

**GENETIC VARIATION IN LOCAL AMAN RICE
GENOTYPES (*Oryza sativa* L.)**

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*This is to certify that thesis entitled, "GENETIC VARIATION IN LOCAL AMAN RICE GENOTYPES (*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. SHAJEDUR HOSSAIN**, Registration No: 11-4720 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 has been availed of during the course of this investigation has duly been acknowledged.

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**DEDICATED TO
MY
BELOVED PARENTS**

List of Abbreviations of Technical Symbols and Terms

FULL NAME	ABBREVIATION
Agro-Ecological Zone	AEZ
And others	<i>et. al.</i>
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Centimeter	cm
Co-efficient of Variation	CV
Days After Sowing	DAS
Degree Celsius	°C
Degrees of freedom	d.f
Etcetera	etc.
Food and Agriculture Organization	FAO
Figure	Fig.
Genetic Advance	GA
Genotypic Co-efficient of Variation	GCV
Genotypic Variance	δ^2_g
Gram	g
Hectare	ha
Heritability in broad sense	h^2_b
Journal	j.
Kilogram	Kg
Meter	m
Mean Sum of Square	MSS
Millimeter	mm
Muriate of Potash	MP
Number	No.
Percent	%
Phenotypic Co-efficient of Variation	PCV
Phenotypic variance	δ^2_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Standard Error	SE
Square meter	m^2
Triple Super Phosphate	TSP
Unites Nations Development Program	UNDP

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GENETIC CHARACTERIZATION OF SOME EXTINCT LOCAL AMAN RICE GENOTYPES (*Oryza sativa* L.)

By

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ABSTRACT

The experiment was conducted with 34 local rice genotypes with one check varieties at the Sher-e-Bangla Agricultural University experimental field to study characterization and genetic diversity of 35 local rice genotypes and to find out the association among the genetic characteristics. Regarding mean performance, the genotype G-4 took the longest period for first flowering is (115) followed by genotype G-35 (114) and the genotype G-12 had the minimum days for first flowering is (99). The highest number of filled grain per panicle was recorded in genotype G-10 was (144.33). The highest number of effective tiller (10.33) was recorded in genotype G-15. The highest 1000 grain weight (26.00) was recorded in the genotype G-15. The highest grain yield per hill was produced by genotype G-24 (35.90g). The highest σ^2_g was found for number of root hair (103415.40) and the lowest magnitude of σ^2_g was observed in number of primary branches per panicle (1.97). The highest σ^2_p was found for number of root hair (109410.31) and the lowest magnitude of σ^2_p was observed in number of primary branches per panicle (2.61). High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield per hill (g) indicated that selection of these traits would be effective. Correlation of Grain yield per hill was found to be highly significant and positive for number of root hair, days to flowering and plant height at both genotypic and phenotypic level and negatively significant for number of secondary branches per panicle at both level. Significant positive correlation of grain yield per hill with number of root hair, days to flowering and plant height implied that selection for these characters would lead to simultaneous improvement of grain yield in rice. Days to flowering had maximum direct effect (0.719) on yield followed by number of effective tiller (0.635), number of unfilled grain per panicle (0.544). Genotypes were grouped into five different clusters. PCA showed the highest inter-cluster distance was observed between the cluster II and V (46.71) followed by III and V (46.40) and IV and V (45.43). Genotypes from these three clusters may be involved in hybridization as wide genetic variations exist among the groups. Cluster IV exhibited the highest intra-cluster distance (38.36), while the lowest distance was observed in cluster V (23.09).

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CHAPTER I

INTRODUCTION



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INTRODUCTION

Rice is a self-pollinated cereal crop belonging to the family Gramineae (synonym-Poaceae) under the order Cyperales and class Monocotyledon having chromosome number $2n=24$ (Hooker, 1979). The genus *Oryza* includes a total of 25 recognized species out of which 23 are wild species and two, *Oryza sativa* and *Oryza glaberrima* are cultivated (Brar and Khush, 2003). It can survive as a perennial crop and can produce a ratoon crop for up to 30 years but cultivated as annual crop and grown in tropical and temperate countries over a wide range of soil and climatic condition.

Rice and agriculture are still fundamental to the economic development of most of the Asian countries. In much of Asia, rice plays a central role in politics, society and culture, directly or indirectly employs more people than any other sector. A healthy rice industry, especially in Asia's poorer countries, is crucial to the livelihoods of rice producers and consumers alike. Farmers need to achieve good yields without harming the environment so that they can make a good living while providing the rice-eating people with a high-quality, affordable staple. Underpinning this, a strong rice research sector can help to reduce costs, improve production and ensure environmental sustainability. Indeed, rice research has been a key to productivity and livelihood.

Rice is the second largest produce cereal in the world in 158.3 million hectare area with annual production of about 685.24 million metric tons (Anonymous, 2011) and also the staple food for over one third of the world's population (Poehlman and Sleper, 1995) and more than 90% to 95% of rice is produced and consumed in Asia (Virmani, 1996). Rice (*Oryza sativa* L.) is the staple food in Bangladesh, and grown in a wide range of environments ranging from the upland areas like Chittagong Hill Tracts, Sylhet and Garo Hills, with little moisture, to situations where the water is 3-4 meter deep (Alim, 1982). Bangladesh is ranked as fourth in rice production with annual production of 47.72 million metric ton in the world (Anonymous, 2011).

Bangladesh has a population density of 977/square km (BBS, 2009) which is the highest in the world. The land scarcity therefore, usually calls for vertical increased in yield or total production. To solve this problem, the production must be increase from less land, with less labor, less water and fewer pesticides.

A plant breeding program consists of building up a gene pool of variable germplasm, selection of individuals from the gene pool and utilization of selected individual to evolve a superior variety (Kempthorne, 1957). The available variability in a population can be partitioned into heritable and non-heritable parts using genetic parameters like variability, heterosis and genetic advance (Miller *et al.*, 1958). Path coefficient analysis provides an effective means of partitioning the correlation coefficient into direct and indirect effects of the component characters on yield on the basis of which crop improvement programs can be logically devised (Kozak *et al.*, 2007). Therefore, correlation in combination with path coefficient analysis will be an important tool to find out the association and quantify the direct and indirect influence of one character upon another (Dewey and Lu, 1959).

Knowledge of genetic diversity among existing cultivars of any crop is essential for long term success of breeding program and maximizes the exploitation of the germplasm resources (Belaj *et al.*2002). Hybridization is one of the major tools for the improvement of a crop that needs the analysis of genetic diversity is important for the source genes of particular traits within the available germplasm (Roy and Panwar, 1993). Multivariate analysis with D^2 technique measures the amount of genetic diversity in a given population in respect of several characters and assesses relative contribution of different components to the total divergence both at intra and inter-cluster levels.

A good knowledge of genetic resources might also help in identifying desirable genotypes for future hybridization program. Considering all these aspects the research has been conducted for achieving the following objectives:

Objectives:

1. To study the variability among the available genotypes,
2. To find out the correlation coefficients among the characters,
3. To assess the direct and indirect effect of component characters on grain yield with the help of path coefficient analysis and
4. To identify the promising genotypes for desirable characters.



CHAPTER II

REVIEW OF LITERATURE

CHAPTER II

REVIEW OF LITERATURE

The identification of suitable parental lines on the basis of their genetic parameters, nature and magnitude of genetic variability, the correlation and genetic diversity of different yield attributing characters are important for successful rice breeding programs. The present study has aimed at studying the variability, heritability, genetic advance, genetic diversity association among characters and yield related characters among the local rice genotypes. The available information relevant to the present study has been reviewed in this chapter.

2.1 Variation for yield and yield contributing characters

2.1.1 Plant height

Plant height is considered as an important plant character related to yield in rice. Plant height has been found to vary from variety to variety in rice.

Sanjeev (2005) conducted an experiment on 19 mutants derived from 2 Bashmati rice cultivars for genetic analysis based on 17 characters and found that plant height had higher heritability.

Satyanarayana *et al.* (2005) studied variability, correlation and path coefficient analysis for 66 restorer lines in rice and observed high variability, heritability and genetic advance for plant height.

Zahid *et al.* (2006) studied phenotypic and genotypic variance, co-efficient of variation, genetic advance, heritability, correlation co-efficient and path analysis for yield and yield components and found that plant height had high heritability coupled with high genetic advance.

Singh *et al.* (2006) conducted an experiment with 32 genotypes of rice and found high heritability and high genetic advance for plant height, indicating the predominance of additive gene action for this trait. Also, Sankar *et al.* (2006) conducted an experiment with 34 genotypes and high heritability and as well as genetic advance was obtained for plant height.

Singh *et al.* (2006) evaluated the genetic variability, heritability, genetic advance and character association in 37 rice genotypes. The estimates of phenotypic co-efficient of variation and genotypic co-efficient of variation were of the same magnitude for plant height except fertility heritability accompanied with moderate genetic advance was recorded for plant height.

2.1.2 Number of effect tillers

Sharma and Bhuiyan (2004) studied genetic variation and divergence in 58 aus rice and found highest genotypic as well as phenotypic co-efficient of variation for numbers of tillers per plant.

Sanjeev (2005) evaluated 19 mutant lines and found that number of panicle-bearing tillers per plant in Taro Basmati had high genetic advance.

Satyanarayana *et al.* (2005) studied variability, correlation and path co-efficient analysis for 66 restorer lines in rice and observed low heritability for number of effective tillers per plant.

Patil and Saragwi (2005) evaluated 128 aromatic rice associations and estimate genetic variations and correlation for 7 traits and found that number of tillers per hill had high genotypic and phenotypic co-efficient of variation. High heritability coupled with high genetic advance was also estimated for the character.

Sankar *et al.* (2006) studied on variability and correlation among its components in 34 rice genotypes. High heritability and genetic advance were obtained for days to 50% flowering, plant height. Positive and significant correlation was reported with days to 50% flowering and productive tillers per plant.

2.1.3 Length of panicle

Pandey and Awasthi (2002) observed significant genetic variability for the character panicle length among 21 genotypes that played a major role in the enhancement of production of grain yield.

Matho *et al.* (2003) studied 26 early maturing upland rice genotypes and found significant difference between genotypic and phenotypic co-efficient of variation for panicle length.

Satyanarayana *et al.* (2005) studied variability, correlation and path co-efficient analysis for 66 restorer lines in rice and observed low heritability for panicle length.

Sankar *et al.* (2006) studied on variability, correlation and path co-efficient among its components in 34 rice genotypes. High heritability and genetic advance were obtained for productive tillers per plant, panicle length. Positive and significant correlation with productive tillers per plant, panicle length and hence these traits can be taken as indices for improving yield in rice.

2.1.4 Days to flowering

Sanjeev (2005) conducted an experiment with 19 mutant lines (M_3) derived from Pusa Basmati and Taraori Basmati and observed higher heritability for days to flowering compared to other characters.

Satyanarayana *et al.* (2005) studied variability, correlation and path co-efficient analysis for 66 restorer lines in rice and observed high variability, heritability and genetic advance for days to 50% flowering.

Singh *et al.* (2006) evaluated the genetic variability, heritability, genetic advance and character association in 37 rice genotypes. The estimates of phenotypic co-efficient of variation and genotypic co-efficient of variation were of the same magnitude for plant height except fertility percentage. Days to 50% flowering exhibited the highest heritability estimates. High heritability accompanied by moderate genetic advance was recorded for days to 50% flowering.

Sankar *et al.* (2006) studied on variability and correlation among its components in 34 rice genotypes. High heritability and genetic advance were obtained for days to 50% flowering, plant height. Positive and significant correlation was reported with days to 50% flowering and productive tillers per plant.

Sanjeev Kumar *et al.* (2007) studied the gene action for grain yield, components and quality traits in 9 parental genotypes hybrids of rice grown in Himachal Pradesh,

India, during the kharif of 2003. The additive and non-additive components were significant for days to 50% flowering.

Adil Jamal *et al.* (2007) studied the eight rice genotypes including six hybrids (HR-41, HR-30, HR-9, HR-10, Arize-403, Dagha-1, KS 282 and Bas-385) in Pakistan to observe genetic variability among different plant traits contributing to yield. A significant negative correlation was obtained between days to 50% flowering and grain yield per plant.

Kishore *et al.* (2007) conducted an experiment during kharif 2004 in Hyderabad, Andhra Pradesh, India, with 70 rice genotypes, including aromatic and non -aromatic lines. Observations were recorded on days to 50% flowering. Path co-efficient analysis revealed that day to 50% flowering showed positive direct effects on grain yield.

2.1.5 Number of primary and secondary branches per panicle

Mahmood *et al.* (2004) release of rice cultivars with improved performance in saline environments is reliant on an understanding of the genetic control of plant and panicle characters in plants exposed to salinity. Plant height and primary branch per panicle are traits that may be readily improved by selection in saline environments.

Yamagishi *et al.* (2004) studied a large panicle with numerous florets is essential for improving rice (*Oryza sativa* L.) yield. Rice panicle size is determined by such underlying morphogenetic processes as: (1) primary branch formation on the panicle axis; (2) floret formation on the primary branches (mainly determined by the secondary branch formation); and (3) pre-flowering abortion of florets in the panicle. These results demonstrate that studying the partitioning of panicle size into these underlying morphogenetic components would be helpful in understanding the complicated genetic control of panicle size.

2.1.6 Number of filled grains per panicle

Sanjeev (2005) studied 19 mutant lines derived from two Basmati rice and observed maximum amount of variability for number of grains per panicle. High heritability coupled with high genetic advance was also observed for this character.

Satyanarayana *et al.* (2005) studied variability, correlation and path co-efficient analysis for 66 restorer lines in rice and observed high variability, heritability and genetic advance for number of grains per panicle.

Patil and Sarawgi (2005) studied genetic variability in traditional aromatic rice accessions and found that the genetic and phenotypic co-efficient of variation were high for number of filled grains per panicle.

Singh *et al.* (2006) conducted an experiment with 37 rice genotypes and reported that there were highly significant differences among the genotypes for number of grains per panicle and the estimates of phenotypic co-efficient of variation and genotypic co-efficient of variation were of the same magnitude for the character. High heritability was recorded for the characters.

Sankar *et al.* (2006) conducted an experiment with 34 rice genotypes and high heritability as well as genetic advance was obtained for grains per panicle.

2.1.7 1000 Grain weight

Singh *et al.* (2000) showed that approximately 38-50% of the hybrids exhibited significant and positive heterobeltiosis and standard heterosis for grain yield per plant. Heterosis for grain yield was mainly due to heterosis for 1000 grain weight.

Patil *et al.* (2003) studied 128 traditional aromatic rice genotypes along with seven improved controls to obtain information on the nature and magnitude of variation. The analysis of variance and genotypic co-efficient of variation revealed genetic variability for the characters. The characters exhibited high heritability associated with high genetic advance for 1000 grain weight.

Chand *et al.* (2004) studied nineteen genotypes of aman paddy (rice) (*Oryza sativa*) emanating from different sources were evaluated for grain yield and their components during kharif. Heritability and genetic advance as percentage of mean were high for 1000 grain weight.

Senapati and Sarkar (2005) were conducted a field experiment in West Bengal, India, during the 1997-2001 kharif season, to evaluate the genetic divergence of 40 tall

indica rice genotypes based on grain yield and yield components. 1000 grain weights were the chief contributors towards genetic divergence.

Zahid *et al.* (2006) were observed high heritability estimates coupled with high genetic advance 1000 grain weight. Hence, 1000 grain weight contributed maximum direct effects on yield indicating that this trait should be given emphasis while selecting high yielding. 1000 grain weight had positive correlations with grain quality characteristics, i.e. grain length and cooked.

2.1.8 Grain yield per hill

Honarnejad and Tarang (2001) evaluated seven local and alien rice cultivars for traits grain yield and other contributing characters. They observed 46% narrow sense heritability for grain yield.

Shanthi and Singh (2001) studied 16 M6 generation of induced mutant along with non-mutant Mahsuri for variation in yield and yield component and found significant variation among the genotypes for all characters studied. Heritability in broad sense was high (more than 80%) for all characters expect grain yield per plant (78.99).

Pandey and Awasthi (2002) studied genetic variability in 21 genotypes of aromatic rice for yield contributing traits. Significant genetic variability was observed among the 21 genotypes for the entire yield contributing traits. They concluded that traits plant height, days to 50% flowering, effective tillers per plant, panicle length, number of grains per panicle, grain weight and grain yield per plant play major roles in the enhancement of grain production.

Sinha *et al.* (2004) evaluated 19 mid land rice land races and found high heritability coupled with high genetic advance for grain yield followed by test weight and panicles per plant. A high genotypic and phenotypic co-efficient of variation was also observed for this character.

Battan *et al.* (2006) studied 25 rice genotypes and observed high co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) coupled with high heritability indicating further scope of improvement in this character grain yield per plant through selection.

2.2 Relationship between yield and yield contributing characters

Grain yield is associated with many yield contributing characters. The major yield components in rice have been identified as number of panicles per plant; number of grain per plant and average grain weight. In addition there are other characters plant height, days to maturity, panicle length etc. which contribute to grain yield. Association of yield contributing characters with grain yield in rice was comprehensively studied by many breeders and based on their results they formulated different selection criteria for yield improvement. Association of yield contributing characters with yield was studied at both genotypic and phenotypic levels. Usually, it was observed that genotypic correlation co-efficient were higher than the phenotypic correlation co-efficient. Some of the important findings those are relevant to correlation study are reviewed here-

2.2.1 Variability

Banumathy *et al.* (2002) evaluated ten cytoplasmic male sterile (CMS) lines for genetic variability for 8 floral traits and their association with outcrossing rate. Genetic variability analysis revealed narrow difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for all the traits. The genetic parameters, PCV, GCV, heritability and genetic advance, were also high for these traits indicating the preponderance of additive gene effects in the inheritance of these traits. The CMS line IR 68281A which had maximum outcrossing rate possessed maximum percentage of exerted stigma. Similarly, IR 68885A with large stigmatic area and maximum style length also recorded high seed set percentage on outcrossing.

Chang-JaeKi *et al.* (2002) tested two rice cultivars, 'Oochikara' with large grain and 'Hwayeongbyeon' and their progenies (F_1 , F_2 , B_1 , and B_2) to understand gene action of morphological traits of rice grain and their relationships. The evaluated traits were 1000-grain weight, grain length, width, thickness, length-width ratio, and chalkiness of brown rice. Correlation between grain weight and chalkiness was highly significant in the all progenies, and grain length was not associated with width and thickness in an F_2 population. Scaling test and joint scaling test revealed that inheritance of grain

traits were fitted to additive-dominance model without epistasis. Additive effects for the traits were much greater than the dominance effects.

Abdel-Ghani *et al.* (2005) investigated the genetic variability and correlation coefficients involving five floral characters in a group of 29 cultivated and wild rice (*Oryza sp.*). Wide variability existed in anther length, stigma length and percent exerted stigma. The genetic variation constituted a high proportion of the total variation for these traits. Thus, selection for these characters is expected to be highly effective.

Ordenez *et al.* (2005) studied the genetic variability of restorer for the development of three-line rice hybrids involving 20 randomly selected restorer lines and three commercially usable CMS lines. Estimates of genetic variance of restorer lines for days to 50% flowering, plant height (cm), grain yield per ha, panicle length (cm), number of spikelets per panicle, percent filled grains and 1000-grain weight (g) were highly significant but not for number of productive tillers. Confidence interval estimates for all traits were also significantly different from zero, except for number of productive tillers, indicating substantial genetic variability for these traits. Combined mean performance across locations revealed several hybrids out-yielding the best check varieties.

Madhavalatha *et al.* (2005) were evaluated fifty-four elite rice genotypes in Tirupati, Andhra Pradesh, India, during rabi 2001-02 for their variability with regards to grain yield, yield components (plant height, number of effective tillers per plant, panicle length, number of grains per panicle, fertility percentage, days to 50% flowering, days to maturity and harvest index) and quality parameters (kernel length (L), breadth (B), L/B ratio and elongation ratio, 1000-grain weight etc.). The results revealed high variability, heritability and genetic advance for number of grains per panicle, grain yield per plant, harvest index and kernel L/B ratio, while days to maturity, fertility percentage, hulling recovery and kernel elongation ratio had high heritability coupled with low genetic advance indicating the need for emphasis on these traits during selections for yield improvement.

Kumar *et al.* (2006) was conducted a study in Himachal Pradesh, India during the kharif seasons of 2003-04 to evaluate the genetic parameters for quality traits in rice cultivars HPR 1164, HPR 2047, China 988, VL 91-1754, VL-93 3613, VL 93-6052,

IR 57893-08, VL Dhan 221 and JD 8; their 36 hybrids (F₁); and their 36 F₂s. Variability was high for grain yield per plant. Additive gene action was found to be important for grain length, grain yield per plant and 100-grain weight, whereas both additive and non-additive gene actions were important for grain breadth, grain length:breadth ratio and protein content. Association analysis revealed that all the traits showed non-significant association with grain yield. Thus, it is evident from the present investigation that all the characters can be improved in a genotype without any adverse effect on grain yield per plant.

Ali *et al.* (2007) evaluated twenty one CMS lines of rice from five different male sterility sources for various morphological, floral and agronomic traits at Rice Research Institute, Kala Shah Kaku, Pakistan. A considerable variation existed among CMS lines for these traits. Anther length and stigma length ranged from 2.0 to 3.0 mm and 1.0 to 2.5 mm, respectively in these lines. This complete pollen sterility was observed in all CMS lines. On the basis of outcrossing ratio (OCR), better panicle exertion ratio (PER) and stigma exertion ratio (SER) and good phenotypic acceptability, CMS lines IR58025A, IR62829A, IR68897A, IR68886A, IR68896A, IR68885A (WA), IR69617A (Basmati type), IR66707A (*Oryza perennis* type) and 913A (Dian type) can be used for their exploitation in commercial hybrid rice seed production in Pakistan.

Adil *et al.* (2007) studied the eight rice genotypes including six hybrids (HR-41, HR-30, HR-9, HR-10, Arize-403, Dagha-1, KS 282 and Bas-385) in Pakistan to observe genetic variability among different plant traits contributing to yield.

2.2.2 Correlation co-efficient

Ganesan (2000) conducted a study to assess the nature and magnitude of association between grain yield and its component characters of cytoplasmic male sterility, at Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore using 48 hybrids derived from 6 lines and 8 testers. Most of the characters studied (days to flowering, plant height, number of tillers, productive tillers/plant, panicle exertions, spikelets per panicle, filled grains per panicle and spikelet fertility) exhibited positive correlations with grain yield at both phenotypic as well as genotypic level. The results

revealed that the direct selection for the above mentioned traits can improve the grain yield in CMS rice hybrids.

Mahto *et al.* (2003) evaluated Twenty-six early maturing upland rice genotypes, collected from Jharkhand, India, for genetic variation, character association and path analysis based on days to 50% flowering, number of branches per panicle, number of filled grains per panicle, 1000-seed weight and grain yield. The association of high heritability with high genetic advance was observed for 1000-grain weight, days to 50% flowering, grain yield, number of branches per panicle. Grain yield was positively and significantly correlated with days to 50% flowering, number of branches per panicle and number of filled grains per panicle. Path coefficient analysis showed that the number of branches per panicle (0.424) had the highest positive direct effect on grain yield followed by number of filled grains per panicle (0.411), and days to 50% flowering (0.07).

Khedikar *et al.* (2003) estimated genetic variability for 9 characters (days to 50% flowering, plant height, effective tillers per plant, panicle length, test weight, sterility percentage, spikelet density, head rice recovery and grain yield per plant) in 20 scented rice genotypes. Analysis of variance showed sufficient variation among genotypes in all environments for the different yield and yield contributing characters studied. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters, indicating that the variation among them is not only due to genetic content but also due to the influence of environment. Days to 50% flowering followed by plant height and head rice recovery recorded low GCV and PCV values in all environments.

Borbora *et al.* (2005) conducted a field experiment with 30 rice genotypes and observed positive and significant correlation of grain yield per plant with grain yield per panicle and significant negative correlation with plant height, panicle number per plant and chaffy grain number per panicle.

De *et al.* (2005) studied correlation and path analysis for 10 characters of 14 diverse aromatic cultivars and observed significant positive correlation on number of panicles per hill with grain yield per panicle.

Sivakumar and KannanBapu (2005) assessed the nature and magnitude of association between grain yield and its component characters of wide compatible gene involving

inter sub-specific rice hybrids. Most of the characters studied (number of tillers per plant, panicle length, pollen fertility, grains per panicle and 100-grain weight) had exhibited positive correlation with grain yield at both phenotypic as well as genotypic levels. The results revealed that the direct selection for the above mentioned traits can improve the grain yield in wide compatible gene involving inter sub-specific rice hybrids.

Patil and Sarawgi (2005) conducted an experiment on 128 aromatic rice accessions for genetic variation and correlation and found positive and significant correlation of grain with number of filled grains per panicle at genotypic and phenotypic level.

Shashidhar *et al.* (2005) reported positive association of grain yield with plant height, number of productive tiller per hill, and dry matter per plant and harvest index at phenotypic and genotypic level.

Vaithiyalingan and Nadarajan (2005) conducted an experiment to assess the nature and magnitude of association between grain yield and its components, and observed positive and significant relation of pollen fertility, plant height, and productive tillers per plant, panicle length, number of grains per panicle and spikelet fertility with grain yield.

Satyanarayana *et al.* (2005) studied correlation and path co-efficient analysis for 66 restorer lines in rice and that yield was positively associated with spike let fertility, panicle length, number of grains per panicle and number of effective tillers per plant.

Battan *et al.* (2006) studied 25 rice genotypes and observed high co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV) coupled with high heritability indicating further scope of improvement in this character grain yield per plant through selection.

Zahid *et al.* (2006) studied 14 Basmati rice genotypes and found negative correlation of plant height with yield indicating that Bashmati plants had low yield.

Singh *et al.* (2006) conducted an experiment with 37 rice genotypes to study character association reported that a grain yield having significant and positive association with number of grains per panicle followed by days to 50% flowering, effective tillers per plant and panicle length.

Sankar *et al.* (2006) conducted an experiment with 34 rice genotypes and reported that single plant yield having positive and significant correlation with days to 50% flowering productive tillers per plant, panicle length and grains per panicle, and hence these traits can be taken as indices for improving yield in yield.

2.2.3 Path co-efficient study

Yang-LianSong *et al.* (2002) studied grown Seeds of eight japonica rice varieties from different countries and seeds of F₁ and F₂ generations of their 56 hybrids (obtained by single cross and reciprocal cross) in Hefei, Anhui, China during 1999-2000. Rice grain shape traits (RGSTs) including grain length (GL), grain width (GW), grain thickness (GT) and grain weight were investigated after harvesting. No significant difference in GL was found among different hybrids, but their differences in GW, GT and grain weight reached a significant level. Significant difference in GL was noted between the hybrids obtained by single cross and reciprocal cross. It is inferred that the RGSTs were obviously controlled by female parent.

Mahto *et al.* (2003) reported that the number of branches per panicle had the highest positive direct effect (0.424) on grain yield followed by number of filled grains per panicle (0.411), number of panicle per plant (0.159) and days to 50% flowering (0.07).

Borbora *et al.* (2005) conducted an experiment with 16 local cultivars and 14 high yielding varieties advance lines under two sowing dates and observed the highest positive direct effect of grain yield per panicle followed by plant height on grain yield per plant under both environments. Chaffy grain number per panicle showed the highest negative direct effect on grain weight showed the highest indirect effects on grain yield per plant.

Patil and Sarawgi (2005) worked out on path co-efficient in 128 aromatic rice accessions for seven traits and observed greatest positive direct effect of 1000-grain weight followed by number of ear-bearing tillers per plant, number of filled grains per panicle and number of days to 50% flowering on grain yield. However, 1000-grain weight had on significant correlation with grain yield per plant due to its negative

indirect on grain yield plant through number of filled grain per panicle and plant height.

Shashidhar *et al.* (2005) carried out an experiment on 20 double haploid lines of rice and yield components. Path analysis showed that dry matter per plant had the greatest positive direct effect on grain yield, followed by harvest index and plant height at the phenotypic level.

Vaithiyalingan and Nadarajan (2005) conducted an experiment to assess the nature and magnitude of association between grain yield and its components, and observed positive and significant relation of pollen fertility, plant height, and productive tillers per plant, panicle length, number of grains per panicle and spikelet fertility with grain yield. Also studied correlation and path analysis in inter sub specific rice hybrids and reported that the number of grains per panicle had the highest positive direct effect on yield followed by productive tillers per plant. The results revealed that the direct selection for the above mentioned traits could improve the grain yield in interracial rice hybrids.

Satyanarayana *et al.* (2005) studied path co-efficient analysis for 66 restorer lines in rice and observed that panicle length and spike let fertility exerted maximum direct effect on grain yield. High indirect effects of the different yield component traits studied were also noticed through spike let fertility on grain yield, indicating the need for emphasis on spike let fertility during selections for yield improvement in restorer lines of rice.

Vaithiyalingan and Nadarajan (2005) studied correlation and path analysis in inter sub specific rice hybrids and reported that the number of grains per panicle had the highest positive direct effect on yield followed by productive tillers per plant. The results revealed that the direct selection for the above mentioned traits could improve the grain yield in interracial rice hybrids.

Zahid *et al.* (2006) observed that the number of tillers per plant, grains per panicle and 100-grain weight contributed maximum direct effect on yield.

2.3 Genetic Diversity

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

Jha *et al.* (1999) studied 20 accessions of wild rice species of Uttar Pradesh, India, were subjected to multivariate analysis following Mahalanobis's D^2 statistics for assessing genetic diversity among them. The 20 accessions could be grouped into three clusters, exclusively of variants of specific species, without any overlap. Cluster 1 represented *Oryza nivara* with fourteen accessions, while cluster, II comprised of five accessions of *O. sativa* var, *spontanea* and cluster III with only accessions of *O. rufipogon*.

Soni *et al.* (1999) reported the genetic divergence of 132 rice genotypes (128 traditional cultivars and 4 standard genotypes) for 18 quality traits led to their grouping 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 clusters VI and VII. Based on mean performance, genetic distance and clustering pattern, hybridization selected 10 genotypes are likely to give desirable segregants for grain quality.

Banasal *et al.* (1999) assessed 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 were identified which might be useful in creating wider variability for early maturity, dwarf and high yielding segregants.

Hegde and Patil (2000) reported the genetic divergence in 40 genotypes of rainfed rice using Mahalanobis's D^2 statistic. The cultivars fall into 7 clusters. Cluster I, II, III and IV comprised 18, 14, 3 and 2 genotypes, respectively, while Cluster V, VI and VII were solitary clusters. The average intercluster D^2 value was the highest (51.88) between the Clusters V and VII, indicating high genetic divergence between the cultivars of these two clusters. The highest contributing characters to D^2 values were spikelet number per panicle, photosynthetic rate and 1000-grain weight. Based on genetic distance, mean performance and clustering pattern, hybridization of Pancaj with CTH-3 or Kanthimori or Chachakki biliakki and CTH-3 with Kanthimori or Jolagabatta or Dodabatta was suggested to be appropriate in breeding.

Rather *et al.* (2001) studied the genetic divergence in 56 rice cultivars in Jammu and Kashmir, India during the rainy season of 1997 and 1998. Significant variations for days to 50% flowering; leaf length; leaf breadth; productive tillers per plant; plant height; days to maturity; total and sterile grains per panicle; panicle length, harvest index; grain yield; length; breadth ratio of the grain, and IQO-grain weight were observed among cultivars. The grouping of cultivars from various regions into the same cluster (as apparent in clusters I, II and VI) indicated that the geographical distribution did not necessarily indicate genetic divergence. The highest mean value for harvest index and the lowest spikelet sterility were observed for K 332. Based on the mean performance for plant height, maturity, spikelet fertility, grain yield and intercluster distance, cultivars from clusters II and IV may be used for initiating hybridization.

Sharma *et al.* (2002) assessed genetic diversity in 28 yield and morphological traits of 100 aromatic rice genotypes, grown using Mahalanobis's D^2 statistics. These genotypes, originating from different countries, were divided into 9 clusters. The pattern of distribution of genotypes within various clusters was random and independent of geographical isolation. Based on mean performance, genetic distance and clustering pattern, inter-crossing of genotypes Gam Poon, Khao Jao Hawam, Basmati Sufaid 187, KCN 80152, Abor Bora and Hara might be useful in creating wider variability for important agronomic and quality traits with high yielding segregants.

Mishra *et al.* (2003) were determined the nature and magnitude of the genetic diversity for 20 quantitative and qualitative characters for 16 rice cultivars and their 72 F₁ hybrids during 1996-97 in Raipur, Madhya Pradesh, India. The genotypes were grouped in 12 clusters based on the relative magnitude of multivariate D² values. The highest number of genotypes was in cluster XII. Based on the cluster means, plant height, flag leaf width, ear bearing tillers per plant, 100-seed weight, hulling and milling percentage, panicle length, biological yield, harvest index, kernel length after cooking, gelatinization temperature and grain yield were the main factors for differentiation. The highest genetic distance was observed between clusters III and VIII and lowest between cluster VII and VIII. No close correspondence was evidenced between geographical distributions to genetic divergence as estimated by multivariate D². Analysis of variance indicated highly significant differences for the most of the characters studied.

Awasthi *et al.* (2005) conducted a field experiment to determine the genetic divergence of 21 Indian aromatic rice genotypes. A total of 21 aromatic rice genotypes were grouped into 6 clusters for different characters. The genotypes of one cluster indicated overall genetic similarity among them. The intercluster distance ranged from 0.00 for clusters IV, V and VI to 40.21 for cluster III. The intercluster distance was observed to be highest between clusters II and III, indicating that the genotypes of these two clusters were genetically more diverse. The number of grains per panicle, grain yield per plant, days to 50% flowering, leaf length and leaf width showed high percent contribution towards total genetic divergence.

Bhutia *et al.* (2005) was carried out assessment of genetic divergence using Mahalanobis D² statistics on 41 high yielding and local genotypes of rice (*Oryza sativa*). The genotypes were grouped into six clusters. Cluster I had the highest number of genotypes (27) followed by cluster II with eight, and cluster III with three genotypes, respectively. Clusters IV, V and VI were monogenotypic. Cluster IV showed the maximum genetic distance from cluster VI followed by its distance from cluster V. The desirable yield and quality characteristics were distributed mainly in clusters III and IV and cluster V showed the highest value for protein. The genotypes included in clusters III and IV may be used as parents in hybridization programme to improve yield and cooking quality, whereas the genotypes in clusters III and V may

be used in hybridization programmes to improve yield and nutritional quality with respect to protein.

Deepak *et al.* (2006) conducted a genetic divergence study to estimate the nature and magnitude of diversity in 50 aromatic rice accessions including five scented improved varieties (Pusa Basmati, Taraori Basmati, Indira 9, Dubraj and Madhuri 11 as controls). The D^2 analysis indicated the presence of appreciable amount of genetic diversity in the material. The 50 genotypes were grouped into 7 clusters. The cluster VI had the highest mean for grain yield per plant and for biological yield per plant. Intercluster distance was recorded highest between cluster III and cluster IV. The least distance was recorded in between cluster I and cluster V. The conclusion drawn by the cluster analysis was that high variability observed between the genotypes in different clusters for different characters in the studied population.

Multivariate analysis was carried out with 30 advanced deep water lines of BRRI and 10 local rice germplasms collected from south-west of Bangladesh by Habib *et al.* (2007). The genotypes were grouped into six clusters. More emphasis should be given on cluster VI for selecting genotypes as parents for crossing with the genotypes for cluster II and III which may produce new recombinants with desired traits.

Khalequzzaman *et al.* (2008) studied genetic diversity of 40 traditional Bangladeshi rice genotypes under rainfed condition through Mahalanobis D^2 statistic for grain yield and yield contributing characters. The genotypes were grouped into six clusters. The inter cluster distances were higher than the intra cluster distances indicating wider genetic diversity among the genotypes of different clusters. The intra cluster distances were lower in all the cases reflecting homogeneity of the genotypes within the clusters. More emphasis should be given on cluster V and III for selecting genotypes as parents for crossing with the genotypes of cluster IV which would be used to produce new recombinants with desired traits.



CHAPTER III

MATERIALS AND METHODS



CHAPTER III

MATERIALS AND METHODS

The study was conducted at the experimental farm of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207 during the period from July 2012 to December 2012 to know the genetic diversity of some extinct local rice genotypes. The materials and methods were adopted for conducting the experiments are discussed under the following heading and sub-headings:

3.1 Field experiment and observations

3.1.1 Experimental site

The experimental field was located at $90^{\circ} 33.5'$ E longitude and $23^{\circ} 77.4'$ N latitude at an altitude of 9 meter above the sea level. The field experiment was set up on the medium high land of the experimental farm.



Plate 1: The experimental plot at SAU



3.1.2 Soil and climate of the experimental site

The soil of the experiment site was a medium high land, clay loam in texture and having pH 5.47-5.63. The land was located in Agro-ecological Zone of 'Madhupur Tract' (AEZ No. 28).

The climate of the experimental site is sub-tropical characterized by heavy rainfall during April to July and sporadic during the rest of the year.

3.1.3 Design and layout

The experimental plots were laid out in randomized complete block design (RCBD). The field was divided into three blocks; representing three replications. Row to row and plant to plant distances were 25cm and 20cm respectively. Thirty five genotypes were distributed to each plot within each block randomly.

3.1.4 Materials

The experimental materials of the study comprised of 35 rice genotypes. The seeds were collected from Bangladesh Institute of Nuclear Agriculture, Mymensingh (BINA). The details of these genotypes are given in Table 1.



Table 1: List of thirty five rice genotypes along with their sources

Sl. No.	Indicating Symbol	Genotypes	Source
1	G-1	Kathi Goccha	BINA
2	G-2	Hamai	BINA
3	G-3	Khak Shail	BINA
4	G-4	Hari	BINA
5	G-5	Tal Mugur	BINA
6	G-6	Dakh Shail	BINA
7	G-7	Moina Moti	BINA
8	G-8	Nona Bokhra	BINA
9	G-9	Bogi	BINA
10	G-10	Patnai	BINA
11	G-11	Ledra Binni	BINA
12	G-12	Lalanamia	BINA
13	G-13	Hogla	BINA
14	G-14	Jamai Naru	BINA
15	G-15	Jota Balam	BINA
16	G-16	Khejur Chori	BINA
17	G-17	Ghunshai	BINA
18	G-18	Malagoti	BINA
19	G-19	Bazra Muri	BINA
20	G-20	Nona Kochi	BINA
21	G-21	Moghai Balam	BINA
22	G-22	Ghocca	BINA
23	G-23	Mondeshor	BINA
24	G-24	Mota Aman	BINA
25	G-25	Golapi	BINA
26	G-26	Bhute Shelot	BINA
27	G-27	Mowbinni	BINA
28	G-28	Kalo Mota	BINA
29	G-29	Ponkhiraj	BINA
30	G-30	Jolkumri	BINA
31	G-31	Lalbiroi-31	BINA
32	G-32	Karengal	BINA
33	G-33	Sada Gotal	BINA
34	G-34	Holde Gotal	BINA
35	G-35	BRRRI Dhan-33	BRRRI

BINA= Bangladesh Institute of Nuclear Agriculture

BRRRI= Bangladesh Rice Research Institute

3.1.5 Germination of seeds

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

3.1.6 Preparation of seedbed and raising seedling

The irrigated land was prepared thoroughly by 3-4 times ploughing and cross ploughing followed by laddering to attain a good puddle. Weeds and stubbles were removed. Thirty five separate strips were made and sprouted seeds were sown on each strip in 14th July of 2012. Seedbed was irrigated with regular interval to maintain moisture.

3.1.7 Preparation of main land

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

3.1.8 Application of fertilizers

The experimental plot was fertilized by applying urea, TSP, MP and Gypsum @180,100,70 & 60 Kg/ha, respectively. Total TSP, MP and Gypsum were applied at final land preparation. Total urea was applied in three installments, at 15 days after transplanting (DAT), 30 DAT and 50 DAT.

3.1.9 Intercultural operation

Necessary intercultural operations were made during cropping period for proper growth and development of the plants. Irrigation with regular interval was given to maintain 5-7 cm water up to hard drought stage of rice.

3.1.10 Plant protection measures

Proper control measures were taken against rats and birds.

3.1.11 Harvest and post-harvest operations

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

3.1.12 Collection of data

Data were collected from 5 hills of each genotype on the following parameters:

- | | |
|--|--|
| a) Plant height at maturity (cm): | Average length of the plants from base to the terminal spikelet including awn in centimeter. |
| b) Number of effective tillers: | Average number of tillers bearing panicles per hill. |
| c) Length of panicle (cm): | Average length of panicles to the top of the terminal spikelet including awn. |
| d) Days to flowering (DAS): | The days required for first flowering after sowing. |
| e) Number of primary branches per panicle: | Average number of primary branches per panicle |
| f) Number of secondary branches per panicle: | Average number of secondary branches per panicle |
| g) Number of unfilled grain per panicle: | Average number of unfilled grain per panicle |
| h) Number of filled grain per panicle: | Average number of filled grain per panicle |
| i) 1000 grain weight: | Weight of well dried and cleaned 1000-grains in gram. |
| j) Root length: | Average length of root per panicle. |
| k) Number of root hair: | Average number of root hair per panicle. |
| l) Root weight: | Average weight of root per panicle. |
| m) Grain yield per hill (g): | Average weight of grains per hill |

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3.2 Statistical Analysis of data

3.2.1 Estimation of genotypic and phenotypic variance

Genotypic and Phenotypic Variances were estimated according to the formula given by Johnson *et al.*, (1955).

$$\text{Genotypic variance } (\sigma^2g) = \frac{\text{GMS} - \text{EMS}}{r} \quad \text{Where,}$$

GMS = Genotypic mean square
EMS = Error mean square
R = Number of replication

$$\text{Phenotypic Variance } (\sigma^2p) = \sigma^2g + \text{EMS} \quad \text{Where,}$$

σ^2g = Genotypic variance
EMS = Error mean square

3.2.2 Estimation of Genotypic and Phenotypic Co-efficient of Variation

Genotypic and Phenotypic co-efficient of variation were estimated according to Burton (1952) and Singh and Chaudhary (1985).

Genotypic co-efficient of variation,

$$(\text{GCV}) = \frac{\sigma^2g}{x} \times 100 \quad \text{Where,}$$

σ^2g = Genotypic variance
x = Population mean

Phenotypic co-efficient of variation,

$$(\text{PCV}) = \frac{\sigma^2p}{x} \times 100 \quad \text{Where,}$$

σ^2p = Phenotypic variance
x = Population mean

3.2.2 Estimation of heritability

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

$$\text{Heritability } (h^2b) = \frac{\sigma^2g}{\sigma^2p} \times 100 \quad \text{Where,}$$

σ^2g = Genotypic variance
 σ^2p = Phenotypic variance

3.2.3 Estimation of genetic advance

Estimation of Genetic Advance was done following formula given by Johnson *et al.*, (1955).

$$\text{Genetic Advance (GA)} = h^2b.K.\sigma_p \quad \text{Where,}$$

h^2b = Heritability
 K = Selection differential, the value of which is 2.06 at 5% selection intensity; and
 σ_p = Phenotypic standard deviation.

3.2.4 Estimation of correlation coefficients

The Genotypic and Phenotypic correlation coefficients between yield and different yield contributing characters were estimated as:

$$\text{Genotypic correlation} = \frac{\text{Cov}(g)_{1.2}}{\sqrt{\sigma^2(g)_1.\sigma^2(g)_2}} \quad \text{Where,}$$

$\text{Cov}(g)(xy)$ = Genotypic covariance between the variables X and Y
 $\sigma^2(g)_1$ = Genotypic variance of the variable X1
 $\sigma^2(g)_2$ = Genotypic variance of the variable X2

Similarly,

$$\text{Phenotypic correlation} = \frac{\text{Cov}(ph)_{1.2}}{\sqrt{\sigma^2(ph)_1.\sigma^2(ph)_2}} \quad \text{Where,}$$

$\text{Cov}(ph)(xy)$ = Phenotypic covariance between the variables X and Y
 $\sigma^2(ph)_1$ = Phenotypic variance of the variable X1
 $\sigma^2(ph)_2$ = Phenotypic variance of the variable X2

3.2.5 Estimation of path coefficients

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects of yield contributing characters on grain yield per hectare.

After calculating the direct and indirect effect of the characters, residual effects (R) was calculated by using the formula given below (Singh and Chaudhary, 1985).

$$P^2_{RY} = 1 - (r_{1,y}P_{1,y} + r_{2,y}P_{2,y} + \dots + r_{12,y}P_{12,y})$$

Where,

$P^2_{RY} = R^2$ and hence residual effect, $R = (P^2_{RY})^{1/2}$
 $P_{i,y}$ = Direct effect of the i th character on yield y .
 $r_{i,y}$ = Correlation of the i th character with yield y .

3.2.6 Genetic diversity

Genetic diversity was analyzed using GENSTAT 5.13 software program (copyright 1987, Lawes Agricultural Trust, Rothamsted Experimental Station, UK). Genetic diversity analysis involves several steps, i.e., estimation of distance between the varieties clustering and analysis of inter-cluster distance. Therefore, more than one multivariate techniques are required to represent the results more clearly and it is obvious from the results of many researchers (Bashar, 2002, Uddin, 2001, Juned *et al.*, 1988, Ariyo, 1987, Patil *et al.*, 1987, Dani and Murthy, 1985, Anand and Rawat, 1984 and Balasch *et al.*, 1984).

3.2.7 Principal component analysis (PCA)

Analysis of genetic diversity in rice following multivariate techniques was used and mean data for each character were subjected to use. Principal components were computed from the correlation matrix and genotype scores obtained from first components (which has the property accounting for maximum variance) and succeeding components with latent roots greater than the unity (Jeger *et al.*, 1983) and contribution of the different morphological characters towards divergence are discussed from the latent vectors of the first two principal components. To divide the varieties of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. The algorithm is used to search for optimum values of chosen criterion. Starting from some initial classification of the varieties into required number of groups, the algorithm repeatedly transfers varieties from one group to another so long as such transfer improve the value of the criterion

the algorithm switches to a second stage which examines the effect of swapping two varieties of different classes and so on.

3.2.8 Principal coordinates analysis (PCO)

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

3.2.9 Canonical vector analysis (CVA)

Canonical vector analysis (CVA) complementary to D^2 statistic is a sort of multivariate analysis where canonical vector and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes, respectively and derived. Canonical vector analysis finds linear combination of original variability than maximize the ratio of between groups to within group's variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus in this analysis a series of orthogonal transformation sequentially maximize the ratio of among groups to within group variation.

3.2.10 Computation of average intra-cluster distances

The average intra cluster distance for each cluster was calculated by taking all possible D^2 values within the members of a cluster obtained from PCO. The formula used to measure the average intra-cluster distance was as follows:

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

Where,

D^2 is the sum of distances between all possible combinations (n) of the genotypes included in a cluster.

The square root of the D^2 values represents the distance (D) within cluster.

3.2.11 Computation of average inter-cluster distances

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

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

Where,

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

n_i = number of population in cluster i

n_j = number of population in cluster j

3.2.12 Cluster diagram

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



CHAPTER IV

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

This chapter comprises the presentation and discussion of the findings obtained from the study.

Characterization of Different Rice Genotypes

Various Characteristics of Different Local Rice Genotypes

The genotype G-13 showed dark red panicle in color (Plate 1). The genotypes G-18 and G-20 showed light red panicle in color and others showed greenish in color.

Variability for Agronomic Traits in Local Rice Genotypes

The mean performances of different quantitative characters of individual genotypes with Duncan's Multiple Range Test (DMRT) and the corresponding analysis of variance and the variability of 35 local rice genotypes with one check varieties are presented in Table 2 and Table 3, respectively.

Variation and Performance of the Genotypes

The analysis of variance of different genotypes of rice for yield and reproductive characters are shown in Table 2. Analysis of variance for the characters showed highly significant variations among the tested genotypes. This indicated that there was a wide genotypic variation among the genotypes for all the characters.



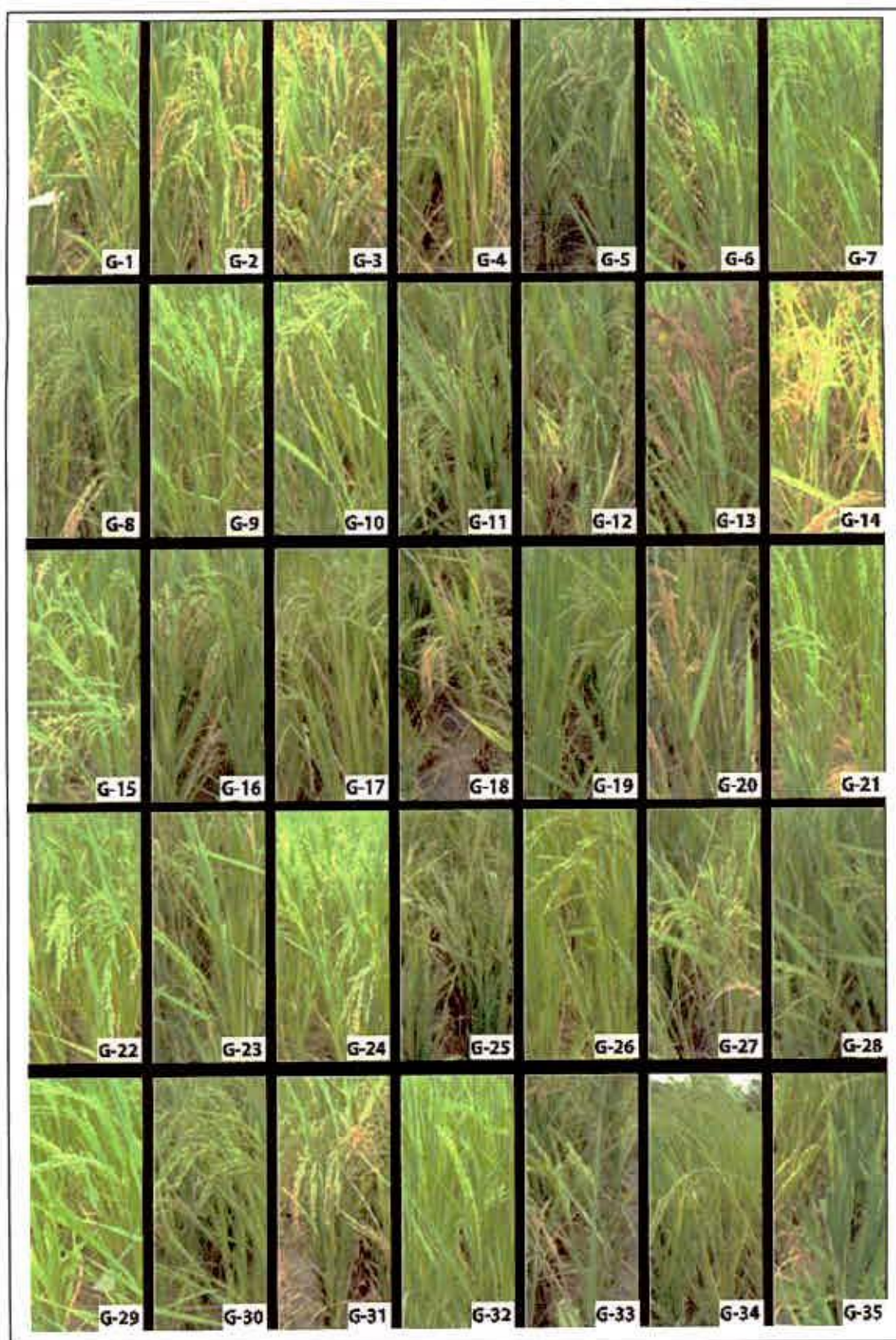


Plate 2: 35 rice genotypes were use in the study



Plate 3: Various types of roots of G-1 to G-10 from left to right



Plate 4: Various types of roots of G-21 to G-30 from left to right



Plate 5: Various types of roots of G-11 to G-20 from left to right



Plate 6: Various types of roots of G-31 to G-35 and G-1 from left to right

Plant height (cm)

The study showed that the range of plant height was 139.00 to 173.33 cm (Table 3). The highest plant height 173.33 cm was recorded for the genotype G-25 followed by G-1 and G-7. The Genotype G-29 was the shortest in plant height (139.00 cm) which was followed by G-12. The rest of the genotypes were different to each other.

Number of effective tiller

The range of number of effective tiller was 1.00 to 10.33. The highest number of effective tiller was produced by genotype G-15 (10.33) which was followed by G-5, G-7 and G-21. On the other hand genotype G-11, G-20, G-22 and G-31 produced the minimum number of effective tiller.

Length of panicle

The study showed that the range of length of panicle was 23.66 to 33.66 cm (Table 3). The highest plant height 33.66 cm was recorded for the genotype G-13 followed by G-20 and G-26. The Genotype G-28 was the shortest in length of panicle (23.66 cm) which was followed by G-12. The rest of the genotypes were different to each other.

Days to flowering

The study showed that the days to flowering for the genotypes ranged from 99.00 to 115.00 days (Table 3). Out of 35 genotypes G-4 (115 days) took longest period for flowering which was closely followed by G-35. The genotype G-12 took the minimum days for flowering. The second minimum days for flowering were recorded in the genotype G-1. The rest of the genotypes were different in flowering time and were medium to long duration in flowering.

Number of primary branches per panicle

The range of number of primary branches per panicle was 8.33 to 13.33. The highest number of primary branches per panicle was produced by genotype G-10 (13.33) which was followed by G-22 and G-29. On the other hand genotype G-9 produced the minimum number of primary branches per panicle.



Plate 7: In the research field showing plant height comparison with a person



Plate 8: G-12 took the minimum days to flowering

Number of root hair

The range of number of root hair was 478.00 to 1809.67. The highest number of root hair was produced by genotype G-4 (1809.67) which was followed by G-2 and G-21. On the other hand genotype G-27 followed by G-3 produced the minimum number of root hair.

Root weight

The study showed that the range of root weight was 15.67 to 122.33 (Table 3). The highest root weight 122.33 was recorded for the genotype G-20 followed by G-2. The Genotype G-35 was the shortest in root weight (15.67) which was followed by G-34 and G-32. The rest of the genotypes were different to each other.

Grain yield per hill (g)

The range of grain yield per hill was 7.20 to 35.90. The highest grain yield per hill was produced by genotype G-24 (35.90) which was followed by G-10. On the other hand genotype G-20 produced the minimum grain yield per hill.



Table 2 Analysis of variance for different plant characters

Source of variation	Replication	Genotypes	Error
Df	2	34	68
Plant height (cm)	10.08	255.65**	2.23
Number of effective tiller	0.867	23.055**	0.543
Length of panicle	5.813	15.929**	1.136
Days to flowering	1.057	39.343**	1.204
Number of primary branches per panicle	2.600	6.552**	0.639
Number of secondary branches per panicle	5.638	129.948**	0.971
Number of filled grain per panicle	4.581	551.086**	5.708
Number of unfilled grain per panicle	4.467	94.238**	1.114
1000 grain weight	4.372	7.461**	0.894
Root length	2.067	9.673**	1.978
Number of root hair	5340.94	316241.10**	5994.91
Root weight	96.86	2545.88**	9.66
Grain yield per hill (g)	0.381	117.245**	0.183

** indicates significant at 0.01 probability, respectively.

Number of secondary branches per panicle

The study showed that the range of number of secondary branches per panicle was 17.33 to 39.33 (Table 3). The highest number of secondary branches per panicle 39.33 was recorded for the genotype G-18 followed by G-26 and G-11. The Genotype G-7 was the shortest in number of secondary branches per panicle (17.33) which was followed by G-31. The rest of the genotypes were different to each other.

Number of filled grain per panicle

The range of number of filled grain per panicle was 98.00 to 144.33. The highest number of filled grain per panicle was produced by genotype G-10 (144.33) which was followed by G-6 and G-25. On the other hand genotype G-1 followed by G-12 produced the minimum number of filled grain per panicle.

Number of unfilled grain per panicle

The study showed that the range of number of unfilled grain per panicle was 21.33 to 41.33 (Table 3). The highest number of unfilled grain per panicle 41.33 was recorded for the genotype G-17 followed by G-15. The Genotype G-28 was the shortest in number of unfilled grain per panicle (21.33) which was followed by G-1. The rest of the genotypes were different to each other.

1000 grain weight

The range of 1000 grain weight was 19.80 to 26.00. The highest 1000 grain weight was produced by genotype G-15 (26.00) which was followed by G-34, G-35 and G-32. On the other hand genotype G-30 produced the minimum 1000 grain weight.

Root length

The study showed that the range of root length was 6.33 to 14.33 cm (Table 3). The highest root length 14.33 cm was recorded for the genotype G-33 followed by G-10. The Genotype G-12 and G-24 was the shortest in root length (6.33 cm) which was followed by G-22. The rest of the genotypes were different to each other.

Table 3 Mean performance of various growth parameter and yield components

Genotypes	PH	NET	LP	DF	NPBP	NSBP
G-1	173.00	6.33	30.50	103.00	9.33	20.33
G-2	162.00	7.33	27.87	105.00	10.33	22.33
G-3	168.60	3.33	29.66	108.00	11.67	27.33
G-4	156.60	7.00	27.66	115.00	12.33	31.33
G-5	144.60	9.33	28.50	109.00	8.67	35.33
G-6	160.30	2.33	30.16	104.00	12.67	31.33
G-7	171.30	9.33	28.83	110.00	10.33	17.33
G-8	170.00	3.33	30.66	112.00	9.67	22.67
G-9	164.00	7.33	25.80	109.00	8.33	26.33
G-10	170.80	6.00	28.50	110.00	13.33	30.00
G-11	158.00	1.00	29.25	111.00	11.67	38.33
G-12	139.50	4.33	25.00	99.00	10.67	33.33
G-13	166.30	6.00	33.66	109.00	9.00	21.67
G-14	163.00	3.33	30.83	112.00	12.33	18.67
G-15	169.50	10.33	27.75	111.00	8.67	27.67
G-16	158.30	7.00	31.66	108.00	12.00	32.33
G-17	162.25	8.33	32.25	104.00	11.67	36.67
G-18	148.25	8.00	26.37	104.00	10.33	39.33
G-19	145.00	4.33	27.66	112.00	9.67	19.33
G-20	168.50	1.00	33.50	113.00	11.67	26.67
G-21	158.50	9.33	28.25	109.00	8.67	23.67
G-22	151.50	1.00	28.33	110.00	13.00	20.67
G-23	170.33	3.33	29.66	110.00	10.67	28.33
G-24	161.66	3.00	30.16	113.00	10.33	24.67
G-25	173.33	4.67	29.16	106.00	8.67	31.33
G-26	165.90	2.00	32.40	110.00	11.33	38.67
G-27	168.50	5.33	28.75	107.00	9.67	31.00
G-28	158.50	7.00	23.66	111.00	12.33	22.67
G-29	139.00	1.33	30.83	104.00	13.00	33.33
G-30	159.66	3.33	25.66	113.00	10.33	36.33
G-31	166.30	1.00	26.83	106.00	8.67	18.00
G-32	159.33	2.33	26.83	110.00	11.33	22.33
G-33	166.30	8.00	28.25	105.00	12.33	21.33
G-34	169.66	5.33	30.50	107.00	9.67	19.33
G-35	165.75	4.00	28.00	114.00	10.67	23.67
Mean	161.54	5.04	28.95	108.66	10.71	27.25
Min.	139.00	1.00	23.66	99.00	8.33	17.33
Max.	173.33	10.33	33.66	115.00	13.33	39.33
LSD _{0.05}	2.43	1.20	1.74	1.78	1.30	1.61

PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUFGP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g),

Table 3 (continued)

Genotypes	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
G-1	98.00	22.00	23.09	9.33	987.00	77.00	22.90
G-2	109.67	26.67	22.40	11.00	1707.33	105.33	25.30
G-3	106.67	31.33	21.85	10.67	578.00	34.33	18.40
G-4	136.33	37.00	21.33	11.00	1809.67	84.00	30.80
G-5	133.67	23.67	23.19	9.33	1260.00	60.33	25.40
G-6	143.00	28.33	22.50	8.33	685.33	72.33	16.60
G-7	105.33	38.67	21.94	7.00	823.00	32.00	21.70
G-8	101.67	30.67	21.66	10.67	1553.00	22.00	31.40
G-9	108.00	25.33	24.25	9.00	956.33	76.33	23.40
G-10	144.33	35.33	23.53	13.33	1442.00	20.00	33.50
G-11	140.33	33.67	23.07	10.00	1428.33	24.33	19.10
G-12	98.33	32.00	22.85	6.33	930.00	46.00	12.70
G-13	111.33	29.67	20.25	11.00	1283.33	51.67	21.60
G-14	102.00	34.33	23.72	10.33	1327.00	60.33	27.40
G-15	121.67	40.67	26.00	11.00	1170.33	84.00	25.10
G-16	116.00	32.67	24.89	12.33	1223.00	82.33	27.30
G-17	113.67	41.33	23.76	10.00	1048.33	80.00	22.30
G-18	111.67	39.33	23.32	8.33	1567.33	52.67	17.60
G-19	127.67	29.33	20.67	9.00	1293.00	52.00	10.30
G-20	117.33	30.00	22.57	10.33	680.67	122.33	7.20
G-21	113.33	32.67	21.17	9.00	1607.33	70.33	26.40
G-22	128.67	39.33	23.63	7.33	1229.00	98.33	31.50
G-23	139.00	29.33	21.80	10.00	1287.33	78.33	28.50
G-24	117.00	25.33	22.13	6.33	1303.67	68.00	35.90
G-25	141.33	24.33	21.87	10.67	963.00	47.00	21.60
G-26	116.67	39.00	23.70	11.00	1407.33	30.00	30.20
G-27	112.33	27.00	20.30	7.33	478.00	90.00	24.30
G-28	123.33	21.33	21.77	9.00	1224.33	20.67	22.10
G-29	125.33	31.33	24.07	9.67	1136.00	26.00	20.60
G-30	110.67	35.67	19.80	10.00	827.33	32.33	26.10
G-31	135.33	33.33	23.77	12.33	887.00	94.33	29.40
G-32	132.00	37.00	25.25	9.00	779.33	18.00	24.30
G-33	124.33	30.33	24.83	14.33	1153.00	52.33	21.70
G-34	114.00	27.67	25.44	11.00	1331.33	16.00	23.60
G-35	132.67	22.67	25.35	9.33	836.00	15.67	18.50
Mean	120.36	31.38	22.91	9.85	1148.66	57.05	23.56
Min.	98.00	21.33	19.80	6.33	478.00	15.67	7.20
Max.	144.33	41.33	26.00	14.33	1809.67	122.33	35.90
LSD _{0.05}	3.89	1.72	1.54	2.29	126.20	5.06	0.70

PH = Plant height (cm), NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUGFP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight, RL = Root length, NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

Genetic Variability in Local Rice Genotypes

Thirteen characters of rice such as plant height (cm), number of effective tiller, length of panicle, days to flowering, number of primary branches per panicle, number of secondary branches per panicle, number of filled grain per panicle, number of unfilled grain per panicle, 1000 grain weight, root length, number of root hair, root weight and grain yield per hill (g) were studied in thirty five genotypes.

Analysis of variance in Table 2; the mean values over three replication for the characters of all genotypes are presented in Table 3; genotypic, phenotypic and environmental variance, genotypic, phenotypic and environmental coefficients of variations in Table 4 showed highly significant variations among the genotypes for all characters indicating wide scope of selection for these characters, i.e., the data revealed substantial variability and thus high possibility of improvement in most of the traits. The variability in the present study indicated the potentiality of the genotypes for selecting out desirable character. The phenotypic variance was partitioned into genotypic and environmental variances for clear understanding of the pattern of variations.

The extent of variability for any character is very important for the improvement of a crop through breeding. The estimates of genotypic variation (σ^2g), phenotypic variation (σ^2p), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance (GA) for different characters have been presented in Table 4. The highest σ^2g was found for number of root hair (103415.40) and the lowest magnitude of σ^2g was observed in number of primary branches per panicle (1.97). The highest σ^2p was found for number of root hair (109410.31) and the lowest magnitude of σ^2p was observed in number of primary branches per panicle (2.61). Abdel-Ghani *et al.* (2005) investigated the genetic variability and correlation coefficients involving five floral characters in a group of 29 cultivated and wild rice (*Oryza sp.*). Wide variability existed in anther length, stigma length and percent exerted stigma. The genetic variation constituted a high proportion of the total variation for these traits. Thus, selection for these characters is expected to be highly effective.

Table 4 Estimation of genetic parameters in thirteen characters of 35 genotypes in rice

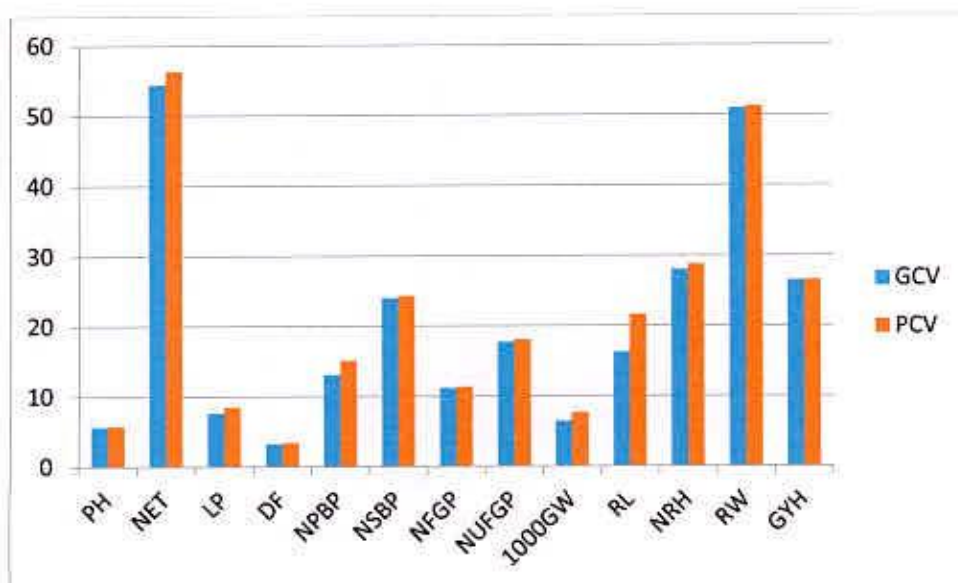
Characters	Grand mean	(σ^2_g)	(σ^2_p)	(σ^2_e)	h^2_b (%)	GCV (%)	PCV (%)	GA	GA (%)
PH	161.54	84.47	86.71	2.24	97.42	5.69	5.76	18.69	11.57
NET	5.04	7.50	8.05	0.54	93.25	54.39	56.33	5.45	108.20
LP	28.95	4.93	6.07	1.14	81.28	7.67	8.51	4.12	14.24
DF	108.66	12.71	13.92	1.20	91.35	3.28	3.43	7.02	6.46
NPBP	10.71	1.97	2.61	0.64	75.52	13.10	15.08	2.51	23.46
NSBP	27.25	42.99	43.96	0.97	97.79	24.06	24.33	13.36	49.02
NFGP	120.36	181.79	187.50	5.71	96.96	11.20	11.38	27.35	22.72
NUFGP	31.38	31.04	32.16	1.11	96.54	17.75	18.07	11.28	35.93
1000GW	22.91	2.19	3.08	0.89	71.00	6.46	7.67	2.57	11.21
RL	9.85	2.57	4.54	1.98	56.46	16.26	21.64	2.48	25.17
NRH	1148.66	103415.40	109410.31	5994.91	94.52	28.00	28.80	644.06	56.07
RW	57.05	845.41	855.07	9.66	98.87	50.97	51.26	59.56	104.40
GYH	23.56	39.02	39.20	0.18	99.53	26.51	26.57	12.84	54.48

PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUGP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g),

σ^2_g = Genotypic variance, σ^2_p = Phenotypic variance, σ^2_e = Environmental variance, h^2_b = Heritability (broad sense), GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, GA = Genetic Advance

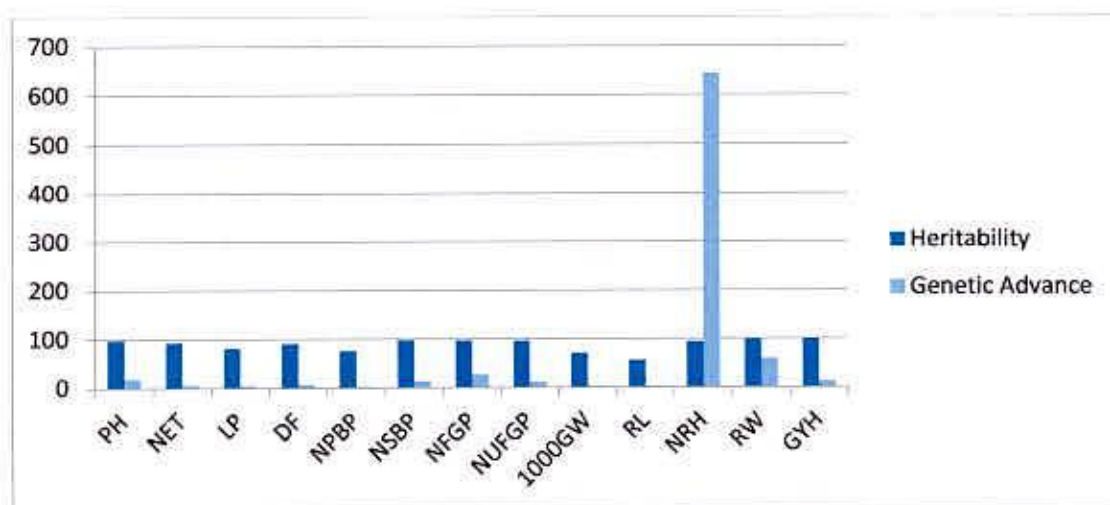
The GCV and PCV were the highest for number of effective tiller (54.39 and 56.33) followed by root weight (50.97 and 51.26), number of root hair (28.00 and 28.80) and grain yield per hill (g) (26.51 and 26.57) (Table 4). High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield per hill (g) indicated that selection of these traits would be effective. The GCV and PCV were the lowest for days to flowering (3.28 and 3.43) and plant height (cm) (5.69 and 5.76). PCV were slightly higher than GCV in case of all the traits, indicating presence of environmental influence to some degrees in the phenotypic expression of the characters. Akanda *et al.* (1997) also reported similar result.

Heritability estimates were high for all the characters studied except root length, 1000 grain weight and number of primary branches per panicle. The values were especially high for grain yield per hill (g), root weight and number of secondary branches per panicle. Johnson *et al.* (1955) suggested that high heritability combined with high genetic advance is an indicative of additive gene action and selection based on these parameters would be more reliable. In the present investigation, high heritability estimates in conjunction with high genetic advance in present of mean were observed for number of effective tiller, root weight and number of root hair.



PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUFGP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

Figure 1 Graphical representation of genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV)



PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUFGP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

Figure 2 Graph showing heritability and genetic advance

Table 5 Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of rice

Characters		NET	LP	DF	NPBP	NSBP	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
PH	Rg	0.201	0.985**	0.648**	-0.624**	-0.996**	-0.158	-0.314	0.030	0.983**	-0.616**	0.151	0.772**
	Rp	0.192	0.882**	0.620**	-0.539	-0.970**	-0.157	-0.302	0.041	0.955**	-0.590**	0.145	0.763**
NET	Rg		-0.638**	-	-0.851**	-0.044	-0.728**	0.038	0.165	0.303	0.802**	0.309	0.161
	Rp		-0.577**	0.427**	-0.810**	-0.041	-0.691**	0.037	0.134	0.209	0.753**	0.289	0.161
LP	Rg			0.103	0.442**	0.110	-0.323	0.235*	0.111	0.829**	0.038	0.514**	0.039
	Rp			0.102	0.325	0.098	-0.281	0.204	0.061	0.565**	0.032	0.459**	0.035
DF	Rg				0.200	-0.543**	0.663**	0.186	-0.516**	0.233	0.598**	-0.309	0.846**
	Rp				0.140	-0.503**	0.614**	0.171	-0.432**	0.157	0.528**	-0.295	0.809**
NPBP	Rg					0.543**	0.817**	0.921**	0.515**	0.426*	0.114	-0.446**	0.060
	Rp					0.470**	0.686**	0.789**	0.403*	0.308	0.106	-0.369*	0.051
NSBP	Rg						0.563**	0.770**	-0.124	-0.127	0.152	-0.214	-0.218
	Rp						0.545**	0.747**	-0.118	-0.081	0.133	-0.210	-0.215
NFGP	Rg							-0.071	0.433**	0.831**	0.182	-0.162	0.288
	Rp							-0.069	0.353*	0.612**	0.175	-0.160	0.282
NUFGP	Rg								0.531**	0.290	0.505**	0.091	0.517**
	Rp								0.442**	0.239	0.478**	0.089	0.507**
1000GW	Rg									0.963**	-0.038	-0.283	0.176
	Rp									0.630**	-0.025	-0.232	0.151
RL	Rg										0.839**	-0.125	0.645**
	Rp										0.630**	-0.088	0.479**
NRH	Rg											-0.094	0.888**
	Rp											-0.092	0.859**
RW	Rg												0.031
	Rp												0.030

** = Significant at 1%. * = Significant at 5%.

PH = Plant height (cm), NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUGP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight, RL = Root length, NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g), Rg = Genotypic correlation, Rp = Phenotypic correlation.

Character Association

Yield is a complex product being influenced by several independent quantitative characters. Breeders always look for variation among traits to select desirable types. Some of these characters are highly associated among themselves and with seed yield. The analysis of the relationships among these characters and their associations with seed yield is essential to establish selection criteria. When more characters are involved in correlation study it becomes difficult to ascertain the characters which really contribute toward yield. The path coefficient analysis under such situations helps to determine the direct contribution of these characters and their indirect contributions via other characters. Selection for yield *per se* may not be effective unless the other yield components were having direct or indirect influence on it and are taken into consideration. When selection pressure is exercised for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated traits. Genotypic and phenotypic correlation coefficients were calculated as according to Miller *et al.* (1958)

Correlation coefficient

The genotypic and phenotypic correlations among yield and yield contributing characters in rice are shown in Table 5. It is evident that in majority of the cases, the genotypic correlation coefficients were higher than their phenotypic correlation coefficients indicating that of a strong inherent association between the characters studied and suppressive effect of the environment modified the phenotypic expression of these characters by reducing phenotypic correlation values. In few cases, however, phenotypic correlation coefficients were same with or higher than their corresponding genotypic correlation coefficients suggesting that both environmental and genotypic correlation in these cases act in the same direction and finally maximize their expression at phenotypic level. Accordingly, Bai *et al.* (1992) reported that the genotypic correlations were greater than the phenotypic values in medium duration rice varieties.

Correlation of grain yield per hill was found to be highly significant and positive for number of root hair, days to flowering and plant height at both genotypic and phenotypic level and negatively significant for Number of secondary branches per panicle at both level (Table 5). Significant positive correlation of grain yield per hill with number of root

hair, days to flowering and plant height imply that selection for these characters would lead to simultaneous improvement of grain yield in rice. Plant height recorded significant negative correlation with number of secondary branches per panicle followed by number of primary branches per panicle and number of root hair at genotypic and phenotypic level. Number of effective tiller showed significant positive correlation with number of root hair at both genotypic and phenotypic level. It is observed that length of panicle was significantly and positively associated with root length followed by root weight at both genotypic and phenotypic level.

Table 6 Genotypic path coefficient analysis showing direct and indirect effects of different characters on yield of 35 rice genotypes

Characters	PH	NET	LP	DF	NPBP	NSBP	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
PH	0.240	0.127	-0.184	0.466	-0.110	0.092	-0.027	-0.170	-0.005	0.182	0.144	0.016	0.772**
NET	0.048	0.635	0.119	-0.307	-0.150	0.004	-0.128	0.020	-0.027	0.056	-0.141	0.033	0.161
LP	0.236	-0.405	-0.186	0.074	0.078	-0.010	-0.057	0.127	-0.018	0.153	-0.008	0.055	0.039
DF	0.155	-0.271	-0.019	0.719	0.035	0.050	0.117	0.101	0.087	0.043	-0.140	-0.033	0.846**
NPBP	-0.149	-0.540	-0.082	0.143	0.177	-0.050	0.144	0.501	-0.087	0.079	-0.026	-0.048	0.060
NSBP	-0.239	-0.027	-0.020	-0.390	0.096	-0.093	0.099	0.419	0.021	-0.023	-0.035	-0.023	-0.218
NFGP	-0.037	-0.462	0.060	0.477	0.144	-0.052	0.176	-0.038	-0.073	0.154	-0.042	-0.017	0.288
NUFGP	-0.075	0.024	-0.043	0.133	0.163	-0.071	-0.012	0.544	-0.090	0.053	-0.118	0.009	0.517**
1000GW	0.007	0.104	-0.020	-0.371	0.091	0.011	0.076	0.289	-0.169	0.178	0.008	-0.030	0.176
RL	0.236	0.192	-0.154	0.167	0.075	0.011	0.146	0.157	-0.163	0.185	-0.197	-0.013	0.645**
NRH	-0.147	0.382	-0.007	0.430	0.020	-0.014	0.032	0.274	0.006	0.155	-0.235	-0.010	0.888**
RW	0.036	0.196	0.096	-0.222	-0.079	0.019	-0.028	0.049	0.048	-0.023	0.022	0.108	0.031

Residual effect: 0.137. ** = Significant at 1%. * = Significant at 5%.

PH = Plant height (cm), NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUGFP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight, RL = Root length, NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

Path Analysis

Associations of characters determined by correlation coefficient may not provide an exact picture of the relative importance of direct and indirect influence of each of yield components on grain yield per plant. As a matter of fact, in order to find out a clear picture of the interrelationship between grain yield per plant and other yield attributes, direct and indirect effects were worked out using path analysis at both genotypic and phenotypic level.

Genotypic path coefficient analysis showing direct and indirect effects of different characters and the results are presented in Table 6. From the path coefficient analysis (Table 6) showed that days to flowering had maximum direct effect (0.719) on yield followed by number of effective tiller (0.635), number of unfilled grain per panicle (0.544). Matho *et al.* (2003) reported that the number of branches per panicle (0.424) had the highest positive direct effect on grain yield followed by number of filled grains per panicle (0.411), and days to 50% flowering (0.07). The lowest direct effect on grain yield was exhibited by root weight (0.108) followed by number of filled grain per panicle (0.176). The highest negative indirect effects on grain yield were obtained by number of root hair (-0.235). Patil and Sarawgi (2005) worked out on path co-efficient in 128 aromatic rice accessions for seven traits and observed greatest positive direct effect of 1000-grain weight followed by number of ear-bearing tillers per plant, number of filled grains per panicle and number of days to 50% flowering on grain yield. However, 1000-grain weight had on significant correlation with grain yield per plant due to its negative indirect on grain yield plant through number of filled grain per panicle and plant height. The results prescribed that highly significant positive correlation with positive direct effect was observed in days to flowering, number of effective tiller, number of unfilled grain per panicle, number of filled grain per panicle and root weight.

The residual effect of the present study was 0.137.

Phenotypic path coefficient analysis showing direct and indirect effects of different characters and the results are presented in Table 7. From the path coefficient analysis (Table 7) showed that number of unfilled grain per panicle had maximum direct effect (0.623) on yield followed by number of effective tiller (0.575), root length (0.543). The lowest direct effect on grain yield was exhibited by number of filled grain per panicle

(0.027) followed by root weight (0.203). The highest negative indirect effects on grain yield were obtained by length of panicle (-0.523). The results prescribed that highly significant positive correlation with positive direct effect was observed in number of unfilled grain per panicle, number of effective tiller, root length, root weight and number of filled grain per panicle.

The residual effect of the present study was 0.0055.

Table 7 Phenotypic path coefficient analysis showing direct and indirect effects of different characters on yield of rice

Characters	PH	NET	LP	DF	NPBP	NSBP	NFGP	NUFGP	1000 GW	RL	NRH	RW	GYH
PH	0.247	0.110	-0.461	0.329	-0.278	0.274	-0.004	-0.188	-0.020	0.519	0.206	0.029	0.763**
NET	0.047	0.575	0.302	-0.203	-0.418	0.011	-0.018	0.023	-0.067	0.113	-0.263	0.058	0.161
LP	0.218	-0.332	-0.523	0.054	0.168	-0.027	-0.007	0.127	-0.030	0.307	-0.011	0.093	0.035
DF	0.153	-0.219	-0.053	0.531	0.072	0.142	0.016	0.106	0.218	0.085	-0.184	-0.060	0.809**
NPBP	-0.133	-0.466	-0.170	0.074	0.517	-0.132	0.018	0.492	-0.203	0.167	-0.037	-0.075	0.051
NSBP	-0.239	-0.023	-0.051	-0.267	0.243	-0.282	0.014	0.466	0.059	-0.044	-0.046	-0.042	-0.215
NFGP	-0.038	-0.397	0.147	0.326	0.354	-0.154	0.027	-0.043	-0.178	0.332	-0.061	-0.032	0.282
NUFGP	-0.074	0.021	-0.106	0.090	0.407	-0.211	-0.001	0.623	-0.223	0.129	-0.167	0.018	0.507**
1000GW	0.010	0.077	-0.031	-0.229	0.208	0.033	0.009	0.275	-0.505	0.342	0.008	-0.047	0.151
RL	0.236	0.120	-0.295	0.083	0.159	0.022	0.016	0.149	-0.318	0.543	-0.220	-0.017	0.479**
NRH	-0.145	0.433	-0.016	0.280	0.054	-0.037	0.004	0.298	0.012	0.342	-0.349	-0.018	0.859**
RW	0.035	0.166	-0.240	-0.156	-0.190	0.059	-0.004	0.055	0.117	-0.047	0.032	0.203	0.030

Residual effect: 0.0055

PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUGFP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

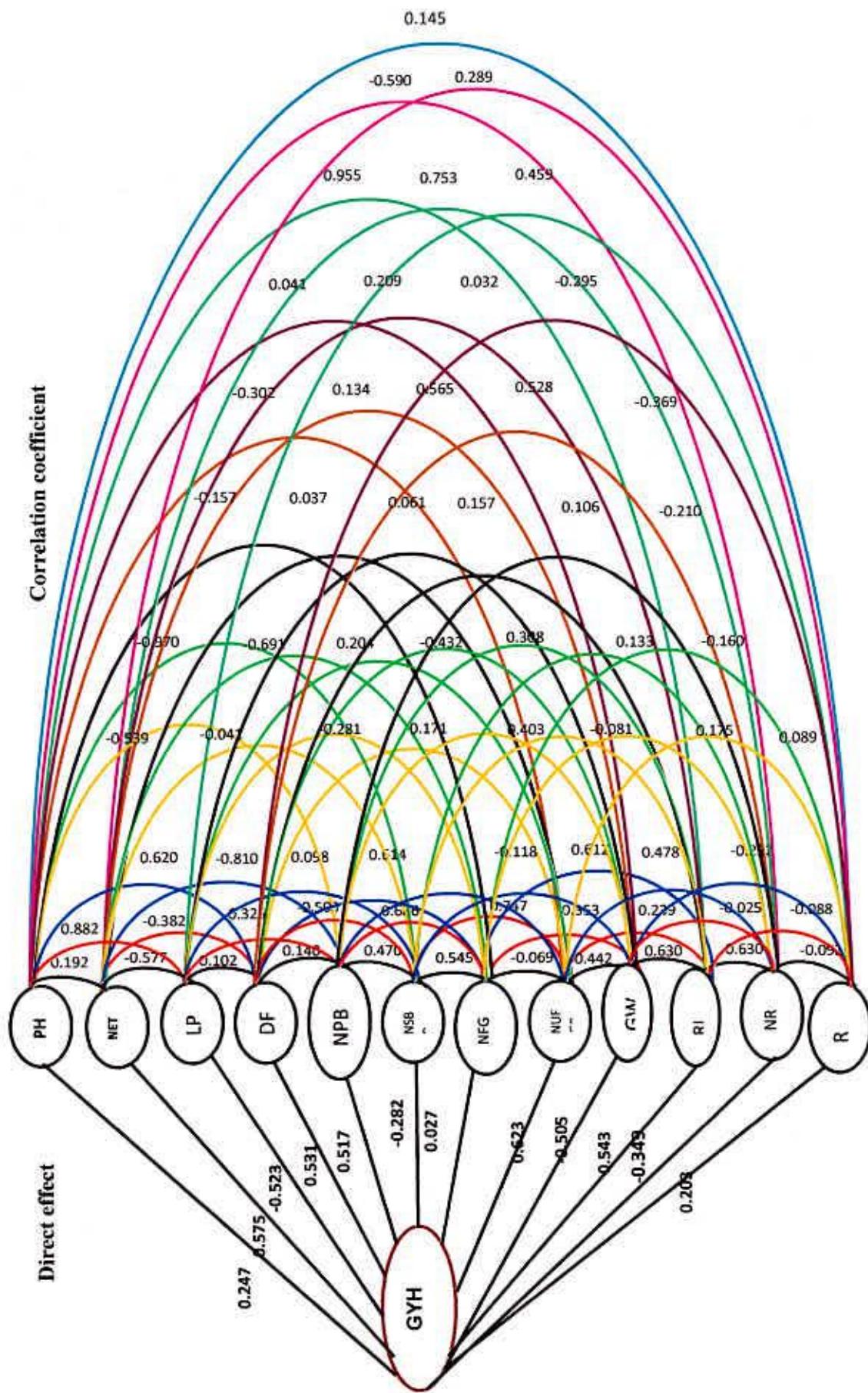


Figure 3: Phenotypic path diagrammatic representation of direct effect and correlation coefficient

Table 8 Distribution of 35 rice genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Percent	Name of genotypes
I	G-1, G-2, G-5, G-9, G-19, G-21 and G-28	7	20.00	Kathi Goccha, Hamai, Tal Mugur, Bogi, BazraMuri, MoghaiBalam and KaloMota
II	G-3, G-7, G-8, G-13, G-14, G-22, G-24, G-27 and G-30	9	25.71	KhakShail, MoinaMoti, Nona Bokhra, Hogla, JamaiNaru, Ghocca, MotaAman, Mowbinni and Jolkumri
III	G-4, G-10, G-11, G-15, G-16, G-17 and G-26	7	20.00	Hari, Patnai, Ledra Binni, Jota Balam, Khejur Chori, Ghunshai and Bhute Shelot
IV	G-6, G-20, G-23, G-25, G-29, G-31, G-32, G-33, G-34 and G-35	10	28.57	Dakh Shail, Nona Kochi, Mondeshor, Golapi, Ponkhiraj, Lalbiroi-31, Karengal, Sada Gotal, Holde Gotal and BRRI Dhan-33
V	G-12 and G-18	2	5.71	Lalanamia and Malagoti

The analysis of variance showed significance differences among 35 genotypes for all 13 characters studied indicating the presence of genetic variability among the genotypes. On the basis of cluster analysis, studied genotypes were grouped into five clusters (Table 8). This distribution pattern indicated that the highest number of genotypes was comprised in cluster IV (10) and the lowest were in cluster V (2).

Intra and inter cluster distances (D^2) for 35 genotypes are shown in Table 9. The highest inter-cluster distance was observed between the cluster II and V (46.71) followed by III and V (46.40) and IV and V (45.43) (Figure 4). Genotypes from these three clusters may be involved in hybridization as wide genetic variations existed among the groups. While the lowest distance was observed in between the cluster I and II (34.25) followed by I and IV (36.02), suggesting a close relationship among these clusters (Figure 4). Cluster IV exhibited the highest intra-cluster distance (38.36), while the lowest distance was observed in cluster V (23.09).

Table 9 Intra (Bold) and inter cluster distances (D^2) for 35 genotypes

Cluster	I	II	III	IV	V
I	1067.58 (32.67)	1172.86 (34.25)	1569.92 (39.62)	1297.77 (36.02)	1683.22 (41.03)
II		1063.08 (32.60)	1320.19 (36.33)	1360.99 (36.89)	2182.20 (46.71)
III			1206.87 (34.74)	1664.34 (40.80)	2153.41 (46.40)
IV				1471.19 (38.36)	2063.57 (45.43)
V					533.10 (23.09)

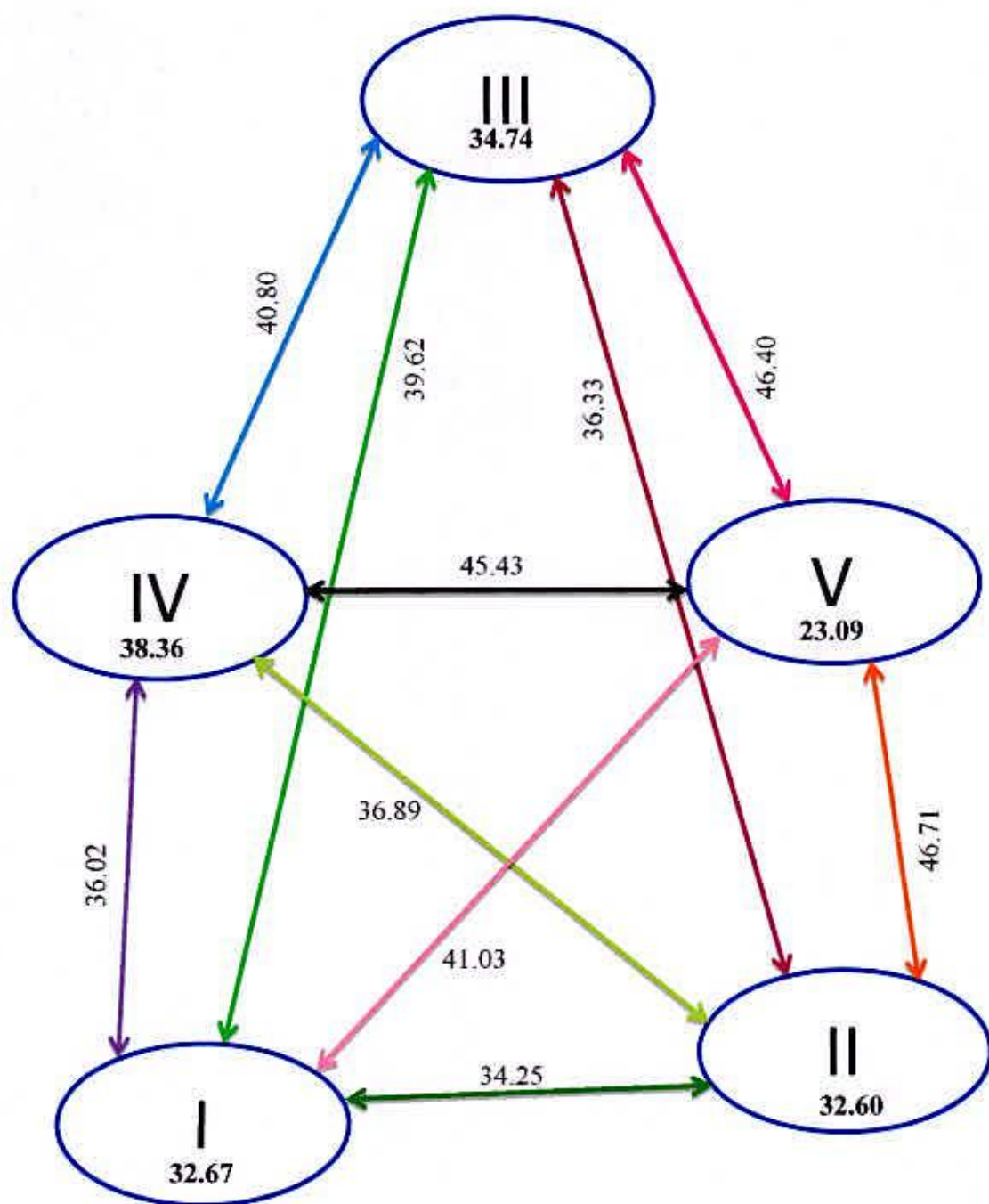


Figure 4 Diagram showing intra and inter-cluster distances of 35 genotypes of rice

Table 10 The nearest and farthest clusters from each cluster between D^2 values

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	II (34.25)	V (41.03)
2	II	I (34.25)	V (46.71)
3	III	II (36.33)	V (46.40)
4	IV	I (36.02)	V (45.43)
5	V	I (41.03)	II (46.71)



In the Table 10 Cluster I consisted of nearest cluster with D^2 values cluster II (34.25) and farthest cluster with D^2 values cluster V (41.03). Cluster II consisted of nearest cluster with D^2 values cluster I (34.25) and farthest cluster with D^2 values V (46.71). Cluster III consisted of nearest cluster with D^2 values cluster II (36.33) and farthest cluster with D^2 values V (46.40). Cluster IV consisted of nearest cluster with D^2 values cluster I (36.02) and farthest cluster with D^2 values V (45.43). Cluster V consisted of nearest cluster with D^2 values cluster I (41.03) and farthest cluster with D^2 values II (46.71).

The cluster mean for 13 characters of 35 genotypes of rice are presented in Table 11. The result revealed that cluster the highest intra cluster means for yield were obtained from cluster III and other most important reproductive characters were obtained from cluster I. Therefore, more emphasis should be given on this cluster for selecting genotypes as a variety and as well as parents in crossing with other genotypes.

Table 11 Cluster mean values of 13 different characters of 35 rice genotypes

Characters	I	II	III	IV	V	Max	Min
PH	157.94	164.50	163.05	163.88	143.88	164.50	143.88
NET	7.28	4.22	5.95	3.33	6.16	7.28	3.33
LP	27.46	29.61	29.92	29.37	25.68	29.92	25.68
DF	108.28	110.44	109.85	107.90	101.50	110.44	101.50
NPBP	9.61	10.70	11.57	10.93	10.50	11.57	9.61
NSBP	24.28	24.48	33.57	25.56	36.33	36.33	24.28
NFGP	116.23	110.63	127.00	130.43	105.00	130.43	105.00
NUFGP	25.85	32.44	37.09	29.43	35.67	37.09	25.85
1000GW	22.36	21.69	23.75	23.74	23.08	23.75	21.69
RL	9.38	8.96	11.23	10.49	7.33	11.23	7.33
NRH	1290.76	1044.70	1361.28	973.89	1248.67	1361.28	973.89
RW	65.99	54.33	57.80	54.23	49.33	65.99	49.33
GYH	22.25	26.47	26.90	21.20	15.15	26.90	15.15

PH = Plant height (cm) , NET = Number of effective tiller, LP = Length of panicle, DF = Days to flowering, NPBP = Number of primary branches per panicle, NSBP = Number of secondary branches per panicle, NFGP = Number of filled grain per panicle, NUGFP = Number of unfilled grain per panicle, 1000 GW = 1000 grain weight , RL = Root length , NRH = Number of root hair, RW = Root weight, GYH = Grain yield per hill (g).

Table 12: Latent vectors for 13 characters of 35 rice genotypes

Characters	Vector 1/PCA1	Vector 2/PCA2
Plant height	0.046	0.374
Number of effective tiller	0.134	-0.011
Length of panicle	0.068	0.309
Days to flowering	0.464	-0.190
Number of primary branches per panicle	0.240	-0.374
Number of secondary branches per panicle	0.447	0.060
Number of filled grain per panicle	-0.069	0.417
Number of unfilled grain per panicle	-0.116	0.337
1000 grain weight	0.118	-0.412
Root length	-0.072	0.058
Number of root hair	0.489	0.254
Root weight	-0.060	0.049
Grain yield per hill (g)	0.472	0.240

Contribution of the characters towards divergence is presented in Table 12. The PCA (Principal Component Analysis) revealed that in vector I; most of the characters were positive divergence except for number of filled grain per panicle, number of unfilled grain per panicle, root length and root weight. Similarly, in vector II most of the characters showed positive divergence except for number of effective tiller, days to flowering, number of primary branches per panicle and 1000 grain weight. Such result indicates that most of the characters contributed maximum towards divergence. It is interesting that greater divergence in the present material due to these characters will offer a good scope for improvement of yield through rational selection of parents.

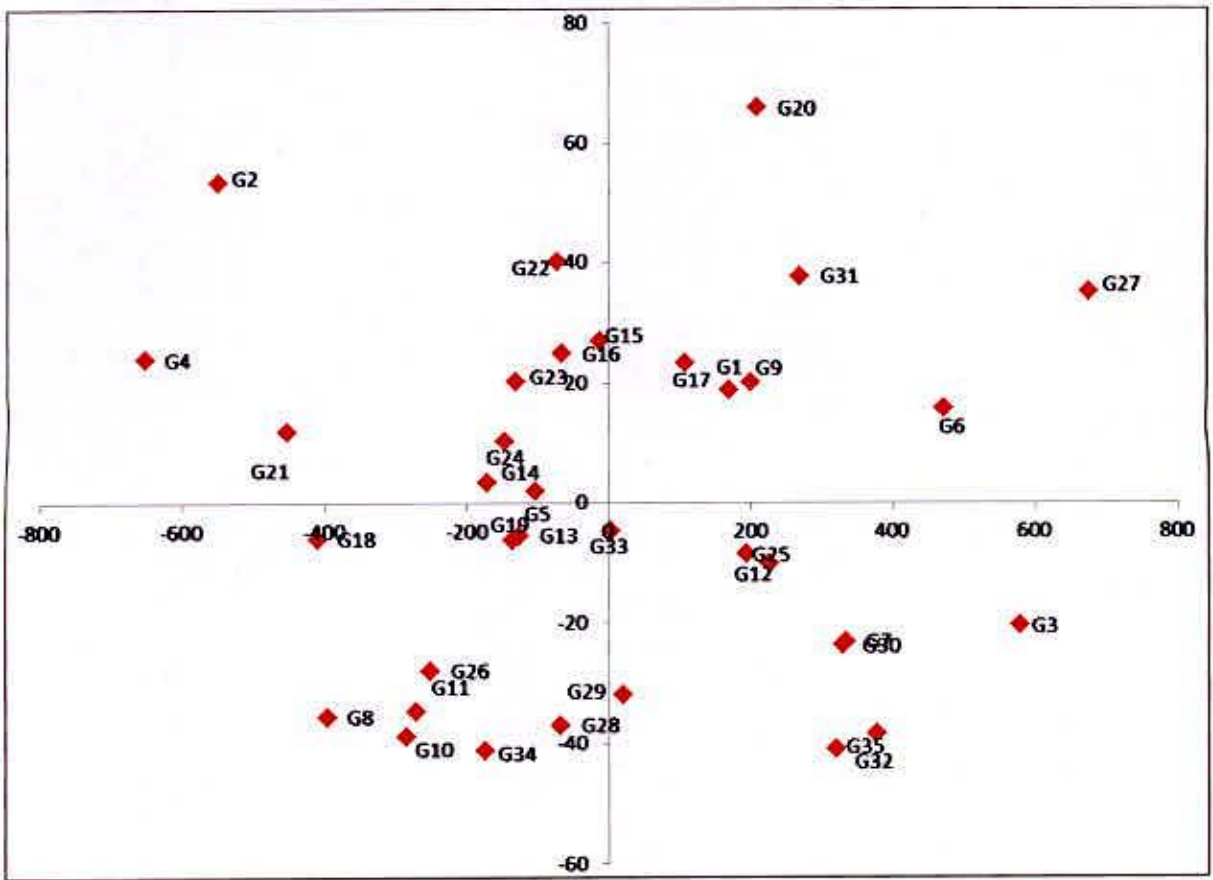


Figure 5 Scattered diagram of 35 rice genotypes based on their principal component scores.

A two-dimensional scattered diagram constructed using principal component I on X-axis and component II on Y-axis, reflecting the relative position of the genotypes (Figure 5).





CHAPTER V

SUMMARY AND CONCLUSION

CHAPTER V

SUMMARY

The experiment was conducted with 34 local rice genotypes with one check varieties at the Sher-e-Bangla Agricultural University experimental field to study characterization and genetic diversity of 35 local rice genotypes and to find out the association among the genetic characteristics. The salient findings of the present study have been summarized below.

The genotypes G-13 showed dark red and G-20 showed light red panicle in color. The genotypes G-25 showed the highest plant height (173.33cm) which is taller than an average height of human and genotype G-29 had the lowest plant height (139.00cm).

Analysis of variance showed significant for all the genotypes in respect to 13 characters, indicating considerable variation among them. Regarding mean performance, the genotype G-4 took the longest period for first flowering is 115 followed by genotype G-35 (114) and the genotype G-12 had the minimum days for first flowering is 99. The highest number of filled grain per panicle was recorded in genotype G-10 was (144.33), while the lowest was recorded in genotype G-1 (98.00). The highest number of effective tiller (10.33) was recorded in genotype G-15. The highest 1000 grain weight (26.00) was recorded in the genotype G-15. The lowest 1000 grain weight (19.80) was recorded in genotype G-30. The highest grain yield per hill produced by genotype G-24 (35.90g), whereas, the lowest grain yield per hill obtained from the genotype G-20 with (7.20g).

The highest σ^2_g was found for number of root hair (103415.40) and the lowest magnitude of σ^2_g was observed in number of primary branches per panicle (1.97). The highest σ^2_p was found for number of root hair (109410.31) and the lowest magnitude of σ^2_p was observed in number of primary branches per panicle (2.61). High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield per hill (g) indicated that selection of these traits would be effective.

Correlation of Grain yield per hill was found to be highly significant and positive for number of root hair, days to flowering and plant height at both genotypic and phenotypic level and negatively significant for number of secondary branches per panicle at both level. Significant positive correlation of grain yield per hill with number of root hair, days to flowering and plant height imply that selection for these characters would lead to simultaneous improvement of grain yield in rice. Days to flowering had maximum direct effect (0.719) on yield followed by number of effective tiller (0.635), number of unfilled grain per panicle (0.544).

Thirteen genetic characteristics of 35 local rice genotypes with one check varieties were evaluated to study the genetic divergence through multivariate analysis. Genotypes were grouped into seven different clusters. PCA showed the highest inter-cluster distance was observed between the cluster II and V (46.71) followed by III and V (46.40) and IV and V (45.43). Genotypes from these three clusters may be involved in hybridization as wide genetic variations exist among the groups. Cluster IV exhibits the highest intra-cluster distance (38.36), while the lowest distance was observed in cluster V (23.09).

CONCLUSION

- ⌘ Analysis of variance showed that there were significant variations among the genotypes for 13 characters studied.
- ⌘ The genotype G-4 took the longest period and genotype G-12 took the minimum days for first flowering. The highest grain yield per hill obtained from G-24.
- ⌘ The highest σ^2_g and σ^2_p was found for number of root hair. High GCV and PCV for number of effective tiller, root weight, number of root hair and grain yield per hill (g) suggested that these characters could be transmitted to the hybrid progeny and phenotypic selection based on these would be effective.
- ⌘ Genotypic path coefficient analysis prescribed that highly significant positive correlation with positive direct effect was observed in days to flowering, number of effective tiller, number of unfilled grain per panicle, number of filled grain per panicle and root weight and phenotypic path coefficient analysis prescribed that highly significant positive correlation with positive direct effect was observed in number of unfilled grain per panicle, number of effective tiller, root length, root weight and number of filled grain per panicle.

RECOMMENDATION

- ▶ Selection procedure would be applied for desired characters such as lowest days to first flowering and increase number of effective tiller, number of filled grain per panicle, 1000 grain weight and grain yield per hill to develop high yielding varieties.
- ▶ The Further collection of rice germplasms would be continued for getting more variability and desired traits in rice.
- ▶ Further study of this experiment is needed in different locations of Bangladesh for accuracy of the results obtained from the present experiment.





CHAPTER VI

REFERENCES

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REFERENCES

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