CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS IN NEW PLANT TYPE RICE (*indica* / *japonica*)

BY

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CERTIFICATE

*This is to certify that thesis entitled, "**Characterization and Genetic Diversity Analysis in New Plant Type Rice (indica / japonica)** " submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **MAFRUHA MOSTARY** , Registration No. **011-84** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated : December, 2008
Place : Dhaka, Bangladesh

(Dr. Md. Sarowar Hossain)
Supervisor

Dedicated to
My
Beloved Parents

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The Author

LIST OF ABBREVIATED TERMS

FULL NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	*et al.*
Bangladesh Rice Research Institute	BRRI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of Variation	CV
Days After Transplanting	DAT
Degree Celsius	^{o}C
Degrees of Freedom	d.f
Etcetera	etc.
Figure	Fig.
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	δ^2_g
Gram	G
Hectare	ha
Heritability in broad sense	h^2_b
Journal	J.
Kilogram	Kg
Meter	M
Mean Sum of Square	MSS
Millimeter	mm
Muriate of Potash	MP
Number	no.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic Variance	δ^2_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Standard Error	SE
Square Meter	m^2
Triple Super Phosphate	TSP
Genotypic Mean Square	GMS

LIST OF ABBREVIATED TERMS (Cont'd)

FULL NAME	ABBREVIATION
Error Mean Square	EMS
Analysis of Variance	ANOVA
Pollen Parent	PP
Advanced Line	AL
Restorer	R
Conventionally Bred	CB
Double Haploid	DH
Dry Matter Production	DMP

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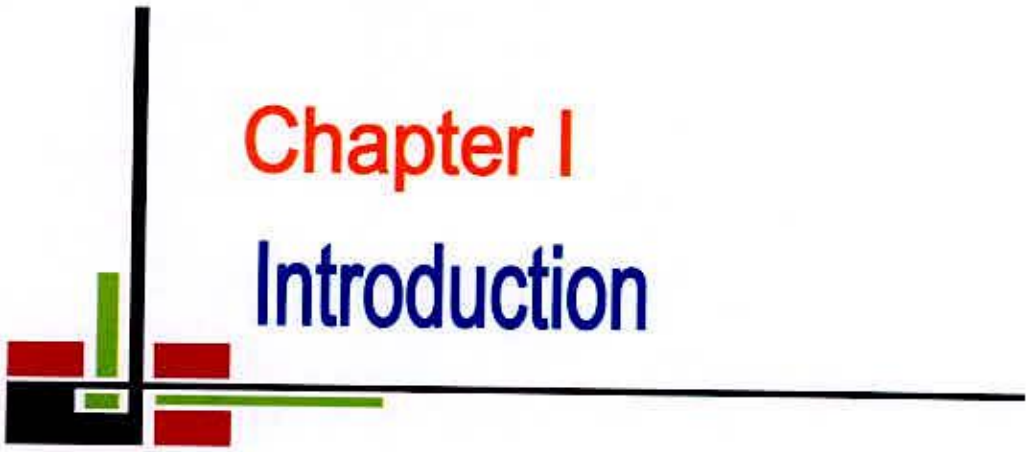
CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS IN NEW PLANT TYPE RICE (*indica / japonica*)

BY

MAFRUHA MOSTARY

ABSTRACT

The morphological characters, genetic diversity, genotypic and phenotypic variance, genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean were studied for 60 NPT genotypes of rice during December 2007 to May 2008 at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka. Significant variation was observed among all the genotypes for all the characters studied. Considering genetic parameters, high genotypic coefficient of variation (GCV) was observed for grain yield per plant followed by filled grains per panicle, effective tillers per plant and total tillers per plant, whereas days to maturity showed very low GCV. High heritability with low genetic advance in percent of mean was observed for days to 50% flowering which indicated that non-additive gene effects were involved for the expression of this character and selection for such trait may not be rewarding. High heritability with moderate genetic advance in percent of mean was observed for plant height indicated that this trait was under additive gene control and selection for genetic improvement for this trait would be effective. Multivariate techniques were used to classify the sixty genotypes and six clusters were formed. Cluster IV had maximum 15 genotypes and cluster I had only four genotypes. The highest intra-cluster distance was observed in cluster II. The highest inter-cluster distance was observed between the cluster I and II and the lowest was between cluster III and V. Analyzing diversity pattern and other agronomic performance, the inter genotypic crosses between G4 and G13, G4 and G27, G13 and G21, G60 and G54 may be used for future hybridization program.



Chapter I

Introduction

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the genus Oryza and family Gramineae (Roy, 1985). It is second most important food crop next to wheat. Rice is a major source of livelihood in terms of providing food income and employment in Bangladesh. Particularly the poor farmers of the country feel that without production of rice there is no food security of their family household.

Rice is the staple food for the people of Bangladesh. Food scarcity has been and will remain a major concern for Bangladesh as population growth is 1.21%. Rice contributes 14.6% to the national GDP (BBS, 2004) and supplies 71% of the total calories and 51% of the protein in a typical Bangladeshi diet (BBS, 1998). Rice accounts for about 40% of the employment and covers about 75% of total cropped area (Choudury, 1999).

In Bangladesh rice is grown in 10.579 million hectares and production is 27.318 million metrictons with average yield is 2.58 tons per hectare (BBS, 2006-2007).

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. 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. "Farmers will have to produce 40 to 50 percent more rice with improved quality to meet consumer demand in 2025," says Ronald Cantrell, IRRI's Director General. To help meet those goal Asian farmers may soon begin planting a new type of rice that could raise global output 15 percent by 2004. IRRI has worked to perfect the new rice plant type since 1990 using conventional breeding techniques. Each of the new plants has six to ten productive stems that can hold upwards of 250 grains. Conventional varieties have just 14 to 15 productive stems that only hold about 100 grains.

Good plant type is the foundation for super high yield. Since the concept of ideotype was proposed by Dr Donald, rice breeders have proposed several models for super high-yielding rice. The most famous is the "new plant type" proposed by Dr Khush. Its main features are: big panicles (250 spikelets per panicle), fewer tillers (3-4 productive tillers per plant), and short and sturdy culm. Experience will show whether or not this model can realize super high yield.

The New Plant Type (NPT) rice has been developed with the target to increase the yield potential of rice by 20-25% (Khush, 1995). One could thus, increase yield by increasing the proportion of heavy or high density grains. Panicle architecture should viewed with equal importance in order to develop yield performance of rice. Larger panicle, a greater number of filled grains would be suitable selection criteria for increasing rice yield. New plant type (NPT) advanced lines are ideal for increasing the biomass per unit area and hence grain yield by planting less profuse tillering but high panicle weight genotypes at high density by manipulating crop geometry. For effective use of advanced lines of NPT (*indica / japonica*) in hybridization program it is necessary to characterize all the advanced lines to know the genetic and morphological nature so as to exploit it

practical breeding program. In order to identify the promising advanced lines of NPT with enhanced genetic yield potential combining grain size for commercial cultivation as well as for use as donors for major yield traits in the breeding program. Therefore, characterization of the advanced NPT rice genotypes is considered to be most important.

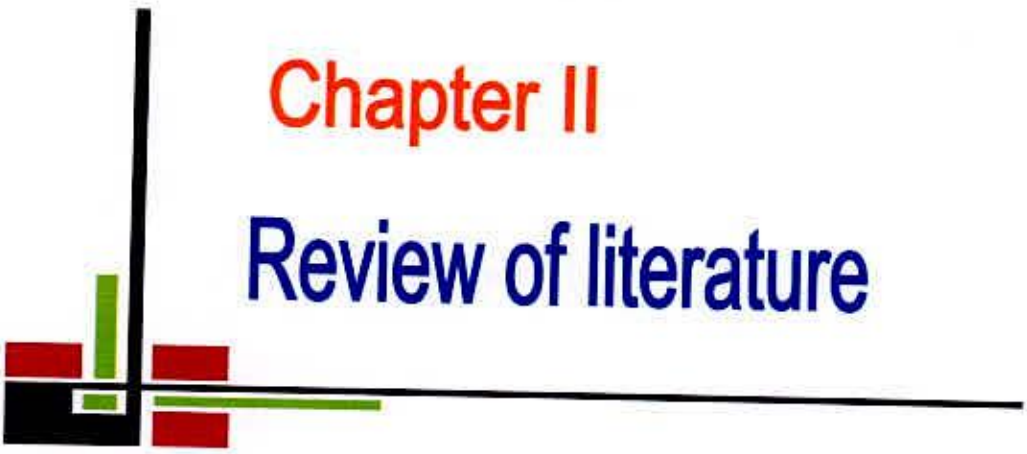
A survey of genetic variability with the help of suitable parameters such as genotypic coefficient of variation, heritability and genetic advance are absolutely necessary to start an efficient breeding programme (Mishra *et al.* 1988).

In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed. Variability and genetic diversity are the fundamental law of plant breeding which is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973). The quantification of genetic diversity through biometrical procedures such as Mahalanobis's D^2 - statistic and Canonical Variate Analysis (CAV) have possible to choose genetically diversed parents. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis. More diverse parents (within a limit) in hybridization is supposed to increase the chance of obtaining maximum heterosis and give broad spectrum of variability in segregating generations.

Keeping the above hypothesis in view the proposed study with NPT advanced lines of rice, therefore undertaken with the following objectives.

Objective(s):

- To characterize the morphological and yield component of NPT rice.
- To study genetic variability of some important quantitative characters among rice germplasms.
- To assess the contribution of the different traits towards divergence.
- To study genetic diversity among genotypes to screen suitable diverse germplasm for the utilization in hybridization programme.



Chapter II

Review of literature

CHAPTER II

REVIEW OF LITERATURE

The present experiment has aimed at studying the genetic variability and genetic diversity of 60 NPT rice genotypes and relationship between yield and yield contributing characters. In this chapter, some of the available information's most relevant to the present study are reviewed under the following headings:

2.1 Characterization of rice genotypes

2.2. Genetic diversity

2.1. CHARACTERIZATION OF RICE GENOTYPES

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.

The first-generation NPT lines based on tropical japonicas were developed in 1993. As intended, the NPT lines had large panicles, few unproductive tillers, and lodging resistance. They did not yield well, however, because of limited biomass production and poor grain filling. It was speculated that the excessive reduction in tillering capacity resulted in low biomass production of the first-generation NPT lines. The first-generation NPT lines were susceptible to diseases and insects, and had poor grain quality, thus the lines could not be released as cultivars but were valuable genetic materials for rice breeding programs (Peng and Khush, 2003).

In 1995, development of the second-generation NPT lines was begun by crossing the first-generation tropical japonica NPT lines with elite indica

parents. Indica parents have effectively increased tillering capacity and reduced panicle size (i.e., number of spikelets per panicle) in the second-generation NPT lines. Indica germplasm also helped improve other NPT attributes such as grain quality and disease and insect resistance. Some second-generation NPT lines (F_5 generation) were planted in a replicated observational trial for the first time in the 1998 wet season). Overall, the second-generation NPT lines showed yield advantage over the first-generation NPT lines. A rigorous comparison between the second-generation NPT lines and indica inbred varieties is needed, however, to determine the progress of improving rice grain yield by NPT breeding (Laza *et al.* 2003).

The development of NPT rice at IRRI was inspired by (Donald, 1968) ideotype breeding approach. The goal was to develop NPT cultivars with a yield potential 20 to 25% higher than current existing semidwarf rice cultivars under a tropical environment during the dry season. The NPT was designed based on the results of simulation modeling and the new traits were mostly morphological since they are easier to select than physiological traits in breeding programs.

Chakraborty and Hazarika (1994) reported high heritability with moderate genetic advance for days to flowering, which was mostly due to non-additive gene action.

Durai *et al.* (2001) studied heritability in 10 conventionally bred (CB) and 9 double haploid (DH) lines in rice and recorded high heritability (broad sense) for days to 50% flowering.

Twenty semi deep water scented local rice varieties were studied by Tripathi *et al.* (1999) for yield components at Ambikapur in kharif 1997-98. Plant height and panicle length exhibited high genotypic and

phenotypic variation. High genotypic coefficient of variation and heritability and genetic advance were observed for grain yield.

Shanthakumar *et al.* (1998) reported that significant genotypic coefficient of variability together with high heritability and genetic advance for plant height, total tillers per hill, flag leaf length and grain yield/ha indicated gene effects were important for those characters.

Gupta *et al.* (1999) studied genetic variability for grain yield and its component traits in 95 genotypes of rice and found high heritability and low genetic advance for days to flowering.

Pattanayak and Gupta (1999) evaluated nine rice genotypes for genetic variability and character association and found days to flowering had high value of heritability and genetic advance.

Sarma *et al.* (1996) evaluated 39 upland rice genotypes for the estimation of genetic variability. The significant mean sum square indicated strong variability for days to 50% flowering. Though the character had high value of heritability (92.8%), it had low (GCV).

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

Binse *et al.* (2004) carried out an experiment on 44 breeding lines and found that low genotypic and phenotypic coefficient of variations for breadth of paddy, panicle length, length of paddy and days to 50 percent flowering. Moderate genotypic and phenotypic coefficient of variations were shown by effective tillers per plant, total number of spikelets per panicle and plant height.

High genotypic and phenotypic coefficients of variations were expressed by harvest index, total number of filled spikelets per panicle, 1000-grain weight and spikelet fertility percentage (Iftekharuddaula *et al.* 2001a).

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.

Information 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 (Niranjana *et al.* 1999).

Iftekharuddaula *et al.* (2001b) studied 24 modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for yield and its component characters. All the characters tested were showed significant variation among the varieties. The highest genetic variability was obtained in spikelets per panicle and grains per panicle. High heritability together with high genetic advance in percentage of mean was observed in plant height, 1000-grain weight, grains per panicle and spikelets per panicle.

Singh and Chaudhury (1996) estimated genetic variability, heritability and genetic advance for 12 characters in 100 genotypes of rice. Plant height showed high heritability together 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.

Thakur *et al.* (1999) studied genetic variability and correlations among grain yield and its attributing traits in an F_2 population in rice. High heritability coupled with high genetic advance were estimated for biological yield, panicle weight, branches per panicle and grains per panicle, and indicated the major contribution of additive gene action for expression of these characters. Correlation studies suggested that grain yield had a positive association with plant height, tillers per plant, panicle weight, biological yield and harvest index.

Both genotypic and phenotypic variances were found highly significant in all the traits little higher phenotypic variations as usual. Similarly the low differences between the genotypic and phenotypic coefficient of variation indicated low environmental influences on the expression of the character. High heritability coupled with high genetic advance of yield, grains per panicle, days to flowering and height suggested effective selection for the improvement of these characters could be made. Direct and indirect effect of these characters through path coefficient analysis supported the significant positive correlation coefficients at genotypic and phenotypic levels for plant height, panicle per hill, panicle length and 1000-grain weight on yield. Thus selection on yield in rice through these characters will be effective as reported by Hossain and Hoque (2003).

Paramasivan (1991) studied the performance of seven yield components and found significant positive correlation for grain yield with plant height, productive tillers, panicle length and 100-grain weight.

Mirza *et al.* (1992) in a study with six crosses and five parental rice genotypes observed that plant height was positively correlated with panicle length and 1000-grain weight. Grain yield was found to be positively correlated with 1000-grain weight and number of grains/panicle and suggested that panicle length, number of grains/panicle and number of panicles/plant should be used as selection criteria.

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 (%).

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 coefficient of variation together with high to moderate heritability and genetic advance were observed for productive tillers/plant.

Shavani and Reddy (2000) reported that high genetic advance was exhibited by harvest index, total number of chaffy spikelets per panicle, grain per plant, total number of filled spikelets per panicle and spikelets fertility percentage. High heritability with high genetic advance indicates heritability due to additive gene effects and selection may be effective for related characters.

Gupta *et al.* (1999) studied the variability and association analysis for grain yield and its components and indicated the improvement of additive gene action. Biological yield per plant, harvest index and grain yield exhibited positive correlation with panicle length and suggested that trail can be used for higher yields.

Diao *et al.* (1999) observed the contribution rates of yield components to grain yield were in order of grain yield per plant, panicles per plant, grains per plant, 1000-grain weight and spikelet fertility. They concluded that higher grain per panicle and 1000-grain weight should be selected.

Cheema *et al.* (1998) reported that yield/plant showed highly significant positive correlation with grains/panicle and panicle length. They also observed that number of grains/panicle had high significant positive correlation with panicle length.

Debi *et al.* (1997) made correlation studies in 29 irrigated rice genotypes. In most cases, genotypic correlations were higher than phenotypic correlations. Plant height and filled grains per plant showed highly significant positive correlation with grain yield/plant both at genotypic and phenotypic levels whereas panicle length showed significant positive association only at genotypic level. Panicles/plant was negatively correlated with grain yield/plant.

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

A field experiment was conducted by Vange *et al.* (1999) at Makurdi during 1994-95 to evaluate 10 early duration rainfed lowland rice genotypes for grain yield and its 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 30.9g, grain per 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.

Li *et al.* (1991) studied path analysis in nine rice cultivars for yield components and showed grains/panicle had the highest direct effect on yield/plant, followed by 1000-grain weight and effective tillers/plant.

Bui Chi Buu *et al.* (1988) studied path coefficient for six characters in rice and reported that number of filled grains/panicle and sterility (%) had the greatest direct effect on yield and are recommended as selection criteria under saline condition.

Akhter *et al.* (2004) concluded that the higher coefficient of variation was found in case of flag leaf area followed by panicles per m^2, 1000-grain weight and spikelets per panicle. High heritability with high genetic advance in percent of mean was found in panicles/m^2, flag leaf area and 1000-grain weight.

Pushpa *et al.* (1999) studied 50 genotypes of gora (upland) rice for 10 quantitative traits in kharif 1995. They observed high heritability for 1000-grain weight, days to 50% flowering, days to 100% flowering and grain per plant.

The nature and magnitude of genetic variability, interrelationship and co-heritability were studied for different yield and quality characters in 11 induced promising mutants along with mother variety- 'Taraori' during kharif, 2001. High genetic coefficient of variation, high to moderately high values of heritability and high genetic advance expressed as percent of mean was observed for grains per panicle, grain weight per panicle, effective tiller per plant and grain yield per plant among quantitative traits, where as for amylase content and alkali digestion value among quality traits. The grain yield/plant had high positive correlation and coheritability values with plant height, days to flowering, days to maturity, 100-grain weight, kernel breadth, amylase content and alkali

digestion values. It revealed that 75 continuous selection of these component traits would be effective for bringing simultaneous improvement in grain yield of basmati rice (Singh and Singh, 2004).

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.

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%).

Genetic variability for yield and its component was calculated in 124 rainfed landraces of rice by Yadav (2001) and found the presence of significant variability for days to maturity.

Kumari *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses and found that plant height exhibited high phenotypic and genotypic coefficient of variation, heritability and genetic advance.

Ali *et al.* (2000) studied genetic variability and broad sense heritability in F_2 population of *Oryza sativa* and found that heritability estimates were maximum for number of tillers/plant.

Yadav (2001) evaluated genetic variability for yield and its components in 124 rainfed landraces of rice for genetic variability and found significant variability for number of tillers/plant.

Kaw *et al.* (1999) evaluated 94 rice genotypes for genetic variability. They observed low genetic variation with high heritability (82.6%).

Shanthi and Singh (2001) studied variability in induced mutants of Mashuri rice and found high heritability (broad sense) for panicle length.

Bhandarkar *et al.* (2002) evaluated genetic parameters of variability in 52 early duration genotypes of rice and found that heritability estimates were high for panicle length. High heritability coupled with high genetic advance as (%) of mean was observed for plant height.

Kumari *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses and found high heritability coupled with moderate genetic advance for panicle length.

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

Yadav (2000) studied genetic variability of yield and yield components in 15 genotypes of rice and found that considerable amount of genotypic coefficient 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.

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

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

Shanthi and Singh (2001) studied variability in induced mutants of Mashuri rice. Heritability in the broad sense was high for plant height.

High heritability coupled with high genetic advance was observed in plant height.

Mishra and Verma (2002) evaluated 16 rice parental cultivars and 72 F_1 progenies in rice and showed high heritability coupled with high genetic advance for plant height.

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.

Genetic variability in 20 genetically diverse irrigated rice genotypes were studied by Shaha *et al.* (1993b). The genotypes revealed significant difference for all the traits with wide range of variability. Heritability estimate and genetic advance were high for filled grains/panicle.

In a study on yield and its component traits in 81 genotypes of rice. Hemareddy *et al.* (1994) observed a higher PCV than GCV for grains/panicle. Grains/panicle had high genetic advance indicating better scope for selection.

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 coefficient 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 six yield related traits in F_4 generation of rice, found that expected genetic advance and heritability

were high for grains/panicle. A high coefficient of variation and high value of heritability together with high expected genetic advance were also observed.

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

Shrirame and Muley (2003) carried out genetic variability study in rice hybrids TNRH 10, TNRN 13, TNRH 18 and cultivar Jaya and found maximum coefficient of variability for number of sterile spikelets per panicle.

Ali *et al.* (2000) observed genetic variability in F_2 population of *Oryza sativa* and found that heritability (broad sense) estimates were maximum for 100 seed weight.

Bidhan *et al.* (2001) studied genetic variability, heritability and genetic advance for yield and yield component in 25 medium duration rice genotypes, and found that heritability ranged from 50% to 90%. High heritability coupled with moderate to high genetic advance for 1000-grain weight.

Mishra and Verma (2002) evaluated 16 rice parental cultivars and 72 F_1 progenies and found that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation (GCV). 100-grain weight showed high heritability coupled with high genetic advance.

Kumari *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses and found high phenotypic and genotypic coefficient of variation, heritability

and genetic advance for 100-grain weight. 100-grain weight showed high heritability coupled with moderate genetic advance indicating the role of non-additive gene effect in the inheritance of this trait.

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

Reddy *et al.* (1997) evaluated 36 genotypes of low land rice and found high coefficient of variation and high heritability for grain yield/plant.

Meenakshi *et al.* (1999) evaluated 10 rice genotypes for eight yield and physiological components and found that productive tillers/plant, grains/panicle, dry matter production (DMP) and harvest index were positively correlated with grain yield.

Vange *et al.* (1999) conducted an experiment to evaluate 10 early duration rainfed lowland rice genotypes for grain yield and its components. Genotypic correlation of yield with grain weight/panicle, grains/panicle were significant and positive but non-significant for 1000-grain weight, panicle length, panicles/m^2 and 50% heading (days), 1000-grain weight had high positive correlation with grain weight/panicle at genotypic level and positively correlated with grains/panicle and grain weight/panicle at phenotypic level but negatively correlated with panicles/m^2 at the both levels.

Kato (1999) estimated correlation coefficient of yield attributes in some rice genotypes and found significant positive relationships between minimum tiller number and panicle number.

Nayak *et al.* (2001) studied genotypic and phenotypic correlation for 10 quantitiative characters of 200 scented rice genotypes and reported that

grain yield/plant showed positive correlation with plant height, panicle number/plant, panicle length, total number of spikelets/panicle and total number of grains/panicle at both genotypic and phenotypic levels.

Shanthi and Singh (2001) conducted an experiment with 17 rice genotypes and studied six quantitative characters. Genotypic correlation coefficients were generally higher than the phenotypic correlation coefficients. They recorded significant negative genotypic correlation coefficient between 1000-grain weight and grain yield/plant. They also found significant negative genotypic and phenotypic correlation coefficient between 1000-grain weight and the number of grains/panicle.

Bhandarker *et al.* (2002) studied correlation analysis in 52 early duration genotypes of rice and found yield per plant had positive significant association with days to 50% flowering, maturity, plant height, number of total grains panicle and number of filled grain per panicle.

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

Bao (1989) performed path analysis for main economic characters in 10 japonica rice. The result showed that the number of filled grains/panicle had the greatest direct effect on grain weight/plant, followed by 1000-grain weight and effective panicles/plant. The indirect effect of panicle length to grain weight/plant via filled grains/panicle was also important.

Bagali *et al.* (1999) studies path coefficient analysis for yield-related attributes in 114 homozygous lines of rice. Panicle weight followed by number of grains/panicle had the greatest positive direct effect on grain yield/plant at the phenotypic level.

Meenakshi *et al.* (1999) studied path analysis and observed high positive direct effects of dry matter production on grain yield.

Path coefficients analysis was studied for eight quantitative characters in 33 rice genotypes by Babu *et al.* (2002). The plant height and productive tillers/plant were the principal characters responsible for single plant yield. Plant height recorded highest positive effect on single plant yield via positive indirect effect of panicle length, number of grains/panicle. Selection based on these characters would be efficients.

2.2. Genetic diversity

Mishra and Das (1997) estimated genetic diversity among 10 promising aromatic genotypes of rice using D^2 values. They grouped 10 genotypes into four clusters.

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

An experiment was conducted by kumar *et al.* (2004) to assess the genetic diversity among 50 restorers. They indicated that all the restorer lines were grouped into eight clusters indicating that the high level of variability exist among the lines. The biological yield contributed height (32%) towards divergence followed by panicle length (28.7%), plant height (27%).

Sreedhar *et al.* (2004) conducted a field experiment during rabi season 2002 for genetic diversity of 114 germplasm of rice and concluded that the maximum inter cluster distance (23.73) was observed between cluster V and cluster X, followed by cluster III and cluster IX (22.27). Based on

the divergence estimates and clustering pattern in the present genetic material, cross could be made between the genotypes of cluster V and cluster X for yielding good recombinants for the character viz., spikelets/panicle, filled grains/panicle, single plant yield, biological yield and harvest index.

Shanthi and Singh (2000) studied genetic divergence using Mahalanobis's D^2 statistic for six quantitive characters in 17 induced mutant genotypes of Masuri rice. The genotypes differ 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 forth clusters were monogenic. The greater cluster distance was observed between genotypes belonging to cluster II and III.

Reddy *et al.* (2004) conducted an experiment to assess the nature and extent of genetic diversity among 36 genotypes of rice for 14 quantitative characters using Mahalanobis's D^2-statistic. The genotypes were grouped into six different clusters adopting Tocher's method indicated the presence of wide rang of genetic variability. Diversity in pedigree of the genotypes was conspicuously reflected in the clustering pattern. Cluster V was evolved as a largest cluster comprising of 10 genotypes followed by cluster I, III and IV each comprising 8 genotypes where as cluster II and VI were consisting one genotype each. Maximum genetic distance was observed between cluster I and VI followed by cluster IV and VI. Hybridization between these clusters is expected to generate a wide range of variability and will facilitate the isolation of desirable genotypes.

An attempt was made to find out the nature and extent of genetic divergence and variability among a set of 54 standard rice varieties with

the objective of selecting genetically divergent parental lines for hybridization. The analysis of variance revealed that highly significant variation for plant height, panicle length, flag leaf length, tillers/hill, spikelets/panicle, days to 50% flowering, maturity duration and grain yield/plot. The genotypes were grouped into nine clusters employing Mahalanobis's D^2 analysis. This indicated the presence of wide genetic diversity in experimental material for majority of the characters. The pattern of clustering indicated no general association between ecological distribution of genotypes and genetic divergence. This might be due to differential adaptation, selection criteria, selection pressure and environment. Plant height contributed maximum towards genetic divergence (40.16%), followed by flag leaf length (20.12%), grain yield/plant (15.79%) and maturity duration (15.58%). Maximum inter cluster distance (7.93) was found between cluster number VI and VIII indicating that hybridization between these two clusters could produce progeny with desirable characters (Devi *et al.* 2004).

Soni *et al.* (1999) conducted an experiment to assess the genetic divergence among 132 rice genotypes for 18 quality traits. They grouped the genotypes into 10 clusters. Grouping of genotypes in different clusters indicated the existence of significant amount of variability among the genotypes for the quality traits studies. Higher order of divergence was recorded between cluster VI and VII. Based on the mean performance, genetic distance and clustering pattern, hybridization of selected 10 genotypes are likely to give desirable segregants for grain quality.

Bansal *et al.* (1999) reported the genetic diversity in 34 rice stocks using D^2 analysis of 10 economic traits. Thirty-four genotypes from seven countries were grouped into 15 clusters. The pattern of distribution of genotypes within various clusters was independent of geographical

distribution. Based on the mean performance, genetic distance and clustering pattern, intervarietal crosses are identified which may be useful in creating wider variability for early maturity, dwarf and high yielding segregants.

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

Genetic diversity was assessed with 34 rice stocks using D^2 analysis of 10 economic traits (Bansal *et al.* 1999). The 34 genotypes were grouped in to 15 clusters.

Genetic divergence studies were carried out by 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.

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.

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.

Mishra *et al.* (2002) determined the nature and magnitude of the genetic diversity for 20 quantitative and qualitative characters in 16 rice cultivers. 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.

Manna *et al.* (2003) reported that the clustering pattern based on genetic diversity did not correlated with the grouping of cultivars based on growing condition.

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

Bidhan *et al.* (2002) found that days to 50% flowering, grain length and grain yield/plant were the major yield contributing characters to genetic diversity.

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.

Zhang *et al.* (1987) reported that multivariate analysis for the genetic distance of 7 yield related characters between the maintainer line Qing B and 31 newly developed restorer line was used predict heterosis. The results, which agreed with the heterosis indices actually determined, showed that 15 restorers were better than other crosses between Qing B and 9 restorer lines, had greater genetic distances, implying higher heterosis than those with similar genetic distances.

Chapter III

Materials and Methods

CHAPTER III
MATERIALS AND METHODS

3.1 Experimental Site

The study was carried out at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207 under the Agro-ecological Zone of Madhupur Tract, AEZ-28 during the period from December 2007 to May 2008. The location of the site is situated at 23^0 41' N latitude 90^0 22' E longitude and 8.6 m above from the sea level.

3.2 Climate and Soil

The experimental site has the sub-tropical climatic zone. It is characterized by high temperature accompanied by moderate high rainfall during Kharif season (April to September) and low temperature in the Rabi season (October to March). Its top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 5.61 and organic carbon content is 0.82%. The record of air temperature humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargoan, Dhaka (Appendix II).

3.3 Planting Materials

Sixty genotypes were used in the study. The seeds of 60 genotypes were collected from the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka. Descriptions of the genotypes are given in Table 1.

Table 1. List of the 60 rice genotypes used in the experiment

Designation	Genotypes	Sources	Designation	Genotypes	Sources
G1	PP-3	SAU	G31	AL-16	SAU
G2	PP-5	SAU	G32	AL-17(III)	SAU
G3	PP-6	SAU	G33	AL-17(III)	SAU
G4	PP-8	SAU	G34	AL-17(III)	SAU
G5	PP-10	SAU	G35	AL-20(II)	SAU
G6	AL-17(I)	SAU	G36	AL-20(II)	SAU
G7	AL-17(II)	SAU	G37	AL-26(II)	SAU
G8	AL-17(III)	SAU	G38	AL-27	SAU
G9	AL-33(II)	SAU	G39	AL-35	SAU
G10	AL-42(I)	SAU	G40	AL-20	SAU
G11	AL-42(II)	SAU	G41	AL-36	SAU
G12	AL-44(I)	SAU	G42	AL-47(I)	SAU
G13	AL-48	SAU	G43	AL-47(II)	SAU
G14	AL-49	SAU	G44	AL-50	SAU
G15	P-5B	SAU	G45	AL-51(I)	SAU
G16	P-6B	SAU	G46	AL-53	SAU
G17	PP-1	SAU	G47	AL-55	SAU
G18	PP-2	SAU	G48	AL-56(I)	SAU
G19	PP-4(B)	SAU	G49	AL-56(II)	SAU
G20	PP-4(B)	SAU	G50	AL-56(III)	SAU
G21	PP-6	SAU	G51	R-2	SAU
G22	PP-8	SAU	G52	PP-2(I)	SAU
G23	PP-9(I)	SAU	G53	AL-57(I)	SAU
G24	PP-9(II)	SAU	G54	P-3B	SAU
G25	PP-9(III)	SAU	G55	AL-29	SAU
G26	AL-1	SAU	G56	R-1	SAU
G27	AL-10	SAU	G57	R-4	SAU
G28	AL-11	SAU	G58	R-5	SAU
G29	AL-12	SAU	G59	R-5	SAU
G30	AL-14(III)	SAU	G60	R-5	SAU

AL = Advanced Line, B = B Line, PP = Pollen Parent, R = Restorer Line, SAU = Sher-e-Bangla Agricultural University.

Plate (1a): Close field view of the experiment

Plate (1b): Field view of the experiment

3.4 Layout of The Experimental Design

The experiment was laid out in Randomized Complete Block Design (RCBD) with 3 replications. The field will be divided into three blocks then the blocks will be further sub-divided into 60 plots where genotypes will be randomly assigned. The individual was plot was 3.5m × 1.5m in size. Plant to plant distance and row to row distance were maintain at 20cm and 25cm, respectively. The genotypes will be distributed to each plot with each block randomly.

3.5 Raising of Seedling

Seeds of all collected rice genotypes were sown on last week of December 2007 in the net house separately and proper tags were maintained.

3.6 Preparation of Main Field

The land was prepared by ploughing with power tiller. Weeds and stubbles were removed from the field. Proper laddering was done to bring the soil at proper tilth condition. The land was finally prepared by the addition of basal dose of fertilizers recommended by BRR1.

3.7 Fertilizer Used

The soil fertility was ensured by applying of Urea, TSP, MP and Gypsum @ 260-77-79-55 kg/ha, respectively. During the final land preparation, total Urea was applied in three installments, at 15 days after transplanting (DAT), 30 DAT and 45 DAT recommended by BRRI (Anonymous, 1999).

3.8 Transplanting of Seedling

Healthy seedlings of 45 days old were transplanted on second week of February 2008 in separate strip of experimental field. In each strip 25 x 20 spacing between row to row and plant to plant, respectively were maintained. Just after transplanting the seedlings were properly watered.

3.9 Intercultural Operation

After 7 days of transplanting, necessary gap filling was done. Weeding was done during top dressing of urea to break the soil crust. The crop was kept weed free throughout the growth period. Hand weeding was done at 25 and 40 days after transplanting.

3.10 Irrigation

The experiment 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.

3.11 Method of Recording of Observations

Observations were recorded on 10 randomly chosen plants from each plot. The plants were selected from middle to avoid border effect and portion of the plot. The mean was estimated. The observations for characterization and genetic diversity analysis were recorded under field condition as follows:

3.11.1. Days to 50% flowering

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

3.11.2. Days to maturity

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

3.11.3. Plant height (cm)

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

3.11.4 Total tillers per plant

Total tiller number per plant was counted in 10 randomly selected plants under study.

3.11.5. Panicle length (cm)

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.

3.11.6. Effective tillers per plant

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

3.11.7. Filled grain per panicle

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

3.11.8. 1000 grain weight (g)

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

3.11.9 Grain yield per plant (g)

Grain yield per plant was estimated as the average weight of grain (g) from 10 randomly selected plants at 14% moisture level by the following formula.

$$\text{Grain Yield per Plant} = \frac{\text{Wd (100-Md)}}{\text{100-14}}$$

Where,

Wd = Weight of sun dried grain

Md = % Moisture of sun dried grain

Each plant was threshed and cleaned separately and grain yield was recorded in g.

3.12 Statistical Analysis

Analysis of variance was done for all the characters under study using the mean values (Singh and Chaudhury, 1985). Mean, range and coefficient of variation (CV) were estimated using MSTAT computer program. Mean data for each character were subjected to both univariate and multivariate analysis. 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).

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

Where,

GMS = Genotypic mean square

EMS = Error mean square

r = Number of replication

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

Where,

$\sigma^2_{(g)}$ = Genotypic variance

EMS = Error mean square

ii. Estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV)

Genotypic and phenotypic coefficient of variation were estimated according to Burton (1952), Singh and Chaudhury (1985).

$$GCV\ (\%) = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

Where,

σ^2_g = Genotypic variance

$\bar{x}$ = Population mean

Similarly, $PCV\ (\%) = \frac{\sqrt{\sigma^2_{ph}}}{\bar{x}} \times 100$

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).

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

Where,

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).

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

Where,

GA = Genetic advance

$\bar{x}$ = 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's $D^{2:}$ 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 Chaudhuty (1979). For each combination the mean deviation, i.e. Y_I^1-Y^2_I with i = I, 2 ... p was estimated and the D^2 was calculated as sum of the squares of these deviations, i.e. $\sum(Y_I^1 - Y_I^2)$. 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 gave 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).

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

Where,

D_I^2 = 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).

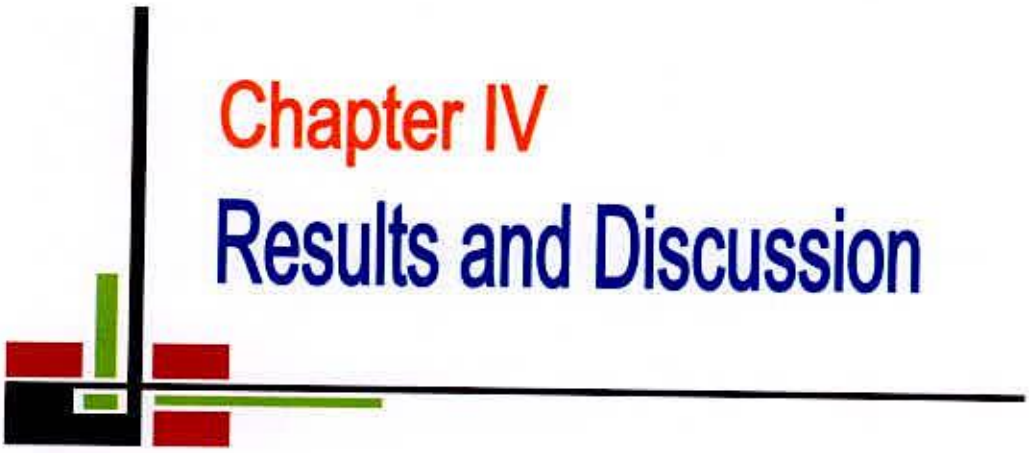
$$\text{Average inter-cluster } D^2 = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

$\sum D_{ij}^2$ = 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 IV

Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the results obtained from the study. The results were in Table 2 to 9, Figures 1 to 3 and necessary discussions have been presented under the following headings:

4.1 Characterization of yield and yield contributing traits of rice genotypes

4.2 Diversity of the rice genotypes

4.1 CHARACTERIZATION OF RICE GENOTYPES ON THE BASIS OF YIELD AND YIELD CONTRIBUTING TRAITS

4.1.1 Analysis of variance, genetic variability, heritability and genetic advance in rice genotypes

The genotypes differed significantly for all the characters (Table-2). The extent of variation among the genotypes in respect of 9 characters were studied and mean value, range, genotypic variance (σ^2_g), phenotypic variance (σ^2_p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2_b), genetic advance (GA) and genetic advance in percent of mean have been presented in (Table-3). The mean values of all genotypes for each character is also shown in Appendix I. Performance of the genotypes are described below for each character.

Table 2. Mean sum of squares from the ANOVA of sixty rice genotypes in respect of nine characters

Characters	d.f			Mean sum of square		
	Replication	Genotype	Error	Replication	Genotype	Error
Days to 50% flowering	2	59	118	204.706**	113.66**	3.852
Plant height (cm)	2	59	118	8.400^{ns}	346.993**	21.386
Panicle length (cm)	2	59	118	8.409^{ns}	23.644**	4.424
Total tillers per plant	2	59	118	8.263^{ns}	28.732**	7.004
Effective tillers per plant	2	59	118	7.832^{ns}	22.455**	3.221
Days to maturity	2	59	118	228.356**	113.66**	16.706
Filled grains per panicle	2	59	118	339.684^{ns}	6902.947**	833.818
Thousand grain weight (g)	2	59	118	2.002^{ns}	29.522**	2.868
Grain yield per plant (g)	2	59	118	70.270^{ns}	208.504**	23.003

** Significant at 1% level of probability
^{ns} Not Significant

Table 3. Variability, genetic parameter, heritability (h^2b), genetic advance (GA) and GA in percent of mean for 9 yield and its related characters in rice

Characters	Range	Mean	MS	σ^2g	σ^2p	GCV	PCV	h^2b	GA(%) (1%)	GA in % of mean (1%)
DFF	110.3-136.7	122.0	113.66**	36.60	40.45	4.96	5.21	90.48	15.19	12.45
PH	71.28-130.67	99.01	346.993**	108.54	129.92	10.52	11.51	83.54	25.14	25.39
PL	15.67-34.11	28.05	23.644**	6.41	10.83	9.02	11.73	59.15	5.14	18.32
TTP	6.78-25.00	12.38	28.732**	7.24	14.25	21.74	30.49	50.84	5.07	40.92
ETP	6.33-19.89	10.43	22.455**	6.41	9.63	24.27	29.75	66.56	5.45	52.27
DDM	140.3-166.7	152.0	113.66**	32.32	49.02	3.74	4.61	65.92	12.19	8.02
FGP	84.7-282.7	180.0	6902.947**	2023.04	2856.86	24.98	29.69	70.81	99.92	55.51
TGW	13.40-27.30	21.24	29.522**	8.88	11.75	14.03	16.14	75.60	6.84	32.21
GYP	5.62-43.77	28.31	208.504**	61.83	84.84	27.77	32.53	72.88	17.72	62.59

** Significant at 1% level of Probability

DFF= Days to 50% flowering (days), PH= Plant height (cm), PL=Panicle length (cm), TTP= Total tillers per plant, ETP= Effective tillers per plant, DDM=Days to maturity (days), FGP= Filled grains per panicle, TGW= Thousand grain weight (g), GYP= Grain yield per plant, MS = Mean sum of square, σ^2g = Genotypic variance, σ^2p= Phenotypic variance, GCV= Genotypic coefficient of variation and PCV = Phenotypic coefficient of variation.

4.1.1.1. Days to 50% flowering

The mean value of days to 50% flowering ranged from 110.3 days (G13) to 136.7 days (G60), where as mean performance was 122 days. The phenotypic and genotypic variances for this trait were moderate (40.45 and 36.60). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (5.21) was higher than genotypic coefficient of variation (4.96) (Table-3). Heritability estimates for this trait was high (90.48) with moderate genetic advance (15.19) and low genetic advance in percent of mean (12.45). Gupta *et al.* (1994) found high heritability with low genetic advance for days to 50% flowering in rice.

4.1.1.2. Plant height (cm)

Plant height ranged from 71.28 (G13) to 130.67 (G33) with mean value 99.01 (Table-3). The phenotypic and genotypic variances for this trait were comparatively high (129.92 and 108.54). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (11.51), which suggested that environment has a significant role on the expression of this trait. Heritability estimates was high (83.54) with moderate genetic advance (25.14) and moderate genetic advance in percent of mean (25.39) was considerable for this trait indicating apparent variation was due to genotypes. So, selection based on this trait would be effective. Kumar *et al.* (1994) found high heritability coupled with moderate genetic advance for plant height.

4.1.1.3. Panicle length (cm)

The highest panicle length was found in G60 (34.11 cm) and lowest panicle length was found in G13 (15.67 cm) with mean value of 28.05 cm (Table-3). The phenotypic variance (10.83) was higher than genotypic variance (6.41). The phenotypic coefficient of variation (11.73) and genotypic coefficient of variation (9.02) were moderate. Heritability estimates was low (59.15). The genetic advance was very low (5.14) with low genetic advance in percent of mean (18.32). Chakraborty and Hazarika (1994) reported a very small difference between phenotypic and genotypic coefficient of variation in panicle length.

4.1.1.4. Total tillers per plant

Total tiller number per plant ranged from 6.78 (G4) to 25.00 (G15) with mean value 12.38. The phenotypic variance (14.25) was much higher than genotypic variance (7.24) as presented in Table-3. This feature indicated higher influence of environment on the expression of the trait and genetic factor had low expressivity on the total tiller number per plant. This character showed high genotypic and phenotypic coefficient of variation (21.74 and 30.49, respectively). Here the phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicating the apparent variation not only due to genotypes but also due to the influence of environment. Estimated heritability (50.84) for this trait was low with moderate genetic advance in percent of mean (40.92). The estimated heritability was the lowest (50.84) among the characters studied. Shanthakumar *et al.* (1998) reported high heritability and genetic advance for total tillers per plant.

4.1.1.5. Effective tillers per plant

Analysis of variance for effect tillers per plant showed highly significant mean sum of square due to genotypic difference (Table-2). The mean value with respect to this trait ranged from 6.33 (G54) to 19.89 (G15). Phenotypic variance (9.63) was higher than the genotypic variance (6.41). The considerable differences between genotypic and phenotypic variance indicating the effect of environment for the expression of the trait (Table-3). The phenotypic coefficient of variation (29.75) was higher than genotypic coefficient of variation (24.27) for this trait. A heritability estimate was also moderate (66.56) with high genetic advance in percent of mean (52.27). Das *et al.* (1992) found high genetic coefficient of variation, high heritability with high genetic advance (%) of mean for number of effective tillers/plant.

4.1.1.6. Days to maturity

Mean sum of square for days to maturity was highly significant (Table-2). The mean value ranged from 140.33 days (G13) to 166.7 days (G60), where as mean performance was 152 days. The phenotypic and genotypic variances for this trait were moderate (49.02 and 32.32). The phenotypic variance appeared to be higher than the genotypic variance, suggested considerable influence of environment on the expression of the genes controlling this trait. The phenotypic coefficient of variation (4.61) and genotypic coefficient of variation (3.74) were low. Heritability estimates for this trait was moderate (65.92) with moderate genetic advance (12.19) and low genetic advance in percent of mean (8.02).

4.1.1.7. Filled grains per panicle

Mean sum of square for filled grains per panicle was highly significant (Table-2). The mean values ranged from 84.7 (G3) to 282.7 (G4). The phenotypic variance (2856.86) was higher than the genotypic variance (2023.04) suggested that the environment had a significant role for the expression of the character. The phenotypic coefficient of variation (29.69) was higher than the genotypic coefficient of variation (24.98). Moderate heritability (70.81) with high genetic advance (99.92) as presented in Table-3. Biswas *et al.* (2000) observed high genetic coefficient of variation and high heritability in broad sense coupled with high genetic advance in percentage of mean. Shavani and Reddy (2000) reported that high genetic advance exhibited by filled spikelets per panicle.

4.1.1.8. 1000 grain weight (g)

Mean sum of square for thousand grain weight was highly significant (Table-2). 1000-grain weight ranged from 13.40g (G24) to 27.30g (G54) with a mean value of 21.24g. The character showed low phenotypic (11.75) and genotypic (8.88) variance. The considerable difference between genotypic and phenotypic variance indicating effect of the environment for the expression of this trait (Table-3). The phenotypic coefficient of variation (16.14) was higher than the genotypic coefficient of variation (14.03) for this trait. 1000-grain weight showed moderate heritability (75.60). The genetic advance was low (6.84) and genetic advance in percentage of mean was moderate (32.21). Sawant *et al.* (1994) observed significant difference between high genotypic and phenotypic coefficient of variation for 1000-grain weight.

4.1.1.9. Grain yield per plant (g)

Grain yield per plant showed a highly significant mean sum of squares due to different genotypes that suggested considerable range of variation for this trait (Table-2). The mean values ranged from 5.62g (G56) to 43.77g (G27). The phenotypic variance (84.84) was much higher than the genotypic variance (61.83) suggested that the environment had a significant role for the expression of the character. This trait showed high genotypic (27.77) and phenotypic (32.53) coefficient variation. Here the phenotypic coefficient of variation was higher than the genotypic coefficient of variation indicating the apparent variation not only due to genotypes but also due to the influence of environment. The estimated heritability was moderate (72.88). The genetic advance was moderate (17.72) and genetic advance in percent of mean was high (62.59). Considerable amount of heritability and genetic advance were observed for yield per plant in rice by Yadav (2000).

4.2 DIVERSITY OF THE RICE GENOTYPES

4.2.1 Principal Component Analysis (PCA)

The principal component analysis yielded Eigen values of principal component axes of coordination of genotypes with the first axes totally accounted for the variation among the genotypes, whereas three of these Eigen values above unity accounted for 90.08% (Table-4). The First two principal axes accounted for 79.54% of the total variation among the 9 characters describing 60 rice genotypes. Based on principal component axes I and II, a two dimensional chart (Z_1-Z_2) of the genotypes are presented (Figure-1). The scatter diagram revealed that apparently there were mainly six apparent clusters. The genotypes were distantly located from each other (Figure- 2).

4.2.2 Principal Coordinate Analysis (PCO)

Principal coordinate analysis was performed on auxiliary of principal component analysis. Inter genotypic distances obtained from principal coordinate analysis showed that the highest distance (2.1417) was observed between the genotypes G56 and G55 followed by G56 and G48 (2.1119), G56 and G21 (2.0767), G56 and G41 (2.0676), G56 and G27 (2.0618) and the lowest distance was observed between the genotypes G53 and G28 (0.1134) followed by G41 and G21 (0.1475), G53 and G31 (0.1898), G25and G9 (0.1911) (Table-5). By using these distances from distance matrix intra-cluster distances were calculated (Table-6) as suggested by Singh and Choudhury (1979). The highest intra-cluster distance was observed in cluster II (0.898) which is composed of 11 genotypes which is almost similar with cluster III (0.534). The cluster V showed the lowest intra-cluster distance (0.418) composed of 9 genotypes.

Table 4. Eigen values and percentage of variation in respect of 9 in 60 rice genotypes

Principal component character	Eigen values	Percentage of total variation accountant for	Cumulative percentage
Days to 50%flowering	10.593	49.92	49.92
Plant height (cm)	6.286	29.62	79.54
Panicle length (cm)	2.236	10.54	90.08
Total tillers per plant	0.848	4.00	94.08
Effective tillers per plant	0.733	3.46	97.54
Days to maturity	0.238	1.12	98.66
Filled grains per panicle	0.191	0.90	99.56
Thousand grain weight (g)	0.094	0.44	100
Grain yield per plant(g)	0.000	0.00	100

Table 5. Ten of each higher and lower inter genotypic distance (D^2) between pair of genotypes

10 higher D^2 values	Genotypes combination	10 lower D^2 values	Genotypes combination
2.1417	G56&G55	0.1134	G53&G28
2.1119	G56&G48	0.1475	G41&G21
2.0767	G56&G21	0.1898	G53&G31
2.0676	G56&G41	0.1911	G25&G9
2.0618	G56&G27	0.1949	G12&G11
2.0484	G56&G6	0.2049	G55&G21
2.0414	G56&G19	0.2065	G24&G8
2.0318	G56&G7	0.2114	G35&G11
2.0061	G59&G55	0.2126	G51&G9
1.9939	G56&G5	0.2163	G50&G31

Table 6. Average intra (Diagonal) and inter cluster distances (D^2) for 60 rice genotypes

Cluster	I	II	III	IV	V	VI
I	**0.544**					
II	18.381	**0.898**				
III	9.759	8.999	**0.534**			
IV	4.969	13.420	5.071	**0.466**		
V	9.259	9.242	2.940	4.313	**0. 418**	
VI	13.802	4.623	4.413	8.863	4.863	**0.606**

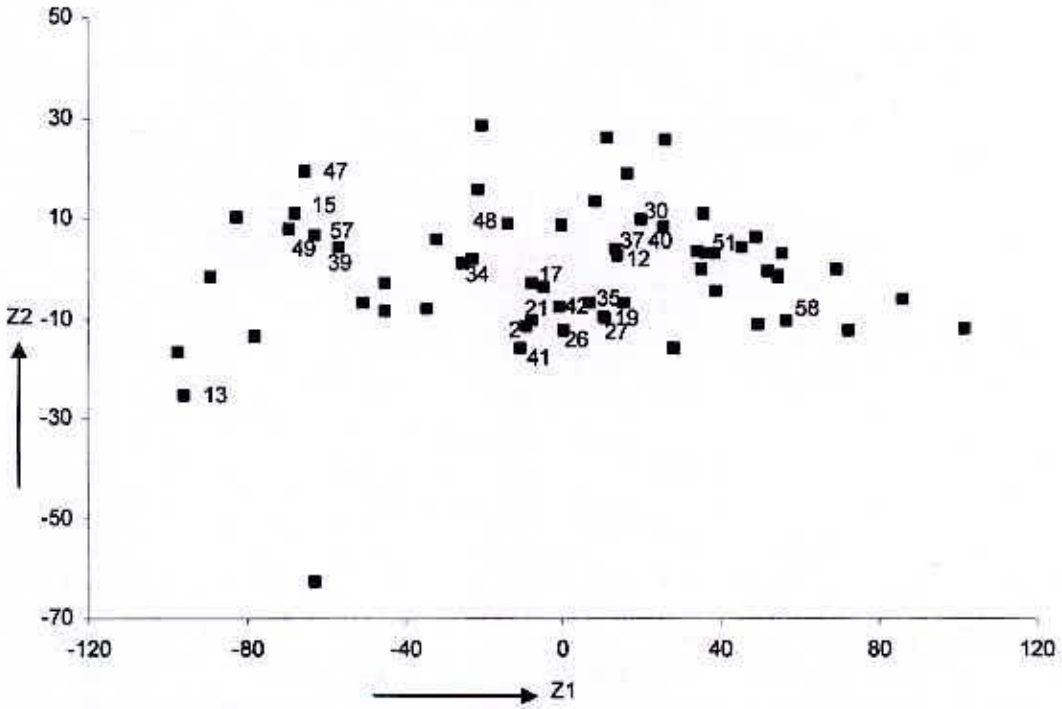


Figure 1. Scatter distribution of 60 rice genotypes based on their principal component scores

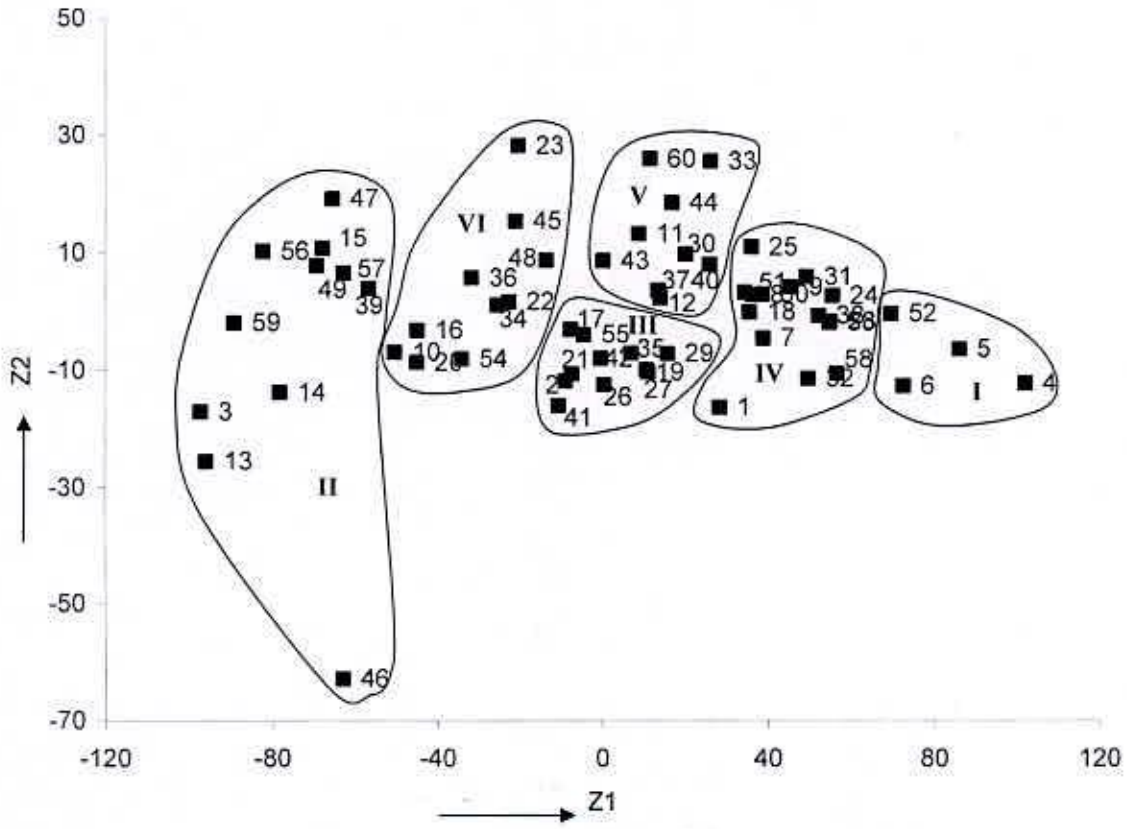


Figure 2. Scatter distribution of 60 rice genotypes based on their principal component scores superimposed with clustering

4.2.3 Non Hierarchical Clustering

By application of non-hierarchical clustering using co-variance matrix, the 60 genotypes were grouped into six clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Chauhan and Chauhan (1994) reported twelve clustering; Arun *et al.* (2002) nine clustering; Reddy *et al.* (2004) six clustering in rice. Composition of different clusters with their corresponding genotypes in each cluster are presented in Table-7.

Cluster IV had maximum number of (15) genotypes followed by II, III, VI, V and I which had 11, 11, 10, 9 and 4 genotypes, respectively. Cluster I composed of only 4 genotypes namely G4, G5, G6 and G52. From the clustering mean values (Table-8), it was observed that the mean value of cluster I ranked first for filled grains per panicle (262.81) and the second for grain yield per plant (31.51). On the other hand these genotypes produced lowest for total tillers per plant (9.06), effective tillers per plant (8.39) and thousand grain weight (19.03).

Cluster II was composed of 11 genotypes namely G3, G13, G14, G15, G39, G46, G47, G49, G56, G57 and G59. This group possessed genotypes with the highest cluster mean for thousand grain weight (23.08) and the lowest for panicle length (25.50), filled grains per panicle (105.69), grain yield per plant (17.46), days to maturity (149.18) and days to 50% flowering (119.18).

Cluster III constituted of 11 genotypes namely G2, G17, G19, G21, G26, G27, G29, G35, G41, G42 and G55. These genotypes produced the highest cluster mean for total tillers per plant (13.76), effective tillers per plant (12.02), grain yield per plant (35.81) and the lowest for plant height (91.58). This cluster contains the shortest plant.

Table 7. Distribution of 60 genotypes of rice in six clusters

Cluster	Member numbers	Genotypes number
I	4	G4(PP-8), G5(PP-10) G6(AL-17(I)), G52(PP-2(I)).
II	11	G3(PP-6), G13(AL-48), G14(AL-49), G15(P-5B), G39(AL-35), G46(AL-53), G47(AL-55), G49(AL-56(II)), G56(R-1), G57(R-4), G59(R-5).
III	11	G2(PP-5), G17(PP-1), G19(PP-4(B)), G21(PP-6), G26(AL-1), G27(AL-10), G29(AL-12), G35(AL-20(II)), G41(AL-36), G42(AL-47(I)), G55(AL-29).
IV	15	G1(PP-3), G7(AL-17(II)), G8(AL-17(III)), G9(AL-33(II)), G18(PP-2), G24(PP-9(II)), G25(PP-9(III)), G28(AL-11), G31(AL-16), G32(AL-17(III)), 38(AL-27), G50(AL-56(III)), G51(R-2), G53(AL-57(I)), G58(R-5).
V	9	G11(AL-42(II)), G12(AL-44(I)), G30(AL-14(III)), G33(AL-17(III)), G37(AL-26(II)), G40(AL-20), G43(AL-47(II)), G44(AL-50), G60(R-5).
VI	10	G10(AL-42(I)), G16(P-6B), G20(PP-4(B)), G22(PP-8), G23(PP-9(I)), G34(AL-17(III)), G36(AL-20(II)), G45(AL-51(I)), G48(AL-56(I)), G54(P-3B).

Table 8. Cluster means for 9 characters of 60 rice genotypes

Characters	Clusters					
	I	II	III	IV	V	VI
Days to 50% flowering	120.92	119.18	119.36	124.02	124.59	123.20
Plant height (cm)	97.35	94.07	91.58	99.72	112.79	99.84
Panicle length (cm)	28.49	25.50	27.75	28.50	30.11	28.50
Total tillers per plant	9.06	13.07	13.76	11.60	11.70	13.20
Effective tillers per plant	8.39	10.45	12.02	9.69	9.73	11.24
Days to maturity	150.92	149.18	149.36	154.02	154.59	153.20
Filled grains per panicle	262.81	105.69	180.59	224.44	194.26	148.62
Thousand grain weight (g)	19.03	23.08	21.27	20.41	20.59	21.92
Grain yield per plant(g)	31.51	17.46	35.81	28.63	28.77	29.85

Cluster IV was composed of 15 genotypes namely G1, G7, G8, G9, G18, G24, G25, G28, G31, G32, G38, G50, G51, G53 and G58. This cluster obtained second position in respect of cluster mean for days to 50% flowering (124.02), days to maturity (154.02), panicle length (28.50), filled grains per panicle (224.44) and the third in plant height (99.72).

Nine genotypes formed cluster V. This cluster contained genotypes G11, G12, G30, G33, G37, G40, G43, G44 and G60. Cluster V had the highest cluster mean for days to 50% flowering (124.59), days to maturity (154.59), plant height (112.79), panicle length (30.11) and the third highest cluster mean for filled grains per panicle (194.26). This cluster contains tallest plant.

Cluster VI constituted of 10 genotypes namely G10, G16, G20, G22, G23, G34, G36, G45, G48 and G54. The mean value of cluster VI ranked second for plant height (99.84), total tillers per plant (13.20), effective tillers per plant (11.24), panicle length (28.50), 1000-grain weight (21.92) and the third for days to 50% flowering (123.20), days to maturity (153.20), grain yield per plant (29.85).

4.2.4 Canonical Variate Analysis (CVA)

Canonical variate analysis was done to compute the inter-cluster Mahalanobis's D^2 values. The Table-6 indicates the intra and inter-cluster distance (D^2) values. The inter-cluster distances were higher than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. Singh *et al.* (1987) obtained larger inter-cluster distances than the intra-cluster distances in a multivariate analysis in rice. Results indicated that the highest inter-cluster distance was observed between clusters I and II (18.381) followed by between cluster II and IV (13.420), I and VI (13.802), I and III (9.759), I and V (9.259), II

and V (9.242), II and III (8.999). The lowest inter-cluster distance was observed between cluster III and V (2.940), followed by IV and V (4.313) (Figure-3).

However, the maximum inter-cluster distance was recorded between the clusters 1 and 11 (18.381). Genotypes from these two clusters, if involved in hybridization may produce a wide spectrum of segregating population. Similar reports were also made by Bansal *et al.* (1999) and Singh *et al.* (1996). Zhang *et al.* (1987) reported that the greater genetic distances implying higher heterosis than those with similar genetic distances. The intra-cluster distance varied from 0.418 to 0.898, maximum for cluster II (0.898), which contained of 11 genotypes, while the minimum distance was found in cluster V (0.418) that comprises 9 genotypes.

Results obtained from different multivariate analysis were superimposed in Figure-2 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed the results of one another.

A two-dimensional scatter diagram was constructed using component I as X-axis and component II as Y-axis, reflecting in the relative position (Figure-1). As per scatter diagram the genotypes were apparently distributed into six clusters. It was also revealed that the genotypes of cluster 1 was more diverse from the genotypes of cluster II genotypes. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve high-level production. In the present study the maximum distance existence between cluster 1 and II. But considering the yield and duration crosses involving cluster I and II may exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed

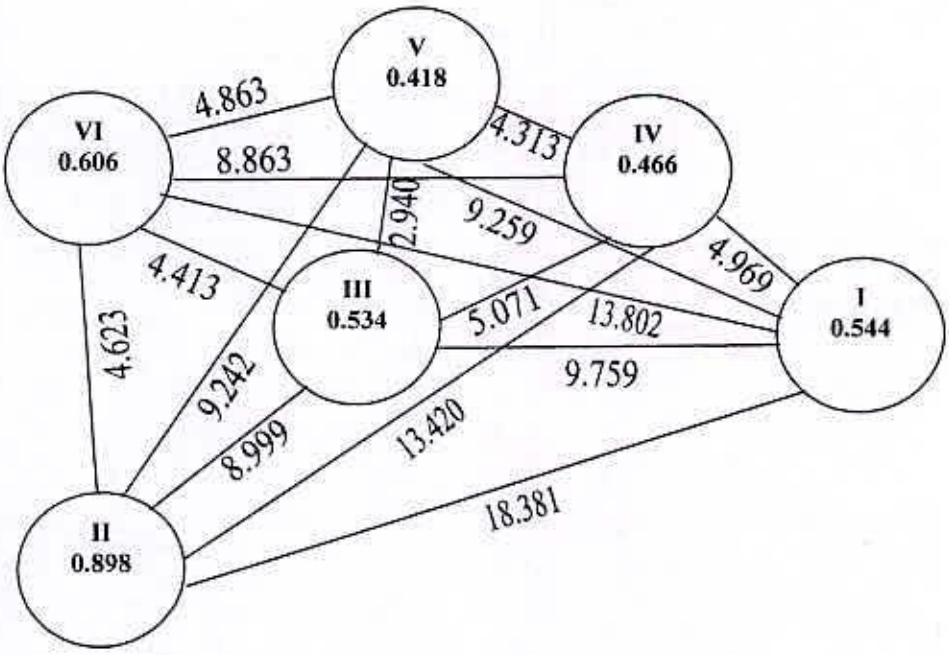


Figure 3. Diagram showing intra and inter cluster distances ($\sqrt{D^2}$) of 60 rice genotypes

higher heterosis. keeping this in view, it appears that the crosses between the crosses between the genotypes belonging cluster I with cluster II might produce high heterosis in yield as well as earliness. Also the crosses between genotypes from cluster I with cluster V, genotypes in cluster II with III and genotypes in cluster V with cluster II have been selected for future hybridization program.

4.3 CONTRIBUTION OF CHARACTERS TOWARDS DIVERGENCE OF THE GENOTYPES

Contribution of characters towards divergence is presented in Table-9. The vector-I (Z_1) obtained form PCA, the important characters responsible for genetic divergence in the axis of differentiation were effective tillers per plant (0.4129), filled grains per panicle (0.1155), days to 50% flowering (0.0014) and days to maturity (0.0014). In vector-11 (Z_2), effective tillers per plant (0.2355), 1000-grain weight (0.1294), plant height (0.1054), days to 50% flowering (.0293), days to maturity (0.0293) and filled grains per panicle (0.0081) were important but plant height, panicle length, total tillers per plant, 1000-grain weight and grain yield per plant played only a minor role in the first axis of differentiation. The role of panicle length, total tillers per plant and grain yield had a minor role in the genetic divergence. The role at days to 50% flowering, days to maturity, effective tillers per plant and filled grains per panicle in both the vectors were important components for genetic divergence in these materials.

Table 9. Latent vectors for 9 characters of rice genotypes

Characters	Vectors I	Vectors II
Days to 50% flowering	0.0014	0.0293
Plant height (cm)	-0.0380	0.1054
Panicle length (cm)	-0.1227	-0.1565
Total tillers per plant	-0.3543	-0.2276
Effective tillers per plant	0.4129	0.2355
Days to maturity	0.0014	0.0293
Filled grains per panicle	0.1155	0.0081
Thousand grain weight (g)	-0.0875	0.1294
Grain yield per plant(g)	-0.0149	-0.1114

4.4 COMPARISION OF DIFFERENT MULTIVARIATE TECHNIQUES

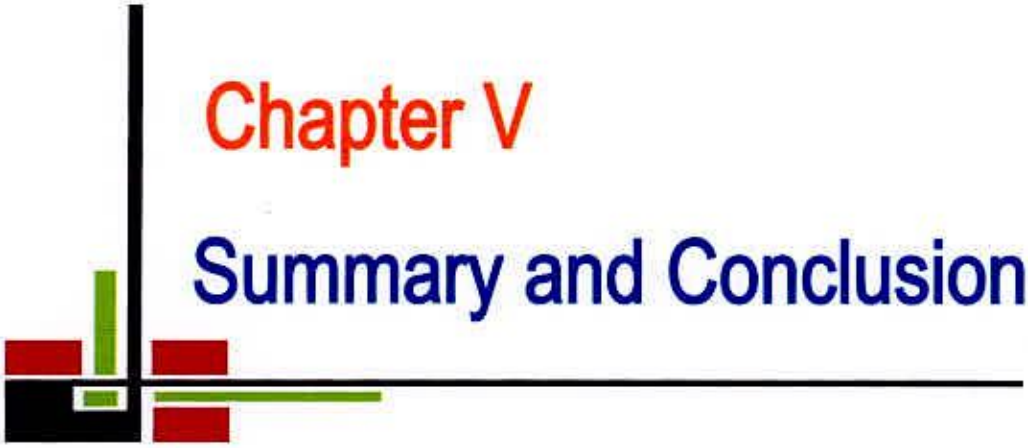
The cluster pattern of D^2 analysis through non-hierarchical clustering has taken care of simultaneous variation in all the characters under study. The distribution of genotypes in different clusters of the D^2 analysis has followed more or less similar trend of the Z_1 (principal component score I) and Z_2 (principal component score II) vectors of the principal component analysis. The D^2 and principal component analysis were found to be alternative methods in giving the information regarding the contribution of characters towards divergence in rice.

4.5 SELECTION OF PARENTS FOR FUTURE HYBRIDIZATION

In hybridization program, selection of genetically diverse parents is an important step. So the genotypes were 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 program. The genotypes G4 for highest number of filled grains per panicle from cluster I; G13 lowest plant height and also for shortest days to 50% flowering from cluster II; G21 for higher number of total tillers per plant, higher number of effective tillers per plant and G27 for highest grain yield per plant from cluster III; G60 for highest panicle length from cluster V and genotypes G54 for highest 1000-grain weight from cluster VI were found promising. 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 other agronomic performance, the inter genotypic crosses between G4 and G13, G4 and G27, G13 and G21, G60 and G54 may be used for future hybridization program.



Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

In order to evaluate the characterization and genetic divergence of rice, the present experiment was carried out during the period December 2007 to May 2008, at the experimental farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka. It involved sixty NPT rice genotypes. The experiment was conducted in a randomized complete block design (RCBD) with three replications. Data on days to 50% flowering (DFF), plant height (PH), panicle length (PL), total tillers per plant (TTP), effective tillers per plant (ETP), days to maturity (DDM), filled grain per panicle (FGP), 1000-grain weight (TGW) and yield grain per plant (GYP) were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

Different genotypes showed better performance for different characters. The highest mean value was observed for filled grains per panicle (180.0). This character also exhibited the highest range of variation (84.7-282.7) indicated that all the genotypes showed wide range of variation in respect of this character. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. However, these differences were in case of plant height, days to maturity, grain yield per plant indicating greater influence on environment for the expression of these characters. Among the characters, days to 50% flowering, total tillers per plant, effective tillers per plant, panicle length, 1000-grain weight, filled grains per panicle showed least difference between phenotypic and genotypic variance, which indicated additive gene action for the expression of the characters. All the characters showed moderate to high phenotypic and genotypic coefficient of variation except days to

50% flowering (5.21 and 4.96, respectively), days to maturity (4.61 and 3.74, respectively). Amongst the characters the highest genotypic coefficient of variation was recorded for grain yield per plant (27.77) followed by filled grains per panicle (24.98), effective tillers per plant (24.27), total tillers per plant (21.74), 1000-grain weight (14.03), plant height (10.52), panicle length (9.02) in order of merit. The highest value of heritability was observed for days to 50% flowering (90.48) and the lowest for total tillers per plant (50.84). The highest genetic advance in percent of mean was observed for grain yield per plant (62.59) followed by filled grains per panicle (55.51), effective tillers per plant (52.27) and total tillers per plant (40.92), whereas the lowest for days to maturity (8.02). Days to 50% flowering showed high heritability (90.48) but low genetic advance in percent of mean (12.45) indicated non-additive gene action for the expression of the characters. Here high heritability was exhibited due to favorable environment rather than genotype.

Significant differences among the clusters were observed. The first three principal component axes accounted for 90.08% variation towards the divergence. As per PCA, D^2 and cluster analysis, the genotypes were grouped into six different clusters. Clusters IV had maximum 15 genotypes followed by clusters II, III, VI, V which had 11, 11, 10, 9 and cluster I had only 4 genotypes, respectively. The highest inter cluster distance was observed between the cluster I and II (18.381) followed by between II and IV (13.420), I and VI (13.802) the lowest inter cluster distance was observed between the cluster III and V (2.940) followed by IV and V (4.313), III and VI (4.413). Cluster II showed highest intra cluster distance (0.898) and cluster V showed the lowest intra cluster distance (0.418). Genotypes included in cluster I were important for highest filled grain per panicle; cluster II for shortest days to 50%

flowering and lowest plant height; cluster III for higher total tillers per plant, effective tillers per plant and also highest for grain yield per plant; cluster V for highest panicle length and cluster VI for highest 1000-grain weight.

Therefore, considering group distance and other agronomic performance, the inter genotypic crosses between G4 and G13, G4 and G27, G13 and G21, G60 and G54 may be used for future hybridization program.

Chapter VI

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CHAPTER VI

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Appendices

Appendix I

Mean values of 9 characters for sixty rice genotypes

Designation	DFF	PH(cm)	PL(cm)	TTP	ETP	DDM	FGP	TGW(g)	GYP(g)
G1(PP-3)	116.33	86.55	25.00	8.56	8.22	146.33	210.11	24.30	21.45
G2(PP-5)	113.33	92.11	25.33	9.00	7.33	143.33	171.56	19.57	31.77
G3(PP-6)	114.33	77.89	22.56	15.45	15.45	144.33	84.67	23.83	23.03
G4(PP-8)	122.33	92.44	31.33	6.78	6.44	152.33	282.67	21.63	30.10
G5(PP-10)	120.33	100.22	28.28	9.44	9.22	150.33	265.89	16.83	35.47
G6(AL-17(I))	112.33	99.39	25.22	9.22	9.11	142.33	252.66	21.47	39.00
G7(AL-17(II))	123.33	97.78	28.33	10.67	10.00	153.33	218.11	23.07	40.83
G8(AL-17(III))	124.33	103.44	29.11	13.78	10.44	154.33	215.45	15.50	34.58
G9(AL-33(II))	123.33	105.11	29.00	12.44	10.55	153.33	225.89	20.07	21.63
G10(AL-42(I))	113.33	95.56	28.50	15.56	14.89	143.33	129.33	26.40	38.95
G11(AL-42(II))	123.33	114.34	29.11	9.45	8.00	153.33	187.56	21.53	31.34
G12(AL-44(I))	120.33	104.56	30.00	10.78	8.67	150.33	193.56	23.60	31.62
G13(AL-48)	110.33	71.28	15.67	10.55	8.56	140.33	87.45	25.53	13.26
G14(AL-49)	110.33	85.89	24.33	9.44	8.22	140.33	103.67	26.97	19.27
G15(P-5B)	126.67	101.39	28.94	25.00	19.89	156.67	112.00	22.20	22.93
G16(P-6B)	120.33	93.66	25.89	13.11	11.67	150.33	135.00	18.87	31.29
G17(PP-1)	116.33	100.33	30.00	11.33	11.33	146.33	171.89	22.90	36.80
G18(PP-2)	126.67	99.17	24.89	11.67	11.67	156.67	214.89	15.53	35.96
G19(PP-4(B))	118.33	92.55	28.33	12.00	12.00	148.33	190.67	20.20	42.03
G20(PP-4(B))	114.33	91.22	30.00	10.67	9.56	144.33	135.56	23.07	27.85
G21(PP-6)	120.33	88.50	26.22	19.11	17.00	150.33	172.78	18.63	37.22
G22(PP-8)	129.67	92.28	28.28	13.67	10.22	159.67	157.55	19.13	22.25
G23(PP-9(I))	123.33	129.17	32.39	14.33	12.89	153.33	156.89	18.20	36.03
G24(PP-9(II))	128.67	100.78	31.72	13.78	11.44	158.67	234.67	13.40	33.93
G25(PP-9(III))	130.67	106.22	29.22	11.78	10.55	160.67	215.78	17.00	20.77
G26(AL-1)	116.33	89.55	25.22	15.55	13.67	146.33	181.33	21.03	30.75
G27(AL-10)	116.33	95.22	29.44	11.55	9.67	146.33	190.22	26.73	43.77
G28(AL-11)	120.33	102.89	30.55	12.22	10.11	150.33	234.67	22.33	32.68
G29(AL-12)	123.33	91.89	28.67	13.33	11.22	153.33	195.89	23.53	34.10
G30(AL-14(III))	125.67	108.89	27.05	14.78	12.89	155.67	199.45	16.53	29.46
G31(AL-16)	130.67	103.00	28.22	12.11	8.67	160.67	228.78	22.47	27.33

Appendix I (Cont'd)

Designation	DFF	PH(cm)	PL(cm)	TTP	ETP	DDM	FGP	TGW(g)	GYP(g)
G32(AL-17(III))	118.33	92.89	27.00	11.56	9.11	148.33	230.22	19.40	31.31
G33(AL-17(III))	120.33	130.67	33.33	11.67	9.00	150.33	204.78	23.20	24.09
G34(AL-17(III))	116.33	103.44	27.55	13.22	10.67	146.33	154.11	22.47	33.09
G35(AL-20(II))	116.33	95.56	30.00	9.44	7.89	146.33	187.44	21.43	28.82
G36(AL-20(II))	126.67	99.44	23.94	14.33	11.67	156.67	148.22	21.07	23.23
G37(AL-26(II))	120.33	105.22	31.72	13.44	10.89	150.33	193.22	23.87	29.00
G38(AL-27)	120.33	101.89	30.11	9.55	7.89	150.33	232.89	20.47	19.50
G39(AL-35)	120.33	100.11	28.06	11.78	9.55	150.33	123.44	24.93	23.23
G40(AL-20)	118.33	113.44	27.67	11.44	9.67	148.33	205.22	20.20	31.22
G41(AL-36)	120.33	82.22	27.00	19.00	15.67	150.33	169.78	20.57	38.14
G42(AL-47(I))	124.33	88.17	26.11	12.78	11.00	154.33	180.22	20.17	28.24
G43(AL-47(II))	127.67	104.44	27.56	10.22	8.11	157.67	179.67	19.97	26.37
G44(AL-50)	128.67	115.11	30.44	10.67	8.44	158.67	195.78	15.50	23.29
G45(AL-51(I))	125.67	111.22	28.28	11.11	8.78	155.67	158.33	19.40	21.21
G46(AL-53)	124.33	89.44	26.61	15.34	12.22	154.33	117.34	25.67	27.56
G47(AL-55)	129.67	109.39	25.50	14.33	9.56	159.67	114.11	25.30	16.63
G48(AL-56(I))	130.67	102.95	29.94	18.11	15.67	160.67	164.78	23.27	41.05
G49(AL-56(II)	126.67	97.78	27.78	10.22	7.33	156.67	110.56	18.53	19.84
G50(AL-56(III))	128.67	99.89	28.83	10.56	8.22	158.67	218.78	24.13	23.57
G51(R-2)	126.67	101.56	27.22	13.67	10.89	156.67	214.44	20.47	25.72
G52(PP-2(I))	128.67	97.33	29.11	10.78	8.78	158.67	250.00	16.17	21.48
G53(AL-57(I))	125.67	98.67	29.78	11.67	9.56	155.67	234.56	23.30	31.43
G54(P-3B)	131.67	79.44	30.22	7.89	6.33	161.67	146.44	27.30	23.59
G55(AL-29)	127.67	91.28	28.95	18.22	15.45	157.67	174.67	19.20	42.22
G56(R-1)	125.67	98.67	26.44	10.67	7.22	155.67	98.67	19.97	5.62
G57(R-4)	111.33	107.72	28.83	10.33	9.11	141.33	117.89	21.40	13.90
G58(R-5)	116.33	95.89	28.45	10.00	8.00	146.33	237.33	24.67	28.77
G59(R-5)	111.33	95.22	25.78	10.67	7.89	141.33	92.78	19.53	6.74
G60(R-5)	136.67	118.44	34.11	12.89	11.89	166.67	189.11	20.87	32.57
CV%	1.61	4.67	7.50	17.38	17.20	2.69	16.04	7.97	16.94

DFF= Days to 50% flowering (days), PH= Plant height (cm), PL=Panicle length (cm), TTP= Total tillers per plant, ETP= Effective tillers per plant, DDM=Days to maturity(days), FGP= Filled grains per panicle, TGW= Thousand grain weight (g), GYP= Grain yield per plant, CV = Coefficient of variation.

Appendix II. Monthly record of air temperature, relative humidity and rainfall of experimental site during the period from November 2007 to May 2008

Month	Year	*Air temperature (°c)		Relative Humidity (%) at 12 p.m.	**Rainfall (mm)
		Maximum	Minimum		
November	2007	29.07	18.80	65.13	0
December	2007	27.07	15.65	63.80	3
January	2008	24.76	13.46	69.53	0
February	2008	31.26	19.42	51.27	0
March	2008	33.20	22.00	46.13	0
April	2008	33.74	23.81	61.40	185
May	2008	33.66	24.95	46.27	180

* Monthly average
** Monthly total
Source: Bangladesh Meteorological Department (Climate Division) Agragoan, Dhaka-1212.

Appendix III

Principle component scores for 60 rice genotypes

Genotypes	Z1	Z2
G1	28.25	-16.30
G2	-9.01	-11.85
G3	-97.17	-17.12
G4	101.99	-12.18
G5	86.01	-6.31
G6	72.43	-12.62
G7	38.81	-4.49
G8	36.21	2.84
G9	45.55	4.20
G10	-50.50	-6.94
G11	8.80	13.18
G12	13.98	2.38
G13	-95.82	-25.57
G14	-78.17	-13.82
G15	-67.92	10.70
G16	-44.96	-3.23
G17	-7.68	-3.04
G18	35.56	-0.10
G19	11.04	-10.33
G20	-45.09	-8.69
G21	-7.43	-10.63
G22	-22.70	1.68
G23	-20.43	28.23
G24	55.46	2.73
G25	36.03	10.95
G26	0.42	-12.51
G27	10.68	-9.92
G28	54.81	-1.65
G29	15.81	-7.13
G30	20.20	9.79

Appendix III (Cont'd)

Genotypes	Z1	Z2
G31	49.13	5.92
G32	49.57	-11.36
G33	26.16	25.61
G34	-25.52	1.05
G35	6.99	-7.08
G36	-31.84	5.66
G37	13.44	3.61
G38	52.08	-0.70
G39	-56.71	3.88
G40	25.93	8.00
G41	-10.71	-16.02
G42	-0.35	-8.00
G43	0.24	8.58
G44	16.86	18.53
G45	-21.07	15.36
G46	-62.98	-2.99
G47	-65.49	19.13
G48	-13.59	8.66
G49	-69.33	7.70
G50	38.62	2.97
G51	34.40	3.30
G52	69.50	-0.31
G53	54.65	-1.84
G54	-34.25	-8.12
G55	-4.47	-3.94
G56	-82.31	10.15
G57	-62.90	6.48
G58	56.46	-10.50
G59	-89.16	-1.96
G60	11.51	25.98