STUDY ON VARIABILITY AND GENETIC DIVERSITY IN BORO RICE GENOTYPES

BY

MUHAMMAD SHAHINUL ISLAM

REGISTRATION NO. 25279/00384

A Thesis
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 & PLANT BREEDING
SEMESTER: JULY-DECEMBER, 2006

Approved by:

(Dr. Mohammad Khalequzzaman)
Principal Scientific Officer
GRS Division (BRRI)
Supervisor

(Dr. Md. Sarowar Hossain)
Associate Professor
Co-supervisor

(Dr. Md. Sarowar Hossain)
Chairman
Examination Committee

Finally, I am ever grateful and express my special appreciation and indebtedness to my beloved parents, my uncles Hazi Aminul Islam &, Ashraful Alam, whose sacrifice, inspiration, encouragement and continuous blessing paved the way to my higher education. I am also grateful to my younger brother Shaha Alam, younger sister Akhi and cuisine Nasir, Suruz, Enamul, Hasan, Firoz, Juyel, Pervin, Papia, Yeasmin, Flora, Faiza for their unquantifiable love and reverend support, their sacrifice and untiring efforts for bringing my dreams to proper shape.

Dated: December, 2006 ***The Author***

Place: SAU, Dhaka

LIST OF CONTENTS

LIST OF CONTENTS (Continued)

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

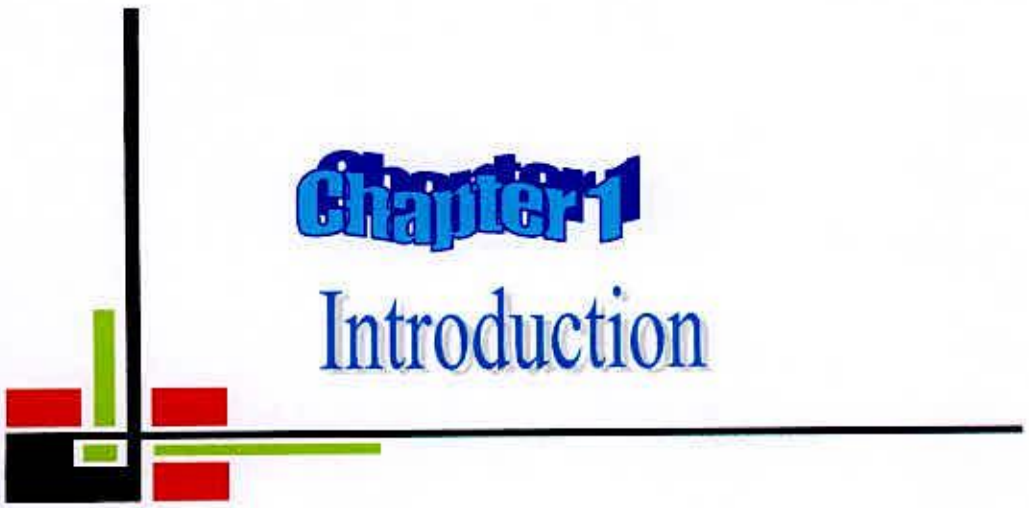
STUDY ON VARIAVILITY AND GENETIC DIVERSITY IN BORO RICE GENOTYPES

BY

MUHAMMAD SHAHINUL ISLAM

ABSTRACT

The experiment was carried out at the research farm of Bangladesh Rice Research Institute (BRRI), Gazipur. The study was conducted during November, 2005 to May, 2006 (Boro season) to obtain information on variability and genetic diversity for yield and yield contributing characters. Significant variation among the genotypes were observed for all the characters. High heritability along with high genetic advance in percent of mean was observed for panicle per plant, fertile grain per panicle. So these characters would be best for selection. Diversity was estimated by cluster distance. Significant variations were observed among the genotypes for all the studied parameters. Multivariate techniques were used to classify the forty genotypes of boro rice and is five clusters were formed. Cluster III had maximum 21 genotypes and cluster I and IV had only one genotype respectively. The highest intra-cluster distance was observed in cluster III followed by cluster II. The highest inter-cluster distance was observed between the cluster IV and V and the lowest was between the cluster II and III. The characters such as yield per plant, days to 50% flowering, days to maturity were the important components of genetic divergence among the forty boro rice genotypes. Analyzing diversity pattern and other agronomic performance, the inter genotypic crosses between G31 and G5, G31 and G34; G1 and G26; G1 and G5, G1 and G34 may be used for future hybridization program.



Chapter 1

Introduction

INTRODUCTION

Rice is the most important cereal crop of the world and is the staple food of many countries. It is consumed by almost half of the world's population. More than 250 million farm households in Asia depend on rice for their livelihood (Hossain, 1998). On a worldwide basis, it provides 20% of the calories and 14% of the protein of human consumption (Chang, 1985).

Globally, rice is cultivated in an area of about 153.12 million hectares of land with an annual production of 586.79 million metric tons (FAO, 1999). The major rice producing countries are China, India, Indonesia, Bangladesh, Thailand, Vietnam and Myanmar. These countries account for nearly 81% of the world rice production (FAO, 1999). Ninety percent of this crop is grown and consumed in South and South East Asia, the major centers of the World's population (Catling, 1992). China is the largest rice producing country of the world, whereas India has the highest cultivated area under rice (FAO, 1999). Bangladesh is the fourth largest producer and consumer of rice in the world with recent annual production of about 25 million metric tons.

Rice is widely cultivated crop of the world. It can be grown in a wide range of agro-ecological conditions. Rice is very versatile tropical and sub-tropical or warm season temperate crop and is cultivated in 111 countries of all continents, from 53^0N to 45^0S latitude and from sea level to over 3000 meter in the Himalayas (Lu and Chang, 1980).

The agriculture of Bangladesh is predominantly crop-based and the cropping in this country is absolutely dominated by rice cultivation because of its suitable geographical and agro-climatic conditions. It grows in all the three crop growing seasons of the year and occupies about 77% of the total cropped

area of about 13.9 million hectare (mha). Presently, rice alone constitutes about 92% of the total food grain production of 18.52 million metric tons (BBS, 2004). The soil and climate of Bangladesh are favourable for its cultivation throughout the year. Over the period of time, farmers have identified four specific ecotypes of rice, namely: Aus, Deep water Aman, Transplant Aman and Boro (Rashid, 1994). Rice plays an important role in the agro-economy and national health of Bangladesh. Per capita consumption of rice is estimated as 153.4 kg/year (BBS, 1998). It covers 94% of the cereals consumed in Bangladesh and contributes 69% of the calories and 54% of protein intake in the average diet of the people (Rashid, 1994).

Today the world is facing an increased demand for food. The obvious cause is the higher growth rate in the world's population (Tonniessen, 1984). Bangladesh is an over populated country and the population problem is increasing day by day. The rice demand is increasing in Bangladesh every year alone with the increasing population. To meet this demand, Bangladesh has to produce additional rice for about 2.2 million tons to feed the people. In Bangladesh the yield of rice is 2.77 ton/ha while it is 6 ton/ha in Japan, Australia, China and North Korea (FAO, 1997). So there is a scope to increase the yield of rice with appropriate technology. To keep peace with the increasing population by the year 2020, the demand for rice in Bangladesh is predicted to increase from 20 millions to over 30 million tons.

Among the major cereal and other grains the nutritional level of rice is high. It supplies 80% carbohydrate, 7-8% protein, 1% fat and 1% minerals (Draper, 1976; Duffus and Slaughter 1980). Rice is rich in energy having 345 kcal/100 g and contains a reasonable amount of thiamine, riboflavin, niacin and vitamin E (Juliano, 1993). Among cereals, rice has comparatively high content of essential amino acids. Though the protein content of rice is less than wheat, the true protein digestibility and the biological value of rice protein are the highest among wheat and other cereals (Juliano, 1993; Eggum, 1979 and Gopalan *et al.* 1980).

Rice yield in Bangladesh has significantly increased after the launching of Green Revolution. The yield of rice in general has increased, yet it is much lower than the genetic potential of yield of about 15-16 ton/ha as obtained from the international trials with a Bangladeshi rice variety BR 11 (BRRI, 1989, BRRI, 1995). However, the full genetic potentiality may not be achieved due to various environmental and socio-economic conditions. Yield is a complex character and various morphological and physiological characters contribute to grain yield. For yield improvement, it is essential to have knowledge on variability of different characters. The variability of a biological population is an outcome of genetic constitution of individuals making up that population in relation to prevailing environment. A survey of genetic variability with the help of suitable parameters such as genotypic co-efficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme (Mishra *et al.* 1988).

A measure of genetic diversity would help to choose parents either to exploit heterosis or to select desirable segregants (Sarathe and Perraju, 1990). Genetic diversity is very important factor for any hybridization programme aiming at genetic improvement of yield, especially in self-pollinating crops (Joshi and Dhawan, 1966). The quantification of genetic diversity through biometrical procedures (Anderson, 1957; Rao, 1952) has made it possible to choose genetically diverse parents for a successful hybridization programme. Moreover, evaluation of genetic diversity is important to know the source of gene for particular trait within the available germplasms (Tomooka, 1991). The genetic diversity is a must for a sound base for selection (De *et al.* 1988). Before starting any breeding programme many genetic materials should be selected from diverse origin with agronomically important characters which are highly heritable and easy to distinguish. Genetic diversity is also essential to meet the diverse goals of plant breeding such as producing cultivars with increased yield (Joshi and Dhawan, 1966), wider adaptation, desirable quality, pest and diseases resistance (Nevo *et al.* 1982).

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

I. To evaluate the performance of forty rice genotypes for yield and yield contributing characters.

II. To study the variability for yield and yield contributing characters.

III. To study genetic diversity among the genotypes.

Chapter 2

Review of literature

REVIEW OF LITERATURE

2.1 Variability

The extent of existing genetic variability of a crop plant is an index of its genetic dynamism. Plant breeding revolves around selection which can be effectively practiced only in the presence of variability of desired traits. Hence, the success of breeding depends entirely upon the variability.

Reddy and Kumar (1996) reported that phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation (GCV), indicating significant genotype environment interactions which were observed on 9 quantitative characters of twelve rice cultivars.

Akter *et al.* (2004) conducted a field experiment to asses the variability in rice genotypes with yield and yield contributing characters and found that all the tested characters showed significant variation. The higher genotypic coefficient of variations were found in case of flag leaf area followed by panicles/m^2, 1000-grain weight and spikelets per panicle. High heritability was observed for all the tested characters except grains/panicle. High heritability with high genetic advance in percent of mean was found in panicles /m^2, flag leaf area and 1000-grain weight.

Narendra and Reddy (1997) studied with 11 rice genotypes and found high levels of variability for all seven yield components recorded. The components grains per panicle and 1000-grain weight were under the influence of additive genetic effects indicating their role in crop improvement. Straight selection of grain yield and straw yield per plant also indicated better scope for crop improvement. Selection through panicle length and plant height was found ineffective as they are highly influenced by environmental effects.

Pushpa *et al.* (1999) studied fifty genotypes of rice for 10 quantitative traits in kharif 1995. The genotypic coefficient of variation was highest for grain yield/plant and also high for spikelets/panicle and grain yield/panicle

Kaw *et al.* (1999) carried out an experiment on 94 rice genotypes for genetic variability and found high genotypic variation was observed at all locations for fertility percentage and fertile spikelet number per panicle, and low genetic variation for flowering duration and panicle length.

According to Venkataramana *et al.* (1999) high values for phenotypic and genotypic variances were observed for grain yield per plant, productive tillers per plant, panicle exertion and epicuticular wax content per leaf.

Dhananjaya *et al.* (1998) studied genetic variability on 121 elite homozygous rice genotypes in kharif 1994. Most variation was observed for productive tillers/plant, number of fertile spikelets and grain yield/plant.

Moon *et al.* (1996) was estimated the variability of 30 genotypes of upland paddy and observed that plant height and the number of grains/panicle recorded the greatest values for all parameters, indicating a high scope of selection. Panicle length, 1000-grain weight and sterility percentage can be improved if the genotypes are grown under different environmental conditions and are subjected to recurrent selection. Selection for the number of tillers/per plant was ineffective, as indicated by low values for all parameters.

According to Kumar *et al.* (1998) high genotypic coefficient of variability together with heritability and genetic advance was observed for plant height, total tillers/hill, flag leaf length, panicle length, spikelet fertility, 1000-grain weight and grain yield.

Significant genotypic coefficient of variability together with high heritability and genetic advance was observed for plant height, total tillers/hill, flag leaf length and grain yield/ha indicating involvement of additive gene effects were important for these character (Shanthakumar *et al.* 1998)

Biswas *et al.* (2000) observed variability on 30 advanced breeding lines and found that panicle weight, 1000-grain weight, panicle length and filled grains per panicle had high genetic coefficient of variation and heritability in broad sense coupled with high genetic advance in percentage of mean.

Iftekharuddaula *et al.* (2001) assessed the genetic variability on 24 modern rice varieties of irrigated ecosystem. All the characters tested showed significant variations in spikelets/panicle and grains/panicle. High heritability together with high genetic advance in percent of mean was observed in plant height, 1000-grain weight, grains/panicle and spikelets/panicle.

Shanthi and Singh (2001) studied for variation in yield and yield components (plant height, number of tillers per plant, panicle length, number of grains per panicle, and 1000-grain weight). The analysis of variance indicated that the genotypes significantly varied for all characters studied. Plant height, panicle length, 1000-grain weight, and number of grains per panicle exhibited low variation between phenotypic and genotypic coefficient of variations.

Hossain *et al.* (2003) conducted an experiment on rice genotypes to find out the genetic variability during dry season of 1997. Both phenotypic and genotypic variances were found highly significant in all the traits with little higher phenotypic variations as usual. Similarly the low difference between the phenotypic and genotypic coefficients of variations indicated low environmental influences on the expression of the characters. High heritability coupled with high genetic advance of yield, grains per panicle, days to flowering and plant height suggested effective selection for the improvement of these characters.

Seventeen rice cultivars collected from drought prone rainfed lowlands from different parts of southern Karnataka, India, during 1994-95 were grown in farmer's field and at the research station in 1995 to assess actual production and potential productivity. Wide variability for height, tiller number, yield, panicle number, test weight, biomass, flowering, and maturity was observed in spite of their narrow geographical origin. The magnitude of variability for yield and related traits narrowed at farmer's fields compared to that in research station. (Venuprasad *et al.* 2002).

Reddy *et al.* (1997) studied heritability and genetic advance in 36 genotypes of lowland rice under intermediate lowland (0-50 cm water depth) conditions at Cuttack, India during the wet season of 1995. Among the different characters studied, number of grains per panicle and 1000-grain weight showed high genetic advance along with moderate to high heritability

Choudhury and Das (1997) stated that high heritability with high genetic advance was found in grains per panicle followed by grain yield.

Singh *et al.* (1998) carried out a study with 45 indigenous rice genotypes in different agro-climatic regions of Uttar Pradesh were evaluated for 13 yield-related traits. Most of the characters exhibited high heritability coupled with high genetic advance.

Pandey and Awasthi (2002) found significant genetic variability was observed among the test genotypes for all yield contributing traits. Thus, they concluded that these traits play a major role in the enhancement of production of grain yield and serve as important criteria for screening germplasm to identify the suitable aromatic rice cultivars.

Choudhury and Das (1998) estimated heritability and genetic advance in eleven deep-water rice varieties for yield and its attributing characters. High heritability with high genetic advance was found for grains per panicle followed by grain yield.

Heritability on 95 rice genotypes native to the hills of Uttar Pradesh in wet season of 1996 was evaluated. High heritability and high genetic advance for grains/panicle and high heritability and low genetic advance for days to flowering, biological yield/plant and grain yield/plant indicated the involvement of additive and non-additive gene action, respectively (Gupta *et al.* 1999)

An experiment was conducted by Vange *et al.* (1999) at Makurdi during 1994-95 to evaluate 10 early duration rain fed lowland rice genotypes for grain yield and its yield components. Significant variation was observed for most of the traits. Grain yield ranged from 2.0 to 4.2 t/ha, 1000-grain weight ranged from 22.4 to 30.9 g, grains/panicle ranged from 116 to 155, panicles/m^2 ranged from 140 to 233 and flag leaf area ranged from 26.3 to 42.3 cm^2.

Niranjana *et al.* (1999) studied on heritability, genetic variation and genetic advance is derived from data on 16 yield-related and physiological traits in 7 genotypes and their 42 hybrids. Variability, heritability and genetic advance were high for grain yield, total dry matter and leaf area at the early stage, while leaf area at flowering, leaf area duration and leaf photosynthetic rate showed high heritability with moderate genetic advance.

High heritability coupled with high genetic advance were estimated by Thakur *et al.* (1998) for biological yield, panicle-weight, branches per panicle and grains per panicle, which indicated the major contribution of additive gene action for expression of these characters.

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

Das *et al.* (1992) evaluated 30 rice genotypes for variability. The highest GCV was found in grain yield per plant. High heritability (Broad sense) with high genetic advance in percent of mean was found for days to 50% flowering, days to maturity, plant height, number of effective tillers/plant for 100-grain weight and yield per plant.

Kumar *et al.* (1994) evaluated 9 genotypes of rice for 10 quantitative traits and found high genotypic variation, high heritability and high to moderate genetic advance for days to flowering, high heritability and genetic advance for plant height. High heritability coupled with high genetic advance was observed for grains/panicle, indicating the predominance of additive gene effect controlling this character.

Bhandarkar *et al.* (2002) evaluated genetic parameters of variability for yield and its components in 52 early duration genotypes in rice. Heritability estimates were high for days to 50% flowering, days to maturity and panicle length. High heritability coupled with high genetic advance as (%) of mean was observed for plant height.

Shaha *et al.* (1993b) evaluated 20 genetically diversed irrigated rice genotypes to study genetic variability. The genotypes revealed significant difference for days to maturity with high heritability but very low genetic advance. Heritability estimate and genetic advance were high for filled grains/ panicle.

Hemareddy *et al.* (1994) studied genetic variability for grain yield and its component traits in 81 rice genotypes. Days to maturity showed high heritability (97.24%) and observed a higher PCV and GCV for grains/panicle. Grains/ panicle had high genetic advance indicating better scope for selection in 81 rice genotypes.

Rao and Shrivastava (1994) evaluated 18 divergent rice genotypes to study genetic variability significant difference for days to maturity with high heritability was found.

Debi *et al.* (1997) studied genetic variability in 29 irrigated rice genotypes. High heritability (H_b) was observed for days to maturity and for panicle length.

Information on genetic variability and heritability was derived from data on 14 yield-related traits in 73 rice genotypes by Marekar *et al.* (1996). High estimate of heritability together with genetic advance was observed for days to maturity.

Paul and Sarmah (1997) studied genetic variability in 13 genotypes of upland Aus rice. Days to maturity and yield/ha showed high heritability above 90% and GCV were high for all the characters. Genetic gain was low for yield/ha.

Yadav (2000) studied genetic variability of yield and yield components in 15 genotypes of rice. Considerable amount of genotypic co-efficient of variation, heritability and genetic advance were observed for grain yield/plant, indicating the role of additive genetic component controlling this trait and scope for selections.

Genetic variability for yield and its component was calculated in 124 rain fed landraces of rice by Yadav (2001) and found the presence of significant variability for days to maturity and for number of tillers/plant.

Jangale *et al.* (1985) studied variability, heritability and genetic advance for some quantitative characters in upland rice and reported that plant height had high heritability. They also found that grain yield had maximum genetic advance followed by plant height.

Kihupi and Doto (1989) reported significant genotypic differences for plant height in selected rice varieties. High estimates of heritability; high expected genetic advance and genotypic and phenotypic co-efficient of variation were numerically higher for plant height.

In a study on yield and its components of 52 late duration pure lines of rice, Sawant *et al.* (1994) observed high genotypic and phenotypic coefficient of variation, high heritability and genetic advance for plant height, high genotypic and phenotypic co-efficient of variation for ear bearing tillers/plant, 100 grain weight. Heritability and genetic advance were high for 100 grain weight, indicating the importance of additive gene effects for the expression of this trait.

Singh and Chaudhury (1996) estimated genetic variability, heritability and genetic advance for 12 characters in 100 genotypes for rice. . Phenotypic co-efficient of variation (PCV) was higher than genotypic co-efficient of variation (GCV) for all the characters studied indicating that they all interacted with the environment to some extent. Plant height showed high heritability together with high genetic advance. High GCV and PCV were observed for grains/panicle, 1000 grain weight. Heritability and genetic advance estimates were high for grains/panicle.

In a study of genetic variability and heritability of 8 yield components in 28 cultivars, Loknathan *et al.* (1991) found expected genetic advance as high as 68.4% for plant height.

Ashvani *et al.* (1997) studied genetic variability in rice which revealed high genotypic co-efficient of variation for plant height. High heritability coupled with high genetic advance was also observed for this character.

Chookar *et al.* (1994) in a study with 73 rice varieties found that effective tillers/plant had high heritability, genotypic and phenotypic co-efficient of variation with high genetic advance indicating additive gene action that provide better scope for selection.

Pattanayak and Gupto (1999) evaluated nine rice genotypes and found high co-efficient of variation for plant height and high value of heritability with high genetic advance.

Sadhukhan and Chattopadhyay (2000) studied variability and character association for yield attributes and several grain quality characters in 26 aromatic rice genotype and found that broad sense heritability estimates were moderate to high for plant height, he also found broad sense heritability estimates were moderate to high for number of grains/panicle.

Kumar *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses and found that plant height and number of tillers/plant exhibited high phenotypic and genotypic co-efficient of variation, heritability, genetic advance. They also found 100-grain weight exhibited high heritability coupled with moderate genetic advance indicating the role of non-additive gene effect in the inheritance of this taint.

Ali *et al.* (2000) observed genetic variability in F_2 population of *Oryza sativa* and found broad sense heritability for plant height and heritability estimates were maximum for number of tillers/plant, 100-seed weight.

Gomathinayagam *et al.* (1990) studied genetic variability in 40 upland rice genotypes and found that the co-efficient of variation was high for number of effective tillers/plant, high heritability coupled with high genetic advance implying additive gene action and suggested the reliability of this trait in the selection programe under rainfed condition.

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

Basavaraja *et al.* (1997) worked on genetic variability of 10 characters to evaluate two F_4 populations of fine grained rice. High estimates of phenotypic co-efficient of variation together with high to moderate heritability and genetic advance were observed for productive tillers/plant.

Borbora and Hazarika (1999) evaluated 30 genotypes of rice for 11 yield related traits and found highly significant variation among the genotypes for different characters. High to moderate genotypic co-efficient of variation together with high heritability and genetic advance were recorded for number of filled grains/panicle, indicating the effectiveness of selection for these characters.

Sawant *et al.* (1995) in a genetic analysis of yield related traits in F_4 generation of rice, found that the expected genetic advance and heritability were high for panicle length indicating predominance of additive gene effect in the expression of this trait. A high co-efficient of variation and high value of heritability together with high expected genetic advance were also observed.

Ramalingam *et al.* (1994) studied panicle characteristics of rice and reported that panicle length had low genetic co-efficient of variation along with high heritability and high genetic advance.

Zeng and Wang (1988) evaluated 59 high yielding cultivars and breeding lines of rice for yield related traits and found that number of filled grains/panicle had broad-sense heritability of more than 85%. The relative expected genetic advance value at 5% selection intensity for grain number/panicle was 35.73.

Mani *et al.* (1997) investigated the extent of genetic variation in 24 genotypes of Basmati rice. A wide range of variation was recorded for all traits studied. A high estimated of heritability coupled with high genetic advance for number of filled grains/ panicle suggested the predominance of additive gene action for this character.

Luji (1998) evaluated 36 rice lines/cultivars and found significant difference for most of the traits wide range of variability. Heritability estimates were high for number of filled grains per panicle.

Bidhan *et al.* (2001) studied genetic variability, heritability and genetic advance for yield and yield components in 25 medium duration rice genotypes and found high phenotypic and genotypic variation for number of filled grains/panicle. They also found that high heritability coupled with moderate to high genetic advance for number of filled grains/panicle and 100-grain weight.

Mishra and Verma (2002) evaluated 16 rice cultivars and 72 F_1 progenies and found that the phenotypic co-efficient of variation was higher than the genotypic co-efficient of variation (GCV) for number of fertile spikelets/panicle. High heritability coupled with high genetic advance was observed for number of fertile spikelets/panicle and 1000-grain weight.

Patwary (1991) studied seven important quantitative characters of 11 promising advanced generation lines of rice and found that sterility/panicle had low genotypic co-efficient of variation.

Wilpred *et al.* (1993) observed high genetic variation for sterility percentage in rice genotypes. The estimates of heritability and genetic advance (%) were high for this trait.

Ahmed and Das (1994) evaluated 85 glutinous rice genotypes for 19 quantitative characters and found high genotypic coefficient of variation and low heritability for spikelet sterility(%).

Babu (1996) estimated high genotypic and phenotypic coefficient of variation and low heritability along with low genetic advance for unfilled grain/panicle. High heritability along with high genetic advance for grain yield/plant.

Paul and Sarmah (1998) reported high genotypic co-efficient of variation, high heritability and high genetic advance for false grains/panicle.

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

Chaubey and Singh (1994) worked with 20 rice varieties and reported that phenotypic co-efficient of variation was greater than genotypic co-efficient of variation for all the traits studied. Heritability was high for all traits but 100-grain weight showed an estimate of heritability near the maximum value showed by total number of spikelets. High heritability together with high genetic advance in percentage of mean for grain yield/plant. Similar result was also found By kumar *et al.* (1994) in nine genotypes of rice for 10 quantitative traits.

In a study with 14 short duration rice genotypes, Paramasivam *et al.* (1995) reported that there was high heritability together with increased genetic advance for 1000-grain weight which indicated the importance of additive gene action.

Vishwakarma *et al.* (1989) estimates heritability and genetic parameters in 82 population of rice and stated that broad sense heritability was moderate and also moderate genetic advance for grain yield.

Li *et al.* (1991) worked on 9 rice cultivars and estimated that genetic co-efficient of variation was high for yield/plant but they gene moderate heritability along with moderate genetic advance for this trait.

Sawant and Patil (1995) evaluated 75 genotypes of rice and found high co-efficient of variation for grain yield/plant. High value of heritability coupled with expected genetic advance was observed for grain yield/plant. A high value of heritability together with genetic advance was also observed by Mononmani *et al.* (1996) in F_1 population of 20 cross combinations of 9 short duration rice genotypes.

Shrirame and Muley (2003) carried out an experiment on rice hybrids TNRH 10, TNRH 13, TNRH 18 and cultivar Jaya and found maximum co-efficient of variability for grain yield/plant (31.1%).

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

In a study carried out by Balan *et al.* (1999) on 15 salt tolerant rice genotypes for 5 characters, high genotypic co-efficient of variation (GCV), genetic advance and moderate heritability was found for grain yield.

2.2 Genetic Diversity:

Pravin *et al.* (2003) conducted a field experiment to asses genetic diversity among 49 rice cultivars grown in Madhya Pradesh, India, using Mahalanobis D^2 statistics. The cultivars were grouped into 9 clusters based on genetic distance. The greatest intra-cluster distance was observed in cluster V, which consisted of cultivars Annada, Aditya, Kranti, Mahamaya, and Ruchi. The cultivars from cluster IV (Safri-17, Bamleshwari, R1037-649-1-1, ND-9730021, Jaldubi, and Basmati-370) had the greatest number of panicles per plant, panicle length, number of fertile spikelets per panicle, biological yield per plant, and grain yield per plant. Vandana, R-1102-2795-3-1, R288-650-2, and Poornina of cluster VIII had the highest amylose percentage, grain yield per plant, harvest index, and starch percentage. Annada, Ruchi, and Kranti of cluster V had the highest 100-seed weight and harvest index. G95-02 of cluster IX had high panicle length and flag leaf area, and intermediate number of tillers per plant, paddy length, 100-seed weight, and grain yield per plant. These cultivars have good potential as parents for the development of hybrids with high yield and quality.

Fifty rice cultivars were evaluated by Roy *et al.* (2002) in Port Blair, Andaman and Nicobar Islands during the rainy seasons of 1998, 1999 and 2000 for genetic diversity in yield-contributing characters (days to 50% flowering, plant height, number of panicles per plant, panicle length, number of grains per panicle, grain density, 100-grain weight, 100-kernel weight, and kernel: grain weight ratio). The grouping of genotypes into 10 clusters was independent of geographical origin or region of adaptation. Days to 50% flowering, grain length, kernel breadth, and grain yield per plant were the major yield-contributing characters. Based on the mean grain yield performance, genetic distance, and clustering pattern, intercrossing among Taipei 309, SIPI 681032, and RP 2669-424-298-18 of cluster IV and Black Jeera, IR 50, and IR 54447 B-B-B 10-2 of cluster IX may be conducted to obtain high-yielding cultivars.

The genetic diversity of humid lowland rice cultivars were estimated by Pereira and Cruz (2003) using canonic and cluster analysis. The latter included Ward methods, single linkage, average linkage and Tocher's, with Euclidean and Mahalonobis distances. The clustering patterns obtained varied both among applied methods and distances. The Mahalanobis distance-based clustering analysis showed 4 groups regardless of the applied method. On the other hand, the Euclidean-based clustering analysis ranged from 6 to 10 groups, depending on the method. Despite the varying number of groups and clustering patterns, the combinations indicated for crossing are more consistent when methods are based on similar types of distance.

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 during 1996-97 in Raipur, Madhya Pradesh, India. The genotypes were grouped in 12 clusters based on the relative magnitude of multivariate D^2 values. The highest number of genotypes was in cluster XII. Based on the cluster means, plant height, flag leaf width, ear bearing tillers per plant, 100-seed weight, hulling and milling percentage, panicle length, biological yield, harvest index, kernel length after cooking, gelatinization temperature and grain yield were the main factors for differentiation. The highest genetic distance was observed between clusters III and VIII and lowest between cluster VII and VIII. No close correspondence was evidenced between geographical distributions to genetic divergence as estimated by multivariate D^2. Analysis of variance indicated highly significant differences for the most of the characters studied (Mishra *et al.* 2003).

Genetic diversity of 62 cultivars of irrigated rice originating from BRRI, IRRI, and China were evaluated by Islam *et al.* (2004) in Satkhira, Bangladesh, during the boro season of 2001-2002 using the Mahalanobis D^2 statistical method. The cultivars were grouped into five clusters. Clusters II and IV contained the highest number of cultivars (16) and cluster I contained the

lowest number (7). The highest intra-cluster distance was recorded from cluster I and the lowest were from cluster III. The highest inter-cluster distance was observed between cluster I and cluster IV followed by cluster I and cluster V, cluster I and cluster III, cluster III and cluster IV, and cluster IV and cluster V. The highest cluster means for yield and the other three yield-contributing characters were obtained from cluster I, the six highest and two second highest means for yield-contributing characters were found in cluster III; however, the lowest cluster mean for yield was also found in this cluster. Therefore, more emphasis should be given to cluster I when selecting cultivars as parents for crossing with the cluster III cultivars, which may produce new recombinants with desired traits.

Nejad *et al.* (2004) conducted an experiment at a research farm of Rice Research Institute of Iran. The genotypes, mostly belonging to Isfahan Province and north of Iran, were evaluated based on morphological traits and yield components. The results of analysis of variance demonstrated that the differences among genotypes were highly significant for all traits. High values of phenotypic and genotypic coefficients of variation were obtained for most traits, indicating high variability in the traits under study. Factor analysis revealed three factors which determined 90% of yield variation and were named grain number, plant type and structure and grain shape, respectively. Cluster analysis by "cubic clustering criterion" and "pseudo-hotelling T2 test" grouped genotypes into four clusters. Analysis of variance showed that the differences among clusters were highly significant for most traits.

The nature and magnitude of genetic divergence in 28 genotypes of rainfed rice by Vivekanadan and Subramanian (1993) using Mahalanobis's D^2 statistics. The population was grouped into five clusters. Plant height grain yield contributed considerably, accounting for 85% of total divergence.

Twenty accessions of wild rice (*Oryza sativa* var. *spontanea*, *O. nivara* and *O. rufipogon*) collected from different parts of Uttar Pradesh, India, were subjected to multivariate analysis of data on 16 quantitative traits using Mahalanobis' D^2 statistic by Jha *et al.* (1999). The 20 accessions could be grouped into 3 clusters representing the 3 species, without any overlap. Cluster I represented *O. nivara* with 14 accessions, cluster II contained 5 accessions of *O. sativa* var. *spontanea* and cluster III contained the only accession of *O. rufipogon*.

Genetic divergence as measured by the D^2 technique was studied for 18 grain quality traits in 132 rice genotypes (128 traditional cultivars and 4 standard genotypes). The analysis of variance revealed significant differences among the genotypes for each character indicating genotypes for characters studied. The genotypes were grouped into 10 clusters and the maximum intra-cluster distance was observed in cluster VIII comprising of a single traditional rice cultivar Gonda Jhul. Clusters VI and VIII were identified as genetically divergent. Considering the cluster means and cluster distances, Bakal-B and Jondhera Dhan of cluster VI, Gonda Jhul of cluster VIII, Poorva and IR-36 of cluster VII, Kranchi, X-12, Moti Bakiya and Assam Chudi of cluster V and Kranti of cluster X were the most promising varieties (Sarawgi *et al.*, 1998).

Isoenzyme variation was analysed at 14 loci in 64 upland varieties. Five of the loci proved to be monomorphic. When the 64 varieties were classified using an algorithm bases on alleles present at 5 polymorphic loci, 35 were classed as indica and 22 as aus. A dendrogram clustering 62 of the varieties was established; this also showed clear-cut differentiation into the 2 varietal groups (Courtois *et al.*, 1997).

Genetic divergence using Mahalanobis' D^2 statistic was estimated in 62 early rice genotypes obtained from sixteen countries and from CIAT, IITA and IRRI. Based on eight important yield contributing characters, these genotypes

were grouped into six clusters. Cluster I was the largest, containing 85% of genotypes from a range of countries and institutions. Cluster II, III, IV and V had two genotypes each. Genotypes in cluster II originated from India, those in cluster III from Romania and IITA, and those in cluster IV from IRRI. Cluster VI contained a single genotype from India. There was no relationship between geographical distribution and genetic diversity. Characters like grain yield per plant, panicle exertion and plant height made the largest contribution to total divergence. It is suggested that these characters could, therefore, form the basis for selection of parents from distantly placed clusters with a view to obtaining highly heterotic combinations (Kumari and Rangasamy, 1997).

An experiment was conducted by Mishra and Dash during the rainy season of 1991-94 to study genetic diversity and stability in 10 genotypes of aromatic rice (Oryza sativa). Pooled data on 9 quantitative characters, viz. days to 50% flowering, plant height, tillers/hill, ears/hill, panicle length, grains/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 D2 statistics. Pooled analysis showed highly significant differences due to genotypes, environments and genotype X environment interaction for all the characters. On the basis of stability parameters, genotype Kasturi was found stable for yield with high mean yield and ORP665-7 was found stable for 4 yield-attributing characters with high mean yield. On the basis of D2 analysis and stability, crossing selected genotypes of cluster II (ORP665-7 and Kasturi) with the genotype of cluster IV (Badena) was useful for recombining genes for stability and high yield.

Seed of 42 waxy rice accessions, collected from various localities in Mukdahan and Yasothon provinces of northeast Thailand, was sown in pots during May-October 1994. On the basis of 12 desirable agronomic traits, the accessions were grouped into 16 varietal types, which were further classified into 5 groups on the basis of 8 grain architecture traits. Cluster analysis also grouped the varieties into 5 clusters (Prathepha, 1995).

Varieties originating from IRRI (21 varieties), India (3), Korea (1), Sri Lanka (1) and Vietnam (6) were subjected to cluster analysis (Mahalonobis's D^2 statistic) based on plant height, days to 50% flowering, panicle length, grains/panicle, unfilled grain percentage, effective tillers/plant, grain weight and grain yield. Five clusters were produced by Tocher's method with cluster I containing 24 varieties. The largest statistical distance (maximum divergence) was shown between clusters IV (IR68) and V (Basmati 370). Plant height and days to 50% flowering contributed the most to divergence (Buu and Tuan 1989).

Mokate *et al.* (1998) studied genetic diversity with 25 genotypes of rice and the genotypes grouped into five clusters on the basis of yield component data. Maximum inter cluster divergence was observed as 63.04 followed by 51.90 and 48.30.

Hanamaratti *et al.* (1998) evaluated 50 rice genotypes for 10 yield components in low land and upland conditions. Cluster analysis grouped the genotypes into 18 and 17 clusters under low and uplant conditions, respectively.

Sawant *et al.* (1995) noticed on the basis of data on 8 yield components, 75 genotypes of rice grown on kharif 1991 and grouped into 10 clusters. Clustering patterns revealed that geographic diversity is not a reasonable index of genetic diversity. The average inter cluster distance was the highest between clusters IX and X (66.58), followed by clusters VI and IX (62.59) and clusters IV and X (56.52), suggesting that these groups of genotypes were highly divergent from each other. The character association study indicated that ear-bearing tillers/plant, 1000 grain weight, panicle length and grains/panicle were positively and significantly correlated with grain yield. Grains/panicle, 1000 grain weight and plant height were the components which influenced grain yield directly.

Genetic diversity was assessed with 34 rice stocks using D^2 analysis of 10 economic traits (Bansal *et al.* 1998). The 34 genotypes were grouped into 15 clusters. Genetic divergence studies were carried out by Singh *et al.* (1999) using 42 genotypes of Boro rice for eleven quantitative characters, including gaind yield. Multivariate analysis revealed considerable genetic diversity in the material and led to their grouping into four clusters. They also found that total number of grains/panicle, number of filled grains/panicle accounted 90.6% of the total divergence.

Shanthi and singh (2001) studied genetic divergence using Mahalanobi's D^2 statistic for six quantitative characters in 17 induced mutant genotypes of Mashuri rice. The genotypes differed significantly for six characters considered collectively and were grouped into four clusters. The first cluster contained nine genotypes, the second contained six genotypes, while third and fourth clusters were monogenic. The greater cluster distance was observed between genotypes belonging to cluster II and III.

Arun *et al.* (2002) assessed genetic diversity in 28 yield and morphological traits of 100 aromatic rice genotypes. These genotypes, originating from different countries, were divided into nine clusters.

Bidhan *et al.* (2002) observed genetic diversity in 50 rice cultivars that the grouping of genotypes into 10 clusters was independent of geographical origin or origin of adoption. They also found that days to 50% flowering grain length and grain yield/plant were the major yield contributing character to genetic diversity.

Jadhav *et al.* (2003) evaluated genetic diversity among 49 rice cultivars using Mahalanobis's D^2-statistics. The cultivars were grouped into nine clusters based on genetic distance. The greatest intra-cluster distance was observed in cluster V.

Mishra *et al.* (2002) determined the nature and magnitude of the genetic diversity for 20 quantitative and quantitative characters in 16 rice cultivars. The genotypes were grouped in 12 clusters based on the relative magnitude of multivariate D^2 values. The highest number of genotypes was in cluster XII. The highest genetic distance was observed between clusters III and VIII and lowest between cluster VII and VIII.

Maurya and singh (1977) found that maturity time, plant height, and number of productive tillers contributed most to the divergence in rice.

Chuhan and Chauhan (1994) studied genetic divergence among 44 breeding lines and two improved cultivars under rainfed upland conditions and grouped them into 12 clusters. They reported that 100-grain weight contributed maximum to the divergence. In rainfed rice, (Vivekanandan and Sukanya, 1993) the characters which contributed maximum to the divergence were grain yield, plant height and number of effective tillers/plant in order of merit.

Bui-chi-Buu and Tran-Minh-Tuan (1998) found that plant height and days to 50% flowering contributed the most to divergence.

Shiv *et al.* (2003) found that plant height contributed the maximum towards genetic divergence (52.24%) followed by days to 50% flowering and grain yield/plant.

An experiment was conducted by Naskar *et al.* (1985) and reported that when cluster analysis was applied to 9 characters in 22 diverse Indian genotypes in 1981 and 1982, all genotypes were grouped into 9 clusters in both years, although the clustering pattern was not consistent over the years. Genetically diverse (as estimated by Mahalanobis's D^2 statistic) use in crosses to give promising sergeants. High heterosis, it was suggested, could be achieved by crosses between members of distant clusters.

Peyne *et al.* (1989) reported that the hierarchical nature of the grouping into various number of classes could impose undue constrains and the statistical properties of the resulting groups were not at all clear. Therefore, they have suggested non-hierarchical classification, as an alternative approach to optimize some suitability choosing criteria directly from the data matrix. They also reported that the squared distance between means were Mahalanobis's D^2 statistics when all the dimensions were used, could be computed using Principal Coordinate Analysis (PCO). They also commended the canonical vector analysis (CVA) for discriminatory purpose.

The coordinates obtained from the Principal Component Analysis (PCA) are used as input at Principal Coordinate Analysis (PCO) to calculate distances among the points reported by Digby *et al.* (1989). PCA is used for the graphical representation of the points while PCO is used to calculate the minimum distance straight line between each pair of points.

Chapter 3

Materials and Methods

MATERIALS AND METHODS

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

3.1 Experimental site and experimental period

The experiment was carried out at the research farm of Bangladesh Rice Research Institute (BRRI), Gazipur. The site is located at 24.00 ^{0} N latitude and 90.25 ^{0} E longitude with an elevation of 8.4 meter from the sea level. The study was conducted during November, 2005 to May, 2006 (Boro season).

3.2 Climate and soil

The experimental site is under the sub- tropical climatic zone. The meteorological data including maximum and minimum mean monthly temperature (^{0}C), total rainfall (mm), relative humidity and sunshine (hour /day) for growing season are presented in Appendix 1. The soil texture of the experimental field was clay loam and pH was 6.2. The land was medium high with uniform topography and almost homogenous in respect to soil fertility.

3.3 Materials

Forty rice genotypes (varieties/lines) were used for the present study. The genetically pure and physically healthy seeds of these genotypes were obtained from the Germplasm Bank of Bangladesh Rice Research Institute (BRRI), Gazipur. The name and origin of these genotypes are presented in Table 1.

Table 1. Source of forty boro rice genotypes

Sl. No.	Genotypes	BRRI ACC Number	Source
1	Banajira	7	Gene bank of BRRI
2	Ghuni boro	181	Gene bank of BRRI
3	Ausha boro	254	Gene bank of BRRI
4	Kaika boro	262	Gene bank of BRRI
5	Khamarang	742	Gene bank of BRRI
6	Deshi boro	1405	Gene bank of BRRI
7	Jamir	1706	Gene bank of BRRI
8	Isamoti	1790	Gene bank of BRRI
9	Sada boro	1791	Gene bank of BRRI
10	Bogra	1802	Gene bank of BRRI
11	Jagli	1806	Gene bank of BRRI
12	Boro	1808	Gene bank of BRRI
13	Tupa	1811	Gene bank of BRRI
14	Sadaboro (awn)	1863	Gene bank of BRRI
15	Sail boro	1970	Gene bank of BRRI
16	Birion	1972	Gene bank of BRRI
17	Boro 66/1	2217	Gene bank of BRRI
18	Boro 66/2	2219	Gene bank of BRRI
19	Boro 135/1	2225	Gene bank of BRRI
20	Boro 391	2229	Gene bank of BRRI
21	Boro 398	2231	Gene bank of BRRI
22	Boro 465	2232	Gene bank of BRRI
23	Boro 522	2237	Gene bank of BRRI
24	Boro 259	2241	Gene bank of BRRI
25	Dhali boro 7/2	2243	Gene bank of BRRI
26	Dhali boro 87/1	2245	Gene bank of BRRI
27	Dhali boro 94	2246	Gene bank of BRRI
28	Dhali boro104/1	2247	Gene bank of BRRI
29	Dhali boro	2248	Gene bank of BRRI
30	Omni boro	2386	Gene bank of BRRI
31	Chinese var 1	3404	Gene bank of BRRI
32	Firooz	3766	Gene bank of BRRI
33	Moghalsail 2	3956	Gene bank of BRRI
34	Fenaful	3984	Gene bank of BRRI
35	Bichi barui	3986	Gene bank of BRRI
36	Toifa boro	4015	Gene bank of BRRI
37	Biroin	4522	Gene bank of BRRI
38	Chengri boro	4535	Gene bank of BRRI
39	Unknown	4595	Gene bank of BRRI
40	Sonali boro 2	4958	Gene bank of BRRI

3.4 Land preparation

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

3.5 Experimental design and layout

A Randomized Complete Block Design (RCBD) was used in the experiment with three replications. The individual plot was of 3m x 0.75 in size.

3.6 Sowing and transplanting

The seeds were sown on 29 November 2005 and 1 seedling/hill was transplanted to the main plot on 20 January 2006 when they were 52 days old. Plant to plant distance and row to row distance were maintained at 20cm and 25cm respectively. Thus, each plot had 3 rows and each row contained 20 plants.

3.7 Fertilizer used

The following recommended doses of fertilizers were used (a) Urea-80kg/ha, (b) TSP-60 kg/ha (c) Mp-40kg/ha. During the final land preparation, one third of the urea, the whole amount of Triple Super Phosphate (TSP) and Muriate of Potash (MP) were applied in the experimental field. Remaining two third of the urea were applied in two splits, one at 15 days after transplanting and the other before panicle initiation.

3.8 Irrigation

The experimental field was irrigated properly and adequate water was ensured through out the whole crop growth period. A good drainage system was also maintained. The experimental field was irrigated as per required to raise healthy crop.

3.9 Intercultural Operation

Weeding was done during top dressing of urea to break the soil crust, keep the crop free from weeds and incorporate fertilizer into the soil for reducing the loss of urea through mineralization. Irrigation was given at a regular interval to maintain 2-3 cm water depth up to hard dough stage. The crop field was weeded twice, one within 20 to 25 days after transplanting and the second within 40-45 days after transplanting.

3.10 Harvesting

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

3.11 Recording of data

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

i. Days to 50% flowering: Recorded as days from sowing to 50% flowering of the plants of each plot.

ii. Days to maturity: Recorded as days on plot basis from sowing time to about 80% of the plants were ready for harvesting.

iii. Plant height: The plant height (cm) was taken from 10 randomly selected plants of each plot. The length of the main culm (cm) from the ground level to the tip of its panicle was measured and the average was taken.

iv. Panicle length: Recorded as the distance (cm) from the last node of the rachis to the tip of the main panicle of each sample plant and the average was taken.

v. Panicle per plant: The total number of effective tillers was counted from 10 randomly selected plants of each plot and the average was taken.

vi. Fertile grain per panicle: The total number of fertile grains was counted from the main panicle of each sample plant and the average was taken.

vii. Unfertile grain per panicle: The total number of sterile grains was counted from the main panicle of each sample plant and the average was taken.

viii. 1000 grain weight: One thousand clean sun dried grains were counted randomly from the sample plant after which the weight (g) and average was taken.

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

3.12 Statistical Analysis

Analysis of variance was done for all the characters under study using the mean values (Singh and Chudhury, 1985). Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the difference between the means of the genotypes following Steal and Torrie (1960). Mean, range, co-efficient of variation (CV) and correlation was estimated using MSTAT computer program. Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT program.

3.12.1 Estimation of Genetic parameters

i. Estimation of genotypic and phenotypic variances

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

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

Where, GMS = Genotypic mean square

EMS = Error mean square

r = Number of replication

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_{(g)} + \text{EMS}$$

Where, $\sigma^2_{(g)}$ = genotypic variance

EMS = Error mean square

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

Genotypic and phenotypic co-efficient of variation were estimated according to Burton, 1952; Singh and Chaudhury, 1985

$$\text{GCV (\%)} = \frac{\sqrt{\sigma^2 g}}{\bar{x}} x100$$

Where, σ^2_g = genotypic variance

$\bar{x}$ = population mean

$$\text{Similarly, PCV (\%)} = \frac{\sqrt{\sigma^2 ph}}{\bar{x}} x100$$

Where, σ^2_{ph} = phenotypic variance

$\bar{x}$ = population mean

iii. Estimation of heritability

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

$$\text{Heritability } (h^2_b\%) = \frac{\sigma^2_g}{\sigma^2_{ph}} \times 100$$

Where, σ^2_g = genotypic variance

σ^2_{ph}= phenotypic variance

iv. Estimation of Genetic Advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advance (GA)} = \frac{\sigma^2_g}{\sigma^2_{ph}} \times k \times \sigma_{ph}$$

σ^2_g = genotypic variance

σ^2_{ph} = phenotypic variance

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

σ_{ph} = phenotypic standard deviation.

v. Estimation of genetic advance in percent of mean

Genetic advance in percent of mean was calculated as proposed by Comstock and Robinson (1952).

$$\text{Genetic advance in percent of mean (GA \%)} = \frac{GA}{\overline{x}} \times 100$$

Where,

GA = genetic advance

$\overline{x}$ = population mean

3.12.2 Analysis of Genetic Divergence

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

i. Principal Component Analysis (PCA)

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

ii. Principal Coordinate Analysis (PCO)

Principal coordinate analysis is equivalent to principal component analysis but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the maximum distances between each pair of the N point using similarity matrix (Digby *et al.*, 1989).

iii. Clustering

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

iv. Canonical Vector Analysis (CAV)

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

v. Calculation of D^2 values

The Mahalanobis`s distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury (1979). For each combination the mean deviation, i.e. Y^1_I-Y^2_I with i=1, 2 ... p was estimated and the D^2 was calculated as sum of the squares of these deviations, i.e.$\sum (Y_{11}$-$Y^2_I)$. The D^2 values were estimated for all possible pairs of combinations between genotypes.

vi. Cluster Diagram

With the help of intra and inter-cluster distances ($D=\sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chaudhury (1979). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

vii. Calculation of average intra cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1979).

$$\text{Average intra-cluster } D^2 = \frac{\sum D^2_1}{n}$$

Where, D^2_1 = sum of distances between all possible combinations (n) of genotypes included in a cluster.

n = number of all possible combinations between the populations in a cluster.

viii. Calculation of average inter cluster distances

Average inter-cluster distances were calculated by using following formula as suggested by Singh and Chaudhury (1979)

$$\text{Average inter-cluster } D^2 = \frac{\sum D^2_{ij}}{n_i X n j_1}$$

Where,

$\sum D^2_{ij}$ = sum of distances between all possible combinations of the populations in cluster i and j.

n_i= number of populations in cluster i.

n_j= number of populations in cluster j.

Chapter 4

Results & Discussion

RESULTS AND DISCUSSION

The mean performance of different quantitative characters such as days to 50% flowering, days to maturity, plant height, panicle length, panicle per plant, fertile grain per panicle, unfertile grain per panicle, 1000 grain weight and yield per plant of forty boro rice genotypes were analyzed by Duncan's Multiple Range Test (DMRT) (Table 2). The corresponding analysis of variances is presented in Table 3. The range, mean, genotypic, phenotypic and environmental variance, genotypic and phenotypic co-efficient of variation, heritability, genetic advance and genetic advance in percent of mean are presented in Table 4. Analysis of genetic divergence for the assessment of genetic distance between the genotypes are presented in Table 5 to Table 10.

The results of various genetic parameters of the test genotypes are presented and interpreted below.

4.1 Performance of the genotypes

The performance of different genotypes of rice for yield and yield contributing characters are given in Table 3. Analysis of variance for the characters showed that there were significant variations among the genotypes for all the characters studied. This indicates that there were genetic variations presented among the genotypes for the characters studied.

Study of performance of different genotypes showed that the genotype Khamarang took longest period for flowering (128.7 days) which was significantly different from the second highest genotype Deshi boro (123 days). The genotypes Boro 135/1 (116.3 days), Boro 398 (116.0 days), Dhali boro 104/1 (116 days), Sada boro (116 days) and Omani boro (115.7 days) which were not significantly different from one another and were characterized as

medium duration variety. The genotype Chinese var1 required minimum (109.3 days) days to 50% flower (Table 2).

Among the genotypes, Chinese var1 was the first early maturing genotype (109.3 days). Genotype Ghuni boro (110.7 days) was next to Chinese var1. Besides, the genotypes Khamarang (128.7 days) was late maturing type which was significantly different from the next variety.

The genotype Chinese var1 was the shortest variety (45.47cm) which was significantly different from Sada boro (86.2cm) and Kaika boro (85.6cm). But no significant differences was observed in Ghuni boro (92.2cm), Ausha boro (89.8cm), Sada boro (86.2cm), Kaika boro (85.6cm) and Sonali boro2 (95.33cm). The genotype Fenaful (129.1cm) was the tallest and was not significantly different from Boro 259 (120.6cm) and Bichi barui (120.5cm).

The genotype Khamarang produced the longest panicle (27.73cm) followed by Fenaful (26.73cm) and they were statistically similar (Table 2). Genotype Chinese var1 produces the shortest type of panicle (16.40cm) which was not significantly different from Kaika boro (17.17cm), Deshi boro (17.67cm), Ausha boro (17.70cm), Ghuni boro (18.07cm) and Sada boro (18.50cm).

The highest number of panicle per plant was produced by Deshi boro (24.93) which was significantly different from the second highest genotype Sada boro (18.57), and the Sada boro was significantly different from the next highest Moghalsail 2 (14.57). Genotype Bichi barui produced the least number of panicle per plant (7.93) which was not significantly different form Chinese var1 (10.70), Firoz (8.73), Boro 522 (9.07), Fenaful (9.20), Boro (9.43), Ghuni boro (9.70), Biroin (9.90), Boro 465 (10.27), Jagli (10.30), Boro 135/1 (10.53), Omani boro (10.63), Boro 398 (10.63), Chengri boro (10.67), Jamir (10.67), Dhali boro 104/1 (10.70), Boro 66/1 (10.83), Toifa boro (10.93), Sail boro (10.97).

Table 2. Mean performance of forty boro rice genotypes in respect of nine quantitative characters

Sl. No.	Genotypes	BRRI ACC Number	Days to 50% flowering	Days to maturity	Plant height	Panicle Length
1	Banajira	7	117.7 c-i	146.0 d-i	102.1 h-k	19.40 i-m
2	Ghuni boro	181	110.7 m-o	140.0 mn	92.20 k-m	18.07 l-o
3	Ausha boro	254	109.7 n-o	140.3 l-n	89.80 lm	17.70 m-o
4	Kaika boro	262	110.7 m-o	141.0 j-n	85.60 m	17.17 no
5	Khamarang	742	128.7 a	162.0 a	112.0 b-h	27.73 a
6	Deshi boro	1405	123.0 b	147.3 c-f	104.0 g-j	17.67 m-o
7	Jamir	1706	112.7 j-o	142.0 h-n	107.1 d-i	21.20 e-j
8	Isamoti	1790	117.0 d-j	145.7 d-i	107.8 d-i	20.53 e-k
9	Sada boro	1791	116.0 e-l	144.3 e-m	86.20 m	18.50 k-o
10	Bogra	1802	115.3 f-l	144.3 e-m	99.40 i-l	18.87 j-n
11	Jagli	1806	113.7 h-o	143.0 f-m	113.5 b-h	20.63 e-k
12	Boro	1808	114.0 g-n	146.0 d-i	105.2 f-j	21.43 e-i
13	Tupa	1811	119.3 b-f	148.0 c-e	118.0 b-d	22.73 b-e
14	Sadaboro (awn)	1863	113.0 j-o	142.7 g-m	106.2 e-j	21.80 c-h
15	Sail boro	1970	114.7 g-m	143.7 e-m	111.9 b-h	20.93 e-j
16	Birion	1972	113.3 i-o	142.7 g-m	105.9 e-j	20.87 e-j
17	Boro 66/1	2217	114.3 g-m	142.7 g-m	114.5 b-g	20.50 e-k
18	Boro 66/2	2219	114.7 g-m	144.0 e-m	111.2 b-h	20.17 f-l
19	Boro 135/1	2225	116.3 e-l	144.7 d-l	105.3 f-j	19.83 g-m
20	Boro 391	2229	112.0 l-o	140.7 k-n	109.0 b-i	20.47 e-k
21	Boro 398	2231	116.0 e-l	144.7 d-l	116.4 b-f	21.87 c-h
22	Boro 465	2232	112.3 k-o	141.7 i-n	105.5 e-j	20.90 e-j
23	Boro 522	2237	116.7 e-k	145.7 d-i	115.1 b-g	22.27 c-f
24	Boro 259	2241	121.7 bc	152.0 b	120.6 ab	24.50 b
25	Dhali boro 7/2	2243	120.0 b-e	150.3 bc	117.2 b-e	21.53 d-i
26	Dhali boro 87/1	2245	115.3 f-l	145.3 d-j	112.7 b-h	20.10 f-l
27	Dhali boro 94	2246	118.0 c-h	147.0 c-g	108.9 c-i	20.10 f-l
28	Dhaliboro104/1	2247	116.0 e-l	144.7 d-l	111.9 b-h	21.00 e-j
29	Dhali boro	2248	119.7 b-f	147.3 c-f	116.0 b-f	22.00 c-g
30	Omni boro	2386	115.7 e-l	144.7 d-l	104.9 f-j	19.53 h-m
31	Chinese var 1	3404	109.3 o	138.0 n	45.47 n	16.40 o
32	Firooz	3766	119.7 b-f	148.0 c-e	102.2 h-k	23.73 b-d
33	Moghalsail 2	3956	118.3 c-g	145.7 d-i	104.9 f-j	19.27 i-n
34	Fenaful	3984	121.3 b-d	149.0 b-d	129.1 a	26.73 a
35	Bichi barui	3986	116.7 e-k	145.0 d-k	120.5 a-c	23.87 bc
36	Toifa boro	4015	119.7 b-f	147.3 c-f	111.5 b-h	22.30 c-f
37	Biroin	4522	113.0 j-o	141.0 j-n	107.9 d-i	20.13 f-l
38	Chengri boro	4535	113.3 i-o	142.7 g-m	112.9 b-h	20.57 e-k
39	Unknown	4595	112.0 l-o	140.7 k-n	107.2 d-i	20.60 e-k
40	Sonali boro 2	4958	117.7 c-i	146.3 c-h	95.33 j-m	19.80 g-m
Mean			**115.98**	**144.95**	**106.32**	**20.84**
CV (%)			**1.94**	**1.55**	**5.51**	**5.65**

Table 2. Continued.

Sl. No.	Genotypes	BRRI ACC Number	Panicle per plant	Fertile grain per panicle	Unfertile grain per panicle	1000 grain weight	Yield per plant
1	Banajira	7	14.17 cd	55.60 g-j	1.94 e	20.16 a-d	10.75 a-f
2	Ghuni boro	181	9.70 f-k	58.47 d-j	2.67 de	18.36 c-h	7.89 c-h
3	Ausha boro	254	12.47 c-g	49.67 h-j	2.34 e	18.31 ch	7.67 e-h
4	Kaika boro	262	11.30 d-j	57.87 e-j	2.14 e	17.80 d-h	8.83 c-h
5	Khamarang	742	11.03 e-j	102.0 b	8.80 cd	20.13 a-d	14.05 a
6	Deshi boro	1405	24.93 a	43.13 ij	2.14 e	16.75 f-h	13.53 ab
7	Jamir	1706	10.67 e-k	65.20 c-h	5.47 de	19.58 a-e	11.85 a-d
8	Isamoti	1790	12.30 c-g	54.87 g-j	3.60 de	21.22 ab	7.98 c-h
9	Sada boro	1791	18.57 b	55.87 f-j	2.33 e	20.73 a-c	9.45 c-g
10	Bogra	1802	13.07 c-e	57.33 e-j	3.53 de	18.46 c-h	9.93 b-g
11	Jagli	1806	10.30 e-k	78.87 c-e	4.73 de	20.36 a-d	10.98 a-f
12	Boro	1808	9.43 g-k	62.20 d-i	3.60 de	19.03 a-h	7.46 e-h
13	Tupa	1811	12.37 c-g	75.27 c-g	4.20 de	16.72 gh	11.16 a-f
14	Sadaboro(awn)	1863	11.07 e-j	79.33 cd	7.33c-e	19.42 a-f	8.84 c-h
15	Sail boro	1970	10.97 e-k	69.67 c-h	1.73 e	18.73 a-h	8.99 c-h
16	Birion	1972	11.27 d-j	63.40 c-i	3.47 de	18.96 a-h	9.26 c-g
17	Boro 66/1	2217	10.83 e-k	60.53 d-j	4.60 de	19.76 a-e	9.04 c-h
18	Boro 66/2	2219	11.50 d-I	74.40 cg	3.80 de	18.54 b-h	10.32 a-g
19	Boro 135/1	2225	10.53 e-k	65.07 c-h	4.93 de	21.27 a	11.15 a-f
20	Boro 391	2229	11.87 c-h	65.73 c-h	3.53 de	18.97 a-h	7.99 c-h
21	Boro 398	2231	10.63 e-k	73.93 c-g	3.53 de	16.79 f-h	9.97 b-g
22	Boro 465	2232	10.27 e-k	70.80 c-h	5.00 de	19.98 a-e	8.41 c-h
23	Boro 522	2237	9.07 h-k	57.67 d-j	3.07 de	20.28 a-d	8.80 c-h
24	Boro 259	2241	11.40 d-j	76.47 c-g	3.73 de	17.33 e-h	9.13 c-g
25	Dhali boro 7/2	2243	12.70 c-f	84.40 c	3.27 de	17.68 d-h	9.52 b-g
26	Dhali boro 87/1	2245	14.20 cd	39.60 j	33.53 a	19.83 a-e	5.03 h
27	Dhali boro 94	2246	11.87 c-h	61.60 d-i	4.73 de	20.21 a-d	7.26 f-h
28	Dhaliboro104/1	2247	10.70 e-k	60.53 d-j	9.00 cd	20.29 a-d	8.24 c-h
29	Dhali boro	2248	11.10 e-j	67.47 c-h	4.47 de	18.32 c-h	11.43 a-e
30	Omni boro	2386	10.63 e-k	62.47 d-i	3.33 de	18.41 c-h	8.09 c-h
31	Chinese var 1	3404	8.40 jk	52.00 h-j	6.87 de	20.79 a-c	6.46 gh
32	Firooz	3766	8.73 i-k	65.07 c-h	5.33 b	21.33 a	7.02 f-h
33	Moghalsail 2	3956	14.57 c	79.53 cd	4.40 de	16.61 gh	12.00 a-c
34	Fenaful	3984	9.20 h-k	140.9 a	12.80 bc	11.54 i	9.37 c-g
35	Bichi barui	3986	7.93 k	67.60 c-h	7.20 c-e	20.06 a-d	8.07 c-h
36	Toifa boro	4015	10.93 e-k	77.60 c-f	3.87 de	19.02 a-h	7.79 d-h
37	Biroin	4522	9.90 f-k	74.93 c-g	4.93 de	19.23 a-g	10.18 a-g
38	Chengri boro	4535	10.67 e-k	64.47 c-i	3.53 de	16.39 h	9.24 c-g
39	Unknown	4595	13.10 c-e	58.53 d-j	4.93 de	20.23 a-d	9.87 b-g
40	Sonali boro 2	4958	13.00 c-e	62.67 d-i	2.20 e	19.99 a-e	10.41 a-g
Mean			**11.683**	**67.32**	**5.42**	**18.94**	**9.34**
CV (%)			**13.11**	**16.02**	**58.20**	**7.12**	**21.85**

Figures followed by same letter(s) (in a column) are not significantly different ($p > 0.05$) from each other and a to o represent as ascending ranking by DMRT.

Table 3. Analysis of variance of nine characters of forty boro rice genotypes

Source of variation	Degrees of freedom (df)			Mean sum of square (MSS)		
	Rep.	Genotype	Error	Replication	Genotype	Error
Days to 50% flowering	2	39	78	0.175NS	46.263**	5.055
Days to maturity	2	39	78	12.025**	49.326**	5.076
Plant height (cm)	2	39	78	838.826*	541.672**	34.331
Panicle length (cm)	2	39	78	10.817**	15.875**	1.385
Panicle per plant	2	39	78	0.134*	24.967**	2.348
Fertile grain per panicle	2	39	78	252.086**	826.965**	116.233
Unfertile grain per panicle	2	39	78	1.767**	85.665**	9.931
1000 grain wt. (g)	2	39	78	1.214NS	9.907**	1.817
Yield per plant (g)	2	39	78	20.007**	10.003**	4.160

** Significant at 1% level of probability, * Significant at 5% level of probability, NS= Non Significant.

Table 4. Genetic variability, genetic parameter, heritability (h_b^2), GA and GA in percent of mean for nine yield contributing characters of forty rice genotypes

Characters	Range	Mean	Mean sum of square	σ^2_g	σ^2_e	σ^2_p	GCV (%)	PCV (%)	h_b^2	GA (5%)	GA(5%) of mean
Days to 50% flowering	109.3-128.7	115.98	46.263**	13.74	5.05	18.79	3.20	3.74	73.10	6.53	5.63
Days to maturity	138.00-162.00	144.95	49.326**	14.75	5.07	19.82	2.65	3.07	74.41	6.82	4.71
Plant height (cm)	45.47-129.1	106.32	541.672**	169.11	34.34	203.44	12.23	13.42	83.12	24.42	22.97
Panicle length (cm)	16.40-27.73	20.84	15.875**	4.83	1.38	6.28	10.55	11.97	77.72	3.99	19.16
Panicle per plant	7.933-24.93	11.68	24.967**	7.54	2.35	9.89	23.5	26.91	76.26	4.94	42.28
Fertile grain per panicle	39.60-140.9	67.32	826.965**	236.90	116.24	353.14	22.86	27.92	67.08	25.97	38.58
Unfertile grain per panicle	1.933-33.53	5.42	85.665**	25.24	9.93	35.18	89.20	92.79	71.77	8.77	161.92
1000 grain wt. (g)	11.54-21.33	18.94	9.907**	2.70	1.82	4.51	8.67	11.22	69.75	2.62	13.81
Yield per plant (g)	5.033-14.05	9.34	10.003**	1.95	4.16	6.11	14.95	26.47	31.89	1.62	17.39

** Significant in 1%, σ^2_g = Genotypic variance, σ^2_e = Environmental variance, σ^2_p = Phenotypic variance, GCV (%) =Genotypic co-efficient of variation, PCV (%) =Phenotypic co-efficient of variation, GA (5%) = Genetic advance in 5% and GA (5%) of mean= Genetic advance in 5 percent of mean.

There was a high range (39.60-140.9) in the number of fertile grain per panicle (Table 2). Genotype Fenaful produced the highest number of fertile grain per panicle (140.9) which was significnatly different from second highest genotype Khamarang (102.0). Khamarang was significantly different from the next highest Dhali boro 7/2 (84.40). The genotype Dhali boro 87/1 produced the lowest number of fertile grain per panicle (39.60) and which was not significantly different from Deshi boro (43.13), Ausha boro (49.67), Chinese var1 (52.00), Isamoti (54.87), Banagira (55.60), Sada boro (55.87), Bogra (57.33), Boro 522 (70.80), Kaika boro (57.87), Ghuni boro (58.47), Unknown (58.53), Boro 66/1 (60.53), Dhali boro 104/1 (60.53).

Generally, the genotypes with lower number of unfertile grain per panicle is expected to be better yielder. The genotype Sailboro produced minimum number of unfertile grain per panicle (1.73) but the genotype Dhali boro 87/1 produced highest number of unfertile grain per panicle (33.53).

The highest 1000 grain weight (21.339g) was observed in Firoz. Boro 135/1 (21.27g) also fell in the same statistical group. Fenaful gave the lowest 1000 grain weight (11.54g) which was significantly different from the second lowest Chengri boro (16.399g).

The genotype Khamarang produced highest yield per plant (14.05g) which was not significantly different from Deshi boro (13.53g), Moghal sail (12.00g), Jamir (11.85g), Dhali boro (11.43g), Tupa (11.16g), Boro 135/1 (11.15g), Jagli (10.98g), Banagira (10.75g), Sonali boro 2 (10.41g), Boro 66/2 (10.32g), Biroin (10.18g). The genotype Dhali boro 87/1 gave the lowest yield per plant (5.03g) which was not significantly different from Chinese var1 (6.46g), Firooz (7.02g), Dhali boro 94 (7.26g), Boro (7.46g), Ausha boro (7.67g), Toifa boro (7.79g), Ghuni boro (7.89g), Isamoti (7.98g), Boro 391 (7.99g), Bichi barui (8.07g), Omni boro (8.09g), Dhali boro 104/1 (8.24g), Boro 465 (8.41g), Boro 522 (8.80g), Kaika boro (8.83g), Sada boro (Awn)

(8.84g), Sail boro (8.99g), Boro 66/1 (9.04g). It is apparent that differences among the varieties are very low in respect of yield which might be due to narrower gene pool of local germplasm.

4.2 Studies on variability and character association

4.2.1 Variability, Heritability and Genetic Advance

The genotypic (σ^2g), phenotypic (σ^2p) and environmental variance (σ^2c), genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), heritability in broad sense (h^2b %) genetic advance (GA) and genetic advance in percent of mean (GA %) for all quantitative characters under study are presented in Table 4. The phenotypic co-efficient of variation (PCV) was higher than their corresponding genotypic co-efficient of variation (GCV) for all the characters, indicating that they all interacted with the environment to some extent.

4.2.2 Genetic parameter in respect of all characters are discussed below:

4.2.2.1 Days to 50% flowering

In the present study, genotypic (3.20%) and phenotypic (3.74%) co-efficient of variation were numerically lower for days to 50% flowering (Table 5). There was a little difference between genotypic and phenotypic co-efficient of variation, indicating least influence of environment on this trait. Such low values of GCV (5.4%) and PCV (5.8%) with least difference was also observed by Katocha *et al.* (1993) for days to 50% flowering in rice. A very little GCV with least difference with PCV was also reported by Das *et al.* (1992).

Days to 50% flowering showed high heritability (73.10%) and low genetic advance (5.63%) in percent of mean, indicating non-additive genetic control of this character. Gupta *et al.*, (1999) found high heritability with low genetic advance for days to flowering in rice. Sing *et al.* (1986) also found high heritability (95.1%) with low genetic advance (14.7%) in percent of mean.

4.2.2.2 Days to maturity

Days to maturity showed the lowest genotypic (3.65%) and phenotypic (3.07%) co-efficient of variation. Difference between genotypic and phenotypic co-efficient of variation was very low which indicates that environment had little influence on the expression of this character in rice. Shaha *et al.* (1993a) found little genotypic (2.58%) and phenotypic (2.62%) co-efficient of variation with negligible difference. Das *et al.* (1992) also found little different between GCV and PCV for days to maturity.

Days to maturity showed high heritability (74.41%) coupled with low genetic advance (4.71%) in percent of mean, indicating non-additive gene effects and expression might be influenced largely by non-genetic factors. Debi *et al.* (1997) found high heritability (96.9%) and low genetic advance (9.07%) in percent of mean for days to maturity in rice. Rao and Shrivastava (1994) also found high heritability for this character.

4.2.2.3 Plant height

In the present study, plant height showed moderate genotypic (12.23%) and phenotypic co-efficient of variation (13.42%). There was a little difference between genotypic and phenotypic co-efficient of variation indicating minor influence of environment in the expression on this character. Maurya *et al.* (1986) found moderate genotypic (10.4%) and phenotypic (11.7%) co-efficient of variation and also reported least influence of environment on this character. Moderate genotypic (16.6%) and phenotypic co-efficient of variation (16.85%) with almost no difference was reported by Wilpeed *et al.* (1993).

Plant height showed high heritability (83.12%) along with moderate genetic advance (22.98%) in percent of mean. The results suggested the importance of additive and non-additive gene effect on the control of plant height. Kumar *et al.* (1994) found high heritability coupled with moderate genetic advance for plant height. Maurya *et al.* (1986) also reported such a high

heritability (79.85%) coupled with moderate genetic advance (19.2%) in percent of mean for this character in rice.

4.2.2. 4. Panicle length

Genotypic and phenotypic co-efficient of variation were moderate for panicle length. There was a little difference between phenotypic (11.97%) and genotypic (10.55%) co-efficient of variation indicating minor environmental influence on this character. Biswas *et al.* (2000) reported that panicle length showed moderate genotypic co- efficient of variation and phenotypic co-efficient of variation. Chakraborty and Hazarika (1994) reported a very small difference between phenotypic and genotypic co-efficient of variation in panicle length.

This character showed high heritability (77.72%) coupled with moderate genetic advance (19.16%) in percent of mean. The results suggested the importance of additive and non- additive gene effect on the control of panicle length. Chakraborty and Hazarika (1994) reported high heritability along with moderate genetic advance for panicle length. Kumari *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses and found high heritability coupled with moderate genetic advance for this trait in rice.

4.2.2.5 Panicle per plant

In the present study, number of panicle per plant showed high genotypic (23.50%) and phenotypic (26.91%) co-efficient of variation. The difference between GCV and PCV indicated considerable influence of environment in the expression of this character. Singh and Choudhury (1996) reported high PCV and GCV and suggested that environmental effect contributed more to phenotypic co-efficient of variation.

This character exhibited high heritability (76.26%) along with high genetic advance (42.28%) in percent of mean, indicating the presence of

additive gene effects that might be expressed consistently in segregating generations, leading to greater efficiency of a breeding programme. Gomathinayagam *et al.* (1990) studied high heritability coupled with high genetic advance implying additive gene action. Chookar *et al.* (1994) reported high heritability with high genetic advance indicating additive gene action that provides better scope for selection. Kumari *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses and found high heritability coupled with high genetic advance for this trait in rice.

4.2.2.6 Fertile grain per panicle

Fertile grain per panicle showed high genotypic (22.86%) and phenotypic (27.92%) co-efficient of variation. The difference between GCV and PCV indicated considerable influence of environment in the expression of this character. Shaha *et al.* (1993b) found high genotypic (26.14%) and phenotypic (27.85%) co-efficient of variation for fertile grain per panicle. Singh *et al.* (1986) also found high GCV (30.7%) and PCV (37.5%) for this trait in rice.

This character also showed high heritability (67.08%) with high genetic advance (38.58%) in percent of mean, indicating the presence of additive gene effects that might be expressed consistently in segregating generations, leading to greater efficiency of a breeding programme. Maurya *et al.* (1994) found high heritability (77.0%) with high genetic advance (39.1%) in percent of mean for fertile grain per panicle. Similar result was also found by Paramasivan and Rangasamy (1988).

4.2.2.7 Unfertile grain per panicle

The genotypic and phenotypic co-efficient of variation was higher for this character. The phenotypic co-efficient of variation (92.79%) was higher than genotypic (89.20%) co-efficient of variation, indicating that this character was slightly influenced by environment. Ahmed and Das (1994) found such

environmental influence on this character. Babu (1996) estimated high genotypic and phenotypic coefficient of variation for this trait in rice. Wilpeed Manual and Prasad (1993) observed high genetic variation for sterility percentage in rice genotypes.

The heritability estimates revealed that unfertile grain per panicle had high heritability (71.77%) along with high genetic advance (61.92%) in per cent of mean. This character might be highly heritable and undesirable in selection programme for yield improvement. De and Surya Rao (1988) also observed high heritability (95.8%) with high genetic advance (69.5%) in percent of mean for this trait in rice. Paul and Sarmah (1998) reported high genotypic co-efficient of variation, high heritability and high genetic advance for unfertile grain per panicle.

4.2.2.8 1000 grain weight

1000 grain weight showed moderate genotypic (8.67%) and phenotypic (11.22%) co-efficient of variation. The phenotypic co-efficient of variation was higher than genotypic co-efficient of variation indicating considerable environmental influence on 1000 grain weight. Sawant *et al.* (1994) observed significant difference between high genotypic and phenotypic co-efficient of variation for 1000 grain weight. Similar results were also found by Reddy *et al.* (1997) and Kumar *et al.* (1998).

Low genetic advance (13.81%) in percent of mean associated with high heritability (69.75%) were recorded for 1000 grain weight, indicating non-additive gene effects and expression might be influenced largely by non-genetic factors. Kumari *et al.* (2003) showed high heritability coupled with moderate genetic advance indicating the role of non-additive gene effect in the inheritance of this trait.

4.2.2.9 Yield per plant

Yield per plant showed high genotypic (14.95%) and phenotypic (26.79%) co-efficient of variation. The phenotypic co-efficient of variation was higher than genotypic co-efficient of variation indicating considerable environmental influence on Yield per plant. Sawant and Patil (1995) reported high genotypic and phenotypic co-efficient of variation for this trait in rice. Similar results were also found by Li *et al.* (1991) and Das *et al.* (1992).

This character showed moderate heritability (31.89%) along with moderate genetic advance (17.39%) in percent of mean, indicating the presence of both additive and non additive genes on controlling this character. Vishwakarma *et al.* (1989) stated that broad sense heritability was moderate and also moderate genetic advance for yield per plant. Li *et al.* (1991) also found the similar result. Considerable amount of heritability and genetic advance were observed for yield per plant in rice by Yadav (2000).

The result on co-efficient of variation, heritability and genetic advance indicated that selection for fertile grain per panicle, unfertile grain per panicle, panicle per plant and plant height are important to improve the values of these characters.

4.3 Diversity of forty Boro rice genotypes

4.3.1 Principal component analysis

The principal component analysis yielded eigen values of each principal component axes of ordination of genotypes with the first axes totally accounting for the variation among the genotypes, while three of these with eigen values above unity accounted for 76.49%. The first two principal axes accounted for 62.56% of the total variation among the 9 characters describing forty genotypes (Table 5). Based on principal component exes I and II, a two dimensional chart (Z_1-Z_2) of the genotypes are presented (Fig. 1). The scattered diagram revealed that apparently there were mainly five clusters (Fig. 1).

Table 5. Eigen values and percentage of variation in respect of nine characters of forty rice genotypes

Principal component characters	Eigen values	Percentage of total variations accounted for	Cumulative percentage
Day to 50% flowering	3.877	43.07	43.07
Day to maturity	1.754	19.49	62.56
Plant height (cm)	1.253	13.93	76.49
Panicle length (cm)	0.904	10.05	86.54
Panicle per plant	0.562	6.24	92.78
Fertile grain per panicle	0.391	4.34	97.12
Unfertile grain per panicle	0.148	1.65	98.77
1000 grain wt. (g)	0.077	0.86	99.63
Yield per plant (g)	0.034	0.37	100.00

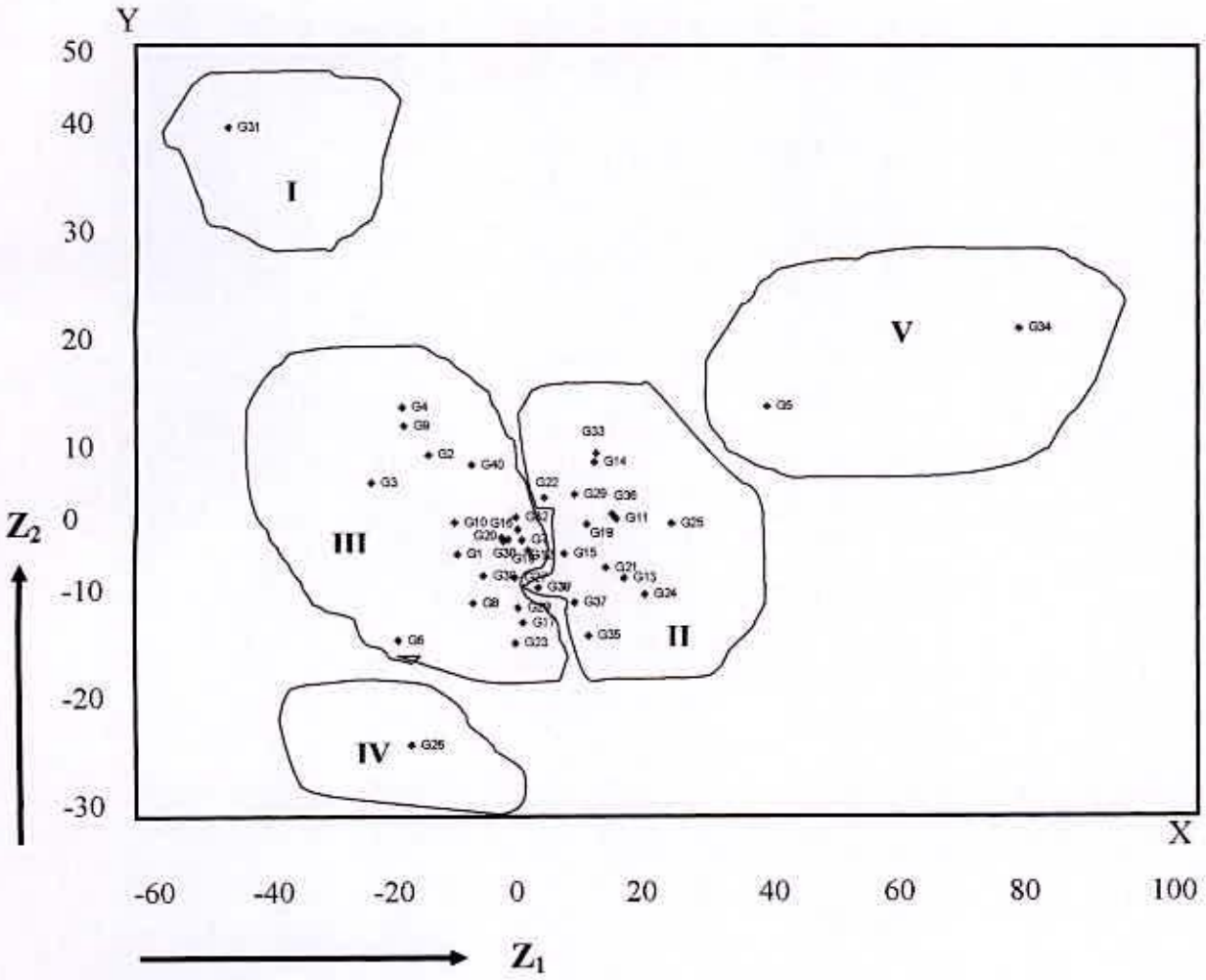


Fig. 1 Scattered diagram of forty boro rice genotypes based on their principal components scores superimposed with clustering

Singh *et al.* (1999) using 42 genotypes of Boro rice for eleven quantitative characters, including grain yield. Multivariate analysis revealed considerable genetic diversity in the material and led to their grouping into four clusters. They also found that total number of grains/panicle, number of filled grains/panicle accounted 90.6% of the total divergence.

Shiv *et al.* (2003) found that plant height contributed the maximum towards genetic divergence (52.24%) followed by days to 50% flowering and grain yield/plant. Singh *et al.* (1996) reported that plant height contributed 16.5% of total divergence in 40 genotypes of scented and fine rice.

4.3.2 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two dimensional scatter diagram (Z_1-Z_2) using component score 1 as X-axis and component score 2 as Y-axis was constructed. The position of the genotypes in the scatter diagram was apparently distributed into five groups, which indicated that diversity among the genotypes were existed (Fig. 1). The scatter diagram for the forty rice genotypes of different clusters revealed that the genotype number 5, 26, 31, 34 were distantly located which suggesting more diverged from rest of the genotypes.

4.3.3 Principal coordinate analysis

Inter genotypic distances as obtained by principal coordinate analysis for selective combination showed that the highest distance 2.667 was observed between the genotype (G) number G15 and G26, followed by G6 and G26 (2.630), G1 and G26 (2.588), G4 and G26 (2.517) and the lowest distance was observed between G11 and G37 (0.127), followed by G20 and G30 (0.143), G7 and G19 (0.147), G16 and G20 (0.157) (Table 6).

Table 6. Ten higher and lower genotypic distance between pair of genotypes

Ten higher D^2 values	Genotypic combination	Ten lower D^2 values	Genotypic combination
2.667	G15 & G26	0.127	G11 & G37
2.630	G6 & G26	0.143	G20 & G30
2.588	G1 & G26	0.147	G7 & G19
2.517	G4 & G26	0.151	G16 & G20
2.509	G26 & G32	0.162	G16 & G38
2.465	G9 & G26	0.166	G18 & G21
2.403	G3 & G26	0.170	G21& G38
2.363	G2 & G26	0.175	G12 & G30
2.326	G25 & G26	0.176	G13 & G29
2.280	G23 & G26	0.179	G21 & G24

By using these inter genotypic distance intra cluster genotypic distances were calculated (Table 7 as suggested by Sing and Choudhury 1989). Cluster I which showed highest intra cluster distance (6.4061) composed of 21 genotypes and cluster I & IV showed the lowest intra cluster distance (0.000) composed of only one genotype which indicated within group diversity of the genotypes was maximum in cluster III and minimum in cluster I & IV.

4.3.4 Canonical variate analysis

Canonical variate analysis was done to compute the inter cluster Mahalanobis's values. The intra and inter cluster distance (D^2) values are presented in (Table 7). Results indicated that the highest inter cluster distance was observed between the cluster IV and V (25.066), followers by between I and IV (21.107), II and IV (20.201), III and IV (18.800).

The lowest inter cluster distance was observed between the cluster II and III (2.696) followed by I and III (4.820) I and II (6.866), suggesting a close relationship among these three clusters (Figure 2). As the maximum inter cluster distance were recorded between the cluster IV and V, followed by between I and IV. So genotypes from these three clusters if involved in hybridization may occur a wide spectrum of segregating population as genetic variation is very distinct among the group. The genotypes belonging to the distant clusters could be used in hybridization programme for obtaining a wide spectrum of variation among the segrigants. Similar reports were also made byBansal *et al.* (1999), Mokate *et al.* (1998), Kumar and Rangasamy (1997) Sing *et al.* (1996).

The intra cluster divergence varied from 0.000 to 6.4061, maximum being from cluster III which comprised of 21genotypes of diverse origin, while the minimum distance was observed in cluster I (0.000) & IV (0.000) both comprise only one genotype.

Table 7. Average intra (Diagonal) and inter cluster D^2 value of five clusters formed by tochers method

Cluster no.	I	II	III	IV	V
I	**0.000**	6.866	4.820	21.107	16.010
II		**3.0744**	2.696	20.201	9.351
III			**6.4061**	18.800	11.985
IV				**0.000**	25.066
V					**0.8297**

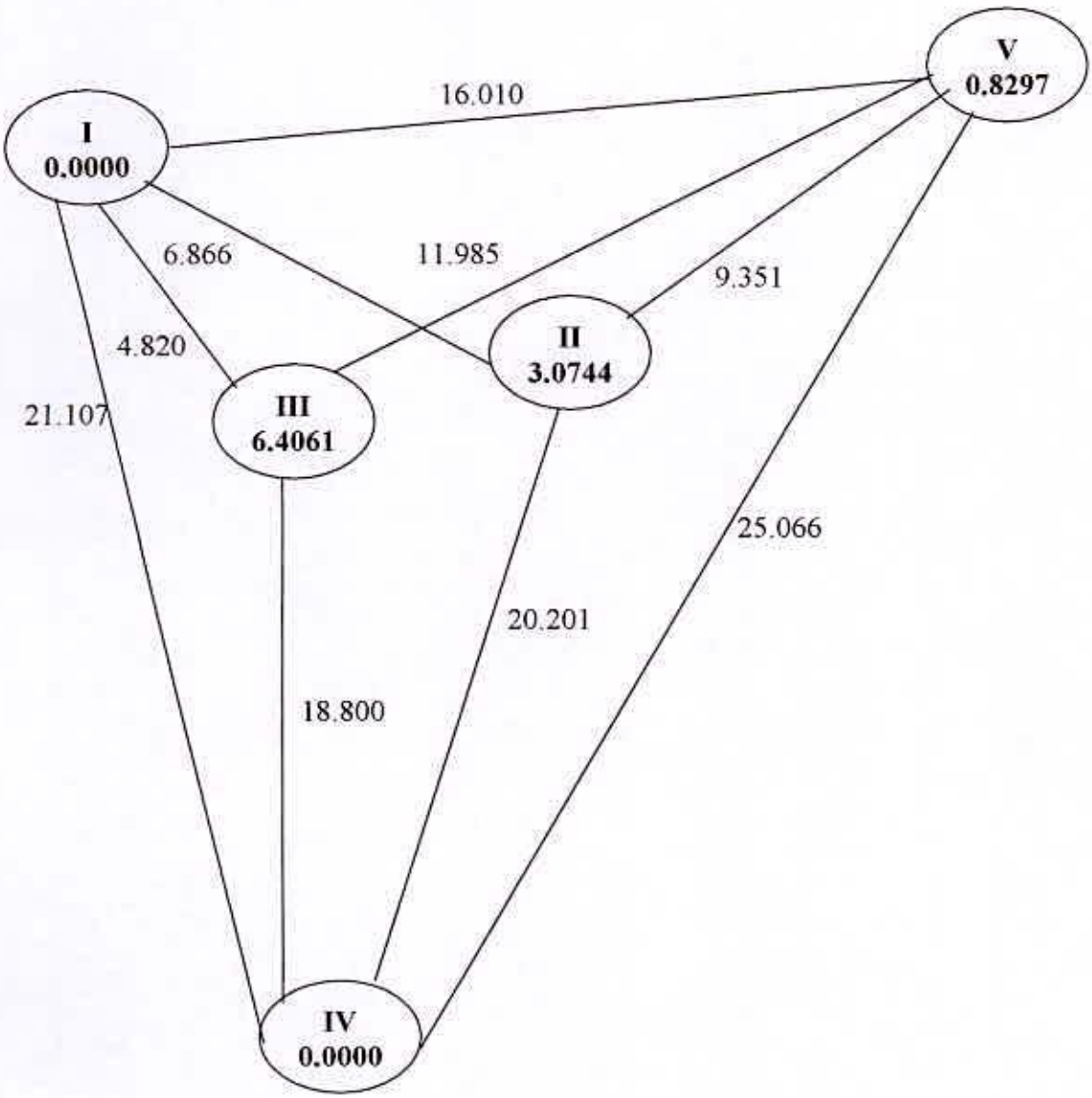


Fig. 2 Diagram showing intra (inside the circle) and inter cluster (out side the circle) distance of forty boro rice genotypes

Results obtained from different multivariate techniques were superimposed in (Figure 2) from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one.

4.3.5 Non-hierarchical clustering

By application of non-hierarchical clustering using co-variance matrix, the forty rice genotypes were grouped into five different clusters. These results confirmed the clustering pattern of the genotype according to the principal component analysis. Sawant *et al.* (1995) carried out principal component analysis and cluster analysis in 75 rice genotypes and stated 75 varieties into 10 clusters. Composition of different clusters with their corresponding genotypes are presented in Table 8. Custer III had maximum 21 genotypes followed by cluster II, V which had 5, 2 and cluster I and IV had only one genotype respectively.

Cluster I composed of only one genotype (Genotype name) Chinese var 1. From the clustering mean values (Table 8), it was observed that cluster I showed the highest mean for 1000 grain weight (20.76), and the lowest values for days to 50% flowering (109.30), days to maturity (138.00), plant height (45.50), panicle length (16.40) and panicle per plant (8.40) (Table 9).

Cluster II was composed of 15 genotypes namely Jagli, Tupa, Sadaboro (awn), Sail boro, Boro 66/2, Boro 398, Boro 465, Boro 259, Dhali boro 7/2, Dhali boro, Moghalsail 2, Bichi barui, Toifa boro, Biroin and Chengri boro. These genotypes produced the second highest mean for days to 50% flowering (116.43), plant height (112.95), panicle length (21.55), fertile grain per panicle (74.28) and yield per plant (2.73).

Table 8. Distribution of forty genotypes in five clusters

Cluster	BRRI Accession no of genotypes with serial no.	No. of Genotypes	Name of genotypes
I	3404 (G31)	1	Chinese var-1
II	1806 (G11), 1811 (G13), 1863 (G14), 1970 (G15), 2219 (G18), 2231 (G21), 2232 (G22), 2241 (G24), 2243 (G25), 2248 (G29), 3956 (G33), 3986 (G35), 4015 (G36), 4522 (G37), 4535 (G38)	15	Jagli,, Tupa, Sada boro Awn, Sail boro, Boro 66/2, Boro 398, Boro465, Boro259, Dhali Boro 7/2, Dhali Boro, Moghal sail 2, Bichi barui, Toifa boro, Birion, Chengri boro
III	7 (G1), 181 (G2), 254 (G3), 262 (G4), 1405 (G6), 1706 (G7), 1790 (G8), 1791 (G9), 1802 (G10), 1808 (G12), 1972 (G16), 2217 (G17), 2225 (G19), 2229 (G20), 2237 (G23), 2246 (G27), 2247 (G28), 2386 (G30), 3766 (G32), 4595 (G39), 4958 (G40)	21	Banojira, Ghuni boro, Ausha boro, Kaika boro, Deshi Boro, Jamir, Isamoti, Sada boro, Bogra, Boro, Birion, Boro 66/1, Boro 135/1, Boro 391, Boro 522 Dhali Boro 94, Dhali Boro104/1, Omni boro, Firooz, Unknown, Sonali Boro 2
IV	2245 (G26)	1	Dhali Boro 87/1
V	742 (G5), 3986 (G34)	2	Khamarang, Fenaful

Table 9. Cluster mean for nine characters in forty rice genotypes

Character	Cluster				
	I	II	III	IV	V
Day to 50% flowering	109.30	116.43	114.96	115.30	124.95
Day to maturity	138.00	145.21	144.00	145.30	155.50
Plant height (cm)	45.50	112.95	102.84	112.70	120.55
Panicle length (cm)	16.40	21.55	19.97	20.10	27.20
Panicle per plant	8.40	11.05	12.25	14.20	10.10
Fertile grain per panicle	52.00	74.28	59.22	39.60	121.40
Unfertile grain per panicle	6.80	4.35	4.20	33.50	10.80
1000 grain wt. (g)	20.76	18.12	19.53	19.83	15.83
Yield per plant (g)	6.45	9.73	9.16	5.03	11.71

Cluster III had 21 genotypes namely Banajira, Ghuni boro, Ausha boro, Kaika boro, Deshi boro, Jamir, Isamoti, Sada boro, Bogra, Boro, Birion, Boro 66/1, Boro 135/1, Boro 391, Boro 522, Dhali boro 94, Dhali boro104/1, Omni boro , Firooz, Unknown and Sonali boro. The genotypes of this cluster produced second highest mean values for panicle per plant but least values for unfertile grain per panicle (4.20).

Cluster IV constituted only one genotype namely Dhali boro 87/1. The genotype of this cluster produced highest mean value for panicle per plant (14.20) and unfertile grain per panicle (33.50). The lowest value was observed for fertile grain per panicle (39.60) and yield par plant (5.03).

Cluster V constituted of 2 genotypes namely Khamarang and Fenaful. From the clustering mean values (Table 8), it was observed that the mean value of cluster V ranked first for days to 50% flowering (124.95), days to maturity (155.50), plant height (120.55), panicle length (27.20), fertile grain per panicle (121.40), yield per plant (11.7) and the second for unfertile grain per panicle (10.80). The lowest clusters mean value for 1000 grain weight (15.83).

The maximum range of variability was observed for fertile grain per panicle (39.60 to 121.40) among all the characters in five clusters. Cluster III indicated second lowest days to 50% flowering, days to maturity and plant height; Second highest panicle per plant, lowest unfertile grain per panicle and moderate 1000 grain weight. The cumulative effect of the above characteristics would lead to high yield per plant (Table 9). Cluster V indicated highest panicle length, highest fertile grain per panicle and highest yield per plant. To develop high yielding as well as early and semi dwarf stature varieties, genotypes of the cluster III and cluster V can be used in hybridization programme.

Pravin *et al.* (2003) reported that the cultivars from cluster IV (Safri-17, Bamleshwari, R1037-649-1-1, ND-9730021, Jaldubi, and Basmati-370) had the greatest number of panicles per plant, panicle length, number of fertile spikelets per panicle, biological yield per plant, and grain yield per plant. Vandana, R-1102-2795-3-1, R288-650-2, and Poornina of cluster VIII had the highest amylose percentage, grain yield per plant, harvest index, and starch percentage. Annada, Ruchi, and Kranti of cluster V had the highest 100-seed weight and harvest index. G95-02 of cluster IX had high panicle length and flag leaf area, and intermediate number of tillers per plant, paddy length, 100-seed weight, and grain yield per plant. These cultivars have good potential as parents for the development of hybrids with high yield and quality.

Genetic diversity of 62 cultivars of irrigated rice originating from BRRI, IRRI, and China were evaluated by Islam *et al.* (2004) in Satkhira, Bangladesh, during the boro season of 2001-2002 using the Mahalanobis D^2 statistical method. The highest cluster means for yield and the other three yield-contributing characters were obtained from cluster I, the six highest and two second highest means for yield-contributing characters were found in cluster III; however, the lowest cluster mean for yield was also found in this cluster. Therefore, more emphasis should be given to cluster I when selecting cultivars as parents for crossing with the cluster III cultivars, which may produce new recombinants with desired traits.

4.3.6 Contribution of characters towards divergence of the genotypes

The PCA revealed that in vector I (Z_1) the important characters responsible for genetic divergence in the major axis of differentiation were panicle length (0.4491), days to 50% flowering (0.4427), days to maturity (0.4348), fertile grain per panicle (0.3971), plant height (37.38), yield per plant (0.2314) and unfertile grain per panicle (0.0733) (Table 10). In vector II (Z_2), which was the second axis of differentiation panicle per plant (0.6059) yield per plant (0.4592), days to 50% flowering (0.1419), days to maturity (0.1023) were

important. The role of yield per plant, days to 50% flowering, days to maturity for both the vectors was positive across two axes indicating the important components of genetic divergence in these materials.

The character contributing maximum to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al.*, 1991).

Julfiquar (1984) also reported similar response for the traits yield, 1000 grain weight, days to maturity and plant height in rice. Plant height and grain yield contributed considerably to the total divergence reported by Vivekanondon and Subramaniam (1993). On the other hand Chauhan and Chauhan (1994) reported that the contribution of 1000 grain weight was the highest followed by days to 50% flowering, panicle weight and spikelet per panicle.

4.3.7 Comparison of different multivariate technique (D^2) analysis and principal component analysis

The cluster pattern of D^2 analysis through Non-hierarchical clustering has taken care of simultaneous variation in all the characters under study. However, the distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the Z_1 and Z_2 vector of the principal component analysis. The D^2 and principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the principal component analysis provides the information regarding the contribution of characters towards divergence of boro rice. Mohapatra *et al.* (1993) reported that group constellation based on Tocher`s method was fairly in good agreement with the scattered points of the Z_1-Z_2 graph as well as the clustering pattern obtained through dendograms.

Table 10. Latent vactors for nine characters of forty rice genotypes

Characters	Vactor I	Vactor II
Day to 50% flowering	+0.4427	+0.1419
Day to maturity	+0.4348	+0.1023
Plant height (cm)	+0.3738	-0.1010
Panicle length (cm)	+0.4491	-0.2719
Panicle per plant	-0.304	+0.6059
Fertile grain per panicle	+0.3971	-0.1350
Unfertile grain per panicle	+0.0733	-0.4283
1000 grain wt. (g)	-0.2367	-0.1214
Yield per plant (g)	+0.2314	+0.4592

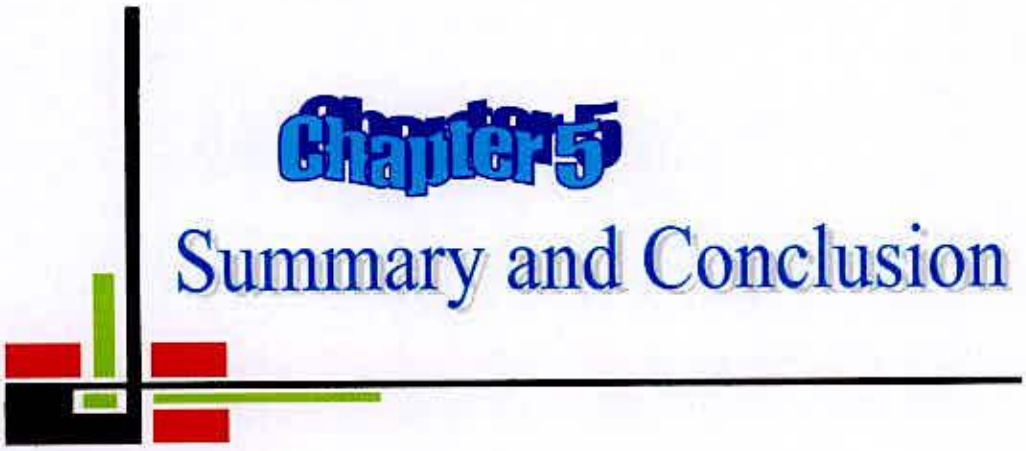
4.3.8 Selection of genotypes for future hybridization purpose

Genotypes are to be selected on the basis of specific objectives. No common criterion is considered for the selection of genotypes. Considering magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster mean for different characters and agronomic performance of the following genotypes were considered to perform better if used in hybridization programme. The genotypes of cluster I can be selected for earliness, lower plant height and higher 1000 grain weight. The genotype of cluster II can be selected for the moderate number of fertile grains per panicle, panicle length, plant height, days to 50% flowering, and yield per plant. The genotypes of cluster III can be selected for the lowest unfertile grains per panicle. The genotypes of cluster IV can be selected for the highest number of panicles per plant. The genotypes of cluster V can be selected for the highest panicle length, fertile grain per panicle and yield per plant.

It is assumed that highest heterosis would be manifested in cross combination involving the genotypes belonging to divergent clusters. However for a practical plant breeder, the objective was not only high heterosis but also to achieve high level of production. Considering this, it appears that the cross between the genotypes belonging cluster III with cluster IV, cluster III with cluster V, and cluster I with cluster V might produce high heterosis in yield as well as earliness and short stature. So, select the better performing genotype G31 from cluster I; G1 from Cluster III; G26 from cluster IV and G5, G 34 from cluster V were selected for future hybridization.

Genotypically distant parents usually able to produce higher heterosis (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Ghaderi *et al.* 1984; Mian and Bhal, 1989).

Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G31 and G5; G31 and G34; G1 and G26; G1 and G5, G1 and G34 may be used for future hybridization program.



Chapter 5

Summary and Conclusion

SUMMARY AND CONCLUSION

The present piece of research was conducted at the field laboratory of the Bangladesh Rice Research Institute (BRRI) Gazipur, during the period from November' 05 to May' 06. The experiment was conducted in a Randomized Complete Block Design (RCBD) with three replications. The present study was undertaken with a view to evaluate the performance of forty boro rice genotypes in order to know the variability and genetic parameters of nine important quantitative characters and finally assessing the genetic diversity among these genotypes.

The performance of the genotypes for yield and yield contributing characters were evaluated. It was revealed that there was a significant variation among the genotypes for all the characters studied. Different genotypes showed better performance for different characters. The genotype Chinese var 1 and Ausha boro were (109.3, 109.7) the earliest in flowering whereas the genotypes Khamarang was (128.7) the late flowering types. The genotypes Chinese var 1, Ghuni boro and Ausha boro was the earliest maturing (138.0) type whereas the genotype Khamarang was the late maturing (162.0) type. Genotype Chinese var 1 was the shortest (45.47) in stature and the genotype Fenaful was the tallest (129.1) one. The genotype Khamarang had the highest panicle length (27.73) and the genotype Chinese var1 produced the shortest panicle (16.40). The genotype Deshi boro produced the highest number of effective tillers per plant (24.93) and the genotype Bichi barui produced the least number of effective tillers per plant (7.93). The genotype Fenaful produced the highest number of fertile grain per panicle (140.9) but the genotypes Sail boro produced the lowest number of unfertile grain per panicle (1.73). The genotypes Firooz produced the highest 1000 grain weight (21.33) whereas the genotype Chengri boro produced the lowest 1000 grain weight (16.39). The Maximum yield per plant was produced by Khamarang (14.05) followed by Deshi boro(13.53) whereas Dhali boro 87/1 produced the lowest yield per plant(5.03).

The phenotypic variance was more or less higher than the corresponding genotypic variance for all the characters. However, these differences were in case of days to 50% flowering, days to maturity, fertile grain per panicle, unfertile grain per panicle, 1000 grain weight and yield per plant indicating greater influence on environment for expression of these characters. Among the characters, plant height, panicle length and panicle per plant showed least difference between phenotypic and genotypic variance, which indicated the preponderance of additive gene action for expression of these characters.

High genotypic and phenotypic co-efficient of variation were observed for panicle per plant, fertile grain per panicle, unfertile grain per panicle and yield per plant. Days to 50% flowering and days to maturity showed low genotypic and phenotypic co-efficient of variation. Medium genotypic and phenotypic co-efficient of variation were observed for plant height and panicle length.

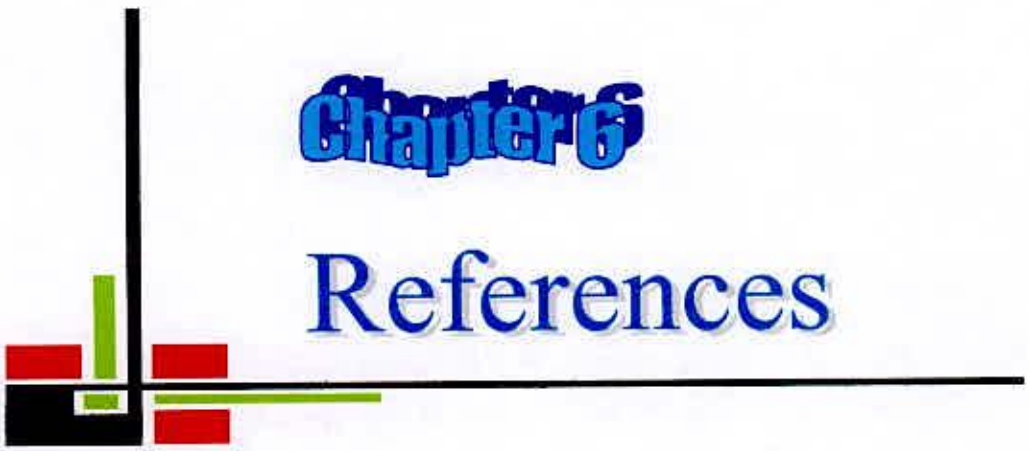
It was observed that all the characters exhibited high heritability except yield per plant, which showed medium heritability. Estimates of genetic advance in percent of mean were high for the characters, panicle per plant, fertile grain per panicle and unfertile grain per panicle. Plant height panicle length and yield per plant showed medium and days to 50% flowering, days to maturity and 1000 grain weight showed low genetic advance in percent of mean. High heritability along with high genetic advance in percent of mean was observed for panicle per plant, fertile grain per panicle and unfertile grain per panicle. So these characters would be best for selection.

Significant differences among the clusters were observed. The first two components with eigen value were greater than unity contributed a total of 62.56% variation towards the divergence. As per PCA, D^2 and Cluster Analysis, the genotypes were grouped into five different clusters. Custer III had maximum 21 genotypes followed by cluster II, V which had 5, 2 and cluster I and IV had only one genotype respectively. The highest inter cluster distance

was observed between the cluster IV and V (25.066), followed by between I and IV (21.107), II and IV (20.201). The lowest inter cluster distance was observed between the cluster II and III (2.696) followed by I and III (4.820), I and II (6.866). Cluster I showed highest intra cluster distance (6.4061), cluster I & IV showed the lowest intra cluster distance (0.000) respectively. The genotypes of cluster I were important for shortest days to 50% flowering, shortest days to maturity, lower plant height and higher 1000 grain weight. The genotype of cluster II were important for the Moderate number of fertile grains per panicle, panicle length, plant height, days to 50% flowering, and yield per plant. The genotypes of cluster III were important for the lowest unfertile grains per panicle. The genotypes of cluster IV were important for the highest number of panicles per plant. The genotypes of cluster V were important for the highest panicle length, fertile grain per panicle and yield per plant.

However for a practical plant breeder, the objective is not only high heterosis but also to achieve high level of production. Considering this, it appears that the cross between the genotypes belonging cluster III with cluster IV, cluster III with cluster V, and cluster I with cluster V might produce high heterosis in yield as well as earliness and short stature. So, select the better performed genotype G31 from cluster I; G1 from cluster III; G26 from cluster IV and G5, G 34 from cluster V selected for future hybridization.

Therefore, considering group distance and the agronomic performance, the inter genotypic crosses between G31 and G5, G31 and G34; G1 and G26; G1 and G5, G1 and G34 might be suggested to use for future hybridization program.



Chapter 6

References

REFERENCES

Ahmed, T., and Das, G.R. (1994). Evaluation and characterization of glutinous rice germplasm of Assam. *Oryza.* **31**: 77-83.

Akter, K., Iftekharuddaula, K.M., Bashar, M.K., Kabir, M.H. and Sarker, M.Z.A. (2004). Genetic variability, correlation and path analysis in irrigated hybrid rice. *J. Subtrop. Agric. Res. Dev.* **2**(1): 17-23.

Ali, S.S., Jafri, S.J.H., Tasleem-Uz-Zamzn, K., Aamir, M. and Butt, M.A. (2000). Heritability of yield and yield components of rice. *Pakistan J. Agril. Res.* **16**(2): 89-92.

Anderson, E., (1957). A Semi-graphical method for the analysis of complex problems. *Proc. Nat. Acad. Sci.* Wash. **43**: 89-92.

Arun, S., Yadav, D.V., Singh, A.K., Gaurav, Y., Surinder, G., Gupta, K.R., Ranghvirendra, S., Deepak, P., Sharma, A., Yadav, G., Gulia, S., Singh, R., and Prem, D., (2002). Genetic divergence in aromatic rice (*Oryza sativa* L.). *Nat. J. Pl. Improve.* **4**(2): 46-49.

Ashvani, P., Sharma, R.K., Arya, K.P.S. and Panwar, A. (1997). Genetic variability and interrelationship in rice. *Advances in Plant Sciences.* **10**(1): 29-32.

Babu, V.R., (1996). Study of genetic Parameters, correlations and path co-efficient analysis of rice (*Oryza sativa* L.) under saline conditions. *Ann. Agril. Res. India.* **17**(4): 370-374.

Balan, A., Muthiah, A.R. and Boopathi, S.N.M.R. (1999). Genetic variability, character association and path co-efficients and analysis in rainfed rice, under alkaline condition. *Madras Agril. J.* **86**(1-3): 122-124.

Bansal, U.K., Saini, R.G., Rani, N.S. and Kuar, A. (1998). Genetic divergence in quality rice. *Orzya.* **36**(1): 20-23.

Basavaraja, P., Rudraradhya, M. and Kulkarni, R.S. (1997). Genetic variability, correlation and path analysis of yield components in two F4 population of fine grained rice. *Mysore J. Agril. Sci.* **31**(1): 1-6.

BBS, (2004). Bangladesh Bureau of Statistics, Statistics Division, Ministry of Planning, Government of the peoples republic of Bangladesh, Dhaka, Bangladesh. p. 52.

BBS. (1998). Statistical Pocket Book of Bangladesh. Bangladesh Bureau of Statistics. p. 385.

Bhandarkear, S., Ravindra, V., Arvind, K., Verma, R. and kumar, A. (2002). Genetic variability and correlation analysis in early duration rice. *Plant Archives.* **2**(1): 95-98.

Bidhan, R., Basu, A.K., Manda, A.B. and Roy, B. (2002). Genetic diversity in rice (*Oryza sativa* L.) genotypes under humid tropic of Andaman based on grain yield and seed characters. *Indian J. Agril. Sci.* **72**(2): 84-87.

Bidhan, R., Hossain, M., Hossain, F and Roy, B. (2001). Genetic variability in yield components of rice (*Oryza sativa* L.). *Env. and Ecol.* **19**(1): 186-189.

Biswas, P.S., Bishwajit P. and Dewan, S.B.A. (2000). Variability, character association and path analysis in rice (*Oryza sativa* L.). *Bangladesh J. Pl. Breed. Genet.* **13**(1): 19-25.

Borbora, T.K. and Hazarika. G.N. (1998). Study of genetic variability, heritability and genetic advance for panicle characters in rice. *Oryza.* **35**(1): 19-21.

BRRI (Bangladesh Rice Research Institute). (1989). Adhunik Dhaner Chash (In Bengali). Bangladesh Rice Res. Inst. Joydebpur, Gazipur. p. 9.

BRRI (Bangladesh Rice Research Institute). (1995). Annual Report for 1992. BRRI pub No.79. Bangladesh Rice Res. Inst. Joydebpur, Gazipur. p. 237.

Bui Chi Buu and Do Zuang Truong. (1988). Path analysis or rice grain yield.

Burton, G.M. (1952). Quantitative inhertance in Grass pea. Proc. of 6th Int. Grassland Cong. **1**: 277-283.

Buu, B.C. and Tuan, T.M. (1989). Genetic diversity in rice (*Oryza sativa* L.). *International Rice Research Newsletter.* **14**(6): 5.

Catling, D. (1992). Rice in Deep water. International Rice Research Institution, Los Banos, Philippines. pp. 121-125.

Chakaraborty, S. and Hazarika, M.H. (1994). Association analysis between grain yield and its components in rice. *Oryza.* **31**: 263-265.

Chang, T.T. (1985). Crop history and genetic conservation; Rice-a case study. *Iowa state J. Res.* **59**: 425-455.

Chaubey, P.K. and Singh, R.P. (1994). Genetic variability, correlation and path analysis of yield components of rice. *Madras Agril.J.* **81**(9): 464- 470.

Chaudhury, P.K.D. and Das, P.K. (1998). Genetic variability, correlation and path co-efficient analysis in deep-water rice. *Ann. Agril. Res.* **19**(2): 120-124.

Chauhan, J.S. and Chauhan, V.S. (1994). Genetic divergence in rainfed upland rice. *Oryza.* **31**: 103-106.

Chauhan, J.S., Chaulian, V.S. and Varriar, M. (1993). Genetic variation and character association in rainfed upland rice. *Oryza.* **30**: 116-119.

Chookar, S.K., Marakar, R.V., and Siddiqui, M.A. (1994). Genetic variability for grain yield and yield contributing characters in rice. *J. Maharashtra Agril. Univ.* **19**(2): 236-238.

Choudhury, P.K.D., and Das, P.K., (1997). Genetic variability, correlation and path analysis in deep water rice. *J. Agril. Sci. Soc.* North-East India. **10**(1): 155-157.

Comstock, R.E. and Robinson, H.F. (1952). Genetic parameters theidr estimation and significance. Proc. of 6th Int. Grassland Cong. **1**: 128-291.

Courtois, B., Sinha, P. K., Prasad, K. and Carandang, S. (1997). Genetic diversity among upland rice varieties from India and Bangladesh. *International Rice Research Notes.* **22**(3): 8-9.

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

De, R.N. and Surya Rao, A.V. (1988). Genetic variability and correlation studies in rice under semi deep water logged situation. *Oryza.* **25**: 360-364.

Debi, B.R., Ray, P.K.S. and Howladar, M. (1997). Variability and genetic association in irrigated rice. *Prog. Agric.* **8**(1 & 2): 165-168.

Dhananjaya, M.V., Rudraradhya, M., Kulkarni, R.S. and Bhushan, H.O. (1998). Variability and character association in elite lines of rice (*Oryza sativa* L.). Current Research University Agric. Sciences Bangalore. **27**(9-10): 166-168.

Digby, P., Galway, M. and Lane, P. (1989). GENSTAT 5. A second course. Oxford Science Publications, Oxford. pp. 103-108.

Draper, S.R., (1976). Biochemical Analysis in Crop Science. Oxford Univ. Press, Lindon, U.K. p. 1-130.

Duffus, C.M. and Slaughter, J.C. (1980). Seeds and Their Uses, John Wiley and Sons Ltd. Chichester, U.K.

Eggum, B.O., (1979). The nutritional value of rice in comparison with other cereals (In) Proceedings of the Workshop on Chemical Aspect of Rice Grain Quality, International Rice Research Institute, Las Banos, Philippines. p. 91.

Falconer, D.S. (1960). Introduction to quantitative genetic. Oliver and Bond, London. p. 304.

FAO, (1997). Production year book. Food and Agricultural Organization. Rome. Italy. p. 51-64.

FAO, (1999). Quarterly Bulletin of Statistics. Food and Agricultural Organization. Vol. **12** (3/4). p. 18-19.

Ghaderi, A., Shishegar, M., Rigai, A. and Ehdaie, B. (1989). Multivariate analysis of genetic diversity for yield and it's Components in Mungbean. *J. Ameri. Soc. Hort. Sci.* **104** (6): 728-732.

Gomathinayagam, P., Natarajan, S. And Subramanian, M. (1990). Genetic variability in drought tolerant genotypes of rice. *Oryza.* **27**: 328-330.

Gopalan, C., Rama Sastri, B.V. and Balasubramaniyan, S.C. (1980). Nutritive value of Indian Foods. National Institute of Nutrition. Hyderabad, India.

Gupta, A., Sharma, R.K., Mani, V.P. and Chauhan, V.S. (1999). Variability and association analysis for grain yield and its components in hill rices. *Indian J. Hill Research.* **12**(2): 99-104.

Hanamaratti, N.G., Patil, S.J., Nadaf, S.K., Naresh, D, And Dronavalli, N., (1998). Genetic divergence in upland rice (*Orzya sativa* L.) genotypes under lowland and upland conditions. *Karnataka J. Agril. Sci.* **11**(1): 220-222.

Hemareddy, H.B., Manjunath, A. and Shadakshair, Y.G. (1994). Genetic variability for grain yield and its components in the hill zone rice (*Oryza sativa* L.) of Karnataka. *Himachal J. Agril. Res.* **20**(1-2): 75-77.

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

Hossain, M. (1998). Sustaining food security in Asia: economic, social and political aspects. **In**: Dowling, N.G., Greenfield, S.M. and Fischer, K.S. (ed). Sustainability of rice in the global food system. IRRI. p.21-34.

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

Islam, M.R., Faruquei, M.A.B., Bhuiyan, M.A.R., Biswas P.S. and Salam. M.A. (2004). Genetic diversity in irrigated rice. *Pakistan J. Bio. Sci.* **7**(2): 226-229.

Jadhav, P., Sarawgi, A.K., Mishra, L.K., and Pravin, J. (2003). Studied on genetic diversity in rice genotype (*Oryza sativa* L.). *Plant Archives.* **3**(1): 15-19.

Jagadev, P.N., Samal, K.M. and Lenka, L. (1991). Genetic divergence in rape mustard. *Indian J. Genet.* **51**: 465-466.

Jangale, R.D., Sangave, R.A., Ugale, S.D. and Dumbre, A.D. (1985). Studies on variability, heritability and genetic advance for some quantitative characters in upland paddy. *J. Maharashtra Agril. Univ.* **10**(1): 69-70.

Jeger, M.I., Garethojones, D. and Griffith, E. (1983). Components of partial resistance of wheat seedlings of septoria nod rum. *Euphytica.* **32**: 575-584.

Jha, S.K., Awasthi, L.P. and Maurya, D.M. (1999). Genetic diversity in wild rice germplasm of eastern U.P. India. *Oryza.* **36**(2): 157-158.

Jhonson, K.F., Robinson, H.F. and Comstock, R.B. (1955). Genotypic and phenotypic correlation in soybeans and their implication in selection. *Agron. J.* **47**(10): 477-483.

Joshi, A.B. and Dhawan, N.L. (1966). Genetic improvement of yield with special reference to self-fertilization crop. *Ind J. Genet. Pl. Breed.* **26A**: 101-113.

Juji-Kihupi, A. (1988). Interrelationship between yield and some selected agronomic characters in rice. *African Crop Sci. J.* **6**(3): 323-328.

Julfiquar, A.W., Virmani, S.S., Kabir, K.A. and Molla, A.H. (1985). Differential heterosis in some growth physiological characters of indica/ japonica and japonica/ japonica crosses of rice. *Progress. Agric.* **5** (2): 149-156.

Juliano, B.O. (1993). IRRI and FAO. IRCN. p. 43:79.

Katocha, A., Katoch, P.C., and Kaushik, R.P. (1993). Selection parameters among tall and semi-dwarf genotypes in rice. *Orzya.* **30**: 106-110.

Kaw, R.N., Aquino, R.C., Moon, H.P., Yae, J.D. and Haque, N. (1999). Variability and interrelationship in rice under cold stree environments. *Oryza.* **36**(1): 1-4.

Kihupi, A.N. and Doto, A.L. (1989). Genotypic and environmental variability in selected rice characters. *Oryza.* **26**: 129-134.

Kumar, G.S. Mahadevappa, M. and Rudraradhya, M. (1998). Studies on genetic variability, correlation and path analysis in rice during winter across the locations. *Karnataka J. Agril. Sci.* **11**(1):73-77.

Kumar, R., Krishanpal, M., Mondal, S.K., Ramashankar, R., Prashad, S. C. and Rai, R. (1994). Genetic studies of major characters in upland rice. *Env. and Ecol.* **12**(2): 363-365.

Kumar, R.U., Rangasmy, P. and Gomex, S.M. (2003). Phenotypic differentiation in Indica-Japonica wide compatible varieties in rice (*Oryza sativa* L.). *Plant Archives.* **3**(1): 141-142.

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

Li,Q.L., G.T. Guo, G.Z., Jiang, G. and Zhu, Y. (1991). Study on high yield breeding and genetic analysis of yield components of main rice cultivars in Jilin. China. *Henrietta's.* **13**(5): 3-6.

Lin, M.S. (1993). Changes in genetic diversity in the japonica rice region of Taiwan. Botanical Bulletin of Academia Sinica. **34**(4): 307-312.

Loknathan, T.R., Sakhare, R.S., Kamble, T.C. and Maheshwari, I.J. (1991). Genetic variability and heritability in upland rice. (*Oryza satuva* L.). *J. Soils and Crops.* **1**(2): 150-153.

Lu, J. and Chang, T.T. (1980). Rice in its temporal and spatial perspectives. **In**: B.S. Luh (ed). Rice production and utilization. AVI, Davis, California, p.1-74.

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

Mani, S.C., Verma, S.K. and Sharma, R.K. (1997). Genetic variability and character association for panicle traits in Basmati rice. *Agril. Sci. Digest Karal.* **17**(3): 155-157.

Marekar, R.V. and Siddiqui, M.A. (1996). Genetic variability and correlation studies in rice. *J. Maharashatra Agril. Univ.* **21**(2): 249-251.

Maurya, D.M. and Singh, D.P. (1977). Genetic divergence in rice. *Ind. J. Genet. Pl. Breed.* **37**(3): 394-402.

Maurya, D.M., Saugh, S.K. and Singh, R.S. (1986). Genetic variability in 48 lowland rice cultivars of Uttar Prodesh, India. *IRRN.* **11**: 4-13.

Miah, M.A.H. and Islam, Z. (1999). Progress and prospects of rice research in Bangladesh. Paper presented in the Central Improvement Workshop held at BRRI, Gazipur on 06 July 1999.

Mian, M.A.K and Bhal, P.N. (1989). Genetic divergence and hybrid performance in Chickpea. *Indian J. Genet.* **49** (1): 119-129.

Mishra, D. and Dash, S.K. (1997). Genetic diversity and stability in aromatic rice (*Oryza sativa* L.). *Indian J. Agric. Sci.* **67**(1): 27-32.

Mishra, L.K. and Verma, R.K. (2002). Correlation and Path co-efficients analysis for morphological and quality traits in rice (*Oryza sativa* L.). *Plant Archves.* **2**(2): 251-256.

Mishra, L.K., Sarawgi, A.K. and Mishra, R.K. (2003). Genetic diversity for morphological and quality traits in rice (*Oryza sativa* L.). *Advances in Plant Sciences.* **16**(1): 287-293.

Mishra, L.K., Sarwgi, A.K., and Mishra, R.K., (2002). Genetic diversity for morphemically and quality traits in rice (*Oryza sativa*L.*). Advances Pl. Sci.* **16**(1): 287-293.

Mishra, R., Rao, S.K. and Koutu, G.K. (1988). Genetic variability, correlation studies and their implication in selection of high yielding genotypes of chickpea. *Ind. J. Agric. Res.* **22**(1): 51-57.

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

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

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

Moon, M.K., Sakhare, R.S. and Patil, A.J. (1996). Variability, heritability and genetic advance studies in upland paddy. *Bioved.* **7** (1): 79-82.

Narendra, C. and Reddy, R. (1997). Variability and heritability in hybrid genotypes of rice. *Agric. Science Digest Karnal.* **17**(2): 139-140.

Naskar, S.K. and Srinivasan, G. (1985). Genetic divergence in sweet potato. *J. Root crops.* **11** (1-2): 57-59.

Nejad, K.Z., Mirlohi, A.F., Zadeh, G.N. and Rezai, A. (2004). Genetic diversity in some of Iranian rice (*Oriza sativa* L.) germplasm based on morphological traits. *J. Sci. Tec. Agril. and Natural Resources.* **7**(4): 199-214.

Nevo, E., Golenberg, E., Beilies, A., Brown, A.H.D. and Zohary, D. (1982). Genetic diversity and environmental associations of wild wheat. *Triticum dicoccoides* in Israel. *Theor. Appel. Genet.* **62**: 241-254.

Niranjana, M., Kulkarni, R.S., Udaykumar, M. and Murthy, N. (1999). Genetic variability, heritability and genetic advance for morpho-physiological traits in rice. *Oryza.* **36**(2): 159-160.

Pandey, V.K. and Awasthi, L.P. (2002). Studies on genetic variability for yield contributing traits in aromatic rice. Crop Research Hisar. **23**(2): 214-218.

Paramasivan, K., Giridharan, S. and Soundararaj, A.P.M.K. (1995). Genetic variability and character association of derived panicle characteristics of rice genotypes. Crop Res. Hisar. **10**(3): 285-290.

Paramasivan, K.S. and Rangasamy, S.R. (1988). Study on variability and genetic advance in quantitative characters in rice. *Oryza.* **25**: 301-306.

Pattanayak, A. and Gupta, H.S. (1999). Genotypic variability and character association in upland rice genotypes developed through anther culture for mid altitude areas of Meghalaya. *Indian. J. Hill farming.* **12**(2): 100-105.

Patwary, A.K. (1991). Yield performance and stability of some promising advanced generation lines of rice under different growing conditions. *Prog. Agric.* **2**(1): 65-70.

Paul, S.K. and Sarmah, A.K. (1998). Interrelationship of yield and yield contributing characters in upland rice. *J. Agril. Sci. Soc.* North-East India. **10**(2): 164-167.

Paul, S.K., and Sarmah, A.K. (1997). Interrelationship of yield and yield contributing characters in upland Aus rice. *J. of the Agril. Sci. Society of North-East India.* **10**(1): 165-168.

Pereira, J.J. and Cruz, C.D. (2003). Comparison of clustering methods for the study of genetic diversity in rice cultivars. *Revista Ceres.* **50**: 41-60.

Peyne, R.W., Lane, P.W., Ainsley, A.E., Bicknell, K.E., Digby, P.G.N., Harding, S.A., Leach, P.K., Simpson, H.R., Todd, A.D., Varrier, P.J. and White, R.P. (1989). GENSTAT 5 Reference manual, Oxford Science publication. pp. 452-490.

Pradhan, B., Mishra, P.K., Sinha, S.K., Muduli, K.C. and. Pradhan, S.K. (1996). Relative efficiency of different numerical methods in assessing genetic diversity of micromutants in rice. *Environment and Ecology.* **14**(2): 394-398.

Prathepha, P. (1995). Genetic diversity of traditional upland rice in northeast Thailand. *Khon Kaen Agriculture Journal.* **23**(1): 24-30.

Pravin, J., Sarawgi, A.K., Mishra, L.K. and Pravin, J. (2003). Studies on genetic diversity in rice genotypes (*Oryza sativa* L.). *Plant Archives.* **3**(1): 15-19.

Pushpa, K., Singh, D.N., Singh, M.P., Maque, M.F. and Kumari, P. (1999). Genetic variability in gora rice (*Oryza sativa* L.). *J. Research, Birsa Agricultural University.* **11**(1): 23-26.

Ramalingam, I., Nadarajan, N., Variarajan, C., Rangasams. P. and Arumugapillai, M. (1994). Character assertion and component analysis for panicle architcture in rice (*Oryza sativa* L). *Agril. Sci. Digest Karnal.* **14**(2): 136-140.

Ramanujam, S., Tiwary, A.S. and Mehra, R.B. (1974). Genetic divergence and hybrid performance in Mungbean. *Theor. App. Genet.* **44** (5): 211-214.

Rao, S.S. and Shrivastava, M.N. (1994). Genetic variation and correlation studies in rainfed uplant rice. *Oryza.* **31**: 288-291.

Rao. C. R. (1952). Advance Statistical Method in Biometrical Research. *Edul. John Willey and Sons.* New York. p. 19.

Rashid, M.M. (1994). Rice production in Bangladesh. Programmes, achievements, potentials and challenges. *IRCN.* **43**: 9-18.

Reddy, J.N., Pani, D. and Roy, J.K. (1997). Variability and character association in lowland rice. *Indian Agricualturist.* **41**(3): 159-165.

Reddy, Y.S. and Kumar, P.V.R. (1996). Studies on genetic variability, correlation and path analysis in rice. *New Botanist.* **23**(1-4): 129-133.

Roy, B., Basu, A.K., Mandal, A.B. and. Roy, B. (2002). Genetic diversity in rice (*Oryza sativa*) genotypes under humid tropics of Andaman based on grain yield and seed characters. *Indian J. Agril. Sci.* **72**(2): 84-87.

Sadhukhan, R.N. and Chattopadhyay, P. (2000). Variability and character association between yield attributes and grain quality in aromatic rice. *J. interacademicia.* **4**(4): 494-497.

Sarathe, M.L. and Perraju, P. (1990). Genetic divergence and hybrid performance in rice. *Oryza.* **27**(3): 227-231.

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

Sawant, D.S. and Patil, S.L. (1995). Genetic variability and heritability in rice. *Ann. Agril. Res.* **16**(1): 59-61.

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

Sawant, D.S., patil, S.L and Sodaye, V.G. (1995). Genetic variability and heritability in segregating generation of rice crosses. *Ann. Agril. Res.* **16**(2): 201-205.

Sawant, D.S., Patil, S.L. and Bhave, S.G. (1994). Variability, heritability and genetic advance in pure lies of low land rice. *Ann. Agril. Res.* **15**(1): 27-30.

Shaha Ray, P.K., Ahmed, H.U., Nahar, K. Bose, G.K. Miah, N.M., Islam, M.A. and Ibrahim, S.M. (1993a). Correlated response and path analysis in irrigated rice. *Bangladesh J. Pl. Breed. Genet.* **6**(1): 19-23.

Shaha Roy, P.K., Nahar, K., Ahmed, H.U., Mia, N.M. and Islam, M.A. (1993b). Genetic variability and character association in irrigated rice. *Bang. J. Pl. Breed. Genet.* **6**(1): 69-74.

Shanthakumar, G., Mahadevappa, M. and Rudraradhya, M. (1998). Studies on genetic variability, correlation and path analysis in rice (*Oryza sativa* L.) over seasons. *Karnataka J. Agric. Sci.* **11**(1): 67-72.

Shanthi, P. and Singh, J. (2001). Genetic divergence for yield and its components in induced mutants of Mahsuri rice (*Oryza sativa* L.). *Res. on . Crops.* **2**(3): 390-392.

Shanthi, P. and Singh, J. (2001). Variability in induced mutants of Mahsuri rice (*Oryza sativa* L.). *Madaras Agril. J.* **188**(10-12): 707-709.

Sharirame, M.D. and Muley, D.M. (2003). Variability and correlation studies in rice (*Oryza sativa* L.). *J. Soils and Crops*. **13**(1): 165-167.

Shiv, D., Dani, S.C. and Datt, S. (2003). Genetic divergence in elite genotypes of basmati rice (*Oryza sativa* L.). *Ind. Genet. Pl. Breed.* **63**(1): 73-74.

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

Singh, R.K. and Chaudhury, B.D. (1979). Biometrical methods in quantitative genetic analysis. Kalyani Publications. New Delhi.

Singh, R.K. and Chaudhury, B.D. (1985). Biometrical Method in Quantitative Genetic Analysis (rev. edition). Kalyani Publishers. New Delhi, India.

Singh, R.S., Chauhan, S.P. and Maurya, D.M. (1986). Genetic variability in 98 upland rice cultivars of India. *IRRN.* **11**(4): 9-10.

Singh, S. and Chaudhury, B.S. (1996). Variability, heritability and genetic advance in cultivars of rice. Crop Res. Hishar. **12**(2): 165-167.

Singh, S.B.; Srivastava, R.K., Giri, S.P. and Yadav, L. (1998). Heritability, genetic advance and correlation studies in indigenous rice (*Oryza sativa* L.). *J. Living World*. **5**(1): 11-14.

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

Steel, R.G.D. and Torrie, J.H. (1960). Principals and procedures of statistics. Mc Grow-Hill Book Co. Inc. New York. pp. 107-109.

Thakur, S.K., Choubey, S.K. and Sharma, N.P. (1998). Genetic variability and character association in F2 (Anupama X IR 36) population in rice (*Oryza sativa* L.). *Agric. Science Digest Karnal.* **19**(3): 187-190.

Toenniessen, I.I. (1984). Review of the World Food Situation and the role of salt tolerant plants. Staples. Richards, C. and Tonniessin, Gray, H. (End). John Wiley and Sons. p.399.

Tomooka, N. (1991). Genetic diversity and landrace differentiaton of mungbean (*Vigna radiate* L.) and evaluation of its wild relatives (the subgenus ceratotrophics) as breeding materials. Tech, Bull, Trop. Res. Centre. Japan. Ministry of Agr. Forestry and Fisheries. Japan. p.28:1.

Vange, T., Ojo, A.A. and Bello, L.L. (1999). Genetic variability, stability and correlation studies in lowland rice genotypes . *Ind. J. Agril. Sci.* **69**(1): 30-33.

Venkataramana, P., Shailaja H. and Hittalamani, S. (1999). Genetic variability on some important traits in two F2 segregants of rice (*Oryza sativa* L.) under non-submergence condition. Crop Research Hisar. **18** (1):53-56.

Venuprasad, R., Latha, J., Shashidhar, H.E. and Hittalmani, S. (2002). Evaluation of genetic diversity among rice cultivars adapted to rainfed low lands of southern Karnataka. I. Yield and related traits. Crop Research Hisar. **23**(3): 501-506.

Vishwakarma, D.N.B., Maurya, D.M. and Maurya, K.N. (1989). Heritability and genetic advance for yield and its components in rice. *Narendra Deva J. Agril. Res.* **4**(1): 37-39.

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

Vivekanandan, P. and Subramanian, S. (1993). Divergence in rainfed rice. *Oryza.* **30**: 60-62.

Wilpeed Manual, W. and Prasad, M.N. (1993). Genetic variability in medium duration rice. *Oryza.* **30**: 355-356.

Yadav, R.K. (1992). Genetic variability, correlation studies and their implication in selection of high yielding genotypes of rice. *Adv. Pl. Sci.* **5**: 306-312.

Yadav, R.K. (2000). Studied on genetic variability for some quantitative characters in rice(*Oryza sativa* L.). *Adv. Agril. Res. India.* **13**: 205-207.

Yadav. R.K. (2001). Variation in local accessions of rice collection under rainfed condition in Chattisgarh. *Indian J. Dry land Agril. Res. Development.* **16**(2): 168-169.

Zeng, X.P. and Wang, L.X. (1988). A study on the genetic parameters for quantitative characters of high yielding rice in Ningxia. *Ningzia J. Agro. Forestry Tech.* **3**: 7-12.

Chapter 7

Appendices

APPENDIX

Appendix I. Monthly average air temperature, relative humidity, rainfall, sunshine of experimental site during the period from November 2005 to May 2006

Month	**Air temperatures(^{0}C)			**Humidity (%)		*Rainfall	**Sunshine (hrs.)
	Max.	Min.	Aver.	9AM	2PM		
November	28.21	15.15	21.05	74.67	55.27	Nil	8.12
December	27.55	14.42	20.98	73.12	52.61	Nil	7.56
January	25.55	12.43	18.99	78.87	45.90	Nil	6.72
February	31.18	18.41	24.80	76.03	45.31	Nil	7.21
March	33.65	20.19	26.92	67.80	39.80	Nil	8.46
April	33.65	22.85	28.25	77.76	61.03	95.2	7.60
May	34.03	24.87	29.45	77.38	62.80	465.0	6.39

*Monthly total, **Monthly average Source: Plant physiology division, BRRI, Gazipur.

Appendix II. Principal components score for forty rice genotypes

Genotype number	Z_1	Z_2
G1	-11.847	-2.962
G2	-16.359	7.607
G3	-25.079	4.628
G4	-20.363	12.652
G5	35.901	12.700
G6	-20.966	-12.111
G7	-1.945	-1.465
G8	-9.495	-8.153
G9	-20.107	10.660
G10	-12.283	0.363
G11	12.694	0.792
G12	-4.834	-1.591
G13	13.795	-5.466
G14	9.223	6.832
G15	4.597	-2.872
G16	-4.051	-1.382
G17	-1.738	-10.191
G18	8.084	0.209
G19	-2.572	-0.349
G20	-1.020	-2.538
G21	10.990	-4.378
G22	1.534	3.035
G23	-2.971	-12.372
G24	17.043	-7.205
G25	21.173	0.301
G26	-18.895	-23.203
G27	-3.014	-5.438
G28	-2.573	-8.647
G29	6.205	-8.094
G30	-5.003	-1.229
G31	-47.159	42.310
G32	-2.811	0.948
G33	9.546	7.721
G34	74.684	21.031
G35	8.317	-11.593
G36	11.999	1.290
G37	6.205	3.393
G38	.616	-6.483
G39	-7.885	-5.269
G40	-9.636	6.524