CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS IN RICE (*Oryza sativa* L.)

BY

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CERTIFICATE

This is to certify that thesis entitled, **"CHARACTERIZATION AND GENETIC DIVERSITY ANALYSIS IN RICE (Oryza sativa L.)"** submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE** in **GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by **MD. ABDUR RAHIM**, Registration No. **26195/00489** 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, 2006
Place: Dhaka, Bangladesh

(Dr. Md. Sarowar Hossain)
Supervisor

Dedicated to
My
Beloved Parents

LIST OF ABBREVIATIONS AND SYMBOLS

Full word	Abbreviation
Agro-Ecological Zone	AEZ
And others	*et al.*
Bangladesh Bureau of Statistics	BBS
Bangladesh Rice Research Institute	BRRI
Centimeter	cm
Coefficient of variation	CV
Days after transplanting	DAT
Degree Celsius	°C
Degrees of freedom	d.f
Etcetera	etc.
Food and Agriculture Organization	FAO
Figure	Fig.
Genetic Advance	GA
Gram	g
Genotypic Coefficient of variation	GCV
Genotypic variance	σ^2_g
Hectare	ha
Heritability in broad sense	h^2_b
Hydrogen ion potentiality	p^H
Journal	*J.*
Kilogram	kg
Leaf area index	LAI
Meter	m
Mean sum of square	MS
Millimeter	mm
Modern variety	MV
Muriate of Potash	MP

LIST OF ABBREVIATIONS AND SYMBOLS

Full word	Abbreviation
Number	no.
Percent	%
Phenotypic coefficient of variation	PCV
Phenotypic variance	σ^2_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Square meter	m^2
Triple Super Phosphate	TSP
United Kingdom	UK

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By

MD. ABDUR RAHIM

ABSTRACT

A field experiment was conducted with 36 rice genotypes at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka to study the characterization and genetic diversity analysis in rice (*Oryza sativa* L.) during November 2005 to May 2006. 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 spikelet sterility % followed by effective tillers per plant, total tillers per plant and grain yield per plant, whereas days to 50% flowering 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. Different multivariate analysis techniques were used to classify 36 rice genotypes. All the genotypes were grouped into five clusters. Principal component analysis, principal coordinate analysis, canonical variate analysis gave similar result. Cluster I had maximum (12) and both cluster III & IV had minimum (2) number of genotypes. The highest intra-cluster distance was found in cluster I and the lowest in cluster IV among five clusters. The highest inter-cluster distance was observed between cluster I and IV and the lowest between cluster II and III. The characters- effective tillers per plant, 1000-grain weight and harvest index contributed maximum towards divergence among the rice genotypes. Considering genetic diversity and other agronomic performance the genotypes G10, G23 and G36 from cluster I; G12, G16 and G33 from cluster II; G31 from cluster III and G21, G22 from cluster IV might be selected as suitable parents for future uses in hybridization program.

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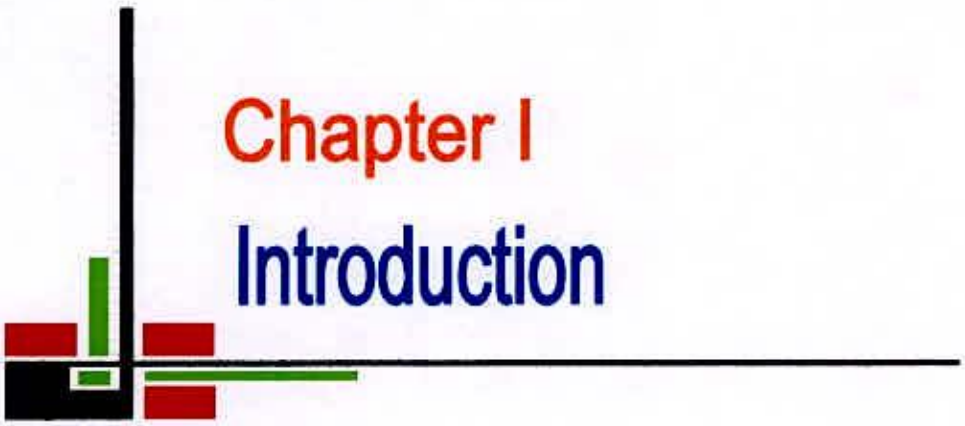


Chapter I

Introduction

CHAPTER I
INTRODUCTION

Rice (*Oryza sativa* L.) is the second most important food crop next to wheat of the world. Over 150 million hectares are planted to rice worldwide with a production of around 375 million tonnes. Feeding more than one half of the world's population, over 90% of rice is produced and consumed in Asia (Chopra, 2001).

Bangladesh is heavily dependent on rice. Rice is and will be the main item in daily food intake by the people of Bangladesh. In Bangladesh, rice is grown on about 11.200 million hectare of land and production is 42.304 million metric tonnes with 3.78 tonnes per hectare average yield in Bangladesh (Anon., 2006). Rice provides, on the average, 76% caloric and 66% protein intake of the people's diet (Haque and Masuduzzaman, 2002).

The demand for rice depends primarily on the size of population that the nation is like to have in the future. Rice is the staple food for her people and will remain so in the future. It grows in all the three crop-growing seasons of the year and occupies about 77% of the total cropped area of about 13.9 million hectare. Presently, rice alone constitutes about 92% of the total food grains produced annually in the country (BBS, 2004).

The total rice growing area did not change much since the independence of Bangladesh in 1971, but there has been a major shift in rice cultivation. Over the last three decades, the area under the high-yielding Boro rice has increased from 0.8 to 3.4 million ha, at the expense of the very low yielding and risky deepwater Aman and upland Aus rice crops. Over this period, the area under Aus rice has

declined from 3.4 to 1.35 million hectare and that of deepwater Aman rice, from 2.1 to 0.77 million hectares. Modern varieties make up of about 94% of Boro (irrigated) rice (Bhuiyan *et al.*, 2002).

Grain yield is the product of the number of panicles per unit area x number of spikelets per panicle x Percent fertility of spikelets x weight of single grain. The grain length is affected least by the environment. 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. Another area of research to break present yield ceiling in rice that merits urgent attention is the improvement of harvest index. Harvest index is the proportion of biological yield that is channelized into usable plant material such as grain, fiber, sugar etc., and thus is a measure of partitioning efficiency of photosynthesis. Increase in harvest index is likely to be more suitable for highly productive environment (Kawano, 1990). For effective use of advanced lines in hybridization program it necessary to characterize al 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 with enhanced genetic yield potential combining desirable 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 rice genotypes is considered to be most importance.

A plant breeding program can be divided into three steps viz., building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Kempthorne, 1957).

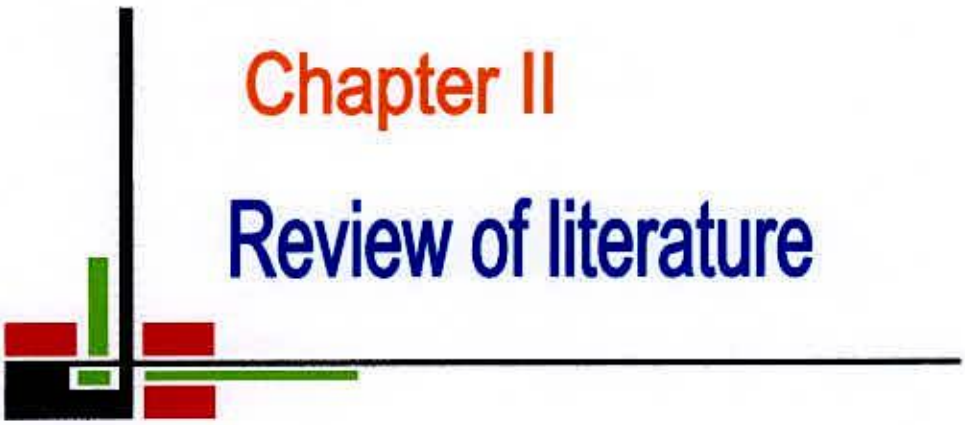
In order to increase the frequency of desired genotypes in breeding progenies, superior parents with high breeding values are needed. Variability and genetic

diversity are the fundamental law of plant breeding which is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973).

Genetic diversity is one of the criteria of parent selection. It is a prerequisite for an efficient plant breeding program. 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. Recent works indicate that the Mahalanobis generalized distance (D^2-statistic) may be an efficient tool in the quantitative estimation of genetic diversity. The divergence analysis has a definite role to play in an efficient choice of divergent parents for hybridization to exploit maximum heterosis. Genetic diversity is essential to meet the diverse goals such as producing cultivars with increased yields, wider adaptation, desirable quality, pest and disease resistance. Inclusion of 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 advanced lines of rice, therefore, was undertaken with the following objectives:

Objective

- To characterize the morphological and yield components of rice germplasm
- To determine the genetic variability of some important quantitative characters among rice germplasm
- To assess the contribution of the different traits towards divergence
- To identify suitable diverse germplasm for the utilization in hybridization program.



Chapter II

Review of literature

CHAPTER II
REVIEW OF LITERATURE

Studies available on characterization and genetic diversity analysis in rice (*Oryza sativa* L). The components of present investigation concerning objectives of present study were studied by number of workers. Thus, after screening wide spectrum of literature available in these aspects, some of the most relevant ones are presented under the following headings:

a) Characterization of rice genotypes

b) Genetic diversity

a) CHARACTERIZATION OF RICE GENOTYPES

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.

Genetic variability and correlation coefficients were studied by Basak and Ganguli (1996) on yield and yield component characters in a set of gamma-radiation induced mutant lines of scented local rice cultivar (*Oryza sativa*) in

two successive generations (M_4 and M_5) during kharif. High genetic advance in percent of mean combined with high genotypic coefficient of variation (GCV) and high heritability were recorded for number of filled grains per panicle, number of tillers and panicles per plant in M_4 generation and number of spikelets per panicle, panicle exsertion, 1st leaf angle, 2nd leaf angle, flag leaf angle and area of flag leaf in M_5 generation. The genotypic correlations, in general, were higher than the corresponding phenotypic correlation coefficients. The estimates of genotypic and phenotypic correlation coefficients between number of filled grains per panicle and harvest index showed strong positive association with grain yield in both M_4 and M_5 generations.

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.

Chaubey and Singh (1994) conducted a field experiment with 20 rice varieties and reported that high heritability for total number of spikelets followed by grain yield per plant and 1000-grain weight. Genetic advance in percent of mean were higher for grain yield per plant followed by panicle length and total number of spikelets.

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 per cent flowering. Moderate genotypic and phenotypic coefficient of variations was 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).

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).

Mani *et al.* (1997) conducted a field experiment with twenty-four genotypes of basmati rice for six panicle characters at Pantnagar during 1993 to investigate the extent of genetic variation and interrelationship among them. A wide range of variation was recorded for all the traits. A high estimate of heritability coupled with high genetic advance for number of filled grains/panicle suggested the predominance of additive gene action for this character. Study of genotypic and phenotypic correlation coefficients indicated that number of secondary branches/panicle and number of filled grains/panicle were positively associated with grain yield/panicle.

A Some 45 indigenous genotypes from different agro-climatic regions of Uttar Pradesh were evaluated Singh *et al.* (1998) for 13 yield-related traits. From the data obtained, information on genetic variability, heritability and correlation coefficients is derived. Most of the characters exhibited high heritability coupled with high genetic advance. Positive and significant genotypic correlations were observed for test weight with grain density, amylose content and grain length; grain breadth with volume expansion; and hulling percentage with milling percentage, water uptake and volume expansion.

The variability, heritability and genetic advance of 30 genotypes of upland paddy were investigated by Moon *et al.* (1996). Plant height and the number of grains/panicle recorded the greatest values for all parameters, indicating a high scope of selection. Panicle length, 1000-grain weight and sterility percentage can be improved if the genotypes are grown under different environmental

conditions and are subjected to recurrent selection. Selection for the number of tillers/per plant was ineffective, as indicated by low values for all parameters.

Thirty genotypes of rice including 16 local varieties and 14 high yielding varieties/advanced lines were evaluated by Borbora and Hazarika (1998) for 11 yield-related traits in trials at Jorhat under 2 sowing dates (10 and 20 July 1995). For the traits studied, information is tabulated on genetic variability, heritability and genotype environment interaction. Highly significant variation among the genotypes was observed for different characters. The differences between genotypic and phenotypic coefficients of variation were relatively low for almost all the characters except grain yield/plant. High to moderate genotypic coefficients of variation together with high heritability and genetic advance were recorded for number of chaffy and filled grains/panicle and 1000-grain weight, grain yield/panicle and number of secondary branches/panicle, indicating the effectiveness of selection for these characters.

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.

Mehetre *et al.* (1996) investigated that information on heritability, yield components and genetic variability was derived from data on 8 characters in the M_2 generation of 8 upland rice varieties treated with gamma radiation (10, 20, 30, 40 or 50 kR). Significant differences occurred among genotypes for all characters. Estimates of heritability ranged from 91.2 (plant height) to 35.6% (sterility). Expected genetic advance ranged from 6.9 (panicle length) to 54.9% (grain yield per plant). Correlation and path analysis showed that filled grain

per panicle, plant height and panicle length are important character for selection in breeding programmes. Multivariate analysis showed that the 75 M_2 families had formed 14 genetically diverse groups.

Shrivastava and Shukla (1996) conducted a field experiment with seven crosses and their F_2 progenies of rice were used to study the genetic variability for seven economic attributes under two fertility levels. The high heritability with high genetic advance as a percentage of mean (GA% mean) were noted for tillers/plant in the cross Madhuri X IR 50, days to 50% of flowering in Madhuri X R-2389 and for biological yield/plant in cross Kranti X IR 50 and Kranti X Poorva. Cross BG 35-2 X Madhuri exhibited high phenotypic covariance (PCV) associated with high genotypic covariance (GCV) and also with high genetic advance as a percentage of mean (GA% mean). It is concluded that mass selection could be practiced on the basis of PCV estimates in non-segregating populations.

Dhananjaya *et al.* (1998) evaluated 121 elite homozygous rice genotypes at Shimoga in kharif 1994. Most variation was observed for productive tillers/plant, number of fertile spikelets and grain yield/plant. Grain yield was positively correlated with harvest index, panicle density, number of fertile spikelets, 1000-grain weight, number of productive tillers and 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).

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 spikelet fertility percentage. High heritability with high genetic advance indicates heritability due to additive gene effects and selection may be effective for related characters.

Bollich (1995) studied the several economic characters in rice and described that the date of 50 percent flowering in rice crosses had the feature of both quantitative and qualitative nature. Earliness was generally expressed with a high degree of parental dominance over lateness. The parental difference was apparently controlled by one major gene pair and a number of modifying genes.

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.

Lu (1988) studied correlation and heritability of quantitative characters and concluded that: 1) correlated heritabilities between grain weight per plant and effective panicle number per plant, grain number per panicle, 1000-grain weight, panicle length, plant height were 0.01, 0.28, 0.01, 0.32 and 0.20, respectively; 2) grain number per panicle had the greatest direct effect on grain weight per plant, followed by 1000-grain weight and effective panicle number per plant.

Narendra and Reddy (1997) conducted an experiment with 11 hybrid rice genotypes exhibited high levels of variability for all 7-yield components. The components grains perpanicle and 1000-grain weight were under the influence of additive genetic effects indicating their role in crop improvement. Straight selection of grain yield and straw yield per plant also indicated better scope for crop improvement. Selection through panicle length and plant height was found ineffective as they are much influenced by environmental effects.

The genetic variability of ten characters, and association and path coefficients among these characters, were evaluated by Basavaraja et al. (1997) in the F_4 populations of 2 crosses (HP32/HP5 and HP32/Pak Basmati) together with the pure line varieties Basmati 370 and Pusa 150 in trials conducted at Shimoga during summer 1992. High estimates of phenotypic coefficient of variation together with high to moderate heritability and genetic advance were observed for total tillers per plant, productive tillers per plant and total spikelets per panicle, while grain yield per plant showed low heritability and genetic advance. Grain yield was positively and significantly associated with plant height, productive tillers pet plant, panicle weight, total spikelets per panicle

and percentage spikelet fertility. Productive tillers per plant had a high positive direct contribution towards grain yield per plant. The indirect effects of other characters through productive tillers were moderate.

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.

Vange and Ojo (1997) studied genetic variation, heritability and genetic advance from data on 12-grain yield-related characters in 10 early and 12 midseason cultivars grown during 1994-95 at Makurdi. Considerable differences were observed for all traits in each maturity group.

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.

Some 34 cold tolerant rice genotypes were evaluated by Kumar *et al.* (1998) over 3 locations in Karnataka in the winter of 1990-91. High genotypic coefficient of variability together with heritability and genetic advance was observed for plant height, total tillers/hill, flag leaf length, panicle length, spikelet fertility, 1000-grain weight and grain yield. High positive correlation was observed of grain yield with plant height, panicle length, spikelet fertility and 1000-grain weight. Path analysis showed high direct effect of spikelet fertility and moderate direct effects of plant height, panicle length and 1000-grain weight to yield. Therefore, direct selection for plant height, panicle length and spikelet fertility is recommended.

Biswas *et al.* (2000) investigated variability on 30 advanced breeding lines of rice for variability study and found that plant height, 1000-grain weight and filled grain per panicle showed high genetic coefficient of variation and heritability in broad sense coupled with high genetic advance in percentage of mean.

Choudhury and Das (1998) studied variability, heritability and genetic advance as well as correlation coefficient and path coefficients in eleven deep-water rice varieties for yield and its attributing characters. High genotypic coefficient of variation was observed in grain yield followed by grains per panicle. High heritability with high genetic advance was found for grains per panicle followed by grain yield. Significant positive correlations were observed for days to 50% flowering, days to maturity, plant height, grains per panicle and panicle length with yield. Direct effects of panicle length, days to maturity, grains per panicle and plant height were high and positive.

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.

An experiment conducted by Reddy *et al.* (1996) with 36 rice genotypes at Cuttack, India during the wet season of 1995. Among the different character studied, number of grains per panicle and 1000-grain weight showed high genetic advance along with moderate to high heritability.

Sarma *et al.* (1996) studied 39 upland rice genotypes for 12 yield components during kharif 1993 at Varanasi, Uttar Pradesh. There was strong variability between the genotypes for the traits studied. Genotypic coefficient of variation (GCV) was the highest for the efective tillers per meter row length, followed by panicle weight, secondary branch per panicle, grain yield per meter row length and spikelets per panicle. Broad sense heritability estimates ranged from 42.2% for grain yield per meter row length to 99.9% for grain length. Effective tillers per meter row length, panicle weight, secondary branch per panicle and spikelets per panicle had high GCV and high heritability. Genetic advance as a percentage of mean was the highest for the effective tillers per meter row length (77.3%), followed by panicle weight (53.9%). The genotypes were grouped into ten distinct clusters. The highest genetic divergence was between cluster V and VI.

Chaubey and Richharia (1993) conducted an experiment to find out genetic variability, simple correlations and path coefficient on 8 quantitative characters in 80 *indica* rice varieties, including HYV and indigenous high quality rices in two environments each at two locations during rainy season. Statistical analyses were done based on character means on pooled data. A wide range of variation was recorded for most of the characters. Heritability in broad sense was very high for all the characters except harvest index. Spikelets per panicle and plant height exhibited high heritability coupled with high genetic advance. Grain yield per plant showed significant positive correlation with plant height, panicle length, spikelets per panicle, panicle weight and test weight. Path analysis indicated a great contribution of panicle weight to grain yield.

Govindaswami *et al.* (1973) concluded that plant height showed very phenotypic and genotypic variance, where as, the variance was average for number of panicles per hill, grain yield per plant and 1000-grain weight.

Information on genotypic and phenotypic coefficients of variability, and on heritability and genetic advance, were derived by Selvarani and Rangasamy (1997) from data on 9 yield related traits in the parents and F_2 progeny of 3 rice crosses (IR50 X TNAU801793, ASD16 X ACM27 and ADT37 X TNAU88022).

The nature and magnitude of genetic variability, interrelationship and coheritability 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 value. 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).

Datke *et al.* (1997) conducted a field experiment with 24 F_6 lines of paddy rice derived from the crosses Taichung Native 1 X Zinia 63, SKL6-1-23 X Zinia 63, SKL6-1-23 X Zinia 31 and RPW6-17 X Iswarkora for 8 quantitative characters at the National Agricultural Research Project, Sakoli, Maharashtra, during kharif 1988-89. All lines showed significant differences for all the characters studied, except number of effective tillers per plant and straw yield/plant. Genetic coefficient of variation was high for grain yield per plant whereas estimates were low to moderate for the remaining traits. High heritability values were associated with high genetic advance with respect to days to 50% flowering, plant height, number of spikelets per panicle and grain

yield/plant, indicating the presence of additive genes. Selection for these characters therefore has the most potential for further improvement.

Saravanan and Senthil (1997) observed heritability from data on 10 yield components in 3 male sterile lines (IR58025A and IR62829A) and their F_1 hybrids. They found high heritability for plant height (99.15%) followed by days to 50% flowering (98.2%) and productive tillers/plant (98.19%).

Anand (1998) investigated genotypic and phenotypic coefficient of variation, heritability, expected genetic advance and character association of grain yield and its contributing characters in 40 F_1 hybrids and their parents under cold stress conditions. Number of filled grains per panicle, seed set percentage, number of chaffy grains per panicle and grain yield/plant showed high variability, heritability and high genetic advance as a percentage of the mean. Correlation studies revealed that grain yield/plant showed positive genotype correlation with number of filled grains per panicle and seed set percentage, while it showed negative correlation with number of chaffy grains per panicle.

b) Genetic Diversity

The knowledge of genetic diversity in crop plants is the key to success of breeding programs. Selection of diverse parents belonging to distant groups leads to wide spectrum of gene recombination for quantitative traits. The multivariate analysis using D^2-statistic can estimate the amount of genetic diversity in a given set of genotypes in respect of several morphological traits considered together.

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.

Reddy *et al.* (2004) conducted an experiment to assess the nature and extent of genetic divergence 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 range 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).

Das *et al.* (1993) reported that genetic divergence among 30 rice genotypes measured by Mahalanobis's D^2-statistic based on plant height, effective tiller per plant, panicle length, fertile spikelet per panicle, 1000-grain weight, days to 50% flowering, days to maturity and grain yield per plant. They were grouped the genotypes into twelve different clusters. No parallel relationship between genetic and geographical divergence was observed. Of the 9 different characters only five viz., days to 50% flowering, days to maturity, plant height, effective tiller per plant and 1000-grain weight contributed as much as 93% of the total divergence.

Chauhan and Chauhan (1994) evaluated 44 breeding lines and two improved cultivars under rainfed upland conditions. They grouped the genotypes into twelve clusters using D^2-statistic. Thousand grain weight contributed maximum (43.3%) to the total divergence. Other traits with appreciable contribution to total divergence were days to 50% flowering, panicle weight and spikelets/panicle.

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.

Vivekananda and Subramanian (1993) reported the nature and magnitude in 28 genotypes of rainfed rice using Mahalanobis's D^2-statistic. The population was grouped into five clusters. Plant height and grain yield contributed considerably, accounting for 85% of total divergence. The geographical diversity has not been found related to genetic diversity.

Mahajan *et al.* (1981) pointed out the genetic diversity (D^2-statistic) for 11 characters related to yield in 60 cultures of rice developed from 14 crosses involving 23 parents. The 60 cultures were grouped into 18 clusters. Mostly the cultures in a cluster came from the cross. The geographical diversity was associated with genetic diversity to some extent. Seven cultures were identified genetic diversity, high yield component and multiple resistances to be utilized as parents in future rice breeding program.

Balram *et al.* (2004) stated that the estimation of D^2 resulted in grouping the germplasm into 6 clusters. Maximum genotypes are in the cluster III followed by cluster II through the survey was conducted in geographically small area, existence of six clusters among these shows that they are not genetically related. Among the characters studied, days to 50% flowering and test weight with 35.8% and 33.0%, respectively contributed maximum to the total

divergence. Panicle length exhibited least contribution of 0.47% to the divergence. The cluster mean for each character indicated that days to 50% flowering was maximum in cluster VI, plant height in cluster II, panicle length in cluster I, productive tillers per plant in cluster V, grain/panicle in cluster IV, test weight in cluster I and grain yield in cluster VI. It would be logical to effect cross among the genotypes belonging to different clusters and selection within cluster with maximum inter-cluster distance to improve the rice grain yield.

Prasad *et al.* (2004) conducted an experiment with 49 genotypes of basmati rice in two consecutive years (1998 and 1999) using Mahalanobis's D^2-statistic to identify the genotypically diverse parental lines and also to study the stability of character expression from year to year. Al the genotypes were grouped into four clusters in year wise analysis. But only three clusters were formed by the pooled analysis of the data over years. Maximum intra-cluster distance was noted in cluster III (D=46.05) in 1998, cluster II (D=43.44) in 1999 and again in cluster II (D=34.87) in the pooled analysis. Cluster I showed minimum intra-cluster distance in both the (26.70 and 20.59 in 1998 and 1999, respectiely) as well as the pooled analysis (D=19.69). Maximum inter-cluster was observed between clusters III and IV during both the years (D=209.54 and 140.2 in 1998 and 1999, respectively) while minimum inter-cluster distance was observed between clusters I and II in year wise analysis (D=37.44 and 34.94 in 1998 and 1999, respectively). However, in the pooled analysis, maximum inter-cluster distance was found between clusters II and III (D=84.99) and minimum between clusters I and II (D=29.24).

Kanwal *et al.* (1983) studied genetic diversity on 100 strains using Mahanobis's D^2-statistic and canonical analysis revealed that panicle weight, days to maturity, height and grain size contributed most towards divergence. The strains were grouped into nine clusters, which were not correlated geographical diversity.

Julfiquar *et al.* (1985) observed divergence among 100 elite lines (67 Restorers and 33 Maintainers from 68 cross made at IRRI) and concluded that these maintainers and restorers, which were grouped under different clusters could be used in crossing programme to produce heterotic F_1 hybrids.

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 lines was used to 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.

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

Genetic divergence studies were conducted by Singh *et al.* (1999) using 42 genotypes of rice in the boro season of 1996-97 at Rajendra Agricultural University farm at Pusa. Eleven quantitative characters, including grain yield

were considered for the study. Multivariate analysis revealed considerable genetic diversity in the material and led to their grouping into four clusters. No relationship between geographic origin and genetic diversity was observed. Harvest index, total number of grains per panicle, number of fertile grains per panicle and standability accounted 90.6% of the total divergence.

Pradhan and Roy (1990) conducted a field experiment on 25 breeding lines of rice from diverse pedigree, undertaken in two levels of water regimes (shallow and intermediate water), revealed six and seven cluster of varying constellations. The composition of clusters differed in two situations due to produce genotype environment interactions. Under both the situations, 1000-grain weight showed the highest contribution to D^2 values.

Sarathe and Perraju (1990) stated genetic diversity and heterosis in 65 rice varieties grouped into 18 clusters. Eight varieties were selected from these clusters on the basis of diversity estimates and popularity of variety. The 28 possible hybrid along with 8 parents fall into as many as 9 clusters. Direct relationship between genetic distance and heterobeltiosis did not occur but parental diversity seems to play an important role in expressing the positive heterobeltiosis. Most of the crosses did not show any relationship with divergence estimates.

Ibrahim *et al.* (1992) investigated that the genetic divergence in upland rice population comprising nine morphologically different genotypes over the different genotypes over the different environment (E) has been assessed through Mahalanobis's D^2 analysis. The analysis revealed considerable genetic diversity among genotypes. The genotypes under study fall into 3 constellations in E_1, E_2 and E_3 in D^2. Poonagar, an indigenous short duration tall stature genotype, consistently occurred either in the same or closely related cluster in both stress (E_1 and E_3) and non-stress condition.

Anandakumar and Subramanium (1989) carried out an experiment with 23 drought resistant varieties during the 1987 wet season, using Mahalanobis' D^2 analysis, for plant height, productive tillers, boot leaf length and breadth, and yield. Using Tochers' clustering technique genotypes were grouped into 6 clusters. Clustering patterns failed to reveal any relationship between geographic divergence and genetic variability. Several clusters were highly divergent and use of these genotypes (E45, IR9575 Sel, Moongil Samba) in breeding programs may result in a large degree of heterosis.

In the basis of D^2 analysis of 10 characters, 67 random genotypes from the Assam Rice Collection (ARC) together with 2 genotypes from each of the subspecies *indica, japonica, javanica* and *ponlai* were grouped into 13 clusters, with 100-grain weight and grains/panicle making the greater contributions to D^2 values. The genetic diversity of the ARC strains indicated the importance of the northwestern region of India as a source of diverse germplasm. It is suggested that *javanica* strains could be synthetic assemblages of *indica* and *japonica* genotypes (De *et al.*, 1988).

Singh *et al.* (1996) showed the nature and magnitude of genetic divergence in 40 genotypes of scented and fine rice using Mahalanobis D^2-statistic for ten characters. The population was grouped into six clusters. Grain yield contribute the most, 40.6% of total divergence and plant height contributed 16.5%. The genotypes belonging to cluster II and V having greater cluster distance are recommended for inclusion in a hybridization program as they are expected to produce good segregants.

Seventeen varieties known to possess some degree of cold tolerance at different stages and their 102 F_1 hybrids with 6 male testers were studied by Glaszmann *et al.* (1990) for isoenzyme variation at 15 loci, spikelet fertility, and cold tolerance at various stages. Multivariate analyses of the data separated the varieties into *japonica* and *indica* groups. The *japonica* group displayed

specific isoenzymes, a low F_1 fertility with *indica* testers, and a high degree of cold tolerance which was expressed in the F_1 progenies. The *indica* group displayed contrasting specific isoenzymes, a high F_1 fertility with *indica* testers and a moderate to low degree of cold tolerance which was not expressed in the F_1 progenies. One variety, ARC6000, displayed unique traits and was classified into a distinct type based on isoenzymes. It is suggested that cold tolerance is a major trait for the classification of rice into 2 varietal groups.

Selvakumar *et al.* (1989) studied 8 yield traits in 40 accessions from various geographical areas using the Mahalanobis D^2-statistic; the clustering pattern indicated that geographic diversity was not a reliable guide to genetic diversity. A wide range of variation in intra- cluster mean values was found for each trait. Yield component traits such as number of grains/panicle and number of fertile tillers contributed most to the genetic divergence between genotypes. Genotypes were grouped in 11 clusters and those related by provenance or pedigree tended to fall into the same cluster. The data are tabulated. Gandakasala, in cluster XI, appeared useful as a parent in breeding programmes.

Sarawgi and Shrivastava (1991) conducted a field experiment with sixteen varieties and their 72 F_1 hybrids under irrigated (set I) and rainfed (set II) conditions during 1985 for 7 yield components in order to determine their genetic divergence and heterosis. Parents and hybrids were grouped into 7 and 15 clusters for set I and II, respectively. In set I, cluster 1 included 79 genotypes of which 12 were parents; the other clusters contained only 1-2 genotypes, which showed limited diversity under irrigated conditions. However, significant diversity was noted in set II; cluster 1 contained 25 and cluster 2 had 30 genotypes (with 6 parents). Clusters that were comprised of only hybrids were found to be quite distant from those that contained the parents. Mean grain yield/plant was the highest for cluster 2 in set I (20.16 g) and cluster 13 in set II (40.52 g) and crosses that included Roti, R68-1 or

Kalimai as one of the parents produced the highest grain yields. IR52 X Samridhi showed high heterosis for grain yield and both parents were in the same cluster. This indicated that genetic diversity may not be related to high heterosis.

Biswas and Sasmal (1990) estimated genetic distance using Mahalanobis D^2 statistic in 7 rice varieties and their 21 F_1 hybrids. They were grouped 28 genotypes into 6 clusters. The grouping of parental genotypes did not follow a geographic pattern. Shoot fresh weight was the main factor contributing to genetic variance.

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

Singh *et al.* (1987) grouped fifty lowland rice cultivars into 10 clusters using D^2 analysis of 15 characters related to yield. Clusters I (23 cultivars), II (8) and III (7) were the largest and together accounted for more than two-thirds of the total population. Genetic diversity was not related to geographical diversity. Plant height, sheath length, grain length and breadth, test weight, panicle length and spikelet number were mainly responsible for the divergence. Cultivars Anandi, Adamchini, Bhatafool, Kanakjiri and Motibadam (cluster IV); Dehradoon and Kesar (cluster V); Lanwangchur (cluster VIII); and Jilhore (cluster X) were selected for hybridization on the basis of their genetic diversity and high yield potential.

On the basis of data on root length, number of roots/plant and root fresh and dry weight, 30 rice varieties were grouped into 7 clusters using the D^2 statistic. Distribution among clusters was not related to ecological or geographic origin. Root dry weight made the highest contribution (52.6%) to total genetic variation. One variety from each of clusters I, II and V and 3 from cluster VI were crossed in a diallel without reciprocals. Significant heterosis was observed for all root characters in Dee-Geo-Woo-Gen X Nira, where the genetic distance of parents was moderate, while in other heterotic crosses genetic distance was low (Sasmal, 1987).

Genetic divergence for five reproductive stage, cold tolerance and adaptability-related characters was assessed by Kaw (1995) in 20 rice genotypes and their 74 F_1 hybrids in 3 cold stress environments (Chuncheon, Korea Republic; Upper Swat, Pakistan; and Banaue, Philippines). The genotypes were grouped into 18 clusters. Genetic and geographical diversity were not necessarily related. Traditional *japonica* varieties and *japonica* X *indica* hybrids were distinct from *indica* varieties and *indica* X *indica* hybrids in cluster analysis. Japonica cultivars K332 and Barkat, and *indica* X *indica* hybrids involving Silewah were divergent from both *indica* and *japonica* clusters.

Multivariate analysis of divergence for 7 quantitative traits among 37 strains of *Oryza sativa* was studied by Mishra *et al.* (1994). They were grouped the genotypes into 5 clusters. The first cluster contained 31 genotypes, the second 3, while the third, fourth and fifth cluster each contained 1 genotype. Number of fertile grains/panicle, number of sterile grains/panicle and plant height were the highest contributors of Mahalanobis' D^2 values. On the basis of cluster distances, UPR485-10-1-1, Basmati 370 and Kamod were identified for use in breeding programmes.

Genetic divergence for bacterial blight (*Xanthomonas oryzae*) resistance, grain yield and 9 yield-related traits was studied by Roy and Panwar (1993) in 99

diverse genotypes during 1990 using multivariate D^2 analysis. They were grouped the genotypes into 16 clusters. Since the 51 genotypes in cluster I were of different origin, no association between ecogeographical distribution and genetic diversity was indicated. Genetic divergence was controlled mainly by panicles/plant, grains/panicle, grain yield/plant, spikelets/panicle and bacterial blight severity. The highest distance was between cluster XVI (IRAT133) and cluster XIV (BKN6819-33-3-2-1-3). The results indicated a significant divergence for the traits measured.

Sharma and Hore (1993) conducted a field experiment with seventeen diverse genotypes of upland rice during 1989 and 1990. They grouped into 5 clusters on the basis of D^2 analysis of data on 11 characters. Inter- and intra-cluster distances are given and their use in the selection of parents for breeding programmes is mentioned.

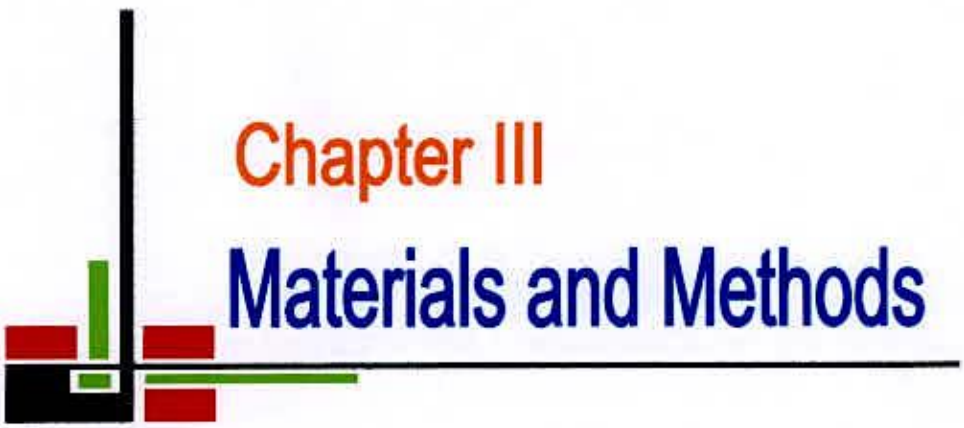
Information on genetic divergence is derived from data on 12 quantitative characters in 28 early maturing genotypes of rice (*Oryza sativa*) grown under direct seeded and transplanted conditions during *rabi*. The genotypes were grouped into 5 and 6 clusters under direct sowing and transplanting conditions, respectively. No correlation was observed between geographical distribution and genetic divergence. Genotype RP670-6-36-14 is recommended as a parent for hybridization and RAU4045-2A for inclusion in a varietal improvement programme (De *et al.*, 1992).

Sinha *et al.* (1991) studied genetic divergence in indigenous upland rice on the basis of the Mahalanobis D^2 statistic calculated for 10 growth and yield related traits. They assigned 30 traditional varieties to one of 6 clusters. Cluster I combined 66.6% of all genotypes while IV, V and VI were monogenotypic. Varieties from the Northeastern region showed the greatest diversity, being represented in all clusters except cluster VI.

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

Bansal *et al.* (1999) studied 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 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.

Kandhola and Panwar observed genetic diversity among 52 indigenous and exotic genotypes of rice using Mahalanobis D^2 statistic in kharif 1996 under 2 sowing dates and 2 nitrogen fertilizer levels. Based on 16 agromorphological and quality characters, these genotypes were grouped into 11 clusters. Cluster I with 26 genotypes was largest, while clusters VII, VIII, IX, X and XI were monogenotypic. There was no association between genetic and geographic diversity. The maximum intercluster distance was observed between genotypes of clusters V and XI (18984.0). It is concluded that hybridization among genotypes drawn from widely divergent clusters with high yield potential is likely to produce heterotic combinations and wide variability in segregating generations.



Chapter III

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

3.1 Experimental Site

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka-1207, during December 2005 to May 2006. The location of the site was situated at 23°41′ N latitude and 90°22′ E longitude with an elevation of 8.6 meter from the sea level (Figure 1).

3.2 Climate and Soil

The experimental site was situated in the sub-tropical zone. The soil of the experimental site lies in Agroecological region of "Madhupur Tract" (AEZ No. 28). Its top soil is clay loam in texture and olive gray with common fine to medium distinct dark yellowish brown mottles. The pH is 4.47 to 5.63 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 Genotypes

Thirty-six genotypes were used in the study. The seeds of 34 genotypes were collected from the Department of Genetics and Plant Breeding, SAU and rest two genotypes were collected from the Genetic Resources and Sub Division (GRSD) of Bangladesh Rice Research Institute (BRRI), Gazipur. Descriptions of the genotypes are given in Table 1.

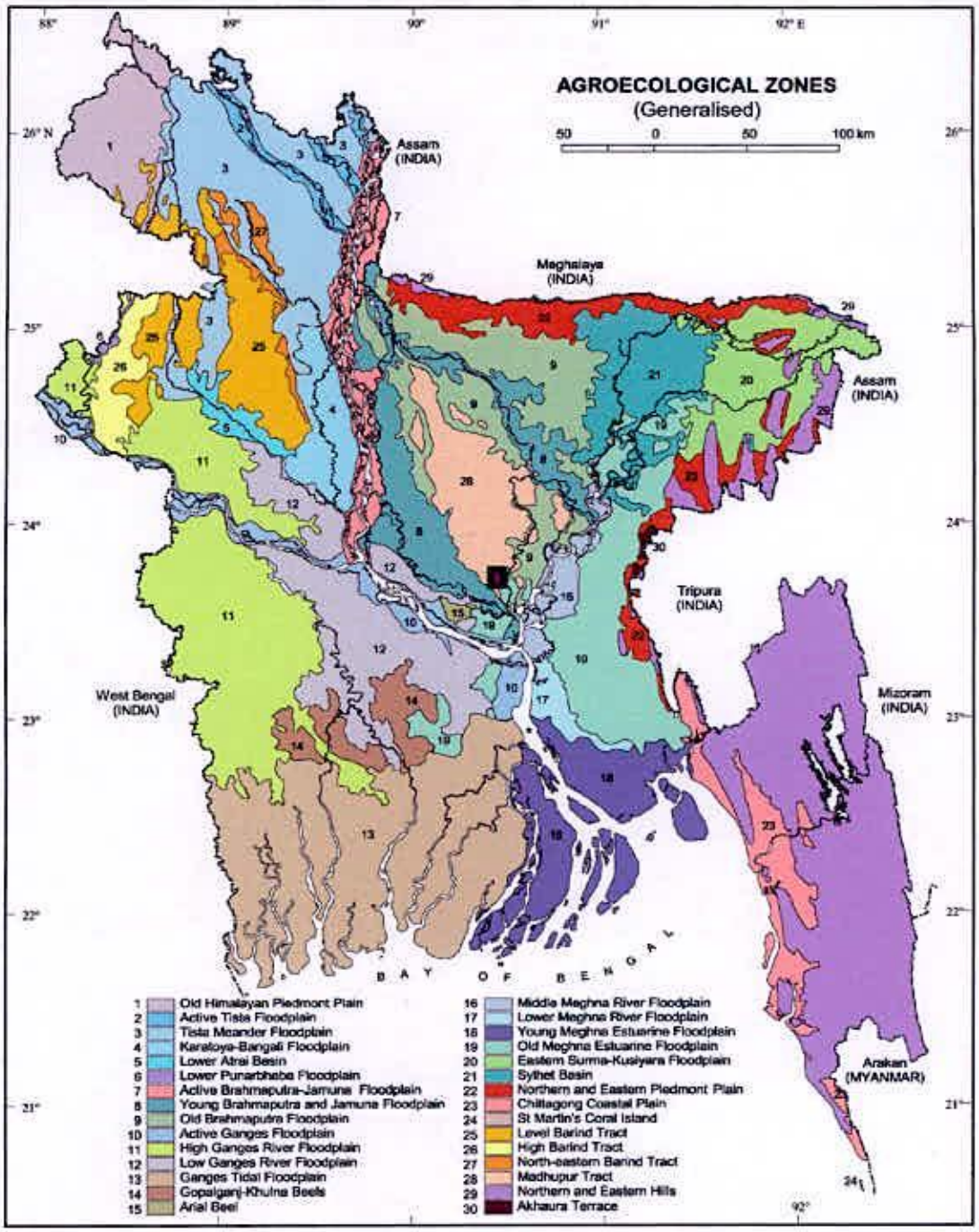


Figure 1. Location of experimental field

Table 1. Sources of 36 rice genotypes

Designation	Genotypes	Sources
G1	AL-1	SAU
G2	AL-9	SAU
G3	AL-10	SAU
G4	AL-12	SAU
G5	AL-13	SAU
G6	AL-14 (I)	SAU
G7	AL- 14 (II)	SAU
G8	AL-16 (I)	SAU
G9	AL-16 (II)	SAU
G10	AL-17 (I)	SAU
G11	AL-17 (II)	SAU
G12	AL-23	SAU
G13	AL-25	SAU
G14	AL-27	SAU
G15	AL-36	SAU
G16	AL-42	SAU
G17	AL-44 (I)	SAU
G18	AL-44 (II)	SAU
G19	AL-45	SAU
G20	AL-47 (II)	SAU
G21	AL-48	SAU
G22	AL-49	SAU
G23	AL-30	SAU
G24	AL-51 (II)	SAU
G25	AL-52	SAU
G26	AL-54	SAU

Table 1. (Cont'd.)

Designation	Genotypes	Sources
G27	R-1	SAU
G28	R-2	SAU
G29	R-4	SAU
G30	R-5 (II)	SAU
G31	R-9	SAU
G32	R-12	SAU
G33	AL-35	SAU
G34	AL-11	SAU
G35	BRRI dhan 28	BRRI
G36	BRRI dhan 29	BRRI

AL = Advanced Line

R = Restorer Line

SAU = Sher-e-Bangla Agricultural University

BRRI = Bangladesh Rice Research Institute

3.4 Design and Layout

The experiment was laid out in Randomized Complete Block Design (RCBD). The field was divided into three blocks; the blocks were sub-divided into 36 plots where genotypes were randomly assigned. The plot size was 3m lengths with single row. Row to row and plant to plant distances were 25cm and 20cm, respectively. The 36 genotypes were distributed to each plot within each block randomly (Plate 1).

3.5 Raising of Seedling

Seeds of all collected rice genotypes were sown on 17th December 2005 in the net house separately and proper tags were maintained.

3.6 Preparation of Main Field

The land was prepared thoroughly by 3-4 ploughing followed by laddering to attain a good puddle. Weeds and stubbles were removed and the land was finally prepared by the addition of basal dose of fertilizers recommended by BRRI.

3.7 Application of Fertilizers

Adequate soil fertility was ensured by applying of Urea, TSP, MP and Gypsum @ 260-77-79-55 kg/ha, respectively. 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 30th January 2006 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.

Plate 1a. Field view of experimental site (Close view)

Plate 1b. Field view of experimental site

3.9 Intercultural Operation and After Care

Necessary gap filling was done within 7 days of transplanting. The crop was kept weed free throughout the growth period. Hand weeding was done at 25 and 40 days after transplanting. Flood irrigation was given to the field when necessary.

3.10 Plant Protection Measure

Proper control measures were taken against rice stem borer during tillering and heading stage of rice. Furadan 5 G @1 kg per square meter was applied at active tillering stage and panicle initiation stage of rice for controlling rice yellow stem borer. Cupravit 80 WP @ 2.5 g per liter water was applied against bacterial leaf blight of rice.

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

Number of days required from date of sowing to 50% plant's panicle emerged from flag leaf.

3.11.2 Plant Height (cm)

Plant height was recorded at the time of maturity from ground level to the tip of main panicle.

3.11.3 Total Tillers per Plant

Total tiller number per plant was counted in all the plants under study.

3.11.4 Effective Tillers per Plant

The tillers having mature grain-bearing panicle was considered as effective tillers.

3.11.5 Panicle Length (cm)

Panicle length was measured from the base to the top of the panicle. The awn part was not measured.

3.11.6 Filled Grains per Panicle

Total number of filled grain of 10 panicles were measured and averaged by dividing with 10.

3.11.7 Percentage of Spikelet Sterility

The number of sterile spikelet of 10 panicle was recorded and sterility percentage was calculated by the following formula:

$$\text{Spikelet Sterility (\%)} = \frac{\text{Number of sterile spikelets of 10 panicles}}{\text{Number of total spikelets of 10 panicles}} \times 100$$

3.11.8 Thousand Grain Weight (g)

Average dry weight (g) of 1000-grains at 14% moisture level was measured.

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.

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

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.

3.11.10 Harvest Index

The dry weight of straw of 10 hills was recorded and harvest index was calculated by the following formula:

$$\text{Harvest Index (HI)} = \frac{\text{Dry weight of grains}}{\text{(Dry weight of grains + Dry weight of straws)}}$$

3.12 Statistical Analysis

All the collected data of the study were used to statistical analysis for each character, analysis of variance (ANOVA), mean, range were calculated by using MSTATC software then analyzed for genotypic and phenotypic variance, genotypic and heritability, genetic advance, and genetic advance in % of mean. Mean data for each character were subjected to both univariate and multivariate analysis. For Univariate Analysis (UA), analysis of variance was done individually by F-test (Panse and Shukatme, 1978). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Vector Analysis (CVA) were done by using GENSTAT[5] software program (Copyright, 1987, Lawes Agricultural Trust, Rothamasted Experimental Station, UK).

3.12.1 CHARACTERIZATION OF RICE GENOTYPES

3.12.1.1 Estimation Phenotypic and Genotypic Variance

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

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

Where,

GMS = Genotypic mean sum of square
EMS = Error mean sum of square
r = Number of replication

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

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

3.12.1.2 Estimation Genotypic and Phenotypic Coefficient of Variation

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

$$\text{Genotypic Coefficient of Variation (GCV)} = \frac{\sigma_g}{\bar{x}} \times 100$$

Where,

σ_g = Genotypic standard deviation
$\bar{x}$ = Grand mean

$$\text{Phenotypic Coefficient of Variation (PCV)} = \frac{\sigma_p}{\bar{x}} \times 100$$

Where,

σ_p = Phenotypic standard deviations
$\bar{x}$ = Grand mean

3.12.1.3 Estimation of Heritability

Broad sense heritability was estimated by the formula suggested by Johnson *et al.* (1955).

$$\% \, h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

h^2_b = Heritability in broad sense
σ^2_g = Genotypic variance
σ^2_p = Phenotypic variance

3.12.1.4 Estimation of Genetic Advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic Advance (GA)} = \frac{\sigma^2_g}{\sigma^2_p} \times K \times \sigma_p$$

Where,

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

σ_p = Phenotypic stander deviation

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.12.1.5 Estimation of Genetic Advance in Percentage of Mean

Genetic advance in percentage of mean was calculated from the formula given by Comstock and Robinson (1952).

$$\text{Genetic in Percentage of Mean} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

3.12.2 Genetic Diversity Analysis

3.12.2.1 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.

3.12.2.2 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).

3.12.2.3 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 examine the effect of swapping two genotypes of different classes, and so on.

3.12.2.4 Canonical Variate Analysis (CVA)

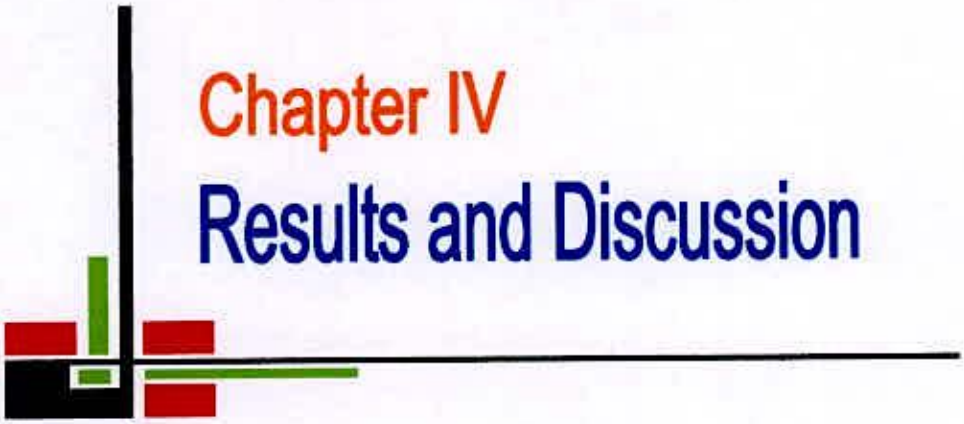
Using canonical vector analysis a linear combination of original variabilities that maximize the ratio in between group to within group variation to be finding out and thereby giving functions of the original variabilities that can be used to discriminate between groups. Thus, in this analysis a series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

3.12.2.5 Computation of Average Intra-cluster Distances

When the clusters were formed, the average intra-cluster distances for each cluster was calculated by taking possible D^2 values within the member of a cluster obtained from the Principal Coordinate Analysis (PCO). The formula used was D^2/n, where D^2 is the sum of distances between all possible combinations (n) of the genotypes included in the cluster. The square root of the average D^2 values represents the distances (D) within cluster.

3.12.2.6 Cluster Diagram

Cluster diagram was drawn using the intra and inter cluster distance. It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.



Chapter IV
Results and Discussion

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study. The data pertaining to ten characters were computed and statistically analyzed and thus obtained results are described below under the following heads:

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 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 10 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.

4.1.1.1 Days to 50% flowering

The analysis of variance (ANOVA) presented in Table 2 showed highly significant value for days to 50% flowering. The highly significant genotypic differences indicated that there was a wide range of variation among the genotypes for days to 50% flowering. The mean value ranged from 95.00 days (G22) to 129.00 days (G35), where as mean performance was 109.90 days. The phenotypic and genotypic variances for this trait were comparatively high (42.02 and 35.80). 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 difference between phenotypic coefficient of variation (5.90) and genotypic coefficient of variation (5.45) was minimum (Table 3). Heritability estimates for this trait was high (85.19) with high genetic advance (14.58) and low genetic advance in percent of mean (13.27). Kaw *et al.* (1999) found low genetic variation for days to flowering. Binse *et al.* (2004) also reported similar result. Pushpa *et al.* (1999) observed high heritability for days to 50% flowering.

4.1.1.2 Plant height

Significant mean sum of square for plant height indicated considerable difference among the genotypes studied (Table 2). Plant height ranged from 85.33 (G33) to 116.72 (G29) with mean value 98.91 (Table 3). The phenotypic and genotypic variances for this trait were comparatively high (60.79 and 44.29). 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 (7.89) was higher than the genotypic coefficient of variation (6.73) (Table 3), which suggested that environment has a significant role on the expression of this trait. Heritability estimates was high (72.87) with high genetic advance (15.00) and moderate genetic advance in percent of mean (15.17) was considerable for this trait indicating apparent variation was due to genotypes. So, selection based on this trait would be effective. This result also have the close agreement with the

Table 2. Mean sum of squres from the ANOVA of 36 rice genotypes in respect of 10 characters

Characters	d.f.			Mean sum of square		
	Replication	Genotype	Error	Replication	Genotype	Error
Days to 50% flowering	2	35	70	10.620^{ns}	113.622**	6.220
Plant height (cm)	2	35	70	88.044**	149.357**	16.499
Total tillers per plant	2	35	70	0.420^{ns}	15.573**	3.558
Effective tillers per plant	2	35	70	2.284^{ns}	14.882**	3.228
Panicle length (cm)	2	35	70	14.973**	10.369**	2.395
Filled grains per panicle	2	35	70	160.225^{ns}	836.886**	324.784
Spikelet sterility %	2	35	70	58.752^{ns}	112.481**	32.687
Thousand grain weight (g)	2	35	70	47.401**	15.861**	3.270
Harvest index	2	35	70	0.002^{ns}	0.005**	0.001
Grain yield per plant (g)	2	35	70	13.909^{ns}	37.608**	11.123

** Significant at 1% level of probability

^{ns} Not significant

findings of Biswas *et al.* (2000), Shanthakumar *et al.* (1998) and Iftekharuddaula *et al.* (2001b).

4.1.1.3 Total tillers per plant

Total tiller number per plant ranged from 8.53 (G22) to 21.80 (G36) with mean value 13.70. The phenotypic variance (7.56) was much higher than genotypic variance (4.01) 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 (14.60 and 20.06, 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 (52.95) for this trait was moderate with high genetic advance in percent of mean (28.05). Shanthakumar *et al.* (1998) reported high heritability and genetic advance for total tillers per plant.

4.1.1.4 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 8.00 (G22) to 20.73 (G26). Phenotypic variance (7.11) was much higher than the genotypic variance (3.88). 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 (22.10) was much higher than genotypic coefficient of variation (16.33) for this trait suggested that environment has a significant role on the expression of this trait. A heritability estimate was also moderate (54.62) with high genetic advance in percent of mean (31.86). Singh and Singh (2004) found high genetic variation, high to moderate value of heritability and high genetic advance in percent of mean.

4.1.1.5 Panicle length

The highest panicle length was found in G30 (26.55) and lowest panicle length was found in G22 (18.67) with mean value of 24.50 (Table 3). The phenotypic variance (5.05) was much higher than genotypic variance (2.66). The phenotypic coefficient of variation (9.18) and genotypic coefficient of variation (6.66) were low. Heritability estimates was moderate (52.60). The genetic advance was very low (3.12) with low genetic advance in percent of mean (12.75). Kaw *et al.* (1999) reported low genetic variation for panicle length. Panicle appearance of some rice genotypes is given in Plate 2.

4.1.1.6 Filled grains per plant

Mean sum of square for filled grains per plant was highly significant (Table 2). The mean values ranged from 123.53 (G12) to 180.20 (G23). The phenotypic variance (495.48) was much higher than the genotypic variance (170.69) suggested that the environment had a significant role for the expression of the character. The phenotypic coefficient of variation (14.87) was much higher than the genotypic coefficient of variation (8.73). Low heritability (34.45) with high genetic advance (20.54) as presented in Table 3. The estimated heritability was the lowest (34.45) among the characters studied. 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.

4.1.1.7 Spikelet sterility percentage

The genotypes showed highly significant differences for spikelet sterility percentage. The mean values ranged from 15.54 (G21) to 39.67 (G33). The component of variation for spikelet sterility percentage showed considerable phenotypic variation (59.29) in comparison to genotypic variation (26.60) suggesting the influence of environment to a great extent for this character (Table 3). The phenotypic coefficient of variation and genotypic coefficient of

Plate 2. Some panicles appearances of different rice genotypes

Plate 2. (Cont'd.)

Table 3. Variability, genetic parameter, heritability (h^2_b), genetic advance (GA) and GA in percent of mean for 10 yield and its related characters in rice

Characters	Range	Mean	MS	σ^2_g	σ^2_p	GCV	PCV	h^2_b	GA (%) (1%)	GA in % of mean (1%)
DFF	95.00-129.00	109.90	113.622**	35.80	42.02	5.45	5.90	85.19	14.58	13.27
PH	85.33-116.72	98.91	149.357**	44.29	60.79	6.73	7.89	72.87	15.00	15.17
TTP	8.53- 21.80	13.70	15.573**	4.01	7.56	14.60	20.06	52.95	3.84	28.05
ETP	8.00- 20.73	12.06	14.882**	3.88	7.11	16.33	22.10	54.62	3.85	31.86
PL	18.67- 26.55	24.50	10.369**	2.66	5.05	6.66	9.18	52.60	3.12	12.75
FGP	123.53-180.20	149.40	836.886**	170.69	495.48	8.73	14.87	34.45	20.24	13.52
SS	15.54-39.67	31.31	112.481**	26.60	59.29	16.48	24.60	44.86	9.12	29.14
TGW	17.83-28.00	22.48	15.861**	4.20	7.47	9.10	12.14	56.21	4.05	18.02
HI	0.32-0.51	0.40	0.005**	0.00	0.00	8.56	12.38	47.75	0.06	15.61
GYP	16.13-30.01	22.36	37.608**	8.83	19.95	13.30	20.00	44.25	5.22	23.36

** Significant at 1% level of probability

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

variation were high, which were 16.48 and 24.60, respectively. The estimated heritability was low (44.86) with high genetic advance in percentage of mean (29.14). High phenotypic coefficient of variation and genotypic coefficient of variation for spikelet sterility percentage was found by Iftekharudaula *et al.* (2001).

4.1.1.8 1000-grain weight

Mean sum of square for thousand grain weight was highly significant (Table 2). 1000-grain weight ranged from 17.83 (G4) to 28.00 (G26) with a mean value of 22.48. The character showed low phenotypic (7.47) and genotypic (4.20) 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 (12.14) was higher than the genotypic coefficient of variation (9.10) for this trait. 1000-grain weight showed moderate heritability (56.21). The genetic advance was low (4.05) and genetic advance in percentage of mean was moderate (18.02). Pushpa *et al.* (1999) observed high habitability for 1000-grain weight. Reddy *et al.* (1996) reported that 1000-grain weight showed high genetic advance along with moderate to high habitability.

4.1.1.9 Harvest index

Analysis of variance for harvest index showed highly significant mean sum of square due to genotypic difference (Table 2). The highest harvest index was observed in G35 (0.51) and the lowest in G28 (0.32). The genotypic and phenotypic variances were nil (0.00). The phenotypic coefficient of variation and genotypic coefficient of variation were 12.38 and 8.56, respectively. The estimated heritability was low (47.75). The genetic advance was low (0.06) and genetic advance in percentage of mean (15.61). Shavani and Reddy (2000) reported high heritability with high genetic advance.

4.1.1.10 Grain yield per plant

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 16.13 (G22) to 30.01 (G23). The phenotypic variance (19.95) was much higher than the genotypic variance (8.83) suggested that the environment had a significant role for the expression of the character. This trait showed high genotypic (13.30) and phenotypic (20.00) 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 low (44.25). The genetic advance was low (5.22) and genetic advance in percentage of mean was high (23.36). Singh and Singh (2004) observed high genetic coefficient of variation and high to moderately high heritability and high genetic advance in % of mean. Pushpa *et al.* (1999) also reported high heritability for grain yield. Grain appearance of different rice genotypes is presented in Plate 3.

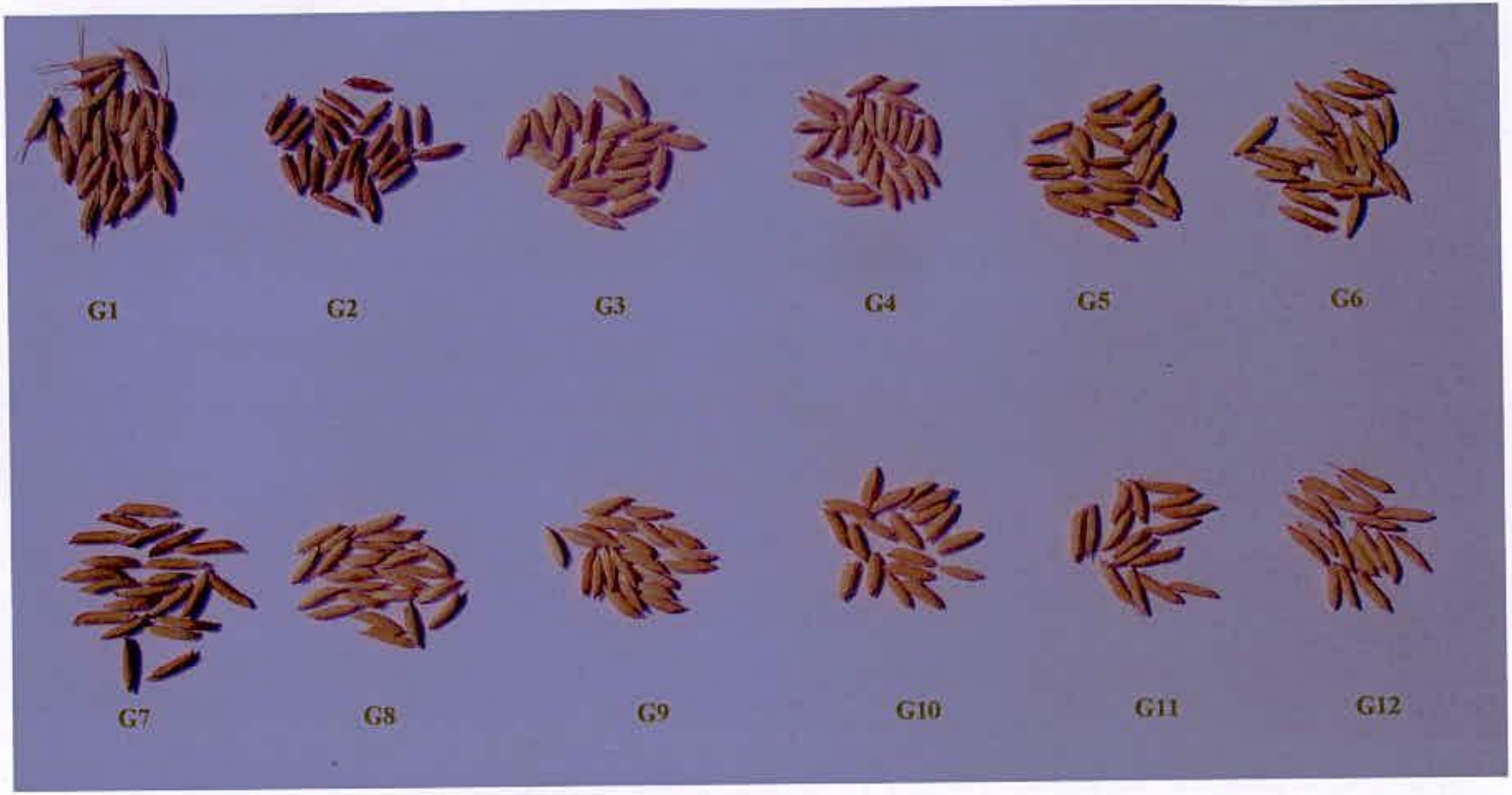


Plate 3. Grain appearance of different rice genotypes

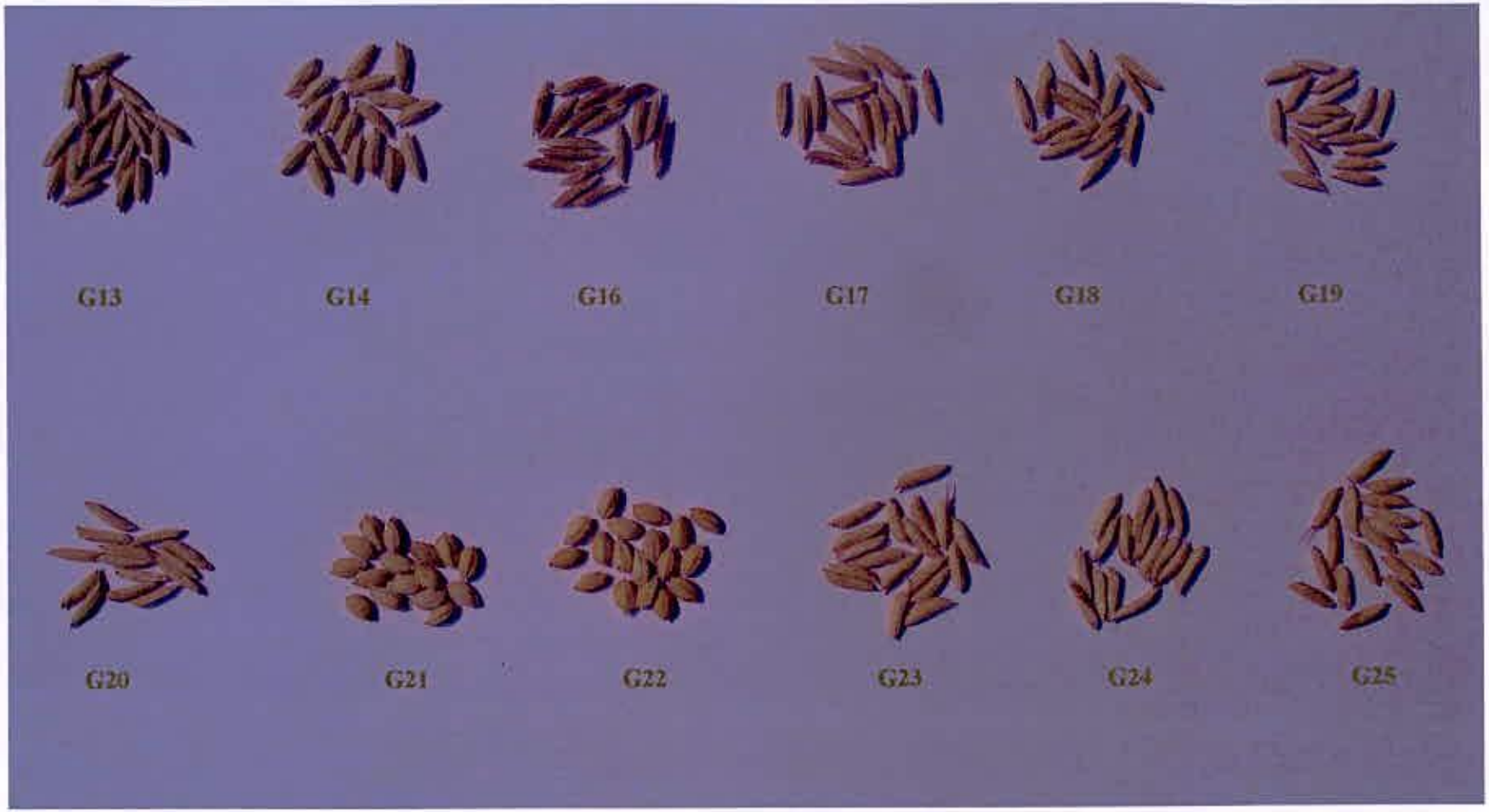


Plate 3. (Cont'd.)

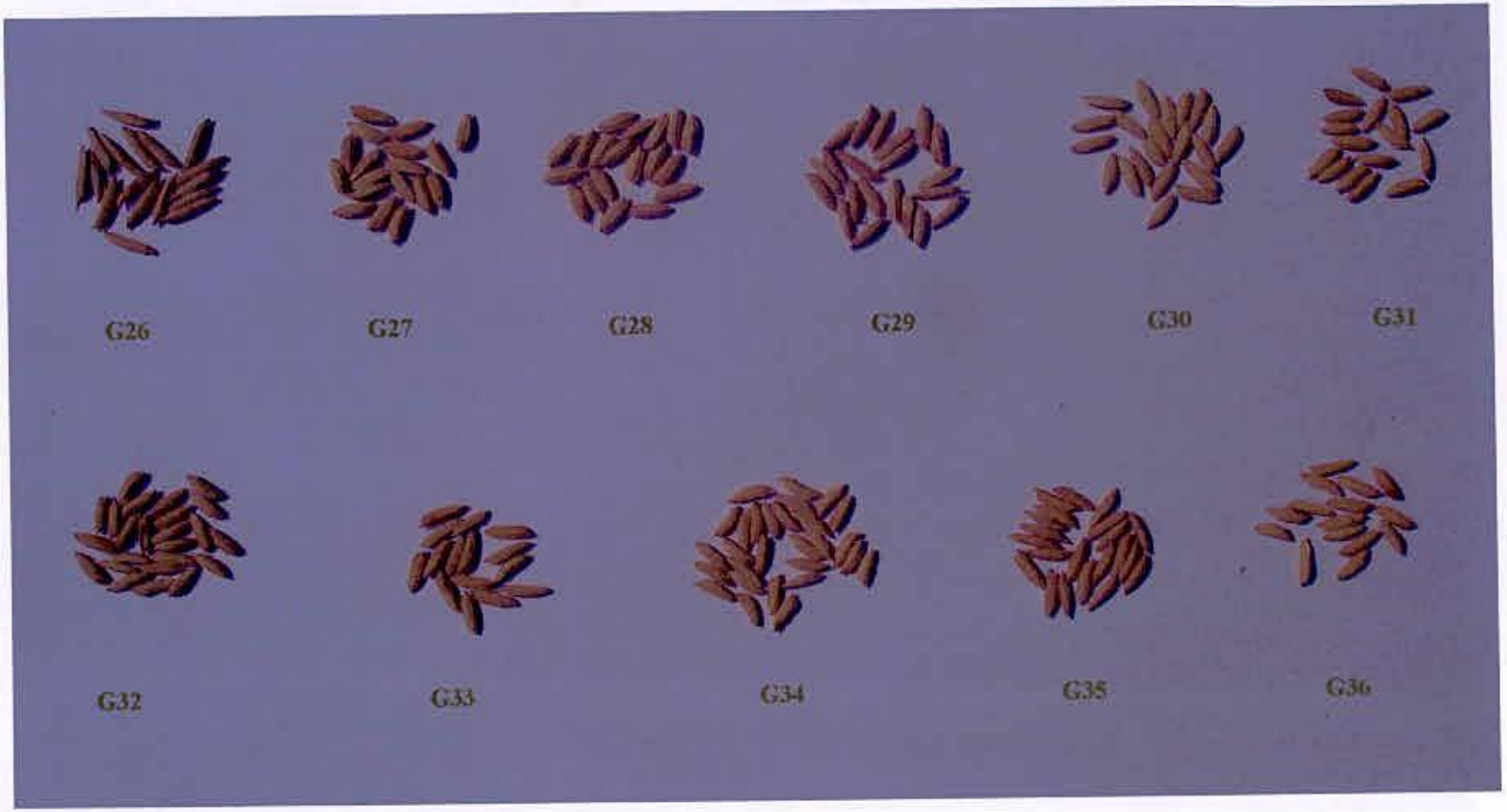


Plate 3. (Cont'd.)

4.2 DIVERSITY OF THE RICE GENOTYPES

The results of the genetic diversity of rice genotypes are presented in Table 4 to 9 and Figure 2 to 4.

4.2.1 Principal Component Analysis (PCA)

The principal component analysis produce 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 70.39% (Table 4). The first two principal axes accounted for 54.87% of the total variation among the 10 characters describing 36 rice genotypes. On the basis of principal axes I and II, a two dimensional chart (Z_1-Z_2) of the genotypes are presented Figure 3. The scatter diagram revealed that there were five apparent clusters. The genotypes were distantly located from each other (Figure 3).

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 (1.5425) was observed between the genotypes G36 and G22 followed by G36 and G21 (1.4260), G24 and G22 (1.2229), G33 and G22 (1.1943), G33 and G21 (1.1630) and the lowest distance was observed between the genotypes G16 and G3 (0.1520) followed by G28 and G9 (0.1630), G16 and G14 (0.1639), G26 and G3 (0.1647) (Table 5). By using these distances from distance matrix intra-cluster distances were calculated (Table 8) as suggested by Singh and Choudhury (1979). The highest intra-cluster distance was observed in cluster I (2.4875), which is composed of 12 genotypes followed by cluster II (1.7902) with 11 genotypes. The cluster IV showed the lowest intra-cluster distance (0.1481) composed of only two genotypes, which is almost similar with cluster III (0.1648). These results revealed that the genotypes in cluster I were distantly related on the other hand the genotypes in cluster III were closely related.

Table 4. Eigen values and percentage of variation in respect of 10 characters in 36 rice genotypes

Principal component characters	Eigen values	Percentage of total variation accounted for	Cumulative percentage
Days to 50% flowering	3.695	36.95	36.95
Plant height (cm)	1.792	17.92	54.87
Total tillers per plant	1.552	15.52	70.39
Effective tillers per plant	0.955	9.55	79.94
Panicle length (cm)	0.623	6.23	86.17
Filled grains per panicle	0.471	4.71	90.88
Spikelet sterility percentage	0.402	4.02	94.90
Thousand grain weight (g)	0.290	2.90	97.80
Harvest index	0.203	2.03	99.83
Grain yield per plant (g)	0.018	0.18	100.00

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

10 higher D^2 values	Genotypes combination	10 lower D^2 values	Genotypes combination
1.5425	G36 & G22	0.1520	G16 & G3
1.4260	G36 & G21	0.1630	G28 & G9
1.2229	G24 & G22	0.1639	G16 & G14
1.1943	G33 & G22	0.1647	G26 & G3
1.1630	G33 & G21	0.1747	G34 & G17
1.1599	G24 & G21	0.1782	G27 & G18
1.1130	G25 & G22	0.1808	G30 & G15
1.1107	G22 & G19	0.1925	G15 & G12
1.0846	G36 & G9	0.1928	G12 & G7
1.0698	G36 & G8	0.1997	G24 & G1

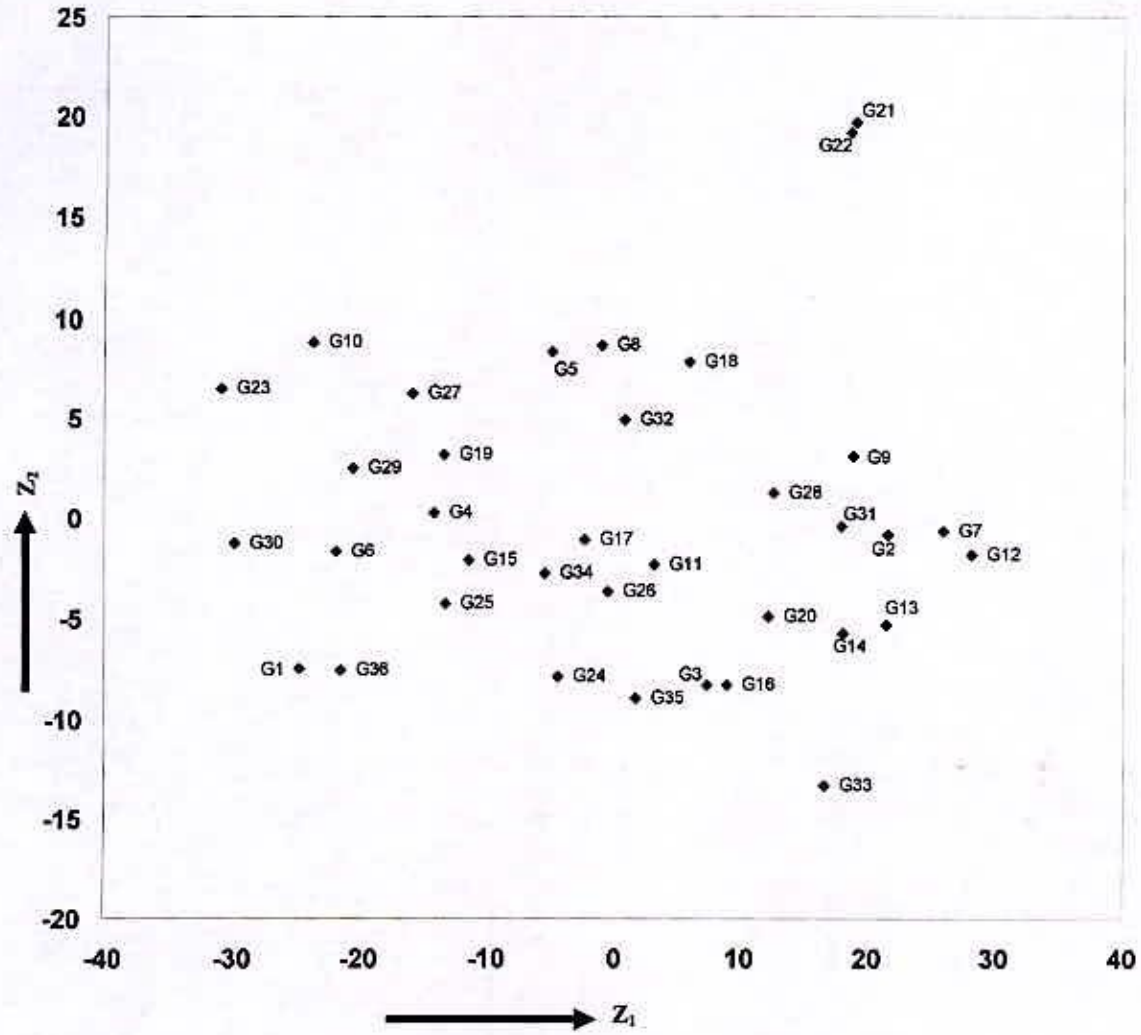


Figure 2. Scatter distribution of 36 rice genotypes based on their principal component scores

4.2.3 Non-Hierarchical Clustering

Using co-variance matrix with the application of non-hierarchical clustering, the 36 genotypes were grouped into five clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Islam *et al.* (2004) reported five clustering; Soni *et al.* (1999) ten clustering; Reddy *et al.* (2004) six clustering in rice. Compositions of different clusters with their corresponding genotypes in each cluster are presented in Table 6.

Cluster I had maximum number of (12) genotypes followed by II, V, III and IV, which had 11, 9, 2, and 2 genotypes, respectively. Cluster I composed of 12 genotypes namely G1, G4, G6, G10, G15, G19, G23, G25, G27, G29, G30 and G36. From the clustering mean values (Table 7), it was observed that the mean value of cluster I ranked first for total tillers per plant (14.66), effective tillers per plant (13.06), filled grains per panicle (168.84), grain yield per plant (24.93) and the second for days to 50% flowering (111.53), plant height (102.38) and panicle length (25.49).

Cluster II was composed of 11 genotypes namely G2, G3, G7, G9, G12, G13, G14, G16, G20, G28 and G33. Cluster II had the second highest cluster mean for total tillers per plant (13.86), Spikelet sterility percentage (34.11) and 1000-grain weight (22.88). Spikelet sterility percentage had negative role in grain yield and ranked third for days to 50% flowering (109.85), effective tillers per plant (11.88) on the other hand cluster mean for filled grains per panicle was the lowest (132.55).

Cluster III constituted of two genotypes namely G31 and G32. This group possessed genotypes with the highest cluster mean for plant height (113.3), spikelet sterility percentage (35.90) and the lowest for harvest index (0.35). This cluster contains tallest plant.

Cluster IV composed of two genotypes namely G21 and G22. These genotypes produced the highest cluster mean for 1000-grain weight (24.70) and harvest index (0.50); lowest for days to 50% flowering (95.15), plant height (93.55), total tillers per plant (9.20), effective tillers per plant (8.60) and spikelet sterility percentage (16.90). This cluster contains the shortest plant.

Nine genotypes formed cluster V. This cluster contained genotypes G5, G8, G11, G17, G18, G24, G26, G34 and G35. This cluster obtained first position in respect of cluster mean for days to 50% flowering (112.30) and the second in filled grains per panicle (149.91), harvest index (0.41) and grain yield per plant (22.86). The maximum range of variability was observed for filled grains per panicle (132.55-168.84) among all the characters in five clusters.

4.2.4 Canonical Variate Analysis (CVA)

To compute the inter-cluster Mahalanobis's D^2 values canonical variate analysis was used. The Table 8 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 IV (13.842), followed by between cluster III and IV (10.968), IV and V (10.431), II and IV (9.205) and I and II (8.520). The lowest inter-cluster distance was observed between cluster II and III (2.238), followed by III and V (3.094) (Figure 4). However, the maximum inter-cluster distance was observed between the clusters I and IV (13.842) maintaining more distance than other clusters. 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 0.1481 to 2.4875,

Table 6. Distribution of 36 genotypes of rice in five clusters

Cluster	Number of genotypes	Name of genotypes
I	12	G1 (AL-1), G4 (AL-12), G6 (AL-14(I)), G10 (AL-17(I)), G15 (AL-36), G19 (AL-45), G23 (AL-50), G25 (AL-52), G27 (R-1), G29 (R-4), G30 (R-5(II)), G36 (BRRI dhan 29).
II	11	G2 (AL-9), G3 (AL-10), G7 (AL-14(II)), G9 (AL-16(II)), G12 (AL-23), G13 (AL-25), G14 (AL-27), G16 (AL-42), G20 (AL-47(II)), G28 (R-2), G33 (AL-35).
III	2	G31 (R-9), G32 (R-12).
IV	2	G21 (AL-48), G22 (AL-49).
V	9	G5 (AL-13), G8 (AL-16(I)), G11 (AL-17(II)), G17 (AL- 44(I)), G18 (AL-44(II)), G24 (AL-51(II)), G26 (AL-54), G34 (AL-11), G35 (BRRI dhan 28).

Table 7. Cluster means for 10 characters of 36 rice genotypes

Characters	Clusters				
	I	II	III	IV	V
Days to 50% flowering	111.53	109.85	104.00	95.15	112.30
Plant height (cm)	102.38	93.65	113.30	93.55	98.70
Total tillers per plant	14.66	13.86	11.20	9.20	13.78
Effective tillers per plant	13.06	11.88	10.20	8.60	12.10
Panicle length (cm)	25.49	23.86	26.40	19.20	24.71
Filled grains per panicle	168.84	132.55	137.60	134.30	149.91
Spikelet sterility percentage	31.93	34.11	35.90	16.90	29.26
Thousand grain weight (g)	22.35	22.88	20.50	24.70	22.10
Harvest index	0.40	0.39	0.35	0.50	0.41
Grain yield per plant (g)	24.93	20.10	22.00	17.50	22.86

maximum for cluster I (2.4875), which contained of 12 genotypes, while the minimum distance was found in cluster IV (0.1481) that comprises 2 genotypes.

Results of different multivariate analysis were superimposed in Figure 3 from which it may be concluded from the above results that different multivariate techniques supplemented and confirmed one another.

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 2). As per scatter diagram the genotypes were apparently distributed into five clusters. It was also revealed that the genotypes of cluster I was more diverse from the genotypes of cluster IV. Islam *et al.* (2004) also observed the similar result. It is assumed that maximum amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. However, for a practical plant 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 I and IV. But considering the yield and duration crosses involving cluster I and IV may exhibit high heterosis for yield. Main and Bahl (1989) reported that the parents separated by D^2 values of moderate magnitude generally showed higher heterosis. Keeping this in view, it appears that the crosses between the genotypes belonging cluster I with cluster II and genotypes in cluster II with cluster IV might produce high heterosis in yield as well as earliness. Also the crosses between genotypes from cluster IV with cluster I and III might produce high level of segregating population. So the genotypes belonging to cluster I and cluster II, cluster I and cluster III and cluster II and cluster IV 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 from PCA, the important characters responsible for genetic divergence in the axis of differentiation were harvest index (3.984), effective tillers per plant (0.720), 1000-grain weight (0.099), Spikelet sterility percentage (0.056), grain yield per plant (0.073) and days to 50% flowering (0.010). In vector-II (Z_2), effective tillers per plant (0.872), filled grains per panicle (0.68), 1000-grain weight (0.057) and harvest index (30.296) were important but plant height, total tillers per plant, panicle length and filled grains per panicle played only a minor role in the first axis of differentiation. The role of plant height, total tillers per plant and panicle length had a minor role in the genetic divergence. The role of effective tillers per plant, 1000-grain weight and harvest index in both the vectors were important components for genetic divergence in these materials. Chauhan and Chauhan (1994) concluded that 1000-grain contributed maximum (43.3%) to the total divergence. Singh *et al.* (1999) reported harvest index, number of filled grains per panicle contributed maximum to the total divergence in rice. Das *et al.* (1993) reported that days to 50% flowering, days to maturity, plant height, effective tillers per plant and 1000-grain weight contributed as much as 93% of the total divergence. Balram *et al.* (2004) also reported days to 50% flowering contributed maximum to the total divergence (35.8%). Pradhan and Roy (1990) reported that 1000-grain weight showed highest contribution to D^2 values.

4.4 COMPARISON 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

Table 8. Average intra (Diagonal) and inter cluster distances (D^2) for 36 rice genotypes

Cluster	I	II	III	IV	V
I	**2.4875**				
II	8.520	**1.7902**			
III	6.816	2.238	**0.1648**		
IV	13.842	9.205	10.968	**0.1481**	
V	4.321	4.294	3.094	10.431	**1.7748**

Table 9. Latent vectors for 10 characters of 36 rice genotypes

Characters	Vector-I	Vector-II
Days to 50% flowering	0.010	-0.097
Plant height (cm)	-0.051	-0.017
Total tillers per plant	-1.051	-0.784
Effective tillers per plant	0.720	0.872
Panicle length (cm)	-0.586	-0.040
Filled grains per panicle	-0.196	0.068
Spikelet sterility percentage	0.056	-0.106
Thousand grain weight (g)	0.099	0.057
Harvest index	3.984	30.296
Grain yield per plant (g)	0.073	-0.164

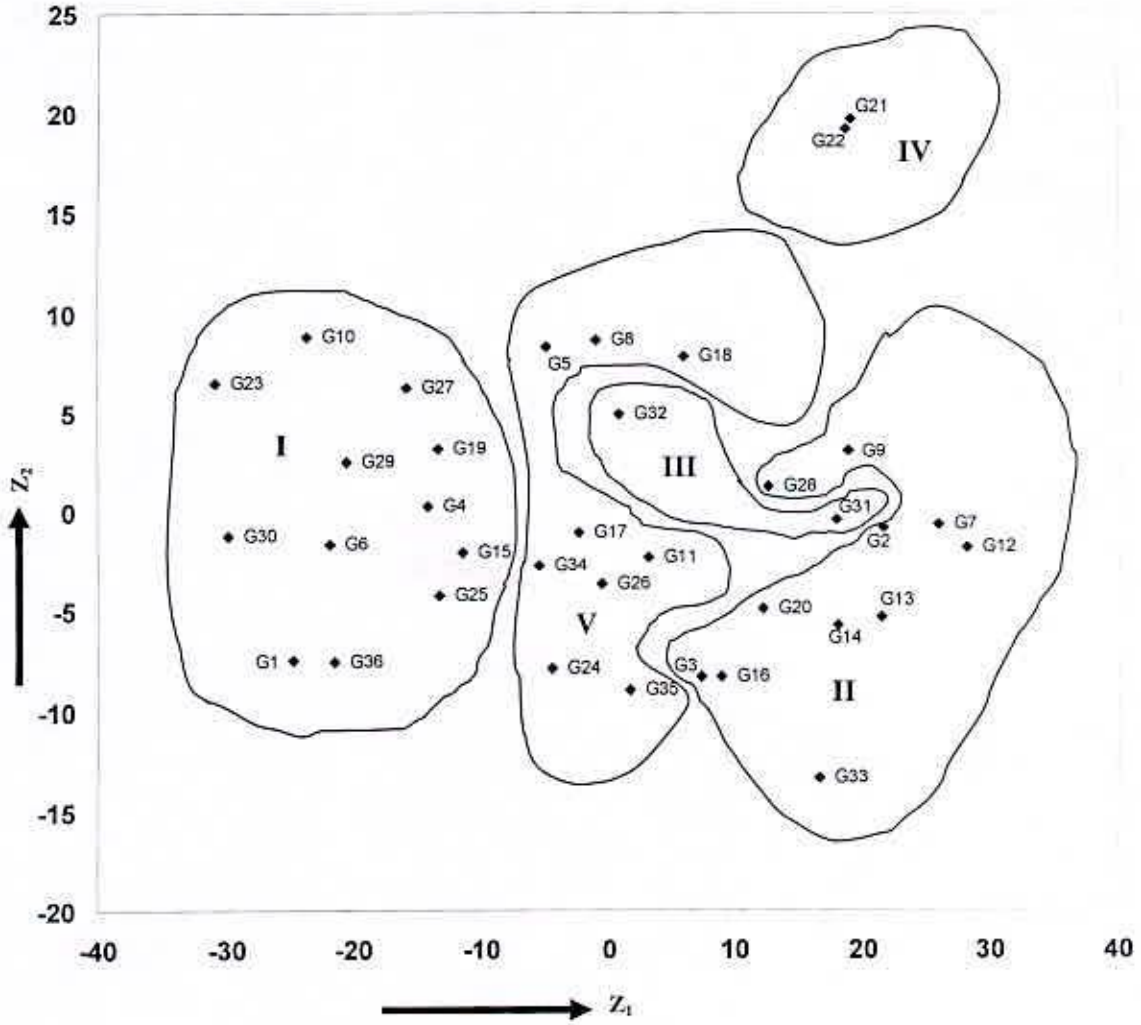


Figure 3. Scatter distribution of 36 rice genotypes based on their principal component scores superimposed with clustering

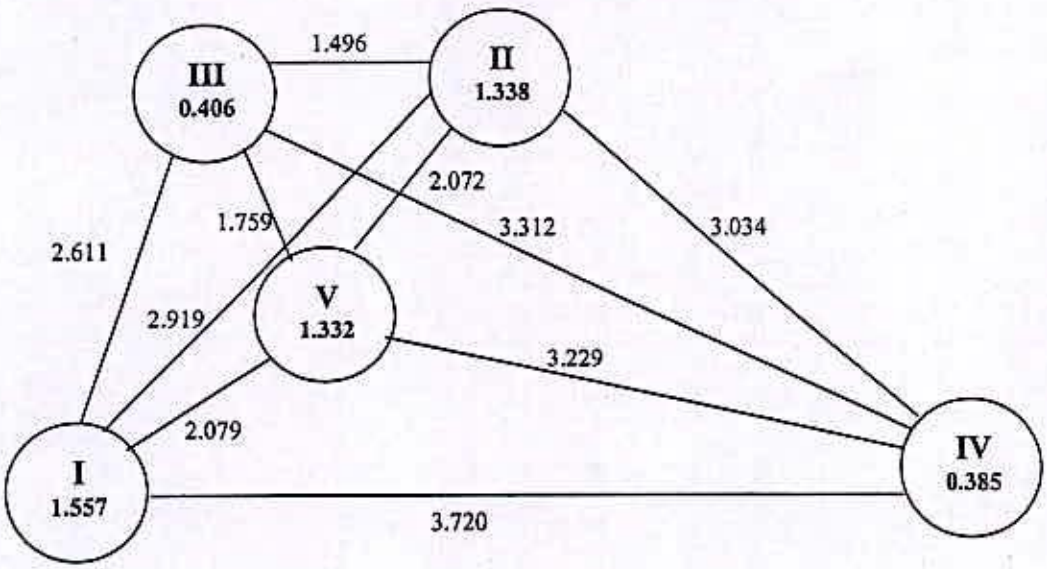
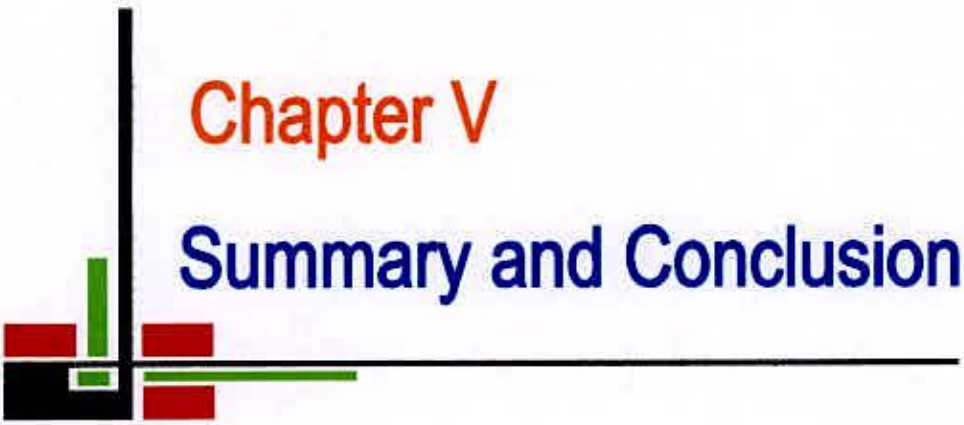


Figure 4. Diagram showing intra and inter cluster distances ($\sqrt{D^2}$) of 36 rice genotypes

giving the information regarding the contribution of characters towards divergence in rice.

4.5 SELECTION OF PARENTS FOR FUTURE HYBRIDIZATION

Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genetically distant parents (Falconer, 1960; Moll *et al.*, 1962; Ramanujam *et al.*, 1974; Ghaderi *et al.*, 1984). Considering the magnitude of genetic distance, contribution of character towards divergence, magnitude of cluster mean and agronomic performance the genotypes G10 for higher filled grains per panicle, yield per panicle, G23 for highest number of filled grains per panicle, higher grain yield per plant and G36 for large number of effective tillers per plant from cluster I; G12 for lower plant height, higher panicle length, G16 for higher panicle length, higher 1000-grain weight and G33 for lowest plant height, large number of effective tillers per plant, higher 1000-grain weight from cluster II; G31 for higher 1000-grain weight, panicle length from cluster III, G21 for lowest plant height, highest 1000-grain weight, highest harvest index and G22 for lowest days to 50% flowering from cluster IV were found promising. Therefore considering group distance and other agronomic performance the inter genotypic crosses between G10 and G31; G10 and G33; G23 and G12; G36 and G31; G36 and G33; G36 and G16; G31 and G21; G31 and G22 may be suggested for future hybridization program.



Chapter V

Summary and Conclusion

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was carried out with 36 rice genotypes at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2005 to May 2006. Seeds were sown separately in the net house and seedlings were transplanted in the main field in Randomized Complete Block Design (RCBD) with three replications. Data on days to 50% flowering (DFF), plant height (PH), total tillers per plant (TTP), effective tillers per plant (ETP), panicle length (PL), Spikelet sterility percentage (SS), filled grains per panicle (FGP), 1000-grain weight (TGW), harvest index (HI), and grain yield per plant (GYP) were recorded. Analysis of variance revealed significant differences among all the genotypes for all the characters under study.

The highest mean value was observed for filled grains per panicle (149.40). This character also exhibited the highest range of variation (123.53-180.20) 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, filled grains per panicle, Spikelet sterility percentage, 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, harvest index 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 (5.90 and 5.45, respectively), plant height (7.89 and 6.73, respectively), panicle length (9.18 and 6.66, respectively). Amongst the characters the highest genotypic coefficient of variation was recorded for Spikelet sterility percentage (16.48) followed by effective tillers per plant (16.33), total tillers per plant (14.60), grain yield per plant (13.30), 1000-grain weight (9.10), filled grains per panicle (8.73), harvest index (8.56) in order of merit. The highest value of heritability was observed for days to 50% flowering (85.19) and the lowest for filled grains per panicle (34.45). The highest genetic advance in percent of mean was observed for effective tillers per plant (31.86) followed by Spikelet sterility percentage (29.14), total tillers per plant (28.05) and grain yield per plant (23.36), whereas the lowest for panicle length (12.75). Days to 50% flowering showed high heritability (85.19) but low genetic advance in percent of mean (13.27) indicated non-additive gene action for the expression of the characters. Here high heritability was exhibited due to favourable environment rather than genotype.

Multivariate analysis was performed through Principal Component Analysis, Principal Coordinate Analysis, Cluster Analysis, Canonical Variate Analysis using GENSTAT 513 software program. The first three principal component axes accounted for 70.39% variation towards the divergence. As per PCA, D^2 and cluster analysis, the genotypes grouped into five different clusters. Five clusters were found from a scatter diagram formed by Z_1 and Z_2 values obtained from PCA. The highest inter genotypic distance was found between G36 & G22 (1.5425) and the lowest between G16 & G3 (0.1520). The highest intra-cluster distance was found in cluster I (2.4875) composed of 12 genotypes and the lowest in cluster IV (0.1481) among five clusters. The highest inter-cluster distance was observed between cluster I and IV (13.842) followed by cluster III and V (10.968). The lowest inter-cluster distance was observed between cluster II and III (2.238) followed by cluster III and IV (3.094). Genotypes included in cluster I were important for filled grains per panicle,

effective tillers per plant, grain yield per plant; cluster III for panicle length; cluster IV for plant height, 1000-grain weight, harvest index, days to 50% flowering; cluster V also important for grain yield and harvest index.

Considering cluster distance, inter genotypic distance and other agronomic performance G10, G23 and G36 from cluster I, G12, G16 and G33 from cluster II, G31 from cluster III, G21 and G22 from cluster IV may be considered to be better parents for future uses in hybridization program.

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CHAPTER VI
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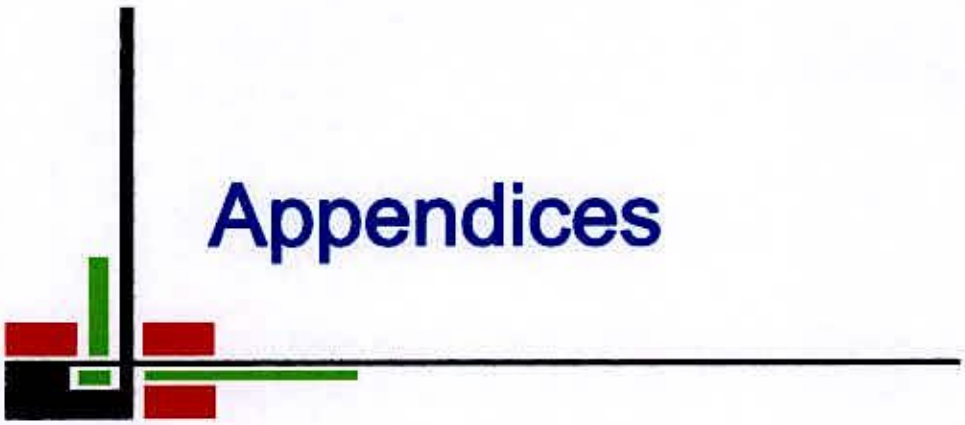

Appendices

Appendix I. Mean values of 10 characters for 36 rice genotypes

Designation	DFF	PH	TTP	ETP	PL	FGP	SS	TGW	HI	GYP
G1	115.33	99.84	16.60	16.00	23.94	173.40	37.82	23.43	0.41	23.59
G2	109.00	92.94	14.87	12.86	22.82	128.46	29.04	18.36	0.40	19.90
G3	113.67	89.98	13.27	11.46	23.84	143.20	37.74	26.30	0.38	20.48
G4	113.00	100.53	14.33	12.27	24.85	163.40	30.41	17.83	0.35	21.98
G5	106.67	96.59	13.67	11.73	21.59	156.33	24.10	20.60	0.39	17.66
G6	113.33	90.87	15.27	13.44	25.27	172.17	30.10	25.12	0.43	28.12
G7	107.33	89.02	14.87	12.87	23.93	125.07	28.68	25.26	0.39	19.51
G8	110.00	102.33	11.53	10.13	22.70	150.40	21.33	22.07	0.36	20.78
G9	106.33	101.72	11.27	9.60	21.54	130.67	30.74	23.30	0.36	17.79
G10	105.33	100.76	14.60	12.00	25.55	173.47	25.19	24.27	0.43	27.62
G11	115.33	104.33	13.93	11.53	25.32	144.60	30.61	24.40	0.35	20.27
G12	105.00	87.05	14.60	11.73	25.78	123.53	32.08	22.96	0.44	18.57
G13	115.00	98.25	13.67	11.33	24.64	126.60	31.04	20.06	0.39	21.54
G14	106.67	93.72	14.93	12.80	23.72	131.80	38.28	25.53	0.40	22.54
G15	114.67	99.48	13.27	11.40	25.49	160.47	32.00	21.35	0.37	21.79
G16	113.33	97.99	13.40	12.203	24.81	139.66	38.79	24.13	0.41	21.70
G17	111.00	97.67	13.20	12.13	25.47	161.66	31.90	20.74	0.41	22.64
G18	103.67	96.41	12.33	10.53	26.37	144.80	24.96	19.61	0.44	21.28
G19	105.00	109.37	15.20	13.93	25.83	161.20	33.50	23.10	0.40	25.51
G20	107.00	94.84	12.93	10.47	24.43	137.87	39.32	20.83	0.43	21.86

Appendix I. (cont'd.)

Designation	DFF	PH	TTP	ETP	PL	FGP	SS	TGW	HI	GYP
G21	95.33	93.21	9.87	9.20	19.72	133.93	15.54	25.43	0.47	18.91
G22	95.00	93.91	8.53	8.00	18.67	134.67	18.32	23.70	0.45	16.13
G23	109.00	101.05	12.33	11.00	24.19	180.20	27.10	21.76	0.40	30.01
G24	113.00	99.49	15.53	14.40	25.92	152.33	38.22	22.55	0.39	27.06
G25	109.00	96.35	13.80	12.40	26.33	163.00	38.77	25.10	0.40	25.49
G26	110.00	97.17	14.27	12.47	25.00	150.33	36.32	28.00	0.41	20.23
G27	109.33	101.48	12.40	10.60	26.00	168.80	26.23	20.70	0.35	22.73
G28	110.00	99.41	11.80	10.20	23.77	137.07	29.79	22.30	0.32	17.38
G29	110.67	116.72	14.40	12.73	26.47	167.20	33.18	22.13	0.35	20.99
G30	118.33	107.35	12.10	10.70	26.55	177.60	32.09	22.12	0.35	22.86
G31	104.33	112.80	12.13	10.53	26.44	129.00	38.86	19.37	0.34	19.79
G32	103.67	113.83	10.33	9.87	26.39	146.20	33.60	21.60	0.37	24.22
G33	115.00	85.33	16.80	15.13	23.38	134.00	39.67	22.60	0.37	19.84
G34	112.00	94.79	13.87	12.26	24.02	154.87	32.47	19.63	0.41	26.23
G35	129.00	99.50	15.73	13.80	26.03	143.93	23.39	21.37	0.51	29.50
G36	115.33	102.88	21.80	20.73	24.73	168.73	35.41	22.41	0.41	27.50
CV%	2.27	4.11	13.76	14.89	6.32	12.04	18.27	8.04	8.95	14.93

DFF = Days to 50% flowering (days), PH = Plant height (cm), TTP = Total tillers per plant, ETP = Effective tillers per plant, PL = Panicle length (cm), FGP = Filled grains per panicle, SS = Spikelet sterility %, TGW = Thousand grain weight (g), HI = Harvest index and GYP = Grain yield per plant.

Appendix II. Monthly record of air temperature, relative humidity and rainfall of the experimental site during the period from November 2005 to May 2006

Month	Year	*Air temperature (°c)		Relative humidity (%) at 12 p.m.	**Rainfall (mm)
		Maximum	Minimum		
November	2005	29.07	18.80	65.13	0
December	2005	27.07	15.65	63.80	3
January	2006	24.76	13.46	69.53	0
February	2006	31.26	19.42	51.27	0
March	2006	33.20	22.00	46.13	0
April	2006	33.74	23.81	61.40	185
May	2006	33.66	24.95	64.27	180

* Monthly average

** Monthly total

Source: Bangladesh Meteorological Department (Climate Division), Agargoan, Dhaka-1212.

Appendix III. Principal component scores for 36 rice genotypes

Designation	Z_1	Z_2
G1	-24.696	-7.489
G2	21.649	-0.844
G3	7.358	-8.269
G4	-14.203	0.256
G5	-4.928	8.326
G6	-21.795	-1.655
G7	25.926	-0.672
G8	-0.985	8.621
G9	18.858	3.072
G10	-23.686	8.807
G11	3.213	-2.332
G12	28.131	-1.825
G13	21.514	-5.281
G14	18.091	-5.747
G15	-11.361	-2.051
G16	8.997	-8.305
G17	-2.249	-1.089
G18	5.891	7.802
G19	-13.402	3.203
G20	12.139	-4.922
G21	19.027	19.704
G22	18.633	19.214
G23	-30.835	6.478
G24	-4.337	-7.861
G25	-13.202	-4.245
G26	-0.407	-3.644
G27	-15.855	6.263
G28	12.589	1.248
G29	-20.562	2.540
G30	-29.849	-1.250
G31	17.919	-0.386
G32	0.850	4.944
G33	16.688	-13.372
G34	-5.396	-2.725
G35	1.740	-8.967
G36	-21.466	-7.543