaluate the genetic divergence of 40 tall indica rice genotypes based on grain yield and yield components, genetic divergence was studied from the pooled data on 8 characters. Based on D^2 values, the genotypes were clustered in 5 groups. Cluster IV showed maximum genetic distance from cluster V suggested wide diversity between these groups. Panicle number per hill, panicle length, sterility percentage, yield per plot and 1000-grain weight were the chief contributors towards genetic divergence (Senapati and Sarkar., 2005).

The assessment of genetic divergence in 43 rice genotypes for 10 yield contributing traits including yield per plant led to their grouping into nine clusters. Grouping of genotypes in different clusters indicated the existing of significant amount of variability among the genotypes for the traits studied. Cluster IV showed highest intra-cluster distance. Based on the mean performance, genetic distance and clustering pattern, hybridization involving genotypes HPR 824 and KC 1 (Achhoo) are likely to give desirable segregants for yield and its component traits (Sood *et al.,* 2005).

Mahalanobis D 22 ^{2} statistics were used to evaluate one hundred fourteen rice genotypes for 16 quantitative characters to quantify the genetic diversity existing among them. The genotypes were grouped into 10 clusters. Among these 16 quantitative characters studied, cluster X had the maximum number of spikelets per panicle, panicle length, filled grains

per panicle, plant yield and biological yield. Cluster III exhibited the lowest means for plant height, days to 50% flowering, panicle length, The genotypes from clusters III and X, which had high and low cluster means for majority of the characters, were recommended as parents for hybridization. Geographical diversity did not relate to genetic diversity (Suman *et al.*, 2005).

Twenty nine strains of rice were collected from different geographical regions of world to analyze the extent of genetic divergence. The genotypes were grouped into four clusters. The clustering pattern was independent of the geographical distribution, cluster II included 23 genotypes and those can be useful in hybridization to create a wide spectrum of variability. Maximum distance (97.34) was observed between clusters III and IV, plant height, single plant yield and 1000-seed weight were found to be important contributors to genetic divergence (Vaithiyalingan, 2005).

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

The fifty-four rice cultivars were collected from various locations in India for genetic diversity for yield and yield components in Allahabad, Uttar Pradesh, during the kharif of 2003. The analysis of variance revealed highly significant variation for plant height, panicle length, and flag leaf length, number of tillers per hill, number of seeds per panicle, number of days to 50% flowering, number and yield per plot. The genotypes were grouped into 9 clusters. Cluster VI recorded high mean values for plant height (140.33 cm), flag leaf length (48.11 cm) and flag leaf width (2.10 cm). Plant height contributed the most to genetic divergence (40.16%), followed by flag leaf width (20.12%), yield per plant (15.79%) (Devi *et al.*, 2006).

55 genotypes were grouped into 12 clusters based on D 23^2 values. High mean values for grain yield/plant, shoot height, panicle length and weight, straw yield/plant, total and fertile grains/panicle, days to 50% flowering and days to maturity were observed in cluster VII. The maximum mean values for grain yield/plant, tillers/plant, 1000-grain weight, grain fineness and seed protein percentage were obtained in clusters V, XII, X and XI, respectively. The highest contribution to divergence was recorded by total grains/panicle (22.6%) panicle weight, days to 50% flowering (7.6%) and shoot weight (7.2%) (Gahalain, 2006).

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

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

Genetic divergence was assessed in 64 early rice genotypes. Based on 10 yield contributing characters, these genotypes were constellated into 13 clusters. There was no relationship observed between geographical distribution and genetic diversity. Percent contribution of characters, i.e. 1000-grain weight, plant height, grain yield per plant and number of spikelets per panicle was highest in to genetic divergence indicating that due

consideration should be given to these characters while selecting parents from distant clusters for hybridization (Reddy *el al.*, 2006) .

The assessment of genetic divergence was carried out among 46 rice genotypes. The genotypes were grouped into seven clusters. Cluster IV showed highest inter-cluster distance from Cluster VI which was immediately followed by Cluster III and Cluster VII. Highest intra-cluster distance was observed in Cluster V and lowest in Cluster I. The desirable yield and its contributing traits were distributed mainly in Cluster III followed by Cluster VII and Cluster I. The genotypes within Cluster III, VII and I may be used as parents in hybridization programme to develop high yielding line (Sarkar *et al.*, 2006).

The investigation on genetic divergence was carried out among 52 traditional lowland rice genotypes from five states of North Eastern Region of India by using Mahalanobis D 2^2 statistic. The genotypes were grouped into six clusters. Genotypes from more than one state were grouped in one cluster, and genotypes from one state were grouped in more than one cluster. Geographical origin was not found to be a good parameter of genetic divergence. Clusters II, III, and IV exhibited high values for most of the characters. Plant height followed by leaf angle and leaf area were highly contributed (32.43%) to the formation of clusters. Clusters II, IV, and V, which had maximum inter-cluster distances and high values of plant height, days to 50% flowering, panicle length, grain yield/plant and milling percent may be used for initiating a hybridization programme (Singh *et al.*, 2006).

The nature and magnitude of genetic divergence were assessed among the fifty-seven upland rice genotypes including 32 local rice germplasm based on 14 agro-morphological traits. On the basis of D^2 values, the 57 genotypes were grouped into five clusters. The most divergent clusters were III and IV (D^2=3387.9) followed by III and V (D2=2808.2) and clusters II and III (D^2=1908.7). The clustering patterns of the genotypes were quite at random indicating that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were 1000-grain weight, grain yield and biological yield (Chandra *et al.*, 2007).

The genetic divergence was studied among 49 genotypes of non-scented rice including three checks, for seven quantitative characters. The significant varietal difference was observed for all the characters studied on the basis of D^2 values. The genotypes were grouped into eight clusters. Characters like kernel length, kernel breadth, days to 50% flowering and plant height had more contribution to total divergence (Chandra *et al.*, 2007).

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

The genetic divergence was assessed among 81 scented rice. Based on D^2 statistics, genotypes were grouped into nine clusters. The genotypes from cluster II having desired mean for characters like hulling %, milling % and head rice recovery and panicle length; cluster VII having high value for kernel length and L/B ratio and cluster V low value for days to 50% flowering but highest value for grain yield Kg./ hac (Sarawgi and Bisne, 2007).

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

2.2 Genetic Diversity in different parts of the world

Agriculture relies heavily on the genetic diversity of crop plants. Ever since the very beginning of agriculture (more than 10000 years ago), during the process of domestication and cultivation of crop plants, a wealth of genetic diversity has been utilized and partly preserved. It is estimated that not even 15 percent of the potential diversity has been utilized. Thousands of valuable allelic variations of traits of economic significance remain unutilized in nearly all crop plants. These can be discovered and effectively used to meet the existing and emerging challenges that threaten world food security. Sadly, this genetic wealth is being eroded due to neglect and over-exploitation. Developmental activities and exploitive land-use planning are destroying natural habitats, and modern varieties are replacing native species and landraces, resulting in a reduction of varietal diversity. Major crop species (rice, wheat and millet) suffered the most during the green revolution. In order to successfully meet future food requirements, it is necessary to manage the continuing genetic erosion and address the issues of genetic conservation and optimum utilization of what remains of the genetic diversity of important crop plants. Most of the genetic diversity found in Asia, Africa and Latin America and are discussed below,

The domestication of rice dates back to antiquity, although the precise time and place of its domestication may never be known. The general consensus, however, is that domestication took place independently in China, India and Indonesia, giving rise to Asia's three varietal groups: *japonica, indica* and *javanica*. There is archaeological evidence that rice was cultivated in India between 1500 and 1000 B.C. With its long history of cultivation and selection under diverse environments, rice acquired wide adaptability enabling it to grow in a range of environments, from deep water to swamps, irrigated and wetland conditions, as well as on dry hill slopes. Probably far more than any other crop, rice can grow under diverse geographical, climatic and cultural conditions.

The quality preferences of rice consumers have resulted in a wide diversity of varieties specific to different localities. Although the exact diversity cannot be gauged, it is estimated to be around 140 000 different genotypes. The IRRI gene bank preserves nearly

100 000 accessions. India alone has 86 330 accessions, of which 42 004 are in the national gene bank (Rai, 1999), which is enriched by further explorations, collections and conservation. Socio-cultural traditions have increased the diversity of Indian rices in terms of morphological and quality traits, especially grain size, shape and colour, as well as aroma and endosperm properties. Ancient *Ayurvedic literature* (Indian *Materia Media*) from the fifteenth and sixteenth centuries A.D. describes different rices, particularly scented varieties with medicinal and curative properties. As far back as 400 B.C., *Susruta*, the great Indian pioneer in medicine, described the medicinal properties of rice.

Indian gene sources provided worldwide gains in production and productivity in both tropical and temperate rices before high-yielding varieties were even introduced. The popular varieties of Indonesia (Intan, Peta and Mas) are derivatives of a cross between the Indian variety Latisail and the Chinese variety Cina. Peta is one of the parents of IR 8, the variety which revolutionized rice production in tropical Asia. IR 8 is the most widely-used parent in several crosses in tropical Asia. More than 80 percent of the semi-dwarf varieties grown in tropical Asia have Latisail as one of their ancestors. Similarly, 35 varieties released by IRRI and grown in several tropical Asian countries have one or another Indian variety or wild species in their ancestry. GEB-24, another famous variety from southern India and known for its grain quality, is in the ancestry of 31 varieties developed and released by IRRI. Other Indian varieties, such as Ptb 18, Ptb 21 and CO-18, known for possessing sources of resistance to planthopper, leafhopper, gall midge and rice tungro virus, are ancestors of between 20 and 25 varieties released from IRRI. An Indian accession of the wild species, *O. nivara* (the only source of resistance for grassy stunt virus), occurs in the parentage of several improved varieties. Thus the rice germplasm collection from primary and secondary centres of diversity - namely: northeastern hills (ARC collection), Koraput region of Orissa, Raipur region of Chattisgarh and peninsular region of India - continues to provide useful genes for rice improvement (Rai, 1999).

In tropical Asia, of several major rice-growing countries, it was India which saw the release of the greatest number (643) of varieties over the last 50 years. India may

therefore be used as a case study to examine the genetic diversity of cultivated varieties. Rice breeding in India started at the beginning of the twentieth century with the establishment of rice research stations in Dacca (now in Bangladesh) and Coimbatore. The rice breeding programme was strengthened during the 1920s and 1930s. Until 1960, there were 69 research stations in the country working on rice breeding. These research stations had developed 430 improved varieties by 1960, 27 of them through hybridization; the rest were from pure line selections in different regions. High yield was the most important objective in all breeding programmes. Additional objectives were strong straw, early maturity and resistance to pests. Some of the outstanding varieties developed during this period are: MTU-1, MTU-15 and HR-19 in Andhra Pradesh; Chinsurah-7 in West Bengal; Kodamba strains in Bombay; GEB 24, CO 2, CO 25, CO 26 and ASD-1 in Tamil Nadu; T 141 and SR 26 B in Orissa; Basmati 170 in Punjab; and T-136 in Uttar Pradesh. The variety, GEB 24, was obtained as a spontaneous mutant in the traditional variety, Konmani. It proved very popular and spread to various parts of southern India. During the 1960s, the semi-dwarf varieties, IR 8 and Jaya, were released, ushering in the era of the green revolution in India. Subsequently, breeding efforts focused on: improvement of grain quality; incorporation of resistance to diseases and insect pests; and reduction of the maturity period. Recently, efforts have been intensified to develop hybrids in rice. Fifteen promising hybrids have already been released for commercial cultivation.

In the last three decades, 632 varieties were developed and released for commercial cultivation in India by central and state variety release committees for different ecosystems. Of the 632 varieties, 374 (59%) were released for the irrigated ecosystem, 123 (19.4%) for rainfed shallow lowlands, 87 (13.7%) for rainfed uplands, 30 (4.7%) for rainfed semi-deep water, 14 (2.2%) for deep-water conditions and 33 (5.2%) for hill ecologies. All together, high-yielding varieties occupy 77 percent of the total area in the country.

By examining the donors utilized in the development of the high-yielding varieties, an indication is obtained of the genetic diversity. Through an FAO-sponsored *indica/japonica* project launched in the 1950s, ADT-27 and Mahsuri (developed in

Malaysia) became popular in India. Subsequently, tropical *japonica* varieties from Taiwan, such as Taichung 65, Taichung Native-1 and Tainan-3, proved to be good donors for developing high-yielding and fertilizer-responsive genotypes. The development of short-duration varieties from the spontaneous dwarf mutant DGWG with *Sd1* genes is a landmark in the history of rice breeding. Using largely IR 8, TN-1 and Jaya as donors of dwarf stature and high yield potential, combined with many of the local selected varieties having adaptability and quality traits, several varieties were developed and released in India.

The parents most often used in recombination breeding in India are listed in Table 17. IRRI's elite germplasm has also been used extensively as a donor in Indian breeding programmes. Details of the germplasm used in breeding for resistance to biotic and abiotic stresses are given in Table 18, while Table 19 lists the varieties developed in the Indian breeding programme for: resistance to insect pests and diseases and to saline/alkaline soils; cold tolerance; and drought resistance.

Genetic diversity among 42 elite Indian rice varieties was evaluated by Davierwala *et al.* (2000) using three different types of DNA markers and parentage analysis. The average genetic similarity coefficient across all 861 cultivars was 0.70 and the average coefficient of parentage was 0.10. A set of 18 accessions from the Indian scented rice collection was subjected to random amplified polymorphic DNA (RAPD) analysis. A dendrogram revealed genetic similarity to be in the range of 25 to 77.5 percent (Raghunathachari *et al.*, 2000).

Examination of the pedigree of 29 rice varieties developed through recombination breeding and released in Kerala State between 1966 and 1995 revealed a narrow genetic base, with only 37 ancestors. Either directly or indirectly, of the 37 ancestors, ten contributed 74.14 percent of the genetic base. Similarly, the cytoplasmic base was also limited, as 41.38 percent of varieties could be traced back maternally to the same ancestor (Ptb-10). All 29 varieties (with the exception of Kayanakulam-1) were interrelated with an average coefficient of parentage of 0.137 for 406 combinations of 29 varieties

(Shivkumar *et al.*, 1998). The extent of genetic uniformity of rice in selected Asian countries is given in Table4.

In the African continent, rice varieties released in Nigeria had varying genetic contributions from across the globe (Maji and Fagade, 2002). Most of the varieties bred in Nigeria since 1986 have parents originating from IRRI: 67 percent of the released varieties in Nigeria originate directly from IRRI materials. FARO 15, a highly adaptable and high-yielding variety, received its high-yielding stiff-straw characteristic from its IR 8 parent. The other parent of FARO 15 is BG 79, used because of its wide adaptability to the Nigerian ecosystem. This combination resulted in the development and release of FARO 30, 31 and 32 as early-maturing, high-yielding varieties for irrigated cropping systems.

However, genetic uniformity is quite common in the upland rice-growing zones of Nigeria where farmers had stuck to growing only one variety (FARO 11) before the introduction of early-maturing FARO 46 only a few years ago. Genetic uniformity is also found in the Bende irrigation scheme area, where FARO 12 and 23 are the only common varieties. The main sources of rice genetic diversity in Nigeria can be classified into three basic categories: *O. sativa, O. glaberrima* and wild species such as *O. bathii* (Maji and Fagade, 2002). *O. glaberrima*, which originated in and is endemic to the subregion, is suited to the soils and harsh climatic conditions of the area and has resistance to biotic stresses, such as drought, rice yellow mottle virus (RYMV), weed competitiveness and acidity. On the other hand, *O. glaberrima*lines are characterized by very low yield potential, grain shattering before full maturity, grain characters which do not appeal to agronomists and consumers, and weak culm that predisposes them to high lodging susceptibility. Other undesirable traits include long awn, black husk at maturity and red seed coat. These limitations are, however, variable, and there is a wide range of materials possessing the positive side of these characters and offering great potential for genetic improvement because of their wide adaptation to various rice-growing ecologies, from uplands to deep water.

Human intervention and the domestication of rice in Africa led to the adoption, selection, development and maintenance of *O.glaberrima* varieties, in contrast with the *O.sativa domestication* in Asia and the Far East. These endemic/indigenous materials were able to compete with major weeds in tropical Africa thanks to their early vegetative growth and vigour. Furthermore, these varieties were flood-tolerant (due to their high elongation ability) and resistant or moderately resistant to various abiotic and biotic stresses. Until about 50 years ago, more than half the rice area in Africa was under *O. glaberrima* varieties; however, *O. sativa* or the Asian rice varieties have now replaced much of the native cultivated rice. The more successful and popular cultivars of *O. glaberrima* during the 1960s included: Badande and Jatau (irrigated/floating); and Dan Zaria, Godongaji and Katsina Ala Shendam (upland). About 2 200 accessions of *O. glaberrima* collected from 22 countries are conserved in the IITA gene bank, with a duplicate set in the IRRI gene bank; the WARDA gene bank has around 300 accessions of *O. glaberrima* collected between 1985 and 1990. Reasons for the replacement of African native rice varieties with Asian cultivars include the high-shattering, short to medium red grain types, as consumers prefer the higher quality materials available. Nevertheless, the *O. glaberrima* accessions could be useful donors for specific traits in future rice breeding programmes. The crossing/segregation behaviour of *sativa x glaberrima* crosses requires further study as there are problems of sterility and persistent segregation with eight or more filial generations; this is also an indication of the existence of multi-allelic loci, probably due to cryptic evolutionary changes in the cultivated *Oryza* species.

The white-grained *O. sativa* cultivars (believed to have been introduced more than 2 000 years ago in Africa) have almost completely replaced the native *O. glaberrima* varieties in recent years. These materials owe their origin to the International Network on Genetic Evaluation in Rice (INGER) under the auspices of FAO. Of the International Agricultural Research Centres, it is the collections of IRRI, IITA and WARDA which have contributed to varietal selection and adaptation, while the countries in Asia which are known to have provided cultivars which have proved successful in Africa are India, Thailand, Sri Lanka, Philippines, Indonesia, Taiwan, Bangladesh and Malaysia.

Prominent donor *O. sativa* cultivars include: Vikram, Mahsuri, Ramadja, ADT-31, Pelitai and Mayang, contributed to INGER by various national programmes. Besides providing high yield and white grain, these and other donor *O. sativa* varieties and lines have contributed towards a number of economic and ecostability traits, for example, good quality and resistance or endurance to various biotic and abiotic stresses (including salinity, acidity, iron toxicity, drought, poor soil, low nutrients, blast and lodging).

The diverse range of *O. sativa* materials introduced in Africa is supplemented with prebreeding, in particular with *O. glaberrima* x *O. sativa*crosses. This has already been carried out at WARD using the backcross method together with anther culture. The new set of germplasm - likely to have good weed competitiveness, drought tolerance and high yield under the low input conditions of resource-poor farmers - should be further developed and promoted through liberal funding and a set of conservation priorities for sustainable use as per the relevant action points under the Global Plan of Action (GPA).

In Latin America, there has been a similar narrowing down of the native genetic diversity in the prevailing rice varieties and breeding materials. Asmall number of indigenous and introduced varieties contributed as much as 70 percent to breeding programmes, including Dee-Geo-Woo-Gen, China, Lati Sail, I Geo Tze, Monge Chim Vang A, Belle Patna and Tetap. A systematic and sustainable approach must be adopted in breeding programmes in or aimed at Latin American countries.

Guimaracs (2002) presents a critical analysis of the Latin American region in general and Brazil in particular. The limited use made of the genetic diversity available worldwide has been a concern in Latin America since the late 1980s. Atotal of 143 commercial varieties released in the region from 1971 to 1989 were analysed: it was found that 101 different landraces were involved in the crosses that produced the varieties, but only 14 ancient cultivars contributed 70 percent of the genes.

Brazil took advantage of the green revolution with the introduction and commercial release of semi-dwarf varieties. The substitution of traditional tall varieties in the state of Rio Grande do Sul and Santa Catarina, the main rice-growing region in Brazil, produced

yield increases of 30 and 66 percent, respectively. While a great number of crosses continued to be performed every year, following the yield jump of the 1970s, the subsequent two decades saw only limited genetic gain. In general, changes were introduced in terms of shortened growth duration, increased disease resistance and improved quality, while yield potential hardly changed, if at all.

The genetic base of the main varieties sown under lowland irrigated conditions in Brazil was analysed and it was concluded that only seven ancestral varieties were responsible for more than 70 percent of the background of these new varieties. In Rio Grande do Sul, this contribution was as high as 86 percent. Under upland conditions, studies reveal a narrow genetic base for the most commonly cultivated varieties. Six native varieties make up the base for the upland varieties released up to 1992. Forty ancestors were involved in crossing to develop varieties, but only 11 of them accounted for 81 percent of the genes for the varieties released between 1971 and 1993.

2.3 Genetic Variability:

Variability refers to the presence of differences among the individuals of plant population. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they have grown. The existence of variability is essential for resistance to biotic and abiotic factors as well as for wider adoptability. Variance is the amount of variation present among the member of a population. Fisher (1918) partitioned the total phenotypic variance into genotypic variance and environmental variance. He further divided the genotypic variance in to additive, dominance and epistatic effects. However, it is only the genetic variation which is heritable. Selection is also effective when there is significant amount of generic variability among the individuals in a population. Hence insight into the magnitude of generic variability present in a population is of paramount importance to plant breeder for staring a breeding programme in any crop including rice.

An experiment was found (Bhattacharaya and Mishra., 1981) high heritability and genetic advance for plant height, number of ear bearing tillers per plant, panicle weight and number of grains per panicle in 22 rice varieties.

A reported was assign (Denge, 1981) high heritability value for 1000-grain weight, palnt height, grain number per panicle, number of tiller, grain weight per plant, panicle length and panicle number per plant.

Singh and Sharma (1982) recorded high hetitability values for plant height and 1000 grain weight and high expected genetic advance for plant height and number of grains per panicle.

An experiment was found high heritability coupled with high genetic advance for kernel length, L/B ratio, flag leaf width, flag leaf length, plant height, grains per panicle and test weight (Maurya *et al.,* 1986).

Reddy (1992) reported highest genotypic and phenotypic coefficient of variability for number of grains per panicle. All the traits exhibited moderate to high estimates of heritability ranging from 67.9% for grain yield per hill to 99.5% for days to 50% flowering. Plant height and number of grains per panicle showed high estimates of genetic advance. Among with high estimates of heritability.

A study was observed high magnitude of heritability along with high genetic advance fro-fertile spikelets per panicle, grain yield, number of tillers per panicle, plant height and spikelets per panicle. High heritability coupled with low genetic advance recorded for 1000- grain weight and panicle length revealed the major role of non –additive gene action in transmission of these characters from parents to offspring (Singh, 1992).

Broad sense heritability and relative expected genetic advance were computed far plant height, number of tillers per plant, panicle length, number of spikelets per panicle, number of grains per panicle, spikelets density, 100 – grain weight and grain yield per plant from F_2 population obtained from twelve rice crosses involving Basmati 385, 4439, 4048 – 3 and IR-6 rice varieties/lines, exhibited high heritability and greater relative expected genetic advance which offered promise for effective selection and high yield potential (Ali *et al.*, 1993).

Sharma and Roy (1993) recorded high heritability and genetic advance for panicle per m2 grains per panicle and grain weight. Plant height, flag leaf length, flag leaf width, panicle length and grains per panicle were significantly and positively correlated with grain yield.

The evaluation of twenty rice varieties for yield related traits and observed that phenotypic coefficient of variation was greater than the genotypic coefficient of variation for all the traits studied and heritability was highest for total number of spikelets followed by grain yield per plant and 100 – grain weight. Genetic advance as percent of mean was highest for grain yield per plant followed by panicle weight and total number of spikelets (Chaubey and Singh, 1994).

The assessment of 28 rice hybrids and their seven very early and four early maturing parents for genetic variability. The characters, grains per panicle, grain yield per plant and dry matter production showed high genotypic co-efficient of variation, indicating the predominance of additive gene effects. Days to panicle emergence showed moderate genetic variability, indicating the existence of scope for further improvement through phenotypic selection (Ganesan, 1994).

Genetic variability for thirty nine rice genotypes were assessed by (Sarma and Richharia, 1995) and reported that secondary branches per panicle, spikelets per panicle, grain yield, panicle weight and effective tillers per plant exhibited high genotypic coefficient of variation and observed high heritability for secondary branches per panicle and spikelets per panicle.

Reddy and De (1996) studied that there were significant differences among 36 genotypes for the 12 characters. Grain yield per hill, grain per panicle and panicle weight had the highest estimates of genotypic and phenotypic variability. They observed high heritability for grain length, followed by 1000 – grain weight, grain breadth, plant height, panicle weight, grain yield and grain per panicle.

The assessment of 39 upland rice genotypes for 12 yield components. Genotypic coefficient of variation (GCV) was highest for effective tillers per meter row length, followed by panicle weight, secondary branches per panicle, grain yield per meter row length and spikelets per panicle (Sharma *et al.*, 1996). They recorded broad sense

heritability which ranged from 42.2% for grain yield per meter row length to 99.9% for grain length. Effective tillers per meter row length, panicle weight, secondary branches per panicle and spikelets per panicle had high GCV and high heritability. Genetic advance as a percent of mean was highest for effective tillers per meter row length followed by panicle weight Ashvani *et. al.* (1997) reported highest genotypic variation for straw yield per plant followed by grain yield per panicle, grain yield per plant, height of plant, total biological yield per plant and number of fertile florets per panicle in 22 genotypes of rice, growing in India. They observed high heritability coupled with high genetic advance for 1000 – grain weight, height of plant, flag leaf area, grain yield per panicle and straw yield per plant.

To evaluated the thirty genotypes of rice for 11 yield related traits. Highly significant variation among the genotypes was observed for different characters. The differences between genotypic and phenotypic coefficient of variation were relatively low for almost all the characters except grain yield per plant. They recorded high to moderate genotypic coefficient of variation together with high heritability and genetic advance for number of filled grains per panicle and 1000 – grain weight, grain yield per panicle and number of secondary branches per panicle (Borbora and Hazarika, 1998).

To evaluated the 56 rice cultivars belonging to three different eco-geographical races *viz.* India Javanica and Japonica for genetic variability and genetic parameters with respect to 14 traits. Spikelets sterility and grains per panicle exhibited high genotypic coefficient of variation associated moderate heritability and high genetic advance (Rather *et al.*, 1998).

A studied was observed by (Lalitha and Sreedhar, 1999) 50 genotypes of groa (upland) rice for 10 quantitative traits in *Kharif 1995*. The genotypic coefficient of variation was highest for grain yield per plant and also high for 1000-grain weight.

The noted of significant variation for plant height, number of tillers per plant, flag leaf length, flag leaf width, number of panicle per plant, Number of spikelets per plant, yield per plant and test weight (Kumar *et al.*, 1999).

Pushpa *et al.* (1999) found that the genotypic coefficient of variation was highest for grain yield/plant and also high for spikelets per panicle and grain yield per panicle in 50

genotypes of gora (upland) rice. High heritability was observed for 1000-grain weight, days to hundred percent flowering, grain yield per plant and days to 50% flowering.

The estimation of genetic component of variances and heritability in a reference population is very crucial if it is utilized for a breeding programme. We were particularly interested in assessing variation for several agronomic traits in a reference population of rice *(Oryza sativa* L.) commonly grown in considerably high level of soil salinity. Fourteen adopted cultivars selected from the area and two high yielding cultivars were evaluated at two levels at salinity in a green house experiment in 1997 (Rasyad, 1999).

Verma *et al.* (2000) observed relatively low magnitude of differences between PCV and GCV for all the traits, except number of sterile spikelets per panicle.

Yadav (2000) reported high genotypic and phenotypic coefficient of variation for spikelets per panicle, grain yield and harvest index in nine rice cultivars at Chattisgarh. High heritability coupled with high genetic advance for total seeds per panicle, total seeds per plant and seed yield per plant in a study including 15 genotypes of rice.

The assessment of genetic variability for yield and its components was studied in 15 genotypes of rice during *Kharif* 1997-98 in Raigarh, Madhya Pradesh. Observation on 5 competitive plants were recorded for 10 characters (days to 50 flowering, days to maturity, plant height, tiller per plant, panicle length, spikelets per panicle, total seeds per panicle and per plant, 1000-seed weight, and seed yield per plant). Appreciable amount of genotypic coefficient of variation, heritability and genetic advance were observed for total grains per panicle, total grains per plant and grain yield per plant. This indicated the role of additive genetic component controlling these traits and scope for selection (Yadav *et al.*, 2002).

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

effect and high heritability coupled with moderate to high genetic advance (Bidhan *et al.*, 2001).

An experiment was carried out (Zen and Bahar., 2001) to study on genetic variability of plant characters and yield of eleven promising lines of highland rice and Batang Sumani at nine location 800- 900 m. *a.s.i.*, the results showed that heritability of all plant characters and yield were high (76.98 percent – 97.96 percent) heritability of filled spikelets per panicle was medium (37.29 percent). Plant height, productive tillers, spikelets per ear, and yield had a wide genetic variability. Selection for those characters could be done at early generation.

A reported were conducted (Mohammad *et al.*, 2002) that phenotypic and genotypic coefficient of variation (PCV and GCV) were of comparable magnitudes except for grain yield./plant and grains per panicle where the environmental coefficient of variation (ECV) contributed more to the PCV than GCV and also observed high heritability along with high relative expected genetic advance for 1000 grain weight, primary branches per panicle and productive tillers in an experiment comprising ten rice varieties or pure lines.

A studied was observed by (Nayak *et al.*, 2002) genetic variability for grain yield and nine yield contributing characters in 200 scented rice genotypes in Cuttack, Orissa. They obtained high estimates of genetic and phenotypic coefficients of variation for number of spikelets per panicle, number of panicles per plant, number of grains per panicle and grain yield per plant. Further they also observed high heritability and high genetic advance for number of spikelets per panicle, number of grains per panicle and grain yield per plant.

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

for number of grains per panicle followed by panicle weight and grain yield per plant in an experiment conducted at Meghalaya.

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

An experiment were conducted (Chaudhary and Motiramant, 2003) fifty four traditional aromatic rice accessions for 19 descriptors to obtain information on genetic variability and character association of grain quality and yield attributes. A wide range of variation as recorded for most of the characters. Heritability in broad sense was very high for all the characters exhibited high heritability coupled with high genetic advance except harvest index. Grain yield per plant showed significant positive correlation with effective tillers per plant, spikelet density and biological yield per plant, path analysis indicated a greater contribution of effective tillers per plant, spikelet density and biological yield per plant towards grain yield.

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

Singhara *et al.* (2003) genetic variability and association of different panicle components with number of grains panicle were determined in 36 genotypes of rice grown under

Kashmir conditions wide range of variability was observed for all characters studied. The PCV and GCV values were larger for number of secondary branches, panicle and grains borne primary branch and low for days to 50% flowering, panicle length, kernel length and kernel breadth. High heritability coupled with high genetic advance were recorded for 1000-seed weight, seeds panicle and primary branch length indicating greater scope for yield improvement through selection.

The estimation of variability, heritability and genetic advance estimates and their correlation coefficient were determined in Ambikapur, Chattisgarh, during the 1998-2000 *kharif* seasons from 19 local midland rice landraces, with IR-36 as the standard control, for yield and its attributing characters (plant height, tillers per hill, panicles per hill, panicle length, days to 50% flowering, days to maturity, test weight and grain yield). A high genotypic coefficient of variation was observed in grain yield followed by test weight and panicles per plant. High heritability with high genetic advance was found for grain yield followed by test weight and panicles per plant. Significant positive genetic correlation were observed for panicles per plant, test weight and grain yield (Sinha *et al.*, 2004).

The estimation of genetic variability for 12 characters in 39 "new plant" tropical Japonica lines from International Rice Research Institute, Philippines along with three control cultivars. The genotypes showed a wide range of variation for all the characters. Grain yield per plant, biological yield per plant, number of tillers and panicles per plant had high values of genetic coefficient of variation and phenotypic coefficient of variation. They reported high heritability with high genetic advance for grain yield per plant, biological yield per plant, panicle in an experiment (Vivek *et al.*, 2004).

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

The observation of high heritability and genetic advance for grain yield per panicle, chaffy grains per panicle, grain yield per plant, filled grains per panicle and secondary branch number per panicle, indicating the effectiveness of selection for these characters.

The nature and magnitude of genetic variability was assessed by Singh *et al.* (2005) for seven characters in 20 rice genotypes including a local check during *kharif* 2004. The analysis of variance revealed significant differences among the genotypes for all the characters. High estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for grain yield (t/ha) and biological yield (t/ha), particle density/sq.m. and harvest index (%) (Panwar, 2005).

The observation of 39 "new plant" tropical Japonica lines during the wet season of 2000 in Pantnagar. The genotypes showed a wide range of all characters. High genotypic and phenotypic coefficient of variation was observed for grain yield, followed by harvest index and biological yield. They observed high heritability coupled with high genetic advance which were also observed for grain yield, followed by harvest index and biological yield.

To assessed a reported (Amudha *et al.*, 2006) that high genetic variability for the number of days to flowering, plant height, number of productive tillers per plant, panicle length, spikelet fertility, number of grains per panicle, 100-grain weight, grain yield per plant, dry matter production and harvest index in biparental progenies of the cross MP x Norungans, for all the characters examined except 100-grain weight, panicle length and root volume in the biparental progenies of cross PM x Mattaikar, and for all the characters examined except 100-grain weight, root volume, number of grain per panicle and grain yield in the biparental progenies of the cross PM x Poonagar.

A experiment were conducted genetic variability and correlation studies in rice during kharif 2002 in Khudwani, Anantnag district, Jammu and Kashmir. Thirty-two genotypes were evaluated for days to 50% heading, days to maturity, plant height, panicles per plant, biological yield, grain yield and harvest index. A wide range of variation was recorded for all traits. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability and high genetic advance were recorded for plant height, indicating the predominance of additive gene action for this trait. Genotypic and phenotypic correlation studies indicated that biological yield per plant and harvest index were significantly and positively correlated with yield. Thus, selection for these two traits might be helpful in enhancing rice grain yield (Singh *et al.*, 2006).

The estimation of genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean in the F_2 and F_3 segregating populations of six crosses of rice for six yield and yield component characters. The F_2 populations of the cross $P_1 P_3$ showed high PCV, GCV coupled with high heritability estimates and high genetic advance as percentage of mean for number of filled grains per panicle, 100-grain weight, biomass per plant and grain yield per plant. Similarly, the F_3 population of the cross $P_2 P_1$ exhibited high genetic parameters for number of productive tillers per plant and grain yield per plant. These populations could be subjected to simple pure line selection to improve grain yield per plant (Kumar *et al.*, 2007).

The estimation of variability and genetic divergence were carried out in rice for 17 characters at RRS, Kaul during kharif 2002-03. Substantial amount of genotypic variability was observed for all the traits under study (Ishwar *et al.*, 2007).

Chapter III

MATERIALS AND METHODS

This chapter contains the details of the materials used and the methods. The detail events of experimental materials and methods employed in the present investigation entitled "Character association and path analysis of T. Aman rice varieties (*Oryza sativa L.*)" were as follows:

- Experimental site and duration
- Soil and climate
- Experimental materials
- Preparation of main land
- Germination of Seed
- Layout plan
- Observations recorded
- Statistical analysis

3.1 Experimental Site and duration

An experiment was conducted at the experiment field (west-byed) of Bangladesh Rice Research Institute (BRRI), Joydebpur, Gazipur during T.Aman 2012. The experimental site is located at the centre of Madhupur Tract (24°09' N latitude and 90°26' E longitude) having an elevation of 8.2m from sea level (Appendix I).

3.2 Soil and climate

The soil type of the experimental field belongs to the Shallow Red Brown Terrace type under Salna Series of Madhupur Tract of Agro ecological Zone (AEZ) 28 which is characterized by silty clay with pH value of 5.92. The climate of the experimental site is subtropical in nature characterized by heavy rainfall during the months from June to

September and scanty in winter with gradual fall of temperature from the month of September (Appendix II & III).

3.3 Experimental materials

The experimental materials for the present study were the 15 rice varieties obtained from the germ-plasm bank of Bangladesh Rice Research Institute (BRRI), Joydebpur, Gazipur. (Table1).

Table1: Name of varieties

Varietal Code	Varieties Name
G_1	BR11
G_2	BR 23
G_3	BRRI dhan33
G_4	BRRI dhan34
G_5	BRRI dhan37
G_6	BRRI dhan38
G_7	BRRI dhan39
G_8	BRRI dhan40
G_9	BRRI dhan41
G_{10}	BRRI dhan44
G_{11}	BRRI dhan46
G_{12}	BRRI dhan49
G_{13}	BRRI dhan51
G_{14}	BRRI dhan52
G_{15}	BINA dhan7

3.4 Method

3.4.1 Preparation of main land

The experimental plot was at a lower elevation with high water holding capacity. The land was prepared thoroughly by 3-4 times ploughing and cross ploughing followed by laddering to attain a good puddle. Weeds and stubbles were removed and land was finally prepared by addition of basal dose of fertilizers recommended by BRRI.

3.4.2 Germination of Seed

Seeds of all genotypes were soaked separately for 48 hours in clothes bag. Soaked seeds were picked out from water and wrapped with straw and gunny bag to increase the temperature for facilitating germination.

3.4.3 Layout plan

- **Design of experiment**

  The experiment was laid out in Randomized Block Design (RCBD) with 15 varieties. The varieties were replicated three times; each variety was grown in a plot of 20 m^2 area.

- **Date of sowing**

  Seed were sown in the seedbed on 30 th June, 2012.

- **Date of transplanting**

  The 26 days old seedlings were transplanted in the main field on 26 th July, 2012.

- **Lay out description**

  The details of the field layout are given below:
  Plot size : 5m x 4m
  Spacing : 25 x 15 cm

  Row to row distance: 25 cm
  Hill to hill distance: 15 cm

Gross area: 1440 m^2 (36 decimal)

Net area: 900 m^2

Drainage area: 540 m^2

No. of genotypes: 15

No. of replications: 03

3.4.4 Fertilizer Application

Urea, TSP, MP, Gypsum and Zinc Sulphate @ 195, 53, 83, 60, 1 kg/ha respectively will be use in the experiment. Total TSP, MP, and Zinc Sulphate will be applied in final land preparation. Total urea will be applied in three installments at 15 days after transplanting (DAT), 35 DAT & 55 DAT respectively.

3.4.5 Transplanting of seedling

Healthy seedlings of 26 days old were transplanted in separate strips of the experimental field. In each strip 25 x 15 cm spacing between plant to plant and row to row, respectively were maintained.

3.4.6 Intercultural operation and after care

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

3.4.7 Plant protection measures

Proper control measures were taken against rice stem borer during tillering and heading stage of rice. Furadan 5G @ 1 g per square meter were applied at active tillering stage and panicle initiation stage of rice for controlling the stem borer. Lani rate and furadan was applied to protect from rat and rice bug respectively. During maturation period a big net was use to cover the hole field to protect the rice from birds.

3.4.8 Irrigation

Thin film of water was given at the time of transplanting; 5 cm depth of water was given at the time of maximum tillering stage. Then field was irrigated as and when required up to physiological maturity.

3.4.9 Harvesting

Different varieties were matured in different times. So crop was harvested on the basis of their physiological maturity.

Plate1. Showing main land preparation and transplanting of seedling

Plate 2.Transplanting of seedling in main experiment field

Plate 3.Putting placard in individual plot of the experiment field

Plate4. Weeding and gap filling in individual plot of the experiment field

Plate5. Supervision of individual plot in the experiment field

Plate6. Naturally perching of individual plot in the experiment field

Plate7. Data collection and field supervision in individual plot of the experiment field

Plate8. Showing stem borer symptom in individual plot of the experiment field

Plate9. Showing stem borer larvae in the rice stem

Plate10. Showing vegetative stage in individual plot of the experiment field

Plate11. Showing mature stage in individual plot of the experiment field

Plate12. Showing harvesting technique in individual plot of the experiment field

3.5 Observations recorded

The data were recorded ten randomly selected plants from each replication leaving the first two border rows from all the four sides, in order to avoid the sampling error. The observations were recorded as per the following procedure. Readings from ten plants were averaged replication wise and the mean data was used for statistical analysis for the 21 characters as follow:

3.5.1 Plant height (cm)

Plant height was measured in centimeter from the ground level to the top of the panice (excluding awn) at the time of maturity.

3.5.2 Flag leaf blade length (cm)

The upper most leaf below the panicle is the flag leaf. The flag leaf generally differs from the others in shape, size and angle. Its length was measured from base to the tip of the leaf in centimeter.

3.5.3 Tillers per hill

The total numbers of tillers are counted as per hill basis.

3.5.4 Panicle length (cm)

Length of main panicle (mother spike) was recorded by measuring from the base of the panicle to the most spikelet's excluding awn in centimeter.

3.5.5 Primary branches per panicle

Number of primary branches per panicle was recorded.

3.5.6 Secondary branches per panicle

Number of secondary branches per panicle was recorded.

3.5.7 No of panicle per m^2

No. of panicle of 24 hills comes form 1 m^2 of area was counted.

3.5.8 Number of filled grains per panicle

Total number of filled grains of the main panicle of each sample plant was counted and the average was taken.

3.5.9 1000 seed weight (g)

1000 seed weight was measured for each treatment. Then grain weight was also adjusted to 14% moisture content.

3.5.10 Grain yield (t/ha)

Grain yield of ten square meters was recorded in gram separately and converted for 1 hectare of land.

3.6 Data analysis

3.6.1 Estimation of genotypic and phenotypic variance

Genotypic and phenotypic variances were estimated by Johnson *et al.* (1955). Genotypic variance (σ^2_g) was obtained by subtracting Error MS from the Genotype MS and dividing by number of replications as shown below:

$$\sigma^2_g = \frac{GMS - EMS}{r}$$

Where, GMS = genotypic mean square

EMS = Error mean square

r = number of replication

The phenotypic variances (σ^2_p) were by adding genotypic variances (σ^2_g) with error variances (σ^2_e) as given by the following formula:

Phenotypic variance = Genotypic variance + error variance

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Where, σ^2_g = Genotypic variance and

σ^2_e = Error variance.

3.6.2 Estimation of genotypic and phenotypic coefficient of variation

The genotypic and phenotypic coefficient of variation were calculated according to the formula suggested by Burton (1952)

$$GCV = \frac{\sigma g}{\text{Population mean}} \times 100$$

Where, GCV= Genotypic coefficient of variation

σ_g= Genotypic standard deviation

$\bar{x}$= Population mean.

$$PCV = \frac{\sigma p}{\text{Population mean}} \times 100$$

Where, PCV=Phenotypic coefficient of variation

σ_p =Phenotypic standard deviation

X=Population mean.

3.6.3 Estimation of heritability

Heritability in broad sense was defined by Lush (1949) as the proportion of genotypic Variance to phenotypic variance and was estimated by using the following formula.

$$h^2_b = \frac{\sigma 2\, g}{\sigma 2\, p} \times 100$$

Where, h^2_b =Heritability in broad sense

σ^2_g=Genotypic variance and

σ^2_p= phenotypic variance

3.6.4 Estimation of genetic advance

The expected genetic advance for different characters under selection were estimated by the formula as suggested by Lush (1949) and Johnson *et al.* (1955).

Genetic advance (GA) = h^2_b. K. σ_p

Where,

h^2_b = Heritability in broad sense

K = Selection intensity, the value of which is 2.06 at 5% selection intensity.

σ_p = Phenotypic standard deviation

3.6.5 Estimation of genotypic and phenotypic correlation coefficients

Genotypic and phenotypic correlation coefficients between different yield contributing morpho-physiological characters contributing to heat tolerance were estimated using the following formula as suggested by Miller *et al.* (1958); Hanson *et al.* (1956) and Johnson *et al.* (1955).

Genotypic correlation,

$$r_{g1.2} = (Cov.g_{1.2}) / \sqrt{\sigma^2 g1 \times \sigma^2 g2}$$

Where,

$Cov.g_{1.2}$ = Genotypic covariance between the variables X1 and X2

$\sigma^2 g1$ = Genotypic variance of the variable X1

$\sigma^2 g2$ = Genotypic variance of the variable X2

Similarly, phenotypic correlation,

$$r_{p1.2} = (Cov.ph_{1.2}) / \sqrt{\sigma^2 p1 \times \sigma^2 p2}$$

Where,

$Cov.ph_{1.2}$ = Phenotypic covariance between the variables X1 and X2.

$\sigma^2 p1$= Phenotypic variance of the variable X1

$\sigma^2 p2$ = Phenotypic variance of the variable X2

3.6.6 Estimation of simple correlation coefficients

Simple correlations between heat stress susceptibility indices and mean of different Characters under late sowing were estimated using the following conventional formula used by Singh and Choudhary (1985).

$$r_{xy} = (Cov._{x.y}) / \sqrt{v_x . v_y}$$

Where,

$Cov._{x.y}$ = Covariance between the variables x and y

V_x = Variance of variable x

V_y = Variance of variable y

The correlation was tested by conventional t-test using following formula

$$t = r \sqrt{n-2} / \sqrt{1-r^2}$$

Where, n = Number of observation

r = Correlation, and tabulated t at n-2. d.f.

3.6.7 Estimation of path coefficients

The components of correlation coefficients of yield contributing characters with yield e further partitioned into components of direct and indirect effects by path coefficient analysis originally developed by Iwey and Lu (1959). In this study, grain yield was considered as the dependent character (effect) and other yield contributing characters

were considered as causal inferiors. The following equations were used depending upon the cause and effect relationships:

$$r_{1y} = P_{1y} + r_{12} P_{2y} + r_{13} P_{3y}$$

$$r_{2y} = r_{12} P_{1y} + P_{2y} + r_{23} P_{3y}$$

$$r_{3y} = r_{13} P_{1y} + r_{23} P_{2y} + P_{3y}$$

where,

Y = Grain yield m^2

1= The character spikes m^2

2= The character grains spike'

3 =The character 1000-grain weight

r_{1y} = Correlation coefficient between grain yield and spikes m^2

r_{2y}= Correlation coefficient between grain yield and grains spike1

r_{3y} = Correlation coefficient between grain yield and 1000-grain weight

r_{12} = Correlation coefficient between spikes m2 and grains spike'

r_{23} = Correlation coefficient between grains spike' and 1000-grain weight

r_{13} Correlation coefficient between spikes m2 and 1000-grain weight

P_{1y} = Path coefficient due to spikes m^2

P_{2y}= 'Path coefficient due to grains spike'

P_{3y} = Path coefficient due to 1000-grain weight

The residual effect was estimated by using the following formula:

$$1 = p^2_{ry} + p_{1y}r_{1y} + p_{2y}r_{2y} + p_{3y}r_{3y}$$

where,

PRY= Residual effect on yield

Similarly, correlation coefficients between grain yield and phenological and physiological characters were studied for path coefficient taking yield as a dependent variable and phenological and physiological characters as independent variables. The

equations were set as the case for 3 primary yield components; only the difference is that there were 6 phenological and physiological characters.

3.6.8 Multivariate analysis (D^2 statistics)

Multivariate analysis was done by computer, using GENSTAT 5.13 and Microsoft Excel 2000 software through four techniques viz, principal component analysis, principal coordinate analysis, cluster analysis and canonical vector analysis.

3.6.8.1 Principal component analysis (PCA)

The technique PCA was used to examine the inter relationships among 21 quantitative characters. The principal components were computed from the correlation matrix (obtained from sum of squares and products matrix of the characters) and genotype scores (obtained from the first component and the succeeding component with latent roots greater than unity). The latent roots are called 'Eigen values'. The first component has the property of accounting for maximum variance. The PCA displays most of the original variability in a smaller number of dimensions, since it finds linear an xbinations of a set of variate that maximize the variation contained within them. Contributions of the different characters towards divergence are discussed from the bent vectors of the first two principal components.

3.6.8.2 Principal Coordinate Analysis (PCO)

PCO was used to calculate the inter genotype distance and it gave the minimum distance between each pair of the N points using similarity matrix through the use of all dimensions of P (Digby et al., 1989).

3.6.8.3 Cluster Analysis (CA)

Cluster analysis was performed by D2 analysis (originally outlined by (Mahalanobis, 1936) and extended by (Rao, 1952), which divides the genotypes based on the data set into more or less homogeneous groups. D2 is the sum of squares of differences between any two populations for each of the uncorrelated variables (obtained by transforming

correlated variables through Pivotal condensation method). Clustering was done using non-hierarchical and hierarchical classification. D2 statistic is defined by

$$D^2x = \sum (\lambda^{ij})\, d_i\, d_j$$

Where, X = Number of metric in point

P = Number of populations or genotypes

λ^{ij} =the matrix reciprocal to the common dispersion matrix

$d_i d_j$ =the differences between the mean values of the two genotypes for the ith and jth characters respectively.

in simpler form D^2 statistic is defined by the formula

$$D^2 = \sum d_i^2 = \sum y^j_i - y^k_j \qquad (j \neq k)$$

Where, Y= uncorrelated variable (character) which varies from i1 to x

X= number of characters.

Superscripts j and k to y= a pair of any two genotypes.

Cluster analysis was performed by computer software Genstat 5.13, which used algorithm to search for optimal values of the chosen criterion. The algorithm did some initial classification of the genotypes into required number of groups and then repeatedly transfers genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer could be found to improve the criterion, the algorithm switched to a second stage, which examined the effect of swooping of two genotypes of different groups, and so on.

3.6.8.4 Canonical Vector Analysis (CVA)

CVA complementary to D2-statitic is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and amount of variation accounted for by each of such axes, respectively are derived. Canonical vector analysis finds linear combination of original variability that maximize the ratio of between groups

to within groups variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformations sequentially maximize the ratio of among groups to within group variations.

3.6.8.5 Computation of average intra-cluster distances

The average intra cluster distance for each cluster was calculated by taking all possible D2 values within the members of a cluster obtained from PCO.

The formula conducted to measure the average intra cluster distance was:

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

Where, D2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster, n = No of all possible combination

3.6.8.6 Cluster diagram

A cluster diagram was drawn using the values of inter and intra cluster distances. The diagram represented the pattern of diversity among the genotypes and relationships between different genotypes included in the clusters.

3.7 Selection of germplasm for future hybridization program

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by the largest statistical distance (D2) express the maximum divergence among the genotypes included into these different clusters.

Singh and Chaudhary (1985) stated the following points should be considered while selecting genotypes for hybridization

i. Choice of cluster from which genotypes are selected for use as parent (s)

ii. Selection of particular genotype (s) from the selected cluster (s)

iii. Relative contribution of the characters to the total divergence

iv. Other important characters of the genotypes (per se performance)

Chapter IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. With the help of suitable genetic parameters like genetic coefficient of variation, genetic advance under selection etc. Ten characters such as plant height, flag leaf blade length, tillers/hill, panicle length, primary branches per panicle, secondary branches per panicle, number of panicles/m^2, filled grains/hill, thousand seed weight and grain yield were studied in respect of 15 genotypes. Results of different studies are described in separate section on character basis.

Variability and other biometrical studies

(1) Variability

(2) Path co-efficient analysis

(3) Multivariate analysis

4.1 Variability

The analysis of variance indicated the existence of highly significant variability for all the characters studied. The variance components, coefficients of genotypic and phenotypic variations, heritability estimates, genetic advance and genetic advance in percent of mean (GAPM) are presented in (Table 2). The results are discussed character wise as follows:

4.1.1 Plant height

Mean sum of square for plant height was highly significant (Table 2) indicating existence of considerable difference for this trait. The maximum plant height was found as 147.6 cm and the minimum was recorded as 92.37 cm with mean value of 118.51 cm (Appendix IV). The genotypic variance (281.42), phenotypic variance (287.04), genotypic co-efficient of variation (13.95) and phenotypic co-efficient of variation (14.09) were close to each other indicating less environmental influence in case of plant

height. Heritability (98.04) estimates for this trait were highly together with considerable moderate genetic advance (34.22) and moderately high genetic advance in percent of mean (28.46) indicated that selection for this character would be more effective.

4.1.2 Flag leaf blade length (cm)

Mean sum of square for flag leaf blade length was highly significant in Rice (Table 2) indicating existence of considerable difference for this trait. The maximum Flag leaf blade length was found 40.82 cm and the minimum was recorded as 27.77 cm with mean value of 34.35 cm (Appendix IV). The genotypic variance (15.88), phenotypic variance (16.00), genotypic co-efficient of variation (11.60) and phenotypic co-efficient of variation (11.65) were close to each other indicating less environmental influence in case of flag leaf blade length. Heritability (99.23) estimates for this trait was very high, genotypic advance (8.18) and genotypic advance in percent of mean (23.80) was found moderately high, indicated that selection for this character would be more effective.

Table2. Genetic parameters of 10 vegetative and yield contributing characters of fifteen rice varieties

Parameters	MSSG	MSSE	Gen.var.	Env.var	Phn.var.	Herit.	G.Ad (5%)	G.Ad (5%) in % mean	GCV	PCV	ECV
PH	849.9**	5.62	281.42	5.62	287.04	98.04	34.22	28.46	13.95	14.09	1.97
FLBL	47.76**	0.12	15.88	0.12	16.00	99.23	8.18	23.80	11.60	11.65	1.02
TH	14.91**	1.53	4.46	1.53	5.99	74.41	3.75	25.04	14.09	16.34	8.26
PL	4.19**	0.47	1.24	0.47	1.71	72.75	1.96	7.50	4.27	5.01	2.61
PBP	3.16**	0.70	0.82	0.70	1.52	53.89	1.37	12.23	8.09	11.02	7.48
SBP	4.84**	0.43	1.47	0.43	1.90	77.26	2.20	25.57	14.12	16.06	7.66
PPM	5960.96**	579.11	1793.95	579.11	2373.05	75.60	75.86	29.99	16.74	19.26	9.51
FGH	55224.86**	10197.32	15009.18	10197.32	25206.50	59.54	14.75	16.83	10.59	13.72	8.73
SS	15.05**	0.17	4.96	0.17	5.13	96.74	4.51	19.19	9.47	9.63	1.74
GY	1.03**	0.07	0.32	0.07	0.39	82.23	1.06	24.88	13.32	14.69	6.19

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

PH=Plant height, FLBL=Flag leaf blade length, TH=Tillers/Hill, PL=Panicle length (cm), PBP=Primary branches per panicle, SBP=Secondary branches per panicle, PPM=Number of panicles/m^2, FGH=Filled grains/hill, SS=Thousand seed weight (1000grain weight in gram), GY=Grain yield (t/ha), G.Ad=Genetic advance, Gen.var=Genotypic variations, Env.var=Environment variations, Phn.var = Phenotypic variations, Herit=Heritability estimates, GCV=Genotypic co-efficient of variation, PCV= Phenotypic co-efficient of variation, ECV = Environment co-efficient of variation.

4.1.3 Tillers per hill

Mean sum of square for tillers per hill was highly significant (Table 2) indicating existence of considerable variability for this trait. The maximum tillers per hill was found 20.67 and the minimum was recorded as 10.33 with mean value of 14.84 (Appendix IV). The genotypic variance (4.46), phenotypic variance (5.99), genotypic co-efficient of variation (14.09) and phenotypic co-efficient of variation (16.34) were close to each other indicating less environmental influence in case of tillers per hill. Heritability (74.41) estimates for this trait was very high, genetic advance (3.75) and genetic advance in percent mean (25.04) were also found moderate, indicated that selection for this character would be effective.

4.1.4 Panicle length (cm)

Mean sum of square for panicle length was highly significant in rice (Table 2) indicating existence of considerable difference for this trait. The maximum panicle length was found 29.77 cm and the minimum was recorded as 23.07 cm with mean value of 26.1 cm (Appendix IV). The genotypic variance (1.24), phenotypic variance (1.71), genotypic co-efficient of variation (4.27) and phenotypic co-efficient of variation (5.01) were close to each other indicating less environmental influence in case of panicle length. Heritability (72.75) estimates for this trait was high, genotypic advance (1.96) and genotypic advance in percent of mean (7.50) was found low, indicated that selection for this character would be less effective.

4.1.5 Number of primary branches per panicle

Mean sum of square for number of primary branches per panicle was highly significant (Table 2) indicating existence of considerable variability for this trait. The maximum number of primary branches per panicle was found 13.67 and the minimum was recorded as 9.33 with mean value of 11.42 (Appendix IV). The genotypic variance (0.82), phenotypic variance (1.52), genotypic co-efficient of variation (8.09) and phenotypic co-efficient of variation (11.02) were close to each other indicating less environmental influence in case of number of primary branches per panicle. Heritability (53.89) estimates for this trait was moderately high, genetic advance (1.37) and genetic advance in percent mean (12.23) were also found low, indicated that selection for this character would be less effective.

4.1.6 Number of secondary branches per panicle

Mean sum of square for number of secondary branches per panicle was highly significant (Table 2) indicating existence of considerable variability for this trait. The maximum number of secondary branches per panicle was found 10.33 and the minimum was recorded as 6.00 with mean value of 8.62 (Appendix IV). The genotypic variance (1.47), phenotypic variance (1.90), genotypic co-efficient of variation (14.12) and phenotypic co-efficient of variation (16.06) were close to each other indicating less environmental influence in case of number of secondary branches per panicle. Heritability (77.26) estimates for this trait was high, genetic advance (2.20) and genetic advance in percent mean (25.57) were also found moderate, indicated that selection for this character would be effective.

4.1.7 Number of panicles per m^2

Mean sum of square for number of panicle per square meter was highly significant in Rice (Table 2) indicating existence of considerable variability for this trait. The maximum number of Panicle per square meter was found 328 gm and the minimum was recorded as 175 with mean value of 252.96 (Appendix IV). The genotypic variance (1793.95), phenotypic variance (2373.05), genotypic co-efficient of variation (16.74) and phenotypic co-efficient of variation (19.26) were close to each other indicating less environmental influence in case of no. of Panicle per square meter. Heritability (75.60) estimates for this trait was high, genetic advance (75.86) was found moderate and genetic advance in percent of mean (29.99) was found moderately high, indicated that selection for this character would be more effective.

4.1.8 Filled grains per hill

Mean sum of square for filled grains per plant was highly significant in Rice (Table 2) indicating existence of considerable difference for this trait. The maximum filled grains per hill was found 1509 and the minimum was recorded as 779.67 with mean value 1173.65 (Appendix IV). The genotypic variance (15009.18), phenotypic variance (25206.50), genotypic co-efficient of variation (10.59) and phenotypic co-efficient of variation (13.72) were close to each other indicating less environmental influence in case of filled grains per hill. Heritability (59.54) estimates for this trait was moderately together with considerable moderately high, genetic

advance (14.75) and genetic advance in percent of mean (16.83) indicated that selection for this character would be less effective.

4.1.9 Thousand Seed Weight (g)

Mean sum of square for thousand seed weight was highly significant in rice (Table 2) indicating existence of considerable difference for this trait. The maximum thousand seed weight was found 26.80 gm and the minimum was recorded as 19.00 gm with mean value of 23.52 gm (Appendix IV). The genotypic variance (4.96), phenotypic variance (5.13), genotypic co-efficient of variation (9.47) and phenotypic co-efficient of variation (9.63) were close to each other indicating less environmental influence in case of thousand seed weight. Heritability (96.74) estimates for this trait was together with considerable very high, genetic advance (4.51) and genetic advance in percent of mean (19.19) indicated that selection for this character would be less effective.

4.1.10 Grain yield (t/ha)

Mean sum of square for grain yield (t/ha) was highly significant in rice (Table 2) indicating existence of considerable difference for this trait. The maximum grain yield was found 5.06 t/ha and the minimum was recorded as 3.31 t/ha with mean value of 4.24 t/ha (Appendix IV). The genotypic variance (0.32), phenotypic variance (0.39), genotypic co-efficient of variation (13.32) and phenotypic co-efficient of variation (14.69) were close to each other indicating less environmental influence in case of yield per plant. The heritability value (82.2) as well as genetic advance (1.06) and genetic advance in percent of mean (24.88) were observed moderately high. The very high heritability with moderate genetic advance in percentage of mean provided opportunity for selecting high valued genotypes for breeding programme.

Plate 13: Photograph showing grain type of different rice varieties

Plate 14: Photograph showing grain type of different rice varieties

4.2 Correlation co-efficient

Genotypic and phenotypic correlation co-efficient between pairs of characters for rice are presented in (Table 3). It is evident that in majority to the case, the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient. This indicated a strong inherent association between the characters studied and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, however, phenotypic correlation co-efficient were same with or higher than their corresponding genotypic correlation co-efficient suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. Rice yield per plant had highest significant positive correlation with Primary branch per panicle (G = 0.709 and P = 0.520) which indicating that, if Primary branch per panicle increase, grain yield per plant also increase (Table 3).

4.2.1 Plant height (cm)

Plant height showed positive significant interaction with flag leaf blade length (G = 0.421, P=0.415) and thousand seed weight (G = 0.512, P=0.507), where as negative interaction were found in tillers per hill (G = -0.775, P = -0.652) and number of panicle per m^2 (G = -0.736, P = -0.633) (Table 3).

4.2.2 Flag leaf blade length

This trait showed highly significant positive correlation with panicle length (G = 0.403) and Thousand seed weight (G = 0.598) at genotypic level (Table 3) and significant positive correlation with panicle length (P = 0.374) and thousand seed weight (P = 0.582) at the phenotypic level. Significant negative correlation was found in tillers per hill (G = -0. 387, P = -0. 329) at genotypic and phenotypic level (Table 3).

4.2.3 Tillers per hill

Tiller per hill showed positive significant interaction with number of panicle per m^2 (G= 0.649, P=0.628), grain yield (G= 0.625, P=0.527) at genotypic level and phenotypic level and showed significant negative interaction with thousand seed weight (G=-0.569, P=-0.475) (Table 3).

4.2.4 Panicle length (cm)

Length of panicle showed positive significant interaction with primary branch per panicle (G= 0.637, P = 0.440), thousand seed weight (G= 0.483, P= 0.396) and grain yield (G= 0.522, P= 0. 581) at both genotypic level and phenotypic level and showed negative interaction with secondary branches per panicle (G = -0.098, P=-0. 052) and number of panicles per m^2 (G = -0.229, P=-0. 145) at both genotypic level and phenotypic level (Table 3).

4.2.5. Number of primary branch per panicle

Primary branches per panicle showed positive significant interaction with filled grains per panicle (G = 0.911, P = 0.601) and grain yield (G = 0.709, P = 0.520) at both genotypic level and phenotypic level. Whereas the negative interaction was found in primary branches per panicle (G= -0.274, P = -0. 115) at both genotypic level and phenotypic level (Table 3).

4.2.6 Number of secondary branches per panicle

Secondary branches per panicle showed positive significant interaction with found filled grains per panicle (G = 0.836, P= 0.648) at both genotypic level and phenotypic level whereas negative significant interaction were found thousand seed weight (G =-0.334) at genotypic level (Table 3).

Table 3: Genotypic and phenotypic Correlations co-efficient among some yield contributing characters in rice

		FLBL	TH	PL	PBP	SBP	PPM	FGP	SS	GY
PH	r_g	0.421**	-0.775**	-0.023	-0.170	-0.214	-0.736**	-0.185	0.512**	-0.652**
	r_p	0.415**	-0.652**	-0.007	-0.110	-0.166	-0.633**	-0.125	0.507**	-0.560**
FLBL	r_g		-0.387*	0.430**	0.298*	0.171	-0.257	0.137	0.598**	0.008
	r_p		-0.329*	0.374*	0.202	0.165	-0.226	0.105	0.582**	0.014
TH	r_g			0.332*	0.124	0.195	0.649**	0.220	-0.569**	0.625**
	r_p			0.247	0.177	0.071	0.628**	0.115	-0.475**	0.527**
PL	r_g				0.637**	-0.098	-0.229	0.249	0.483**	0.522**
	r_p				0.440**	-0.052	-0.145	0.188	0.396**	0.581**
PBP	r_g					0.554**	-0.274	0.911**	0.110	0.709**
	r_p					0.241	-0.115	0.601**	0.095	0.520**
SBP	r_g						0.445**	0.836**	-0.334*	0.307*
	r_p						0.258	0.648**	-0.277	0.264
PPM	r_g							0.150	-0.692**	0.443**
	r_p							-0.011	-0.583**	0.375**
FGP	r_g								-0.316*	0.545**
	r_p								-0.209	0.383**
SS	r_g									-0.211
	r_p									-0.183

PH=Plant height, FLBL=Flag leaf blade length, TH=Tillers/Hill, PL=Panicle length (cm), PBP=Primary branches per panicle, SBP=Secondary branches per panicle, PPM=Number of panicles/m^2, FGP=Filled grains/panicle, SS=Thousand seed weight (1000grain weight in gram), GY= Grain yield (t/ha)

** Significant at the 1% level of probability * Significant at the 5% level of probability

4.2.7 Number of panicles per m^2

Number of panicles per m^2 showed positive significant interaction with grain yield (G = 0.443, P= 0.375) at genotypic level and phenotypic level and showed negative interaction with thousand seed weight (G=-692, P=-0. 583) (Table 3).

4.2.8 Field grains per hill

Filled grains per panicle showed positive interaction with grain yield (G=0.545, P=0. 383) and negative significant interaction with thousand seed weight (G = -0.316) at genotypic level (Table 3).

4.2.9 Thousand seed weight

Thousand seed weight showed no significant negative interaction with yield per plant (G =-0. 211, P =-0. 183) (Table 3).

4.3 Path co-efficient

Path coefficient analysis was done with plant height, flag leaf blade length, tillers per hill, panicle length, primary branches per panicle, secondary branches per panicle, number of panicles per square meter, filled grains per hill, 1000 seed weight and grain yield. The direct and indirect effects of different characters on yield are present in (Table 4 and Fig.1). Path co-efficient analysis revealed that, filled grains per hill had the highest direct positive effect (0.891) on seed yield followed by panicle length (0.785), number of panicles per square meter (0.336), which indicated true relationship between them and direct selection for this trait will be rewarding for yield improvement.

4.3.1 Plant height

Path analysis revealed that plant height had negative direct effect (-0.739) on grain yield and positive indirect effect through tiller per hill (0.450), number of primary branches per panicle (0.054), number of secondary branches per panicle (0.085), (Table 4). On the other hand, plant height showed negative indirect effect on grain yield via Flag leaf blade length (-0.026), Panicle length (-0.018), Number of panicles per square meter (-0.247), Filled grains per panicle (-0.165) and thousand seed weight (-0.046).

4.3.2 Flag leaf blade length

Flag leaf blade length showed negative direct (-0.063) effect on grain yield (t/ha) and positive indirect effects through tillers per hill (0.225), panicle length (0.337) and filled grains per hill (0.122). Flag leaf blade length had negative indirect effect on all other characters. (Table 4).

4.3.3 Tillers per hill

Tillers per hill had negative direct effect -0.581) on grain yield and positive indirect effect on plant height (0.573), flag leaf blade length (0.024), panicle length (0.261), number of panicle per square meter (0.218) and filled grain per plant (0.196) and thousand seed weight (0.051). On the other hand this trait showed negative indirect effect on primary branch per panicle (-0.039) and secondary branch per panicle (-0.078) (Table 4).

4.3.4 Panicle length

Path analysis revealed that panicle length had direct positive effect (0.785) on grain yield (t/ha). This trait had also indirect positive effect on plant height (0.017), secondary branches per panicle (0.039) and filled grains per plant (0.221). Panicle length had negative indirect effect on all other characters (Table 4).

4.3.5 Number of primary branches per panicle

Number of primary branches per panicle had negative direct effect (-0.316) on grain yield and positive indirect effect on plant height (0.125), panicle length (0.500) and field grain per plant (0.812). On the other hand this trait showed negative indirect effect on all other parameters (Table 4).

4.3.6 Number of secondary branches per panicle

Number of secondary branches per panicle had negative direct effect (-0.398) on grain yield and positive indirect effect on plant height (0.158), Number of panicle per square meter (0.149), field grain per plant (0.744) and thousand seed weight (0.030). On the other hand this trait showed negative indirect effect on all other parameters (Table 4).

4.3.7 Number of panicle per square meter

Number of panicles per square meter had positive direct effect (0.336) on grain yield and negative indirect effect on tillers per hill (-0.377), panicle length (-0.180) and number of secondary branches per panicle (-0.177). On the other hand this trait showed positive indirect effect on all other parameters (Table 4).

4.3.8 Field grains per hill

Field grains per plant had positive direct effect (0.891) on grain yield and negative indirect effect on tiller per hill (-0.128), primary branches per panicle (-0.288) and number of secondary branches per panicle (-0.333). On the other hand this trait showed positive indirect effect on all other parameters (Table 4).

Table 4. Direct (Diagonal) and indirect effect of some yield contributing characters in rice

	PH	FLBL	TH	PL	PBP	SBP	PPM	FGH	SS	Grain yield (t/ha)
PH	**-0.739**	-0.026	0.450	-0.018	0.054	0.085	-0.247	-0.165	-0.046	-0.652**
FLBL	-0.311	**-0.063**	0.225	0.337	-0.094	-0.068	-0.086	0.122	-0.053	0.008
TH	0.573	0.024	**-0.581**	0.261	-0.039	-0.078	0.218	0.196	0.051	0.625**
PL	0.017	-0.027	-0.193	**0.785**	-0.201	0.039	-0.077	0.221	-0.043	0.522**
PBP	0.125	-0.019	-0.072	0.500	**-0.316**	-0.221	-0.092	0.812	-0.010	0.709**
SBP	0.158	-0.011	-0.113	-0.077	-0.175	**-0.398**	0.149	0.744	0.030	0.307*
PPM	0.544	0.016	-0.377	-0.180	0.086	-0.177	**0.336**	0.134	0.061	0.443**
FGH	0.137	-0.009	-0.128	0.195	-0.288	-0.333	0.050	**0.891**	0.028	0.545**
SS	-0.379	-0.038	0.330	0.379	-0.035	0.133	-0.232	-0.282	**-0.089**	-0.211

R= 0.406 **Significant at 1% level of probability * Significant at 5% level of probability

PH=Plant height, FLBL=Flag leaf blade length, TH=Tillers/Hill, PL=Panicle length (cm), PBP=Primary branches per panicle, SBP=Secondary branches per panicle, PPM=Number of panicles/m^2, FGH=Filled grains/hill, SS=Thousand seed weight (1000grain weight in gram)

4.3.9 Thousand seeds weight

Thousand seeds weight had high negative direct effect (-0.089) on grain yield and positive indirect effect on tillers per hill (0.330), Panicle length (0.379) and secondary branches per panicle (0.133). Thousand seed weight had negative indirect effect on all other parameter. (Table 4).

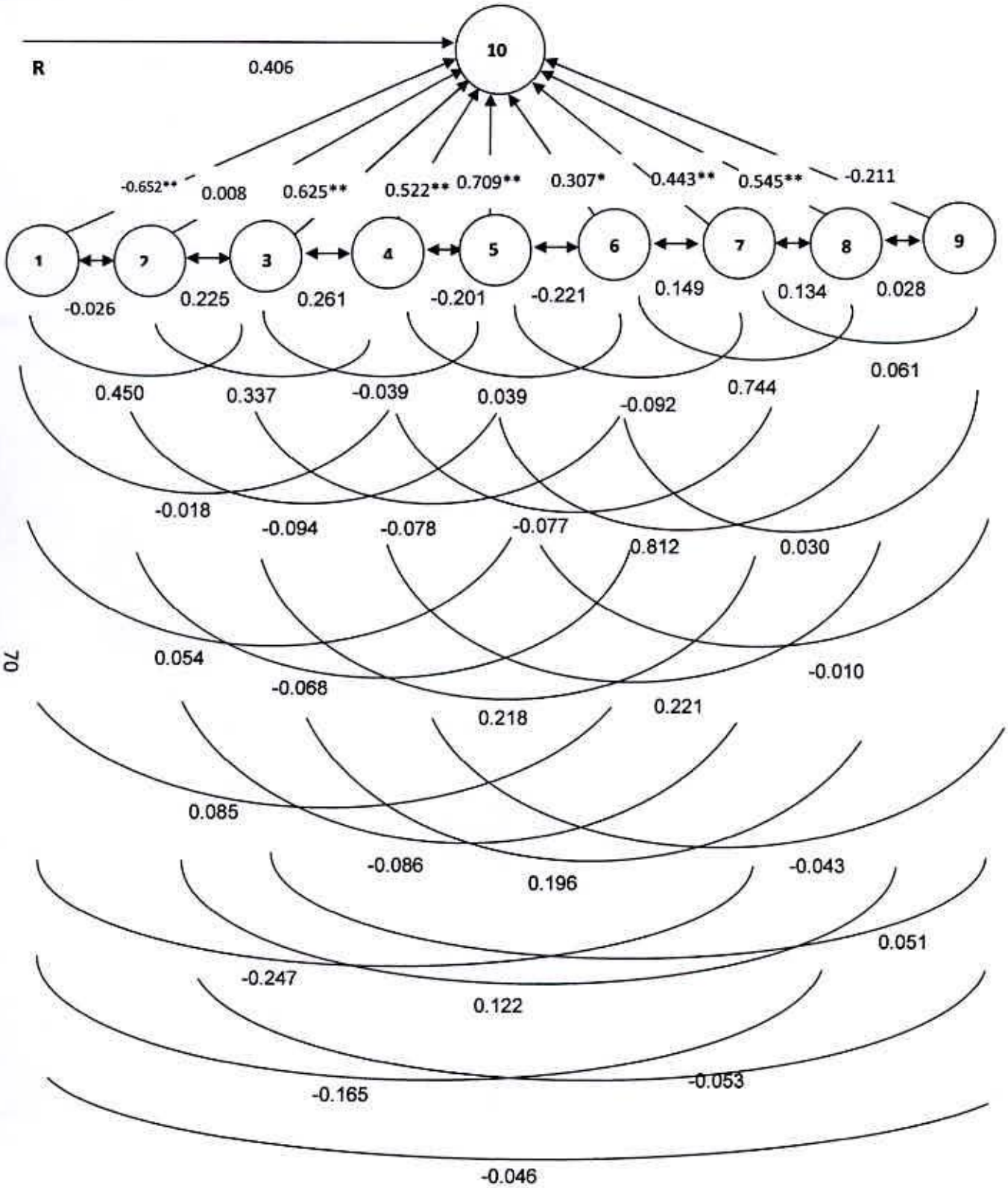

Fig. 1 Path diagram of yield contributing traits in 15 rice varieties.

1=Plant height, 2=Flag leaf blade length, 3=Tiller/Hill, 4=Panicle length (cm), 5=Primary branches per panicle, 6=Secondary branches per panicle, 7=Number of panicle/sm^2, 8=Filled grains/hill, 9=Thousand seed weight (1000grain weight in gram), 10=Grain yield (t/ha).

4.4 MULTIVARIATE ANALYSIS

4.4.1 Principal component analysis (PCA)

Principal component analysis was carried out with 15 genotypes of rice. First 3 Eigen values for 3 principal coordination axes of genotypes accounted for 69.46% variation (Table 5). A two dimensional scattered diagram Fig.2 was developed on the basis of the principal component score, Z_1 and Z_2 score (Appendices V).

4.4.2 Principal coordinates analysis (PCO)

The results obtained from principal coordinate analysis showed that the highest inter genotypic distance was observed between genotypes BRRI dhan46 and BRRI dhan49 (1.8221) followed by BRRI dhan34 and BRRI dhan46 (1.7335) and the lowest distance was observed (0.4084) between genotypes BRRI dhan37 and BRRI dhan38 followed by the distance (0.4426) between genotypes BRRI dhan44and BRRI dhan52 (Table 6). The difference between the highest and the lowest inter genotypic distance indicated the moderate variability among the 15 genotypes of rice. The highest intra-cluster distance was recorded in cluster IV (1.3053) containing Four genotypes BRRI dhan40, BRRI dhan46, BRRI dhan49 and BRRI dhan51. The lowest intra-cluster distance was observed in cluster I (0.000) having one genotypes BINA dhan7. It favored to decide that intra-group diversity was the highest in cluster IV and the lowest in cluster I. The cluster II consisted six genotype viz. BRRI dhan33, BRRI dhan34, BRRI dhan37, BRRI dhan38, BRRI dhan44, BRRI dhan52 and had an intra-cluster distance 0.6772. Cluster III having four genotypes viz. BR16, BR23, BRRI dhan39, BRRI dhan41 and had an intra-cluster distance 0.7144 (Table 7 and 8).

Table 5. Eigen value and percent contribution of 10 yield contributing characters of fifteen rice varieties

Principal component axis	Eigen values	% total variation account for	Cumulative percent
Plant height	5.2929	31.13	31.13
Flag leaf blade length	2.5420	14.95	69.46
Tillers per hill	1.1027	6.49	82.99
Panicle length	0.8096	4.76	87.75
Primary branches per panicle	0.4793	2.82	95.22
Secondary branches per panicle	0.2830	1.66	96.88
Number of panicle / m^2	0.1827	1.07	99.28
Number of filled grains per hill	0.0766	0.45	99.73
1000 seed weight	0.0007	0.00	100
Grain yield (t/ha)	0.0000	0.00	100

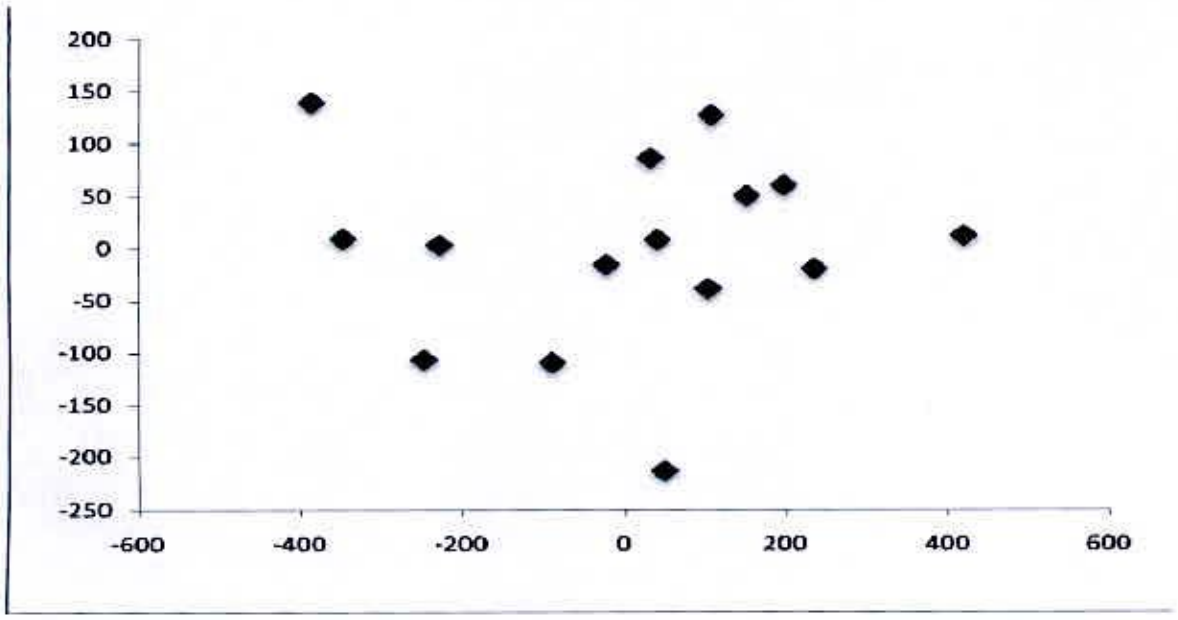

Fig 2. Scatter diagram of 15 varieties of rice based on their principal component scores superimposed with cluster.

Table 6. Ten highest and ten lowest inter genotypic distance among the fifteen rice varieties

Sl. No.	Genotypic combination	Distances
10 highest inter genotypic distance		
01.	BRRI dhan46 – BRRI dhan49	1.8221
02.	BRRI dhan34 – BRRI dhan46	1.7335
03.	BR23 – BRRI dhan49	1.7294
04.	BRRI dhan37 – BRRI dhan46	1.6880
05.	BRRI dhan46 – BINA dhan7	1.6547
06.	BRRI dhan38 – BRRI dhan46	1.6235
07.	BRRI dhan46 – BRRI dhan51	1.5867
08.	BRRI dhan33 – BRRI dhan46	1.5704
09.	BRRI dhan41 – BRRI dhan49	1.5025
10.	BRRI dhan49 – BINA dhan7	1.5021
10 lowest inter genotypic distance		
01.	BRRI dhan37 – BRRI dhan38	0.4084
02.	BRRI dhan44- BRRI dhan52	0.4426
03.	BRRI dhan40 - BRRI dhan41	0.5009
04.	BR16 - BRRI dhan52	0.5026
05.	BR23 - BRRI dhan41	0.5649
06.	BR16 - BRRI dhan39	0.5912
07.	BRRI dhan33 - BRRI dhan44	0.5999
08.	BRRI dhan33 - BRRI dhan52	0.6096
09.	BR16 - BRRI dhan51	0.6189
10.	BRRI dhan39 - BRRI dhan41	0.6223

Table 7. Distribution of fifteen rice varieties of rice in four clusters

Cluster	Number of members	Varieties Numbers	Name of the varieties
I	1	15	BINA dhan7
II	6	3, 4, 5, 6, 10, 14	BRRI dhan33, BRRI dhan34, BRRI dhan37, BRRI dhan38, BRRI dhan44, BRRI dhan52
III	4	1, 2, 7, 9	BR16, BR23, BRRI dhan39, BRRI dhan41
IV	4	8, 11, 12, 14	BRRI dhan40, BRRI dhan46, BRRI dhan49, BRRI dhan51,

Table 8. Average Inter and intra cluster distance of fifteen rice varieties

	I	II	III	IV
I	**0.000**			
II	3.790	**0.6772**		
III	8.155	5.053	**0.7144**	
IV	10.531	10.812	9.227	**1.3053**

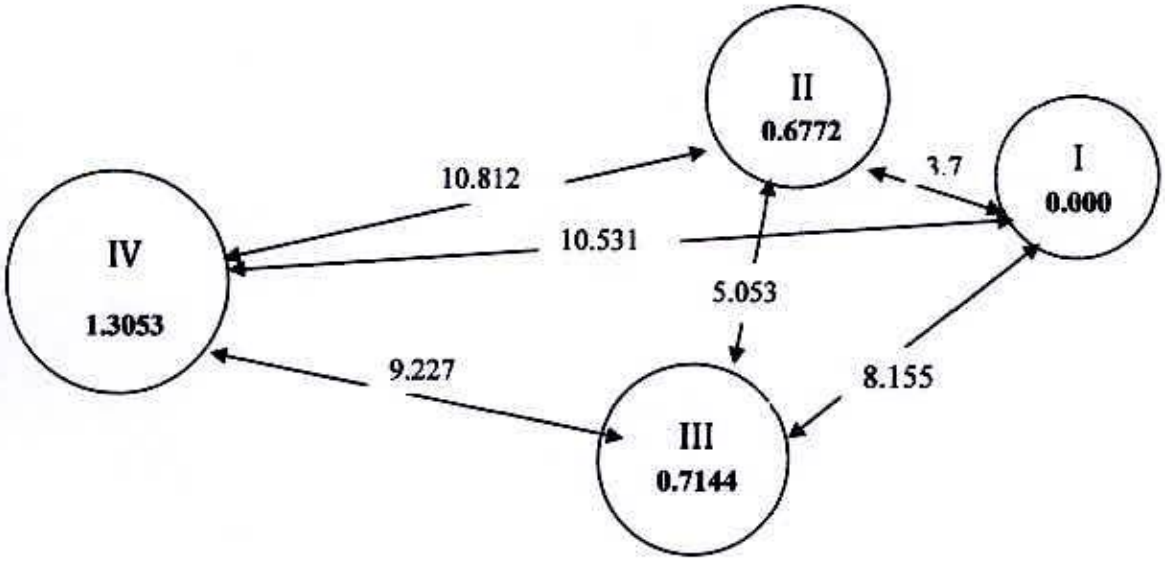

Figure 3. Diagram showing intra and inter cluster distances of 15 varieties of rice

4.4.3 Non-hierarchical clustering

The computations from covariance matrix gave non-hierarchical clustering among fifteen genotypes of rice and grouped them into four clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA. So the results obtained through PCA were confirmed by non-hierarchical clustering. (Table 8) represents the clusters occupied by fifteen genotypes of rice. It explains that's cluster I contained the number of genotype one, cluster II constitute by six genotypes, cluster III constitute by four genotypes and cluster IV constitute by four genotypes. Cluster I was composed of BINA dhan7. The genotypes of cluster I are collected from BINA, Mymensingh. Cluster mean for 45 traits are presented in (Table 9). Cluster IV was formed by 4 genotypes viz. BRRI dhan40, BRRI dhan46, BRRI dhan49, BRRI dhan51. They were collected from BRRI, Gazipur. These clusters were unable to lead in respect of the highest cluster mean value for maximum characters.

Among 10 characters cluster IV produced the maximum cluster mean for the five characters viz. plant height (121.50), flag leaf blade length (36.2) primary branches per panicle (12.7), secondary branches per panicle (9.8) and number of filled grains per plant (1454.9). Similarly, cluster III ranked first for panicle length (26.5) and 1000 seed weight (24.3). Cluster I ranked first for no. number of panicle per square meter (328.0) and grain yield (4.7). Cluster II ranked tillers per hill (16.2) (Table 9).

4.4.4 Canonical variate analysis

The highest inter-cluster distance was observed (Table 7 or Figure 3) between cluster II and IV (10.812) followed by between cluster I and IV (10.531).The intra cluster distance was the highest (1.3053) in cluster IV. The lowest inter-cluster distance was observed between cluster I and II (3.79) followed by cluster II and III (5.053). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used for hybridization program. However, the highest inter-cluster distance was observed between cluster II and IV indicated the genotypes in these clusters were far diverged than those of other clusters. Similarly, the lowest inter-cluster distance was observed between the cluster I and II. Moderate or intermediate distance was found between cluster I and

III (8.155), cluster III and IV (9.227). The inter cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotype of different groups.

Result of different multivariate analysis were superimposed in figure 3 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another. As per scatter diagram the genotypes were apparently distributed into four clusters. (Islam *et al.*, 2004) also similar result was found. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant breeding, the objective is not only high heterosis but also to achieved high-level production. In the present study the maximum distance existence between cluster cluster II and IV. But considering the yield and duration crosses involving cluster cluster II and IV may be exhibit high heterosis for yield. (Main and Bahl, 1989) reported that the parents separated by D^2 values of maderate generally showed higher heterosis.

Table 9. Cluster mean distance of 15 rice varieties

Parameter	I	II	III	IV
Plant height	96.5	119.0	120.0	121.5
Flag leaf blade length	31.6	34.3	33.3	36.2
Tillers per hill	14.7	16.2	13.2	14.6
Panicle length	24.5	26.0	26.5	26.2
Primary branches per panicle	10.7	10.6	11.7	12.7
Secondary branches per panicle	7.7	7.7	9.1	9.8
Number of panicles / m^2	328.0	244.6	240.4	259.3
Number of filled grains per hill	779.7	1035.3	1198.4	1454.9
1000 seed weight	21.4	24.2	24.3	22.3
Grain yield (t/ha)	4.7	4.0	4.3	4.4

4.5.5 Contribution of characters towards divergence of the varieties

The values of Vector I and Vector II are presented in (Table 10). Vector I obtained from PCA expressed that plant height (0.3644), Flag leaf blade length (0.3002), Panicle length (0.3755), Primary branches per panicle (0.2477), Number of filled grains per plant (0.1710) and thousand seed weight (0.3415) were major characters that contribute to the genetic divergence. It was the reflection of first axis of differentiation. In vector II days to plant height (0.0854), Tillers per hill (0.0394), and thousand seed weight (0.0924), showed their important role toward genetic divergence. Negative values in both vectors for, secondary branches per panicle, number of panicles/m^2 and grain yield had lower contribution towards the divergence.

Table 10. Latent vectors for 10 principal component characters of fifteen varieties of rice

	Vector I	Vector II
Plant height	0.3644	0.0854
Flag leaf blade length	0.3002	-0.1243
Tillers per hill	-0.1800	0.0394
Panicle length	0.3755	-0.0532
Primary branches per panicle	0.2477	-0.3434
Secondary branches per panicle	-0.0079	-0.3329
Number of panicles / m^2	-0.3254	-0.1748
Number of filled grains per hill	0.1710	-0.3350
1000 seed weight	0.3415	0.0924
Grain yield	-0.1279	-0.4116

4.5.6 Selection of varieties as parent for hybridization programme.

Selection of generically diverse parents is an important step for hybridization program. So the varieties were to be selected on the basis of specific objectives. A high heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.*, 1974; Ghaderi *et al.* 1984).

Considering the magnitude of cluster mean and agronomic performance the variety G8 (BRRI dhan40) for maximum plant height, and panicle length from cluster IV: G10 (BRRI dhan44) for maximum thousand seed weight and yield form cluster II. Therefore considering group distance and other agronomic performance the inter varietal crosses between G6 and G10; G6 and G8; G6 and G12: G8 and G10: G8 and G12, G8 and G15, G10 and G12, G10 and G15, G15 and G6, G11 and G12, G12 and G15 may be suggested for future hybridization program.

Chapter V

SUMMARY AND CONCLUSION

The experiment was conducted with a view to identify divergent parents for hybridization programme, identify the characters contributing to genetic diversity, asses the magnitude of genetic divergence in genotypes and determine the variability in respect of yield and some yield contributing characters, the degrees of association among the characters and their direct and indirect effects on yield in 15 varieties of rice at the experimental farm (west-byed) of Bangladesh Rice Research Institute (BRRI), Joydebpur, Gazipur during T.Aman June 2012 to December 2012. The salient findings of the present study have been summarized on the basis of the characters studied.

The analysis of variance showed significant differences among the genotypes for all the characters. The maximum plant height (147.6 cm) was recorded from the variety BRRI dhan40 and the lowest plant height (92.367cm) was recorded by BRRI dhan51. Maximum flag leaf blade length was recorded in BRRI dhan40 and BRRI dhan51 produce the minimum flag leaf blade length. Maximum tillers per plant were recorded in BRRI dhan38. Maximum panicle length was recorded in BRRI dhan40 and minimum panicle length in BRRI dhan49.

The minimum number of primary branches per panicle was recorded by the BRRI dhan34 and BRRI dhan40 showed the maximum number of primary branches per panicle. The variety BRRI dhan34 showed the minimum number of secondary branches per panicle and the maximum number of secondary branches per panicle was recorded in BRRI dhan49. The minimum number of panicle per m^2 was observed in BR 23 while maximum number of panicles per m^2 was found in the variety BINA dhan7. The variety BRRI dhan49 had highest filled grains per plant while it was lowest in BINA dhan7. The highest thousand seed weight was recorded in BRRI dhan44 while BRRI dhan49 had the lowest thousand seed weight. The variety BRRI dhan44 had highest grain yield (t/ha) and the lowest was in BRRI dhan34.

The phenotypic variance was higher than genotypic variance in all the characters studied. High heritability (>60%) was observed for the most of characters except primary branches per panicle

and filled grains per panicle. The high heritability coupled with high genetic advance in percent of mean was observed in plant height, flag leaf blade length, tiller per hill, secondary branches per panicle, number of panicles per m^2 and grain yield which suggested that effective selection may be done for these characters.

The significant positive correlation at the 1% level was observed for seed yield per plant with tiller per hill, length of panicle, primary branch per panicle, number of panicle per m^2, Filled grains per panicle at genotypic level both genotypic and phenotypic level. The significant negative correlation at the 1% level was observed for seed yield per plant with plant height.

Filled grains per plant showed the highest positive direct effect (0.891) with grain yield. On the other hand negative direct effect on grain yield was show by plant height, flag leaf blade length, tillesr per hill, primary branches per panicle, secondary branches per panicle and thousand seed weight. Panicle length and number of panicles/m^2 also showed positive direct effect on seed yield. Filled grains per plant showed high direct effect on seed yield indicated that direct selection for this trait might be effective and there is a possibility of improving grain yield through selection based on those characters.

Genetic diversity of fifteen rice varieties based on ten characters was measured through multivariate analysis. The 15 variety fell into four distant clusters. The cluster II comprised the maximum number (6) of variety followed by cluster III and IV (4). The cluster I comprised one variety. The highest inter-cluster distance (10.812) was observed between the cluster II and IV and the highest distant varieties were G_{11} (BRRI dhan46) and G12 (BRRI dhan49). The lowest inter-cluster distance (3.79) was observed between the cluster I and II and the lowest distance varieties were G_5 (BRRI dhan37) and G_6 (BRRI dhan38).

The inter-cluster distances were larger than the intra-cluster distances. The intra-cluster distance in the entire four clusters was more or less low indicating that the varieties within the same cluster were closely related. Plant height and number of filled grains per plant were the important component characters having higher contribution to the genetic divergence.

The result of the present study revealed that a wide variability exists among the collected rice varieties. From the findings of the present study, the following conclusions could be drawn:

1. Wide range of genetic diversity existed among the rice varieties. Wide genetic diversity was observed in 15 varieties of rice, which were grouped into four clusters and most diverse varieties were BRRI dhan46 and BRRI dhan49. That variability could be used for breeding materials of future breeding programme of rice in Bangladesh.

2. High heritability coupled with high genetic advance in percent of mean was observed in plant height and thousand seed weight. Hence, yield improvement in rice would be achieved though selection of these characters.

3. The varieties of clusters IV were more diversed from the varieties of cluster I.

4. Further collection of rice germplasms would be continued for getting more variability and desired traits in rice.

Based on the results of the study, the following recommendations may be drawn:

1. The rice varieties G8 (BRRI dhan40), G10 (BRRI dhan44), G11 (BRRI dhan46), G12 (BRRI dhan49) and G15 (BINA dhan7) could be included in future research towards improvement of grain yield.

2. The varieties of cluster II and IV could be used as parents for future breeding programme to develop rice variety.

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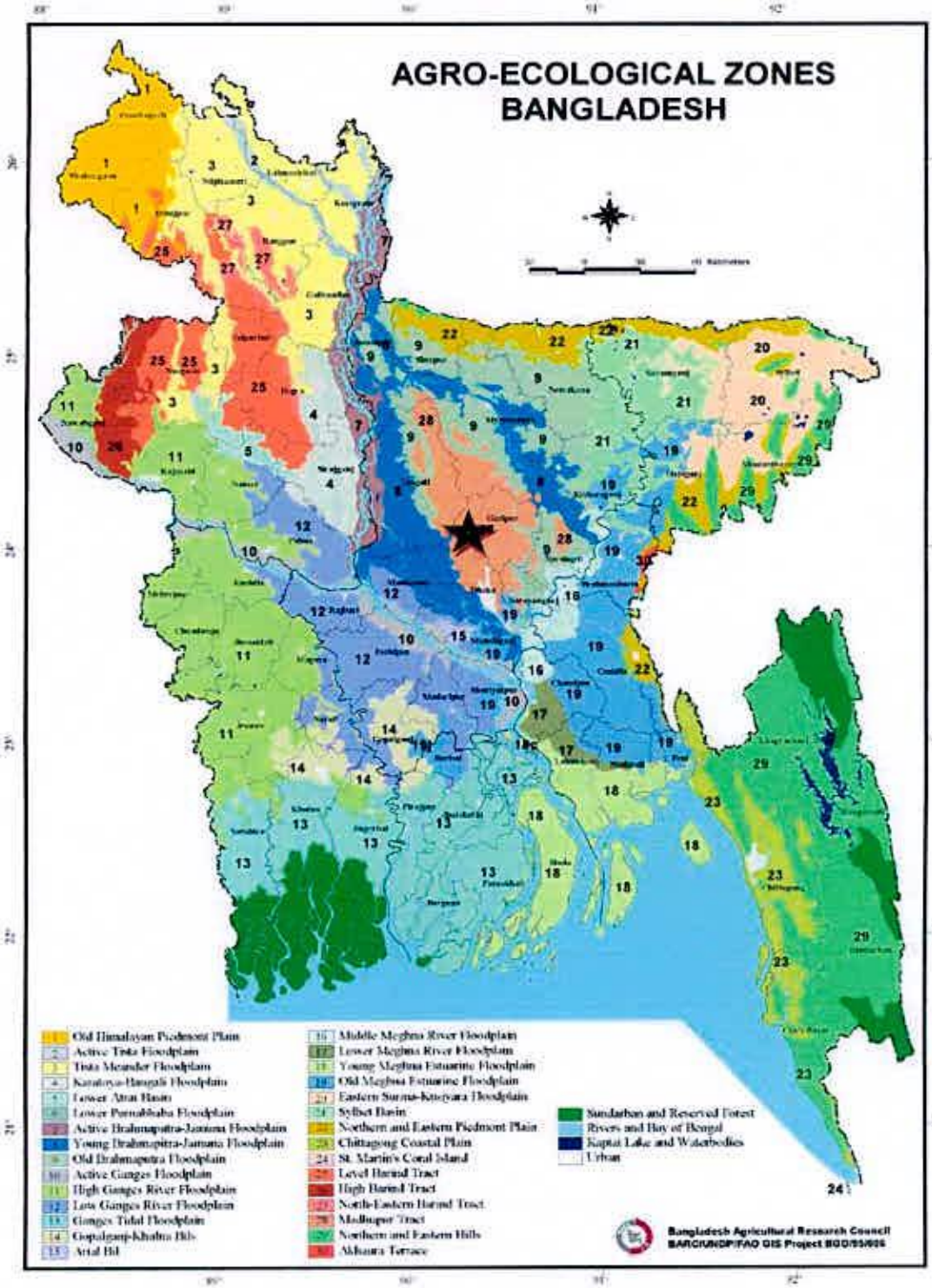
APPENDICES

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



★ **The experimental site under study**

Appendices II. Monthly average Temperature, Relative Humidity and Total Rainfall of The experimental site during the period from July, 2012 to December, 2012

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)	Sunshine (hr)
	Maximum	Minimum			
July, 2012	32.3	26.7	82	356	4.55
August, 2012	31.1	26.5	77	409	5.61
September, 2012	32.4	26.4	73	207	4.28
October, 2012	32.7	24.7	67	112	6.69
November, 2012	29.7	19.2	73	0	6.60
December, 2012	24.7	15.0	70	0	4.56

Source: Bangladesh Rice Research Institute (Phylogy Division), Joydebpur, Gazipur.

Appendices III: Physical Characteristics and chemical composition of soil of the experimental plot

Soil Characteristics	Analytical Results
Agrological Zone	Madhupur Tract
P^H	5.92
Organic Matter (%)	0.82
Total N (%)	0.8
Available phosphorous	6 mg/ kg
Exchangeable K	0.26 meq / 100g soil

Source: Bangladesh Rice Research Institute (Soil Science Division), Joydebpur, Gazipur.

Appendix IV: Mean performance of different parameters of fifteen varieties of rice

Identifier	Minimum	Maximum	Mean
Plant height	92.367	147.6	118.513
Flag leaf blade length	27.767	40.823	34.349
Tillers per hill	10.333	20.667	14.844
Panicle length	23.067	29.767	26.102
Primary branches per panicle	9.333	13.667	11.422
Secondary branches per panicle	6	10.333	8.622
Number of panicle / m^2	175	328	253
Number of filled grains per panicle	780	1509	1174
1000 seed weight	19	27	23
Grain yield (t/ha)	3.31	5.057	4.243

Appendix V. Principal component score fifteen varieties of rice

Serial no.	Genotypes	Z_1	Z_2
1	BR11	39.7	8.7
2	BR 23	50.4	-212.4
3	BRRI dhan33	195.3	60.7
4	BRRI dhan34	232.8	-18.7
5	*BRRI dhan37*	149.5	50.5
6	BRRI dhan38	105.2	127.5
7	BRRI dhan39	-23.3	-15
8	BRRI dhan40	-247.4	-106
9	BRRI dhan41	-89.4	-109.2
10	BRRI dhan44	31.3	86.2
11	BRRI dhan46	-348.8	9.9
12	BRRI dhan49	-388	139.8
13	BRRI dhan51	-228.8	3.5
14	BRRI dhan52	103.1	-37.9
15	BINA dhan7	418.5	12.5