VARIABILITY AND INTERRELATIONSHIP AMONG VARIOUS TRAITS OF AROMATIC RICE LAND RACES

BY

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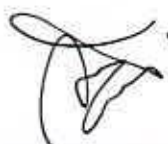for the degree of

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CERTIFICATE

This is to certify that thesis entitled, " **Variability and interrelationship among various traits of aromatic rice land races"** 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 **HELENA AKTAR HAPPY,** Registration No. **09-03461**under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2015
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ABSTRACT

The experiment was conducted at the experimental field of Sher-E-Bangla Agricultural University, Dhaka with 30 aromatic rice land races to study thegenetic varibility, diversity and association of correlation during June 2014 to February 2015. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Analysis of variance revealed significant differences among the genotypes for all the characters studied. Highest grain yield was observed by the thirty genotypes (G1 to G30) followed by G8 and G29. High estimates of GCV and PCV were observed in flag leaf length, secondary branches per panicle, filled grain per panicle, total grain per panicle, thousand grain weight and grain yield per plant. High heritability along with high GA as percent of mean was observed in flag leaf length, secondary branches per panicle, filled grain per panicle, total grain per panicle, thousand grain weight and grain yield per plant.The genotypes were grouped into five clusters.In (figure 9) Cluster IV contained the highest 10 genotypes and the cluster V contained the lowest (1). The highest inter-cluster distance was observed between clusters I and IV (table 10) indicating genotypes from these two clusters are diverse, if involved in hybridization might produce a wide spectrum of segregating population while the lowest inter-cluster distance was observed between cluster II and III.Correlation coefficients among the characters were studied to determine the association between yield and yield components. The significant positive correlations of grain yield per plant were found with effective tillers per hill, filled grain per panicle, total grains per panicle and thousand grain weight in both genotypic and phenotypic level suggesting that genotypes with high partitioning efficiency gave increase in grain yield per plant.Path coefficient analysis revealed that filled grain per panicle, thousand grain weight, secondary branches per panicle, panicle length andclum length had the greatest direct contribution on grain yield.Considering group distance and other agronomic performance genotypes G21, G30, G27, G11, G7, G5, G10 and G12 could be used as open pollinated aromatic rice varities and could be used as parents in future hybridization program.

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LIST OF ABBREVIATED TERMS

Full word	Abbreviation
Percent	%
Degree Celsius	^{0}C
At the rate	@
Phenotypic variance	σ^2_p
Genotypic variance	σ^2_g
Environmental variance	σ^2_e
Heritability in broad sense	h^2_b
Agro Ecological Zone	AEZ
Agriculture	Agric.
Agricultural	Agril.
Agronomy	Agron.
Analysis of variance	Anova
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh	BD
Centimeter	cm
Percentage of Coefficient of Variation	CV%
Cultivars	cv.
Degrees of Freedom	Df
And others	*et al.*
Etcetera	etc.
The third generation of a cross between two dissimilar homozygous parents	F_3
Food and Agricultural Organization	FAO
Gram	g
Genotype	G
Genetic Advance	GA
Genotypic coefficient of varioantion	GCV
Harvst Index	HI
Indian Agricultural Research Institute	IARI
International Center for Agricultural Research in Dry Areas	ICARDA
Journal	J.
Kilogram	kg
Meter	m

LIST OF ABBREVIATED TERMS (*Continued...*)

Abbreviation	Full word
MS	Mean sum of square
MP	Murate of Potash
MOA	Ministry of Agriculture
m^2	Square meter
PCV	Phenotypic coefficient of variantion
RCBD	Randomized Complete Block Design
SAU	Sher-e-BnaglaAgicultural University
TSP	Triple Super Phosphate

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L.) belongs to the grass family named Grameneae (Poaceae). Its chromosome number is 24 in diploid condition. The genome of rice was well mapped and well characterized (Eckardt, 2000). The genome size of indica rice is 420 Mb and contains between 32,000 and 50,000 genes. The japonica genome is larger (466 Mb) and contains around 46,022-55,615 genes (Yu, 2002). Rice has smallest genome size among the cereal crops (Khush, 1997). So its genome is one of the imperative tools to the breeders for its varietal improvement.

Rice occupies the unique position in many nations because of its importance in traditional diets and the main source of income of many people in the world. Among the most cultivated cereals in the world, rice ranks second to wheat (Abodolereza and Racionzer, 2009) and shares equal importance as leading food source for humankind. Rice is a staple food for nearly one-half of the world's population (FAO, 2011; Garris *et al.*, 2005). It is intimately associated with tradition, culture and customs of Bangladesh. Among the rice growing countries of the world, Bangladesh is ranked third in respect of growing area and fourth in production (Huke and Huke, 1999).

The global production of rice is 650 million tones and the area under rice cultivation is 156 million hectares (FAOSTAT, 2008).Bangladesh produced 33.54 million metric tons of rice in 11.52 million hectares of land and total demand is 37.2 million metric tons (BBS, 2012). At present,cropping intensity is 191% (BBS, 2012). Therefore, to fill up the gap between production and demand, we need to increase cropping intensity nearly 300% (Sarker *et al.*, 2014).

For the people of Asia in particular, rice serves as the main source of calories and it creates the field of income and employment (Janaiah, 1997). It provides 40% of the calorie requirement of the of the world's population and almost 80% for the people of some Asian countries (Bhattacharjee *et al.*, 2002). Basically, it is associated with the economic development of the Asian sub-continent. In our country, rice has furnished our culture,society

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even our civilization. Nowadays, the consumption, cultivation, marketing and trading of rice is altering faster than ever before.

Bangladesh is mainly a rice growing country and some of arable lands are used only for rice cultivation here. In Bangladesh, it is grown in three seasons named Aus, Aman and Boro. Though Aman season provides lower yield than Boro season, huge arable lands are utilized under Aman rice cultivation in our country. But nowadays, we are losing huge amount of cultivable land every year for infrastructure and accommodation for ever-growing population. Different Aman rice varieties have already been developed. Many plans have already been taken for further development by different national organizations.

Yield is a complex polygenic character which is controlled by many genes and influenced by the components of its characters. Therefore, direct genome application for yield may often misleaded (Selvaraj *et al.*, 2011). One point should be considered that yield in rice is correlated with different yield contributing traits as well as environmental factors (Yousida, 1983). So, common objective of a rice breeder should be based upon the successive intimacy of yield.

Information on the nature and magnitude of variability present in the existing material and association among the various morphological characters is a pre-requisite for any breeding programme to be initiated by the local breeder for high yields. However, seed yield, a complex character is usually controlled by non-additive gene actions and it is not only influenced by a number of other morphological characters which are governed by a large numbers of genes, but also environment to a great extent. Thereby, the heritable variation creates difficulty in a selection programme. Therefore, it is necessary to partition the overall variability into heritable and non-heritable components which enables the breeders to adopt suitable breeding procedure for further improvement of genetic stocks.

A plant breeding program can be divided into three steps viz. building up a gene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior genotype (Chauhan and Singh, 1985). The knowledge of genetic variability present in the population, heritability of economically important characters and correlation coefficients of those characters is very important before launching an effective breeding program.

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There is plenty of scope in rice to increase yield per unit of area through breeding superior varieties. Information on genetic variability and character association is a prerequisite for initiating a successful breeding program aiming to develop high yielding varieties.

Landraces, also known as local populations, traditional cultivars, or farmers varieties, provide a valuable resource for plant breeding as well as for the preservation of genetic diversity. Landraces have been shown to be excellent sources of genes for novel alleles. (McCouch et al., 1997; Hoisington et al., 1999). They are precious genetic resources, because they contain huge genetic variability which can be used to complement and broaden the gene pool of advanced genotypes.

The extent of genetic diversity in a crop population depends on recombination, mutation, selection and random genetic drift. Mutation and recombination bring new variations to a population, whereas selection and genetic drift remove some alleles, often from agronomically important lines. The use of adapted rice landraces, as the primary source of variation into which desired characters present in modern cultivars are introgressed may be an effective strategy for producing cultivars adapted to difficult production environments.

The demand for productivity and homogeneity in crops has resulted in a limited number of standard, high-yielding varieties and a loss of heterogeneous traditional local varieties (landraces), a process known as genetic erosion. Landraces and older crop varieties preserve much of this lost diversity and comprise the genetic resources for breeding new crop varieties to cope with environmental and demographic changes (Zhu et al., 2004).

Rice landraces, maintained through traditional farming practices, possess high genetic diversity and specific traits such as disease resistance, environmental constraint tolerance and nutritional quality which are often used in crop improvement (Camacho-Villa *et al.*, 2005). Furthermore, landraces are adapted to local agro-environmental conditions which contributes to yield stability and hence, they continue playing an important role in traditional and subsistence farming (Camacho-Villa *et al.*, 2005).Thus, landraces of rice play a very important role in the local food security and sustainable development of agriculture.

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The association among different traits can be evaluated by correlation analysis (Akhtar *et al.*, 2011). Generally, relationship between grain yield and different yield contributing characters establishes a complex chain, which can be further analyzed in more simple way through path co-efficient (Mohsin *et al.*, 2009). Path co-efficient helps to partition the correlation of co-efficient of the yield within its contributing traits into direct and indirect effects (Ahmadizadeh *et al.*, 2011). Such analysis can explain the real cause of relationship (Ganapathy *et al.*, 1994). Often undesirable characters have negative impacts on desirable characters. Therefore, selection of desirable traits and elimination of undesirable traits is essential for a successful breeding program. In this aspect, discriminant function based on desirable characters for selection has been proven to be very useful to eliminate undesirable genotypes on the basis of their performance (Kempthorne and Nordskog, 1959). The technique of discriminant function was developed by Fisher (1936). It was adopted for selection by Smith (1936), which opened a supreme dimension in plant breeding. Nowadays, Molecular markers have been used extensively to evaluate the degree of genetic diversity in most species (Islam *et al.*, 2007).

Genetic diversity is the basic for genetic improvement. It is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding ((Mukhtar *et al.*, 2002 and Khaleque, 1985). Genetic diversity is very important factor for any hybridization program aiming at genetic improvement of yield especially in self pollinated crops (Joshi and Dhawan, 1966). Different methods have been used to assess genetic diversity. This can be obtained from pedigree analysis, morphological traits or using molecular markers. With the development of advanced biometrical method such as multivariate analysis (Rao, 1952) based on Mahalanobis' (1936) D^2 statistics and Ward's no-hierarchical squared Euclidean distance method have become possible to quantity magnitude of diversity among germplasm for their evaluation in respect of breeding program.

Keeping these in mind, this research was undertaken with following objectives:

 ➤ To study the variability of important quantitative and qualitative characters of aromatic rice land races;
 ➤ To study the interrelationships of yield contributing characters among themselves and with yield; and their direct and indirect effects;
 ➤ To assess the contribution of different traits towards divergence; and
 ➤ To select promising genotypes considering high yield.

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CHAPTER II

REVIEW OF LITURATURE

Rice is an important cereal crop and widely cultivated both in tropical and sub-tropical regions of the world. Identification of suitable land race based on their genetic parameters, nature and magnitude of genetic variability, diversity and the correlation of different yield attributing characters are important for successful rice breeding programs. Thosecriteria create the opportunities for a successful breeding program by theassociation of different traits. On that point of view, this experiment was conducted for development ofgenotypes considering yield and related characters in thirty aromatic rice land races.In this chapter, an attempt has been taken to review the relevant literatures, whichfocuses the basic features of rice plant and associated genetic variability, natureand magnitude of genetic divergence, association among different traits; and cause and effect analysis in riceunder the following subheads:

2.1 Rice as crop plant

2.2 Genetic variability, heritability and genetic advance

2.3 Correlation among different characters

2.4 Path Co-efficient analysis

2.5 Genetic Diversity analysis

2.1 Rice as crop plant

Rice (*Oryza sativa*) belongs to the family Gramineae. It serves as the staple diet ofabout half of the world's population. Globally 156 million hectares of land areused to produce 650 million tons of rice (FAOSTAT, 2008). Ninety percent ofworld's rice produced in Asia. This sub-continent has a long historyof rice cultivation. Among the rice growing countries of the world, Bangladeshranked third in respect of growing area and fourth in production (Huke andHuke, 1999). The country produced 33.54 million metric tons rice in 11.52 millionhectares of land (BBS, 2012).

2.1.1 Taxonomy
Rice is a member of the grass family (Gramineae) and belongs to the genus *Oryza*under tribe Oryzeae. The genus *Oryza*has 25 recognized species, in which 23 arewild species and two are cultivated species; *O. glaberrima*Steud and *O. sativa* L.African rice (*O. glaberrima*Steud.) is

confined to West Africa, whereas common orAsian rice (*O. sativa* L.) is now commercially grown in 112 countries, covering allcontinents (Bertin*et al.*, 1971). It is widely grown in Asia, North and South America, Europe, Middle Eastand Africa. However, *O. glaberrima*is grown in West African countries. Biologicaltaxonomy of rice is given below.

Taxonomy of rice:

Name: Rice

Kingdom: Plantae

Division: Magnoliophyta

Class: Liliopsida

Order: Poales

Family: Gramineae (Poaceae)

Tribe: Oryzeae

Genus: *Oryza*

Species: *Sativa*

2.1.2 Origin

The origin and evolution of rice was long masked by desperate postulation of thedifferent postulers because of the pantropical but disjunct distribution of the 20wild species across four continents, different naming and variations incharacterizing specimens and the traditional disputation concerning the relativeantiquity of rice (XU *et al.*, 1998). More than 100 million years ago, during theCretaceous Period, Gondwana divided into land masses and Africa, SouthAmerica, Australia and India were evolved separately from those masses. Early*Oryza*species were present in Gondwana. It seems that variation generated inGondwana rice and several wild rice had evolved. Then those wild species aredifferentiated into several cultivated species (www.nics.go.kr). That's the reason ofscattering rice species across the continents. Scientists, researchers and archaeologistscame to an agreement about the centre of origin and centers of diversity of two cultivatedspecies- *O. sativa* and *O. glaberrima*by observing and following the genetic diversity,historical and archaeological evidences. River valleys of Yangtze, Mekonriver could suppose to be the primary centers of origin of *O. sativa* while Delta of Niger river in Africa was the primary centers of origin of *O. glaberrima*(Porteres, 1956: OECD,1999).

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2.1.3 Evolution and Geographic distribution

It is generally agreed that *O. sativa* and *O. glaberrima*evolved independently fromtwo different progenitors, viz., *O. nivara*and *O. barthii*. *O. nivara*is believed to bedomesticated in South or South East Asia. *O. barthii*is domesticated in tropicalWest Africa. The progenitors of *O. sativa* are considered to have the Asian AAgenome and *O. glaberrima*to have African AA genome. *The genus Oryza*is splittedinto two groups, viz.-*O. sativa* complex and *O. officinalis*complex(www.nhm.ac.uk). *O. sativa* and *O. glaberrima*and their wild relatives are in thefirst complex. Those are very closely related diploid species. Those concepts werereviewed by Chang, 1976; Siddiq and Viraktamath, 2001 and NBPGR, 2006.

Table 1 Table Showing major rice types and their derivatives (www.nhm.ac.uk)

Rice type	Wild perennial	Wild annual	Cultivated annual
Asian	*O. rufipogon*	*O. nivara*	*O. sativa*
African	*O. longistaminata*	*O. barthii*	*O. glabrrima*

Domestication of Asian rice *O. sativa* is considered to have occurred in 7,000 BC(OECD, 1999). Domestication may had occurred independently at about sametime in many places along a broad belt extending from the Ganges Plains belowthe Himalayas, across northern Burma, northern Thailand, Laos and Vietnam toSouth west and South China (Chang, 1976). Then It has spread and diversified.Two ecological groups, Indica and Japonica (Oka, 1988) were evolved eventually.There are other studies indicating that the two groups were derivedindependently from the domestication of two divergents wild rice in China andIndia respectively (Second, 1982; 1986).

2.2 Genetic variability, heritability and genetic advance

Information on genetic variation, heritability and expected genetic advance of different characters of a set of aromatic rice populations is important because these genetic parameters are reported to be influenced by growing environmental conditions. As a matter of fact different workers reported various magnitude of the extent of genetic variation, heritability and genetic advance for the same character. In the present study these genetic parameters were estimated in aromatic rice and the information would be helpful for breeding programs.

2.2 Genetic variability, heritability and genetic advance

2.2.1 Genetic variability

Total variability is a metric trait which is divided into genotypic variability and phenotypic variability. The assessment of genetic variability for yield and its components is a pre-requisite for improvement of the crop to the desired level. Genotypic variability comprises both additive and non-additive variance heritability in broad sense was proposed by Robinson *et al.* (1949); as the ratio of genetic variance to the total variance, while the narrow sense heritability has been defined as the ratio of additive variance to the total (Singh and Chaudhary (1985).

The genetic gain that can be expressed for a particular character through selection is the product of its heritability, phenotypic standard deviation (sp) and selection differential was proposed by Burton (1952). Though, heritability value indicates the relative effectiveness of selection based on phenotypic expression of a trait, the genetic advance is more useful in predicting the actual value of selection as shown by Johnson *et al.* (1955).

Genetic variability refers to the potentiality for a given characteristic or genotype tovary within a population. If a population lacks sufficient genetic variability, it alsolacks the potential to evolve and adapt. Adequate variability also increases fitness.High degree of variability in a plant population leads the opportunities to selectthe desirable plant (Bhuiya, 2006).

Studied on 150 genotypes including five check varieties of rice with 11 characters and found significant differences were observed for all the characters except leaf width and 100-seed weight among the genotypes. GCV and PCV were high for all the characters except days to 50% flowering and panicle length (Padmaja*et al.*, 2008).

Studied on 60 NERICA varieties & 18 promising lines for 23 agromorphological trait. The analysis of variance showed highly significant differences (P<0.0001) between the variables and revealed the structure of the different genotypes from eleven quantitative discriminate traits (Moukoumbi*et al.*, 2011).

Subbaiah*et al.* (2011) were conducted experiment on 16 parents and 48 hybrids with nine yield and its component and 25 quality characters and revealed that the magnitude of difference between PCV and GCV was relatively low for all the traits, indicating less environmental influence.

The discrepancy among the genotypes was found to be highly significant for all traits reported by Yaqoob*et al.* (2012) on ten rice genotypes with yield and yield components.

An experiment on fifty one rice genotypes for grain quality traits by Chakravorty and Ghosh (2012) and showed significant differences among grain quality traits. GCV ranged from 8.66 to 35.28.

Twenty one rice genotypes were studied by Bhadru*et al.* (2012) for yield and yield contributing traits and found that the genotypes were significant for all the traits studied except for plant height and panicle bearing tillers. Phenotypic co-efficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits.

An experiment was conducted on forty four lowland traditional rice genotypes with 23 characters. ANOVA revealed highly significant mean squares due to genotypes for all characters (Chakravorty*et al.*, 2012).

Five local and seven exotic genotypes studied for agro morphological traits and revealed that the selected progenies showed highly significant difference for most of the agro-morphological characters (Sanghera and Kashyap, 2012).

Osman *et al.* (2012) studied experiment on 13 rice genotypes with Morphology and yield contributing traits and found that the highest genotypic co-efficient of variation and genetic advance were recorded for number of tillers per plant and plant height.

40 rice genotypes of rice analyzed for studied genetic variation and found that the highest variability was observed in plant height, tillers per plant, panicle length and flag leaf area (Ashfaq*et al.* 2012).

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Gana *et al.* (2013) studied genetic variability on 39 accessions of rice with 12 morphophysiological traits and found that high variability were expressed among thevarieties and the characters.

An evaluation by Chakravorty*et al.* (2013) on twenty sixrice genotypeswith 18 characters and revealed that the discrepancy amongthe genotypes wasfound to be highlysignificant for all traitsexcept culm diameter.

Studied on fiftyMalaysianupland riceaccessionswith 12 growth traits and revealed that all of the traits weresignificant and highlysignificant among theaccessions(Sohrabi*etal.*, 2013).

2.2.2 Heritability

Heritability is the proportion of phenotypic variance attributable to geneticvariance. As heritability is a proportion, its numerical value will range from 0.0 to1.0. Phenotypic expression of any individual depends on its both geneticcharacteristics and environmental effects. Heritability can separate the contributionof genetic and environmental effects. Thus a selective breeding program can bemore realistic. Moreover, heritability can measure the amount of inheritedquantitative traits (Bhuiya, 2006).

Broad-sense heritability for salinity tolerance in F_2 generation was estimated by Ray and Islam (2008). The heritability for salinity tolerance score was very low to medium. The average estimate of heritability for the six crosses was 46.7%. Heritability was very low in the crosses Rajasail/BR29 and Purbachi/BR29.

Broad sense heritability estimates were high (ranged between 86 to 99.4%) for all traits when studied on 24 rice varieties by Sedeek*et al.* (2009).

An experiment was conducted by Subbaiah*et al.* (2011) on 16 parents and48 hybrids rice with nine yieldcontributingcomponents & 25quality characters. High heritability coupledwith high genetic advanceas per cent of mean wererecorded for differentcharacters.

Akhtar*et al.*(2011) studied on 10 ricegenotypesfor analysis of yield and yieldcontributing traits and found high heritability valuesrelated to days to maturity,grains per panicle, tiller perplant & height.

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Experiment conducted on 40 ricegenotypesfor yield and yieldcontributing traitsby Yadav*et al*. (2010) and revealed that high heritability wasobserved for differentcharacters.

High heritability estimates were observed for yield, days to 50% flowering & filled grains per panicle by Babu*et al.* (2012) on popular rice hybrids of India.

Sohrabi*et al.* (2012) conducted an experiment on 50 Malaysian upland rice accessions with 12 growth traits, yield and yield components and found heritability was registered for yield, days to flowering & flag leaf length.

18 diverse rice genotypes were studied by Hosseini*et al.* (2012) for yield and yield contributing traits and observed genotypes showed high heritability in height, root dry weight & shoot length.

Experiment was conducted by Vanisree*et al.* (2013) on 21 rice genotypes and found high heritability in productive tiller per hill, panicle density, filled grain, 1000 seed weight, karnel length and grain yield.

Chakravorty*et al.* (2013) studied on 26 rice genotypes with 18 characters. High heritability estimates were observed for all the traits. Heritability was over 50% in the characters.

2.2.3 Genetic advance

Phenotypic variation of a plant population depends on genetic variation of itsindividual and environmental effects. Higher genetic variation leads higherphenotypic variation. It is the preliminary base of selection. In a large mandelianpopulation gene frequencies remain constant in absence of selection, migration,mutation and genetic drift. Changing in genetic frequencies by successful selectionin this population is known as genetic advance (Bhuiya, 2006).

Thirty rice genotypes were evaluated for variability by Das *et al.* (1992) and found that fertile tillers per plant showed high GCV high heritability with high genetic advance in percent of mean.

Awasthi and Sharma (1996) recorded considerable genetic variability for plant height in 15 of high quality aromatic *Oryza sativa* genotypes.

Debi et al. (1997) studied genetic variability in 29 irrigated rice genotypes. High heritability (Hb) was observed for days to maturity.

Sharma (1997) studied genetic variability in 13 genotypes of upland Aus rice. Days to maturity showed high heritability (above 90%) and GCV were high for all the characters.

Luzi (1998) evaluated 36 rice lines and found that the genotypes differed significantly for most of the traits. Heritability estimates were high for filled grains per panicle.

Twenty-four genotypes of Basmati rice were evaluated by Mani et al. (1997) to investigate the extent of genetic variation. A wide range of variation was recorded for all traits studied. A high estimate of heritability coupled with high genetic advance for filled grains per panicle suggested the predominance of additive gene action for this character.

Basavaraja et al. (1997) reported high phenotypic co-efficient of variation, high to moderate (Broad sense) heritability and genetic advance for filled grain per panicle.

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

Tripathi et al. (1999) estimated genetic variability for yield components in 20 deep water rice genotypes. Plant height showed high genotypic and phenotypic variation.

Rao and Shrivastava (1999) evaluated 18 divergent rice genotypes to study genetic variability and significant difference for days to maturity with high heritability was found.

Study conducted by Yadav (2000) on 15 genotypes revealed that genotypic coefficient of variation, heritability and genetic advance estimate was not appreciable for days to maturity.

Kumar et al. (2001) evaluated 42 genotypes derived from seven crosses of rice and found that the phenotypic co-efficient of variation comparatively higher than the corresponding

genotypic coefficient of variation for number of panicle per plant, plant height and days to maturity.

Panday and Awasthi (2002) observed genetic variability in 21 genotypes of aromatic rice and significant genetic variability was observed for all the yield contributing traits including plant height.

Chand *et al.* (2004) studied nineteen genotypes of aman paddy emanating from different sources and heritability and genetic advance as percentage of mean were high for 1000 grain weight.

The 3rd most important yield attributes, thousand seed weight had wide variability in existing rice cultivars as reported by Rahman and Ali (2004).

Shashidhar*et al.* (2005) reported positive association grain yield with plant height, number of productive tillers hill-1and harvest index at phenotypic and genotypic level.

Senapati and Sarkar (2005) conducted a field experiments to evaluate the genetic divergence of 40 tall indica rice genotypes based on grain yield and yield components. 1000 grain weights were the chief contributors towards genetic divergence.

Patil and Sarawgi (2005) evaluated 128 aromatic rice accessions and estimate genetic variation and correlation for seven traits and found that effective tillers per hill had high genotypic and phenotypic co-efficient of variation. High heritability coupled with high genetic advance was also estimated for effective tillers per hill.

Singh *et al.* (2006) conducted an experiment with 37 rice genotypes and reported that therewere highly significant differences among the genotypes for plant height and the estimates of
phenotypic coefficient of variation.

High heritability coupled with high genetic advance for 1000 grain weight was observed byZahid*et al.* (2006). Hence, 1000 grain weight contributed maximum direct effects on yieldindicating that these traits should be given emphasis while selecting high yielding. 1000 grain

weight had positive correlations with grain quality characteristics, i.e. grain length andcooked.

150 rice genotypes and five check varieties were studied with yield contributing traits for analysis of genetic advance. GA was high for all the characters except days to flowering, panicle length (Padmaja*et al.*, 2008)

Bisne*et al.* (2009) studied forty-four rice genotypes and observed low genotypic andphenotypic coefficient of variations for breadth of spikelet, panicle length, length of spikelet,and days to 50 % flowering. Moderate genotypic and phenotypic coefficient of variations wasobserved by effective tillers plant-1, total number of spikelets panicle-1 and plant heightwhereas, high genotypic and phenotypic coefficient of variations were expressed by harvestindex, total number of filled spikeletsper panicle, 1000 grain weight, and spikelet fertilitypercentage.

High GA was exhibited by harvest index, yield, chaffyspikelets per panicle & filled spikelets when studied on four CMS lines, eight testers and 32 hybrids with 13 characters by Bisne*et al.* 2009.

Anbanandan*et al.* (2009) observed high heritability and genetic advance for the characters viz, number of productive tillers plant-1, 1000 grain weight and grain yield plant-1 in both F_3 and F_4 generations of four crosses of rice genotypes.

Bisne*et al.* (2009) studied forty-four rice genotypes and observed high heritability were forall the characters studied viz., days to 50 % flowering, plant height, panicle length, effectivetillers plant-1, total number of filled spikelets panicle-1, total number of chaffy spikeletspanicle-1, total number of spikelets panicle-1, spikelet fertility percentage and 1000 grainweight.

Siddiqui and Singh (2010) observed induced genetic variability for yield and yield traits in M2 and M3 generation in the two cultivars of Basmati rice. The observation mean range and coefficient of variation (CV) suggest that the mutagen treatment had wider values than the control.

Yadav*et al.* (2010) studied on 40 rice genotypes with yield contributing traits for estimating GA. High to moderate GA was observed for seed yield, yield, harvest index, weight &spikelets per panicle.

Pandey and Anurag (2010) observed high broad sense heritability among 22 genotypes ofindigenous rice for grain yield per hill (97.90 %) and length breadth ratio (96.72 %).

Pandey and Anurag (2010) observed highest genetic advance among 22 genotypes of indigenous rice for number of spikelets per panicle (30.77).

High broad sense heritability in days to 50% flowering, effective tillers per plant, paniclelength, number of spikeletsper panicle, number of fertile spikelets and grain yield per plant wasobserved by Tiwari*et al.* (2011). High heritability coupled with high genetic advance wasrecorded for number of fertile spikelets.

16 parents and 48 hybrids were evaluated with nine yield contributing components & 25 quality characters for heritability. High heritability coupled with high genetic advance as per cent of mean were recorded for different characters (Subbaiah*et al.* 2011).

Moukoumbi*et al.* (2011) studied the phenotypic variability of 60 lowland NERICA varieties and 18 promising lines for better management of their genetic inheritance. Data on 23 agro morphological traits were collected and analyzed. The analysis of variance showed highly significant differences (P<0.0001) between the variables and revealed the structure of the different genotypes from 11 quantitative discriminate traits.

Heritability in ten rice genotypes was studied by Akhtar*et al.* (2011). High heritability valuesrelated to days to maturity, number of grains panicle-1, number of tiller per plant and plantheight were obtained which indicated reasonable variation for these traits.

Selvaraj*et al.* (2011) estimated high genetic advance in number of tillers plant-1 followed by number of productive tillers plant-1, plant height and grain yield plant-1 of twenty one rice genotypes.

Twenty one genotypes of rice were investigated by Bhadru*et al.* (2012) and the analysis of variance for stability revealed that the genotypes were significant for all the traits studied except for plant height and panicle bearing tillers. Phenotypic coefficient of variation (PCV)

were higher than those of genotypic coefficient of variation (GCV) for all the traits studied, indicating that they all interacted with the environment with the same degree.

Khalid *et al.* (2012) estimated high heritability (>85%) for plant height, number of tillers plant-1 and 100 grain weight.

Sanghera and Kashyap (2012) evaluated the F3 population of eighteen different cross combinations using five local and seven exotic genotypes under temperate conditions. The selected progenies showed highly significant difference for most of the agro-morphological characters. Comparatively high phenotypic coefficients of variation were observed for all the character than genotypic coefficient variation.

Osman *et al.* (2012) evaluated thirteen genotypes of upland rice to estimate the genotypic and phenotypic variability. The highest genotypic coefficient of variation and genetic advance were recorded for number of tillers plant-1 and plant height.

Patel *et al.* (2012) estimated heritability in 24 rice genotypes and the highest heritabilityestimates was observed for days to 50% flowering, plant height, total tillers, panicle length,total number of spikeletsper panicle, number of filled spikelets panicle-1, number of unfilledspikeletsper panicle and grain yield per plant.

Babu*et al.* (2012) estimated heritability in the popular rice hybrids of India. The charactersthey studied expressed low to high heritability, ranging from 25.5 to 98.4 percent. Among theyield characters, highest heritability was recorded by days to 50% flowering followed bynumber of chaffy grains panicle-1, number of filled grains per panicle, whereas, and head rice
recovery percentage recorded lowest heritability value.

Osman *et al.* (2012) evaluated thirteen genotypes of upland rice to estimate broad sense heritability for maturity, morphological and yield associated traits. High heritability estimates (>85%) were recorded for plant height, number of tillers plant-1 and 1000 grain weight and high heritability estimates with low genetic advance observed for days to 50% flowering and days to maturity.

Genetic advance in 24 rice genotypes was estimated by Patel *et al.* (2012) and the highestgenetic advance percentage of mean was observed for number of unfilled spikelet per

panicle.The estimates of genetic advance as percentage of mean (>30%) were also observed for othercharacters viz., total tillers , total number of spikelets panicle-1 and number of filled spikelets per panicle.

Sanghera and Kashyap (2012) studied on five local and seven exotic genotypes for analysis of genetic advance with yield contributing traits and found that high genetic advance were observed for yield & harvest index.

Patel *et al.* (2012) observed genetic advance on 24 rice genotypes with yield contributing traits and found that highest genetic advance as percentage of mean for unfilled spikelets per panicle. >30% GA were observed for other characters.

Studied heritability by Hosseini*et al.* (2012) on 18 diverse rice genotypes with yield contributing traits and found that high heritability estimates in height, root dry weight & shoot length.

Sanghera and Kashyap (2012) studied genetic advance in the F_3 population of eighteendifferent cross combinations using five local and seven exotic genotypes. High geneticadvance were observed for grain yield (47%) followed by biological yield per plant (27%) andharvest index (25%).

An experiment was carried out by Vanisree*et al.* (2013) on 21 rice genotypes for Quality and yield associated characters studied. High genetic advance were recorded in no. of productive tiller, panicle density, filled grain, 1000 seed weight, karnel length and yield.

50 Malaysian upland rice accessions with 12 growth traits was observed for genetic advance with yield and yield components. It was found that high genetic advance for yield, days to flowering & flag leaf length-towidth ratio (Sohrabi*et al.*, 2013).

Paikhomba*et al.* (2014) studied on 30 F_1 hybrids along with 13 parents & checks for 14 characters and found that moderate genetic advance were observed in pollen fertility, yield, harvest index and no. of filled grain.

2.3 Correlation co-efficient

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters. It resolves the complex relations between the events into simple form of association.

Since grain yield is the ultimate product of rice, information on it association with other characters contributing towards yield is necessary to identify the best characters combination for high yield. Grain yield is associated with many yield contributing characters. The major yield components in rice have been identified as panicles per plant; grain per plant and average grain weight. In addition there are other characters plant height, days to maturity, panicle length etc. which contribute to grain yield. Association of yield contributing characters with grain yield in rice was comprehensively studied by many breeders and based on their results they formulated different selection criteria for yield improvement. Association of yield contributing characters with yield was studied both genotypic and phenotypic levels. Relationship between yield and yield contributing characters are usually studied by correlation and path coefficient (Ahmed *et al.*, 2007). Information on the nature of magnitude of association between yield and yield contributing characters is therefore helpful for selection of high yielding genotypes in aromatic rice.

Shamsuddin (1985) studied character association for panicle and grain characteristics inrelation to grain yield in 53 rice genotypes and found that grain yield per plant was positivelyand significantly correlated with 100-grain weight and panicle length at genotypic level.

Ismail and Aleverez (1986) calculated phenotypic and genotypic correlation among the chiefcomponents of yield in nine varieties. Yield showed significant positive correlation with filledgrains per panicle (r = 0.79).

Sampath*et al.* (1989) derived correlation from the data on grain yield and its related traitsand found that yield was significantly and positively correlated with 1000 grain weight,panicle length, grains per panicle and days of flowering.

Majumder*et al.* (1990) studied 18 important characters of rice and observed that yield wassignificantly and positively correlated with plant height, productive tillers, panicle length andgrains per panicle.

Sawant*et al.* (1995) estimates character association of grain yield with six components traitsThey found that grain yield was positively and significantly correlated with panicle length,ear bearing tillers per plant and grains per panicle but grain yield positively and insignificantlyassociated with 1000 grain weight.

Cheema*et al.* (1998) reported highly significant positive correlation of yield per plant withgrains per panicle and panicle length. They also observed that number of grains per panicle hadhigh significant positive correlation with panicle length.

Rahman and Ali (2004) worked with 21 genotypes of rice during Rabi season in 2001 andobserved that seed yield per plant was strongly and positively correlated with number of seed per plant. They also indicated that seed yield was significantly correlated with plant height andseeds per plant was correlated with plant height only.

Thirty rice genotypes was studied by Wattoo*et al.* (2010) in order to determine theassociations among yield components and their direct and indirect influence on grain yield.Grain yield was significantly correlated with its component characters; number of productivetillers perplant, number of grains per panicle and flag leaf area.

Laxuman*et al.* (2011) conducted experiment on 188 backcrossed inbred lines from Swarna x NERICA-L- 20 of rice. Days to heading, days to 50 % flowering, number of productive tiller per plant and panicle length exhibited significant positive correlation with grain yield at both phenotypic and genotypic level.

Grain yield per plant had positive significant correlation with leaf width, days to 50% flowering, plant height, panicle length, number of filled grains per panicle, 100 seed weight and paddy (grain) length observed by Ekka*et al.* (2011).

Akinwale*et al.* (2011) mentioned that grain yield exhibited significantly positive correlationwith the number of tillers per plant (r = 0.58**), panicle weight (r =0.60*) and number of grains per panicle (r= 0.52*).

An experiment was carried out on 20 BRRI released HYV'S and one local variety named Rajasail. Significant positive genotypic and phenotypic correlation was found between flag leaf area and days to flowering, days to flowering and growth duration, days to flowering and LAI at flowering, flag leaf area and growth duration, flag leaf area and LAI at flowering,

growth duration and LAI at flowering, CGR at flowering and RGR at flowering, CGR at flowering and NAR at flowering, RGR at flowering and NAR at flowering and harvest index and yield. Only genotypic correlation was found significant between seedling vigor and CGR at flowering (Rahman*et al.*, 2012).

Haider*et al.* (2012) were carried out an experiment on 20 rice genotypes and found that grains per panicle (0.733**), spikelet fertility (0.709**), thousand grain weight (0.476**), root length (0.465**), root to shoot length ratio (0.242*), drought response index (0.642**) has significant and positive relation with grain yield per plant.

Grain yield per plant was significantly and negatively correlated with percent of unfilled grains per panicle. It was highly significantly and positively correlated with panicle length, number of tillers per plant, number of filled grains per panicle and 1000 grain weight. This experiment was carried out by Osman *et al.* (2012) on 13 genotypes of upland rice.

Correlation in the F_3 population of eighteen different cross combinations using five local andseven exotic genotypes was studied by Sanghera and Kashyap (2012). Days to 50% floweringwas positively and significantly correlated with days to maturity, grain length with LB ratioflag leaf length with grain breadth and panicle length with grain breadth at genotypic level.

Kiani and Nematzadeh (2012) performed a study to determine the association between grainyield and yield components in fifty-four selected rice genotypes at F_2 populations. Resultsshowed that traits, the panicles per plant (r = 0.751) and filled grains per panicle (r = 0.458)correlated significantly with grain yield, while grain yield was negatively associated withnon-filled grains per panicle (-0.297).

2.4 Path Co-efficient analysis

Direct contribution of each component to the yield and the indirect effects it has through its association with other components cannot be differentiated from mere correlation studies. Path coefficient analysis fulfills this study.

It was first developed and described by Wright (1921)and employed first time in plant by Dewey and Lu (1959), as a tool in genetic analysis which partition the association of the

components on yield and indirect effects of the characters on yield through other components. In case of correlated characters, change of one variable can change another variable. Path co-efficient refers to the degree of influences of one variable to the others (Ahmed *et al.*, 2007).The association between the various characters in a rice and the direct and indirect effects of a variable over the dependent variable has been studied by a number of investigators are reviewed here.

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

Chaubey and Singh (1994) observed the greatest direct effect on grain yield for ear bearing tillers (0.44) followed by plant height (0.34), 1000 grain weight (13.0) and total number of spikelets (0.09). They suggested that ear bearing tillers per plant can be used as a selection criterion for rice hybridization program.

Satpute (1996) observed high positive direct effect on yield was exerted by seed weight, followed by number of filled grains per panicle, and number of ear-bearing tillers.

Path co-efficient analysis was studied by Mani *et al.* (1997) in 280 F3 generation of rice found that tillers per plant, 1000 grain weight and grains per panicle had a high positive direct effect on grain yield per plant.

Thirty six rice lines were evaluated using path analysis by Kihupi (1998) and the result revealed that there was high direct effect of number of filled grains per panicle, number of panicles per plant and moderate direct effects of 1000 grain weight on yield.

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

Kole*et al.* (2008) carried out experiment on 18 morphologically distinct mutants in M4 generation of rice and found that panicle number had the highest positive direct effect on grain yield followed by grain number, test weight, plant height, days to flower and straw weight.

An experiment was carried out on 30 rice genotypes and found that days to maturity had the highest direct effect (0.751) on grain yield per plant. In addition, the yield components had positive direct effect on grain yield except the days to heading (-0.834). The order of yield components was the number of productive tillers per plant, flag leaf area and 1000 grain weight (Wattoo*et al.*, 2010).

Yadav*et al.* (2010) estimated path coefficient at genotypic level revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of spikelet's per panicle, plant height and test weight had direct positive effect on seed yield per hill, indicating these are the main contributors to yield.

Bagheri*et al.* (2011) determined the relationship between grain yield and yield component in twenty-six rice genotypes. Path coefficient analysis revealed that panicle length had the highest positive direct effect (0.510) on grain yield. Grain yield linearly correlated with panicle length, the number of panicle per plant, and the number of filled grains per panicle. Therefore, these traits may be used in the selection for grain yield in rice.

Ekka*et al.* (2011) performed path analysis in traditional rice accessions of Chhattisgarh and path coefficient analysis revealed that direct selection for days to 50% flowering, 100 seed weight, panicle length, leaf length and milling percentage would likely be effective for increasing grain yield. Direct selection for days to 50% flowering and number of filled grains per panicle would increase head rice recovery percentage.

An experiment was conducyed by Akhtar*et al.* (2011) on 10 rice genotypes and revealed that 1000-grain weight (0.6556) has highest positive direct effect on grain yield, followed by days to maturity (0.0914) which indicated that these two traits were more contributors towards paddy yield in these rice genotypes.

Sanghera and Kashyap (2012) carried out experiment on five local and seven exoticrice genotypes and revealed that harvest index and biological yield has highestdirect effect on grain yield followed by days tomaturity and number of grain per panicle.Biological yield per plant has highest indirecteffect on yield via days to flowering followed bygrain weight via biological yield per plant, grainbreadth via days to 50% flowering and flag leaflength via biological yield per plant.

Twenty rice genotypes were studied for path coefficient of morphological traits under simulated drought stress condition. Grains per panicle had negative but negligible direct effect (-0.302) on yield per plant. Direct effect of thousand grain weight was positive and high (0.805) (Haider*et al.* 2012).

Pandey*et al.* (2012) mentioned that path analysis identified days to maturity, effective tillers per plant, and 1000 grain weight and flag leaf area and panicle length as major direct contributors.

Path co-efficient was studied on 21 rice genotypes and indicated maximum direct positive effect of plant height, productive tiller, filled grain, karnel length & breadth on grain yield (Vanisree*et al.* 2013).

2.5 Genetic divergence

Evaluation of germplasm through genetic divergence which quantifies variation among genotypes on the basis of a group of characters (yield and yield contributing) helps in identification of promising materials for crop improvement. Germplasm collections are also valuable gene pools providing diverse genetic material that may be applied for the improvement of cultivars and advanced agronomic productivity. An assessment of genetic diversity within these collections can be used to assign land races and populations to diverse groups.

D^2 statistic developed by Mahalanobis (1936), provides a measure of magnitude of divergence between biological populations and relative contribution of each component character to the total divergence (Nair and Mukherjee, 1960). Mahalanobis D^2 statistic is more reliable in selection of potential genotype for hybridization programme using these D^2 values cluster are formed. A summary of literature reviewed on mustard and other allied species are in presented below.

Genetic divergence facilitates the selection of parental genotypes from aMandelian population. Proper assessment of degree, level and pattern of geneticdivergence can help in genetic variability analysis of germplasms (Smith, 1984; Cox*et al.*, 1986). It helps identification of diverse parental combinations for creatingsegregating progenies (Barrett & Kidwell, 1998) as well as to introgression ofdesirable genes from wild germplasm into the adapted high yielding specimens(Thomson *et al.*, 1998).

An experiment was conducted by Zia-Ul-Qamar*et al.* (2012) on 50 ricegenotypes for cluster analysis (D^2) and exhibited six distinct clusters withthe range of two genotypes in cluster VI to thirteengenotypes in cluster I and III each. Interclusterdistance was larger than the intra-clusterdistance suggesting wider genetic diversity among thegenotypes. Maximum intercluster distance wasobserved between cluster I and VI (79.81) followed bycluster I and V (71.90).

Bhadru*et al.* (2012) carried out experiment on 21 ricegenotypes. They revealed that the D^2 values were significant among genotypes,which were grouped into six clusters. Most of thegenotypes with same pedigree either male or femaleparent involved cross combination came under thesame cluster and few genotypes in different cluster andgenotypes of quite different pedigree may all into thesame cluster.

Generally principal component analysis (PCA) is an approach used by breeders toevaluate and characterize germplasm. It is an exploratory tool designed by Pearson(1901) to identify unknown trends in a multi-dimensional data set. However, in atypical micro-array experiment, the expression of thousands of genes is measuredacross many conditions such as treatments or time points. Therefore, it becomesimpossible to make a visual inspection of the relationship between genes orconditions in such a multi-dimensional matrix. One way to make meaningful ofthis data is to reduce its dimensionality (Hotelling, 1933). PCA reduces the datainto two dimensions (Smith, 2002; Raychaudhuri*et al.*, 2000).

36 accessionsof riceanalysis for PCA and showed the combination of first five principalcomponent axes of firstyear. In second year it was 65.4%of the total variation(Gana*et al.*,2013).

123 ricegermplasmincludingchecksPCA resulted in the first two components withEigen value greater than 1 accounting for 78% of thetotal variationMaji andShaibu (2012).

Chakravorty and Ghosh (2012) were carried out experiment on 44 lowlandtraditionalricegenotypesfor PCA and revealed that six quantitative characters viz.,leaf length, culm number, culm diameter, number ofgrains per panicle, grain length/breadth ratio andgrain length significantly influenced the variation inthese cultivars.

Zia-Ul-Qamar*et al.* (2012) studied on 50 ricegenotypesand revealed that two principal components presented 65%information of the raw dataof the yield relatedtraits.

146accessionsof uplandricewas analyzed for PCA of quantitative traits and showed great dispersionof the accessions. The most divergent group ofaccessions included the genotypes Mitsukasane,Mie, Tomoe mochi, Ooba kirishima and Nourinmochi 6, which showed a higher number ofspicklets per plant(Nascimento*et al.*, 2011).

Sanni*et al.* (2010) carried out an experiment on 434accessionsof riceand revealed that the first three principal components explained about58.41% of the total variation among the 14characters.

40 riceaccessionswere analyzed and found that the first principal component accounted for thehighest proportion (26.26%) of total variation was mostlycorrelated with total number of tillers, filled tiller,flowering and maturity dates and grain yield. Charactersthat were mostly correlated with the second principalcomponent, viz.- height, tiller diameter, leaf length, grainlength and grain width. The third principal componentwas dominated by traits such as grain length, 100-grainweight and to lesser extend by leaf width, plant height,flowering and maturity dates and panicle length. Leafand panicle lengths made substantial contribution to thefourth principal component(Ogunbayo*etal.*, 2005).

CHAPTER III

MATERIALS AND METHODS

This chapter deals with the information on the subject of materials and methods that were used in conducting the experiment. It consists of a short explanation of locations of the experimental site, soil characteristics, climate, materials used in the experiment, layout and design of the experiment, land preparation, manuring and fertilizing, transplanting of seedlings, intercultural practices, harvesting, data recording procedure and statistical analysis etc., which are presented as follows:

3.1   Experimental site:

The experiment was conducted at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207 during June 2014 to February 2015. Geographically the experimental area is located at $23^074'$ N latitude and $90^035'$ E longitude with an elevation of 8.6 meter from the sea level. Photograph showing the experimental site (Appendix II).

3.2   Soil and Climate:

The experimental site was situated in the subtropical zone. The soil of the experimental site belongs to the Agro-ecological zone of "The Modhupur Tract" (AEZ-28) (FAO/UNDP, 1988). The texture of the soil was clay loam and olive gray with common fine to medium distinct dark yellowish brown mottles. The p^H ranges from 4.47 to 5.63 and organic carbon content is 0.82% (Appendix III). The climate was characterized by relatively high temperature and high rainfall during Kharif season and low temperature and little rainfall during Rabi season. The record of air temperature, humidity and rainfall during the period of experiment were noted from Bangladesh Meteorological Department (Climate & Weather Division), Agargoan, Dhaka -1207 (Appendix IV).

3.3   Experimental materials:

The healthy seeds of thirty aromatic land races collected from the Dept. of Genetics and Plant Breeding, Sher-E-Bnalga Agricultural University, Dhaka-1207 which were used as experimental materials in the present study. A list of the genotypes is presented in the Table 2.

Table 2. Materials used for the experiment

Code	Genotypes	Source	Code	Genotypes	Source
G1	RCO-538	SAU	G16	RCO-491	SAU
G2	RCO-539	SAU	G17	RCO-484	SAU
G3	RCO-433	SAU	G18	RCO-500	SAU
G4	RCO-441	SAU	G19	RCO-477	SAU
G5	RCO-460	SAU	G20	RCO-531	SAU
G6	RCO-470	SAU	G21	RCO-490	SAU
G7	RCO-456	SAU	G22	RCO-530	SAU
G8	RCO-466	SAU	G23	RCO-441	SAU
G9	RCO-495	SAU	G24	RCO-463	SAU
G10	RCO-487	SAU	G25	RCO-464	SAU
G11	RCO-464	SAU	G26	RCO-498	SAU
G12	RCO-428	SAU	G27	RCO-484	SAU
G13	RCO-453	SAU	G28	RCO-524	SAU
G14	RCO-480	SAU	G29	RCO-501	SAU
G15	RCO-511	SAU	G30	RCO-485	SAU

3.4   Methods

The following precise methods have been followed to carry out the experiment:

3.4.1 Seedbed Preparation

Seed bed was prepared by raising soil up to 5-10 cm from the field surfaces followed by puddling. Before puddling cowdung was applied @ 2 kg per square meter. The entire seed bed was then divided into three seed beds and small plots (50 cm x 50 cm) were prepared considering the 30 rice genotypes. Between the plots 10 cm distance was maintained. Drainage channels (30 cm) were prepared between seed beds to drain out excess water whenever needed.

3.4.2 Sowing of pre-germinated seeds

The seeds were soaked into water on 11 June 2014 for 24 hours and incubated in moist cloth sacks for 48 hours for quick germination. The pre-germinated seeds were sown in seedbed on 14 June 2014.

3.4.3   Land preparation

The experimental plot was prepared by ploughing with power tiller followed by laddering to bring about good tilth. Weeds and stubbles were removed from the experimental field. The land was mudded and leveled well before transplanting. At the final land preparation by addition of basal dose of fertilizers recommended by BRRI.

3.4.4 Application of Fertilizers

Adequate soil fertility was ensured by applying of Urea, TSP, MP and Gypsum @ 260-77-79-55 kg/ha, respectively. Total Urea was applied in three installments, at 15 days after transplanting (DAT), 30 DAT and 45 DAT recommended by BRRI.

3.4.5 Experimental design and layout

The experiment was laid out in Randomized Complete Block Design (RCBD). The field was divided into three blocks; the blocks were sub-divided into 30 plots where genotypes were randomly assigned. The experimental field size was 26 m x 16 m where 1m boarder was maintained surrounding the field and every block. The experimental field was designed such a way where intra varietal row to row distances and inter varietal row to row distances were

Plate 1. Experimental field showing different genotypes at flowering stage.

25 cm and 50 cm respectively and plant to plant distance was 15 cm. The 30 genotypes were distributed to each plot within each block randomly. A pictorial view of experimental field at flowering stage is presented in plate 1.

3.4.6 Transplanting

Healthy seedlings of 20 days old were transplanted on 04 July 2014 in separate strip of experimental field. Water level was maintained properly after transplanting.

3.4.7 Intercultural operations

Gap filling was done within seven days after transplanting with the seedlings from same source to obtain uniform plant population. Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots when required. Hand weeding was done at 25 and 40 days after transplanting. Flood irrigation was given to the field when necessary.

3.4.8 Plant Protection Measure

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

3.4.9 Crop harvesting

Different genotypes matured at different times. Harvesting was done when 80% of the plant population of each plot reached maturity. The harvesting was done by my supervision and also present my research supervisor. 10 hills were selected at randomly from in each replication. The plants were harvested by cutting by sickle and then they were tagged properly. Data were recorded on different parameters from these plants.

3.5 Recording of data

Data were recorded on individual plant basis from 10 randomly selected hills from each replication. The plants were selected from middle to avoid border effect and portion of the plot. Seven qualitative and thirteen quantitative traits were recorded using IBPGR-IRRI Rice Descriptors (2007). The descriptors are appended in the Table 2. In addition to the

descriptors, the test genotypes were classified according to Panse and Sukhatme (1995) and Naseem (2005). The observations for characterization were recorded under field condition as follows.

3.5.1 Qualitative Traits Evaluation Methods

The experimental plots were visited every day and required data were collected as per schedule. An appropriate data record book was used for keeping records of data related to identification of the genotypes. The IBPGR-IRRI Rice Descriptors (2007) (Table 3) were used for data collection and recording. The photographs of specific trait considered to be helpful for identification of the genotypes were taken from the experimental field at appropriate times for different traits to compare the distinctness among the aromatic rice genotypes. Photographs and data related to distinctness in morphological traits were taken on each of the 30 aromatic rice genotypes. This was done particularly to find out the expression of the qualitative traits of the genotypes irrespective of ecotypes when grown under constant environment.

3.5.1.1 Basal leaf sheath color

Data was collected at late vegetative Stage on basal leaf sheath color and the aromatic rice genotypes were classified into four groups with codes according to guided descriptors as per follows.

Green-1
Green with purple lines-2
Light purple-3
Purple-4

3.5.1.2 Green color intensity of leaf blade

Observations with respect to green coloration of leaf blade at late vegetative stage the aromatic rice genotypes were classified into four groups with codes according to guided descriptors as per follows.

No green-0: No green color visible due to anthocyanin
Light green-3
Medium green-5
Dark green-7

Table 3. Descriptors with codes for qualitative characteristics

SL. NO.	Characteristics	Descriptors with Codes
1	Basal leaf sheath color	Green-1, Green with purple lines-2, Light purple-3, Purple-4
2	Grain color intensity of leaf blade	No green-0, Light green-3, Medium green-5, Dark green-7
3	Leaf blade attitude	Erect-1, Horizontal-5, Drooping-7
4	Leaf blade pubescence	Glabrous-1, Intermediate-2, Pubescent-3
5	Ligule shape	Absent-0, Truncate-1, Acute to acuminate-2, 2-cleft-3
6	Presence of Awns	Absent-0, Partly awned-1, Fully awned-2
7	Panicle: attitude of branches	Erect (compact panicle)-1,Semi-erect (semi-compact panicle)-3, Spreading (open panicle)-5, Horizontal-7 Drooping-9

Source: IBPGR-IRRI, 2007, Rice Advisory Committee

3.5.1.3 Leaf blade attitude

Leaf blade attitude refers the position of the tip of the blade relative to its base, scored on the leaf below the flag leaf at late vegetative (prior to heading) stage and the aromatic rice genotypes were classified into four groups with codes according to guided descriptors as per follows.

Erect-1
Horizontal-5
Drooping-7

3.5.1.4 Leaf blade pubescence

It was assessed both visually and by touch, rubbing fingers over the leaf surface from the tip to downwards at late vegetative stage and the test genotypes were categorized into three groups as per descriptors by following way.

Glabrous-1 (smooth—including ciliated margins)
Intermediate-2
Pubescent-3

3.5.1.5 Ligule shape

Shape of the penultimate leaf ligule was observed and the genotypes were categorized as following which are also shown hypothetically in figure 1.

Absent-0
Truncate-1
Acute to acuminate-2,   2-cleft-3
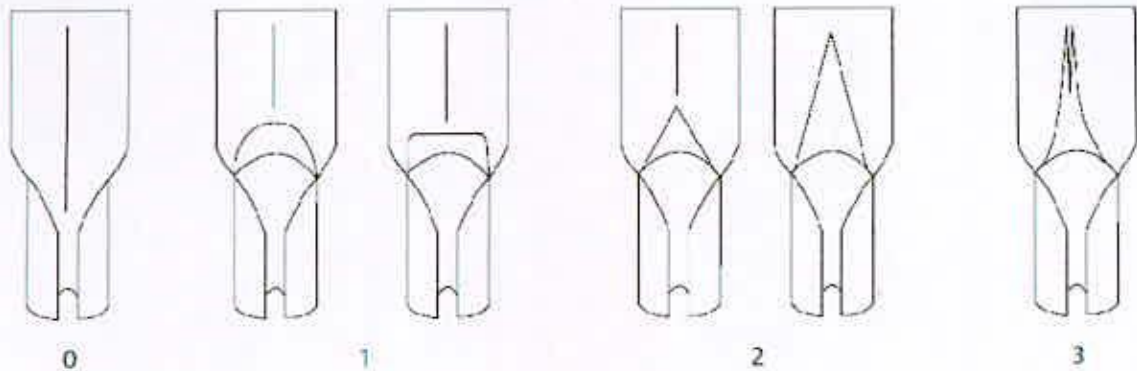
Figure 1. Ligule Shape

3.5.1.6 Presence of Awns

It was observed after maturity and normally a character of wild species of rice and grouped as per descriptors.

Absent-0
Partly awned-1
Fully awned-2

3.5.1.7 Panicle: attitude of branches

The compactness of the panicle was classified according to its mode of branching, angle of primary branches, and spikelet density by the following groups.

Erect (compact panicle)-1, Semi-erect (semi-compact panicle)-3
Spreading (open panicle)-5, Horizontal-7, Drooping-9
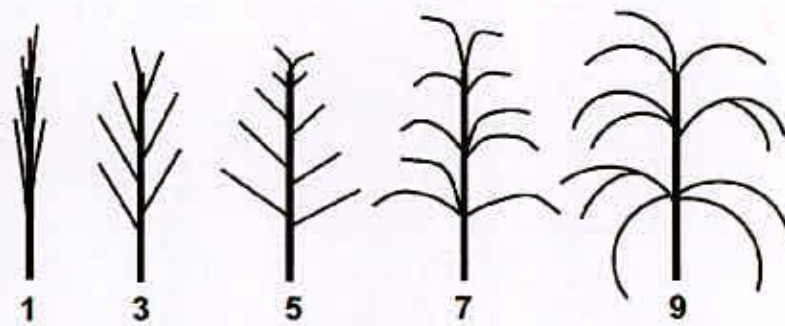
Figure 2. Attitude of panicle branches
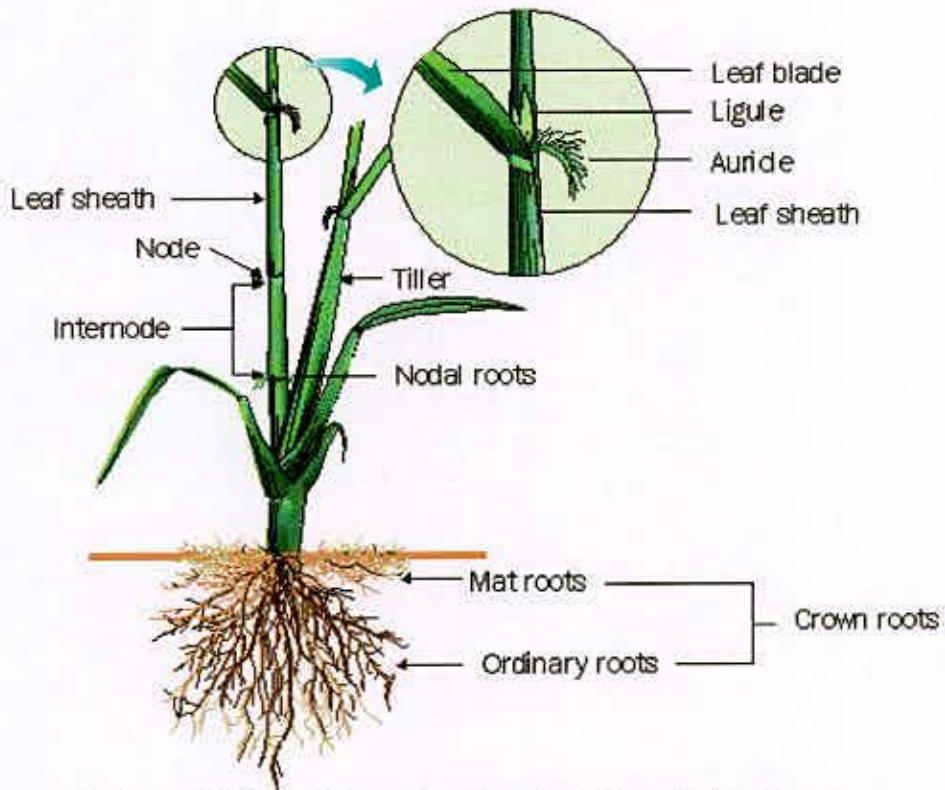
Figure 3. Morphology of a rice plant (Vegetative stage)

3.5.2 Quantitative Traits Evaluation Methods

3.5.2.1 Culm Length
It was measured from ground level to the base of the panicle at maturity stage.
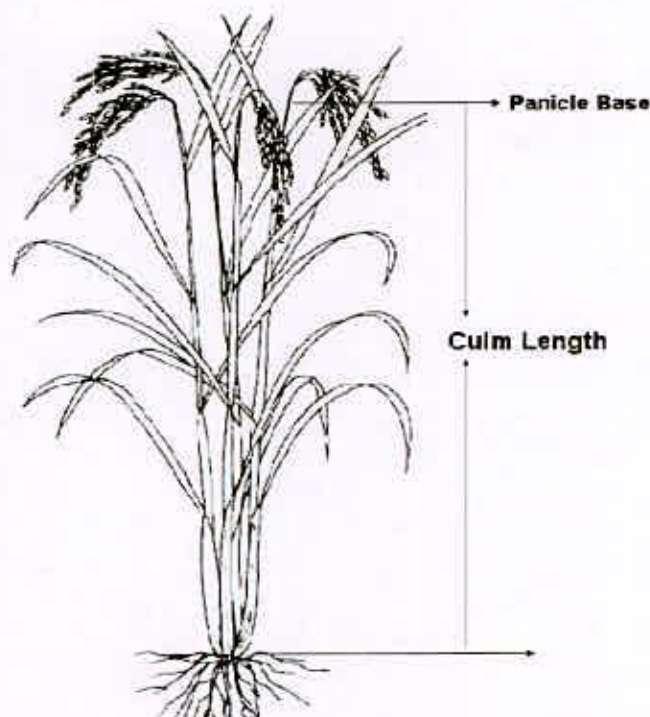
Figure 4. Culm Length

3.5.2.2 Flag Leaf Length

It was measured in centimeter scale from the jointing point of flag leaf and panicle to the tip point of flag leaf after panicle initiation.

3.5.2.3 Flag Leaf Breadth

Flag leaf breadth was measured in cm scale at the middle of flag leaf after panicle initiation.

3.5.2.4 Total tillers per hill

The total number of tillers was counted from each of the sample plants and the average was taken.

3.5.2.5 Effective tiller per hill

Effective tillers are the tillers which bears panicle and the number of effective tillers was counted from each of the sample plants and the average was taken.
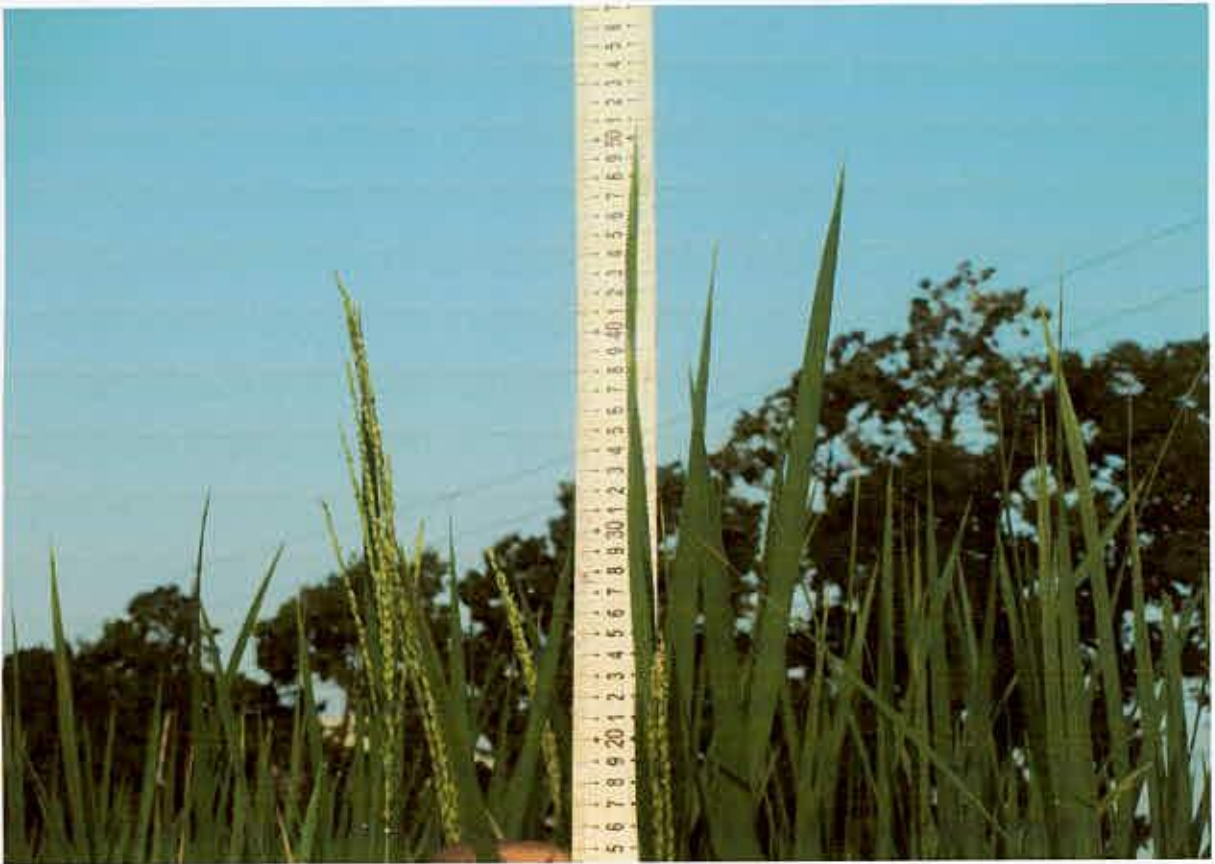
Plate 2. Flag leaf length.

Plate 3. Panicle length of genotypes

3.5.2.6 Panicle Length

The mean length often randomly selected panicles of main tillers from ten hills was measured from neck to the tip of the panicle of main tiller without awn in centimeters.

3.5.2.7 Primary branches per panicle

Observations with respect to number of total primary branches per particle were recorded at maturity stage.

3.5.2.8 Secondary branches per panicle

Observations with respect to number of total secondary branches per particle were recorded at maturity stage.

3.5.2.9 Filled Grain per panilce

The number of filled grains of ten randomly selected panicles of main tillers from ten hills was recorded and then averaged.

3.5.2.10 Total grains per panicle

The total number of grains of ten randomly selected panicles of main tillers from ten hills was recorded and then averaged.

3.5.2.11 Days to Maturity

The number of days from date of sowing until 80% seeds become matured considering each replication was recorded on each individual plot and the genotypes.

3.5.2.12 Thousand grain weight (Dry)

After threshing and recording the net yield, a random sample of fully grown 1000 seeds were counted and weighed at 12% moisture content to record the test weight.

3.5.2.13 Grain yield per plant

Panicles of randomly selected plants per replication were threshed, seeds were sun dried for two days and weighed and then averaged. Seed yield was adjusted at 12% moisture content.

3.6 Statistical analysis

The qualitative data in relation to morphological traits are just presented in tabular form for easier description according to IBPGR-IRRI, 2007. The data were arranged as per IBPGR-IRRI formulation with the help of Microsoft-XL program. For quantitative data analysis mean data of the characters were used to statistical analyze like analysis of variance (ANOVA), mean, range were calculated by using MSTATC software program. Genotypic and phenotypic variance was estimated by the formula used by Johnson *et al.* (1955). Heritability and genetic advance were measured using the formula given by Singh and Chaudhary (1985) and Allard (1960). genotypic and phenotypic coefficient of variation were calculated by the formula of Burton (1952). genotypic and phenotypic correlation coefficient was obtained using the formula suggested by Miller et al. (1958), Johnson et al. (1955) and Hanson et al. (1956); path coefficient analysis was done following the method outlined by Dewey and Lu (1959). Multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Vector Analysis (CVA) were done by using GENSTAT 5.13 and Microsoft Excel 2007 software.

3.6.1 Estimation of genotypic and phenotypic variances

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

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

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

Phenotypic variance (σ^2_p) $= \sigma^2_g + \sigma^2_e$

Where,

σ^2_g = Genotypic variance

EMS = Error mean sum of square

σ^2_e = Error variance

3.6.2 Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation were calculated by the formula suggested by Burton (1952)

Genotypic co-efficient of variation (GCV %) = $\sqrt{\dfrac{\sigma^2_g}{x}} \times 100$

Where,

σ^2_g = Genotypic variance

$\overline{x}$ = Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula.

Phenotypic co-efficient variation (PCV) $= \sqrt{\dfrac{\sigma^2_{ph}}{\overline{x}}} \times 100$

Where,

σ^2_p = Phenotypic variance

$\overline{x}$ = Population mean

3.6.3 Estimation of heritability

Broad sense heritability was estimated (Lush, 1943) by the following formula, suggested by Johnson *et al.* (1955).

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

Where,

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.6.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Lush (1943) and Johnson *et al.* (1955).

Genetic advance, $GA = K. h^2. \sigma_p$

Or Genetic advance, $GA = K. \dfrac{\sigma^2_g}{\sigma^2_p}. \sigma_p$

Where,

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

σ_p = Phenotypic standard deviation

h^2_b = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.6.5 Estimation of genetic advance mean's percentage

Genetic advance as percentage of mean was calculated from the following formula as proposed by Comstock and Robinson (1952):

Genetic advance (% of mean) $= \dfrac{\text{Genetic Advance (GA)}}{\text{Population mean (x)}} \times 100$

3.6.6 Estimation of genotypic and phenotypic correlation co-efficient

The calculation of genotypic and phenotypic correlation co-efficient for all possible combinations through the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956) were adopted. The genotypic co-variance component between two traits and have the phenotypic co-variance component were derived in the same way as for the corresponding variance components. The co-variance components were used to compute genotypic and phenotypic correlation between the pairs of characters as follows:

$$\text{Genotypic correlation, } r_{gxy} = \frac{GCOVxy}{\sqrt{GVx \cdot GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx} \cdot \sigma^2_{gy})}}$$

Where,

σ_{gxy} = Genotypic co-variance between the traits x and y
σ^2_{gx} = Genotypic variance of the trait x
σ^2_{gy} = Genotypic variance of the trait y

$$\text{Phenotypic correlation } (r_{pxy}) = \frac{PCOVxy}{\sqrt{PVx \cdot PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px} \cdot \sigma^2_{py})}}$$

Where,

σ_{pxy} = Phenotypic co-variance between the trait x and y
σ^2_{px} = Phenotypic variance of the trait x
σ^2_{py} = Phenotypic variance of the trait y

3.6.7 Estimation of path co-efficient

It was done according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985), using phenotypic correlation coefficient values. In path analysis, correlation coefficients between yield and yield contributing characters were partitioned into direct and indirect effects on yield per hectare. In order to estimate direct and indirect effects of the correlated characters, i. e. 1, 2, 3….and 13 on yield y, a set of simultaneous equations (eight equations in this example) is required to be formulated as shown below:

$r_{1.y} = P_{1.y} + r_{1.2} P_{2.y} + r_{1.3} P_{3.y} + r_{1.4} P_{4.y} + r_{1.5} P_{5.y} + r_{1.6} P_{6.y} + r_{1.7} P_{7.y} + r_{1.8} P_{8.y} + r_{1.9} \quad P_{9.y} + r_{1.1} P_{10.y} + r_{1.11} P_{11.y} + r_{1.12} P_{12.y} + r_{1.13} P_{13.y}$

$r_{2.y} = r_{1.2} P_{1.y} + P_{2.y} + r_{2.3} P_{3.y} + r_{2.4} P_{4.y} + r_{2.5} P_{5.y} + r_{2.6} P_{6.y} + r_{2.7} P_{7.y} + r_{2.8} P_{8.y} + r_{2.9} P_{9.y} + r_{2.10} P_{10.y} + r_{2.11} P_{11.y} + r_{2.12} P_{12.y} + r_{2.13} P_{13.y}$

$r_{3.y} = r_{1.3} P_{1.y} + r_{2.3} P_{2.y} + P_{3.y} + r_{3.4} P_{4.y} + r_{3.5} P_{5.y} + r_{3.6} P_{6.y} + r_{3.7} P_{7.y} + r_{3.8} P_{8.y} + r_{3.9} P_{9.y} + r_{3.10} P_{10.y} + r_{3.11} P_{11.y} + r_{3.12} P_{12.y} + r_{3.13} P_{13.y}$

$$r_{4.y} = r_{1.4}\,P_{1.y} + r_{2.4}\,P_{2.y} + r_{3.4}\,P_{3.y} + P_{4.y} + r_{4.5}\,P_{5.y} + r_{4.6}\,P_{6.y} + r_{4.7}\,P_{7.y} + r_{4.8}\,P_{8.y} + r_{4.9}\,P_{9.y} +$$
$$r_{4.10}P_{10.y} + r_{4.11}\,P_{11.y} + r_{4.12}\,P_{12.y} + r_{4.13}\,P_{13.y}$$

$$r_{5.y} = r_{1.5}\,P_{1.y} + r_{2.5}\,P_{2.y} + r_{3.5}\,P_{3.y} + r_{4.5}\,P_{4.y} + P_{5.y} + r_{5.6}\,P_{6.y} + r_{5.7}\,P_{7.y} + r_{5.8}\,P_{8.y} + r_{5.9}\,P_{9.y} +$$
$$r_{5.10}P_{10.y} + r_{5.11}\,P_{11.y} + r_{5.12}\,P_{12.y} + r_{5.13}\,P_{13.y}$$

$$r_{6.y} = r_{1.6}\,P_{1.y} + r_{2.6}\,P_{2.y} + r_{3.6}\,P_{3.y} + r_{4.6}\,P_{4.y} + r_{5.6}\,P_{5.y} + P_{6.y} + r_{6.7}\,P_{7.y} + r_{6.8}\,P_{8.y} + r_{6.9}\,P_{9.y} +$$
$$r_{6.10}P_{10.y} + r_{6.11}\,P_{11.y} + r_{6.12}\,P_{12.y} + r_{6.13}\,P_{13.y}$$

$$r_{7.y} = r_{1.7}\,P_{1.y} + r_{2.7}\,P_{2.y} + r_{3.7}\,P_{3.y} + r_{4.7}\,P_{4.y} + r_{5.7}\,P_{5.y} + r_{6.7}\,P_{6.y} + P_{7.y} + r_{7.8}\,P_{8.y} + r_{7.9}\,P_{9.y} +$$
$$r_{7.10}P_{10.y} + r_{7.11}\,P_{11.y} + r_{7.12}\,P_{12.y} + r_{7.13}\,P_{13.y}$$

$$r_{8.y} = r_{1.8}\,P_{1.y} + r_{2.8}\,P_{2.y} + r_{3.8}\,P_{3.y} + r_{4.8}\,P_{4.y} + r_{5.8}\,P_{5.y} + r_{6.8}\,P_{6.y} + r_{7.8}\,P_{7.y} + P_{8.y} + r_{8.9}\,P_{9.y} +$$
$$r_{8.10}P_{10.y} + r_{8.11}\,P_{11.y} + r_{8.12}\,P_{12.y} + r_{8.13}\,P_{13.y}$$

$$r_{9.y} = r_{1.9}\,P_{1.y} + r_{2.9}\,P_{2.y} + r_{3.9}\,P_{3.y} + r_{4.9}\,P_{4.y} + r_{5.9}\,P_{5.y} + r_{6.9}\,P_{6.y} + r_{7.9}\,P_{7.y} + r_{8.9}\,P_{8.y} + P_{9.y} +$$
$$r_{9.10}P_{10.y} + r_{9.11}\,P_{11.y} + r_{9.12}\,P_{12.y} + r_{9.13}\,P_{13.y}$$

$$r_{10.y} = r_{1.10}\,P_{1.y} + r_{2.10}\,P_{2.y} + r_{3.10}\,P_{3.y} + r_{4.10}\,P_{4.y} + r_{5.10}\,P_{5.y} + r_{6.10}\,P_{6.y} + r_{7.10}\,P_{7.y} + r_{8.10}$$
$$P_{8.y} + r_{9.10}\,P_{9.y} + P_{10.y} + r_{10.11}\,P_{11.y} + r_{10.12}\,P_{12.y} + r_{10.13}\,P_{13.y}$$

$$r_{11.y} = r_{1.11}\,P_{1.y} + r_{2.11}\,P_{2.y} + r_{3.11}\,P_{3.y} + r_{4.11}\,P_{4.y} + r_{5.11}\,P_{5.y} + r_{6.11}\,P_{6.y} + r_{7.11}\,P_{7.y} + r_{8.11}$$
$$P_{8.y} + r_{9.11}\,P_{9.y} + r_{10.11}\,P_{10.y} + P_{11.y} + r_{11.12}\,P_{12.y} + r_{11.13}\,P_{13.y}$$

$$r_{12.y} = r_{1.12}\,P_{1.y} + r_{2.12}\,P_{2.y} + r_{3.12}\,P_{3.y} + r_{4.12}\,P_{4.y} + r_{5.12}\,P_{5.y} + r_{6.12}\,P_{6.y} + r_{7.12}\,P_{7.y} + r_{8.12}$$
$$P_{8.y} + r_{9.12}\,P_{9.y} + r_{10.12}\,P_{10.y} + r_{11.12}\,P_{11.y} + P_{12.y} + r_{12.13}\,P_{13.y}$$

$$r_{13.y} = r_{1.13}\,P_{1.y} + r_{2.13}\,P_{2.y} + r_{3.13}\,P_{3.y} + r_{4.13}\,P_{4.y} + r_{5.13}\,P_{5.y} + r_{6.13}\,P_{6.y} + r_{7.13}\,P_{7.y} + r_{8.13}$$
$$P_{8.y} + r_{9.13}\,P_{9.y} + r_{10.13}\,P_{10.y} + r_{11.13}\,P_{11.y} + r_{12.13}\,P_{12.y} + P_{13.y}$$

Where,

r_{1y} = Genotypic correlation coefficients between y and I th character (y = Fruit yield)

P_{iy} = Path coefficient due to i th character (i= 1, 2, 3,….13)

1 = Clum length(cm)

2 = Flag Leaf length (cm)

3 = flag leaf breath (cm)

4 = Total tillers per hill

5 = Effective tiller per hill

6 = Panicle length (cm)

7 = Primary branches per panicle

8 = Secondary branches per panicle

9 = Filled grain per panicle

10 = Total grain per panicle

11= Days to maturity

12 = Thousand grain weight

13 = Grain yield per plant (g)

Total correlation, say between 1 and y i.e., r_{1y} is thus partitioned as follows:

$P_{1.y}$ = the direct effect of 1 on y

$r_{1.2}\,P_{2.y}$ = indirect effect of 1 via 2 on y

$r_{1.3}\,P_{3.y}$ = indirect effect of 1 via 3 on y

$r_{1.4}\,P_{4.y}$ = indirect effect of 1 via 4 on y

$r_{1.5}\,P_{5.y}$ = indirect effect of 1 via 5 on y

$r_{1.6}\,P_{6.y}$ = indirect effect of 1 via 6 on y

$r_{1.7}\,P_{7.y}$ = indirect effect of 1 via 7 on y

$r_{1.8}\,P_{8.y}$ = indirect effect of 1 via 8 on y

$r_{1.9}\,P_{9.y}$ = indirect effect of 1 via 9 on y

$r_{1.10}\,P_{10.y}$ = indirect effect of 1 via 10 on y

$r_{1.11}\,P_{11.y}$ = indirect effect of 1 via 11 on y

$r_{1.12}\,P_{12.y}$ = indirect effect of 1 via 12 on y

$r_{1.13}\,P_{13.y}$ = indirect effect of 1 via 13 on y

Where,

$P_{1.y}$, $P_{2.y}$, $P_{3.y}$ .... $P_{13.y}$ = Path coefficient of the independent variables 1, 2, 3,.....,13 on the dependent variable y, respectively.

$r_{1.y}$, $r_{2.y}$, $r_{3.y}$, ..., r_{13y} = Correlation coefficient of 1, 2, 3,...., 13 with y, respectively.

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

$$P^2_{RY} = 1 - (r_{1.y}P_{1.y} + r_{2.y}P_{2.y} + \ldots\ldots\ldots\ldots + r_{13.y}P_{13.y})$$
Where,
$$P^2_{RY} = R^2$$
and hence residual effect, $R = (P^2_{RY})^{1/2}$

$P_{1.y}$ = Direct effect of the i th character on yield y.

$r_{1.y}$ = Correlation of the i th character with yield y.

3.6.8 Multivariate analysis

The genetic diversity among the genotypes was assessed by Mahalanobis's (1936) general distance (D^2) statistic and its auxiliary analyses. The parents selection in hybridization programme based on Mahalanobis's D^2 statistic is more reliable as requisite knowledge of

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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 programme. Multivariate analysis viz. Principal Component analysis, Principal Coordinate analysis, Cluster analysis and Canonical Vector analysis (CVA), which quantify the differences among several quantitative traits, are efficient method of evaluating genetic diversity. These are as follows:

3.6.8.1 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 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.

3.6.8.2 Principal Coordinate analysis (PCO)

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

3.6.8.3 Cluster analysis (CA)

Clustering was done by Tocher method (Rao, 1952). The genotypes were arranged in order of their relative distance from each other. In this method, the two genotypes having the smallest distance from each other were considered first to which a third population having the smallest average D2 value from the first two genotypes was added. Then comes the nearest fourth population and so it goes on. At certain stage when it was felt that after adding a particular population, there was a abrupt increase in the average D2, this population was not added in that cluster. Similarly, a second cluster was formed. Thus the process was continued till all the genotypes were included into one or other cluster.

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.

3.6.8.4 Canonical Vector analysis (CVA)

Canonical vector analysis (CVA) finds linear combination of original variabilities that maximize the ratio of between group to within group variation, thereby giving functions of the original variables that can be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of among groups to the within group variations. The canonical vector are based upon the roots and vectors of WB, where W is the pooled within groups covariance matrix and B is the among groups covariance matrix.

3.6.8.5 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 (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statistic is defined by the formula

$$D^2 = \sum_i^x d_i^2 = \sum_i^x (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where,
Y = Uncorrelated variable (character) which varies from $i = 1$ ------to x
x = Number of characters.

3.6.8.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

$$\text{Average intra-cluster distance} = \frac{\sum D_i^2}{n}$$

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

3.6.8.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chuadhury (1985).

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

Where,

$$\sum D_{ij}^2 = \text{The sum of distances between all possible}$$
        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

3.6.8.8 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.

CHAPTER IV

RESULTS AND DISCUSSIONS

The present study was conducted with a view to characterizing and evaluating thirty aromatic land races as per the guided descriptors developed by IBPGR-IRRI. Seven quantitative characters were observed for characterization. Results have been compiled in tabular form according to descriptors. Studied of thirteen quantitative traits for measurement of genetic variability, diversity, character association and path analysis of thirty aromatic rice landraces carried out in T. Aman season 2014 are presented in the following sections:

4.1 Qualitative Characteristics

4.2 Analysis of variance

4.3 Genetic variability

4.4 Genetic diversity

4.5 Association analysis

4.6 Path coefficient analysis

4.1 Qualitative Characteristics

4.1.1 Basal leaf sheath color:

On the basis of basal leaf sheath coloration the test genotypes were categorized as Green, Green with purple lines, Light purple, Purple as presented in Table 4. But only three types of color was found in this investigation i.e. Green, Green with purple lines and light purple. Sixteen genotypes (G3, G5, G6, G8, G10, G11, G12, G13, G14, G17, G19, G21, G23, G25, G26, G30) showed green color and thirteen genotypes (G1, G4, G7, G9, G15, G16, G18, G20, G22, G24, G27, G28, G29) showed green color with purple lines. Only one genotype (G2) was shown light green colour. Shahidullah (2009) also found only two types of leaf sheath color working with 40 aromatic varieties.

Table 4. Categorization and grouping based on qualitative characteristics.

Sl No.	Characteristics	Grouping based on Descriptors
1	Basal leaf sheath color	Green: G3, G5, G6, G8, G10, G11, G12, G13, G14, G17, G19, G21, G23, G25, G26, G30 Green with purple lines: G1, G4, G7, G9, G15, G16, G18, G20, G22, G24, G27, G28, G29 Light purple: G2 Purple:Nil
2	Green color intensity of leaf blade	No green:Nil Light green: G4, G5, G6, G7, G8, G9, G10, G11, G16, G19, G23, G24, G27, G28, Medium green: G1, G3, G13, G14, G17, G21, G22 Dark green: G2, G12, G15, G18, G20, G25, G26, G29, G30
3	Leaf blade attitude	Erect: G1, G2, G4, G5, G6, G8, G10, G11, G12, G13, G15, G16, G18, G21, G22, G23, G24, G25, G26, G27, G28, G29, G30 Horizontal: G7, G9, G19 Drooping: G3, G14, G17, G20
4	Leaf blade pubescence	Glabrous: Nil Intermediate:Nil Pubescent:All are pubescent
5	Ligule shape	Absent: Nil Truncate: Nil Acute to acuminate: Nil 2-cleft: All are 2-cleft type
6	Presence of Awns	Absent: G1, G2, G3, G4, G5, G6, G7, G9, G10, G11, G13, G14, G15, G17, G18, G19, G20, G21, G22, G23, G25, G26, G27, G28, G29, G30 Partly awned: G8, G12, Fully awned: G16, G24,
7	Panicle: attitude of branches	Erect (compact panicle): G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G24, G26, G27, G28, G29, G30 Semi-erect (semi-compact panicle): Nil Spreading (open panicle): G25 Drooping:Nil

4.1.2 Green color intensity of leaf blade:

Based on green color intensity of leaf blade the test genotypes were categorized in four groups like No green, Light green, Medium green and Dark green. Here fourteen genotypes (G4, G5, G6, G7, G8, G9, G10, G11, G16, G19, G23, G24, G27, G28) showed light green color, seven genotypes (G1, G3, G13, G14, G17, G21, G22) showed medium green color and rest nine genotypes (G2, G12, G15, G18, G20, G25, G26, G29, G30) showed dark green color on leaf blade.

4.1.3 Leaf blade attitude

Based on leaf blade attitude our test genotypes were categorized into three groups as Erect, Horizontal and Drooping nature. 23 genotypes (G1, G2, G4, G5, G6, G8, G10, G11, G12, G13, G15, G16, G18, G21, G22, G23, G24, G25, G26, G27, G28, G29, G30) were erect type, three genotypes (G7, G9, G19) were horizontal type and rest four genotype (G3, G14, G17, G20) were drooping in nature.

4.1.4 Leaf blade pubescence

On the basis of leaf blade pubescence, aromatic rice genotypes were classified as Glabrous, Intermediate and Pubescent. But there was no variation among the genotypes tested and all the genotypes were pubescent type.

4.1.5 Ligule shape

On the basis of ligule shape, aromatic rice genotypes were classified as Absent, Truncate, Acute to acuminate and 2-cleft type. But our all genotypes were 2-cleft type that means there was no significant difference among the genotypes. According to IRRI most of the cultivated rice have 2-cleft type ligule shape and wild type genotypes may show others type. From the below figure we can see the 2-ceft type ligule where figure-5 is a hypothetical view and figure-9 shows real view taken from my experimental field.

4.1.6 Presence of Awns

This character was observed at maturity stage and based on presence of awns our test genotypes were categorized into three groups as Absent, Partly awned and fully awned where 23 genotypes (G1, G2, G3, G4, G5, G6, G7, G9, G10, G11, G15, G17, G18, G19, G20, G21, G23, G25, G26, G27, G28, G29, G30) were awnless, two genotypes (G12 and G22) were partly awned and five genotypes (G8, G13, G14, G16 and G24) were fully awned.

Plate 4. Real view of 2-cleft type ligule.
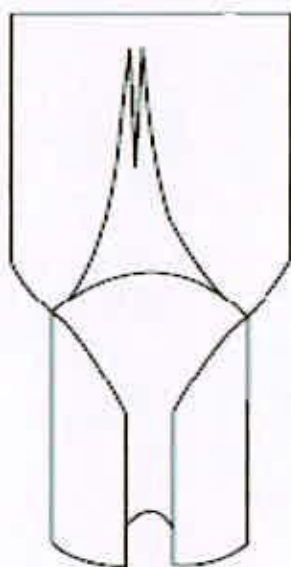
Figure 5. Hypothetical view of 2-cleft type ligule.
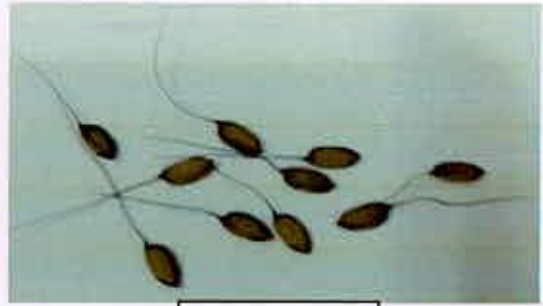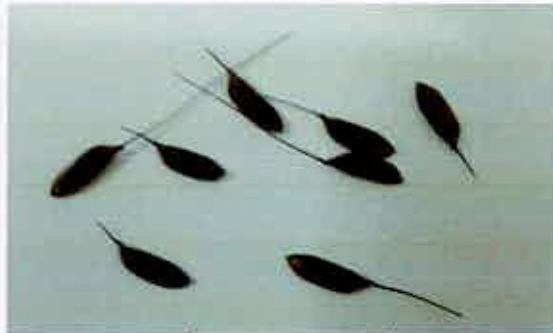
Plate 5. The above pictures showing fully awned genotypes (G8, G13, G14, G16, G24)

4.1.7 Panicle: attitude of branches

The compactness of the panicle was classified according to its mode of branching, angle of primary branches, and spikelet density in five groups as Erect (compact panicle)-1, Semi-erect (semi-compact panicle)-3, Spreading (open panicle)-5, Horizontal-7 and Drooping-9 type panicle where 29 genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20, G21, G22, G23, G24, G26, G27, G28, G29, G30) showed compact type and only one genotype (G25) was showed for open panicle. Semi-compact panicle, horizontal and drooping natured panicles were not found among the genotypes.

Plate 6. Showing different panicle of gentypes (G1 to G20)

Plate 8. Showing different panicle of genotypes (G21 to G30)

4.2 Analysis of variance

The analysis of variance of 30 aromatic rice genotypes for different quantitative traits are shown in Table 5. Analysis of variance indicated that the difference among genotypes for all the traits under study *viz.*, clum length, flag lea length, flag leaf breadth, total tillers per hill, effective tiller per hill, panicle length, primary branches pee panicle, secondary branches per panicle, filled grain per panicle, total grain per panicle, days to maturity, thousand grain weight and grain yield per plant were highly significant. Yaqoob *et al.* (2012) also observed similar results among his genotypes for days to maturity, total number of tillers per plant, effective tillers per plant, plant height, panicle length, 100-grain weight and yield per plant. Tiwari *et al*, (2011) also observed significant variation among genotypes for effective tillers per plant, length of panicle, number of spikelets per panicle, number of fertile spikelets and grain yield per plant. These results suggest that all the studied traits were highly correlated with each other. Thus opportunity exists to use these experimental materials as precious breeding tools.

4.2.1 Trait-wise mean performance of the genotypes

Univariate statistical analysis gave an excellent opportunity to identify and group the genotypes into different categories with respect to various traits individually. The mean performances of the 30 rice genotypes for their traits are shown in Table 6. Clum length had mean value of 143.55 cm with a wide variation from 121.90 cm (G12) to 162.47 cm (G21). Maximum flag leaf length (55.13 cm) was observed in genotype G2 while minimum (26.87 cm) was observed in genotype G25. The mean value of flag leaf length was 38.74 cm. Flag leaf breadth ranged from 0.90 cm to 1.53 cm with mean value of 1.15 cm. The maximum flag leaf breadth was observed in genotype G2 (1.53 cm) while minimum flag leaf breadth was observed in genotype G8 (0.90 cm).

Total tiller per hill ranged from 8.90 to 21.03 with a mean value of 13.09. The maximum total tiller per hill was observe in genotype G1 (21.03) while minimum total tiller per hill was observed in the genotype G22 (8.90). Highest effective tiller per hill was observed in genotype G1 (14.43) while lowest effective tiller number per hill was observed in genotype G22 (6.70).

Table 5. Analysis of variance of different characters in aromatic Rice.

Source	Df	Mean sum of square												
		CL	FLL	FLB	TPH	ETH	PL	PBP	SBP	FGP	TGP	DM	TGW	GYP
Replication	2	54.55	60.29	0.01	1.45	1.55	4.01	1.21	51.76	275.97	943.68	150.43	1.12	0.38
Treatment	29	255.41**	205.22**	0.03**	13.57**	9.51**	16.91**	3.93**	321.07**	6,884.57**	12,675.40**	60.90**	45.52**	102.94**
Error	58	42.04	12.06	0.02	5.13	3.33	1.97	0.78	25.80	833.17	978.79	16.16	1.01	1.90

** = Significant at the 0.01 level.

CL = clum length(cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tillers per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight, GYP = grain yield per plant (g)

Table 6. Mean performance of various growth parameter.

Genotype	CL	FLL	FLB	TPH	ETH	PL	PBP	SBP	FGP	TGP	DM	TGW	GYP
G1	147.67	45.80	1.25	21.03	14.43	29.83	12.87	16.60	143.90	156.37	159.67	17.16	20.14
G2	137.73	55.13	1.53	16.53	12.33	28.10	13.67	31.93	166.53	179.80	171.33	19.40	20.67
G3	160.63	54.00	1.09	14.20	9.93	28.00	12.77	45.03	284.33	332.07	161.00	18.87	26.14
G4	151.07	45.37	1.27	12.70	9.57	23.70	13.53	43.60	224.03	242.50	166.33	18.63	22.53
G5	143.43	42.67	1.17	13.67	11.13	27.60	12.30	42.00	173.17	225.40	165.00	22.67	29.79
G6	143.97	36.13	1.13	12.90	10.60	27.53	12.67	34.00	224.70	290.63	162.67	18.03	25.10
G7	151.87	29.27	1.10	13.63	11.40	30.57	10.17	17.93	106.70	115.20	162.00	12.07	13.82
G8	138.43	33.00	0.90	13.47	10.70	26.90	11.73	30.70	185.00	198.23	158.00	23.47	32.67
G9	140.83	45.07	1.24	12.97	10.33	29.77	10.90	37.10	208.03	246.00	164.67	16.63	26.48
G10	153.73	36.20	1.26	13.00	11.80	25.00	10.67	33.37	165.57	201.50	153.67	15.43	16.67
G11	151.02	34.53	1.14	12.50	8.83	31.57	12.97	25.33	133.73	142.47	172.00	20.67	20.75
G12	121.90	34.13	1.19	12.93	11.37	28.77	12.13	27.70	154.90	177.33	161.33	26.13	25.87
G13	131.00	29.03	1.10	12.97	10.33	33.53	15.50	42.80	209.60	234.60	161.00	21.87	22.60
G14	137.27	33.97	1.03	12.40	8.80	25.90	13.07	43.97	242.80	272.93	158.00	20.07	20.93
G15	133.68	53.90	1.05	13.47	9.93	29.83	13.53	27.80	174.40	186.63	160.00	15.73	16.60
G16	147.82	31.80	1.12	12.00	7.23	27.11	12.33	40.03	236.50	264.77	169.33	23.03	22.57
G17	143.07	32.67	1.14	13.27	8.53	28.07	12.40	33.73	203.03	251.17	159.33	15.77	16.29
G18	135.68	36.00	1.20	9.80	8.13	29.47	12.07	44.87	242.07	274.73	165.67	14.47	18.03
G19	153.85	47.43	1.27	14.80	13.00	26.90	12.67	33.53	199.83	153.90	162.67	15.67	24.30
G20	141.96	54.43	1.14	12.93	10.33	26.87	12.40	46.07	202.47	236.50	162.67	15.20	21.20

CL = clum length (cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tiller per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight and GYP = grain yield per plant (g).

Table 6. (contd.)

Genotype	CL	FLL	FLB	TPH	ETH	PL	PBP	SBP	FGP	TGP	DM	TGW	GYP
G21	162.47	40.67	1.21	12.10	8.93	30.43	15.47	60.40	186.17	375.50	154.00	13.20	13.87
G22	137.10	34.17	1.10	8.90	6.70	28.80	13.37	56.20	268.33	311.00	159.33	13.57	17.95
G23	133.58	27.87	1.21	10.00	9.50	23.10	12.73	53.43	269.87	303.17	165.67	15.23	22.15
G24	137.00	39.80	1.08	15.73	10.97	28.60	11.93	24.43	140.67	156.00	162.00	11.27	13.41
G25	142.18	26.87	1.19	13.07	7.40	29.90	12.87	24.53	124.80	133.47	161.67	13.37	12.24
G26	147.51	33.93	0.97	12.60	9.20	22.97	13.33	38.00	156.83	173.43	159.33	16.13	17.99
G27	136.13	31.73	1.09	12.20	10.03	27.30	13.47	37.60	257.67	298.30	157.67	19.37	29.97
G28	136.87	34.57	1.13	12.30	7.17	27.87	12.83	40.20	234.30	276.30	158.67	15.83	24.61
G29	153.87	43.47	1.14	12.70	11.70	26.27	12.53	38.57	251.53	269.40	158.00	25.20	32.53
G30	153.03	38.63	1.07	12.00	9.27	28.90	11.30	41.97	255.20	275.23	168.33	21.00	33.07
Min.	121.90	26.87	0.90	8.90	6.70	22.97	10.17	16.60	106.70	115.20	153.67	11.27	12.24
Max.	162.47	55.13	1.53	21.03	14.43	33.53	15.50	60.40	284.33	375.50	172.00	26.13	33.07
Mean	143.55	38.74	1.15	13.09	9.99	27.97	12.67	37.11	200.89	231.82	162.03	17.84	22.03
LSD	10.60	5.67	0.08	3.70	2.29	1.45	1.45	8.30	47.18	51.13	6.57	1.64	2.25
CV (%)	4.52	8.96	4.66	17.31	18.28	5.02	7.00	13.69	14.37	13.50	2.48	5.64	6.26

CL = clum length (cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tiller per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight and GYP = grain yield per plant (g).

Maximum panicle length was observed in genotype G13 (33.53 cm) while minimum was observed in genotype G26 (22.97 cm). The mean value of panicle length was 27.97 cm.

The primary branches per panicle among the genotypes ranged from 10.17 to 15.50 with a mean value of 12.67. The maximum primary branches per panicle was observed in genotype G13 (15.50) and the minimum primary branches per panicle was observed in genotype G7 (10.17).Secondary branches per panicle among the genotypes ranged from 16.60 to 60.40 with a mean value of 37.11. The maximum secondary branches per panicle was found in genotype G21 (60.40). The minimum secondary branches per panicle was found in genotype G1 (16.60).The maximum filled grains per panicle was observed in genotype G3 (284.33) while minimum filled grains per panicle was observed in genotype G7 (106.70). Those values ranged from 106.70 to 284.33. Since, greater number of filled grains per panicle was one of the major criteria which contribute to higher grain yield and could be utilized in further program.Total grain per panicle ranged from 115.20 to 375.50 with mean value of 231.82. The highest total grain per panicle was found in the genotype G21 (375.50) while the lowest total grain per panicle was found in genotype G7 (115.20).

Days to maturity varies from 153.67 days to 172.00 days with a mean value of 162.03 days. The minimum days to maturity was found in genotype G10 (153.67). The maximum days to maturity was found in genotype G11 (172.00).

The maximum thousand grain weight was observed in genotype G12 (26.13 g) while minimum thousand grain weight was observed in genotype G24 (11.27 g). Those values ranged from 11.27 g to 26.13 g. Since, greater number of filled grains per panicle was one of the major criteria which contribute to higher grain yield as well grain quality and could be utilized in further program.Regarding the grain yield per plant, maximum value was obtained in genotype G30 (33.07 g) which was followed by G8 (32.67 g) and G29 (32.53 g) and minimum value was obtained in genotype G25 (12.24 g). The yield of G30 (33.07 g) was high may be due to long growth duration (168.33 days), more panicle length (28.90 cm), more thousand grain weight (21.00 g), more filled grain per panicle (255.20) and less unfilled grain per panicle (20.03).

Plate 8. Showing different seed coat colour of 30 aromatic rice genotypes.

4.3 Estimation of genetic parameters of aromatic rice

Genotypic variances, phenotypic variances, heritability, genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance and genetic advance as percent of mean, GA (%) for all the yield contributing traits are presented in Table 7.

4.3.1 Variability parameters

A wide range of variation was observed among 30 aromatic rice (*Oryza sativa* L.) genotypes for thirteen yield contributing traits. The perusal of data revealed that variance due to genotype was highly significant for all the traits (Table 7) which suggested there were inherent genetic differences among the genotypes. Phenotypic variance was higher than the genotypic variances for all the traits thus indicated the influences of environmental factor on these traits. Devi *et al.* (2006) and Prajapati *et al.* (2011) reported similar findings earlier.

Table 7. Estimation of genetic parameters in eight characters of 30 genotypes in aromatic Rice.

Parameters	V_P	V_G	V_E	PCV	GCV	ECV	Heritability	Genetic advance (5%)	Genetic advance (% mean)
CL	113.16	71.12	42.04	7.41	5.88	4.52	62.85	13.77	9.59
FLL	76.45	64.39	12.06	22.57	20.71	8.96	84.22	15.17	39.16
FLB	0.01	0.01	0.00	10.53	9.44	4.66	80.44	0.20	17.45
TPH	7.95	2.81	5.14	21.54	12.81	17.31	35.38	2.06	15.70
ETH	5.39	2.06	3.33	23.26	14.37	18.28	38.20	1.83	18.30
PL	6.95	4.98	1.97	9.43	7.98	5.02	71.60	3.89	13.90
PBP	1.84	1.05	0.79	10.69	8.08	7.00	57.13	1.59	12.58
SBP	124.23	98.42	25.80	30.03	26.73	13.69	79.23	18.19	49.01
FGP	2850.31	2017.13	833.18	26.58	22.36	14.37	70.77	77.83	38.74
TGP	4877.67	3898.87	978.80	30.13	26.94	13.50	79.93	115.00	49.61
DM	31.08	14.91	16.17	3.44	2.38	2.48	47.98	5.51	3.40
TGW	15.85	14.84	1.01	22.32	21.59	5.64	93.60	7.68	43.04
GYP	35.59	33.68	1.90	27.08	26.34	6.26	94.65	11.63	52.79

CL = clum length(cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tiller per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight, GYP = grain yield per plant (g).

Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the traits (Table 7) indicating that they all interacted with the environment to some extent. Among the traits total grain per panicle (30.13% and 26.94%) exhibited high estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV). Flag leaf length (22.57% and 20.71%) showed very close results of PCV and GCV to thousand grain weight (22.32% and 21.59%) and flag leaf breadth (10.53% and 9.44%) showed very close results of PCV and GCV to primary branches per panicle (10.69% and 8.08%). A depicted PCV and GCV was presented in Figure 6.

On the other hand, less differences between PCV and GCV were observed in the traits flag leaf breadth (10.53% and 9.44%), thousand grain weight (22.32% and 21.59%), grain yield per plant (27.08% and 26.34%) and days to maturity (3.44% and 2.38%). They showed very close GCV and PCV. Clum length (7.41% and 5.88%), days to maturity (3.44% and 2.38%) exhibited lower level of PCV and GCV value. The high values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed in flag leaf length (22.57% and 20.71%), secondary branches per panicle (30.03% and 26.73%), filled grain per panicle (26.58% and 22.36%), total grain per panicle (30.13% and 26.94%), thousand grain weight (22.32% and 21.59%) and grain yield per plant (27.08% and 26.34%) suggesting that the possibility of yield improvement through selection of these traits.
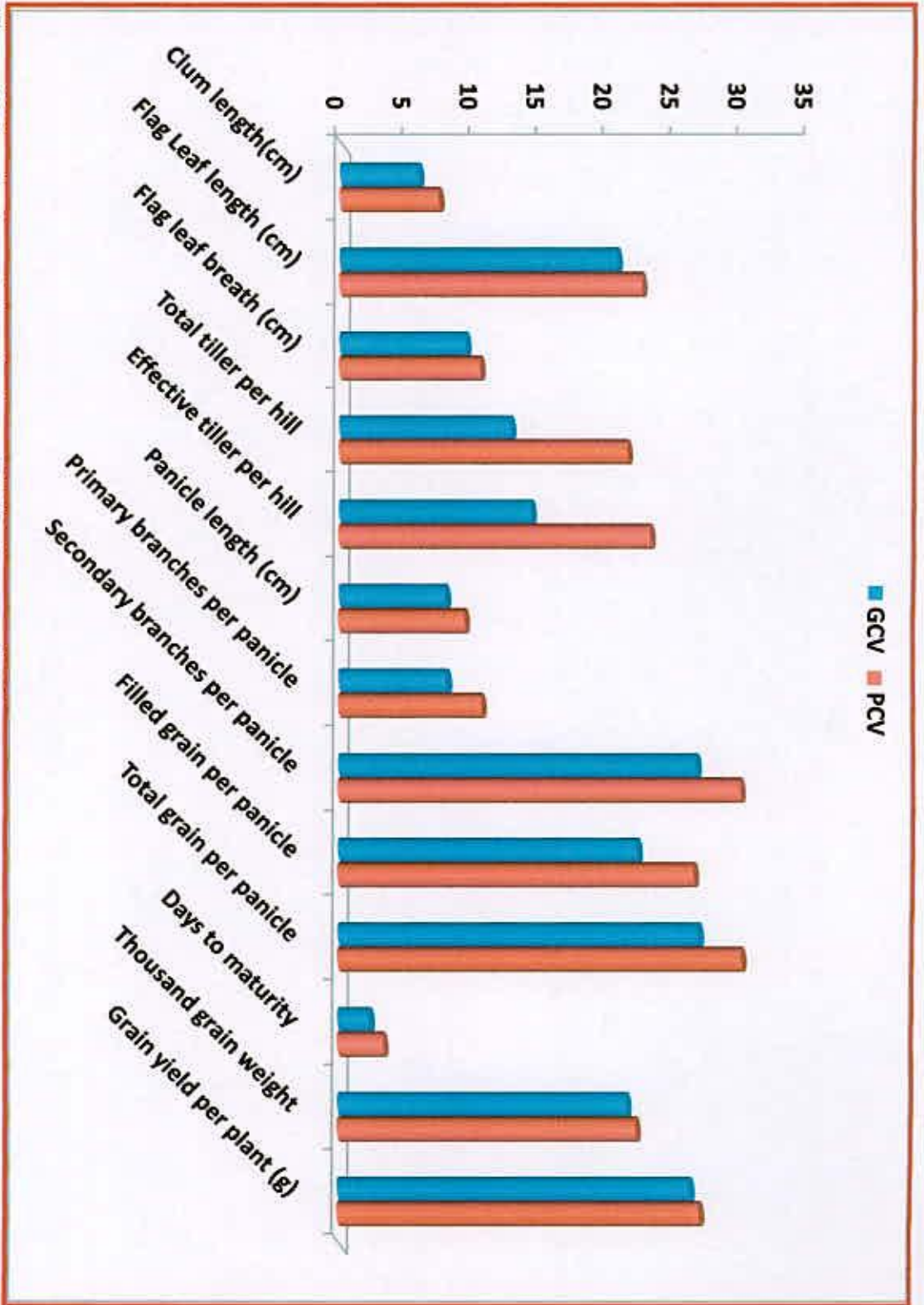
Figure 6. Genotypic and phenotypic variability in aromatic Rice.

4.3.2 Heritability

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait. Heritability was classified as low (below 30%), medium (30-60%) and high (above 60%) as suggested by Johnson *et al.* (1955). The traits studied in the present investigation expressed moderate to high heritability estimates ranging from 35.38 to 94.65 percent. Among the traits, highest heritability was recorded by grain yield per plant (94.65%) followed by thousand grain weight (93.60%), flag leaf length (84.22%), flag leaf breadth (80.44%), total grain per panicle (79.93%), secondary branches per panicle (79.23), panicle length (71.60%), Lowest heritability value was recorded by total panicle per hill (35.38) (Table 7). A depicted heritability and genetic advance in percent of mean was presented in Figure 7.

High heritability values indicate that the traits under study are less influenced by environment in their expression. It also indicates the scope of genetic improvement of these traits through selection. Thus a breeder may make his selection securely on the basis of phenotypic expression of these traits on the individual plant. Patel *et al.* (2012) observed highest heritability for plant height, total tillers, panicle length, total number of spikelets per panicle, number of filled spikelets per panicle, number of unfilled spikelets per panicle and grain yield per meter square.

4.3.3 Genetic advance

The genetic advance is a useful indicator of the progress that can be expected as result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al.*, 1955). In the present study genetic advance was highest for total grain per panicle (115.00) followed by filled grain per panicle (77.83), secondary branches per panicle (18.19) and lowest for flag leaf breadth (0.20) among yield contributing traits. The genetic advance as percent of mean was the highest in case of grain yield per plant (52.79%), total grain per panicle (49.61%), secondary branches per panicle (49.01%), thousand grain weight (43.04%) and filled grain per panicle (38.74%), while it was lowest in days to maturity (3.40%) (Table 7).

If selection is made for improving the particular trait under study, one should focus on heritability and genetic advance. The information on genetic variation, heritability and
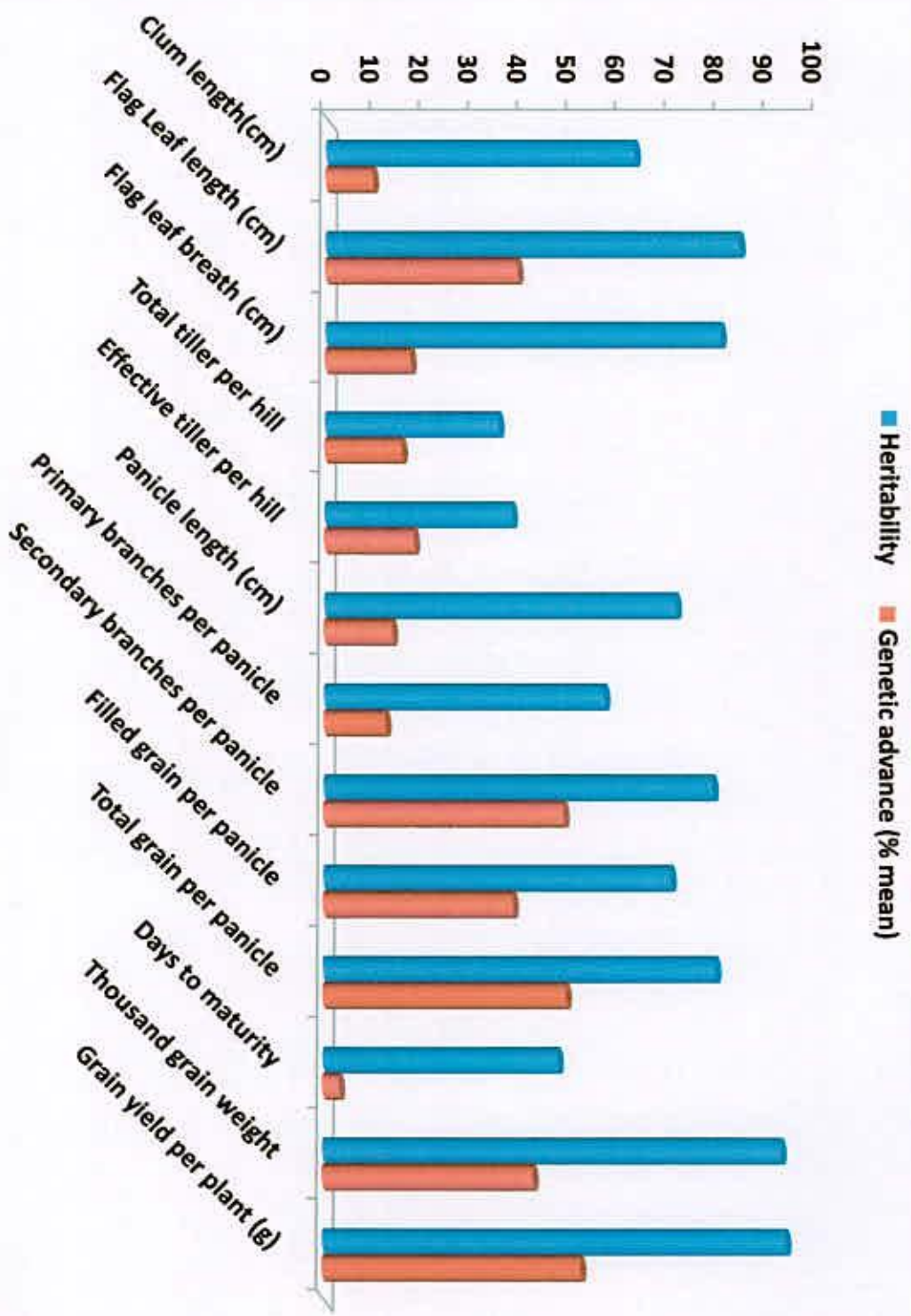
Figure 7. Heritability and genetic advance over mean in aromatic Rice.

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genetic advance help to predict the genetic gain that could be obtained in later generations. High heritability with high genetic advance exhibited by the traits are controlled by additive gene action (Panse and Sukhatme, 1957) and can be improved through simple or progeny selection methods. Selection for the traits having high heritability associated with high genetic advance leads to accumulate more additive genes. It can enhance the opportunities for further improvements of their performance. In the present study, high heritability along with high genetic advance was noticed for the traits flag leaf length, secondary branches per panicle, filled grain per panicle, total grain per panicle, thousand grain weight and grain yield per plant. Other traits showed high heritability along with moderate or low genetic advance which can be improved by inter mating superior genotypes of segregating population (Samadia, 2005). Babu *et al.* (2012) also found highest genetic advance for number of filled grains per panicle and highest genetic advance as per cent of mean in case of number of unfilled grains per panicle.

4.4 Genetic diversity

The knowledge of available genetic diversity is an important factor for any heritable improvement and its nature and degree is useful for selecting desirable parents from a germplasm for the successful breeding programme. There is still much scope for improving of genetic architecture desirable for hybrid through heterosis breeding. Its magnitude in desirable direction is preferable. The success of hybridization depends upon the selection of suitable parental genotypes and performance of their cross combinations.

The amount of diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. In the present investigation, 30 genotypes of aromatic rice were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanobis' (1936) concept of generalize distance (D^2) considering eight important quantitative characters. Based on D^2-value, the genotypes were grouped into five clusters (Table 8).

Table 8. Distribution of thirty genotypes in different clusters

Cluster no.	No. of Genotypes	No. of populations	Name of genotypes
I	1, 7, 11, 24, 25	5	RCO-538, RCO-456, RCO-464, RCO-463, RCO-464
II	2, 5, 8, 10, 12, 15, 26	7	RCO-539, RCO-460, RCO-466, RCO-487, RCO-428, RCO-511, RCO-498
III	4, 6, 9, 13, 17, 19, 20	7	RCO-441, RCO-470, RCO-495, RCO-453, RCO-484, RCO-477, RCO-531
IV	3, 14, 16, 18, 22, 23, 27, 28, 29, 30	10	RCO-433, RCO-480, RCO-491, RCO-500, RCO-530, RCO-441, RCO-484, RCO-524, RCO-501, RCO-485
V	21	1	RCO-490
	Total	30	

4.4.1 Nonhierarchical clustering

With the application of covariance matrix for nonhierarchical clustering, 30 aromatic rice land races were grouped into five different clusters. It is stated that 33.33% genotypes were included in cluster IV and it was followed by 23.33% in clusters both II & III, 16.67% in cluster I and the remaining were in cluster V. The composition of clusters with different genotypes is presented in Table 8. The cluster IV included 10 genotypes, which is the highest followed by cluster II & III whose are contained seven genotypes each. Cluster I contained six genotypes and only one genotype included in cluster V. Zia-Ul-Qamar *et al.* (2012) reported on 50 rice genotypes and exhibited six distinct clusters with the range of two genotypes in cluster VI to thirteen genotypes in cluster I and III each.

4.4.2 Principal component analysis

Eigen values of principal component axis, percent of total variation and cumulative variation accounted for them obtained from principal component analysis are presented in Table 9. The results showed that the first principal axis, clum length largely accounted for the variation among the genotypes which alone contributed 25.94% of the total variation among the genotypes. The first five characters of the principal component axes with eigen values above unity accounted for 78.57% of the total variation among the thirteen characters. The rest eight characters contributed remaining 21.43% of total variation. Based on principal component scores I and II obtained from the principal component analysis, a two-dimensional scatter diagram (Z_1-Z_2) using component score 1 as X axis and component score 2 as Y axis was constructed, which has been presented in Figure 8. Gana *et al.* (2013) analyzed 36 accessions of rice for PCA and showed the combination of first five principal component axes of first year. In second year it was 65.4% of the total variation. 123 rice germplasm including checks PCA resulted in the first two components with Eigen value greater than 1 accounting for 78% of the total variation Maji and Shaibu (2012). Zia-Ul-Qamar *et al.* (2012) studied on 50 rice genotypes and revealed that two principal components presented 65% information of the raw data of the yield related traits. Sanni *et al.* (2010) carried out an experiment on 434 accessions of rice and revealed that the first three principal components explained about 58.41% of the total variation among the 14 characters.

Table 9. Eigen values and yield percent contribution of thirteen characters of 30 genotype.

Characters	Eigen values	Percent variation	Cumulative % of Percent variation
Clum length(cm)	3.1133	25.94	25.94
Flag Leaf length (cm)	2.1555	17.96	43.90
Flag leaf breath (cm)	1.6558	13.80	57.70
Total tiller per hill	1.3417	11.18	68.88
Effective tiller per hill	1.1632	9.69	78.57
Panicle length (cm)	0.8446	7.04	85.61
Primary branches per panicle	0.5809	4.84	90.45
Secondary branches per panicle	0.4785	3.99	94.44
Filled grain per panicle	0.2711	2.26	96.70
Total grain per panicle	0.2376	1.02	97.72
Days to maturity	0.2001	0.87	98.59
Thousand grain weight	0.1007	0.34	99.93
Grain yield per plant (g)	0.0946	0.07	100.00

Z1-Z2 Graph
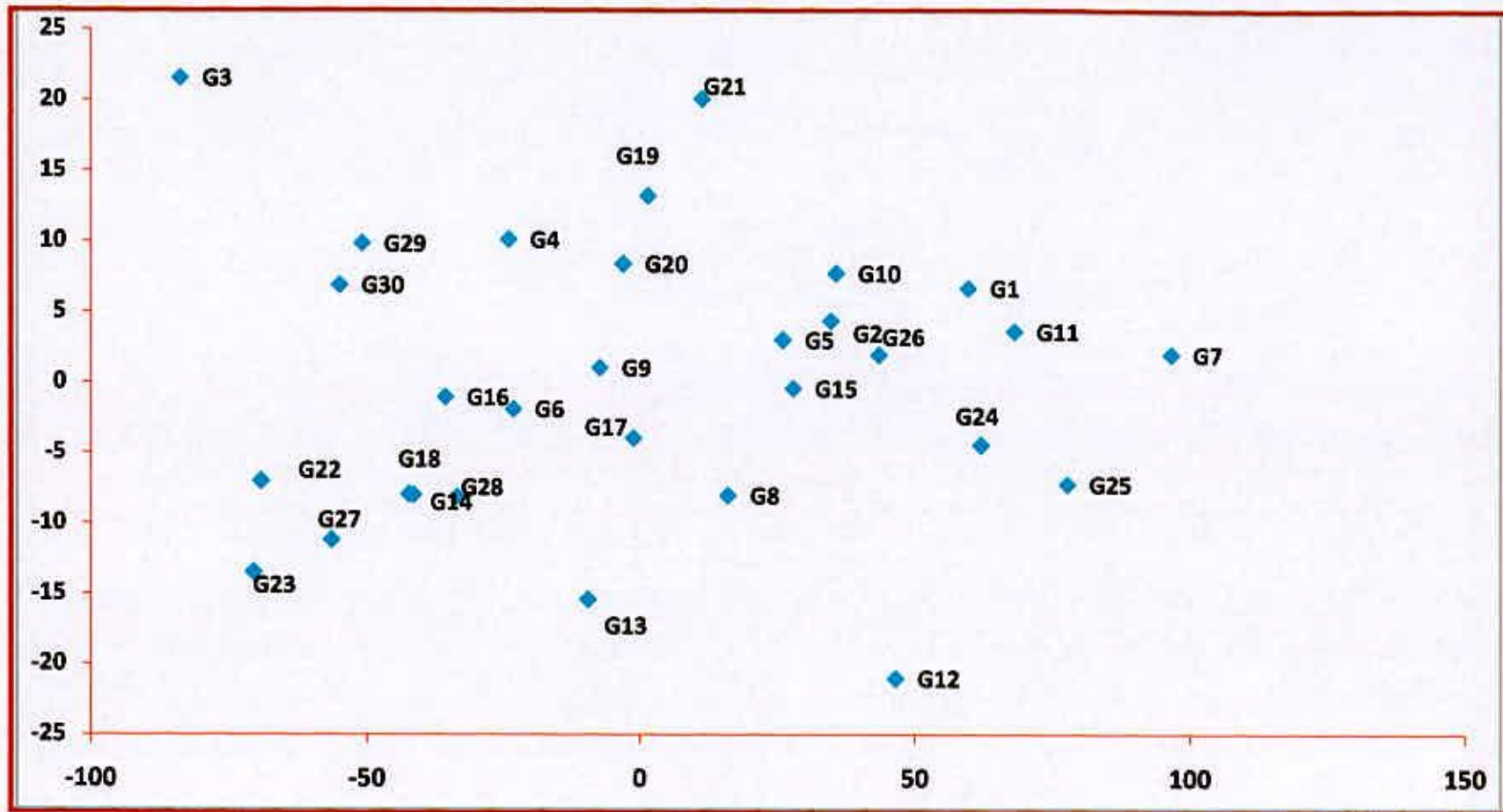
Figure 8.Scatter diagram of aromatic Rice genotypes of based on their principal component scores.

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4.4.3 Inter cluster distance

The average intra and inter cluster D^2 values are given in Table 10 and the nearest and farthest cluster from each cluster based on D^2 value is given in Table 11. It was observed that inter cluster distance was always higher than those of intra cluster distance. Zia-Ul-Qamar *et al.* (2012) observed larger inter cluster distance than the intra-cluster distance suggesting wider genetic diversity among the genotypes. The maximum inter cluster distance was observed between genotypes of cluster I and IV (10.080) followed by clusters III and V (10.997) and II and III (8.944) (Table 9). Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding programme. Zia-Ul-Qamar *et al.* (2012) reported maximum inter cluster distance was observed between cluster I and VI (79.81) followed by cluster I and V (71.90). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum variability of population. However, the highest inter cluster distance was observed between clusters I and IV indicated the genotypes in these clusters were diversed than those clusters. Cluster IV was the most diverse as many other clusters showed maximum inter cluster distance with it. The minimum distance observed between clusters II and III (3.941) indicated close relationship among the genotypes included.

4.4.4 Intra cluster distance

The intra cluster D^2 values were given in Table 10. The intra cluster distance was observed in the clusters I, II, III and IV. The intra cluster distance was higher in cluster III (0.876) followed by cluster IV (0.545) and lowest in cluster V (0.00). The intra cluster distances in all the five clusters were lower than the inter cluster distances and which indicated that genotypes within the same cluster were closely related. The inter cluster distances were larger than the intra cluster distances which indicated wider genetic diversity among the genotypes of different groups. Hence, there is a lot of scope for exchange of genes among genotype within these clusters. Table 10 showed average intra and inter cluster D^2 values of five clusters. The mutual relationships among the five clusters are presented in the diagram (Figure 8). The average inter and intra cluster distance have been used to denote cluster distance.

Table 10. Intra (Bold) and inter cluster distances (D^2) for 30 genotypes.

Cluster	I	II	III	IV	V
I	**0.234**	5.279	7.121	11.080	10.065
II		**0.345**	3.941	7.796	8.944
III			**0.876**	4.297	8.613
IV				**0.545**	10.997
V					**0.00**

Table 11. The nearest and farthest clusters from each cluster between D^2 values in aromatic Rice.

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	II (5.279)	IV (11.080)
2	II	III (3.941)	V (8.944)
3	III	II (3.941)	V (8.613)
.4	IV	III (4.297)	I (11.080)
5	V	III (8.613)	IV (10.997)

4.4.5 Cluster diagram

The positions of the genotypes in the scatter diagram were apparently distributed into four groups, which indicated that considerable diversity existed among the genotypes (Figure 8).
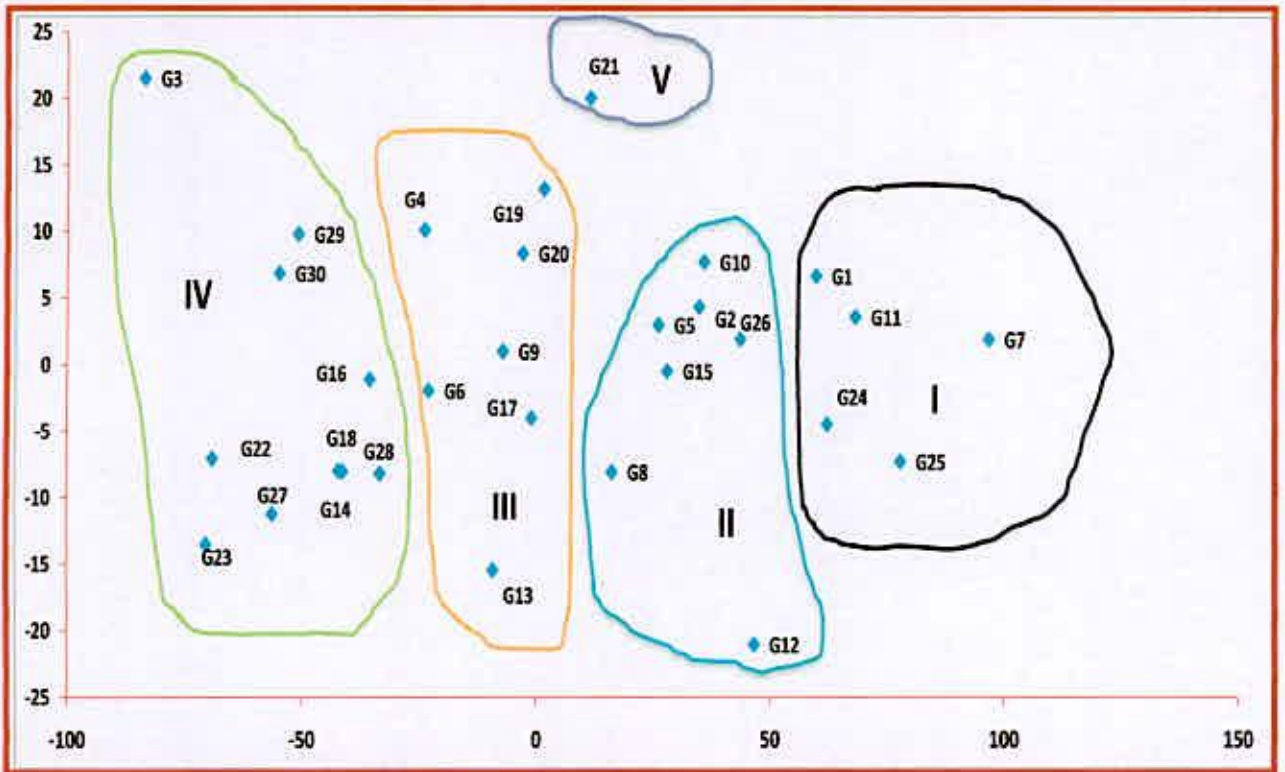
Figure 9. Cluster diagram of aromatic Rice genotypes of based on their principal component scores.

4.4.6 Characterization of individual clusters

The mean values of each cluster for eight characters are presented in Table 12. There was wide range of variation in the cluster mean values for all the characters. The mean values of all characters for the respective clusters were categorized into low (L), intermediate (I) and high (H) classes.

Minimum clum length was observed in cluster II (139.49 cm) and Cluster I, III and IV showed intermediate values (145.95 cm, 143.68 cm and 143.20, respectively) and maximum clum length by cluster V (162.47 cm). Cluster III had highest flag leaf length (41.45 cm) and cluster I had lowest flag leaf length (35.25 cm). Maximum (1.21 cm) and minimum (1.12) flag leaf breadth was observed in cluster V and IV respectively. For total tillers per hill, cluster I showed maximum value (15.19) and cluster IV showed minimum value (11.65).

Effective tillers per hill was the highest in cluster II with a mean value of (10.92) and it was least in genotypes belongs to the cluster IV (8.85). Highest panicle length was recorded by the cluster V (30.43) while cluster II (27.02) showed the least panicle length. The maximum primary branches per panicle was observed in cluster V (15.47), whereas minimum primary branches per panicle was observed in cluster I (12.16). Highest secondary branches per panicle was recorded by the cluster V (60.40) while cluster I (21.76) showed the least secondary branches per panicle. Filled grain per panicle was the highest in cluster IV with a mean value of (254.26) and it was least in genotypes belongs to the cluster I (129.96). The maximum total grain per panicle was observed in cluster V (375.5), whereas minimum total grain per panicle was observed in cluster I (140.70). Highest days to maturity was recorded by the cluster I (163.47) while cluster V (154.00) showed the least days to maturity.

For thousand grain weight, cluster II showed maximum value (19.85) and cluster V showed minimum value (13.20). A highest grain yield er plant was recorded by the genotype making up cluster IV (24.79 g) while cluster V showed the least grain yield (13.87 g) per plant.

Table 12. Cluster mean values of thirteen different characters of 30 genotypes

Characters	I	II	III	IV	V
Clum length(cm)	145.95 (I)	139.49 (L)	143.68 (I)	143.20 (I)	162.47 (H)
Flag Leaf length (cm)	35.25 (L)	41.28 (H)	41.45 (H)	36.62 (I)	40.67 (I)
Flag leaf breath (cm)	1.15 (I)	1.15 (I)	1.18 (I)	1.12 (L)	1.21 (H)
Total tiller per hill	15.19 (H)	13.67 (I)	13.22 (I)	11.65 (L)	12.10 (I)
Effective tiller per hill	10.61 (I)	10.92 (H)	10.38 (I)	8.85 (L)	8.93 (L)
Panicle length (cm)	30.09 (H)	27.02 (L)	28.05 (I)	27.27 (L)	30.43 (H)
Primary branches per panicle	12.16 (L)	12.48 (I)	12.87 (I)	12.65 (I)	15.47 (H)
Secondary branches per panicle	21.76 (L)	33.07 (I)	38.69 (I)	44.19 (I)	60.40 (H)
Filled grain per panicle	129.96 (L)	168.06 (I)	210.24 (I)	254.26 (H)	186.17 (I)
Total grain per panicle	140.70 (L)	191.76 (I)	236.47 (I)	287.79 (I)	375.5 (H)
Days to maturity	163.47 (H)	161.24 (I)	162.76 (I)	162.17 (I)	154.00 (L)
Thousand grain weight	14.91 (I)	19.85 (H)	17.40 (I)	18.66 (I)	13.20 (L)
Grain yield per plant (g)	16.07 (I)	22.89 (I)	22.64 (I)	24.79 (H)	13.87 (L)

H= High value
I=Intermediate value
L= Low value

The present study revealed that the cluster V with high mean values for maximum desirable traits are desired to be crossed with cluster I and cluster II whose possessed low mean values of many characters for getting high heterosis. Same cross between clusters IV and I; and cluster IV and II for two characters. This finding was strongly supported with identification of similar cluster combinations from interpretation of inter cluster distance made in the present study and thereby the expected progenies inculcate traits in a positive direction and further selection would be more effective.

4.4.7 Contribution of characters towards divergence

Contribution of characters towards the divergence obtained from canonical variates analysis is presented in Table 13. The character, which gave high absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Likewise, the characters, which gave higher absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If the same character given equal magnitude for both the vectors than the character was considered responsible for primary as well as secondary differentiation.

In vector (Z_1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were clum length (0.0146), flag Leaf length (0.0062), total tiller per hill (0.1139), effective tiller per hill (0.2161), panicle length (0.0153), primary branches per panicle (0.3437), secondary branches per panicle (0.0130), total grain per panicle (0.0543), days to maturity (0.0489) and grain yield per plant (0.0363). In vector 2 (Z_2), the second axis of differentiation clum length (0:0680), flag leaf breadth (3.1762), total tiller per hill (0.0099), Panicle length (0.2057), primary branches per panicle (0.3551), secondary branches per panicle (0.1731), total grain per panicle (0.0753) and grain yield per plant (0.0550) were important because all these characters had positive signs. Clum length, total tillers per hill, panicle length, primary branches per panicle, secondary branches per panicle, total grain per panicle and grain yield per plant had positive signs in both the vectors, which indicated they were the important component characters having higher contribution to the genetic divergence among the aromatic rice land races studied.

Table 13. Relative contributions of the thirteen characters of 30 land races to the total divergence.

Characters	Principal Component	
	Vector-1	Vector-2
Clum length (cm)	0.0146	0.0680
Flag Leaf length (cm)	0.0062	-0.0021
Flag leaf breath (cm)	-2.9574	3.1762
Total tiller per hill	0.1139	0.0099
Effective tiller per hill	0.2161	-0.0280
Panicle length (cm)	0.0153	0.2057
Primary branches per panicle	0.3437	0.3551
Secondary branches per panicle	0.0130	0.1731
Filled grain per panicle	-0.0847	-0.0261
Total grain per panicle	0.0543	0.0753
Days to maturity	0.0489	-0.1523
Thousand grain weight	-0.1076	-0.0163
Grain yield per plant (g)	0.0363	0.0550

4.5 Association analysis

Relationships among yield and yield contributing traits were studied through analysis of correlation among them. Phenotypic and genotypic correlation co-efficient among thirteen traits of 30 aromatic rice genotypes are presented in Table 14. In the present study out of 78 associations, 34 associations were significant both at genotypic and phenotypic level. Among the 34 associations, 23 associations were positively significant and the rest 11 were negatively significant. The significant and positive association between the traits suggested additive genetic model thereby less affected by the environmental fluctuation. Besides, 20 associations were positive and non significant both at genotypic and phenotypic level. The positive and non-significant association referred information of inherent relation among the pairs of combination. On the other hand 24 relationships were found negative and non significant both at genotypic and phenotypic level. The negative and non significant association referred a complex link of relationships among the pair of combinations.

Due to masking or modifying effect of environment, genotypic correlation coefficients may be higher in magnitude than the corresponding phenotypic correlation coefficients (Singh, 1980). It was also supported by the observations of Meenakshi *et al.* (1999) and Bhattacharya *et al.* (2007). Very close values of genotypic and phenotypic correlations were also observed between some character combinations. These might be due to reduction in error (environmental) variance to minor proportions as reported by Dewey and Lu (1959). Similar findings were also reported by Prasad *et al.* (2001), Surek and Beser (2003) and Yogamenakshi *et al.* (2004).

Table 14. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of aromatic Rice.

	CL	FLL	FLB	TPH	ETH	PL	PBP	SBP	FGP	TGP	DM	TGW	GYP
CL	1												
FLL	0.285**	1											
FLB	0.057	0.408**	1										
TPH	0.303**	0.627**	0.407**	1									
ETH	0.229*	0.605**	0.459**	0.713**	1								
PL	-0.168	-0.064	0.026	0.247*	-0.013	1							
PBP	-0.096	0.073	0.099	-0.098	-0.341**	0.162	1						
SBP	0.101	0.019	-0.016	-0.868**	-0.622**	-0.321**	0.456**	1					
FGP	-0.009	0.063	-0.143	-0.673**	-0.506**	-0.370**	0.166	0.760**	1				
TGP	0.149	0.019	-0.113	-0.680**	-0.544**	-0.190	0.367**	0.894**	0.862**	1			
DM	-0.040	0.199	0.430**	-0.019	-0.098	0.174	-0.139	-0.136	-0.039	-0.290**	1		
TGW	-0.157	0.002	-0.108	0.055	0.219*	-0.055	0.053	-0.025	0.213*	0.071	0.236*	1	
GYP	-0.024	0.134	-0.176	-0.093	0.217*	-0.212*	-0.163	0.144	0.509**	0.286**	0.174	0.768**	1

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

CL = clum length(cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tiller per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight, GYP = grain yield per plant (g).

Table 15 Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of aromatic Rice.

	CL	FLL	FLB	TPH	ETH	PL	PBP	SBP	FGP	TGP	DM	TGW	GYP
CL	1												
FLL	0.222*	1											
FLB	0.106	0.319**	1										
TPH	0.018	0.269*	0.191	1									
ETH	0.006	0.268*	0.229*	0.766**	1								
PL	-0.007	0.010	0.032	0.099	-0.016	1							
PBP	-0.056	0.084	0.057	0.027	-0.043	0.175	1						
SBP	0.078	0.015	-0.044	-0.453**	-0.343**	-0.176	0.366**	1					
FGP	0.014	0.017	-0.108	-0.361**	-0.220*	-0.216*	0.170	0.678**	1				
TGP	0.097	-0.000	-0.059	-0.367**	-0.315**	-0.114	0.284**	0.784**	0.806**	1			
DM	-0.081	0.066	0.253*	0.005	-0.045	0.018	-0.099	-0.062	0.010	-0.113	1		
TGW	-0.105	-0.003	-0.094	0.001	0.121	-0.038	0.061	-0.007	0.199	0.067	0.174	1	
GYP	-0.014	0.108	-0.145	-0.007	0.196	-0.143	-0.094	0.159	0.468**	0.279**	0.106	0.745**	1

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

CL = clum length(cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tiller per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight, GYP = grain yield per plant (g).
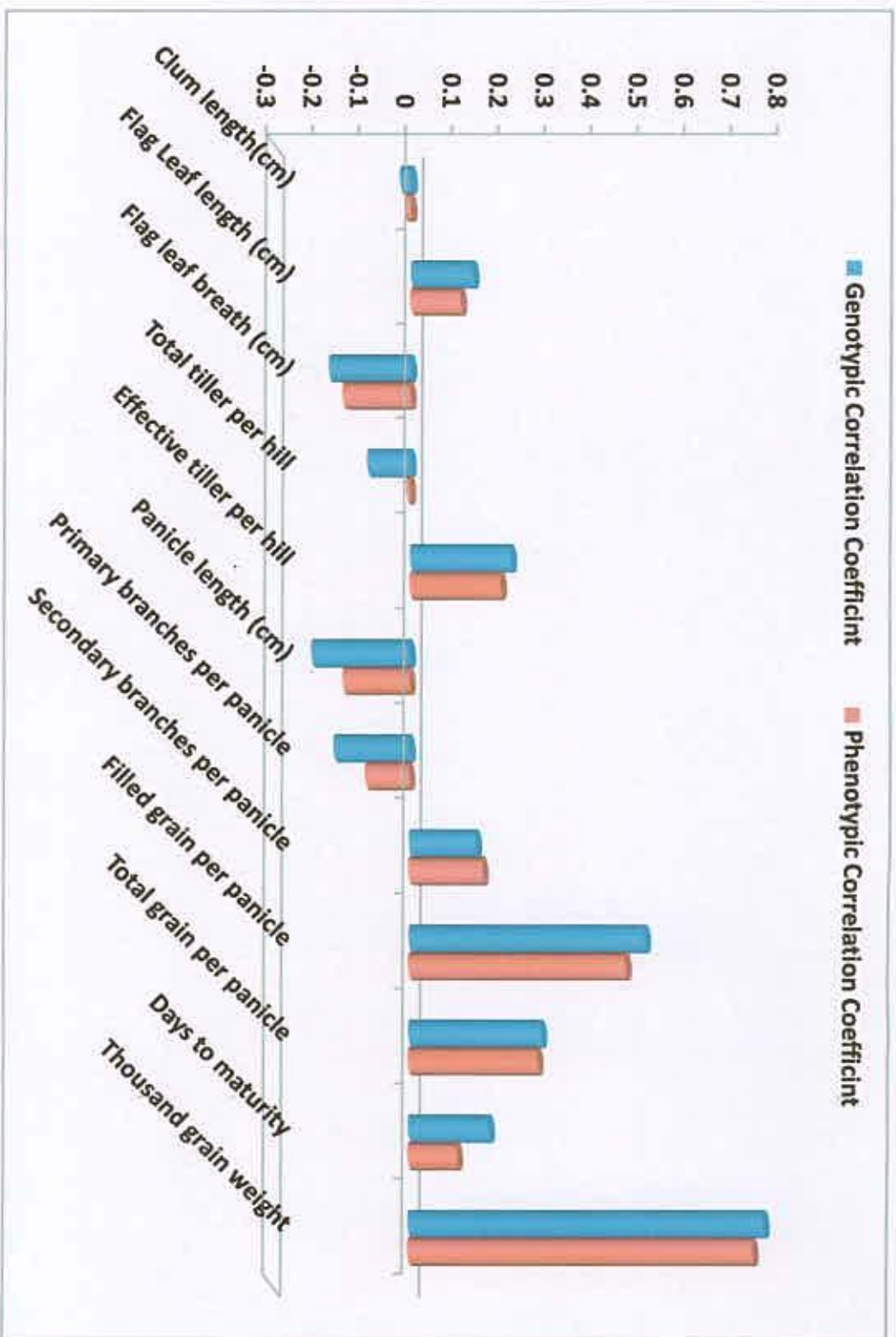
Figure 10. Genotypic & Phenotypic Correlation Coefficient for twelve characters with yield of aromatic rice.

Grain yield per plant was significant positive correlation with effective tillers per hill (0.217), filled grain per panicle (0.509), total grains per panicle (0.286) and thousand grain weight (0.768) in both genotypic and phenotypic level (Table 14 & Table 15) suggesting that genotypes with high partitioning efficiency gave increase in grain yield per·plant. Kiani and Nematzadeh (2012) reported that panicles per plant ($r = 0.751$) and filled grains per panicle ($r = 0.458$) correlated significantly with grain yield. Grin yield was highly significantly and positively correlated with panicle length, number of tillers per plant, number of filled grains per panicle and 1000 grain weight reported by·Osman *et al.* (2012). Haider *et al.* (2012) were found that grains per panicle (0.733**) and thousand grain weight (0.476**) has significant and positive relation with grain yield per·plant. That were supported this findings.

4.6 Estimation of path co-efficient

The correlation coefficient alone is inadequate to interpret the cause and effect relationships among the traits and ultimately with yield. Path analysis technique furnishes a method partitioning the correlation coefficients into direct and indirect effects and· provides the information on actual contribution of the independent variables to the dependent variable. In the present study, all the twelve traits were considered as causal variables of grain yield per plant and genotypic correlation coefficients of these traits with grain yield per plant were partitioned into the direct and indirect effects through path coefficient analysis. The results are shown in Table 16.

Path coefficient analysis revealed that clum length, flag leaf length, flag leaf breadth (0.056), total tiller per hill (0.054), panicle length, secondary branches per panicle, filled grain per panicle, thousand grain weight had direct positive effect on grain yield per plant. It indicates that these are the main contributors to grain yield. The highest positive direct effects on grain yield per plant were obtained by filled grain per panicle (1.251) followed by thousand grain weight (0.862), secondary branches per panicle (0.787), panicle length (0.448), clum length (0.246) and flag leaf length (0.108). Prasad *et al.* (2001) observed the highest positive direct effect of the number of fertile grains per panicle on grain yield. Habib *et al.* (2005) observed the high positive direct effect of culm length on yield. Again the highest negative direct effect on grain yield per plant was obtained by total grain per panicle (-1.505), followed by days to maturity (-0.519) and primary branches per panicle (-0.384). The highest indirect positive effect on grain yield per plant was found in total grain per panicle via filled grain per panicle (1.078) followed by total tiller per hill via total grain per panicle (1.023), secondary branches

per panicle via filled grain per panicle (0.951), effective tiller per hill via total grain per panicle (0.819), total grain per panicle via secondary branches per panicle (0.704).

The residual effect determines how best the causal factors account for the variability of the dependent factor. In this case, the dependent factor was grain yield per plant. In the present study the residual effect was 0.177 indicating that the thirteen traits explain 82.3% of variability in grain yield per plant.

Table 16. Partitioning of genotypic correlations into direct and indirect effects of eight important characters by path analysis of aromatic Rice

Characters	Direct effect	Indirect effect via												Genotypic correlation with yield
		CL	FLL	FLB	TPH	ETH	PL	PBP	SBP	FGP	TGP	DM	TGW	
CL	0.246	-	0.031	0.008	0.016	-0.016	-0.075	0.037	0.080	-0.011	-0.225	0.021	-0.135	-0.024
FLL	0.108	0.070	-	0.056	0.034	-0.041	-0.029	-0.028	0.015	0.079	-0.028	-0.103	0.001	0.134
FLB	0.056	0.070	0.108	-	0.034	-0.041	-0.029	-0.028	0.015	0.079	-0.028	-0.103	0.001	-0.176
TPH	0.054	0.075	0.068	0.056	-	-0.049	0.111	0.038	-0.683	-0.841	1.023	0.010	0.047	-0.093
ETH	-0.068	0.056	0.065	0.063	0.038	-	-0.006	0.131	-0.489	-0.633	0.819	0.051	0.189	0.217*
PL	0.448	-0.041	-0.007	0.004	0.013	0.001	-	-0.062	-0.253	-0.462	0.285	-0.090	-0.048	-0.212*
PBP	-0.384	-0.024	0.008	0.014	-0.005	0.023	0.073	-	0.359	0.207	-0.552	0.072	0.046	-0.163
SBP	0.787	0.025	0.002	-0.002	-0.046	0.042	-0.144	-0.175	-	0.951	-1.345	0.070	-0.021	0.144
FGP	1.251	-0.002	0.007	-0.020	-0.036	0.034	-0.166	-0.064	0.599	-	-1.298	0.020	0.183	0.509**
TGP	-1.505	0.037	0.002	-0.016	-0.036	0.037	-0.085	-0.141	0.704	1.078	-	0.150	0.061	0.286**
DM	-0.519	-0.010	0.021	0.059	-0.001	0.007	0.078	0.053	-0.107	-0.048	0.436	-	0.204	0.174
TGW	0.862	-0.039	0.000	-0.015	0.003	-0.015	-0.025	-0.021	-0.019	0.266	-0.107	-0.123	-	0.768**

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

Residual effect: **0.177**

CL = clum length(cm), FLL = flag Leaf length (cm), FLB = flag leaf breath (cm), TPH = total tiller per hill, ETH = effective tiller per hill, PL = panicle length (cm), PBP = primary branches per panicle, SBP = secondary branches per panicle, FGP= filled grain per panicle, TGP = total grain per panicle, DM = days to maturity, TGW = thousand grain weight, GYP = grain yield per plant (g).

4.7 Selection of genotypes

The genotypes of cluster I best in terms of the highest value of total tillers per hill, highest panicle length and late maturity (Table 17). The genotypes of cluster II produced highest value for flag leaf length, most effective tiller per hill and most thousand grain weight. The genotype of cluster III possessed the highest flag leaf length. The genotypes of cluster IV produced highest filled grain per panicle and the highest grain yield per plant. The genotypes of cluster V possessed the highest clum length, most flag leaf breadth, highest panicle length, most panicle length, most primary branches per panicle, most secondary branches per panicle, most total grain per panicle and early maturity. Considering diversity pattern and other agronomic performance G21 from cluster V, G30; G27 and G11 and G7 from cluster I and G5, G10 and G12 from cluster II could be considered suitable genotypes for open pollinated varieties and further use for efficient hybridization in future. Involving of such diverse lines in inter cluster genotypes crossing program could produce desirable segregants. So, more divergent genotypes are recommended to use as parents in future hybridization program.

Table 17. Salient features of genotypes in four different clusters

Cluster	Salient features
I	Highest total tillers per hill Highest panicle length Late maturity
II	Highest flag Leaf length Highest effective tiller per hill Highest thousand grain weight
III	Highest flag Leaf length
IV	Highest filled grain per panicle Highest grain yield per plant
V	Highest clum length Highest flag leaf breath Highest panicle length Most primary branches per panicle Highest secondary branches per panicle Most total grain per panicle Early maturity

CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted with the objective to assess the selection of superior genotypes from 30 aromatic rice land races through study the characterization, genetic variation and morphological diversity among the genotypes for improvement of yield. The experiments were carried out at the experimental Farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from June 2014 to February 2015. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Data on different morphological characters were recorded time to time and analyzed statistically. The results of the studies have been summarized as follows:

The performance of 30 rice genotypes for yield and different yield contributing traits were evaluated and observed that there were significant variations for all the traits studied among the genotypes. The phenotypic coefficient of variation (PCV) of all studied traits were found higher than genotypic coefficient of variation (GCV) which indicating that they all interacted with the environment to some extent. The traits studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among all of the traits, total grain per panicle exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) followed by secondary branches per panicle and grain yield per plant. The lowest PCV and GCV values were recorded for days to maturity.

The studied traits expressed moderate to high heritability estimates ranging from 35.38 to 94.65 percent. Among the traits, the highest heritability was recorded by grain yield per plant followed by thousand grain weight, flag leaf length, flag leaf breadth, secondary branches per panicle, total grains per panicle, panicle length and filled grain per panicle. The lowest heritability value was recorded by total tillers per hill. High heritability values indicate that the traits under study are less influenced by environment in their expression.

Genetic advance was the highest for grain yield per plant, followed by secondary branches per panicle, total grains per panicle, thousand grain weight, filled grain per panicle and flag leaf length. The lowest genetic advance was obtained in days to maturity. In this study, high heritability along with high genetic advance was noticed for grain yield per plant, secondary

branches per panicle, total grains per panicle, thousand grain weight, filled grain per panicle and flag leaf length. These traits can be improved through simple or progeny selection methods. Other traits showed high heritability along with moderate or low genetic advance. These traits can be improved by intermating superior genotypes of segregating population developed from combination breeding.

Relationship among yield and yield contributing traits was studied through analysis of correlation among them. Yield was significantly and positively correlated with effective tillers per hill, filled grain per panicle, total grains per panicle and thousand grain weight in both genotypic and phenotypic level. The significant and positive association between the traits suggested that those traits are less affected by the environmental fluctuation. The positive and non-significant association referred information of inherent relation among the pairs of combination and the negative and non significant association referred a complex linked of relation among the pair of combinations.

The path coefficient analysis was performed using genotypic correlation to determine direct and indirect influence considering thirteen traits. The results revealed that the highest positive direct effects on grain yield per plant was observed by filled grain per panicle followed by thousand grain weight, secondary branches per panicle, panicle length, clum length and flag leaf length. It indicates that these are the main contributors to grain yield.

Based on D^2 values 30 genotypes were grouped into five clusters. Maximum number of genotypes were under cluster IV and whereas cluster V included minimum number of genotypes. In all the cases the inter-cluster distances were greater than the intra-cluster distances suggesting wider diversity among the genotypes of the distant groups. Cluster I showed maximum genetic distance from cluster IV followed by the distance between cluster III and V and cluster II and V. Minimum distance was found between the genotypes of the cluster II and III. Thus hybridization among genotypes belonging to cluster I and III with those of cluster IV and V would exhibit higher heterosis for improvement of desirable traits in segregating populations. However, the objective of a plant breeder is not only to get high heterosis but also to achieve high level of production and reducing the life span of a variety so that, it can be fitted in existing cropping pattern. In this study, the mean yield and number of filled grain per panicle was highest in cluster IV but the minimum days to maturity was found in cluster V. So, the crosses involving the genotypes from this cluster with those from cluster I and III may exhibit high heterosis for earliness in maturity and number of grain per

panicle. Principal component analysis revealed that first five components account for more than 78% of total variation. The first principal component accounted for more than 25% of total variance.

In conclusion, the results of the present experiment revealed that the variability existed among the selected aromatic rice genotypes for all the characters studied. Among this cultivar the superior G21, G27, G11, G7, G5, G10 and G12 may use as open pollinated verities and parents in future hybridization program.

CHAPTER VI
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CHAPTER VII
APPENDICES

Appendix I. Principal component score 1 & 2.

Genotypes	Z_1	Z_2
1	59.70	6.65
2	34.72	4.32
3	-83.81	21.51
4	-23.99	10.09
5	25.99	2.97
6	-23.13	-1.94
7	96.54	1.91
8	15.99	-8.07
9	-7.28	1.00
10	35.72	7.70
11	68.11	3.58
12	46.50	-21.05
13	-9.42	-15.44
14	-42.37	-7.99
15	27.84	-0.47
16	-35.67	-1.09
17	-1.17	-4.01
18	-41.54	-8.03
19	1.50	13.18
20	-3.01	8.36
21	11.33	20.04
22	-69.23	-7.06
23	-70.54	-13.53
24	62.02	-4.48
25	77.68	-7.27
26	43.46	1.92
27	-56.48	-11.23
28	-33.54	-8.18
29	-50.92	9.79
30	-54.98	6.85

Appendix II. Map showing the experimental site under the study

AGROECOLOGICAL ZONES
(Generalised)

1	Old Himalayan Piedmont Plain	16	Middle Meghna River Floodplain
2	Active Tista Floodplain	17	Lower Meghna River Floodplain
3	Tista Meander Floodplain	18	Young Meghna Estuarine Floodplain
4	Karatoya-Bangali Floodplain	19	Old Meghna Estuarine Floodplain
5	Lower Atrai Basin	20	Eastern Surma-Kusiyara Floodplain
6	Lower Punarbhaba Floodplain	21	Sylhet Basin
7	Active Brahmaputra-Jamuna Floodplain	22	Northern and Eastern Piedmont Plain
8	Young Brahmaputra and Jamuna Floodplain	23	Chittagong Coastal Plain
9	Old Brahmaputra Floodplain	24	St Martin's Coral Island
10	Active Ganges Floodplain	25	Level Barind Tract
11	High Ganges River Floodplain	26	High Barind Tract
12	Low Ganges River Floodplain	27	North-eastern Barind Tract
13	Ganges Tidal Floodplain	28	Madhupur Tract
14	Gopalganj-Khulna Beels	29	Northern and Eastern Hills
15	Arial Beel	30	Akhaura Terrace

★ **The experimental site under the study**

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

A. Physical composition of the soil

Soil separates	%	Method employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.90	Do
Clay	36.66	Do
Texture class	Clay loam	DO

B. Chemical composition of the soil

Sl No.	Soil characteristics	Analytical data	Method employed
1	Organic carbon (%)	0.82	Walkley and black, 1947
2	Total N (Kg/ha)	1790.00	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 (Kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (Kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	p^H (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-E-Bangal Agricultural University, Dhaka.

Appendix IV. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from June, 2014 toJanuary, 2015

Month	Air temperature (°c)		Relative humidity (%)	Rainfall (mm) (total)
	Maximum	Minimum		
June,2014	30.30	21.80	71.08	2.89
July,2014	33.45	25.50	65.43	4.55
August,2014	35	24.20	58	2.63
September,2014	30.30	21.80	71.08	2.89
October,2014	33.45	25.50	65.43	4.55
November, 2014	31.45	24.65	58.54	3.23
December, 2014	29.56	23.54	50.34	3.12
January, 2015	27.34	20.55	45.65	2.54

Source: Bangladesh Meteorological Department (Climate & Weather Division),Agargoan, Dhaka -1207

Appendix V. Descriptors with codes for qualitative characteristics

SL. NO.	Characteristics	Descriptors with Codes
1	Basal leaf sheath color	Green-1, Green with purple lines-2, Light purple-3, Purple-4
2	Grain color intensity of leaf blade	No green-0, Light green-3, Medium green-5, Dark green-7
3	Leaf blade attitude	Erect-1, Horizontal-5, Drooping-7
4	Leaf blade pubescence	Glabrous-1, Intermediate-2, Pubescent-3
5	Ligule shape	Absent-0, Truncate-1, Acute to acuminate-2, 2-cleft-3
6	Presence of Awns	Absent-0, Partly awned-1, Fully awned-2
7	Panicle: attitude of branches	Erect (compact panicle)-1, Semi-erect (semi-compact panicle)-3, Spreading (open panicle)-5, Horizontal-7 Drooping-9

Source: IBPGR-IRRI, 2007, Rice Advisory Committee