ASSESSMENT OF GENETIC DIVERSITY IN BORO RICE GENOTYPES

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DHAKA-1207

JUNE, 2021

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BY

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REGISTRATION NO.: 19- 10135

A Thesis
Submitted to the Faculty of Agriculture,
Sher-e-Bangla Agricultural University, Dhaka,
in partial fulfillment of the requirement
for the degree of

MASTER OF SCIENCE

IN

GENETICS AND PLANT BREEDING

SEMESTER: January-June, 2019

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CERTIFICATE

This is to certify that thesis entitled, **"Assessment of genetic diversity in Boro rice genotypes"** 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 **Saurin Shahid**, Registration No. **19-10135** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: June, 2021
Place: Dhaka, Bangladesh

(Dr. Md. Harun-Ur-Rashid)
Supervisor

Dedicated

To

My Honorable Teachers

&

Beloved Parents

Whose Blessings Always

With Me

ACKNOWLEDGEMENTS

All praises are due to the Almighty and Merciful "Allah Subhana Wa Ta La" the supreme ruler of the universe who kindly enabled me to complete the thesis for the degree of Master of Science (M.S) in Genetics and Plant Breeding.

The author would like to express her deepest sense of gratitude to the honorable course supervisor, Dr. Md. Harun-Ur-Rashid, Associate Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh for his scholastic guidance, support, encouragement and valuable suggestions for successfully completing the research work and writing the manuscript.

I would like to express my heartiest respect and profound appreciation to my Co-Supervisor, Dr. Shahanaz Parveen, Associate Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for her utmost cooperation and constructive suggestions to conduct the research work as well as preparation of the thesis.

I am expressing my sincere respect to the teachers of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for providing the facilities to conduct the experiment and for their valuable advice and sympathetic consideration in connection with the study.

I also express my thankful gratitude to the farm and office staffs of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka.

I would like to thank all my senior brothers and sisters, roommates and friends for helping me in this research work. Mere diction is not enough to express my profound gratitude and deepest appreciation to my parents, brothers, sister and friends for their ever-ending prayer, encouragement, sacrifice and dedicated efforts to educate me to this level.

June, 2021

SAU, Dhaka **The Author**

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ABSTRACT

An experiment was carried out at Sher-e-Bangla Agricultural University in Boro season with thirty two local varieties of Boro rice to identify the diversity among the genotypes. The varieties were examined for eighteen yield and yield contributing characters. Significant variation was observed among all the genotypes for all the characters under studied.

High heritability along with high genetic advance in percentage of mean were observed for culm diameter and yield/plant. High heritability along with moderate genetic advance in percentage of mean were observed for 50% heading, plant height and1000 seed weight. High heritability along with low genetic advance in percentage of mean were observed for 1st heading and days to maturity. Highly significant positive correlation of yield per plant observed for 1st heading (r_g=0.538, r_p=0.422,), 50% heading (r_g=o.529, r_p=0.440), days to maturity (r_g=0.603, r_p=0.413), culm diameter (r_g=0.258, r_p=0.216), length of flag leaf (r_g=0.214, r_p=0.226), no. of filled grain of main tiller (r_g=0.617, r_p=0.502) and 1000 seed weight (r_g=0.386, r_p=0.286) at both genotypic and phenotypic level. Path analysis indicated that, yield per plant had positive and direct effect through 50% heading, culm length, culm diameter, length of flag leaf, no. of effective tiller/plant and no. of filled grain of main tiller and 1000 seed weight. On the basis of D^2-value the genotypes were grouped into six clusters. Cluster V was the largest and containing twelve genotypes followed by cluster II with seven genotypes and cluster III with only five genotypes. The highest inter cluster distance was observed between cluster III and cluster IV (13.985). The intra cluster distance was maximum (0.367) in cluster IV. The lowest inter-cluster distance was recorded between cluster II and VI (1.486). Cluster I showed maximum performance for no. of effective tiller/plant (13.64). Cluster II showed maximum performance for 1st heading (114), 50% heading (120) and culm diameter (0.60 cm). Cluster III recorded highest mean performance for days to maturity (161.33), length of flag leaf (27.980 cm), no. of filled grain of main tiller (198.67), 1000 seed weight (30.33 g) and yield/plant (33.01 g). Cluster IV showed maximum performance for plant height (123.28 cm) and culm length (72.510 cm). Cluster V did not show maximum performance for any character. Cluster VI showed maximum performance for length of panicle (25.65 cm).

Considering the degree of variability, heritability, genetic advance in percent of mean, correlation with grain yield, path analysis, magnitude of distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and performance, the genotypes G15, G26, and G27 for yield per plant from cluster III; G20 for earliness from cluster IV might be considered better parents for efficient hybridization program.

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SOME COMMONLY USED ABBREVIATIONS

FULL WORD	ABBREVIATION
Agro Ecological Zone	AEZ
Analysis of variance	ANOVA
and others (at elli)	*et al.*
At the rate	@
Bangladesh	BD
Bangladesh Agricultural Research Institute	BARI
Bangladesh Agricultural University	BAU
Bangladesh Institute of Nuclear Agriculture	BINA
Centimeter	cm
Degree Celsius (Centigrade)	^{0}C
Coefficient of variation	CV
Days after sowing	DAS
Degree of freedom	df
Environmental variance	σ_e^2
Et cetera	etc.
Food and Agricultural Organization	FAO
Financial Year	FY
Genetic Advance	GA
Genotypic coefficient of variation	GCV
Genotypic correlation	r_g
Genotypic variance	σ_g^2
Gram	g
Heritability in broad sense	h^2b
Kilogram	kg
Meter	m
Milliliter	mL
Mean sum of square	MS
Market Year	MY

FULL WORD	ABBREVIATION
Metric ton	MT
Muriate of Potash	MOP
Number	No.
Percent	(%)
Percentage of coefficient of variation	CV%
Phenotypic variance	σ_p^2
Phenotypic coefficient of variation	PCV
Phenotypic correlation	r_p
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Species	*sp.*
Square meter	m^2
Standard error	SE
Triple Super Phosphate	TSP
Variety	Var.
United States Department of Agriculture	USDA
Zinc Oxide	ZnO

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.) is the main staple food crop of Asia where it is consumed by more than half of the world's population. It is mainly grown in large areas of Asia, Latin America and Africa that are characterized by a semitropical climate with alternating rainy and dry seasons (Rao *et al.,* 2016). Rice (2n = 24) belonging to the family *Gramineae* and subfamily *Oryzoidea* occupies almost one-fifth of the total land area covered under cereals (Chakravarthi and Naravaneni, 2006) and is rich in diversity regarding structure, function and properties.

Both agronomically and nutritionally, such cereal occupies an important place among the food crops. It is well known that during early domestication and evolutionary selection, cultivated rice differentiated into two major subspecies, indica and japonica (Chang,1976, Oka, 1988 and Morishima *et al.,*1992*).* Although significant differences exist in morphological and physiological characters between the two subspecies (Liu,1993) of indica and japonica varieties, it appears to be a major source of genetic diversity in the cultivated rice gene pool.

Rice accessions are a rich reservoir of useful genes that rice breeder can harness for rice improvement program (Rasmi *et al.,* 2017). Genetic diversity is the prerequisite for any crop improvement program because it helps in the development of superior recombinants (Manonmani and Khan, 2003), through selection of parents having wider variability for different characters (Nayak *et al.,* 2004). Since, the last few centuries, rice has faced loss in diversity due to replacement of native varieties with high yielding varieties (Choudhary *et al.,* 2013; Heal *et al.,* 2004). Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence (Iftekharuddaula *et al,* 2002). A higher heterosis could be achieved from crosses between genetically distant parents (Falconer 1960).

Genetic diversity in crop plants may be analyzed at different levels: individual genotypes such as inbreed lines or pure lines or clones, populations, germplasm

accessions, and species. Diversity can occur at three levels: genetic diversity (variation in genes and genotypes), species diversity (species richness) and ecosystem diversity (communities of species and their environment). The importance of biodiversity for humankind has been well recognized in the recent decades and it is essential for allowing sustainable development of various human activities. Plant breeding has a long history of integrating the latest innovations in agro-biology and genetics to enhance crop improvement. Plant breeding with agri-horticultural crops has typically aimed at improved yields, nutritional qualities and other traits of commercial values. The plant breeding paradigm has been enormously successful on a global scale, with such examples of the development of hybrid maize (*Zea mays*), the introduction of wheat (*Triticum aestivum*) and rice (*O. sativa*) varieties that spawned the Green Revolution (Duvick, 2001, Everson and Golin, 2003) and the recent commercialization of transgenic crops (James, 2007). Many of these products have been contributed numerous benefits to the global society through the plant breeding approaches.

Rice is grown in more than a hundred countries, with a total harvested area of approximately 158 million hectares, producing more than 700 million tons annually (470 million tons of milled rice). Nearly 640 million tons of rice are grown in Asia, representing 90% of global production. Sub-Saharan Africa produces about 19 million tons and Latin America some 25 million tons. In Asia and sub-Saharan Africa, almost all rice is grown on small farms of 0.5−3 ha.

The world's largest rice producers by far are China and India. China is the top country by rice, paddy production in the world. As of 2019, rice, paddy production in China was 211 million tons that accounts for 27.92% of the world's rice, paddy production. The top 5 countries (others are India, Indonesia, Bangladesh, and Vietnam) account for 71.53% of it. The world's total rice, paddy production was estimated at 757 million tons in 2019.

Winter (Boro) season rice area is forecast to increase as farmers are expected to switch to rice from wheat and minor vegetables. Farmers will continue cultivating Boro season rice considering it to be a comparatively lower risk crop. In 2018/19, total rice area and production is revised down to 11.77 million ha and 34.9 MMT. During the Boro season, a significant number of farmers use two varieties: BRRI dhan

28 and BRRI dhan 29, which in some context becoming more vulnerable to insects and disease. Some farmers use Indian-developed varieties because they believe it is hardier or drought tolerant.

Boro season rice is harvested in March-April and marketed in May, so rice harvested in Boro season is considered as the first rice crop in Market Year (MY) (May-April). On the other hand, Boro rice is considered as the last rice crop of Financial Year (FY) (July-June) in Bangladesh. In an attempt to increase productivity, the Government encouraged hybrid rice cultivation through a series of measures, including financial support and provision of hybrid seeds.

In Bangladesh, development of high yield potential variety is one of the ways to satisfy the future demand. Irrigated modern rice contributes 41% of the total rice production in Bangladesh (Anon, 2000). The performance of two Boro rice varieties of BRRI dhan 28 and BRRI dhan 29 are highly commendable. The hybrid varieties mostly cultivated in Bangladesh are imported from China by private seed companies and only one hybrid varieties BRRI hybrid 1 has developed by Bangladesh Rice Research Institute (Anon, 2004). The population of Bangladesh is increasing day by day and that is why horizontal expansion of rice area is not possible due to high population pressure on land, to ensure the food security for her increasing population. Therefore, it is an urgent need of the time to increase rice production through increasing yield. Proper practices are the most effective means for increasing yield of rice at farmers level using inbred and hybrid varieties (Alauddin, 2004). Hence the proposed research investigation aimed to assess the nature and magnitude of genetic divergence present in the thirty two rice germplasm and to select suitable diverse genotypes as parents for further utilization in crop improvement programs.

Objectives:

- To study the genetic variability among different Boro rice genotypes, and
- To study the interrelationship between yield and yield contributing characters and their direct and indirect effect on yield

CHAPTER II

REVIEW OF LITERATURE

2.1 Center of genetic diversity and biology of rice

Rice belongs to family Poaceae and genus *Oryza* and most probably originated in India or southeastern Asia. It is the world's second most important cereal crop next to wheat. The cultivated species are the Asian rice, *O. sativa L*. and the African rice, *O. glaberrima*. The Asian rice is grown all over the world while African rice has originated and been cultivated in West Africa for about more than 3500 years (Martin *et al.* 2006). Rice, a diploid species with a chromosome number of 2n = 24, is normally a self-pollinated crop but up to 3% natural out crossing may occur depending on the cultivar and the environment, although about 0.5% is the average out-crossing level (Poehlman and Sleper,1995). *O. sativa* is a grass with a genome consisting of 466 Mb across 12 chromosomes with an estimated 46,022 to 55,615 genes (Jun *et al.*, 2002).

Hossain and Haque (2003) reported that both genotypic and phenotypic variances were found highly significant in all the traits with little higher phenotypic variations as usual. Similarly the low differences between the phenotypic and genotype coefficient of variations indicated low environmental influences on the expression of the characters. High heritability coupled with high genetic advance of yield, grains per panicle. Days to flowering and height suggested elective selection for the improvement of these characters could be made.

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

Chaubey and Singh (1994) evaluated 20 rice varieties and reported high heritability for total number of spikelets followed by grain yield per plant and 1000-grain weight. Genetic advances in percent of mean were higher than grain yield per plant followed

by panicle weight and total number of spikelets. Heritability in broad sense was the highest for 1000-grain weight followed by panicle length. Filled grains per panicle, plant height, number of panicle per hill, timber of primary branches and yield per plant showed moderate heritability. Bisne *et al.,* (2009) conducted an experiment on 44 rice genotypes in Raipur.

Subbaiah *et al.* (2011) studied the extent of variability and genetic parameters with 16 parents and 48 hybrids for nine yield and its components and twenty-five quality characters. The magnitude of difference between PCV and GCV was relatively low for all the traits, indicating less environmental influence. High GCV and PCV were recorded for harvest index, total number of productive tillers per plant and gelatinization temperature in parents and for total number of productive tillers per plant, number of grains per panicle. Gelatinization temperature and amylose content in hybrids. High heritability coupled with high genetic advance as percent of mean were recorded for gelatinization temperature, harvest index, total number of productive tillers per plant.

Singh *et al.* (2011) evaluated eighty one rice (*O. sativa L.)* genotypes during kharif 2010 for thirteen quantitative traits to examine the nature and magnitude of variability, heritability (broad sense) and genetic advance. Analysis of variance revealed that the differences among eighty one genotypes were significant for all the characters except flag leaf width. Among all the traits number of spikelets per panicle exhibited high estimates of genotypic coefficient of variation and phenotypic coefficient of variation followed by harvest index, grain yield per hill and number of panicles per hill. Broad sense heritability was highest for biological yield per hill, which suggested that this trait would respond to selection owing their high genetic variability and transmissibility. Maximum genetic advance as percent of mean was recorded for number of spikelets per panicle with high value of heritability.

Chandra and Pradhan (2003) studied genetic variability, heritability and genetic advance in 65 low land rice genotypes. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the 12 studied characters indicating the influence of environment on the characters. Grains per panicle had maximum CCV followed by plot yield, grain yield per plant, harvest index, panicle number, plant height and 1000-seed weight. A moderate to high degree of heritability estimates and

genetic advance was for days to 50% flowering, plant height and grains per panicle. Moderate heritability values with low genetic advance was observed for panicle length, plot yield, 1000 grain weight, grain weight per plant and harvest index.

Padmaja *et al*. (2008) reported genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance for eleven characters in one hundred and fifty genotypes including five check varieties of rice were studied. The analysis of variance revealed that there were highly significant differences for all the characters except leaf width and 100- seed weight among the genotypes. The estimates of genotypic and phenotypic coefficients of variation were high for all the characters except days to 50% flowering and panicle length. Heritability and genetic advance were high for all the characters except days to 50% flowering and panicle length which had moderate genetic advance along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Fifty four rice varieties of diverse origin were studied for genetic variability in the coastal saline low lands by Sahesan *et al.,* (2009). The PCV values are slightly greater than GCV, revealing little influence of environment in character expression. High values of heritability along with genetic advance were observed for grain yield per plant, grain weight, productive tillers per plant, grain per panicle, grain length, grain breadth, kernel length, panicle length and plant height.

Ashura (1998) studied 36 genotypes and concluded that heritability estimates revealed plant height, number of filled grains per panicle and grain weight to the highly heritable characters Jayasudha and sharma (2010) carried out an experiment on 47 rice genotypes revealed that a high genotypic and phenotypic coefficient of variation was observed for grain yield per plant, harvest index, pollen fertility (%) and spikelet fertility (%). Characters like pollen fertility (%), spikelet fertility (%), days to 50% flowering and grain yield per plant showed high value of heritability coupled with high genetic advance.

Jaiswal *et al.* (2007) made an investigation to study the variability for yield and quality traits in twenty-five indigenous aromatic rice genotypes. Highest genetic coefficient of variation was recorded for grain yield per plant and number of panicle bearing tillers among yield traits and length/breadth ratio for quality traits. High

heritability (broad sense) coupled with high genetic advance was observed for yield plant, number of panicle bearing tillers and number of grains per panicle.

Seyoum *et al.* (2012) conducted a field experiment using thirteen rice genotypes during the rainy seasons of 2009 and 2010 at three rainfed upland locations of Southwest Ethiopia to estimate the genetic variability, heritability of grain yield and yield contributing traits in upland rice. Days to 50% flowering, plant height, grains per panicle. spikelets per panicle, thousand grains weight and grain yield showed relatively high GCV and PCV estimates. High heritability was obtained for plant height (92.1 7%) followed by 50% flowering (90.16%), thousand grains weight (83.17%), days to 85% maturity (82.45%), panicle length (79.25%) and spikelet per panicle (60.25%) which indicates high heritable portion of variation. High to medium estimates of heritability and genetic advance were obtained for plant height, days to 50% flowering, panicles per plant, spikelets per panicle, grains per panicle and thousand grain weight.

Ghosal *et al.* (2010) evaluated eighteen advanced breeding lines for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield during Boro season in 2009. All the tested characters showed significant variation. Effective tillers/plant and spikelet sterility (%) had high genotypic variance, high heritability, high genetic advance and high genotypic coefficient of variation. Effective tillers/plant, panicle length, thousand grain weight and growth duration (days) showed significant positive association with grain yield.

Yadav *et al*. (2010) carried out a field experiment was to establish the extent of association between yield and yield components and other characters in rice. They found high heritability coupled with high to moderate genetic advance as percent of mean was observed on plant height, seed yield per plant, biological yield, harvest index, test weight and number of spikelets per panicle suggesting preponderance of additive gene action in the expression of these characters.

Dhaliwal and Sharma (1992) evaluated seventy-eight diverse rice genotypes were in a randomized complete block design to estimate genetic variation and heritability for grain and agronomic characters. Number of grains per panicle, number of panicles per plant and 100-grain weight showed high genotypic and phenotypic coefficient of variation. Good amount of genetic variability also existed for grain yield, plant height

and panicle length. Heritability estimates were high (greater than 80 percent) for all characters, except grain yield. Estimates of expected genetic advance (as percent of mean) were high for number of grains per panicle, number of panicles per plant and 100-grain weight.

Vange (2009) conducted a field experiment in 2005 in the experimental Farm Station of the University of Agriculture, Makurdi, Nigeria to evaluate the performance and genetic diversity of some upland rice accessions. Genotypic coefficient of variability was generally lower than phenotypic coefficient of variability. Days to 50% heading, days to maturity, flag Leaf area, panicle weight, panicle length, number of branches per panicle, number of seeds/panicle, grain weight/panicle and seed yield showed very low differences between their PVC and GCV values. Also these traits had high estimates for heritability and genetic advance.

Nandeshwar *et al.* (2010) evaluated twenty five F_2 progenies derived from the crosses involving HYV and quality rices during kharif 2005. High GCV and PCV were observed for grain yield per plant, panicle number per plant and panicle weight. High heritability was observed against all the characters studied except panicle weight, grain number per panicle and grain breadth. Grain yield per plant showed maximum genetic advance as percentage of mean followed by panicle number per plant, plant height and panicle weight, respectively.

Nandan *et al.* (2010) did an experiment to evaluate thirty three genotypes by identifying their efficiency with respect to 20 yield and quality traits. They found high heritability with high genetic advance as percent of mean was registered for number of effective tillers per plant, panicle weight, number of grains per panicle. number of spikelets per panicle,1000 grain weight, kernel length before cooking (KLBC), length breadth (L/B ratio, water uptake ratio and grain yield per plant.

Sadeghi (2011) used 49 rice varieties (*O. sativa* L.) in experiment to determine variability, heritability and correlation between yield and yield components for 2 years. He found broad sense heritability range from 69.21% (plant height) to 99.53% (grain width).

Akinwale *et al.* (2011) evaluated twenty rice genotypes in the International Institute of Tropical Agriculture, Nigeria during 2008/2009 cropping season. Genotypic coefficient of variations were lower than the corresponding phenotypic coefficients in

all the traits studied indicating considerable influence of the environment on the expression of the traits. High to medium broad sense heritability estimates observed on days to heading, days to maturity, plant height, grain yield and number of grains per panicle, panicle weight, number of panicles per plant and panicle length. The low broad sense heritability observed for the number of tillers per plant and 1000 grain weight is indicative of the influence of the environment on these traits. Low heritability of these traits indicates the ineffectiveness of direct selection for these traits. High to medium heritability and genetic advance were recorded for the number of grains per panicle, grain yield, panicle weight and the number of panicles per plant.

Sankar *et al.* (2006) studied on variability on single plant yield and its components in 34 rice genotypes. High heritability and genetic advance were obtained for the traits days to 50% flowering, plant height, productive tillers/plant, particle length, grains/panicle, 1000 seed weight and single plant yield. Spikelet fertility exhibited high heritability and moderate genetic advance.

Selvaraj *et al.* (2011) studied variability, correlation and path coefficient on 21 rice genotypes for grain yield and other yield attributes. Analysis of variance revealed considerable variability among the genotypes for all the characters. The phenotypic coefficient of variation values were slightly greater than genotypic coefficient of variation, revealing negligible influence of environment in character expression. High heritability coupled with high genetic advance and high GCV was observed for number of tillers/plant followed by number of productive tillers per plant, plant height and grain yield / plant.

Prajapati *et al.* (2013) assessed thirty-eight rice genotypes at Field experimentation Centre of Department of Genetics and Plant Breeding, Alahabad School of Agriculture, Alahabad during kharif-2009. The experiment was conducted to study the 12 quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance. High estimates of heritability coupled with high genetic advance as percent of mean was observed for harvest index followed by number of spikelets per panicle, number of panicles per hill and number of tillers per hill. High estimates of heritability coupled with moderate genetic advance as percent of mean was observed for flag leaf width followed by days to 50% flowering, panicle length and biological yield per hill.

Kumar *et al.* (2014), conducted experiment with 40 genotypes of rice. Analysis of variance revealed significant difference among 40 rice genotypes for all characters indicating the existence of variability. High GCV and PCV were observed for grain yield per plant and biological yield per plant.

On the other hand, Rafiqul (2014), conducted experiment with 19 genotypes of rice, existence of variance in 14 yield contributing character including days to maturity, no. of effective tiller per plant, no. of filled grain of main tiller and yield (ton/ha).

2.2 Correlation coefficient

Hossain and Haque (2003) carried out an experiment in which they showed that direct and indirect effects of characters through path coefficient analysis supported the significant positive correlation coefficient at both genotypic and phenotypic levels for plant height, panicles per hill, panicle length and 1000-grain weight on yield. Thus selection of yield in rice through these characters will be effective.

Iftekharuddaula *et al.* (2001) studied twenty-four modern rice varieties of irrigated ecosystem with a view to finding out variability and genetic association for grain yield and its component characters. Genotypic correlation coefficients were higher than the 16 corresponding phenotypic correlation coefficients in most of the traits. Days to flowering, days to maturity, grains/panicle, 1000-grain weight and harvest index showed significant positive correlation with grain yield.

Sahesan *et al.* (2009) evaluated fifty four rice varieties of diverse origin for correlation analysis under coastal saline low lands. The 1000-grain weight was positively significantly correlated with plant height, grains per panicle and grain breadth.

Ullah *et al.* (2011) studied ten traditional Boro rice and found that genotypic correlations were higher than the phenotypic correlations in most of the cases. Grains per panicle, panicle length, leaf area index, harvest index and chlorophyll content were the major characters contributing to grain yield as these traits were significantly and positively associated with grain yield per plant. Thirty six rice lines of cultivars were evaluated for yield and other components at two sites within the University farm of Sokoine University of Agriculture, Morogoro.

Agahi *et al.* (2007) conducted an experiment to investigate correlation coefficient of grain yield and sixteen yield-related traits among 25 lines. The results showed that grain yield was significantly correlated with days to heading, total tillers, number of productive tillers, days to maturity, number of grain per panicle, flag leaf length, flag leaf width and plant height.

Seyoum *et al.* (2012) conducted a field experiments using fourteen rice genotypes during the main rainy seasons of 2009 and 2010 at three rainfed to upland locations of Southwest Ethiopia to estimate the correlation coefficient of grain yield and yield contributing traits in upland rice. Grains per panicle had highly significant (r= 0.906**) genotypic correlation coefficient with grain yield.

Tomar *et al.* (2000) found that the correlation estimates were highest between harvest index and 1000-grain (48.71) followed by yield/plant and number of grains/panicle (44.71), flag leaf' length and plant height (43.15), and number of grains/panicle and panicle length (41.72). A negative correlation was found between biological yield and harvest index (-39.41), 1000-grain weight and number of grains/panicles (-33.31). The yield/plant had positive association with plant height, number of effective tillers, panicle length, primary branches/panicle, number of grains/panicle and 1000-grain weight, harvest index, biological yield, flag leaf length, width, and days to 50% flowering.

Prasad *et al.* (2001) conducted an experiment where eight rice line genotypes were studied. Correlation coefficient study revealed high positive correlation of grain yield with effective tillers/plant, fertile grains/panicle and 1000-grain weight. A significant negative correlation was obtained between grain yield and plant height.

Yadav *et al.* (2010) carried out a field experiment was to establish the extent of association between yield and yield components and others characters in rice. They found that the correlation coefficient between seed yield per plant and other quantitative attributing to yield showed that grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicles per plant, panicle length, number of spikelets per panicle and weight at both genotypic and phenotypic levels.

Vange (2009) conducted a field experiment in 2005 in the experimental farm station of the University of Agriculture, Makurdi, Nigeria to evaluate the performance and

genetic diversity of some upland rice accessions. Genotypic correlation analysis of yield with other traits revealed that yield had a significantly positive correlation with flag leaf area, number of tillers, number of panicles, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle, seed weigh/panicle, grain length and 1000 seed weight.

Sadeghi (2011) also observed positive significant association of grain yield with grains per panicle, days to maturity, number of productive tillers and days to flowering.

2.2.1 Days to 50% flowering

Most Scientists indicated that days to 50% flowering has direct and indirect effect on yield, grains/panicle and also tillering height.

Ganesan (2001) said that days to flowering, plant height, number of tillers/plant, and productive tillers/plant had both positive and negative indirect effects on yield.

Sathya *et al.* (1999) studied of eight quantitative traits in rice (*O. sativa).* Days to 50% flowering was the principal character responsible for grain yield per plant followed by 1000-grain weight, plant height and harvest index as they had positive and significant association with yield.

Iftekharuddaula *et al.* (2001) reported that days to flowering, days to maturity, plant height and spikelets/panicle had positive and higher indirect effect on grain yield through grains/panicle.

2.2.2 Days to maturity

Ma *et al.* (2001) experimented that ADTRH1 is a rice hybrid. This hybrid is semi dwarf and matures in 115 days.

Parvez *et al.* (2003) observed that shorter field duration was observed in Sonarbangla-1 than the control.

Ma *et al.* (2001) studied a comparative performance of 8 rice hybrids. All hybrids showed shorter growth duration (97-107 days) than the controls (110-116 days).

2.2.3 Plant height (cm)

Dwarfness may be one of the most important physical characters, because it is often accompanied by lodging resistance and there by adapts well to heavy fertilizer application. Plant height is negatively correlated with lodging resistance; positive for plant height in hybrids would not be desirable, particularly with high nitrogen fertilizer.

Haque *et al.* (1991) reported positive association of plant height with yield per plant but negative association with panicle per plant in modern varieties.

Qiu *et al.* (1994) suggested that enhancing biological yields by increasing plant height would be effective in improving hybrid rice yields.

Yu *et al.* (1995) concluded that hybrid where it reaches a height of 90 cm and proved resistant to *Magnaporthe grisea* and *Nilaparvata lugens.*

Cristo *et al.* (2000) observed 8 morphological traits. The highest correlation was between the final height and panicle length, and full grains per panicle and yield.

Wang (2000) reported that plant height was 88-89 cm directly related to yields.

Mrityunjay (2001) concluded hybrids, in general, gave higher values for plant height at harvest, panicle length and number of filled grains per panicle, performed better compared to the others in terms of yield and yield components.

Ganesan (2001) reported that plant height, days to flowering, number of tillers/plant, and productive tillers/plant had both positive and negative indirect effects on yield.

De *et al.* (2002) experimented that plant height ranged from 80 to 132 cm, whereas panicle length ranged from 22 to 29 cm. which is responsible for grain yield per plant.

2.2.4 Length of panicle (cm)

Cristo *et al.* (2000) observed that highest correlation was between the final height and panicle length, and full grains per panicle and yield. There were associations between rice hybrids and their parents.

Ganesan (2001) conducted that panicle length (0.167) had the highest significant positive direct effect on yield/plant followed by number of tillers/plant (0.688), panicle exertion (0.172), and plant height (0.149).

Laza *et al.* (2004) study was measured with yield-related traits, panicle size had the most consistent and closest positive correlation with grain yield.

2.2.5 Total grain per panicle

Ma *et al.* (2001) examined under 20 x 10 cm spacing, producing 142 grains/panicle, and with more than 90% spikelet fertility. The hybrid recorded the highest grain yield 11.4 t/ha.

Yuan *et al.* (2005) studied the variation in the yield components of 75 high-quality rice cultivars. Among the yield components, the greatest variation was recorded for number of grains per panicle in indica rice, and number of panicles in japonica rice.

2.2.6 No. of filled grain per panicle

Cristo *et al.* (2000) observed the highest correlation between full grains per panicle, final height and panicle length and yield.

Mrityunjay (2001) to study the performance of 4 rice hybrids and 4 high yielding rice cultivars. Hybrids, in general, gave higher values for number of filled grains per panicle, plant height at harvest, panicle length compared to the others.

Ganesan (2001) conducted that an experiment of 48 rice hybrids. Filled grains/panicle (0.895) had the highest significant positive direct effect on yield/plant followed by number of tillers/plant (0.688), panicle length (0.167), and plant height (0.149).

Liu and Yuan (2002) studied the relationships between high yielding potential and yielding traits. Filled grains per panicle was positively correlated with biomass, harvest index and grain weight per plant.

Parvez *et al.* (2003) studied the yield advantage for the hybrid rice was mainly due the proportion of filled grains per panicle, heavier grain weight (35%) and increased values than the control (28%).

Chaudhary and Motiramani (2003) Filled grain yield per panicle showed significant positive correlation with effective tillers per plant, spikelets density and biological yield per plant.

Yuan *et al.* (2005) found that the variation in fertile grain percentage/panicle in indica was greater than that in japonica.

2.2.7 1000 seed weight (g)

Sathya *et al.* (1999) reported that 1000-grain weight, days to 50% flowering, plant height and harvest index as they had positive and significant association with yield.

Iftekharuddaula *et al.* (2001) reported that genotypic correlation co-efficient were higher than the corresponding phenotypic correlation coefficient in most of the traits. Days to flowering, days to maturity, grains per panicle, 1000-grain weight and harvest index showed significant positive correlations with grain yield.

2.2.8 Yield/plant (g)

Thakur *et al.* (1999) stated that high heritability coupled with high genetic advance were estimated for biological yield, panicle-weight, branches per panicle and grains per plant, and indicated the major contribution of additive gene action for expression of these characters.

Ganesan (2001) concluded that grains/plant had the least significant positive direct effect on number of tillers/plant (0.688), panicle exertion (0.172), panicle length (0.167) and plant height (0.149).

Pruneddu and Spanu (2001) data are tabulated on grains per plant, days from sowing to maturity, grain yield, and plant height, number of fertile stems per meter, 1000-grain weight and yield percentages. Yields were generally lower mainly due to unfavorably high temperatures.

Chaudhary and Motiramani (2003) reported that grain yield per plant showed significant positive correlation with effective tillers per plant, spikelets density and biological yield per plant. Almost all characters exhibited high heritability coupled with high genetic advance, except harvest index.

CHAPTER III

MATERIALS AND METHODS

The present research work was designated as "**Assessment of genetic diversity in Boro rice genotypes**'' was carried out in the experimental field of Sher-e-Bangla Agricultural University, Dhaka during Boro season December 2018 to May 2019. The explicit information regarding the materials and methods of this experiment is discussed below:

3.1 Experimental site

The study was conducted at the experimental plot of Sher-e-Bangla Agricultural University, Dhaka under the Agro-ecological Zone of Madhupur Tract, The experimental site location was located at 23^0 77' N latitude and 90^0 37' E longitudes with an elevation of 13.03 meters from the sea level (www.distancesfrom.com). The experimental field belongs to the Agro ecological zone AEZ 28 (The Madhapur Tract)

3.2 Soil and climate

The experimental land was clay loam in texture; medium-high with medium fertility level. The pH of the soil was 5.47 to 5.63, and it contains 0.82% organic carbon content (Appendix II). The experimental site was located in the subtropical climatic zone with wet summer and dry winter. Generally, moderate rainfalls, high temperature and long day length are observed during the Boro season. The records of air temperature, humidity and rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix III).

3.3 Experimental materials

The Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, provided the healthy and vigorous seeds of thirty two (32) genotypes of *O. sativa* were used as experimental materials. The materials used in the experiment are showed in Table 1.

Table 1. List of the genotypes used in the study and their sources

Sl. NO.	Genotype No.	Genotypes Name	Source
1.	G-1	Q-19	GEPB, SAU
2.	G-2	Q-66	GEPB, SAU
3.	G-3	Q-16	GEPB, SAU
4.	G-4	Q-15	GEPB, SAU
5.	G-5	Q-4 (Bandarban)	GEPB, SAU
6.	G-6	Q-5 (Bandarban)	GEPB, SAU
7.	G-7	Q-3 (Bandarban)	GEPB, SAU
8.	G-8	Q-6 (Bandarban)	GEPB, SAU
9.	G-9	AYT-11	GEPB, SAU
10.	G-10	AYT-1	GEPB, SAU
11.	G-11	AYT-5	GEPB, SAU
12.	G-12	AYT-3	GEPB, SAU
13.	G-13	AYT-8	GEPB, SAU
14.	G-14	BRRI DHAN-58	GEPB, SAU
15.	G-15	BRRI DHAN-29	GEPB, SAU
16.	G-16	SL-8H	GEPB, SAU
17.	G-17	BRRI DHAN-74	GEPB, SAU
18.	G-18	BRRI DHAN-28	GEPB, SAU
19.	G-19	BINA DHAN 10	GEPB, SAU
20.	G-20	Jagli	GEPB, SAU
21.	G-21	BRRI DHAN-63	GEPB, SAU
22.	G-22	BRRI DHAN-60	GEPB, SAU
23.	G-23	BRRI DHAN-41	GEPB, SAU
24.	G-24	BINA DHAN 8	GEPB, SAU
25.	G-25	NERICA 1	GEPB, SAU
26.	G-26	AYT-2	GEPB, SAU
27.	G-27	AYT-7	GEPB, SAU
28.	G-28	AYT-10	GEPB, SAU
29.	G-29	AYT-9	GEPB, SAU
30.	G-30	AYT-12	GEPB, SAU
31.	G-31	AYT-6	GEPB, SAU
32.	G-32	BR 26	GEPB, SAU

3.4 Experimental design and layout

The research was laid out in a Randomized Complete Block Design (RCBD) with three replications. The experimental field was divided into three blocks, representing three replications. Two to three seedlings per hill were transplanted maintaining 25 cm × 20 cm spacing from row to row and plant to plant, respectively. Thirty-two lines of Boro rice were distributed in each of the block through randomization process.

3.5 Methods

The following specific methods have been used to carry out the experiment:

3.5.1 Germination of seeds

Seeds were soaked separately in a water container using clothbags in 11th December, 2018 for 48 hours. The seed bags were kept inside the straw heap for increasing of the temperature for facilitating germination.

3.5.2 Preparation of seedbed, seed sowing and seedling raising

The irrigated land was prepared by three times ploughing and cross ploughing followed by laddering. Weeds and stubbles were removed from the field. Thirty-two separate strips were made and sprouted seeds were sown in December, 2019. The seedlings were raised by maintaining proper irrigation with regular intervals and protecting from birds and insects pest.

3.5.3 Preparation of main land

Organic matter was applied to the experimental plot and the plot was ploughed by two ploughing and cross ploughing followed by harrowing with a tractor drawn to attain a good puddle. After four days the final ploughing and cross ploughing was done, and weeds and stubbles were removed from the field. First split of urea and full portion of all other fertilizers recommended by BRRI (2009) (Adhunic Dhaner Chach) were applied to the mainland before final ploughing and laddering. Urea, TSP, MoP and Gypsum were applied at 152, 100, 70 and 61 kg/ha, respectively. The rest two splits of urea were applied at 30 and 45 days after transplanting (DAT), respectively (BRRI, 2008).

Plate 1. The pictorial view of experimental field during land preparation

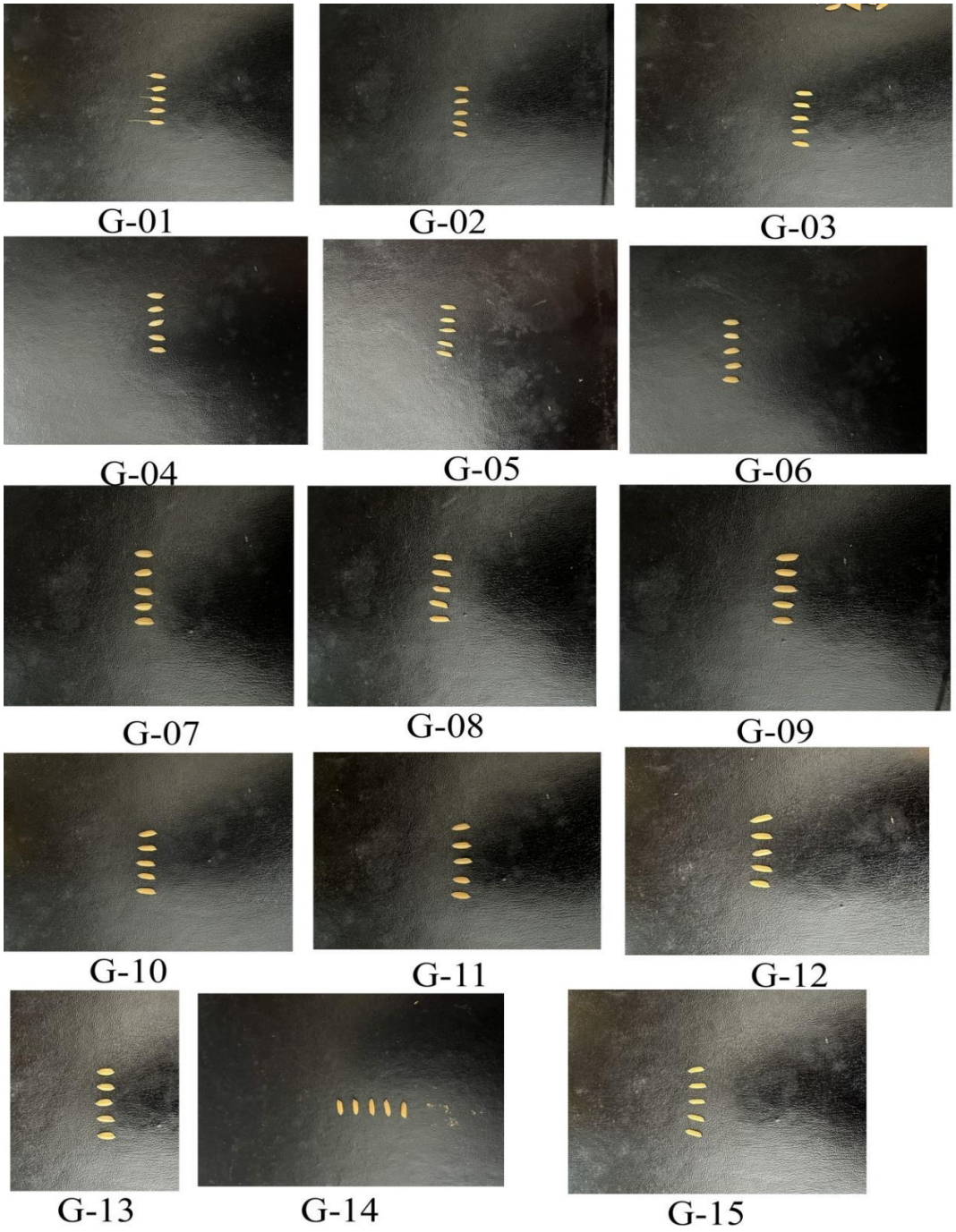


Plate 2: Picture showing seeds of 32 rice genotypes

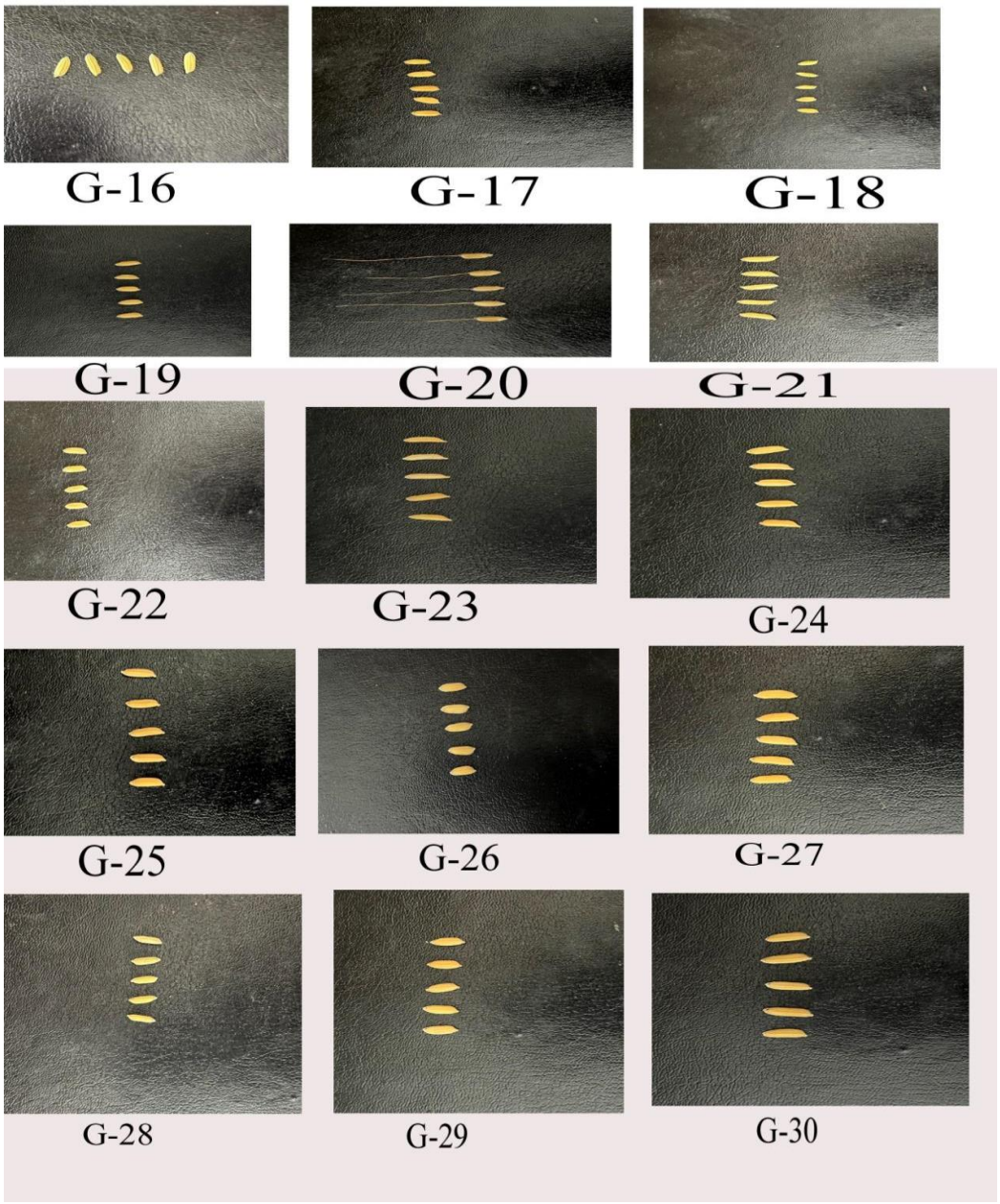


Plate 2: **Picture showing seeds of 32 rice genotypes**

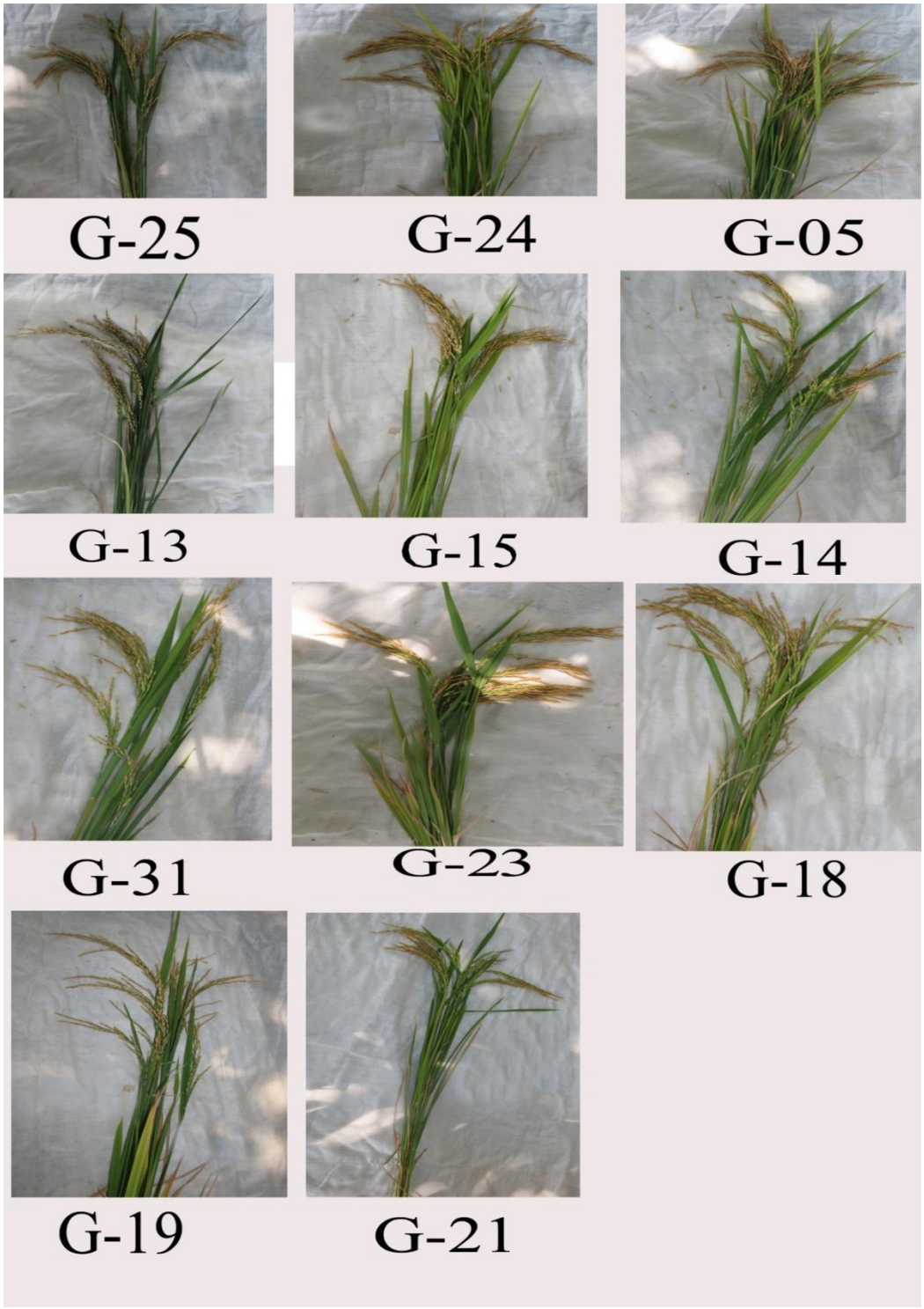
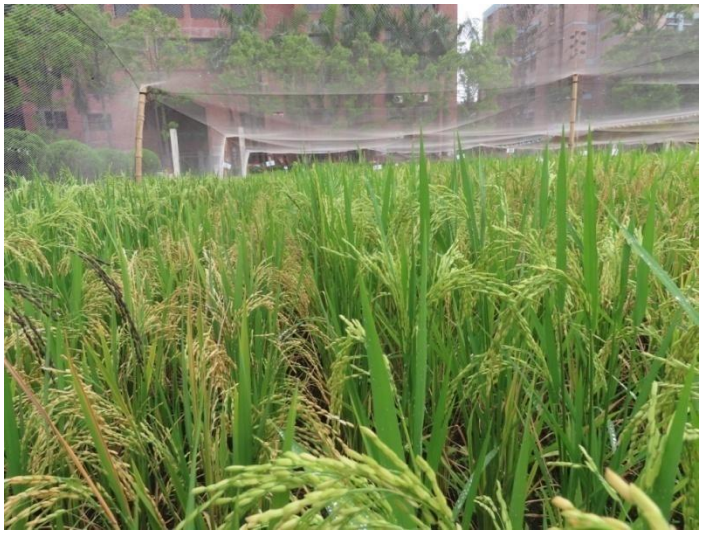
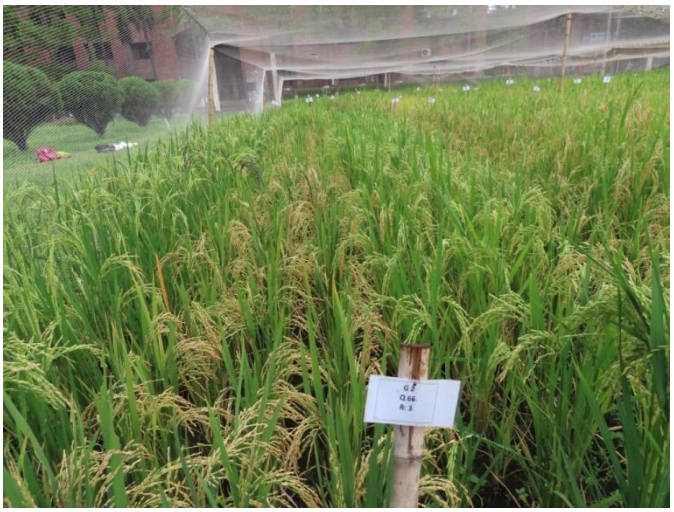


Plate 3: Showing plants of rice genotypes





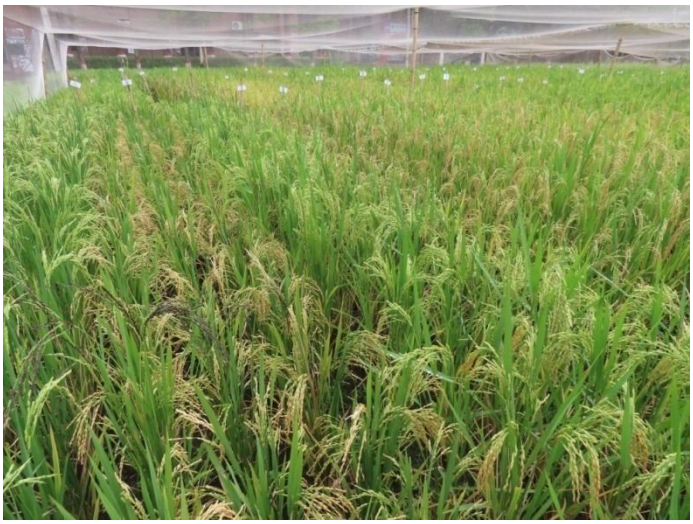


Plate.4: **Pictorial view of research field**

Table 2: Dose and method of application of fertilizers used in rice field

Fertilizers	**Dose (kg/ha)**	**Application (%)**	**Application (%)**	**Application (%)**
Basal	**1st installment**	**2nd installment**	**3rd installment**	**4th installment**
Urea	127	33.33	33.33	33.33
TSP	52	100	--	--
MoP	60	100	--	--
Gypsum	0	100	--	--
Borax	0	100	--	--

Source: BRRI (2014)

3.5.4 Transplanting of seedlings

Thirty-four days old and healthy seedlings were transplanted at the main field in 26th January, 2019, maintaining 25 cm × 20 cm spacing from row to row and plant to plant respectively followed by proper irrigation.

3.5.5 Intercultural operations and aftercare

After establishment of seedlings, various intercultural operations were accomplished for better growth and development of the rice seedlings.

i. Irrigation and drainage

Flood irrigation was given to maintain a constant level of standing water up to 6 cm in the early stages to enhance tillering, proper growth and development of the seedlings and 10-12 cm in the later stage to discourage late tillering. The field was finally dried out 15 days before harvesting.

ii. Gap filling

First gap filling was done for all the plots at 10 days after transplanting (DAT).

iii. Weeding

Weeding was done to keep the plots free from weeds, which ultimately ensured better growth and development. The newly emerged weeds were uprooted carefully at tillering stage and at panicle initiation stage by mechanical means.

iv. Top dressing

After basal dose, the remaining doses of urea were top-dressed in two equal installments. The fertilizers were applied on both sides of seedlings rows with the soil.

v. Plant Protection

Diazinon 57 EC (include active ingredient) was applied at the time of final land preparation and other insecticides were applied when necessary.

3.5.6 Crop harvesting

Harvesting was done depending upon the maturity. When 80% of the plants showed symptoms of maturity i.e., straw color of panicles, leaves, stems, desirable seed color, the crop was assessed to attain maturity. Ten plants were selected at random from the progenies in each replication. The plants were harvested by uprooting and then they were tagged properly. Data were recorded on different parameters from these plants.

3.5.7 Data collection

For studying different genetic parameters and inter-relationships, thirteen characters were taken into consideration. The data were recorded on ten selected plants for each genotype on the following traits

i. Days to flowering

Difference between the dates of transplanting to the date of 50% flowering of genotype was counted and was recorded when 50% plant of a genotype was at the flowering stage.

ii. Days to maturity

Maturities of the crops of different combination were recorded considering the symptom such as moisture content of rice, color changing of the plant from greenish to straw colored appearance color and hardiness of the grain.

iii. Plant height (cm)

The height of plant was recorded in centimeter (cm) at the time of harvesting. The height was measured from the ground level to the tip of the panicle.

iv. Number of total tillers per plant

The total number of panicle bearing tillers were counted from each of the sample hills and average was taken.

v. Number of effective tillers per plant

The number of effective tiller per plant was counted as the number of panicle bearing tillers per plant and average value was recorded.

vi. Panicle length (cm)

The length of panicle was measured with a meter scale from ten selected plants and the average value was recorded as per plant.

vii. Number of primary branches per panicle

Primary branches were counted from one panicle of each of the randomly selected ten plants and the average value was recorded.

viii. Number of secondary branches per panicle

Secondary branches were counted from one panicle of each of the randomly selected ten plants and the average value was recorded.

ix. Number of filled grains per panicle

Presence of endosperm in spikelet was considered as filled grain and total number of filled grains present on main panicle was counted and average was taken.

x. Total number of spikelet per panicle

The total number of filled grains and unfilled grains were collected randomly from selected ten plants of a genotype and then average numbers of total spikelet per panicle was recorded.

xi. Yield per plant (g) Grains obtained from each plant were sun dried and weighted carefully. The dry weight of gains per plant was then recorded.

xii. 1000-seed weight (g)

One thousand seeds were counted randomly from the total cleaned harvested seeds and then weighted in grams and recorded.

3.5.8 Statistical analysis

The data obtained for different traits were analyzed statistically by using Statistix 10 software (www.Statistix.com) to find out the significance of the difference among the advanced populations of *O. sativa*. After evaluating all the characters' mean values, analysis of variance was performed by the F test. The significant differences among the treatments were estimated by the least significant difference (LSD) test at 5% level of probability (Gomez and Gomez, 1984). The genotypic and phenotypic variance was estimated by Johnson *et al.* (1955). Genotypic and phenotypic coefficients of variation were counted with Burton's (1952). Heritability in a broad sense was computed by using the procedure given by Singh and Chaudhary (1985). The genetic advance was measured by Allard (1960) while the genetic advance in the percentage of mean was computed by Comstock and Robinson (1952). The genotypic and phenotypic correlation was obtained by Al-Jibouri *et al.* (1958). Path coefficient analysis was done by following the outlined method of Dewey and Lu (1959).

3.5.8.1 Analysis of variance:

The variance analysis for different characters was carried out utilizing mean data. The level of significance was tested at 5% and 1% using the F test. The model of ANOVA used is presented below:

Sources of variation (S.V)	Degree of freedom (d.f.)	Mean sum of squares (MS)	Expected MS (EMS)
Replication	(r-1)	Mr	$p\,\sigma_r^2 + \sigma_e^2$
Population	(p-1)	Mp	$r\,\sigma_p^2 + \sigma_e^2$
Error	(p-1) (r-1)	Me	σ_e^2
Total	(rp-1)		

Where, p = number of treatments (population)

r = number of replications

σ_r^2 = variance due to replications

σ_p^2 = variance due to treatments (population)

σ_e^2= variance due to error

To test the significance of the difference between any two-adjusted genotypic mean, the standard error of the mean was computed using the formula**:**

$$S.E = \sqrt{\frac{2Me}{r}}\ (1 + \frac{rqu}{q+1})$$

Where, S. E = Standard error of mean

Me = Mean sum of square for error (Intra block)

r = Number of replications

q = Number of population in each sub-block

u = Weightage factor computed

3.5.8.2 Estimation of Least Significant Differences (LSD)

Least Significant Differences were estimated according to the formula of Gomez and Gomez (1984).

$$LSD_\alpha = t_\alpha \sqrt{\frac{s^2}{r}}$$

Here, α = Level of significance, t= tabulated t value with concerned df at same level of significance, s^2= Error Mean Sum of Square, and r = Number of replications.

3.5.8.3 Study of variability parameters

Estimation of the variability among the populations for traits related to yield per plant in *O. sativa* L. were narrated below:

3.5.8.3.1 Estimation of Genotypic variance and phenotypic variance

To estimate phenotypic and genotypic components of variance, Johnson *et al.* (1955) suggested a formula which is mentioned below:

a. Genotypic variance, $\sigma_g^2 = \frac{MSG-MSE}{r}$

Where,

MSG = Mean sum of square for genotypes

MSE = Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\sigma_p^2 = \sigma_g^2 + \sigma_e^2$

Where,

σ_p^2= Phenotypic variance

σ_g^2= Genotypic variance

σ_e^2 = Environmental variance = Mean square of error (MSE)

3.5.8.3.2 Estimation of genotypic and phenotypic coefficient of variation

To compute the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for all the characters, the following formula was given by Burton, (1952):

$$GCV = \frac{\sigma_g \times 100}{\underline{x}}$$

$$PCV = \frac{\sigma_p \times 100}{\underline{x}}$$

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

σ_g= Genotypic standard deviation

σ_p= Phenotypic standard deviation

$\underline{x}$ = Population mean

Sivasubramanian and Madhavamenon (1973) categorized phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) as
Low (0-10%),
Moderate (10-20%), and
High (>20%)

3.5.8.3.3 Estimation of heritability in broad sense

Singh and Chaudhary (1985) suggested a formula to estimate broad sense heritability which is given below:

$$h_b^2(\%) = \frac{\delta_g^2}{\delta_p^2} \times 100$$

Where, h_b^2= Heritability in broad sense

σ_g^2= Genotypic variance

σ_p^2= Phenotypic variance

Robinson *et al.* (1966) suggested the following categories for heritability estimates in cultivated plants:

Categories: Low: 0-30%

Moderate: 30-60%

High: >60%

3.5.8.3.4 Estimation of genetic advance

Allard (1960) suggested the following formula, which was used to estimate the expected genetic advance for different characters under selection:

$$GA = \frac{\sigma_g^2}{\sigma_p^2} . K . \sigma_p$$

Where,

GA = Genetic advance

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

σ_p= Phenotypic standard deviation

K= Standard selection differential which is 2.06 at 5% selection intensity.

Categories: Low (<10%)

Moderate (10-20%)

High (>20%)

3.5.8.3.5 Estimation of genetic advance in percentage of mean

Following formula was given by Comstock and Robinson (1952) to compute genetic advance in the percentage of mean:

GA in percent of mean = $\frac{GA}{Grand\ mean} \times 100$

Johnson *et al.* (1955) suggested that genetic advance in percent of mean was categorized into following groups:

Categories:

Less than 10% - Low

10-20% -Moderate

More than 20% High

3.5.8.4 Correlation coefficient analysis

To determine the level of relationship of characters with yield and among the yield parts, the correlation coefficients were computed. Both genotypic and phenotypic correlation coefficients between two characters were determined by utilizing the variance and covariance components, as suggested by Al-Jibouri *et al.* (1958).

$$r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\sigma^2_{gx}}.\sqrt{\sigma^2_{gy}}} \qquad r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\sigma^2_{px}}.\sqrt{\sigma^2_{py}}}$$

Where,

$r_g(xy), r_p(xy)$ the genotypic and phenotypic correlation coefficients of x and y, respectively.

Cov_{gxy}, Cov_{pxy} are the genotypic and phenotypic covariance of x and y, respectively.

σ^2_{gx}= Genotypic variance of the trait x and σ^2_{gy} = Genotypic variance of the trait y.

σ^2_{px}= Phenotypic variance of the trait x and σ^2_{py}= Phenotypic variance of the trait y.

The calculated value of 'r' was compared with table 'r' value with n-2 degrees of freedom at 5% and 1% level of significance, where, n refers to the number of pairs of observation. Thus, the data obtained from various experimental objectives were subjected to pertinent statistical analysis to draw meaningful inference towards the genetic divergence of rice populations.

3.5.8.5 Path coefficient analysis

According to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), Path coefficient analysis was done utilizing simple correlation values. In path analysis, the correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$ +……..+ $P_{yx11}.r_{x1x11}$

$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$+……..+ $P_{yx11}.r_{x2x11}$

$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$+……..+ $P_{yx11}.r_{x3x11}$

To estimate direct and indirect effect of the correlated characters, say x1, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

Where r's denoted simple correlation coefficient and P's indicate path coefficient (unknown).

P's in the above equations may be conveniently solved by arranging them in matrix form. Total correlation, say between x1 and y is thus partitioned as follows:

P_{yx1} = the direct effect of x1 on y.

$P_{yx2}r_{x1x2}$ = the indirect effect of x1 via x2 on y.

$P_{yx3}r_{x1x3}$ = the indirect effect of x1 via x3 on y.

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

$$P_{RY}^2 = 1 - \sum P_{iy} \cdot r_{iy}$$

Where, $P^2_{RY} = (R^2)$

Hence, residual effect, $R = (P^2_{RY})^{\frac{1}{2}}$

P_{iy}= Direct effect of the character on yield

r_{iy}=Correlation of the character with yield

Categories:

Negligible (0.00 to 0.09);

Low (0.10 to 0.19);

Moderate (0.20 to 0.29);

High (0.30 to 1.0);

Very High (>1.00)

3.5.9 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parent's selection in hybridization program based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a hybridization program. Multivariate analysis viz. Principal Component Analysis (PCA) and Cluster Analysis (CA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows,

3.5.9.1 Principal Component Analysis (PCA)

Principal Component Analysis, one of the multivariate techniques, is used to examine the inter-relationships among several characters and can be done from the sum of squares and products matrix for the characters. Thus, PCA finds linear combinations of a set variate that maximize the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Therefore, Principles components were computed from the correlation matrix and genotypes scores obtained for first components (which has the property of accounting for the maximum variance) and succeeding components with latent roots greater than unity.

Contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.5.9.2 Cluster Analysis (CA)

Cluster Analysis divides the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTAT, the algorithm is used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examines the effect of swooping two genotypes of different classes and so on.

Calculation of D^2 values

The Mahalanobis's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952), and Singh and Chaudhury (1977). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_{i}^{x} d_i^2 = \sum_{i}^{x} \left(Y_i^j - Y_j^k\right)(j \neq k)$$

Where,

Y = Uncorrelated variable (character) which varies from i = 1 to x

x = Number of characters.

Superscript j and k to Y = A pair of any two genotypes.

Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh *et al.* (1985).

Average intra-cluster distance $= \frac{\sum \boldsymbol{d_i^2}}{\boldsymbol{n}}$

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

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

Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh *et. al.* (1985)

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

Where,

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

n_i = number of populations in cluster i.

n_j = number of populations in cluster j.

Cluster diagram

Using the values of intra and inter-cluster distances (D =$\sqrt{D^2}$), a cluster diagram was drawn as suggested by Singh and Chuadhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

3.5.10 Selection of genotypes for future hybridization program

Divergence analysis is usually performed to identify the diverse genotypes for hybridization purposes. The genotypes grouped together are less divergent among themselves than those, which fall into different clusters. Clusters separated by largest statistical distance (D^2) express the maximum divergence among the genotypes included into these different clusters. Variety (s) or line(s) were selected for efficient hybridization program according to Singh and Chaudhury (1985).

CHAPTER IV

RESULT AND DISCUSSION

The experiment was conducted to identify the breeding values in respect of genotypic effects and comparative performances of different rice genotypes. Heritability of a trait is important in determining its response to selection. Character association derived by correlation coefficient gives the basis for selecting desirable plant, aiding in evaluation of relative influence of various component characters on yield. Path coefficient analysis discerns correlation into direct and indirect effects. Diversity is the function of parent selection and also heterosis. The availability of transgressive segregates in a breeding program depends upon the divergence of parents. Thus, the accurate information on the nature and degree of diversity of the parents is the prerequisite of an effective breeding program. Data pertaining to eighteen yield and its contributing characters were computed and statistically analyzed and the results of the present investigation are presented under the following headings:

4.1 Genetic variability
4.2 Heritability, genetic advance and genetic advance percentage of mean,
4.3 Correlation coefficient studies
4.4 Path coefficient analysis and
4.5 Assessment of genetic diversity

4.1 Genetic variability

4.1.1 1st heading

Analysis of variance (Table 3) revealed significant differences among the genotypes (80.50**) for 1st heading. The highest 1st heading was recorded in G3 (114 days), whereas the minimum 1st heading was recorded in G20 (94days) and the mean value is 106.56 (Table 4).

Phenotypic variance (27.50) was slightly different from the genotypic variance (26.50) that indicated slight environmental effect over the trait. Least difference between PCV (4.92%) and GCV (4.83%) values indicated that less variability was found on this character (Table 5).

4.1.2 50% heading

From the ANOVA (Table 3), it was found that 50% heading showed highly significant variations among the genotypes (98.08**). The 50% heading was maximum in G3 (120 days) and minimum was observed in G20 (96 days) and the mean value was 110.88 (Table 4) among 32 genotypes.

The phenotypic and genotypic variances for 50% heading were 33.38 and 32.35, respectively. The phenotypic variance was slightly higher than the genotypic variance suggested that slight influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 5.21% and 5.13%, respectively for 50% heading which indicating that slightly high variation exists among different genotypes (Table 5). The less GCV values of this characters suggested that the less possibility of improving this trait through selection, Iftekharuddaula *et al.* (2001).

4.1.3 Days to maturity

Highly significant variation (118.60**) among 32 genotypes for days to maturity (Table 3) was found. The G15 showed the highest (161.33) days to maturity among 32 genotypes whereas the G20 showed the minimum (127.67) days to maturity and the mean value was 142.85 (Table 4).

The value of phenotypic (45.80) and genotypic (36.40) variance for days to maturity with high difference between them suggested significant role of environment on the character. The difference between phenotypic (4.74%) and genotypic (4.22%) coefficient of variances were low for days to maturity which indicated the existence of less variation among the genotype (Table 5). The less GCV values of this character suggested that there was less possibility of improvement of this trait through selection, Ma *et al.* (2001).

4.1.4 Plant height (cm)

The mean square due to genotype was found significant (184.68**) at for plant height indicating the presence of genotypic differences present among 32 genotypes (Table 3). The highest plant height was recorded in G20 (123.28 cm) and the lowest was found in G2 (87.39 cm) and the mean value was 100.46 cm (Table 4).

The phenotypic (77.06) and genotypic (53.81) variance for rice plant height suggests that high influence of environment on the expression of the genes controlling this trait. Same result was also found by Seyoum *et at.* (2012) for rice. The values of PCV and GCV were 8.74% and 7.30%, respectively which indicated that the genotype has less variation for this trait (Table 5), De *et al.* (2002).

4.1.5 Culm length (cm)

Highly significant variations were observed among the genotypes (33.99**) for culm length (Table 3). The highest culm length was taken in G20 (72.51 cm) and the minimum culm length was taken in G2 (55.52 cm) among 32 genotypes (Table 4) and the mean value was 67.77cm.

The phenotypic and genotypic variance for culm length was observed (23.59) and (5.20), respectively with high differences between them, suggested that the environment had significant roles in the expression of trait. The phenotypic coefficient of variation (7.17%) was higher than genotypic coefficient of variation (3.36%) (Table 5) suggested that environment had higher influence on the expression of the genes controlling this trait.

4.1.6 Culm diameter (cm)

Analysis of variance (Table 3) revealed highly significant differences among the genotypes (0.010**) for culm diameter. The highest culm diameter was recorded in G3 (0.60 cm) whereas the minimum culm diameter was recorded in G20 (0.38 cm) and the mean value was 0.47cm (Table 4).

Phenotypic variance and the genotypic variance were found. Least difference between PCV (12.80%) and GCV (11.63%) values indicated that less influence of environment and moderate variability present on this character (Table 5).

Table 3. Analysis of variance of 18 characters of 32 genotypes of rice

Source of variation	DF	FH	FPH	DM	PH	CL	CD	LFL	LP	LPL
Replication	2	1.13	0.13	2.20	105.72	47.89	0.001	5.77	3.73	15.87
Genotype	31	80.50**	98.08**	118.60**	184.68**	33.99**	0.010**	6.88**	2.49**	15.82 ^{ns}
Error	62	1.00	1.03	9.40	23.25	18.39	0.001	2.75	1.18	11.02

***= 5% level of significant **= 1% level of significant, ^{ns}=Non-significant**

Table 5 (contd.)

Source of variation	DF	NPBPP	NSBPP	TNTPP	NETPP	NNETPP	NFGMT	NUGMT	TSW	YP
Replicaton	2	4.29	1.81	6.97	1.87	0.23	175.41	23.27	0.36	1.00
Genotype	31	4.77^{ns}	22.10 ^{ns}	4.41 ^{ns}	6.16**	0.09 ^{ns}	1260.19**	25.94*	14.67**	58.92**
Error	62	3.44	17.67	2.98	1.95	0.08	337.00	15.26	1.81	8.64

*** =5% level of significant **= 1% level of significant, ^{ns}=Non-significant**

FH= 1st heading, FPH= 50% heading, DM= Days to maturity, PH= Plant height (cm), CL= Culm length (cm), CD= Culm diameter (cm), LFL= Length of flag leaf (cm), LP= Length of panicle (cm), LPL= Length of penultimate leaf (cm), NPBP= No. of primary branches/panicle, NSBPP= No. of secondary branches/panicle, TNTPP= Total no. of tiller/plant, NETPP= No. of effective tiller/plant, NNETPP= No. of non-effective tiller/plant, NFGMT= No. of filled grain of main tiller, NUGMT= No. of unfilled grain of main tiller, TSW= 1000 seed weight (g), YP= Yield/plant (g).

4.1.7 Length of flag leaf (cm)

From the ANOVA (Table 3), it was found that length of flag leaf (cm) showed highly significant variations among the genotypes (6.88**). The length of flag leaf was maximum in G26 (27.98 cm) and minimum was observed in G7 (19.36 cm) and the mean value was 24.57cm (Table 4) among 32 genotypes.

The phenotypic and genotypic variances for length of flag leaf were 4.13 and 1.38, respectively. The phenotypic variance was higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 8.27% and 4.78%, respectively for length of flag leaf which indicating that less variation exists among different genotypes (Table 5). The less GCV and PCV values of this characters suggested that the less possibility of improving this trait through selection.

4.1.8 Length of panicle (cm)

Highly significant variation (2.49**) among 32 genotypes for length of panicle (Table 3) had been found. The G13 showed the highest (25.65 cm) length of panicle among 32 genotypes whereas the G11 showed the minimum (20.58 cm) length of panicle and the mean value was 23.93cm (Table 4).

The value of phenotypic (1.62) was higher than the genotypic (0.44) variance for length of panicle suggests that role of environment on the character. The difference between phenotypic (5.31%) and genotypic (2.77%) coefficient of variances were high for length of panicle which indicated the existence of less variation among the genotype (Table 5), Laza *et al.* (2004).

4.1.9 Length of penultimate leaf (cm)

The mean square due to genotype was found significant (15.82*) at for length of penultimate leaf indicating the presence of genotypic differences present among 32 genotypes (Table 3). The highest length of penultimate leaf was recorded in G26 (40.73 cm) and the lowest was found in G1 (32.11 cm) and the mean value was 36.77cm (Table 4).

The phenotypic (12.62) and genotypic (1.60) variance for length of penultimate leaf suggested that high influence of environment on the expression of the genes

controlling this trait. The values of PCV and GCV were 9.66% and 3.44%, respectively which indicates that the genotype has less variation for this trait (Table 5).

4.1.10 No. of primary branches/panicle

Significant variations were observed among the genotypes (4.77*) for no. of primary branches/panicle (Table 3). The highest no. of primary branches/panicle was taken in G1 (12.27) and the minimum no. of primary branches/panicle was taken in G24 (6.50) among 32 genotypes (Table 4) and the mean value is 10.58.

The phenotypic and genotypic variance for no. of primary branches/panicle was observed (3.89) and (0.44), respectively with slightly differences between them, suggested that the environment had role in the expression of trait. The phenotypic coefficient of variation (18.62%) was higher than genotypic coefficient of variation (6.28%) (Table 5) suggested that environment has high influence on the expression of the genes controlling this trait.

4.1.11 No. of secondary branches/panicle

Analysis of variance (Table 3) revealed significant differences among the genotypes (22.10*) for no. of secondary branches/panicle. The highest number of secondary branches/panicle was recorded in G26 (36.27) whereas the minimum number of secondary branches/panicle was recorded in G24 (22.67) and the mean value is 30.82 (Table 4).

Phenotypic variance (19.15) was highly difference from the genotypic variance (1.48) that indicated high environmental effect over the trait. Large difference between PCV (14.20%) and GCV (3.94%) values indicated that less influence of environment on this character (Table 5).

4.1.12 Total no. of tiller/plant

From the ANOVA (Table 3), it was found that total no. of tiller/plant showed significant variations among the genotypes (4.41*). Total no. of tiller/plant was maximum in G20 (13.27) and minimum was observed in G29 (8.27) and the mean value is 10.66 (Table 4) among 32 genotypes.

The phenotypic and genotypic variances for total no. of tiller/plant were 3.45 and 0.48, respectively. The phenotypic variance was higher than the genotypic variance suggested higher influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 17.44% and 6.48%, respectively for total no. of tiller/plant which indicating that high variation existed among different genotypes (Table 5). The moderate GCV values of this character suggested that there was slightly high possibility of improving this trait through selection.

4.1.13 No. of effective tiller/plant

Highly significant variation (6.16**) among 32 genotypes for no. of effective tiller/plant (Table 3) was found. The G24 showed the highest (13.64) no. of effective tiller/plant among 32 genotypes whereas the G16 showed the minimum (6.90) no. of effective tiller/plant and the mean value was 9.99 (Table 4).

The value of phenotypic (3.35) was higher than the value of genotypic (1.40) variance for no. of effective tiller/plant suggests role of environment on the character. The difference between phenotypic (18.32%) and genotypic (11.86%) coefficient of variances were high for no. of effective tiller/plant which indicateed the existence of adequate variation among the genotype (Table 5).

4.1.14 No. of non-effective tiller/plant

The mean square due to genotype was found significant (0.09*) at for no. of non-effective tiller/plant indicating the presence of genotypic differences present among 32 genotypes (Table 3). The highest no. of non-effective tiller/plant was recorded in G20 (1.13) and the lowest was found in G8 (0.30) and the mean value was 0.62 (Table 4).

The phenotypic (0.08) and genotypic variance for no. of non-effective tiller/plant suggests that low influence of environment on the expression of the genes controlling this trait. The values of PCV and GCV were 46.34% and 10.56%, respectively which indicated that the genotype had considerable variation for this trait (Table 5).

Table 4. Mean performance of eighteen characters of thirty two genotypes of rice

GENOTYPES	FH	FPH	DM	PH	CL	CD	LFL	LP	LPL
G1	109ef	116bc	150.33bc	101.96c-g	65.53a-f	0.48d-g	23.68d-g	23.89a-f	32.11f
G2	110de	115cd	143.33d-g	87.39k	55.52 g	0.41j-l	23.37fg	22.99ef	33.12ef
G3	114a	120a	144.00d-g	99.15e-i	69.79a-f	0.60a	24.45c-g	24.34a-e	35.91a-f
G4	107gh	114de	144.00d-g	87.47k	69.11a-f	0.42h-l	24.28c-g	23.92a-f	39.16a-c
G5	97k	101l	146.00c-e	99.60e-i	67.46a-f	0.48d-g	22.56g	24.07a-e	35.08b-f
G6	105i	107j	143.00e-g	105.83c-e	67.73a-f	0.45f-i	24.05c-g	23.95a-f	35.54a-f
G7	111cd	114de	141.67e-g	98.61e-j	69.49a-f	0.44g-j	19.363h	22.28fg	33.67d-f
G8	110de	114de	144.33d-f	105.32c-e	70.10a-e	0.39kl	23.56d-g	24.59a-e	40.25ab
G9	105i	112fg	141.00e-g	104.91c-f	70.54a-d	0.39kl	24.25c-g	24.48a-e	38.06a-e
G10	106hi	109i	139.33f-h	98.68e-j	67.74a-f	0.45f-i	25.42a-f	23.51c-f	39.59a-c
G11	114a	117b	142.67e-g	104.46c-f	68.89a-f	0.50b-d	26.23a-d	20.58g	33.657d-f
G12	113ab	117b	143.67d-g	107.96cd	68.49a-f	0.540b	27.29 ab	25.21a-c	38.97a-d
G13	96k	101l	139gh	100.17d-h	71.18a-c	0.46e-h	24.29c-g	25.65a	39.67a-c
G14	108fg	114de	153.33b	102.67c-g	69.48a-f	0.51b-d	26.51a-c	24.25a-e	39.88a-c
G15	113ab	117b	161.33a	96.20g-j	71.91a	0.54b	23.70d-g	24.65a-e	35.36a-f
G16	108fg	114de	139gh	96.32g-j	64.33c-f	0.44g-j	24.62bc-g	24.00a-f	37.51a-f
G17	109ef	113ef	148.33b-d	97.43f-j	64.83b-f	0.48d-g	23.52e-g	23.57c-f	33.33ef
G18	105i	109i	139.67f-h	91.00jk	66.35a-f	0.46e-h	25.01b-g	23.60c-f	35.37a-f
G19	110de	114de	131.00ij	103.75c-g	62.93f	0.51b-d	23.71d-g	24.14a-e	36.99a-f
G20	94l	96m	127.67j	123.28a	72.51a	0.38l	26.17a-e	23.21ef	40.13a-c
G21	105i	111gh	148.33b-d	88.11k	63.22ef	0.49c-f	24.62b-g	23.38d-f	37.38a-f
G22	109ef	114de	151.33b	98.00e-j	63.863d-f	0.52bc	23.20fg	24.16a-e	37.74a-e
G23	96k	101l	148.33b-d	116.33ab	70.81a-d	0.59a	24.89b-g	23.75b-f	37.01a-f
G24	105i	107j	135.33hi	92.22i-k	70.21a-e	0.39kl	24.74b-fg	23.83b-f	34.79c-f

G25	103j	105k	143.33d-g	92.84h-k	66.78a-f	0.46e-h	24.60b-g	23.85b-f	35.42a-f
G26	107gh	111gh	141.00e-g	103.59c-g	69.97a-e	0.43h-k	27.98a	25.03a-d	40.73a
G27	105i	107j	139.00gh	104.90c-f	67.18a-f	0.43h-k	25.16b-g	23.95a-f	36.66a-f
G28	108fg	113ef	142.00e-g	102.67c-g	67.95a-f	0.50b-e	25.05b-g	25.38ab	35.77a-f
G29	102j	104k	139.00gh	93.30h-k	67.67a-f	0.53bc	25.51a-f	23.88a-f	37.93a-e
G30	112bc	117b	141.00e-g	109.48bc	67.31a-f	0.43h-k	24.88b-g	23.80b-f	35.96a-f
G31	109ef	114de	141.00e-g	104.94c-f	71.587ab	0.41i-l	25.42a-f	24.05a-f	36.67a-f
G32	105i	110hi	139.00gh	96.07g-j	68.16a-f	0.46e-h	24.06c-g	23.75b-f	37.28a-f
MIN	94	96	127.67	87.39	55.52	0.38	19.36	20.58	32.11
MAX	114	120	161.33	123.28	72.51	0.60	27.98	25.65	40.73
MEAN	106.56	110.88	142.85	100.46	67.77	0.47	24.57	23.93	36.77
SE	0.81	0.83	2.50	3.94	3.50	0.02	1.35	0.89	2.71
LSD (%)	1.63	1.66	5.00	7.87	7.00	0.04	2.71	1.77	5.42

Table 4. (contd.)

GENOTYPES	NPBPP	NSBPP	TNTPP	NETPP	NNETPP	NFGMT	NUGMT	TSW	YP
G1	12.27a	32.90a-d	9.37d-h	8.80f-k	0.57b-e	142.43e-j	25.07a	23.76c-i	21.64ef
G2	10.27ab	28.77b-e	12.60ab	11.67a-c	0.40de	139.20e-k	15.43c-f	22.05h-l	21.37ef
G3	11.27ab	32.13a-d	10.60a-h	9.300d-j	0.63b-e	152.53c-i	21.43a-c	25.16b-e	26.97b-d
G4	10.33ab	29.70a-d	9.63d-h	9.40c-j	0.67b-e	125.73h-k	19.27a-f	23.08e-k	21.82ef
G5	10.33ab	30.00a-d	12.20a-c	9.33d-j	1.00ab	112.23k	14.433d-f	22.557g-l	20.834f
G6	11.80ab	31.43a-d	9.07f-h	8.47g-k	0.60b-e	144.77d-j	17.40b-f	24.11c-h	20.27f
G7	10.20ab	27.90c-e	10.20b-h	9.57c-j	0.80a-d	135.90e-k	14.37ef	26.95b	20.06f
G8	10.63ab	32.37a-d	9.90b-h	10.57b-h	0.30e	178.63a-c	19.27a-f	24.31c-g	22.71d-f

G9	11.73ab	32.17a-d	11.27a-g	8.87e-k	0.60b-e	155.80c-g	19.067a-f	24.39c-g	29.64a-c
G10	11.10ab	33.47a-d	10.03b-h	9.57c-j	0.57b-e	163.53b-f	18.40b-f	24.10c-h	26.05b-e
G11	11.03ab	31.67a-d	11.67a-f	10.57b-h	0.80a-d	172.97a-d	20.80a-d	24.00cd-h	29.04a-c
G12	12.10a	33.63a-d	11.40a-f	10.43b-h	0.57b-e	155.27c-h	23.73ab	21.06k-n	25.82c-e
G13	9.80ab	30.67a-d	9.80b-h	10.23b-i	0.37de	165.67b-e	17.97b-f	20.77l-n	22.84d-f
G14	9.533ab	29.20b-e	11.33a-f	10.73b-g	0.60b-e	146.07d-j	16.37c-f	21.92h-m	30.77ab
G15	11.40ab	32.30ad	11.73a-f	11.00b-f	0.73a-e	178.63a-c	19.33a-f	25.44b-d	33.01a
G16	9.30a-c	29.40b-e	9.50c-h	6.90k	0.57b-e	132.60g-k	13.70f	25.35bd	23.05d-f
G17	10.27ab	28.77b-e	9.57c-h	8.30h-k	0.63b-e	132.63g-k	17.53b-f	22.59g-l	30.67ab
G18	9.73ab	29.70a-d	11.50a-f	11.13b-e	0.57b-e	121.83jk	16.40c-f	22.03h-m	26.09b-e
G19	8.97bc	28.80b-e	10.27b-h	10.17b-i	0.60b-e	131.27g-k	16.43c-f	21.65i-m	23.63d-f
G20	10.20ab	27.03de	13.27a	12.10ab	1.13a	120.40jk	21.13a-c	19.83mn	15.00g
G21	11.13ab	30.53a-d	10.63a-h	10.00b-j	0.63b-e	146.33d-j	17.83b-f	21.46j-n	29.22a-c
G22	8.97bc	28.33b-e	12.07a-d	10.97b-f	0.47c-e	148.10d-j	19.67a-f	25.95bc	31.96a
G23	12.17a	35.07ab	10.60a-h	11.03b-f	0.57b-e	125.84g-k	16.20c-f	19.33n	19.97f
G24	6.50c	22.67e	11.77a-f	13.64a	0.73a-e	123.43i-k	14.40ef	23.66d-j	22.55d-f
G25	9.30a-c	28.47b-e	11.33a-f	12.15ab	0.40de	143.63d-j	18.87a-f	20.66l-n	26.12b-e
G26	12.23a	36.27a	8.47gh	7.97i-k	0.50c-e	198.67a	24.87a	24.86b-f	30.04a-c
G27	10.83ab	33.27a-d	11.93a-e	11.30b-d	0.73a-e	187.70ab	18.47b-f	30.33a	29.35a-c
G28	10.53ab	30.93a-d	10.70a-h	9.63c-j	0.90a-c	140.37e-k	16.77c-f	22.64g-l	21.89ef
G29	11.17ab	33.13a-d	8.27h	7.83jk	0.47c-e	134.37f-k	16.73cd-f	24.87b-f	20.64f
G30	12.23a	32.70a-d	11.10a-g	10.40b-h	0.73a-e	152.57c-i	21.33a-c	24.44c-g	28.69a-c
G31	11.87ab	34.17a-c	9.23e-h	8.67g-k	0.57b-e	153.00c-i	20.30a-e	22.82f-l	23.43d-f
G32	9.50a-c	28.67b-e	10.00b-h	9.00e-k	0.57b-e	139.13e-k	15.13c-f	22.80f-l	19.23fg
MIN	6.50	22.67	8.27	6.90	0.30	112.23	13.70	19.33	15.00
MAX	12.27	36.27	13.27	13.64	1.13	198.67	25.07	30.33	33.01

MEAN	10.58	30.82	10.66	9.99	0.62	146.91	18.38	23.41	24.83
SE	1.52	3.43	1.41	1.14	0.23	14.99	3.19	1.10	2.40
LSD (%)	3.03	6.86	2.82	2.28	0.46	29.96	6.38	2.20	4.80

FH= 1st heading, FPH= 50% heading, DM= Days to maturity, PH= Plant height (cm), CL= Culm length (cm), CD= Culm diameter (cm), LFL= Length of flag leaf (cm), LP= Length of panicle (cm), LPL= Length of penultimate leaf (cm), NPBP= No. of primary branches/panicle, NSBPP= No. of secondary branches/panicle, TNTPP= Total no. of tiller/plant, NETPP= No. of effective tiller/plant, NNETPP= No. of non-effective tiller/plant, NFGMT= No. of filled grain of main tiller, NUGMT= No. of unfilled grain of main tiller, TSW= 1000 seed weight (g), YP= Yield/plant (g).

4.1.15 No. of filled grain of main tiller

Highly significant variations were observed among the genotypes (1260.19**) for no. of filled grain of main tiller (Table 3). The highest no. of filled grain of main tiller was taken in G26 (198.67) and the minimum no. of filled grain of main tiller was taken in G5 (112.23) among 32 genotypes (Table 4) and the mean value was 146.91. The phenotypic and genotypic variance for no. of filled grain of main tiller was observed (644.73) and (307.73), respectively with high differences between them, suggested that the environment had significant role in the expression of trait. The phenotypic coefficient of variation (17.28%) was higher than genotypic coefficient of variation (11.94%) (Table 5) suggested that environment had influence on the expression of the genes controlling this trait.

4.1.16 No. of unfilled grain of main tiller

Analysis of variance (Table 3) revealed significant differences among the genotypes (25.94*) for no. of unfilled grain of main tiller. The highest no. of unfilled grain of main tiller was recorded in G1 (25.07) whereas the minimum no. of unfilled grain of main tiller was recorded in G16 (13.7) and the mean value was 18.38 (Table 4). Phenotypic variance (18.82) was higher than the genotypic variance (3.56) that indicated high environmental effect over the trait. Large difference between PCV (23.61%) and GCV (10.27%) values indicated that high influence of environment and considering variability present on this character (Table 5).

4.1.17 1000 seed weight (g)

From the ANOVA (Table 3), it was found that 1000 seed weight showed highly significant variations among the genotypes (14.67**). The 1000 seed weight was maximum in G27 (30.33 g) and minimum was observed in G23 (19.33 g) and the mean value was 23.41g (Table 4) among 32 genotypes. The phenotypic and genotypic variances for 1000 seed weight were 6.10 and 4.29, respectively. The phenotypic variance was higher than the genotypic variance suggested influence of environment on the expression of the genes controlling this trait. The value of PCV and GCV were 10.55% and 8.85%, respectively for 1000 seed weight which indicating that medium variation exists among different genotypes (Table 5). The moderate GCV values of this characters suggest that the possibility of improving this trait through selection, Iftekharuddaula *et al.* (2001).

4.1.18 Yield/plant (g)

Highly significant variation (58.92**) among 32 genotypes for yield/plant (Table 3) were found. The G15 showed the highest (33.01 g) yield/plant among 32 genotypes whereas the G20 showed the minimum (15g) and the mean value was 24.83g (Table 4).

The value of phenotypic (25.40) and genotypic (16.76) variance for yield/plant with high difference between them suggested significant role of environment on the character. The difference between phenotypic (20.30%) and genotypic (16.49%) coefficient of variances were high for yield/plant which indicated the existence of adequate variation among the genotype (Table 5). The high GCV values of this character suggested the possibility of improvement of this trait through selection, Chaudhary and Motiramani (2003).

4.2 Heritability and Genetic Advance

4.2.1 1st heading

1st heading showed high heritability (96.38%) coupled with moderate genetic advance (10.41) and low genetic advance in percentage of mean (9.77%) (Table 5). The result revealed that character was controlled by additive genes the selection based on this character would be effective.

4.2.2 50% heading

High heritability (96.92%) accompanied with moderate genetic advance (11.53) and moderate genetic advance in percentage of mean (10.40%) was calculated in respect of 50% heading (Table 5). These findings discovered the action of additive gene effects on the expression of this trait. The high heritability was being exhibited due to high environmental effects. Selection may be effective in such character.

4.2.3 Days to maturity

Days to maturity showed high heritability (79.47%) coupled with moderate genetic advance (11.08) and low genetic advance in percentage of mean (7.76%) (Table 5). These finding exposed the predominance of non-additive genes for controlling days to maturity. Thus, selection based on this character will not be rewarding for improvement.

4.2.4 Plant height (cm)

The magnitude of heritability in broad sense of plant height was high (69.83%) with moderate genetic advance (12.63) and moderate genetic advance in percentage of mean (12.57%) (Table 5). These findings revealed that this trait was controlled by additive gene and selection for this character would be effective.

4.2.5 Culm length (cm)

Low heritability (22.04%) along with low genetic advance (2.21) and low genetic advance in percentage of mean (3.25%) was calculated in culm length (Table 5). It was indicated that presence of non-additive gene action and selection for further improvement of the trait might not be effective.

4.2.6 Culm diameter (cm)

Culm diameter showed high heritability (82.51%) coupled with low genetic advance (0.10) and high genetic advance in percentage of mean (21.76 %) (Table 5). Genetic advances in percent of mean were higher which was in accordance with the findings of Singh *et al.* (1977).

4.2.7 Length of flag leaf (cm)

Moderate heritability (33.34%) accompanied with low genetic advance (1.40) and low genetic advance in percentage of mean (5.68%) was calculated in respect of length of flag leaf (Table 5). These findings discovered the action of non-additive gene effects on the expression of this trait. Selection may not be effective in such character.

4.2.8 Length of panicle (cm)

Length of panicle showed low heritability (27.14%) coupled with low genetic advance (0.71) and low genetic advance in percentage of mean (2.97%) (Table 5). These finding exposed the predominance of no additive genes for controlling length of panicle. Thus, selection based on this character will not be rewarding for improvement.**4.2.9 Length of penultimate leaf (cm)**The magnitude of heritability in broad sense of length of penultimate leaf was low (12.66%) with low genetic advance (0.93) and low genetic advance in percentage of

Table 5. Estimation of genetic parameter of eighteen characters of thirty two rice genotypes

Characters	$\sigma^2 g$	$\sigma^2 p$	Genotypic coefficient of variations	Phenotypic coefficient of variations	Heritability %	Genetic advance	Genetic advance of % mean	CV(%)
FH	26.50	27.50	4.83	4.92	96.38	10.41	9.77	0.94
FPH	32.35	33.38	5.13	5.21	96.92	**11.53**	10.40	0.91
DM	36.40	45.80	4.22	4.74	79.47	11.08	7.76	2.15
PH	53.81	77.06	7.30	8.74	69.83	12.63	12.57	4.80
CL	5.20	23.59	3.36	7.17	22.04	2.21	3.25	6.33
CD	0.00	0.00	11.63	12.80	82.51	0.10	21.76	5.35
LFL	1.38	4.13	4.78	8.27	33.34	1.40	5.68	6.75
LP	0.44	1.62	2.77	5.31	27.14	0.71	2.97	4.53
LPL	1.60	12.62	3.44	9.66	12.66	0.93	2.52	9.03
NPBPP	0.44	3.89	6.28	18.62	11.37	0.46	4.36	17.53
NSBPP	1.48	19.15	3.94	14.20	7.72	0.70	2.26	13.64
TNTPP	0.48	3.45	6.48	17.44	13.80	0.53	4.96	16.19
NETPP	1.40	3.35	11.86	18.32	41.88	1.58	15.81	13.97
NNETPP	0.00	0.08	10.56	46.34	5.19	0.03	4.96	45.13
NFGMT	307.73	644.73	11.94	17.28	47.73	24.97	16.99	12.50
NUGMT	3.56	18.82	10.27	23.61	18.92	1.69	9.20	21.26
TSW	4.29	6.10	8.85	10.55	70.26	3.57	15.27	5.76
YP	16.76	25.40	16.49	20.30	65.99	6.85	27.60	11.84

FH= 1st heading, FPH= 50% heading, DM= Days to maturity, PH= Plant height (cm), CL= Culm length (cm), CD= Culm diameter (cm), LFL= Length of flag leaf (cm), LP= Length of panicle (cm), LPL= Length of penultimate leaf (cm), NPBP= No. of primary branches/panicle, NSBPP= No. of secondary branches/panicle, TNTPP= Total no. of tiller/plant, NETPP= No. of effective tiller/plant, NNETPP= No. of non-effective tiller/plant, NFGMT= No. of filled grain of main tiller, NUGMT= No. of unfilled grain of main tiller, TSW= 1000 seed weight (g), YP= Yield/plant (g).

mean (2.52%) (Table 5). These findings revealed that this trait was controlled by non-additive gene and selection for this character would not be effective.

4.2.10 No. of primary branches/panicle

Low heritability (11.37%) along with low genetic advance (0.46) and low genetic advance in percentage of mean (4.36%) was calculated in no. of primary branches/panicle (Table 5). It is indicated that presence of non-additive gene action and selection for further improvement of the trait might not be effective.

4.2.11 No. of secondary branches/panicle

No. of secondary branches/panicle showed low heritability (7.72%) coupled with low genetic advance (0.70) and low genetic advance in percentage of mean (2.26%) (Table 5). The result showed that due to presence of no additive gene effect and no scope of selection of this trait.

4.2.12 Total no. of tiller/plant

Low heritability (13.80%) accompanied with low genetic advance (0.53) and low genetic advance in percentage of mean (4.96%) was calculated in respect of total no. of tiller/plant (Table 5). These findings discovered the action of non-additive gene effects on the expression of this trait. The low heritability was being exhibited due to low environmental effects. Selection may not be effective in such character.

4.2.13 No. of effective tiller/plant

No. of effective tiller/plant showed moderate heritability (41.88%) coupled with low genetic advance (1.58) and moderate genetic advance in percentage of mean (15.81%) (Table 5). These finding exposed the predominance of non-additive genes for controlling total no. of effective tiller/plant. Thus, selection based on this character will not be rewarding for improvement.

4.2.14 No. of non-effective tiller/plant

The magnitude of heritability in broad sense of no. of non-effective tiller/plant was low (5.19 %) with low genetic advance (0.03) and low genetic advance in percentage of mean (4.96%) (Table 5). These findings revealed that this trait was controlled by non-additive gene and selection for this character would not be effective.

4.2.15 No. of filled grain of main tiller

Moderate heritability (47.73%) along with high genetic advance (24.97) and moderate genetic advance in percentage of mean (16.99%) was calculated in no. of filled grain of main tiller (Table 5). It is indicated that presence of additive gene action and selection for further improvement of the trait might be effective.

4.2.16 No. of unfilled grain of main tiller

No. of unfilled grain of main tiller showed low heritability (18.92%) coupled with low genetic advance (1.69) and low genetic advance in percentage of mean (9.20%) (Table 5). The result showed that due to presence of non-additive gene effect and no scope of selection of this trait.

4.2.17 1000 seed weight (g)

High heritability (70.26%) accompanied with low genetic advance (3.57) and moderate genetic advance in percentage of mean (15.27%) was calculated in respect of 1000 seed weight (Table 5). These findings discovered the action of non-additive gene effects on the expression of this trait.

4.2.18 Yield/plant (g)

Yield/plant showed high heritability (65.99%) coupled with low genetic advance (6.85) and high genetic advance in percentage of mean (27.60%) (Table 5). These finding exposed the predominance of non-additive genes for controlling yield/plant. Thus, selection based on this character will not be rewarding for improvement.

4.3 Correlation coefficient analysis

Improvement of a particular character in the breeding programs can be achieved by indirect selection via different characters. This wants a good understanding of the association of various characters with the target character and among the different characters themselves. It's necessary to have the estimates of correlation of yield with different characters that the genotype might be assessed visually. The makeup and constitution correlation reveals the extent of association between completely different characters, thus, it helps to base choice procedure to a needed balance, once two opposite fascinating characters moving the principal characters are being selected. A positive correlation happens because of coupling section of linkage and correlation

arises because of repulsion section of linkage of genes dominant completely different traits. No correlation indicates that genes involved are situated so much apart on identical chromosome or they're situated on completely different bodies. Yield being a fancy character is governed by an outsized range of genes. The influence of every character on yield might be well-known through correlation studies with a view to see the extent and nature of relationships prevailing among yield and yield attributing characters. Hence, the constitution and phenotypic correlation coefficient values for eighteen characters in rice genotypes studied are given in (Table 6).

4.3.1 1st heading

1st heading showed highly significant and positive correlation with 50% heading (r_g=0.972, r_p=0.98), days to maturity (r_g=0.327, r_p=0.306), no. of filled grain of main tiller (r_g=0.435, r_p=0.299), thousand seed weight (r_g=0.455, r_p=0.385) and yield/plant (r_g=0.538, r_p=0.422). It also observed that highly significant but negative correlation with height (cm) (r_g=-0.239, r_p=-0.215) and culm length (r_g=-0.347). It showed non-significant and positive correlation with culm diameter (r_g=0.166, r_p=0.148). It also found non-significant but negative correlation with culm length (r_p=-0.149), length of flag leaf (r_g=-0.095, r_p=-0.037), length of panicle (r_g=-0.195, r_p=-0.108) and no. of effective tiller/plant (r_g=-0.168, r_p=-0.099) (Table 6).

4.3.2 50% heading

50% heading showed highly significant and positive correlation with days to maturity (r_g=0.407, r_p =0.363), no. of filled grain of main tiller (r_g=0.364, r_p=0.272), 1000 seed weight (r_g=0.374, r_p=0.319) and yield/plant (r_g=0.529*, r_p=0.440). It also observed that significant but negative correlation with plant height (r_g=-0.259, r_p=-0.240*), culm length (r_g=-0.393**) and no. of effective tiller/plant (r_g=-0.261*). It showed that non-significant and positive correlation with culm diameter (r_g=0.189, r_p=0.170). It also found non-significant but negative correlation with culm length (r_p=-0.140), length of flag leaf (r_g=-0.103, r_p=-0.056), length of panicle (r_g=-0.086, r_p=-0.041) and no. of effective tiller/plant (r_p=-0.170) (Table 6).

Table 6. Genotypic (r_g) and phenotypic (r_p) correlation coefficient among different pairs of yield and yield contributing characters in rice genotypes

Characters		FH	FPH	DM	PH	CL	CD	LFL	LP	NETPP	NFGMT	TSW
FPH	r_g	0.972**										
	r_p	0.948**										
DM	r_g	0.327**	0.407**									
	r_p	0.306**	0.363**									
PH	r_g	-0.239*	-0.259*	-0.260*								
	r_p	-0.215*	-0.240*	-0.199								
CL	r_g	-0.347**	-0.393**	-0.094	0.774**							
	r_p	-0.149	-0.140	0.008	0.299**							
CD	r_g	0.166	0.189	0.495**	0.014	0.008						
	r_p	0.148	0.170	0.452**	0.028	-0.013						
LFL	r_g	-0.095	-0.103	-0.260*	0.404**	0.365**	0.113					
	r_p	-0.037	-0.056	-0.082	0.203*	0.171	0.025					
LP	r_g	-0.195	-0.086	0.161	-0.003	0.335**	0.101	0.167				
	r_p	-0.108	-0.041	0.062	0.129	0.148	0.099	0.225*				
NETPP	r_g	-0.168	-0.261*	-0.060	0.069	-0.032	-0.125	0.053	-0.249*			
	r_p	-0.099	-0.170	-0.054	0.039	0.057	-0.060	0.011	-0.077			
NFGMT	r_g	0.435**	0.364**	0.280**	0.135	0.270**	-0.028	0.411**	0.132	-0.128		
	r_p	0.299**	0.272**	0.132	0.144	0.194	-0.044	0.265**	0.220*	-0.020		
TSW	r_g	0.455**	0.374**	0.096	-0.137	0.037	-0.122	-0.427**	-0.133	-0.282**	0.574**	
	r_p	0.385**	0.319**	0.112	-0.148	-0.023	-0.106	-0.059	-0.056	-0.182	0.355**	
YP	r_g	0.538**	0.529**	0.603**	-0.226*	-0.098	0.258*	0.214*	0.004	0.034	0.617**	0.386**
	r_p	0.422**	0.440**	0.413**	-0.132	-0.042	0.216*	0.226*	0.151	0.014	0.502**	0.286**

*=5% level of significant **= 1% level of significant ^{ns}, Non-significant. FH= 1st heading, FPH= 50% heading, DM= Days to maturity, PH= Plant height (cm), CL= Culm length (cm), CD= Culm diameter (cm), LFL= Length of flag leaf (cm), LP= Length of panicle (cm), NETPP= No. of effective tiller/plant, NFGMT= No. of filled grain of main tiller, TSW= 1000 seed weight (g), YP= Yield/plant (g).

4.3.3 Days to maturity

Days to maturity showed highly significant and positive correlation with culm diameter (r_g=0.495, r_p=0.452), no. of filled grain of main tiller (r_g=0.280) and yield/plant (r_g=0.603, r_p=0.413). It also observed that significant but negative correlation with plant height (r_g=-0.260*) and length of flag leaf (r_g=-0.260). It showed non-significant and positive correlation with culm length (r_p=0.008), length of panicle (r_g=0.161, r_p=0.062), no. of filled grain of main tiller (r_p=0.132) and 1000 seed weight (r_g=0.096, r_p=0.112). It also found non-significant but negative correlation plant height (cm) (r_p=-0.199), culm length (r_g=-0.094), length of flag leaf (r_p=-0.082), no. of effective tiller/plant (r_g=-0.060, r_p=-0.054) (Table 6).

4.3.4 Plant height (cm)

Plant height showed highly significant and positive correlation with culm length (r_g=0.774**, r_p=0.299**) and length of flag leaf (r_g=0.404**, r_p=0.203*). It also observed that highly significant but negative correlation with yield/plant (r_g=-0.226*). It showed that non-significant and positive correlation with culm diameter (r_g=0.014, r_p=0.028), length of panicle (r_p=0.129), no. of effective tiller/plant (r_g=0.069, r_p=0.039) and no. of filled grain of main tiller (r_g=0.135, r_p=0.144). It also found non-significant but negative correlation with length of panicle (r_g=-0.003), 1000 seed weight (r_g=-0.137, r_p=-0.148) and yield/plant (r_p =-0.132) (Table 6).

4.3.5 Culm length (cm)

Culm length showed highly significant and positive correlation with length of flag leaf (r_g=0.365), length of panicle (r_p=0.335) and no. of filled grain of main tiller (r_g=.270). It showed non-significant and positive correlation with culm diameter (r_g=0.008), length of flag leaf (r_p=0.171), length of panicle (r_p=0.148), no. of effective tiller/plant (P=0.057) and no. of filled grain of main tiller (r_p=0.194) and 1000 seed weight (r_g=0.037). It also found non-significant but negative correlation with culm diameter (r_p=-0.013), no. of effective tiller/plant (r_g=-0.032), 1000 seed weight (r_p=-0.023) and yield/plant (r_g=-0.098, r_p=-0.042) (Table 6).

4.3.6 Culm diameter (cm)

Culm diameter showed highly significant and positive correlation with yield/plant (r_g=0.258, r_p=0.216). It showed non-significant and positive correlation with length of flag leaf (r_g=0.113, r_p=0.025) and length of panicle (r_g=0.101, r_p=0.099). It also found non-significant but negative correlation with no. of effective tiller/plant (r_g=-0.125,

r_p=-0.060), no. of filled grain of main tiller (r_g=-0.028, r_p=-0.044) and 1000 seed weight (r_g=-0.122, r_p=-0.106) (Table 6).

4.3.7 Length of flag leaf (cm)

Length of flag leaf showed highly significant and positive correlation with length of panicle (r_p=0.225*), no. of filled grain of main tiller (r_g=0.411**, r_p=0.265**) and yield/plant (r_g=0.214*, r_p=0.226*). It also observed that highly significant but negative correlation with1000 seed weight (r_g=-0.427). It showed non-significant and positive correlation with length of panicle (r_g=0.167) and no. of effective tiller/plant (r_g=0.053, r_p=0.011). It also found non-significant but negative correlation with 1000 seed weight (g) (r_p=-0.059) (Table 6).

4.3.8 Length of panicle (cm)

Length of panicle showed significant and positive correlation with no. of filled grain of main tiller (r_p=0.220). It also observed that significant but negative correlation with no. of effective tiller/plant (r_g=-0.249). It showed non-significant and positive correlation with no. of filled grain of main tiller (r_g=0.132) and yield/plant (r_g=0.004, r_p =0.151). It also found non-significant but negative correlation with no. of effective tiller/plant (r_p=-0.077) and 1000 seed weight (r_g=-0.133, r_p=-0.056) (Table 6).

4.3.9 No. of effective tiller/plant

No. of effective tiller/plant showed highly significant but negative correlation with 1000 seed weight (r_g=-0.282). It showed non-significant and positive correlation with yield/plant (r_g=0.034, r_p=0.014). It also found non-significant but negative correlation with no. of filled grain of main tiller (r_g=-0.128, r_p=-0.020) and 1000 seed weight (r_p=-0.182) (Table 6).

4.3.10 No. of filled grain of main tiller

No. of filled grain of main tiller showed highly significant and positive correlation with 1000 seed weight (r_g =0.574, r_p=0.355) and yield/plant (r_g=0.617, r_p=0.502) (Table 6).

4.3.11 1000 seed weight

1000 seed weight showed highly significant and positive correlation with yield/plant (r_g=0.386, r_p=0.286) (Table 6).

4.4 Path coefficient Analysis

Correlation analysis indicates the association pattern of component traits with yield, they merely represent the influence of a selected attribute on yield instead of

providing cause and impact relationship. The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. it's standardized partial parametric statistical analysis. As such, it measures the direct influence of one variable upon another. Such data would be of good value in enabling the breeder to specifically determine the necessary component traits of yield and utilize the genetic stock for improvement in a planned way. The direct and indirect effects of yield contributing characters on yield were found out by using path analysis. Here yield per plant was considered as effect (dependent variable) and days to maturity, plant height, culm length, culm diameter, length of flag leaf, length of panicle, length of penultimate leaf, no. of primary branches/panicle, no. of secondary branches/panicle, total no. of tiller/plant, no. of effective tiller/plant, no. of non-effective tiller/plant, no. of filled grain of main tiller, no. of unfilled grain of main tiller and 1000 seed weight were treated as independent variables. Path coefficient analysis was showed direct and indirect effects of different characters on yield of rice in (Table 7).

4.4.1 1st heading:

Path co-efficient analysis revealed that 1st heading had a negative direct effect (-3.200) on yield/plant. 1st heading had positive indirect effect on plant height (0.763), culm length (1.111), length of flag leaf (0.303), length of panicle (0.623) and no. of effective tiller/plant (0.538) while negative indirect effect on 50% heading (-3.112), days to maturity (-1.045), culm diameter (-0.531), no. of filled grain of main tiller (-1.390) and 1000 seed weight(-1.457) with yield/plant. It showed that highly significant and positive genotypic correlation (0.538) with yield/plant (Table 7).

4.4.2 50% heading

Path co-efficient analysis revealed that 50% heading had a positive direct effect (3.528) on yield/plant. 50% heading had positive indirect effect on 1st heading (3.431), days to maturity (1.437), culm diameter (0.668), no. of filled grain of main tiller (1.283) and 1000 seed weight (1.320) while negative indirect effect on plant height (-0.912), culm length(-1.387), length of flag leaf (-0.362), length of panicle (-0.303) and no. of effective tiller/plant (-0.919) with yield/plant. It showed that highly significant and positive genotypic correlation (0.529) with yield/plant (Table 7).

4.4.3 Days to maturity

Path co-efficient analysis revealed that days to maturity had a negative direct effect (-0.093) on yield/plant. Days to maturity had positive indirect effect on plant height (0.024), culm length (0.009), length of flag leaf (0.024) and no. of effective tiller/plant (0.006) while negative indirect effect on 1st heading (-0.030),50% heading (-0.038),culm diameter(cm) (-0.046), length of panicle (cm) (-0.015), no. of filled grain of main tiller (-0.026) and 1000 seed weight(-0.009) with yield/plant. It showed that highly significant and positive genotypic correlation (0.603) with yield/plant (Table 7).

4.4.4 Plant height

Path co-efficient analysis revealed that plant height (cm) had a negative direct effect (-0.936) on yield/plant. Plant height had positive indirect effect 1st heading (0.223), 50% heading (0.242), days to maturity (0.243), length of panicle (0.003) and 1000 seed weight (0.128) while negative indirect effect culm length (-0.725), culm diameter (-0.013), length of flag leaf (-0.378), no. of effective tiller/plant (-0.065) and no. of filled grain of main tiller (-0.127). It showed that significant but negative genotypic correlation (-0.226) with yield/plant (Table 7).

4.4.5 Culm length

Path co-efficient analysis revealed that culm length had a positive direct effect (0.847) on yield/plant. Culm length had positive indirect effect on plant height (0.656), culm diameter (0.007), length of flag leaf (0.309), length of panicle (0.284), no. of filled grain of main tiller (0.229) and 1000 seed weight(g) (0.032) while negative indirect effect on 1st heading (-0.294), 50% heading (-0.333), days to maturity (-0.079) and no. of effective tiller/plant (-0.027). It showed that non-significant but negative genotypic correlation (-0.098) with yield/plant (Table 7).

4.4.6 Culm diameter

Path co-efficient analysis revealed that culm diameter had a positive direct effect (0.319) on yield/plant. Culm diameter had positive indirect effect on 1st heading (0.053), 50% heading (0.060), days to maturity (0.158), plant height (0.004), culm length (0.003), length of flag leaf (0.036), length of panicle (0.032) while negative indirect effect no. of effective tiller/plant (-0.040), no. of filled grain of main tiller (-

0.009) 1000 seed weight (-0.039) with yield/plant. It showed that significant and positive genotypic correlation (0.258) with yield/plant (Table 7).

4.4.7 Length of flag leaf

Path co-efficient analysis revealed that length of flag leaf had a positive direct effect (0.266) on yield/plant. Length of flag leaf (cm) had positive indirect effect on plant height (0.107), culm length(0.097), culm diameter (0.030), length of panicle (0.044), no. of effective tiller/plant (0.014) and no. of filled grain of main tiller (0.109) while negative indirect effect on 1st heading (-0.025), 50% heading (-0.027), days to maturity (-0.069) and 1000 seed weight(g) (-0.114) with yield/plant. It showed that significant and positive genotypic correlation (0.214) with yield/plant (Table 7).

4.4.8 Length of panicle

Path co-efficient analysis revealed that Length of panicle had a negative direct effect (-0.557) on yield/plant. Length of panicle had positive indirect effect on 1st heading (0.108), 50% heading (0.048), plant height (0.002) no. of effective tiller/plant (0.139) and 1000 seed weight(g) (0.074) while negative indirect effect on days to maturity (-0.090), culm length (-0.187), culm diameter (-0.056), length of flag leaf (-0.093) and no. of filled grain of main tiller (-0.074). It showed non-significant but positive genotypic correlation (0.004) with yield/plant (Table 7).

4.4.9 Number of effective tiller/plant

Path co-efficient analysis revealed that no. of effective tiller/plant had a positive direct effect (0.542) on yield/plant. No. of effective tiller/plant had positive indirect effect on plant height (0.038) and length of flag leaf (0.028) while negative indirect effect on 1st heading (-0.091), 50% heading (-0.141), days to maturity (-0.033), culm length (-0.017), culm diameter (-0.068), length of panicle (-0.135), no. of filled grain of main tiller (-0.069) and 1000 seed weight (-0.153) with yield/plant. It showed that non-significant and positive genotypic correlation (0.034) with yield/plant (Table 7).

4.4.10 No. of filled grain of main tiller

Path co-efficient analysis revealed that no. of filled grain of main tiller had a positive direct effect (0.514) on yield/plant. No. of filled grain of main tiller had positive indirect effect on 1st heading (0.224), 50% heading (0.187), days to maturity (0.144), plant height (0.070), culm length (0.139), length of flag leaf (0.211), length of panicle (0.068) and 1000 seed weight (0.296) while negative indirect effect on culm diameter

(-0.014) and no. of effective tiller/plant (-0.066). It showed that highly significant and positive genotypic correlation (0.617) with yield/plant (Table 7).

4.4.11 1000 seed weight (g)

Path co-efficient analysis revealed that 1000 seed weight had a positive direct effect (0.308) on yield/plant. 1000 seed weight had positive indirect effect on 1st heading (0.140), 50% heading (0.115), days to maturity (0.030), culm length (0.012), no. of filled grain of main tiller (0.177) while negative indirect effect on plant height (-0.042), culm diameter (-0.038), length of flag leaf (-0.132), length of panicle (-0.041) and no. of effective tiller/plant (-0.087). It showed that highly significant and positive genotypic correlation (0.386) with yield/plant (Table 7).

4.4.12 Residual Effects

The residual effect (R) of path co-efficient analysis was 0.19which reported that the traits under study contributed 81% of the yield per plant. It is said that there were some other factors those contributed 19% to the yield per plant that are not included in the present study could have significant effect on yield per plant.

Table 7. Path analysis showing direct and indirect effects of different characters on yield per plant of thirty two rice genotypes

Traits	FH	FPH	DM	PH	CL	CD	LFL	LP	NETPP	NFGMT	TSW	Genotypic correlation with YP
FH	**-3.200**	3.431	-0.030	0.223	-0.294	0.053	-0.025	0.108	-0.091	0.224	0.140	0.538**
FPH	-3.112	**3.528**	-0.038	0.242	-0.333	0.060	-0.027	0.048	-0.141	0.187	0.115	0.529**
DM	-1.045	1.437	**-0.093**	0.243	-0.079	0.158	-0.069	-0.090	-0.033	0.144	0.030	0.603**
PH	0.763	-0.912	0.024	**-0.936**	0.656	0.004	0.107	0.002	0.038	0.070	-0.042	-0.226*
CL	1.111	-1.387	0.009	-0.725	**0.847**	0.003	0.097	-0.187	-0.017	0.139	0.012	-0.098^{ns}
CD	-0.531	0.668	-0.046	-0.013	0.007	**0.319**	0.030	-0.056	-0.068	-0.014	-0.038	0.258*
LFL	0.303	-0.362	0.024	-0.378	0.309	0.036	**0.266**	-0.093	0.028	0.211	-0.132	0.214*
LP	0.623	-0.303	-0.015	0.003	0.284	0.032	0.044	**-0.557**	-0.135	0.068	-0.041	0.004^{ns}
NETPP	0.538	-0.919	0.006	-0.065	-0.027	-0.040	0.014	0.139	**0.542**	-0.066	-0.087	0.034^{ns}
NFGMT	-1.390	1.283	-0.026	-0.127	0.229	-0.009	0.109	-0.074	-0.069	**0.514**	0.177	0.617**
TSW	-1.457	1.320	-0.009	0.128	0.032	-0.039	-0.114	0.074	-0.153	0.296	**0.308**	0.386**

*= 5% level of significant, **= 1% level of significant, ^{ns}= Non-significant

Residual effect 0.19

FH= 1st heading, FPH= 50% heading, DM= Days to maturity, PH= Plant height (cm), CL= Culm length (cm), CD= Culm diameter (cm), LFL= Length of flag leaf (cm), LP= Length of panicle (cm), NETPP= No. of effective tiller/plant, NFGMT= No. of filled grain of main tiller, TSW= 1000 seed weight (g), YP= Yield/plant (g).

4.5 Genetic Diversity

4.5.1 Principal component analysis

Principal components were computed from the correlation matrix from genotype scores obtained from first components and succeeding components with latent roots greater than the unity. The Principal Components analysis yielded eigen values of each principal component axes of coordination of genotypes in which the first axes accounted 28.17% of the total variation among the genotypes, whereas five of these eigen values above unity accounted for 75.12%. The first four principal axes accounted for 67.14% of the total variation among the 12 characters describing in 32 rice genotypes (Table 6: Principal component analysis in the second, third, fourth and fifth components accounted for 17.12%, 12.34%, 9.51%, and 7.98% of the total variation, respectively. The rest of the components accounted for only 24.88% of the total variation (Table 8). Based on principal component axis I and II, a two-dimensional chart (Z1-Z2) of the genotypes are presented in Figure 1. The scatter diagram (Figure 1) represented that apparently there were mainly four clusters, and the genotypes were distantly located from each other.

4.5.2 Construction of scatter diagram

Based on the values of principal component scores 2 and 1 obtained from the principal component analysis, a two-dimensional (Z1-Z2) scatter diagram was constructed, using component score 1 as X-axis and component score 2 as Y-axis, which is presented in figure 1. The positions of the genotypes in the scatter diagram were random, which indicated the considerable diversity among the genotypes included in the cluster.

Table 8. Eigen values and percent of variation in respect of 12 characters of 32 germplasm of rice genotypes

Principal component axes	Eigen values	Percent variation	Cumulative % of variation
I	3.3798	28.17	28.17
II	2.0546	17.12	45.29
III	1.4811	12.34	57.63
IV	1.1417	9.51	67.14
V	0.9576	7.98	75.12
VI	0.9473	7.89	83.01
VII	0.6483	5.4	88.41
VIII	0.4787	3.99	92.4
IX	0.416	3.47	95.87
X	0.2749	2.29	98.16
XI	0.1993	1.66	99.82
XII	0.0207	0.17	100

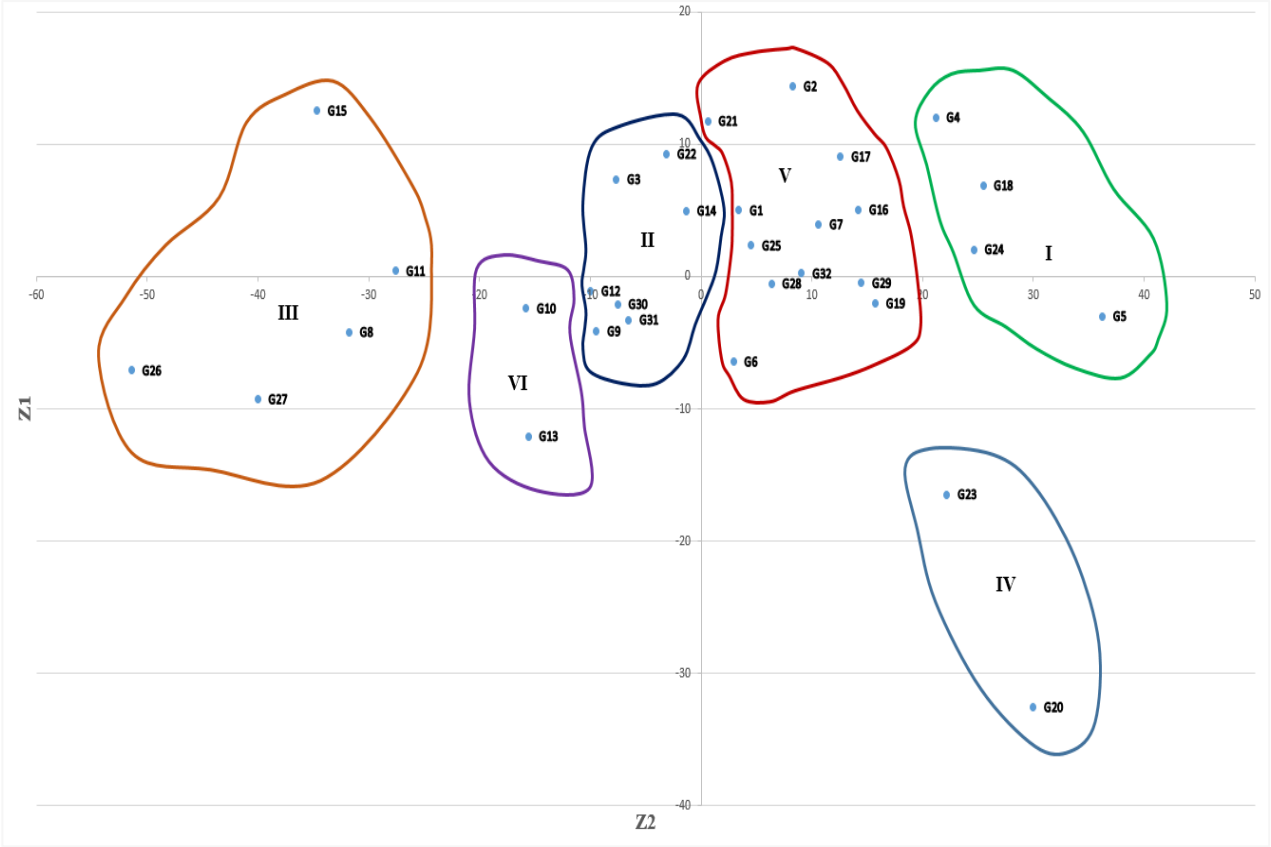


Figure 1. Scatter distribution of 32 rice genotypes based on their principal component scores superimposed with clustering

Table 9. Distribution of 32 rice genotypes in six different clusters with their place of collection

Cluster no.	Genotypes	No. of genotypes
I	G4, G5, G18, G24	4
II	G3, G9, G12, G14, G22, G30, G31	7
III	G8, G11, G15, G26, G27	5
IV	G20, G23	2
V	G1, G2, G6, G7, G16, G17, G19, G21, G25, G28, G29, G32	12
VI	G10, G13	2
Total		**32**

4.5.3 Cluster analysis

The experiment was conducted to investigate the genetic diversity of thirty-two genotypes of rice. The genotypes were divided into six different clusters according to D^2 analysis (Table 9). The cluster V had (G1, G2, G6, G7, G16, G17, G19, G21, G25, G28, G29 and G32) maximum number of genotypes (12) followed by cluster II which had 7 genotypes. Cluster III and I had 5 and 4 genotypes respectively. Remarkably cluster III had five (G8, G11, G15, G26, and G27) and cluster I had four (G4, G5, G18, and G24) genotype. Where, cluster IV and VI carried the lowest number (2) of genotypes. Cluster IV contained (G20, G23) and cluster VI had (G10, G13). Two genotypes each clustering was done at random that indicate a broad genetic base of the genotypes.

4.5.4 Non-hierarchical clustering

By using covariance matrix with the application of Non-hierarchical clustering, the 32 rice genotypes were grouped into six different clusters. These results confined the clustering pattern of the genotype according to the principal component analysis. Compositions of different clusters with their corresponding genotypes in each cluster were presented in Table 8. These results confirmed the clustering pattern of the genotypes according to the principal component analysis. So, the results obtained through PCA were confirmed by non-hierarchical clustering.

4.5.4.1 Cluster I

Cluster I had four genotypes namely G4, G5, G18 and G24 (Table 9). From the clustering mean values (Table 10), it was observed that cluster I produced the highest mean for days to maturity (141.25) followed by no. of filled grain of main tiller (120.81), 50% heading (107.75), first heading (103.5), plant height (92.57) and culm length (68.28).

4.5.4.2 Cluster II

Cluster II was composed of seven genotypes namely G3, G9, G12, G14, G22, G30 and G31 (Table 9). These genotypes produced the highest mean for no. of filled grain of main tiller (151.91) followed by days to maturity (145.05), 50% heading (115.43), 1 heading (110), plant height (103.87) and culm length (68.72).

4.5.4.3 Cluster III

Cluster III consists of five genotypes (G8, G11, G15, G26 and G27) (Table 9). From the clustering mean values (Table 10), it was observed that cluster III produced the highest mean values for no. of filled grain of main tiller (183.32) followed by days to maturity (145.67), 50% heading (113.2), 1st heading (109.8), plant height (102.89) and culm length (69.61).

4.5.4.4 Cluster IV

Cluster IV was constituted of two genotype (G20 and G23) (Table 9). From the clustering mean values (Table 10), it was observed that cluster III produced the highest mean values for no. of filled grain of main tiller (123.12) followed by days to maturity (138), plant height (119.81), 50% heading (98.5), 1st heading (95), and culm length (71.66).

4.5.4.5 Cluster V

Cluster V had maximum number (12) of genotypes namely G1, G2, G6, G7, G16, G17, G19, G21, G25, G28, G29 and G32 (Table 9). From the clustering mean values (Table 10), it was observed that cluster I produced the highest mean for days to maturity (142.36) followed by no. of filled grain of main tiller (138.55), 50% heading (111.33), 1st heading (107.08), plant height (97.02) and culm length(cm) (65.34). The lowest mean value for cluster I (0.47) was the culm diameter.

4.5.4.6 Cluster VI

Cluster VI was composed of two genotypes namely G10 and G13 (Table 9). These genotypes produced the highest mean for no. of filled grain of main tiller (164.6) followed by days to maturity (139.17), 50% heading (105), 1st heading (101), plant height (99.43) and culm length (69.46).

Table 10. Cluster mean of 12 characters of 32 genotypes of rice

Characters	I	II	III	IV	V	VI
FH	103.5	110	109.8	95	107.08	101
FPH	107.75	115.43	113.2	98.5	111.33	105
DM	141.25	145.05	145.67	138	142.36	139.17
PH	92.57	103.87	102.89	119.81	97.02	99.43
CL	68.28	68.72	69.61	71.66	65.34	69.46
CD	0.44	0.49	0.46	0.48	0.47	0.46
LFL	24.15	25.14	25.33	25.53	23.85	24.86
LP	23.85	24.33	23.76	23.48	23.76	24.58
NETPP	10.88	9.91	10.28	11.57	9.37	9.9
NFGMT	120.81	151.91	183.32	123.12	138.55	164.6
TSW	22.83	23.68	25.79	19.58	23.24	22.44
YP	22.82	28.18	28.83	17.48	23.15	24.44

*= 5% level of significant **= 1% level of significant ^{ns}, Non-significant

FH= 1st heading, FPH= 50% heading, DM= Days to maturity, PH= Plant height (cm), CL= Culm length (cm), CD= Culm diameter (cm), LFL= Length of flag leaf (cm), LP= Length of panicle (cm), NETPP= No. of effective tiller/plant, NFGMT= No. of filled grain of main tiller, TSW= 1000 seed weight (g), YP= Yield/plant (g).

4.5.5 Principal coordinate analysis

Principal coordinate analysis (PCA) was estimated on auxiliary principal component analysis. This analysis helps in estimating distances. PCA indicated that the highest inter genotypes distance (0.999) was observed between the rice genotypes G15 and G20 followed by (0.983) between the genotypes G20 and G26. The tenth highest pair distance was (0.808) observed between G3 and G20. The lowest distance (0.137) was observed between the genotypes G1 and G6 followed by (0.144). The tenth lowest distance (0.185) was showed between the genotypes G9 and G10. The difference between the highest and the lowest inter-genotypes distance indicated the prevalence of variability among the 32 genotypes of rice (Table 9).The hybrids of genotypes with maximum distance resulted in high yield and the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. The maximum intra-cluster distance was presented in cluster IV (0.367) which had two genotypes (G20 and G23). The minimum intra-cluster distance was recorded in cluster IV (0.259**)** which containing two genotypes (G10 and G13).

4.5.6 Canonical variate analysis

Conical variate analysis (CVA) was done to identify the inter-cluster distance. (Table 12) were presented intra and inter-cluster distance (D^2) values. In this experiment the inter-cluster distances were higher from intra-cluster distances. It showed that the wide range of genetic variability among genotypes of rice. The intra and inter clusters D^2 values among 32 genotypes presented in Table 12 revealed that cluster VI showed minimum intra cluster D^2 value (0.259) distance whereas, maximum intra cluster D^2 value (0.367) was shown by cluster IV followed by cluster III (0.361) indicated that genotypes included in this cluster are very diverse and was due to both natural and artificial selection forces among the genotypes. Minimum inter cluster D^2 value was observed between the clusters II and VI (1.486) indicated close relationship among the genotypes included in these clusters. Maximum inter-clusters D^2 value was observed between the clusters III and IV (13.985) indicated that the genotypes belongings to these groups were genetically most divergent and the genotypes included in these clusters can be used as a parent in hybridization program to get higher heterotic hybrids from the segregant population. Several authors also reported profound diversity in the germplasm of rice by assessing genetic divergence on the

Table 11. Ten highest and ten lowest inter genotypic distance of 32 genotypes of rice

Highest Distance			Lowest Distance		
Genotypes		Distance	Genotypes		Distance
G15	G20	0.999	G1	G6	0.137
G20	G26	0.983	G6	G32	0.144
G20	G27	0.917	G1	G28	0.144
G20	G22	0.900	G28	G31	0.175
G17	G20	0.872	G1	G32	0.176
G11	G20	0.844	G19	G28	0.178
G9	G20	0.829	G28	G32	0.179
G20	G21	0.819	G1	G31	0.180
G14	G20	0.809	G6	G28	0.184
G3	G20	0.808	G9	G10	0.185

basis of quantitative traits following Mahalanobis D^2 statistics (Ovung *et al*. 2012,Thomas and Lal 2012 and Chakrovorty *et al*. 2013).

Average inter and intra-cluster distance revealed that inter-cluster distance were much higher than those of intra-cluster distances, suggesting homogenous and heterogeneous nature of the germplasm lines within and between the clusters, respectively. These results are in accordance with the findings of Ovung *et al*. (2012). Results obtained from different multivariate techniques from which it may be concluded that all the techniques gave more or less similar results and one technique supplemented and confirmed the results of another one. The clustering pattern of the genotypes revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. This indicated that geographic diversity was not related to genetic diversity that might be due to continuous exchange of genetic materials among the countries of the world. Same results have been reported by Murty and Anand (1966); Anand and Rawat (1984) in brown mustard; Patel *et al*. (1989) in sunflower; Verma (1970) in groundnut and soybean.

It had been observed that geographic diversity was not always related to genetic diversity and therefore, it was not adequate as an index of genetic diversity. Murty and Arunachalam (1966) studied that genetic drift and selection in different environment could cause greater diversity than geographic distance. Furthermore, there was a free exchange of seed material among different region, as a consequence, the character's constellation that might be associated with particular region in nature, lose their individually under human interference, and however, in some cases effect of geographic origin influenced clustering that was why geographic distribution was not the sole criterion of genetic diversity. The free clustering of the genotypes suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favor constancy of the associated characters would thus indiscriminate clustering. This would be suggested that it was not necessary to choose diverse parents for diverse geographic regions for hybridization.

Table 12. Intra (Bold) and inter cluster distances (D^2) for 32 genotypes of rice

	I	II	III	IV	V	VI
I	**0.312**					
II	7.700	**0.261**				
III	13.979	6.393	**0.361**			
IV	7.567	8.504	13.985	**0.367**		
V	4.603	3.803	9.599	8.791	**0.303**	
VI	8.877	1.486	5.103	9.950	4.591	**0.259**

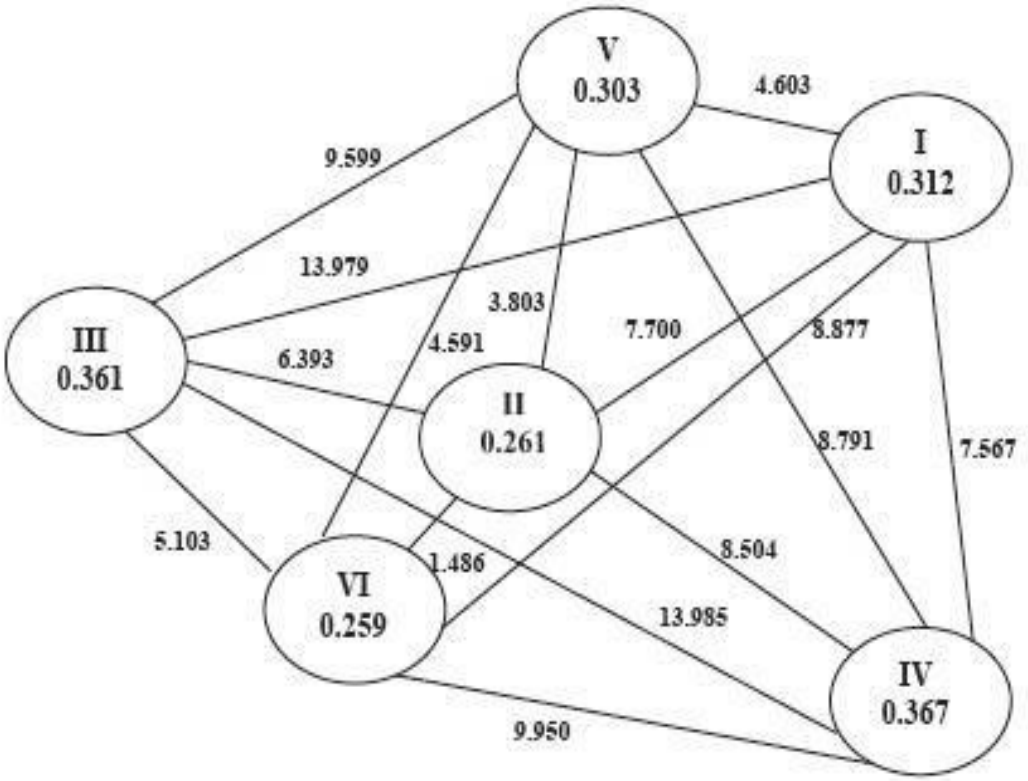


Figure 2. Figure showing cluster distances among cluster

Table 13. Latent vectors of 12 characters of 32 genotypes of rice

Characters	Vector 1	Vector 2
FH	-0.1864	0.6257
FPH	0.1163	-0.4678
DM	-0.0089	-0.0311
PH	-0.0759	-0.1892
CL	0.018	-0.1133
CD	-3.8957	-5.1667
LFL	0.2088	-0.3135
LP	0.3214	0.5362
NETPP	0.0766	-0.6169
NFGMT	-0.1976	0.0066
TSW	0.0096	-0.1209
YP	-0.0626	0.014

4.5.7 Contribution of characters towards divergence of the cultivars

For deciding on the cluster for the purpose of further selection and choice of parents for hybridization the character contributing maximum to the divergence were given greater emphasis (Jagadev *et al*. 1991). The PCA revealed that in vector I (Z1) the important characters responsible for genetic divergence in the major axis of differentiation were 50% heading, culm length, length of flag leaf, length of panicleno. of effective tiller/plant and 1000 seed weight. In vector II (Z2) that was the second axis of differentiation were 1st heading, length of panicle, no. of filled grain of main tiller, yield/plant were important. The role of length of panicle in both the vectors was positive across two axes indicating the important component of genetic divergence in those materials (Table 13).

4.5.8 Comparison of different multivariate techniques

The cluster pattern of D^2 analysis though non-hierarchical clustering has taken care of simultaneous variation in all the character under study. However, the distribution of genotypes in different cluster of the D^2 analysis has followed more or less similar trend of Principal component analysis were found to be alternative methods in giving the information regarding the clustering pattern of genotypes. However, the Principal component analysis provides the information regarding the contribution of characters towards divergence of rice genotypes.

4.5.9 Selection of genotypes for future hybridization

Genotypically distant parents were able to produce higher heterosis (Falconer, 1960; Moll *et al.* 1962; Ramanujam *et al.* 1974; Chauhan and Singh, 1982; Arunachalam 1981; Ghaderi *et al*. 1984; Mian and Bhal, 1989). Beside this, Arunachalam (1981) reported in groundnut that the higher heterosis for yield and its components could be obtained from the crosses between the intermediate divergent parents than extreme ones. Mian and Bahl (1989) also reported the same in chickpea that medium divergent genotypes showed higher heterosis in crosses for different yield contributing characters. Considering this idea and other agronomic performances, G15, G26 and G27 for yield per plant from cluster III; G20 for earliness from cluster IV might be considered better parents for efficient hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was undertaken to evaluate a set of genotypes for variability in morphological characters, extent of character association and genetic diversity to find out the variability regarding yield and some yield contributing characters, the degrees of association among the characters under study and their indirect and direct effects. The material for this study comprised of 32 rice genotypes at the experimental plot of Sher-E-Bangla Agricultural University farm, Dhaka, during November 2018 to March 2019.The experiment was laid out in randomized complete block design with three replications. The 1st heading, 50% heading, days to maturity, plant height, culm length, culm diameter, length of flag leaf, length of panicle, length of penultimate leaf, no. of primary branches/panicle, no. of secondary branches/panicle, total no. of tiller/plant, no. of effective tiller/plant, no. of non-effective tiller/plant, no. of filled grain of main tiller, no. of unfilled grain of main tiller, 1000 seed weight, and yield/plant, were recorded. The most important findings of the present study have been summarized on the basis of the characters under study.

The highest first heading was recorded in G3 (114 days) whereas the minimum first heading was recorded in G20 (94 days). The 50% heading was maximum in G3 (120 days) and minimum was observed in G20 (96 days). The days to maturity were highest in G15 (161.33 days) and lowest was observed in G20 (127.67 days). The plant height was maximum in G20 (123.28 cm) and minimum was observed in G2 (87.39 cm). The culm length was maximum in G20 (72.510 cm) and minimum was observed in G2 (55.52 cm). The culm diameter was maximum in G3 (0.60 cm) and minimum was observed in G20 (0.380 cm). The length of flag leaf was maximum in G26 (27.98cm) and minimum was observed in G7 (19.363 cm). The length of panicle (cm) was maximum in G13 (25.65 cm) and minimum was observed in G11 (20.58 cm). The length of penultimate leaf was maximum in G26 (40.73 cm) and minimum was observed in G1 (32.11 cm). The no. of primary branches/panicle was maximum in G1 (12.27) and minimum was observed in G24 (6.50). The no. of secondary branches/panicle was maximum in G26 (36.27) and minimum was observed in G24 (22.67). The total no. of tiller/plant was maximum in G20 (13.27) and minimum was observed in G29 (8.27). The no. of effective tiller/plant was maximum in G24 (13.64) and minimum was observed in G16 (6.90). The no. of non-effective tiller/plant was

maximum in G20 (1.13) and minimum was observed in G8 (0.30). The no. of filled grain of main tiller was maximum in G26 (198.67) and minimum was observed in G5 (112.23). The no. of unfilled grain of main tiller was maximum in G1 (25.07) and minimum was observed in G16 (13.70). The 1000 seed weight was maximum in G27 (30.33 g) and minimum was observed in G23 (19.33 g). The yield/plant was maximum in G15 (33.01 g) and minimum was observed in G20 (15 g).

The phenotypic variance was higher than genotypic variance in all the characters under study. Phenotypic coefficients of variation were also near to genotypic coefficients of variation for all the characters under study. The high heritability coupled with high genetic advance didn't observe in any character. Heritability coupled with low genetic advance was found in culm diameter and 1000 seed weight. Low heritability and low genetic advance was observed in culm length, length of panicle, length of penultimate leaf, no. of primary branches/panicle, no. of secondary branches/panicle, total no. of tiller/plant, no. of non-effective tiller/plant and no. of unfilled grain of main tiller.

Correlation revealed that highly significant positive association of seed yield per plant with 1st heading, 50% heading, days to maturity, culm diameter, length of flag leaf, no. of filled grain of main tiller and 1000 seed weight at both genotypic and phenotypic level. Genotypic correlation coefficients were larger in values as compared to their respective phenotypic correlation coefficient. This indicates greater contribution of genetic factor in the development of the association.

The path coefficient analysis revealed the positive direct effect on yield per plant by 50% heading, culm length, culm diameter, length of flag leaf, no. of effective tiller/plant and no. of filled grain of main tiller and 1000 seed weight.

Multivariate analysis was performed through Principal component analysis, Principal coordinate analysis, Cluster analysis and canonical variety analysis. The PCA showed 75.12% variation against first five values. Based on the PCA, D^2 and cluster analysis thirty-two genotypes were grouped into six different clusters.

The highest intra cluster distance was estimated for cluster IV (0.367) consisted of 2 genotypes followed by cluster III (0.361) consisted of 5 genotypes, cluster I (0.312) consisted of 4 genotypes, cluster V (0.303) consisted of 12 genotypes cluster II (0.261) consisted of 7 genotypes and cluster VI (0.259) consisted of 2 genotypes.

The highest inter cluster distance was observed between cluster III and cluster IV (13.985) followed by cluster I and cluster III (13.979), whereas distance was minimum between cluster II and cluster VI (1.486).

Cluster I showed maximum performance for no. of effective tiller/plant (13.64). Cluster II showed maximum performance for 1st heading (114.00), 50% heading (120) and culm diameter (0.60). Cluster III recorded highest mean performance for days to maturity (161.33), length of flag leaf (27.98), no. of filled grain of main tiller (198.67), 1000 seed weight (30.33) and yield/plant (33.01). Cluster IV showed maximum performance for plant height (123.28) and Culm length (72.51). Cluster V did not show maximum performance for any character. Cluster VI showed maximum performance for length of panicle (25.65).

Considering the degree of variability, heritability, genetic advance in percent of mean, correlation with grain yield, path analysis, magnitude of distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and performance, the genotypes G15, G26 and G27 for yield per plant from cluster III; G20 for earliness from cluster IV might be considered better parents for efficient hybridization program.

CHAPTER VI

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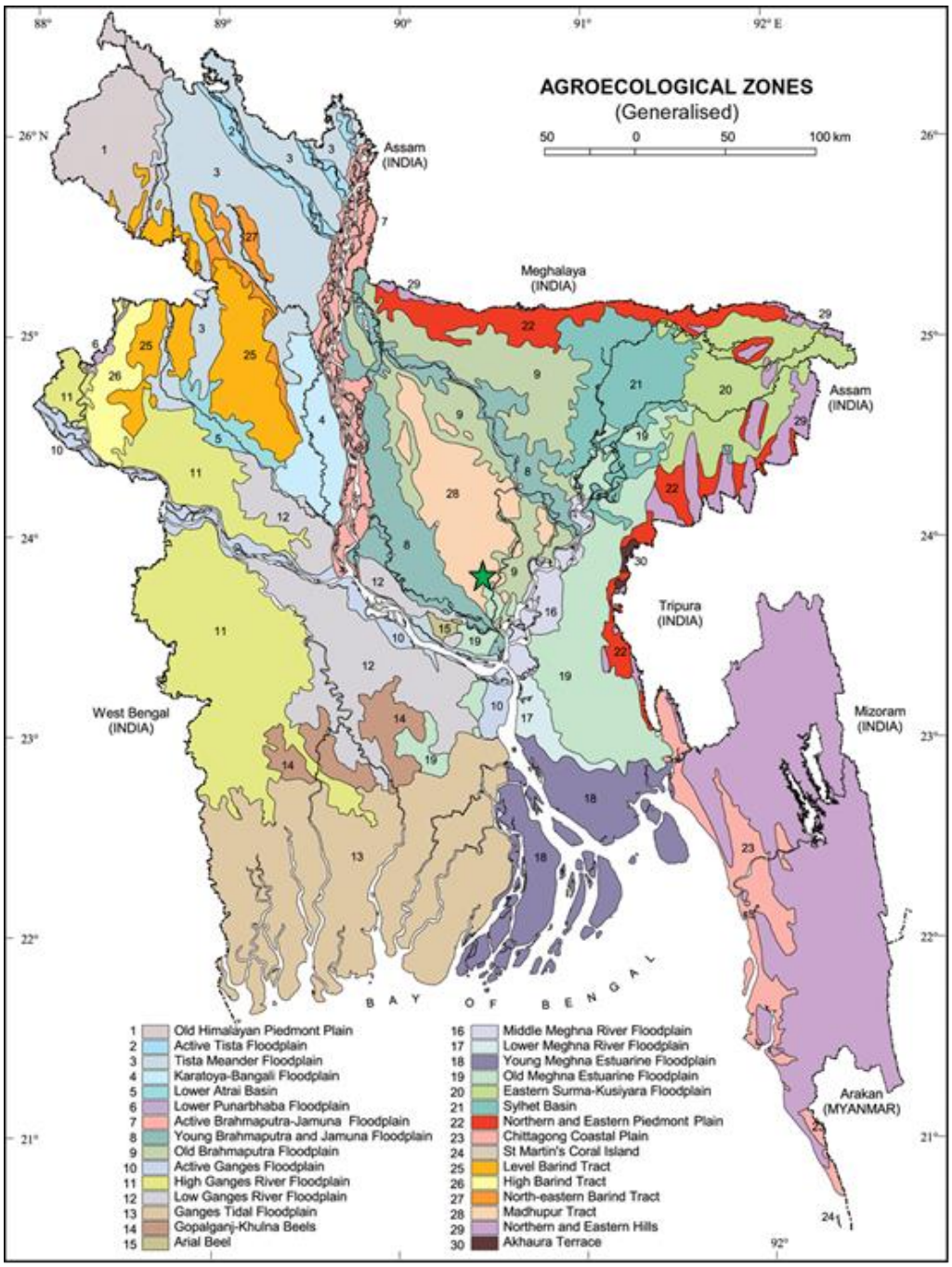
APPENDICES

Appendix I. Map showing the experimental site under the study



Appendix II. Morphological, physical and chemical characteristics of initial soil (0- 15 cm depth) of the experimental site

A. Morphological characteristics of the experimental field

Morphological features	**Characteristics**
Location	Sher-e-Bangla Agricultural University Research Farm, Dhaka
AEZ	AEZ-28, Modhupur Tract
General Soil Type	Deep Red Brown Terrace Soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled

B. Physical composition of the soil

Soil separates	**%**	**Methods employed**
Sand	26	Hydrometer method (Day, 1915)
Silt	45	Do
Clay	29	Do
Texture class	Silty loam	Do

Appendix II. (Cont'd)

C. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.45	Walkley and Black, 1947
2	Total N (%)	0.03	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (ppm)	20.54	Olsen and Dean, 1965
7	Exchangeable K (me/100 g soil)	0.10	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.6	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Soil Resource and Development Institute (SRDI), Farmgate, Dhaka

Appendix III. Monthly records of air temperature, relative humidity, rainfall and sunshine hours during the period from January 2019 to October 2020

Monthly & Yearly Average Humidity (%):

Year	Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.	Sep.	Oct.	Nov.	Dec.	Annual
2019	59	63	61	69	73	78	82	79	80	78	74	74	72
2020	76	59	57	72	80	81	85	84	81	81			

Source: Bangladesh Meteorological Department Climate Division, Agargaon, Dhaka-1207

Monthly average Sea Level Pressure (milliber):

Index	Year	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.
11111	2019	1015.4	1013.7	1010.8	1007.7	1004.4	1001.2	1000.4	1000.7	1006.2	1010.1	1011.5	1015.2
11111	2020	1014.7	1014.5	1010.7	1008.9	1005	1002.1	1002.1	1000.4	1003.9	1006		

Source: Bangladesh Meteorological Department Climate Division, Agargaon, Dhaka-1207

Monthly & Yearly Total Rainfall (mm):

Year	Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.	Spt.	Oct.	Nov.	Dec.	Annual
2019	1	115	39	212	231	242	383	223	161	188	37	5	1837
2020	21	1	30	127	301	271	404	285	140	300			

Source: Bangladesh Meteorological Department Climate Division, Agargaon, Dhaka-1207

Monthly average Dry-bulb Temperature (degree Celsius)

Index	Year	Jan.	Feb.	Mar.	Apr.	May	June	July	Aug.	Sep.	Oct.	Nov.	Dec.
11111	2019	20.2	22	26	28.3	29.8	29.9	29.3	29.9	29.1	27.6	24.9	19.3
11111	2020	18.5	21.6	26.4	27.9	28.7	29.5	29.4	29.5	29.6	28.8		

Source: Bangladesh Meteorological Department Climate Division, Agargaon, Dhaka-1207

Month	Year	Monthly average air temperature (^{o}C)			Average relative humidity (%)	Total rainfall (mm)	Total sunshine (hours)
		Maximum	Minimum	Mean			
Nov	2019	31	18	24	63	Trace	216.4
Dec	2019	27.12	11.56	19.34	61	Trace	212.50
Jan.	2020	28	10	14	65	Trace	212.50
Feb	2020	32	12	22	73.23	4.0	195.00
Mar.	2020	34	16	25	67.23	4.5	225.50

Source: Bangladesh Meteorological Department (Climate division), Agargaon, Dhaka-1212.