CHARACTERIZATION OF 18 F_5 LINES OF AUS RICE

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CERTIFICATE

This is to certify that the thesis entitled ***"CHARACTERIZATION OF 18 F_5 LINES OF AUS RICE"*** *Sher-e-Bangla Agricultural University (SAU), Dhaka in partial fulfillment of the requirements for the degree of* ***MASTER OF SCIENCE IN SEED TECHNOLOGY****, embodies the results of a piece of bona fide research work carried out by* ***MD. KAMRUL ISLAM, Registration no. 10-03836*** *under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

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

Dated: June, 2016
Place: Dhaka, Bangladesh

Prof. Dr. Md. Shahidur Rashid Bhuiyan
Supervisor

Dedicated To

My Respectable

Parents and

Teachers

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ABSTRACT

The investigation was carried out under field conditions to characterize eighteen advanced aus rice lines (F_5) during the period of transplanting aus season (2015-2016) at the experimental field of Sher-e-Bangla Agricultural University, Dhaka-1207. The eighteen genotypes of rice were characterized for 10 quantitative and 31 qualitative traits. All the genotypes were characterized and categorized as per the descriptors developed by Biodiversity International, IRRI and WARDA-2007 for DUS test of inbred rice. Among the qualitative characteristics, no variation was observed in case of anthocyanin coloration of leaf sheath, penultimate leaf ligule shape, microscopic observation of pollen with I_2-KI solution, anthocyanin coloration of lemma and palea, anthocyanin coloration of nodes, anthocyanin coloration of internodes, color of stigma, awns in the spikelet and decorticated grain aroma. Among all the quantitative characters, characters like panicle length, thousand grain weight, number of effective tillers per plant, culm length, time of maturity and grain length provided better agronomic performance which resulted in ultimate higher yield per plant. The average days to maturity was 111 days and the average culm length of the tested genotypes was 79.57 cm and most of the genotypes resulted in early maturity and lodging resistance. The most of the genotypes showed average panicle length 24.33 cm and average thousand grain weight 22.67gm resulted in higher yield per plant. These G1, G3, G6, G8, G9, G10, G12, G16 and G18 were the most promising lines in respect of yield and quality which could be released as variety in future.

LIST OF CONTENTS

LIST OF CONTENTS (CONT'D)

LIST OF TABLES

LIST OF TABLES (CONT'D)

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

LIST OF ABREVIATIONS

Full Name	Abbreviation
Agricultural	Agril.
Agriculture	Agric.
Agro-Ecological Zone	AEZ
At the rate	@
And others	*et al.*
Bangladesh	BD
Bangladesh Agricultural Research Institute	BARI
Bangladesh Bureau of Statistics	BBS
Bangladesh Rice	BR
Bangladesh Rice Research Institute	BRRI
Biological	Biol.
International Rice Research Institute	IRRI
Biodiversity International	WARDA
Seed Certification Agency	SCA
Centimeter	Cm
Days After Transplanting	DAT
Department of Agricultural Extension	DAE
Degree Celsius	ºC
Etcetera	etc.
Food and Agricultural Organization	FAO
Genotype	G
Genetics	Genet.
Gram	gm
High Yielding Variety	HYV
Journal	J.
Kilogram	Kg
Meter	m
Ministry of Agriculture	MoA
Murate Potash	MP
Percent	%
Randomized Complete Block Design	RCBD
Sher-e-Bangla Agricultural University	SAU
Square meter	m^2
Science	*Sci.*
The fifth generation of a cross between two dissimilar homozygous parents	F_5
Ton	t
Triple Super Phosphate	TSP

CHAPTER I

INTRODUCTION

Rice (*Oryza sativa* L., 2n = 24) is one of the most extensively cultivated cereal crops in the world spreading across a wide range of geographical, ecological and climatic regions. It belongs to the family Poaceae and sub family Oryzoidea is the staple food for more than half of the world‘s population and occupies almost one-fifth of the total land area covered by cereals. High genotypic and phenotypic diversity exists and about 1,20,000 different accessions are reported in rice globally as a consequence of varied adaptations (Das *et al*. 2013). Most of the world‘s rice is cultivated and consumed in Asia which constitutes more than half of the world population. It provides 75% of the calories consumed by more than three billion asians. Approximately 11% of the world's arable land is under rice cultivation and it ranks next to wheat (Chakravarthi and Naravaneni, 2006).

Rice belongs to the genus *Oryza* and has two cultivated and 22 wild species. The cultivated species are *Oryza sativa* and *Oryza glaberrima*. *Oryza sativa* is grown all over the world while *Oryza glaberrima* has been cultivated in West Africa for the last ~3500 years (IRRI, 2001). Rice is grown under many different conditions and production systems, but submerged in water is the most common method used worldwide. Rice is the only cereal crop that can grow for long periods of time in standing water (IYR, 2004). About 57% of rice is grown on irrigated land, 25% on rainfed lowland, 10% on the uplands, 6% in deep water, and 2% in tidal wetlands (Chopra and Prakash, 2002).

Asia can be considered as ‘Rice Basket’ of the world, as more than 90 percent of the rice is produced and consumed in Asia. World paddy production area was 163.3 million hectares and production was 749.7 million tons (FAO, October, 2016). Bangladesh is the fourth largest producer of rice in the world with the annual production of 345.81 lac metric tons (USDA, 2016). During aus season in Financial Year (FY) 2015-16, total cultivated area, production and yield rate of rice was10,17,969 hectares, 22,88,642 metric tons and 2.248 metric ton, respectively. During T. aman season in Financial Year (FY) 2015-16, total cultivated area, production and yield rate of rice was 55,90,340 hectares, 1,12,39,943 metric tons and 2.412 ton respectively. During boro season in Financial Year (FY) 2015-16, total cultivated area, production and yield rate of rice was 47,72,576 hectares, 1,89,37,581metric tons and 3.968 ton respectively (BBS, 2016).

Qualitative characters are important for plant description (Kurlovich, 1998) and are influenced by consumer preference, socio-economic scenario and natural selection. Several morphological characters are the major determining factors of rice grain yield. Genetic diversity probably serves as an insurance against crop failure (Subba Rao *et al.,* 2001). Landraces and wild species possess immense potential of most valuable genes which can be effectively utilized in the present day breeding programs to evolve miracle varieties in rice that possess not only high yield potential and quality, but also resistant to biotic and abiotic stresses (Saxena *et al.,* 1988).

The total cultivable land is decreasing at a rate of more than 1% per year due to urbanization. The population growth rate is 2 million per year and if the population increases at this rate, the total population will reach 238 million by 2050 (Shelley *et al*., 2016). An increase in total rice production is required to feed this ever-increasing population. Aus, aman, and boro rice were recently reported to account for 7%, 38%, and 55%, respectively, of the total rice production in Bangladesh (Risingbd, 2014). Now, modern high yielding varieties in aus season are essential to increase the total rice production of Bangladesh. The high yielding varieties of aus rice are developed through crossing between aus rice and boro rice with the intension to increase yield of aus rice having genes from boro rice without much affecting the days to maturity. Eighteen F_4 lines were selected in the previous year which will be used in the present study. The present study was undertaken to characterize the F_5 lines which is the prerequisite to release rice variety. It will pave the ways for selection of high yielding and short duration T. aus rice genotypes from eighteen (18) genotypes.

OBJECTIVES:

1. To characterize rice genotypes as per descriptors used for rice.
2. To find out high yielding genotypes with their different growth parameters and yield contributing characters.
3. To select short duration and high yielding T. aus materials for further trial.

CHAPTER II

REVIEW OF LITERATURE

Rice has wide adaptability to different environmental conditions, as it is evident from its worldwide distribution. Yield of rice variety is determined by the morphological parameters such as 50% flowering, days to 80% maturity, plant height (cm), total no. of tiller per plant, no. of effective tiller/plant, panicle length (cm) per plant, no. of primary branches per plant, no of secondary branches per plant, total no. of spikelet per panicle, no. of filled grain of main tiller, no. of unfilled grain of main tiller, yield per plant (gm), thousand grain weight (gm) and yield (ton/hectare). The identification of suitable combinations of genotypes in comparison to the best parent varieties for yield and some important yield contributing characters are essential tool for a successful assessment. The present study has aimed to assess the performance of genotypes as compared to the check varieties. The literature relevant to the present investigation entitled “Characterization of 18 F_5 lines of Aus Rice” through morphological traits has been reviewed in this section.

Kumar *et al.* (2014) conducted experiment with 40 genotypes of rice**.** Analysis of variance revealed significant difference among 40 rice genotypes for all characters indicating the existence of variability. High GCV and PCV were observed for grain yield per plant and biological yield per plant. On the other hand, Rafiqul (2014) conducted experiment with 19 genotypes of rice, existence of variance in 14 yield contributing character including days to maturity, number of effective tiller per plant, number of filled grain of main tiller and yield (ton/ha) were found in analysis of variance. Sadeghi (2011) also observed positive significant association of grain yield with grains per panicle, days to maturity, number of productive tillers and days to flowering.

Dutta *et al.* (2013) studied 68 genotypes for twelve agronomical important characters to estimate variability and genetic parameters. Considering genetic parameters, high genotypic and phenotypic coefficient of variations, high heritability (broad sense) and genetic advance as percentage of mean were observed viz. tillers per plant, days to flowering, harvest index, spikelet per panicle, spikelet density, panicle per plant and spikelet yield. Thus, these characters were under the influence of additive gene action and a satisfactory selection program.

Singh *et al.* (2013) observed forty-eight genotypes to examine genetic variability. High genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent of mean was recorded for total number of spikelet per panicle, filled grains per panicle, number of effective tillers, leaf width and spikelet yield per plant. Positive and significant association was recorded by days to 50% maturity, leaf length, leaf width, filled grains per panicle and total number of spikelet per panicle. Spikelet yield per plant showed positive and significant correlation at genotypic and phenotypic levels. Days to maturity, plant height, number of filled grains per panicle and test weight exhibited positive direct effect both at genotypic and phenotypic levels.

Satheesh Kumar *et al.* (2012) estimated correlation in fifty three genotypes of rice for fifteen characters. It revealed grain yield per plant exhibited high significant and positive genotypic correlation with number of productive tillers per plant, filled grains per panicle and total number of grains. According to Yadav *et al.* (2011) it is apparent that information of morphological and physiological aspects of crop is also a key feature to plan a creative breeding program. Thus, the genetic reconstruction of plant architecture is required for developing high yielding crop varieties.

Rangare *et al.* (2012) evaluated forty exotic and Indian rice germplasm including one local check for their efficiency with respect to eleven yield and yield contributing characters from Kharif, 2009 under normal conditions. Associated studies have indicated that for an improvement in grain yield, the intensive selection should be positive for biological yield per plant, number of fertile tillers per plant, number of spikelet per panicle, test weight, panicle length and days to maturity as these traits showed significantly strong positive association with grain yield, but days to 50% flowering, days to initial flowering, harvest index and plant height through had positively non-significant association with grain yield.

Akhtar *et al.* (2011) studied on the variance and heritability for yield contributing characters in ten rice genotypes. The heritability was found to be high for number of grains per panicle, days to maturity, plant height and paddy yield while lower for number of tillers per plant.

Prajapati *et al.* (2011); assessed thirty eight rice genotypes at field experimentation centre, Department of Genetics and Plant Breeding, Allahabad School of Agriculture, Allahabad during kharif, 2009. The experiment was conducted to study the 12 quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance. High estimates of heritability coupled with high genetic advance as percent of mean was observed for harvest index followed by number of spikelet per panicle, number of panicles per hill and number of tillers per hill. High estimates of heritability coupled with moderate genetic advance as percent of mean was observed for flag leaf width followed by days to 50% flowering, panicle length and biological yield per hill.

Sadeghi (2011) studied on the nature and magnitude of variation for yield and yield contributing characters in 49 rice varieties. Broad sense heritability ranged from 69.21% for plant height to 99.53% for grain width.

Subbaiah *et al.* (2011) studied the extent of variability and genetic parameters with 16 check varieties and 48 hybrids for nine yield and yield related components and twenty five quality characters. The magnitude of difference between phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was relatively low for all the traits. There was less environmental effect. High GCV and PCV were found for harvest index, total number of productive tillers per plant in check varieties and for total number of productive tillers per plant, number of grains per panicle in hybrids. High heritability coupled with high genetic advance as percent of mean were recorded for harvest index, total number of productive tillers per plant, number of grains per panicle and grain yield per plant in case of check varieties and total number of productive tillers per plant, number of grains per panicle and harvest index in case of hybrids indicating the additive gene effects in the genetic control of these traits and can be improved by simple selection in the present breeding material.

Akhtar *et al.*(2011) studied the genotypic and phenotypic correlation for yield contributing characters in ten rice genotypes. Paddy yield had strong genetic correlation with number of grains per panicle, days to maturity and 1000 grain weight. Paddy yield had significant positive correlation with number of grains per panicle and 1000 grain weight.

Pandey *et al.* (2010) studied the genetic variability among forty rice genotypes for yield and yield contributing components. High significant difference was found for all the characters for the presence of substantial genetic variability. The maximum genotypic and phenotypic coefficient of variability was found for harvest index, grain yield per hill, plant height and biological yield per hill. High heritability coupled with high genetic advance was found for plant height and number of spikelet per panicle.

Kumar *et al.* (2009) carried out an experiment to study the selection criteria for selecting high yielding genotypes in two different early segregating F_2 and F_3 populations by estimating heritability and genetic correlation between yield and its main economic traits in their subsequent F_3 and F_4 generations of two crosses in rice. The heritability estimates were high for spikelet/main panicle and 100 grain weight, whereas it was medium to low for grain yield and low for panicles/plant.

Shahidulla *et al.* (2009) conducted an experiment to assess the genetic divergence of aromatic rice for grain quality and nutrition aspects. Forty genotypes composed of 32 local aromatic, five exotic aromatic and three non-aromatic rice varieties were used. Univariate and multivariate analyses were done. Enormous variations were observed in majority of characters viz. grain length, breadth, kernel weight, milling yield, kernel length, L/B ratio of kernel and volume expansion ratio (VER). In multivariate analysis, genotypes were grouped into six clusters. In the discriminant function analysis (DFA) function 1 alone absorbed 6l.7% of the total variance. The most contributing variables were kernel weight, kernel length and L/B ratio in function 1. The inter-cluster D^2 value was maximum (26.53) between I and VI followed by 21.28 (between I and V). Minimum D^2 value was found (5.90) between II and III. Majority of the local aromatic rice varieties with smaller kernels were included in the cluster l. The cluster III contains Elai, Sarwati and Sugandha-I with long-slender kernel and very good appearance. Thus, they concluded that these varieties can be used in breeding program for improvement of germplasms in cluster-I.

An investigation was carried out by Shehata *et al.* (2009) to evaluate the morphological variation among Egyptian Jasmine and its 10 M_5 derived mutants. The results showed that all tested genotypes including Egyptian Jasmine and its new derived mutants were significantly varied in their growth duration, yield and yield components except number of tillers. Interestingly, derived mutants significantly headed earlier than Egyptian Jasmine. The results clearly showed the existence of considerable amount of variation at the morphological level and demonstrate the significance of mutation breeding in enhancing genetic variability in the breeding programs.

Rita *et al.* (2009) observed high genotypic and phenotypic coefficient of variations with harvest index, total number of filled grain per panicle, 100-spikelet weight and spikelet fertility percentage. High heritability coupled with high genetic advance was exhibited by harvest index, total number of chaffy spikelet per panicle, spikelet yield per plant, total number of filled grain per panicle and spikelet fertility percentage and selection may be effective for these characters.

Sarhadi *et al.* (2008) worked with the most important agronomic attributes and aroma of 26 cultivars from Afghanistan, Iran, and Uzbekistan, and controls from Japan, Thailand and India were characterized. Diversity for some traits of agronomic importance, such as plant height was detected among countries, e.g. Afghan cultivars classified as tall, and Iranian and Uzbek intermediate and short, respectively. Differentiations of panicle, grain, leaf, basal internodes, and culm dimension among rice cultivars, indicating the source of rice diversity in Central Asia. According to the results, 6 of 10, 2 of 7, and 0 of 6 of Afghan, Iranian, and Uzbek rice cultivars were scored as aromatic, respectively. Therefore. Afghan cultivars are a good source of aromatic rice germplasm for Central Asia.

Bisne and Sarawgi (2008) characterized thirty two aromatic rice accessions of Badshahbhog group from IGKV. Raipur, Chhattisgar germplasm. These germplasm accessions were evaluated for twenty-two morphological, six agronomical and eight quality characters viz. leaf blade pubescence, leaf blade color, basal leaf sheath color, flag leaf angle, Ligule color, collar color, auricle color, secondary branching of panicle, panicle thresh ability, awning, awn color, stigma color, lemma and palea color, lemma and palea pubescence etc. The specific genotypes B: 1340, B: 2039, B: 2495, B: 2816, B: 16930, B: Z354, B: 1163, B: 2094 were identified for quality and agronomical characteristics. It was concluded that these accessions may be used in hybridization program to achieve desired segregant for good grain quality with higher yield.

Vcasey *et al*. (2008) characterized the genetic variability among species and populations of South American wild rice, eleven populations of *Oryza glumeapatula*, seven of *O. grandiglumis,* four of *O. latifolia* and one of *O. alta* from Brazil and Argentina. Univarate analyses were performed with 16 quantitative traits with the partitioning of populations within species. The high genetic variation among populations of *Oryza glumeapatula* was observed especially for the traits tiller number, plant height at flowering, days to heading, number of particles, panicle length, spikelet length and awn length. Significant differences ($p<0.001$) between species were observed for all the traits as well as among populations within the species. The most variable was *Oryza glumeapatula* followed by *O. latifolia.* Multivariate discriminant canonical and cluster analyses confirmed the separation of the highly diverse *Oryza glumeapatula* populations from the tetraploid species and the high genetic variation among *O. latifolia* populations.

Kole *et al.* (2008) studied variability for twelve morphological characters of 18 morphologically distinct mutants in M_4 generation along with their two mother genotypes (IET 14142 and IET 14143), which were developed from Tulaipanja, an aromatic non-basmati rice cultivar of West Bengal. Genotypic and phenotypic coefficients of variation were high for flag leaf angle and panicle number; moderate for grain number per panicle, straw weight, harvest index and grain yield per plant; and low for days to flower, plant height, panicle length, spikelet number, spikelet fertility (%) and test weight. High heritability accompanied by high to moderate genetic advance for flag leaf angle, panicle number, grain number, straw weight and grain yield indicated the predominance of additive gene action for the expression of these characters.

Akter *et al.* (2007) evaluated thirty advanced breeding lines of deep-water rice during T. aman season with a view to finding out variability and genetic association for grain yield and its component characters. The highest genetic variability was obtained in filled grains/panicle followed by plant height. Panicles/plant, filled grains/panicle and grain yield had genetic coefficient of variation and heritability in broad sense coupled with high genetic advances in percentage of mean. Panicle length, panicles/plant, plant height, filled grains/panicle and harvest index showed significant positive association with grain yield. Path coefficient analysis also revealed the maximum positive and direct contribution of filled grain yield followed by panicles/plant, 1000-grain weight and flag leaf area. Moreover, plant height had the highest indirect effect on grain yield through filled grains/panicle. Flag leaf area, harvest index and panicle length also had higher positive indirect effect on grain yield through filled grains/panicle.

An investigation was conducted by Hien *et al.* (2007) to determine the extent of diversity and relationships among 36 aromatic rice cultivars collected from Asia. Characterization for 22 morphological characters with 101 morphometric descriptors was carried out. High and comparative levels of phenotypic variation using phenotypic frequency distribution and Shannon-Weaver diversity index were found between Countries of origin. Most traits were polymorphic except to ligule color, grain size, grain shape, culm strength, plant height and secondary branching contributed the highest mean diversity indices.

Ingale *et al.* (2007) conducted an experiment to study the effect of seedling age on 50% flowering of parental lines of sahyadri rice hybrid. The experiment was formulated to assess the effect of seedling age at transplanting on 50% flowering of A, B, and R lines of sahyadri rice hybrid. The 50% flowering was delayed in both younger and older aged seedlings than the recommended age of seedling (25 days old) at transplanting by approximately half the number of days by which the seedlings are younger and older than the recommended age.

Karim *et al*. (2007) studied 40 different new rice genotypes for variability and genetic parameter analysis and found highly significant mean sum of square due to genotypes for days to maturity. They reported that variation for days to maturity was attributed by genetic constituent rather than environment.

Forty-six rice cultivars and lines in Liaoning, Jilin and Heilongjiang provinces of China in 2004 were used to study particle characteristics and their relationship with yield and quality traits in Shenyang city, Gongzhuling city and Jiamusi city. The panicle length in Liaoning was 2 cm shorter than that in Jilin and Heilongjiang. Grain density, number of primary branches and number of grains in the primary branch in Liaoning were much higher than those in Jilin and Heilongjiang (Xu-Zheng Jin *et al*., 2007).

Singh *et al.* (2006) evaluated thirty two genotypes of rice for seven traits to estimate genetic variability and interrelationship among them. There was found a wide range variation for all the characters. Highest genotypic and phenotypic coefficients of variations were recorded for grain yield. High heritability and high genetic advance for height suggested the predominance of additive gene action for this trait.

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

Five aromatic and two non-aromatic milled rice samples were used by Sharp (2006) to compare the quality of U.S. produced aromatic rice with that of India and Thailand. Jasmine (Thailand) was whiter than all other rice samples tested. Della rice samples (U.S.) were not as white as Basmati (India). Della AR (Arkansas) was less red and less yellow than Della LA (Louisiana). While the uncooked kernels of Della were as long as Basmati or Jasmine, the greater length: width ratio caused Basmati to appear longer than Della. Della and Jasmine were greater than Basmati in 1000 kernel weight. Della samples were classified as having intermediate to high intermediate gelatinization temperature. Medium gel consistency, intermediate amylose content and cooking quality, which are characteristic of typical U.S. long grain non-aromatic rice. A sensory panel could not detect a flavor difference between Della AR and either Basmati or Jasmine.

A study was conducted by Hossain *et al.* (2005) in order to investigate the relationship between grain yield with the morphological parameters of five local and three modern aromatic rice varieties. Among the aromatic rice varieties the highest grain yield was obtained from BRRI dhan 34 which identically followed by Kataribhog. The highest plant height was observed in Chinigura which was statistically similar to Kataribhog. The highest number of effective tillers/hill was observed in BRRI dhan 37 and it was identically followed by Radhunipagal. Badshabhog, Chinigura, BRRI dhan 38 and the lowest fertile tillers per hill was obtained from Kalijira which was statistically similar to Kataribhog. The highest number of grains per panicle was found in BRRI dhan 34 and that was the lowest in BRRI dhan 38. Maximum 1000-grains weight was observed in BRRI dhan 38. In respect of yield BRRI dhan 34 and Kataribhog are suitable for Dinajpur region in Bangladesh during T. aman season.

Fifty four elite rice genotypes were evaluated by Madhavilatha *et al.* (2005) for their variability with regards to grain yield, yield components (plant height, number of effective tillers per plant, panicle length. number of grains per panicle, fertility percentage, days to 50% flowering, days to maturity and harvest index) and quality parameters (hulling recovery, kernel length (L), breadth (B), L/B ratio and elongation ratio, volume expansion ratio and 1000 grains weight). Estimation of heritability and genetic advance were also obtained for the above traits.

Sharief *et al.* (2005) observed morphological characters of four rice cultivars. The varieties were identified through their flag leaf area, angle of the flag leaf, plant height, time of heading, lemma and palea pubescence, culm diameter, number of secondary branches per to particle, number of grains per panicle, panicle density, particle weight, presence of awn, number of tillers, filled grain yield. 1000-grains weight, seed width and grain color.

Shashidhar *et al.* (2005) reported positive association of spikelet yield with plant height, number of productive tillers hill-1, dry matter plant-1 and harvest index at15 phenotypic and genotypic level.

The assessment of genetic diversity is an integral part of any successful breeding program. Usually breeders have been employing morphological markers for genetic diversity estimation and a number of morphological descriptors in various crops are in vogue for characterization purpose (Rana and Bhat, 2004).

Morphological characters of seeds such as seed coat color, seed shape, seed length, seed width, kernel length, kernel breadth, kernel shape, presence of awn, thousand seed weight etc. and traits of plants such as culm length, time of heading, time of maturity, number of primary branches, number of secondary branches, panicle length, number effective tillers per plant, grain per panicle etc. can invariably be used in characterization of rice genotypes. Genetic studies have revealed that these characters are simply inherited and highly heritable and therefore, could be readily used in distinguishing varieties.

Chaudhary *et al.* (2004) studied genetic variability, heritability and genetic advance for 17 quality and plant traits viz. kernel length, kernel length-breadth ratio, kernel length after cooking, length-breadth ratio of cooked rice, elongation ratio, elongation index, alkali spreading value, head rice recovery, milling percentage, panicle length, number of effective tillers per plant, number of fertile spikelet per panicle, spikelet density, spikelet sterility, biological yield, harvest index and grain yield per plant in 54 aromatic rice accessions. The phenotypic and genotypic coefficient of variation, heritability and genetic advance indicated that selection of genotypes may be carried out for kernel length-breadth ratio, length-breadth ratio of cooked rice and alkali spreading, value for quality traits in all the genotypes. All the traits exhibited high heritability coupled with high genetic advance and genetic variability.

Kisandu and Mghogho (2004) characterised two hundred and seventy five accessions collected from all rice growing regions of the Southern Highlands of Tanzania using morphological characters. Other assessments included grain colour, 1000 grains weight and milling characteristics were conducted. Using simple statistics, an analysis of variances for different characters was done and reported that a large number of names exist for rice cultivars. Different naming of varieties relates with differences in location and morphological appearance. In some cases, a single name can be given to different genotypes at different locations. High genetic diversity was observed for grain color, plant height (63 cm to l70 cm) and disease resistance. Grain color ranged from cream to blackish brown. On the other hand, cultivars did not show statistical differences on 100-grains weight. Indigenous cultivars showed small differences on heading and maturity rates. Some are highly aromatic and some had better milling quality.

A total of 124 landrace genotypes of rice were evaluated by Nabeela *et al.* (2004) for seven quantitative and eight qualitative characters. A significant amount of genetic variation was displayed for most of the traits. The coefficient of variation was more than 10% for all the characters with the exception of grain length. Compared with the modern cultivars the landrace genotypes were on average delayed in heading and maturity but had lower values for panicle and grain length. Days to heading was positively correlated with maturity (r=0.833) and grain length (r=0.452). Plant height showed positive and significant correlation with panicle length (r=0.452), indicating the importance of plant height in improving panicle length. Seven accessions with the best performance for individual character were identified.

Souresh *et al.* (2004) studied the genetic diversity of quantitative and qualitative traits of 36 lines and cultivars of rice using 17 traits including grain yield, number of particles per plant, number of filled grains per panicle, 1000-grainsweight, leaf length, leaf width, leaf area, plant height, culm length, amylose content of the grain, gel consistency, panicle weight, grain length, grain width, grain shape, days to 50% flowering and maturity.

Zaman *et al.* (2004) evaluated 8 agro-morphological characters of 20 modern rice varieties for the magnitude of genetic divergence using Mahalanobis's D^2 statistics and reported that days to flowering and plant height contributed consistently to total divergence.

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

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

Mahto *et al*. (2003) evaluated twenty six early maturing upland rice genotypes for genetic variation, character association and path analysis based on days to 50% flowering. Plant height, number of panicle per plant, panicle length, number of branches per particle. Number of filled grains per panicle, 1000 seed weight and grain yield. The genotypic variance ranged from 5.36 cm for panicle length to 24.83 gm for grain yield. The difference between phenotypic and genotypic coefficient of variation was minimum for 1000 grain weight (0.12) and days to 50% flowering (0.13). High values of heritability were observed for 1000-grains weight (98.30%) and days to 50% flowering (97.33%). The number of grains per panicle and panicle length showed a significant difference between phenotypic and genotypic coefficient of variation. The association of high heritability with high genetic advance was observed for 1000 grain weight, days to 50% flowering, grain yield, number of branches per particle and plant height. Grain yield was positively and significantly correlated with days to 50% flowering, number of panicles per plant, number of branches per panicle and number of filled grains per panicle.

Mishra *et al.* (2003) evaluated 16 rice cultivars and their 72 F_1 hybrids for genetic diversity and grouped in twelve clusters using Mahalanobis's D^2 statistics. The values revealed that plant height, ear bearing tillers per plant, panicle length, 1000 grain weight, hulling and milling percentage, biological yield, harvest index, kernel length after cooking, gelatinization temperature and grain yield were the main factors for differentiation.

Patil and Sarawgi (2003) studied genetic variation and correlation analyses in 128 aromatic rice accessions for 7 traits. The genetic and phenotypic coefficients of variation were high for number of unfilled grains per panicle, unfilled grain percentage, grain yield per plant, 1000 grains weight, number of ear-bearing tillers per plant, and number of filled grains per particle. High heritability estimates coupled with high genetic gain were recorded for grain yield per plant, number of ear-bearing tillers per plant, number of filled grains per panicle and unfilled grain percentage. The grain yield showed a positive and significant correlation with number of days to 50% flowering, plant height, number of ear-bearing tillers per plant and number of filled grains per panicle at the genetic and phenotypic levels. Path analysis revealed that 1000 grains weight had the greatest positive direct effect on grain yield followed by number of ear-bearing tillers per plant, number of filled grains per particle and number of days to 50% flowering. However 1000 grains weight had no significant correlation with grain yield per plant due to its negative indirect effect on grain yield per plant through the number of filled grains per particle and plant height.

Shiv and Mani (2003) evaluated genetic divergence in elite genotypes of Basmati rice and found that plant height contributed maximum towards genetic divergence (52.2) followed by days to 50% flowering and grain yield /plant.

Itani (2002); evaluated the agronomic characteristics of aromatic rice collected from all over Japan, 71 randomly selected cultivars were cultivated along with 21 foreign aromatic cultivars from 7 countries and l8 Japanese non-aromatic cultivars. In addition, 44 Japanese aromatic cultivars and 6 old and I2 new non-aromatic cultivars were examined for their leaf characteristics. The local Japanese aromatic cultivars had a greater height, fewer and larger panicles, greater straw weight, lower yield, less tolerance to lodging and more awns than the new cultivars. Morphologically, the local Japanese aromatic cultivars were divided into eastern and western groups. The former showed earlier heading, shorter culm, smaller panicle, lower yield, thinner stem and less tolerance to lodging than the latter. Foreign aromatic cultivars were similar to the Japanese ones in terms of long culm, heavy panicle and low yield, but they had poorer biomass and harvest index with later maturing and larger panicle. Local

Japanese aromatic cultivars had longer and wider flag leaf, larger flag leaf angle, faster leaf senescence and longer neck inter node of panicle than the new cultivars.

Basher (2002) studied genetic divergence among 36 genotypes by using D^2 statistics for 15 characters related to yield and its contributing characters. The genotypes were grouped into six clusters. The results revealed that the harvest index had the highest contribution followed by tillers per plant, panicle length, 1000 grains weight, filled grains per panicle, days to maturity and leaf photosynthetic rate towards genetic divergence.

Roy *et al.* (2002) evaluated 50 rice cultivars for genetic diversity and responded that plant height, tiller numbers, panicle length, 1000 grains weight. 1000 kernel weight, filled grains/panicle and kernel-grain ratio contributed most towards divergence.

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

Yield per hectare is the most important consideration in rice breeding program, but yield is a complex character in inheritance and may involve several related components. Rice yield is a product of number of panicles per unit area, number of spikelets per panicle, percentage of filled grains and weight of 1000 grains (Datta and Khanam 2002).

Thayamanavan *et al*. (2001) evaluated genetic diversity among twenty six rice genotypes from four states of South Eastern Region of India using Mahalanobis's D^2 statistics. Based on 12 morphological and quality characters namely, days to first flower, productive tillers per plant. panicle length, number of grains per panicle, 1000- grain weight, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant. These genotypes were grouped into 13 clusters. Genotypes from more than one place of origin were grouped in one cluster and genotypes from one state were grouped in more than one cluster. Geographical origin was not found to be a good parameter of genetic divergence. Cluster XII recorded highest mean value for grain yield per plant and lowest mean value for days to first flower. Number of grains per panicle followed by days to first flower contributed maximum to total divergence. Hybridization among genotypes AUR 4, Annamalan mutant poumani, Karnoolsona, Jecraga samba, AUR 7 and PY 5 from clusters Ill, ll, XII and IX which had maximum inter-cluster distances and desirable values for days to first flower, number of grains per panicle, kernel length, kernel breadth, 1000 grain weight and grain yield per plant is likely to produce heterotic combinations and wide variability is segregating generations.

Jiang *et al.* (2000) observed the importance of number of tillers/plant influencing yield. Productive tillers/hill showed significant positive correlations with correlations with grain yield (Reddy and Kumar, 1996).

Choudhury *et al.* (1999) studied 64 indigenous rice varieties to know the nature and magnitude of genetic divergence among them. Based on nine agro-morphological characters, these genotypes were grouped into five clusters and found that plant height, tiller number, earliness, grain size and grain yield contributed considerably to total divergence.

Li and Yuan (1998) reported the parental genotype divergence had a relatively low impact on heterosis for panicle number and 1000 grain weight. Plant height, panicle per plant, grain per panicle and 1000 grain weight increase the yield in modern varieties (Saha Ray *et al.,* 1993).

Vijaya kumar *et al.* (1997) found that hybrids out yielded than their check varieties when their days to 50% flowering were similar or more than their respective restorers. They concluded that superior hybrids could be early by comparing their tiller number, plant height and days to 50% flowering with those of their respective restorers.

Considerable genetic variability was recorded by Awasthi and Sharma (1996) for morphological traits in fifteen high quality aromatic rice genotypes grown at Faisabad. Maximum and minimum plant heights were recorded for Type-3 and Pusa-33, respectively, and maximum and minimum leaf lengths for Kasturi and Pusa-33 respectively. Highest number of nodes and internodes were recorded in Type-3 and Tilakchandan respectively. Colour of leaves and magnitude of aroma also varied greatly with genotypes.

Sawant *et al.* (1994) studied 6 yield related traits in F_4 generation of rice found that expected genetic advance and heritability were high for grains per panicle. A high coefficient of variation and high value of heritability together with high expected genetic advance were also observed by Sawant and Patil (1995).

Mohapatra *et al.* (1993) evaluated 13 agro-morphological characters of 34 mutant lines for the magnitude of genetic divergence using Mahalanobis‘s D^2 statistics. The population was grouped into seven clusters. Plant height (24.6%) and 1000 grains weight (18.3%) contributed considerably, accounting for 43% of total divergence.

Vivekzuradan and Subramanian (l993) evaluated 28 rice genotypes for the magnitude of genetic divergence using Mahalanobis's D^2 statistics. The population was grouped into five clusters. Plant height and grain yield

contributed considerably, accounting for 85% of total divergence. The geographic diversity has not been found related to genetic diversity.
Das *et al*. (l992) evaluated 30 rice genotypes for variability analysis and found that plant height, days to 50% flowering, number of filled grains per panicle, panicle length, 1000-grains weight and days to maturity had high genetic coefficient of variation.

Twenty-six aromatic rice germplasms collected from different parts of Orissa were evaluated for seed protein variability by Dikshit *et al.* (1992). Highly significant differences were reported for protein content, grain weight and L/B ratio. Some of the land races (Kalajira, Kanakpure etc.) were found to have protein content in the range of 9-10 percent and more. The L/B ratio varied from l.6 to 3.5 with six collections characterized as long slender grain type most notable among them were (Gidhanpakshi, Barhampuri, Badshahbhog and Durgabhogs) litming kernel length of 7.7 mm and 6.6 mm, respectively.

Rice tillering is a major determinant for panicle production (Miller *et al*. 1991) and as a consequence affects total yield (Gallagher and Biscoe, 1978). The high tillering capacity is considered as a desirable trait in rice production, since number of tillers per plant is closely related to number of panicles per plant. To some extent, yield potential of a rice variety may be characterized by tillering capacity. On the other hand, it was reported that the plants with more tillers showed a greater inconsistency in mobilizing assimilates and nutrients among tillers. Moreover, grain quality could be also affected by tillering ability due to different grain developmental characteristics. It has been well documented that either excessive or insufficient tillering is unfavorable for high yield.

Sarma *et al.* (1990) studied the grain characteristics of 13 traditional aromatic rice varieties of Assam and reported wide variation in grain length (566 - 994 mm), breadth (180 - 296 mm), L/B ratio (2.44) and 1000 grains weight (8.44 -

25.48 gm). Obviously, some of the collections had extra ordinarily high grain length and could be used as donors in breeding programs.

Ghosh and Hossain (1988) reported that effective tillers/plant, number of grains/panicle and grain weight as the major contributory characters for grain yield it had positive correlations with number of productive tillers/plant.

Miyagawa and Nakamura (1984) classified 85 aromatic rice cultivars based on the regional differences in varietal characteristics. Using principal component analysis, they divided the material into four major groups and found that the cultivars from Tohoku and Kanto area showed early maturity having shorter culms, longer awn, larger angle of flag leaf, less straw weight and yield. In Kinkind and Kyushu, the cultivars showed late maturity, and had longer culms, more straw height and yield. Cultivars from Shikoku differed from those of the warm areas of Kinkind and Kyushu. Similarly the cultivars from Hokuriku area were different from that of the other regions. Yield in cereals is a complex character and determined by some yield component. Grafius (1964) suggested that these yield components express their genetic and environmental effects finally through spikelet yield. Allard (1960) stated that the broad sense heritability is the relative magnitude of genotypic and phenotypic variance for the traits and it gives an idea of the total variation accounted to genotypic effect. Ghose and Ghatge (1960) also stated that tiller number, panicle length contributed to yield with grain yield (Reddy and Kumar, 1996).

CHAPTER III

MATERIALS AND METHODS

The details of different populations used and methodology followed during the experimental period are described in this chapter as follows:

Experimental treatments and sources of plant populations:

3.1 Experimental Site

The experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during April 2015 to August 2015. The location of the site was situated at 23°41’ N latitude and 90°22’ E longitude. Geographically the experimental field is located at 8.4 metre above the mean sea level (Anon., 1989). The experimental site was shown in the map of AEZ of Bangladesh in Appendix I.

3.2 Climate and Soil

The experimental site was medium high land belonging of old Madhupur tract (AEZ-28) (UNDP, 1988) and the soil series was Tejgaon (FAO, 1988).The soil of the experimental plot was clay loam in texture having pH around 6.5 and organic carbon content is 0.84%. The experiment area was above flood level and having available irrigation and drainage system and has been presented in Appendix VI.

The experimental site was under the subtropical climate. It is characterized by three distinct seasons, winter season from November to February and the pre-monsoon or hot season from March to April and the monsoon period from May to October (Edris *et al.*, 1979). Details of the metrological data of air temperature, relative humidity, rainfall and sunshine hour at the time of experiment was collected from the weather station of Bangladesh, Sher-e-Bangla Nagar, Dhaka and has been presented in Appendix VII.

3.3 Planting Materials (Genotypes)

Eighteen (18) genotypes of F_5 generation with three check varieties (BR 24, BRRI dhan 48 and BRRI dhan 55) were used as experimental materials in the study. Descriptions of the genotypes are given in Table l.

Table 1. List of materials used for the experiment

Genotypes	Populations	Source
G1	BR 21× BRRI dhan 29 F_5S_7 P_5	GEPB, SAU
G2	BR 24× BRRI dhan 28 F_5S_{10} P_{10}	GEPB, SAU
G3	BR 21× BRRI dhan 29 F_5S_6 P_3	GEPB, SAU
G4	BR 21× BRRI dhan 29 F_5S_7 P_2	GEPB, SAU
G5	BR 24× BR 26 F_5S_6 P_4	GEPB, SAU
G6	BR 21× BRRI dhan 29 F_5S_6 P_{10}	GEPB, SAU
G7	BR 21× BRRI dhan 29 $F_5S_7P_1$	GEPB, SAU
G8	BR 21× BRRI dhan 29 F_5S_6 P_9	GEPB, SAU
G9	BR 21× BRRI dhan 29 F_5S_7 P_4	GEPB, SAU
G10	BR 24× BRRI dhan 28 F_5S_{10} P_8	GEPB, SAU
G11	BR 21× BRRI dhan 36 F_5S_1 P_9	GEPB, SAU
G12	BR 21× BRRI dhan 29 F_5S_6 P_3(a)	GEPB, SAU
G13	BR 24× BRRI dhan 29 F_5S_5 P_{10}	GEPB, SAU
G14	BR 21× BRRI dhan 29 $F_5S_6P_{10}$	GEPB, SAU
G15	BR 21× BRRI dhan 29 F_5S_6 P_2	GEPB, SAU
G16	BR 21× BRRI dhan 29 F_5S_1 P_2	GEPB, SAU
G17	BR 21× BRRI dhan 29 F_5S_6 P_3(b)	GEPB, SAU
G18	BR 21× BRRI dhan 29 F_5S_6 P_5	GEPB, SAU
G19	BRRI dhan 48	BRRI
G20	BRRI dhan 55	BRRI
G21	BR 24	BRRI

G=Genotypes

3.4 Design and Layout

The experiment was laid out in randomized complete block design (RCBD). The field was divided into three blocks; the blocks were sub-divided into 9 plots (lines) where genotypes were randomly assigned. The experimental field size was 27 m x 14 m where 1m boarder was maintained surrounding the field and every block. The same size of crop field was used for another nine lines. The experimental field was designed such a way where row to row distance was 25 cm and plant to plant distance was 25 cm. The 18 genotypes and 3 check varieties were distributed to each plot within each block randomly.

3.5 Collection of Seed

The seeds of 18 aus lines were collected from germplasm center of Sher-e-Bangla Agricultural University (SAU). Three check varieties (BR 24, BRRI dhan 48 and BRRI dhan 55) were collected from Bangladesh Rice Research Institute (BRRI).

3.6 Germination of Seed

Seed of all collected rice genotypes soaked separately for 24 hours in clothes bag. Soaked seeds were picked out from water and wrapped with straw and gunny bag to increase the temperature for facilitating germination. After 72 hours seeds were sprouted properly.

3.7 Seedbed Preparation and Seedling Raising

The seed bed was prepared well by puddling the wetland with repeated ploughing following by laddering. Sprouted seeds were sown seperately in the previously wet seedbed on 25 April, 2015. Proper care was taken so that there was no infestation of pest and diseases and no damage by birds.

3.8 Preparation of Main Field

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

3.9 Application of Fertilizers

The fertilizers N, P, K, S and B in the form of urea, TSP, MP, Gypsum and Borax respectively were applied. The entire amount of TSP, MP, Gypsum, Zinc Sulphate and Borax were applied during final preparation of field. Urea was applied in three equal installments during ploughing, vegetative stage and before flowering. The dose and method of application of fertilizer are sown in Table 2.

Table 2. Dose and method of application of fertilizers in rice field

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

Source: BRRI (2015), Jodebpur, Gazipur.

3.10 Transplanting of Seedling

Healthy seedlings of 25 days old were transplanted on 20 May 2015 in separate strip of experimental field. Water level was maintained properly after transplanting.

3.11 Intercultural Operation and After Care

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

3.11.1. Irrigation and Drainage

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

3.11.2. Gap Filling

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

3.11.3. Weeding

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

3.11.4. Top Dressing

After basal dose, the remaining doses of urea were top dressed in 2 equal installments. The fertilizers were applied on both sides of seedlings rows with the soil.

3.11.5. 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 gm per liter water was applied against bacterial leaf blight of rice.

3.11.6. Harvesting, Threshing and Cleaning

The rice was harvested depending upon the maturity of plant and harvesting was done manually from each plot. The harvested crop of each plot was bundled separately. Properly tagged and brought to threshing floor. Enough care was taken for threshing and also cleaning of rice seed. Fresh weight of grain was recorded. The grains were cleaned and finally the weight was adjusted to moisture content 14%.

3.12 Methods of Recording of Observations

To study the stable diagnostic characteristics data and morphological characters were collected from ten randomly selected hills from each replicated plots. The plants were selected from middle of each plot to avoid border effect and portion of the plot. The mean was estimated. Thirty one qualitative and ten quantitative traits were recorded using the descriptors developed by BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007. The descriptors are shown in the Appendix II & III. In addition to the descriptors, the observed genotypes were classified according to Panse and Sukhatme (1995) and Naseem (2005). The observations for characterization were recorded under field condition as follows.

3.12.1 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. Rice descriptors developed by The BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007 (Appendix II & III) 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 rice genotypes. Photographs and data related to distinctness in morphological traits were taken on each of the 18 rice genotypes.

3.12.1.1 Leaf Sheath: Anthocyanin color

Data was collected at early vegetative stage on leaf sheath anthocyanin color and the rice genotypes were classified into two groups with codes according to guided descriptors as per follows.

Absent-1 and Present-9.

3.12.1.2 Leaf Color

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

Pale green-1, Green-2, Dark green-3,

Purple tip-4, Purple margins-5,

Purple blotch-6 and Purple-7.

3.12.1.3 Penultimate Leaf 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 observed genotypes were categorized into three groups as per descriptors by following way.

Absent or very weak-1,

Weak or only on the margins-3,

Medium hairs on the medium portion of the leaf-5,

Strong hairs on the leaf blade-7 and

Very strong-9.

3.12.1.4 Penultimate Leaf: Anthocyanin coloration of auricles and collar

Data was collected at late vegetative stage on penultimate leaf anthocyanin coloration of auricles and collar and the rice genotypes were classified into two groups with codes according to guided descriptors as per follows.

Absent-1 and Present-9.

Table 3. Descriptors with codes for qualitative characteristics

SL. No.	Characteristics	Descriptors with Codes
1	Leaf sheath: anthocyanin color	Absent-1, Present-9.
2	Leaf color	Pale green-1, Green-2, Dark green-3, Purple tip-4, Purple margins-5, Purple blotch-6, Purple-7.
3	Penultimate leaf pubescence	Absent or very weak-1, Weak or only on the margins-3, Medium hairs on the medium portion of the leaf-5, Strong hairs on the leaf blade-7, Very strong-9.
4	Penultimate leaf: anthocyanin coloration of auricles and collar	Absent-1, Present-9.
5	Penultimate leaf: ligule	Absent-1, Present-9.
6	Penultimate leaf: shape of the ligule	Truncate-1, Acute-2, Split or two-cleft-3.
7	Flag leaf: attitude of the blade	Erect (<30^0)-1, Intermediate or Semi-erect (30^0-45^0)-3, Horizontal (46^0-90^0)-5, Reflexed or descending (>90^0)-7.
8	Male sterility	Absent-1, CMS-3, TGMS-5, PGMS-7, P(T)GMS-9.
9	Microscopic observation of pollen with I_2-KI solution	Completely sterile with TA pollen-1, Completely sterile with 80% TA pollen-2, Completely sterile with 50% TA pollen-3, Sterile (91-99%)-4, Partial sterile(31-70%)-5, Partial fertile (31-70%)-6, Fertile (21-30%)-7 and Fully fertile (0-20%)-8.
10	Lemma and Palea: anthocyanin coloration	Absent or very weak-1, Weak-3, Medium-5, Strong-7, Very strong-9.
11	Lemma: anthocyanin coloration of area below apex	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
12	Lemma: anthocyanin coloration of apex	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
13	Color of stigma	White-1, Light green-2, Yellow-3, Light purple-4 and Purple-5.
14	Stigma exertion	No or a few (>5%)-1, Low (5-20%)-3, Medium (21-40%), High (41-60%)-7, Very high (>61%)-9.
15	Stem: anthocyanin coloration of nodes	Absent-1, Present-9.
16	Stem: intensity of anthocyanin coloration of nodes	Weak-3, Medium-5, Strong-7 and Very strong-9.

Table 3. Descriptors with codes for qualitative characteristics(cont'd)

SL. No.	Characteristics	Descriptors with Codes
17	Stem: anthocyanin coloration of internodes	Absent or very weak -1, Weak-3, Medium-5, Strong- 7,Very strong-9.
18	Panicle: curvature of main axis (i.e. recurved main axis)	Absent or very weak -1, Weak-3, Medium-5, Strong- 7.
19	Spikelet: pubescence of lemma and palea	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
20	Spikelet: color of the tip of lemma	White-1, Yellowish-2, Brownish-3, Red-4, Purple-5, Black-6.
21	Spikelet: awns in the spikelet	Absent-1, Present-9.
22	Spikelet: Length of the longest awn	Very short (<2 mm)-1, Short (2-5 mm)-3, Medium (5-10 mm)-5, Long (11-20 mm)-7 and Very long (>20 mm)-9.
23	Panicle: Distribution of awns	Tip only-1, Upper half only-3 and Whole length-5.
24	Panicle: Color of awns	Yellow white-1, Brown-3, Reddish-5, Purple-7 and Black-9.
25	Panicle: attitude of branches	Erect-1, Semi-erect-3, Spreading-5.
26	Panicle: exertion	Enclosed-1, Partly exerted-3, Just exerted-5, Moderately exerted-7, Well exerted-9.
27	Leaf senescence: Penultimate leaves are observed at the time of harvest.	Late and slow (2 or more leaves retain green color at maturity)-1, Intermediate-5 and Early and fast (leaves are dead at maturity)-9.
28	Decorticated grain: shape (length-width ratio of de-hulled grain)	Round (L:W<1.5)-1, Bold (L:W=1.5-2.0)-3, Medium (L:W=2.1-2.5)-5, Medium slender (L:W=2.6-3.0)-7 and Slender (L:W>3.0)-9.
29	Decorticated grain (bran): color	White-1, Light brown-2, Variegated brown-3, Dark brown-4, Red-5, Variegated purple-6 and Purple-7.
30	Polished grain: size of white core or chalkiness (% of kernel area)	Absent or very small-1, Small (<10%)-3, Medium (11-20%)-5 and Large (11-20%)-7.
31	Decorticated grain: aroma	Absent-1, Lightly present-5 and Strongly present-9.
32	Other distinct special character (if any)	

Source: BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007. Descriptors for wild and cultivated rice (*Oryza spp*.)

3.12.1.5 Penultimate Leaf: Ligule

Data was collected at late vegetative stage on penultimate leaf ligule and the rice genotypes were classified into two groups with codes according to guided descriptors as per follows.

Absent-1 and Present-9.

3.12.1.6 Penultimate Leaf: Shape of the ligule

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 and

Split or two-cleft-3.

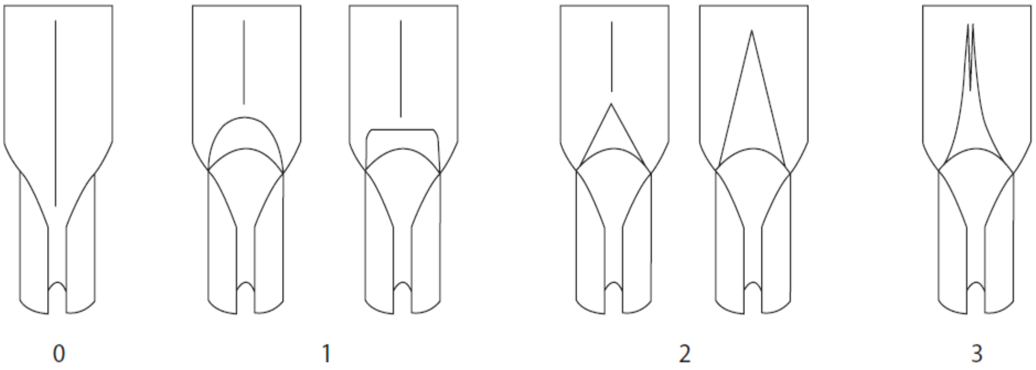

Figure 1. Ligule shape.

3.12.1.7 Flag Leaf: Attitude of the blade

Attitude of the blade of flag leaf is angle of attachment between the flag leaf blade and the main panicle axis. It was just visually observed at anthesis period and classified into following four groups.

Erect ($<30^0$)-1,

Intermediate or Semi-erect (30^0-45^0)-3,

Horizontal (46^0-90^0)-5 and

Reflexed or descending ($>90^0$)-7.

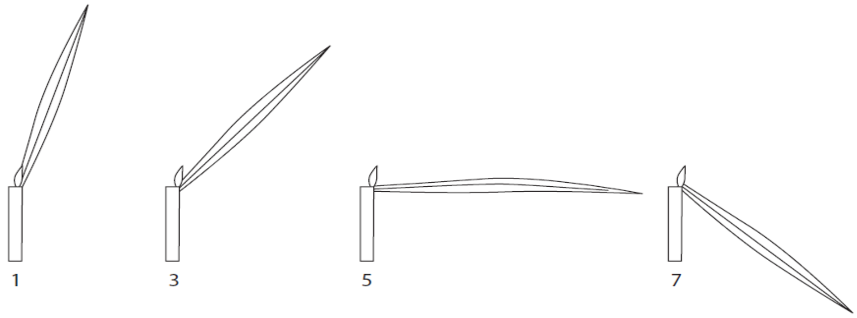

Figure 2. Flag leaf attitude

3.12.1.8 Male Sterility

It was observed at anthesis period of rice and grouped as per descriptors.

Absent-1,

CMS-3, TGMS-5,

PGMS-7 and P (T) GMS-9.

3.12.1.9 Microscopic Observation of Pollen with I_2-KI solution

It was observed at anthesis period of rice using microscope and the rice genotypes were classified into eight groups with codes according to guided descriptors as per follows.

Completely sterile with TA pollen-1,

Completely sterile with 80% TA pollen-2,

Completely sterile with 50% TA pollen-3,

Sterile (91-99%)-4,

Partial sterile (31-70%)-5,

Partial fertile (31-70%)-6,

Fertile (21-30%)-7 and

Fully fertile (0-20%)-8.

3.12.1.10 Lemma and Palea: Anthocyanin coloration

Data was collected at pre-ripening stage on grain anthocyanin coloration of lemma and palea and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Absent or very weak-1,

Weak-3, Medium-5,

Strong-7 and Very strong-9.

3.12.1.11 Lemma: Anthocyanin coloration of area below apex

Data was collected at pre-ripening stage on grain anthocyanin coloration of lemma and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Absent or very weak-1,

Weak-3, Medium-5,

Strong-7 and Very strong-9.

3.12.1.12 Lemma: Anthocyanin coloration of apex

Data was collected at pre-ripening stage on grain anthocyanin coloration of lemma and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Absent or very weak-1,

Weak-3, Medium-5,

Strong-7 and Very strong-9.

3.12.1.13 Color of Stigma

Data was observed at anthesis period using a hand lens or magnifying glass and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

White -1, Light green-2,
Yellow-3, Light purple-4 and
Purple-5.

3.12.1.14 Stigma Exertion

Data was observed at anthesis period using a hand lens or magnifying glass and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

No or a few (>5%)-1, Low (5-20%)-3,

Medium (21-40%)-5, High (41-60%)-7 and

Very high (>61%)-9.

3.12.1.15 Stem: Anthocyanin coloration of nodes

Data was collected after flowering to near maturity stage on stem anthocyanin coloration of nodes and the rice genotypes were classified into two groups with codes according to guided descriptors as per follows.

Absent-1 and

Present-9.

3.12.1.16 Stem: Intensity of anthocyanin coloration of nodes

Data was collected after flowering to near maturity stage on stem anthocyanin coloration of nodes and the rice genotypes were classified into four groups with codes according to guided descriptors as per follows.

Weak-3, Medium-5,

Strong-7 and Very strong-9.

3.12.1.17 Stem: Anthocyanin coloration of internodes

Data was collected at near coloration maturity stage on stem anthocyanin coloration of internodes and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Absent or very weak-1,

Weak-3, Medium-5,

Strong-7 and Very strong-9.

3.12.1.18 Panicle Curvature of Main Axis (i.e. recurrent main axis)

Data was collected at near maturity stage and the rice genotypes were classified into four groups with codes according to guided descriptors as per follows.

Absent or very weak (upright)-1,

Weak (semi-upright)-3,

Medium (slightly drooping)-5 and

Strong (strongly dropping)-7.

3.12.1.19 Spikelet: Pubescence of lemma and palea

Data was collected after anthesis to hard dough stage or pre-ripening stage on spikelet with pubescence of lemma and palea and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Absent or very weak-1,

Weak-3, Medium-5,

Strong-7 and Very strong-9.

3.12.1.20 Spikelet: Color of the tip of lemma

Data was collected after anthesis to hard dough stage or pre-ripening stage on spikelet with color of the tip of lemma and the rice genotypes were classified into six groups with codes according to guided descriptors as per follows.

White-1, Yellowish-2,

Brownish-3, Red-4,

Purple-5 and Black-6.

3.12.1.21 Spikelet: Awns in the spikelet

It was observed at flowering to maturity stage and normally a character of wild species of rice and grouped as per descriptors.

Absent-1 and

Present-9.

3.12.1.22 Spikelet: Length of the longest awn

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

Very short (<2 mm)-1,

Short (2-5 mm)-3,

Medium (5-10 mm)-5,

Long (11-20 mm)-7 and

Very long (>20 mm)-9.

3.12.1.23 Panicle: Distribution of awns

It was observed at flowering to maturity stage and normally a character of wild species of rice and grouped as per descriptors.

Tip only-1,

Upper half only-3 and

Whole length-5.

3.12.1.24 Panicle: Color of awns

It was observed at flowering to maturity stage and normally a character of wild species of rice and grouped as per descriptors.

Yellow white-1, Brown-3,

Reddish-5, Purple-7 and

Black-9.

3.12.1.25 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 and Drooping-9.

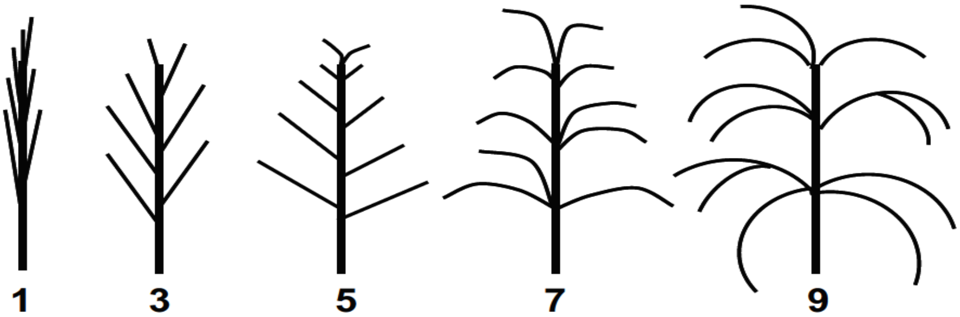

Figure 3. Attitude of panicle branches

3.12.1.26 Panicle: Exertion

Extent to which the panicle is exerted above the flag leaf sheath is known as panicle exertion. Data was collected at near maturity stage and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Enclosed-1, Partly exerted-3

Just exerted-5, Moderately exerted-7 and

Well exerted-9.

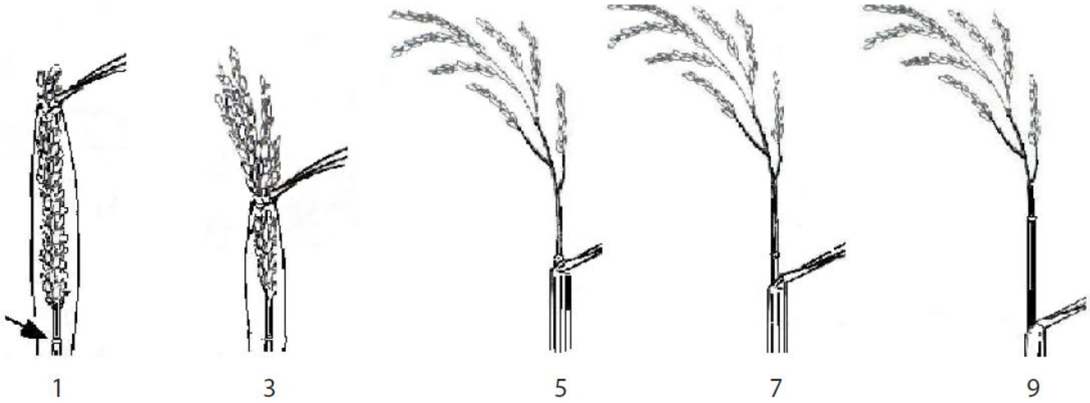

Figure 4. Panicle exertion.

3.12.1.27 Leaf Senescence: Penultimate leaves are observed at the time of harvest.

Data was collected at the time of harvest and the rice genotypes were classified into three groups with codes according to guided descriptors as per follows.

Late and slow (2 or more leaves retain green color at maturity)-1,

Intermediate-5 and

Early and fast (leaves are dead at maturity)-9.

3.12.1.28 Decorticated Grain: Shape (length-width ratio of de-hulled grain)

Data was collected at the time of harvest and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows.

Round (L: W<1.5)-1

Bold (L: W=1.5-2.0)-3

Medium (L: W=2.1-2.5)-5

Medium slender (L: W=2.6-3.0)-7 and

Slender (L: W>3.0)-9.

3.12.1.29 Decorticated Grain (bran): Color

Data was collected at the time of harvest and the rice genotypes were classified into seven groups with codes according to guided descriptors as per follows.

White-1, Light brown-2,

Variegated brown-3,

Dark brown-4, Red-5

Variegated purple-6 and

Purple-7.

3.12.1.30 Polished Grain: Size of white core or chalkiness (% of kernel area)

Data was collected at the time of harvest and the rice genotypes were classified into four groups with codes according to guided descriptors as per follows.

Absent or very small-1,

Small (<10%)-3,

Medium (11-20%)-5 and

Large (11-20%)-7.

3.12.1.31 Decorticated Grain: Aroma

Data was collected at the time of harvest and the rice genotypes were classified into three groups with codes according to guided descriptors as per follows.

Absent-1,

Lightly present-5 and

Strongly present-9.

3.12.1.32 Other Distinct Special Character (if any)

3.12.2 Quantitative Traits Evaluation Methods

3.12.2.1 Stem: Culm diameter (from 5 mother tillers in the lowest internode)

Culm diameter of the stem was measured in millimeter scale at the lowest internode of the stem during flowering or late reproductive stage by using digital caliper and categorized as per descriptors.

Small (<5.0 mm)-1, Medium (5.1-6.0 mm)-3,

Large (6.1-7.0 mm)-5 and Very Large (>7.0 mm)-7

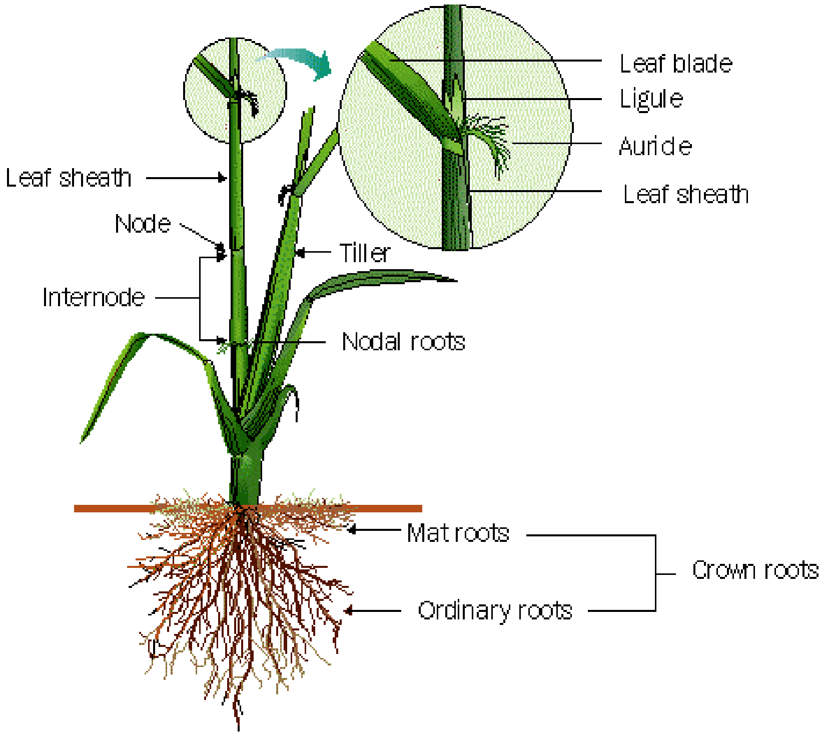

Figure 5. Morphology of a rice plant (vegetative stage)

3.12.2.2 Stem Length (culm length): Measure from the base of the plants to the neck of the panicles

Stem length (culm length) was measured in centimeter from the base of the plants to the neck of the panicles after flowering to maturity stage and categorized as per descriptors.

Very short (<40 cm)-1,

Short (41–60 cm)-3,

Medium (61–80 cm)-5,

Long (81-110 cm)-7 and

Very long (>110 cm)-9.

3.12.2.3 Panicle Length: Measured from the neck to the tip of the panicle of main tillers without awns

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. Data was collected at 7 days after anthesis or full panicle exertion stage According to their length, the observed rice genotypes were classified into four groups with codes.

Short (<20 cm)-3, Medium (21-25 cm)-5,

Long (26-30 cm)-7 and Very long (>30 cm)-9.

3.12.2.4 Panicle: Number of the effective tillers per plant

Effective tillers are the tillers which bears panicle and the total number of tillers were counted from each of the sample plants and the average was taken. Based on this character, all the genotypes were grouped into following groups.

Few (>6)-3,

Medium (6-10)-5 and

Many (>10)-7.

3.12.2.5 Time of 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 were classified as per the guided descriptors.

Very early (>100 days)-1, Early (101-115 days)-3,

Medium (116-135 days)-5, Late (136-150 days)-7 and

Very late (>150 days)-9.

3.12.2.6 Grain: Weight of 1000 fully developed grains (adjusted of 12% of moisture)

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. According to test weight, the genotypes were categorized into five different groups as following.

Very low (<15 gm)-1, Low (16-19 gm)-3,
Medium (20-23 gm)-5, High (24-27 gm)-7 and Very high (>27 gm) – 9.

Table 4. Descriptors with codes for quantitative characteristics

SL. No.	Characteristics	Descriptors with Codes
1	Time of heading (50% of plants with heads)	Very early (< 70 days)-1, Early (70-85 days)-3, Medium (86-105 days)-5, Late (106-120 days)-7, Very late (>120 days)-9.
2	Stem: culm diameter (from 5 mother tillers in the lowest internode)	Small (<5.0 mm)-1, Medium (5.1-6.0 mm)-3, Large (6.1-7.0 mm)-5, Very Large (>7.0 mm)-7.
3	Stem length (culm length): Measure from the base of the plants to the neck of the panicles	Very short (<40 cm)-1, Short (41–60 cm)-3, Medium (61–80 cm)-5, Long (81-110cm)-7, Very long (>110 cm)-9.
4	Panicle length: measured from the neck to the tip of the panicle of main tillers without awns	Short (<20 cm)-3, Medium (21-25 cm)-5, Long (26-30 cm)-7 and Very long (>30 cm)-9.
5	Panicle: number of the effective tillers per plant	Few (>6)-3, Medium (6-10)-5, Many (>10)-7.
6	Time of maturity	Very early (>100 days)-1, Early (101-115 days)-3, Medium (116-135 days)-5, Late (136-150 days)-7, Very late (>150 days)-9.
7	Grain: weight of 1000 fully developed grains (adjusted of 12% of moisture)	Very low (<15 gm)-1, Low (16-19 gm)-3, Medium (20-23 gm)-5, High (24-27 gm)-7, Very high (>27 gm)- 9.
8	Grain: length (without dehulling)	Very short (<6.0 mm)-1, Short (6.1-7.0 mm)-3, Medium (7.1-8.0 mm)-5, Long (8.1-9.0 mm)-7 and Very Long (>9.0 mm)-9.
9	Sterile lemma length: Measure at postharvest stage	Short (<1.5 mm)-1, Medium (1.5-2.5 mm)-3, Long (2.6-3.0 mm)-5 and Very Long (>3.0 mm)-7.
10	Decorticated grain: length (After dehulling, before milling)	Short (<5.5 mm)-1, Medium (5.6-6.5 mm)-3, Long (6.6-7.5 mm)-5 and Very Long (>7.5 mm)-7.

Source: BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007. Descriptors for wild and cultivated rice *(Oryza spp.)*

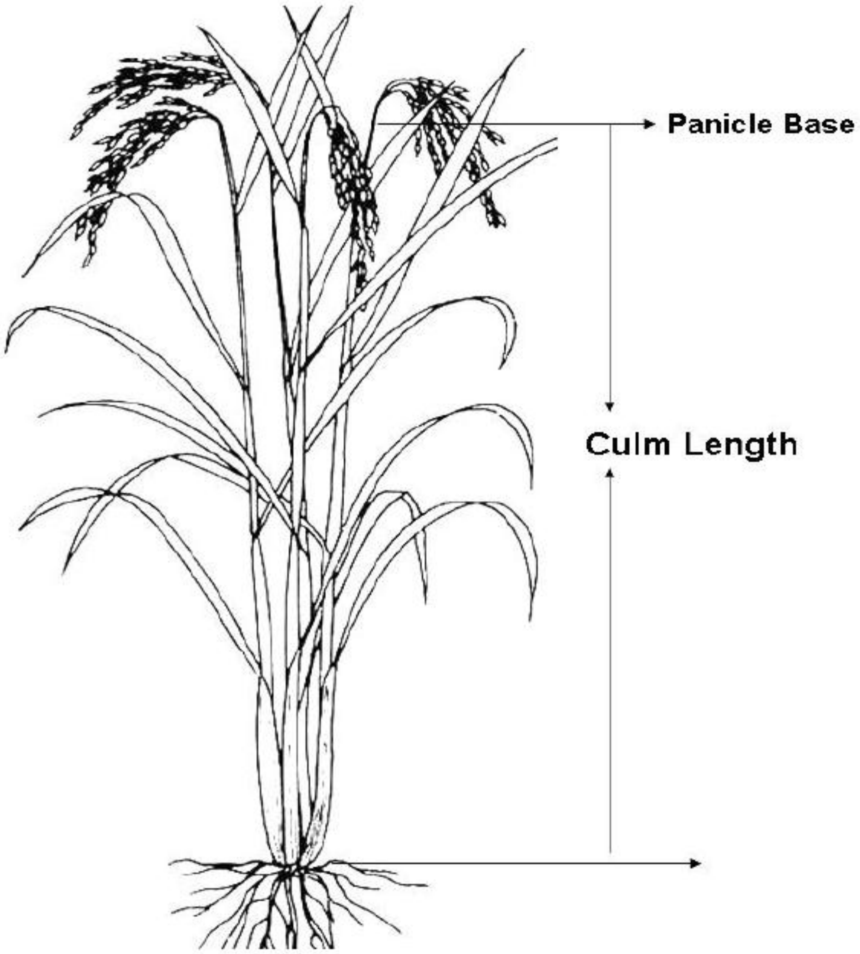

Figure 6. Culm length

3.12.2.7 Grain: Length (without dehulling)

Grain length was measured in mm and a digital caliper was used for clear visualization. Ten grains from every genotypes were measured and the mean value was recorded. The genotypes were classified as per the guided descriptors.

Very short (<6.0 mm)-1,

Short (6.1-7.0 mm)-3,

Medium (7.1-8.0 mm)-5,

Long (8.1-9.0 mm)-7 and

Very Long (>9.0 mm)-9.

3.12.2.8 Sterile Lemma Length: Measure at post-harvest stage

Sterile lemma length was measured in mm and a digital caliper was used for clear visualization. Ten grains from every genotypes were measured and the mean value was recorded. The genotypes were classified as per the guided descriptors.

Short (<1.5 mm)-1,

Medium (1.5-2.5 mm)-3,

Long (2.6-3.0 mm)-5 and

Very Long (>3.0 mm)-7.

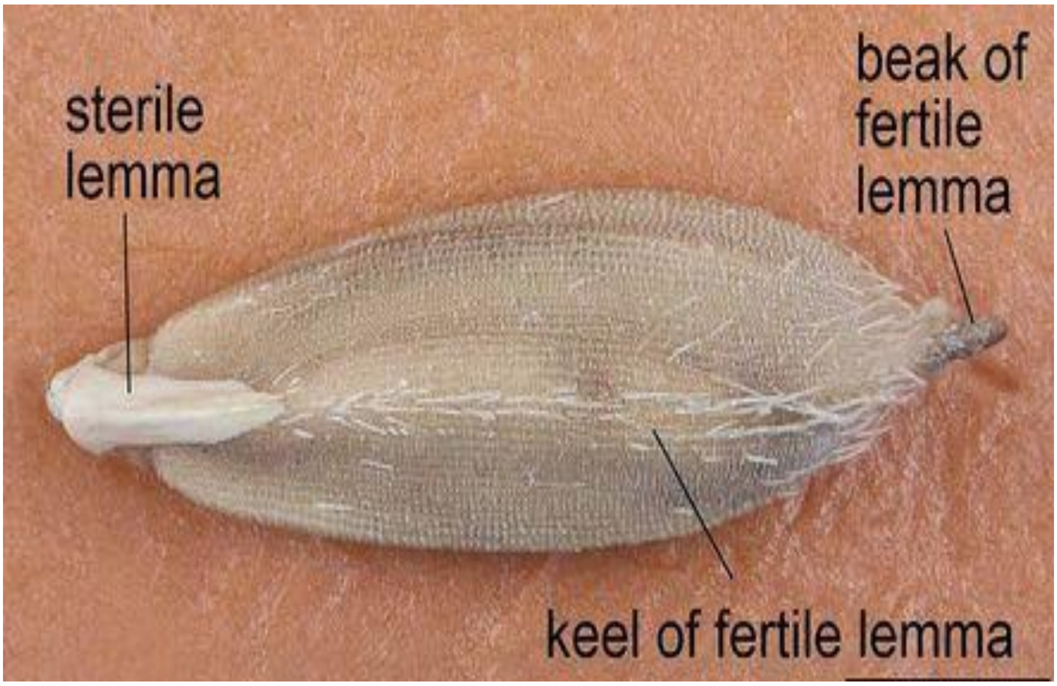

Figure 7. Rice grain with sterile lemma.

3.12.2.9 Decorticated Grain: Length (After dehulling, before milling)

Decorticated grain length was measured in mm and a digital caliper was used for clear visualization. Ten grains from every genotypes were measured and the mean value was recorded. The genotypes were classified as per the guided descriptors.

Short (<5.5 mm)-1,

Medium (5.6-6.5 mm)-3,

Long (6.6-7.5 mm)-5 and

Very Long (>7.5 mm)-7.

3.12.3 Statistical Application

The qualitative and quantitative data in relation to morphological traits are just presented in tabular form for easier description according to the descriptors developed by BIOVERSITY INTERNATIONAL, IRRI AND WARDA-2007. The data were arranged as per IBPGR-IRRI formulation with the help of Microsoft-XL program.

CHAPTER IV

RESULTS AND DISCUSSION

The study was conducted with a view to characterizing and evaluating eighteen F_5 lines of aus rice as per the guided descriptors developed by BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007. Thirty one qualitative and ten quantitative characters were observed. Results have been compiled in tabular form according to descriptors and described by the following ways:

- Qualitative Characteristics
- Quantitative Characteristics

4.1 Qualitative Characteristics

4.1.1 Leaf Sheath: Anthocyanin color

On the basis of leaf sheath anthocyanin coloration the observed genotypes were categorized as absent-1 and present-2 according to guided descriptors as per follows. But no coloration was found in this investigation (Table 5). A pictorial view of leaf sheath anthocyanin color is present in Plate 1.

4.1.2 Leaf Color

Based on leaf color the observed genotypes were categorized in 7 groups like pale green-1, green-2, dark green-3, purple tip-4, purple margins-5, purple blotch-6 and purple-7 according to guided descriptors as per follows. Here 2 genotypes (G9, and G13) showed pale green color, 15 genotypes (G1, G2, G4, G6, G7, G10, G11, G12, G14, G15, G16, G17, G18, G19 and G21) showed green color and rest 4 genotypes (G3, G5, G8 and G20) showed dark green color on leaf. Purple tip, purple margins, purple blotch and purple green type leaf were not found in any genotypes (Table 6). Pictorial view of leaf color is present in Plate 2, 3 and 4.

Table 5. Categorization and grouping based on leaf sheath anthocyanin color

Types	Code	Genotypes
Absent	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Present	2	Nil

Table 6. Categorization and grouping based on leaf color

Types	Code	Genotypes
Pale green	1	G9 and G13
Green	2	G1, G2, G4, G6, G7, G10, G11, G12, G14, G15, G16, G17, G18, G19 and G21
Dark Green	3	G3, G5, G8 and G20
Purple tip	4	Nil
Purple margins	5	Nil
Purple blotch	6	Nil
Purple	7	Nil

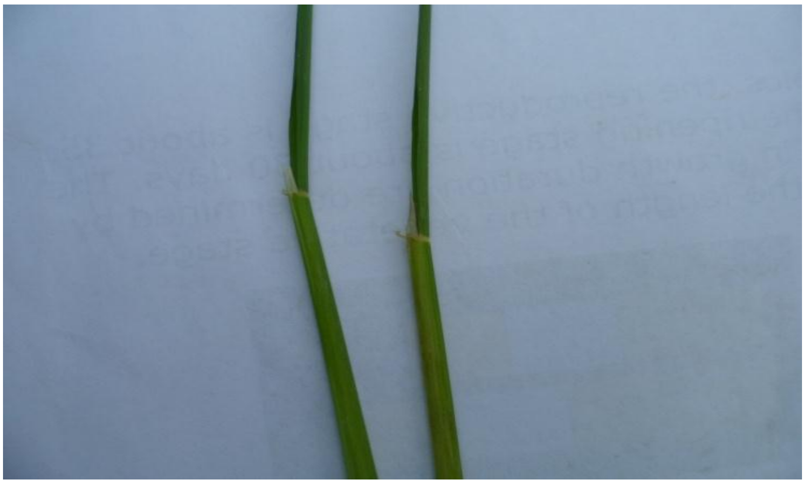

Plate 1. Leaf sheath anthocyanin color.

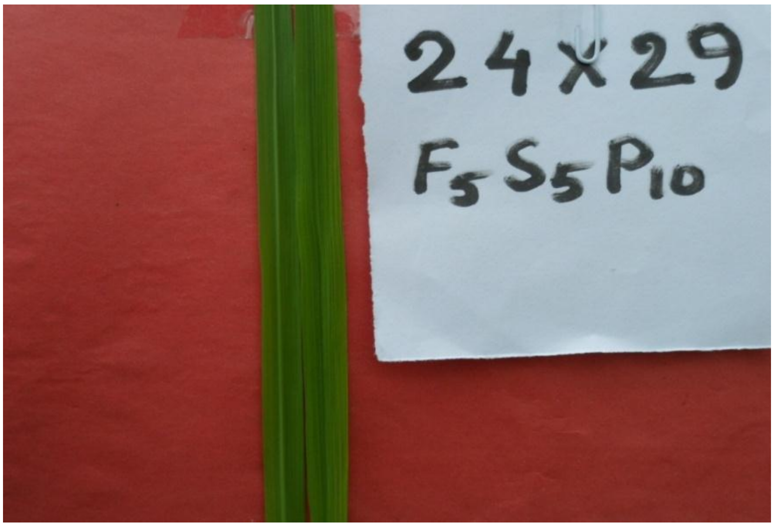

Plate 2. Pale green color leaf

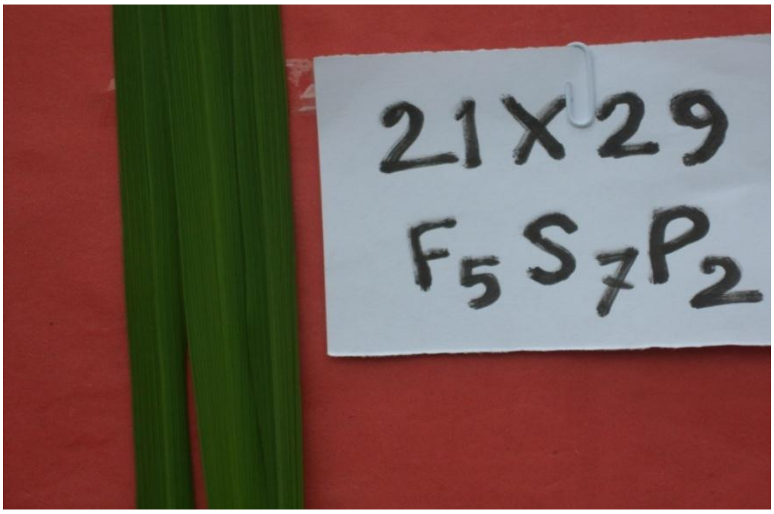

Plate 3. Green color leaf

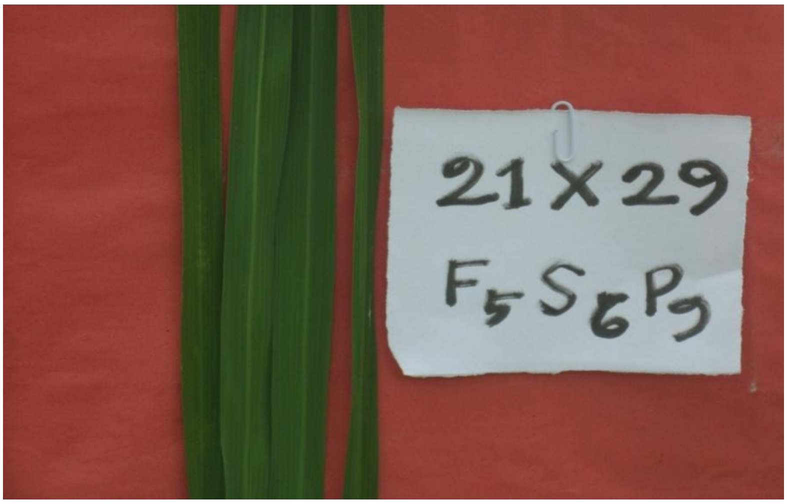

Plate 4. Dark green color leaf

4.1.3 Penultimate Leaf Pubescence

Based on penultimate leaf pubescence our observed genotypes were categorized into 5 groups as absent or very weak-1, weak or only on the margins-3, medium hairs on the medium portion of the leaf-5, strong hairs on the leaf blade-7 and very strong-9 nature. Nineteen genotypes (G1, G2, G3, G4, G5, G6, G7, G9, G10, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were strong hairs on the leaf blade type and 2 genotypes (G8 and G11) were very strong type. Absent or very weak, weak or only on the margins and medium hairs on the medium portion of the leaf were not found in any genotypes (Table 7).

4.1.4 Penultimate Leaf: Anthocyanin coloration of auricles and collar

On the basis of penultimate leaf anthocyanin coloration of auricles and collar, rice genotypes were classified as absent-1 and present-2. Only one genotype (G16) absence penultimate leaf anthocyanin coloration of auricles and collar and twenty genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G17, G18, G19, G20 and G21) presence penultimate leaf anthocyanin coloration of auricles and collar (Table 8). A pictorial view of anthocyanin coloration of auricles and color of penultimate leaf is present in Plate 5.

4.1.5 Penultimate Leaf: Ligule

On the basis of penultimate leaf ligule shape, rice genotypes were classified as absent-1 and present-9. All genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) presence ligule of the penultimate leaf (Table 9).

Table 7. Categorization and grouping based on penultimate leaf pubescence

Types	Code	Genotypes
Absent or very weak	1	Nil
Weak or only on the margins	3	Nil
Medium hairs on the medium portion of the leaf	5	Nil
Strong hairs on the leaf blade	7	G1, G2, G3, G4, G5, G6, G7, G9, G10, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Very strong	9	G8 and G11

Table 8. Categorization and grouping based on penultimate leaf anthocyanin coloration of auricles and collar

Types	Code	Genotypes
Absent	1	G16
Present	2	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G17, G18, G19, G20 and G21

Table 9. Categorization and grouping based on penultimate leaf ligule

Types	Code	Genotypes
Absent	1	Nil
Present	9	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21

4.1.6 Penultimate Leaf: Shape of the ligule

On the basis of ligule shape of penultimate leaf, rice genotypes were classified as truncate-1, acute to acuminate-2 and split or two-cleft-3 type. But our all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were two-cleft type that means there was no significant difference among the genotypes (Table 10). According to IRRI most of the cultivated rice have two-cleft type ligule shape and wild type genotypes may show others type. From our observation the two-cleft type ligule was found. A pictorial view of shape of the ligule of penultimate leaf is present in Plate 6.

4.1.7 Flag Leaf: Attitude of the blade

Based on angle of attachment between the flag leaf blade and the main panicle axis the observed genotypes were categorized in 4 groups like erect ($<30^0$)-1, intermediate or semi-erect (30^0-45^0)-3, horizontal (46^0-90^0)-5, reflexed or descending ($>90^0$)-7 type. Here 15 genotypes (G1, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G17, G19 and G20) showed erect type flag leaf, 5 genotypes (G2, G3, G4, G16 and G18) showed intermediate or semi-erect type and rest one genotype (G21) showed horizontal type flag leaf (Table 11). Pictorial view of attitude of the blade of flag leaf is present in Plate 7 and 8.

4.1.8 Male Sterility

Male sterility was observed at anthesis period of rice and grouped as per descriptors. On the basis of male sterility, rice genotypes were classified as absent-1, CMS-3, TGMS-5, PGMS-7 and P (T) GMS-9. But all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21)had absence of male sterility (Table 12).

Table 10. Categorization and grouping based on ligule shape of penultimate leaf

Types	**Code**	**Genotypes**
Truncate	1	Nil
Acute to acuminate	2	Nil
2-Cleft	3	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21

Table 11. Categorization and grouping based on attitude of the blade of flag leaf

Types	**Code**	**Genotypes**
Erect	1	G1, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G17, G19 and G20
Semi-erect	3	G2, G3, G4, G16 and G18
Horizontal	5	G21

Table 12. Categorization and grouping based on male sterility

Types	**Code**	**Genotypes**
Absent	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
CMS	3	Nil
TGMS	5	Nil
PGMS	7	Nil
P(T) GMS	9	Nil

Plate 5. Anthocyanin coloration of auricle and collar

Plate 6. Split or two-cleft type of ligule

Plate 7. Erect type attitude of the flag leaf blade

Plate 8. Semi-erect type attitude of the flag leaf blade

4.1.9 Microscopic Observation of Pollen with I_2-KI solution

It was observed at anthesis period of rice using microscope and the rice genotypes were classified into eight groups with codes according to guided descriptors as per follows. Completely sterile with TA pollen-1, completely sterile with 80% TA pollen-2, completely sterile with 50% TA pollen-3, sterile (91-99%)-4, partial sterile (31-70%)-5, partial fertile (31-70%)-6, fertile (21-30%)-7 and fully fertile (0-20%)-8. In this situation all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were fertile (Table 13).

4.1.10 Lemma and Palea: Anthocyanin color

On the basis of lemma and palea anthocyanin coloration the observed genotypes were categorized as absent or very weak-1, weak-3, medium-5, strong-7 and very strong-9 as presented according to descriptors. Lemma and palea combinedly indicates the seed coat color actually. But all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed no anthocyanin coloration of lemma and palea or very weak anthocyanin coloration of lemma and palea for seed coat color (Table 14).

4.1.11 Lemma: Anthocyanin coloration of area below apex

On the basis of lemma anthocyanin coloration of area below apex the observed genotypes were categorized as absent or very weak-1, weak-3, medium-5, strong-7 and very strong-9 as presented according to descriptors. Lemma indicates the seed coat color actually. But all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed no anthocyanin coloration of area below apex of lemma or very weak anthocyanin coloration of area below apex of lemma for seed coat color (Table 15).

Table 13. Categorization and grouping based on microscopic observation of pollen with I_2-KI solution

Types	Code	Genotypes
Completely sterile with TA pollen	1	Nil
Completely sterile with 80% TA pollen	2	Nil
Completely sterile with 50% TA pollen	3	Nil
Sterile (91-99%)	4	Nil
Partial sterile (31-70%)	5	Nil
Partial fertile (31-70%)	6	Nil
Fertile (21-30%)	7	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Fully fertile (0-20%)	8	Nil

Table 14. Categorization and grouping based on lemma and palea anthocyanin color

Types	Code	Genotypes
Absent or very weak	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Weak	3	Nil
Medium	5	Nil
Strong	7	Nil
Very strong	9	Nil

Table 15. Categorization and grouping based on anthocyanin coloration of area below lemma apex

Types	Code	Genotypes
Absent or very weak	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Weak	3	Nil
Medium	5	Nil
Strong	7	Nil
Very strong	9	Nil

4.1.12 Lemma: Anthocyanin coloration of apex

On the basis of lemma anthocyanin coloration of apex the observed genotypes were categorized as absent or very weak-1, weak-3, medium-5, strong-7 and very strong-9 as presented according to descriptors. Lemma indicates the seed coat color actually. But all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed no anthocyanin coloration of apex of lemma or very weak anthocyanin coloration of apex of lemma for seed coat color (Table 16).

4.1.13 Color of Stigma

Data was observed at anthesis period using a hand lens or magnifying glass and the rice genotypes were classified into five groups with codes according to guided descriptors as white -1, light green-2, yellow-3, light purple-4 and purple-5. All genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed white color of stigma. Light green, yellow, light purple and purple color of stigma were not observed (Table 17).

4.1.14 Stigma Exertion

Data was observed at anthesis period using a hand lens or magnifying glass and the rice genotypes were classified into five groups with codes according to guided descriptors as no or a few (>5%)-1, low (5-20%)-3, medium (21-40%)-5, high (41-60%)-7 and very high (>61%)-9. In this case 6 genotypes (G6, G7, G9, G14, G16 and G18) were no or few type, 4 genotypes (G2, G4, G5 and G12) were low type, 6 genotypes (G3, G8, G15, G17, G19 and G20) were medium type and rest 5 genotypes (G1, G10, G11, G13 and G21) were high type for exertion of stigma (Table 18). A pictorial view of stigma exertion of rice is present in Plate 9.

Table 16. Categorization and grouping based on anthocyanin coloration of lemma apex

Types	**Code**	**Genotypes**
Absent or very weak	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Weak	3	Nil
Medium	5	Nil
Strong	7	Nil
Very strong	9	Nil

Table 17. Categorization and grouping based on color of stigma

Types	**Code**	**Genotypes**
White	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Light green	2	Nil
Yellow	3	Nil
Light purple	4	Nil
Purple	5	Nil

Table 18. Categorization and grouping based on stigma exertion

Types	**Code**	**Genotypes**
No or a few (>5%)	1	G6, G7, G9, G14, G16 and G18
Low (5-20%)	3	G2, G4, G5 and G12
Medium (21-40%)	5	G3, G8, G15, G17, G19 and G20
High (41-60%)	7	G1, G10, G11, G13 and G21
Very high (>61%)	9	Nil

4.1.15 Stem: Anthocyanin coloration of nodes

Data was collected after flowering to near maturity stage on stem anthocyanin coloration of nodes and the rice genotypes were classified into two groups with codes according to guided descriptors as absent-1 and present-9. In this case all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed no anthocyanin coloration of nodes (Table 19). A pictorial view of anthocyanin coloration of nodes is present in plate 10.

4.1.16 Stem: Intensity of anthocyanin coloration of nodes

Data was collected after flowering to near maturity stage on stem anthocyanin coloration of nodes and the rice genotypes were classified into four groups with codes according to guided descriptors as weak-3, medium-5, strong-7 and very strong-9. In this case there was no anthocyanin coloration of nodes on the stem present in all the genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21). So intensity of anthocyanin coloration of nodes on the stem of all genotypes was not present.

4.1.17 Stem: Anthocyanin coloration of internodes

Data was collected at near coloration maturity stage on stem anthocyanin coloration of internodes and the rice genotypes were classified into five groups with codes according to guided descriptors as absent or very weak-1, weak-3, medium-5, strong-7 and very strong-9. In this case all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed no anthocyanin coloration of internodes (Table 20). A pictorial view of anthocyanin coloration of internodes is present in Plate 11.

Table 19. Categorization and grouping based on stem anthocyanin coloration of nodes

Types	Code	Genotypes
Absent	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Present	9	Nil

Table 20. Categorization and grouping based on stem anthocyanin coloration of internodes

Types	Code	Genotypes
Absent	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Present	9	Nil

Plate 9. High type stigma exertion of rice

Plate 10. Anthocyanin coloration of nodes

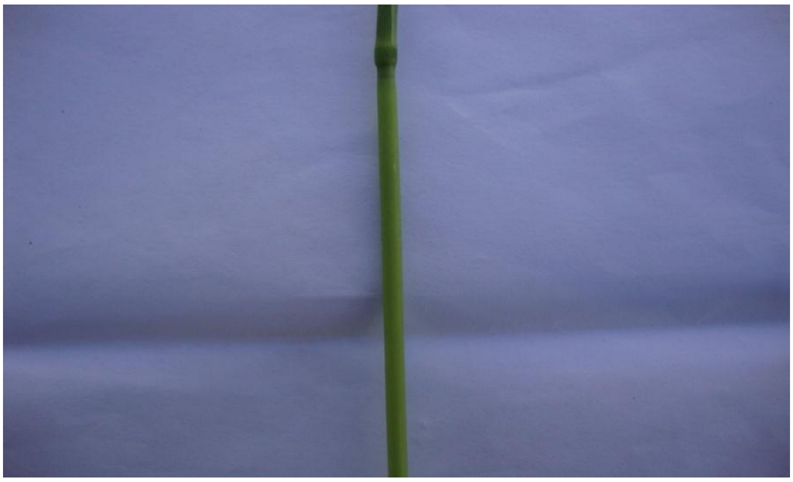

Plate 11. Anthocyanin coloration of internodes

4.1.17 Panicle Curvature of Main Axis (i.e. recurrent main axis)

Data was collected at near maturity stage and the rice genotypes were classified into four groups with codes according to guided descriptors as absent or very weak (upright)-1,weak (semi-upright)-3, medium (slightly drooping)-5 and strong (strongly dropping)-7. In this case one genotype (G11) was observed weak type, 8 genotypes (G2, G4, G6, G7, G9, G10, G18 and G20) were observed medium type and 12 genotypes (G1, G3, G5, G8, G12, G13, G14, G15, G16, G17, G19 and G21) were observed strong type of panicle curvature of main axis (Table 21). Pictorial view of panicle curvature of main axis is present in Plate 12, 13 and 14.

4.1.18 Spikelet: Pubescence of lemma and palea

Data was collected after anthesis to hard dough stage or pre-ripening stage on spikelet with pubescence of lemma and palea and the rice genotypes were classified into five groups with codes according to guided descriptors as absent or very weak-1, weak-3, medium-5, strong-7 and very strong-9. In this case all genotypes(G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G20 and G21) were observed medium type pubescence of lemma and palea of the spikelet without only one genotype (G19) which was strong type (Table 22).

4.1.19 Spikelet: Color of the tip of lemma

Data was collected after anthesis to hard dough stage or pre-ripening stage on spikelet with color of the tip of lemma and the rice genotypes were classified into six groups with codes according to guided descriptors as white-1, yellowish-2, brownish-3, red-4, purple-5 and black-6. In this case two genotype (G3 and G20) were observed white color type, 13 genotypes (G1, G2, G4, G5, G7, G8, G9, G11, G12, G14, G15, G17 and G18) were observed yellowish color type and 6 genotypes (G6, G10, G13, G16, G19 and G21) were observed brownish color type of the tip of lemma. Red, purple and black coloration of the tip of lemma was not observed (Table 23).

Table 21. Categorization and grouping based on panicle curvature of main axis (i.e. recurrent main axis)

Types	Code	Genotypes
Absent or very weak (upright)	1	Nil
Weak (semi-upright)	3	G11
Medium (slightly drooping)	5	G2, G4, G6, G7, G9, G10, G18 and G20
Strong (strongly dropping)	7	G1, G3, G5, G8, G12, G13, G14, G15, G16, G17, G19 and G21

Table 22. Categorization and grouping based on pubescence of lemma and palea of the spikelet

Types	Code	Genotypes
Absent or very weak	1	Nil
Weak	3	Nil
Medium	5	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G20 and G21
Strong	7	G19
Very strong	9	Nil

Table 23. Categorization and grouping based on color of the tip of lemma of the spikelet

Types	Code	Genotypes
White	1	G3 and G20
Yellowish	2	G1, G2, G4, G5, G7, G8, G9, G11, G12, G14, G15, G17 and G18
Brownish	3	G6, G10, G13, G16, G19 and G21
Red	4	Nil
Purple	5	Nil
Black	6	Nil

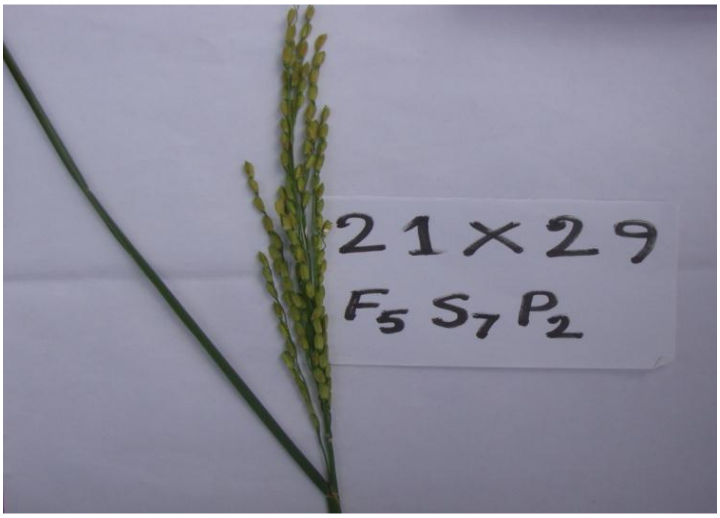

Plate 12. Weak type panicle curvature of main axis

Plate 13. Medium type panicle curvature of main axis

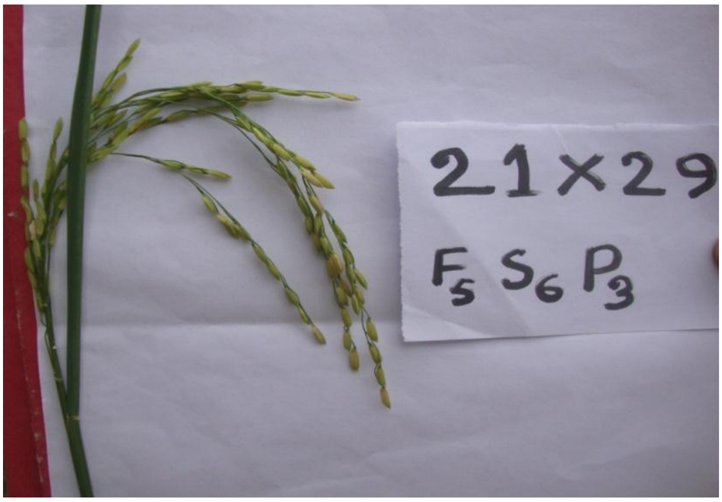

Plate 14. Strong type panicle curvature of main axis

4.1.20 Spikelet: Awns in the spikelet

It was observed flowering to maturity and normally a character of wild species of rice and grouped as absent-1 and present-9. But all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were not observed awns in the spikelet (Table 24).

4.1.22 Spikelet: Length of the longest awn

It was observed at maturity stage and normally a character of wild species of rice and grouped as per descriptors such as very short (<2 mm)-1, short (2-5 mm)-3, medium (5-10 mm)-5, long (11-20 mm)-7 and very long (>20 mm)-9. In this case there was no awns in the spikelet present in all the genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21). So length of the longest awn in the spikelet of all genotypes was not present.

4.1.23 Panicle: Distribution of awns

It was observed at flowering to maturity stage and normally a character of wild species of rice and grouped as per descriptors such as tip only-1, upper half only-3 and whole length-5. In this case there was no awns in the spikelet present in all the genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21). So distribution of awns in the panicle of all genotypes was not present.

4.1.24 Panicle: Color of awns

It was observed at flowering to maturity stage and normally a character of wild species of rice and grouped as per descriptors such as yellow white-1, brown-3, reddish-5, purple-7 and black-9. In this case there was no awns in the spikelet present in all the genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21). So color of awns in the panicle of all genotypes was not present.

4.1.25 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 3 groups as erect (compact panicle)-1, semi-erect (semi-compact panicle)-3 and spreading (open panicle)-5 type panicle where 20 genotypes (G1, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) showed semi-erect type and rest 1 genotype (G2) showed spreading type panicle. Erect typed panicles were not found among the genotypes (Table 25)**.** Pictorial view of attitude of branches of panicle is present in Plate 15 and 16.

4.1.26 Panicle: Exertion

Extent to which the panicle is exerted above the flag leaf sheath is known as panicle exertion. Data was collected at near maturity stage and the rice genotypes were classified into five groups with codes according to guided descriptors as enclosed-1, partly exerted-3, just exerted-5, moderately exerted-7 and well exerted-9. In this case one genotype (G9) was observed partly exerted type, 7 genotypes (G4, G6, G8, G12, G13, G16 and G18) were observed just exerted type, 4 genotypes (G1, G3, G14 and G20) were observed moderately exerted type and 9 genotypes (G2, G5, G7, G10, G11, G15, G17, G19 and G21) were observed well exerted type of the panicle exertion. Enclosed type of panicle exertion was not found (Table 26).

Table 24. Categorization and grouping based on awns in the spikelet

Types	Code	Genotypes
Absent	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Present	9	Nil

Table 25. Categorization and grouping based on panicle attitude of branches

Types	Code	Genotypes
Erect	1	Nil
Semi-erect	3	G1, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Spreading	5	G2

Table 26. Categorization and grouping based on panicle exertion

Types	Code	Genotypes
Enclosed	1	Nil
Partly exerted	3	G9
Just exerted	5	G4, G6, G8, G12, G13, G16 and G18
Moderately exerted	7	G1, G3, G14 and G20
Well exerted	9	G2, G5, G7, G10, G11, G15, G17, G19 and G21

Plate 15. Semi-erect type panicle attitude

Plate 16. Spreading type panicle attitude

4.1.27 Leaf Senescence: Penultimate leaves are observed at the time of harvest.

Data was collected at the of harvest and the rice genotypes were classified into three groups with codes according to guided descriptors as per follows. Late and slow (2 or more leaves retain green color at maturity)-1, intermediate-5 and early and fast (leaves are dead at maturity)-9 where 16 genotypes (G1, G3, G4, G5, G7, G9, G10, G11, G12, G13, G14, G15, G16, G17and G20) showed 2 or more leaves retain green color at maturity level and rest 5 genotypes (G6, G8, G18, G19 and G21) showed intermediate type of leaf senescence. Early and fast (leaves are dead at maturity) type of leaf senescence was not found among the genotypes (Table 27).

4.1.28 Decorticated Grain: Shape (length-width ratio of de-hulled grain)

Data was collected at the time of harvest and the rice genotypes were classified into five groups with codes according to guided descriptors as per follows round (L:W<1.5)-1, bold (L:W=1.5-2.0)-3, medium (L:W=2.1-2.5)-5, medium slender (L:W=2.6-3.0)-7 and slender (L:W>3.0)-9 where 16 genotypes (G1, G2, G4, G5, G7, G8, G9, G11, G13, G15, G16, G17, G18, G19, G20 and G21) showed slender type and rest 5 genotype (G3, G6, G10, G12 and G14) showed medium slender type decorticated grain shape. Round, bold and medium type decorticated grain were not found among the genotypes (Table 28).

4.1.29 Decorticated Grain (bran): Color

Data was collected at the time of harvest and the rice genotypes were classified into seven groups with codes according to guided descriptors as per follows white-1, light brown-2, variegated brown-3, dark brown-4, red-5, variegated purple-6 and purple-7 where 10 genotypes (G3, G4, G7, G8, G9, G13, G17, G19, G20 and G21) showed white colored decorticated grain (bran) and rest 11 genotypes (G1, G2, G5, G6, G10, G11, G12, G14, G15, G16 and G18) showed light brown decorticated grain (bran) color. Variegated brown, dark brown, red, variegated purple and purple decorticated grain (bran) coloration were not found among the genotypes (Table 29). Pictorial view of decorticated grain (bran) color is present in Plate 17 and 18.

Table 27. Categorization and grouping based on leaf senescence of penultimate leaves are observed at the time of harvest.

Types	**Code**	**Genotypes**
Late and slow (2 or more leaves retain green color at maturity)	1	G1, G3, G4, G5, G7, G9, G10, G11, G12, G13, G14, G15, G16, G17and G20
Intermediate	5	G6, G8, G18, G19 and G21
Early and fast (leaves are dead at maturity)	9	Nil

Table 28. Categorization and grouping based on decorticated grain shape

Types	**Code**	**Genotypes**
Round	1	Nil
Bold	3	Nil
Medium	5	Nil
Medium slender	7	G3, G6, G10, G12 and G14
Slender	9	G1, G2, G4, G5, G7, G8, G9, G11, G13, G15, G16, G17, G18, G19, G20 and G21

Table 29. Categorization and grouping based on decorticated grain (bran) color

Types	**Code**	**Genotypes**
White	1	G3, G4, G7, G8, G9, G13, G17, G19, G20 and G21
Light brown	2	G1, G2, G5, G6, G10, G11, G12, G14, G15, G16 and G18
Variegated brown	3	Nil
Dark brown	4	Nil
Red	5	Nil
Variegated purple	6	Nil
Purple	7	Nil

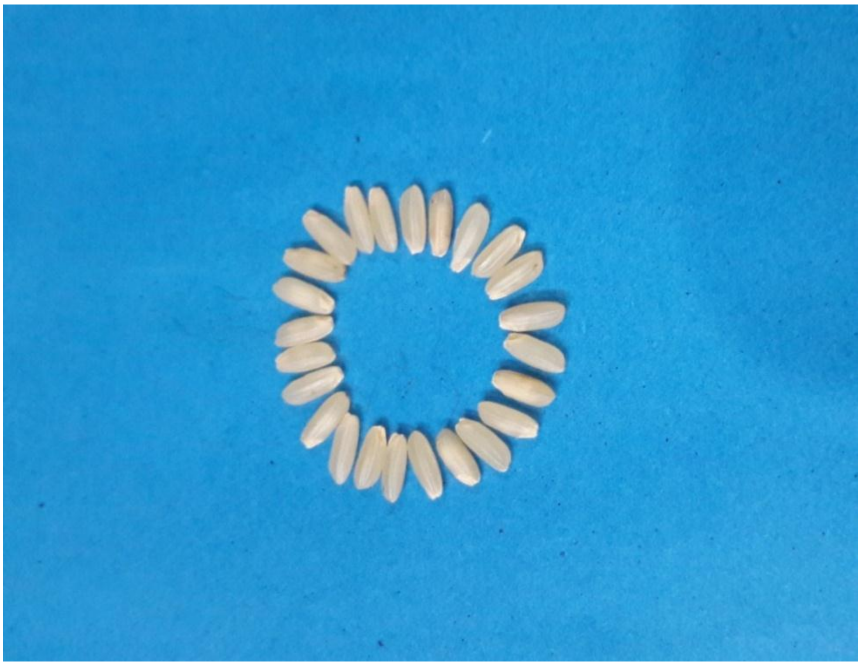

Plate 17. White colored decorticated grain

Plate 18. Light brown colored decorticated grain

4.1.30 Polished Grain: Size of white core or chalkiness (% of kernel area)

Data was collected at the time of harvest and the rice genotypes were classified into four groups with codes according to guided descriptors as per follows absent or very small-1, small (<10%)-3, medium (11-20%)-5 and large (11-20%)-7 where 19 genotypes (G1, G2, G3, G4, G5, G6, G8, G9, G10, G11, G12, G13, G14, G16, G17, G18, G19, G20 and G21) showed absent or very small size of white core or chalkiness (% of kernel area) of polished grain and rest 2 genotypes (G7 and G15) showed small size of white core or chalkiness (% of kernel area) of polished grain. Medium and large small size of white core or chalkiness (% of kernel area) of polished grain were not found among the genotypes (Table 30).

4.1.31 Decorticated Grain: Aroma

Data was collected at the time of harvest and the rice genotypes were classified into three groups with codes according to guided descriptors as per follows absent-1, lightly present-5 and strongly present-9. In this case all genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21) were observed no aroma present in decorticated grain (Table 31).

4.1.32 Other Distinct Special Character (if any)

In this experiment there were no distinct special characters found.

Table 30. Categorization and grouping based on size of white core or chalkiness (% of kernel area) of polished grain

Types	**Code**	**Genotypes**
Absent or very small	1	G1, G2, G3, G4, G5, G6, G8, G9, G10, G11, G12, G13, G14, G16, G17, G18, G19, G20 and G21
Small (<10%)	3	G7 and G15
Medium (11-20%)	5	Nil
Large (11-20%)	7	Nil

Table 31. Categorization and grouping based on aroma of decorticated grain

Types	**Code**	**Genotypes**
Absent	1	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21
Lightly present	5	Nil
Strongly present	9	Nil

4.2 Quantitative Characteristics

4.2.1 Time of Heading (50% 0f the plants with heads)

Date on which 50% of panicle emergence is done of the rice fields known as heading. It is specified either as the number of days from seed sowing date to 50% heading date. Time of 50% heading of the observed genotypes ranged from 97 days to 71 days with a mean value of 79 days (Appendix-V). On the basis of time of 50% heading, rice genotypes were classified into 5 groups viz. very early (<70 days), early (70-85 days), medium (86-105 days), late (106-120 days) and very late (>120 days). Sixteen genotypes (G1, G2, G3, G4, G6,G7, G8, G9, G10, G11, G12, G14, G16, G18, G20 and G21) showed early, five genotypes (G5, G13, G15, G17 and G19) showed medium but no genotypes were found as very early, late and very late type for 50% heading formation (Table 32). A pictorial view of time of heading (50% of the plants with heads) is present in plate 19.

4.2.2 Stem: Culm diameter (from 5 mother tillers in the lowest internode)

Culm diameter of the stem was measured in millimeter scale at the lowest internode of the stem during flowering or late reproductive stage. Culm diameter of observed genotypes ranged from 7.93 mm to 5.18 mm with a mean value of 6.38 mm (Appendix-V). On the basis of this character, the genotypes were categorized into 4 groups as small (<5.0 mm), medium (5.1-6.0 mm), large (6.1-7.0 mm) and very large (>7.0 mm) as the guided descriptors where there was no small type genotypes on the other hand, six medium type genotypes (G2, G10, G11, G12, G13 and G18), 13 large type genotypes (G1, G3, G4, G6, G7, G8, G9, G14, G15, G16, G19, G20 and G21) and 2 very large type genotypes (G5 and G17) were found (Table 33). From the figure-8 we also can distinguish different groups of observed genotypes based on culm diameter where genotypes and culm diameter has been presented horizontal and vertical axis respectively.

Table 32. Categorization and grouping based on time of heading

Groups	Scale (Days)	Code	Genotypes
Very early	<70	1	Nil
Early	70-85	3	G1, G2, G3, G4, G6,G7, G8, G9, G10, G11, G12, G14, G16, G18, G20 and G21
Medium	86-105	5	G5, G13, G15, G17 and G19
Late	106-120	7	Nil
Very Late	>120	9	Nil
Range	(G13, G15) 97 - (G12, G16) 71		
Average	79		

Table 33. Categorization and grouping based on culm diameter

Groups	Scale	Code	Genotypes
Small	<5.0 mm	1	Nil
Medium	5.1-6.0 mm	3	G2, G10, G11, G12, G13 and G18
Large	6.1-7.0 mm	5	G1, G3, G4, G6, G7, G8, G9, G14, G15, G16, G19, G20 and G21
Very Large	>7.0 mm	7	G5 and G17
Range	(G5) 7.93 mm - (G10) 5.18 mm		
Average	6.38 mm		

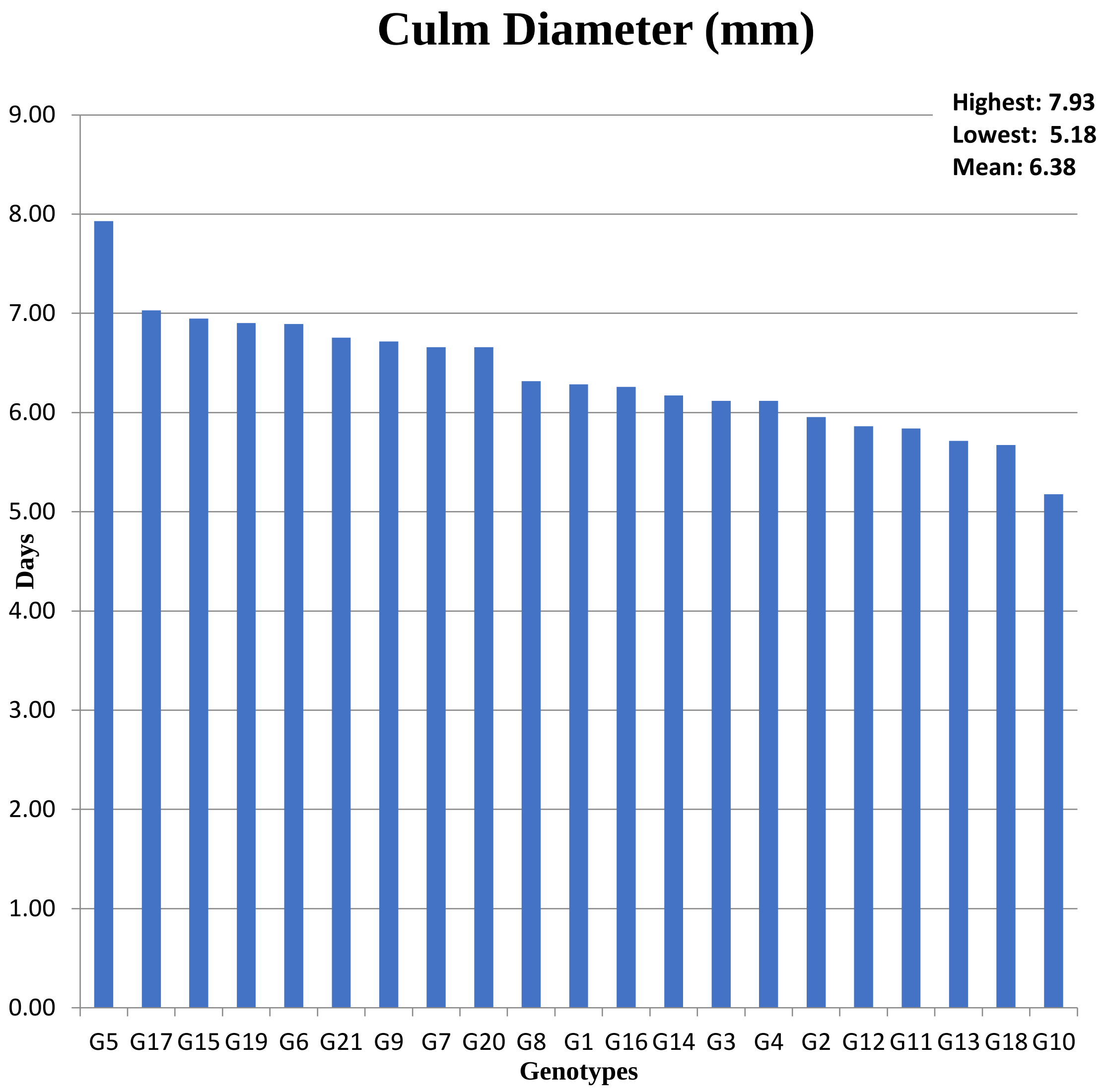

Figure 8. Grouping of observed genotypes based on culm diameter.

Plate 19. Time of heading (50% of plants with heads).

4.2.3 Stem Length (culm length): Measure from the base of the plants to the neck of the panicles

Culm length means the length of a stem from ground level to panicle base. Stem length (culm length) was measured from the base of the plants to the neck of the panicles after flowering to maturity stage. Culm lengths of observed genotypes ranged from 99.46 cm to 57.43 cm with a mean value of 79.57 cm (Appendix-V). On the basis of this character, the genotypes were categorized into 5 groups as very short (<40 cm), short (41–60 cm), medium (61–80 cm), long (81-110 cm) and very long (>110 cm) as the guided descriptors where there were no very short type and very long type genotypes on the other hand, only one short type genotypes (G11), 15 medium type genotypes (G1, G2, G3, G4, G6, G7, G8, G9, G10, G12, G14, G16, G18, G19 and G20) and 5 long type genotypes (G5, G13, G15, G17 and G21) were found (Table 34). From the figure-9 we also can distinguish different groups of observed genotypes based on culm length where genotypes and culm length has been presented horizontal and vertical axis, respectively.

4.2.4 Panicle Length: Measured from the neck to the tip of the panicle of main tillers without awns

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. Panicle length of observed genotypes ranged from 26.40 cm to 20.21 cm with a mean value of 24.33 cm (Appendix-V). Data was collected at 7 days after anthesis or full panicle exertion stage. On the basis of this character, the genotypes were categorized into 4 groups as short (<20 cm), medium (21-25 cm), long (26-30 cm) and very long (>30 cm) as the guided descriptors where there were no short type and very long type genotypes, on the other hand 13 medium type genotypes (G4, G5, G10, G11, G12, G13, G14,G15,G16, G17, G19, G20 and G21) and 8 long type genotypes (G1, G2, G3, G6, G7, G8, G9 and G18) were found (Table 35). From the figure-10 we also can distinguish different groups of observed genotypes based on panicle length where genotypes and panicle length has been presented horizontal and vertical axis, respectively.

Table 34. Categorization and grouping based on culm length

Groups	**Scale**	**Code**	**Genotypes**
Very short	<40 cm	1	Nil
Short	41-60 cm	3	G11
Medium	61-80 cm	5	G1, G2, G3, G4, G6, G7, G8, G9,G10, G12, G14, G16, G18, G19 and G20
Long	81-110 cm	7	G5, G13, G15, G17 and G21
Very long	>110 cm	9	Nil
Range	(G17) 99.46 cm - (G11) 57.43 cm		
Average	79.57 cm		

Table 35. Categorization and grouping based on panicle length

Groups	**Scale**	**Code**	**Genotypes**
Short	<20 cm	1	Nil
Medium	21-25 cm	5	G4, G5, G10, G11, G12, G13, G14, G15,G16, G17, G19, G20 and G21
Long	26-30 cm	7	G1, G2, G3, G6, G7, G8, G9 and G18
Very long	>30 cm	9	Nil
Range	(G9) 26.40 cm - (G11) 20.21 cm		
Average	24.33 cm		

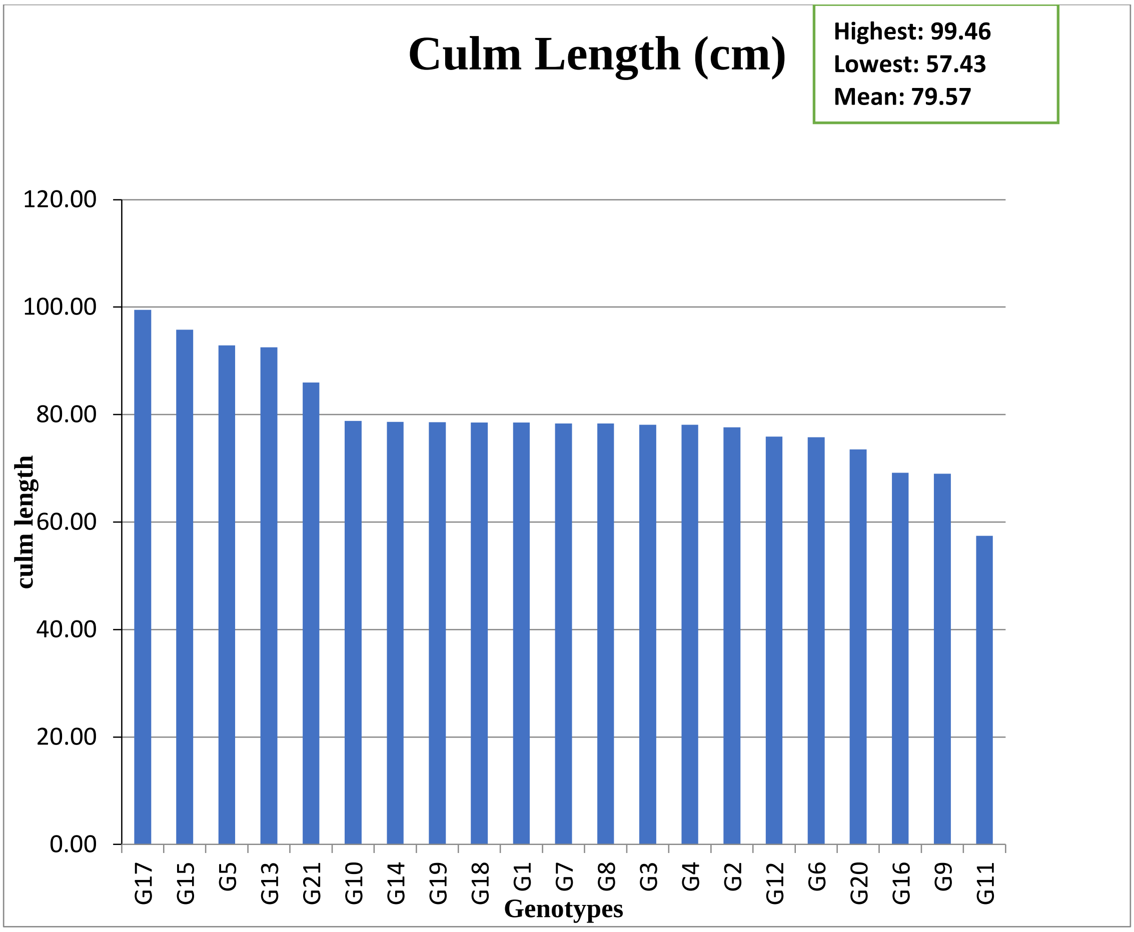

Figure 9. Grouping of observed genotypes based on culm length.

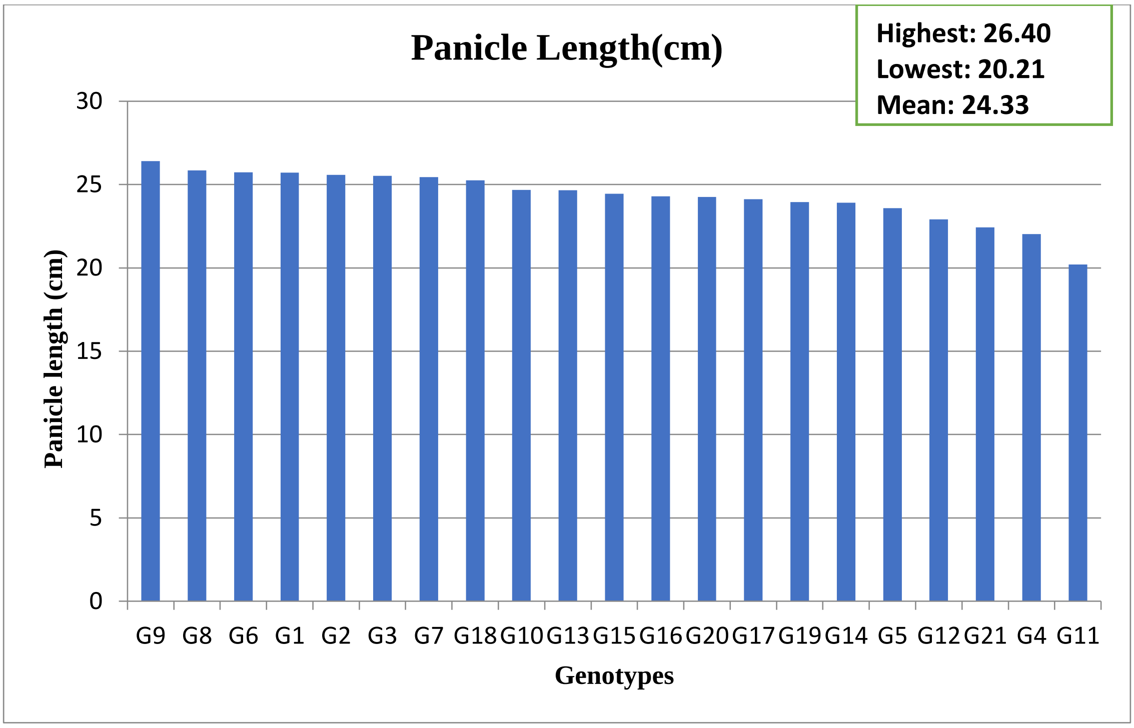

Figure 10. Grouping of observed genotypes based on panicle length.

4.2.5 Panicle: Number of the effective tillers per plant

The number of effective tillers per plant of the observed genotypes ranged from 15.03 to 9.80 with a mean value of 12.55 (Appendix-V) and considering this character, the observed genotypes were categorized as few (>6), medium (6-10) and many (>10) effective tillers per plant. There was no genotype showed few type of effective tillers per plant. On the other hand only two genotypes (G14 and G18) had medium type of effective tillers per plant and rest genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G15, G16, G17, G19, G20 and G21) showed many type of effective tillers per plant (Table 36).

4.2.6 Time of Maturity

Time of maturity was calculated as days required from sowing to maturity. Time of maturity of the observed genotypes ranged from 130.33 days to 103 days with a mean value of 110.98 days (Appendix-V) and on the basis of this character, all the genotypes were classified into 5 groups as very early (>100 days), early (101-115 days), medium (116-135 days), late (136-150 days) and very late (>150 days). There was no genotype showed very early, late and very late maturity of plant. On the other hand 17 genotypes (G1, G2, G3, G4, G6, G7, G8, G9, G10, G11, G12, G14, G16, G18, G19, G20 and G21) showed early type maturity of plants and rest genotypes (G5, G13, G15 and G17) showed medium type maturity of plants (Table 37). This grouping based on time of maturity is also shown in bar graph for more easy perception by the following figure-11 where genotypes has been shown horizontal axis and time of maturity along vertical axis.

Table 36. Categorization and grouping based on number of effective tillers per plant

Groups	Scale	Code	Genotypes
few	<6 tillers	3	Nil
medium	6-10 tillers	5	G14 and G18
many	>10 tillers	7	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G15, G16, G17, G19, G20 and G21
Range	(G11) 15.03 tillers - (G18) 9.80 tillers		
Average	12.55 tillers		

Table 37. Categorization and grouping based on time of maturity

Groups	Scale (Days)	Code	Genotypes
Very early	>100	1	Nil
Early	101-115	3	G1, G2, G3, G4, G6, G7, G8, G9, G10, G11, G12, G14, G16, G18, G19, G20 and G21
Medium	116-135	5	G5, G13, G15 and G17
Late	136-150	7	Nil
Very Late	>150	9	Nil
Range	(G13, G15) 130.33 - (G1) 103		
Average	110.98		

4.2.7 Grain: Weight of 1000 fully developed grains (adjusted of 12% of moisture)

Thousand grain weight of the observed genotypes ranged from 26.27 gm to 19.67 gm with a mean value of 22.67 gm (Appendix-V) and considering this character, the genotypes were grouped as 4 types such as very low (<l5 gm), low (l6-19 gm), medium (20-23 gm), high (24-27 gm) and very high (>27 gm). In this situation, there was no genotype showed very low and very high type of 1000 grain weight. On the other hand 2 genotypes (G5 and G11) showed low type of 1000 grain weight, 13 genotypes (G1, G2, G3, G4, G6, G7, G8, G9, G12, G13, G14, G18 and G21) showed medium type of 1000 grain weight and rest genotypes (G10, G15, G16, G17, G19 and G20) showed high type of 1000 grain weight (Table 38). From the figure-12 we also can distinguish different groups of observed genotypes based on thousand grain weight (adjusted of 12% of moisture) where genotypes and thousand grain weight has been presented horizontal and vertical axis, respectively.

4.2.8 Grain: Length (without dehulling)

Grain length was measured in mm and a digital caliper was used for clear visualization. Ten grains from every genotypes were measured and the mean value was recorded. Grain length of 21 rice genotypes ranged from 10.63 mm to 7.81 mm with a mean value of 8.49 mm (Appendix-V). On the basis of grain length, the observed genotypes were grouped as very short (<6.0 mm), short (6.1-7.0 mm), medium (7.1-8.0 mm), long (8.1-9.0 mm) and very Long (>9.0 mm). Two genotypes (G17 and G20) were recorded as very long, 16 genotypes (G1, G2, G3, G4, G5, G8, G9, G10, G11, G13, G14, G15, G16, G18, G19 and G21) as long and rest 3 genotypes (G6, G7 and G12) as medium (Table 39). No genotypes were found as very short and short type. Pictorial view of grain length is present in Plate 20, 21, 22, 23 and 24.

Table 38. Categorization and grouping based on thousand grain weight (adjusted of 12% of moisture)

Groups	Scale	Code	Genotypes
Very Low	<15 gm	1	Nil
Low	16-19 gm	3	G5 and G11
Medium	20-23 gm	5	G1, G2, G3, G4, G6, G7, G8, G9, G12, G13, G14, G18 and G21
High	24-27 gm	7	G10, G15, G16, G17, G19 and G20
Very High	>27 gm	9	Nil
Range	(G17) 26.27 gm- (G11) 19.67 gm		
Average	22.67 gm		

Table 39. Categorization and grouping based on grain length (without dehulling)

Groups	Scale	Code	Genotypes
Very Short	<6.0 mm	1	Nil
Short	6.1-7.0 mm	3	Nil
Medium	7.1-8.0 mm	5	G6, G7 and G12
Long	8.1-9.0 mm	7	G1, G2, G3, G4, G5, G8, G9, G10, G11, G13, G14, G15, G16, G18, G19 and G21
Very Long	>9.0 mm	9	G17 and G20
Range	(G20) 10.63 mm - (G12) 7.81 mm		
Average	8.49 mm		

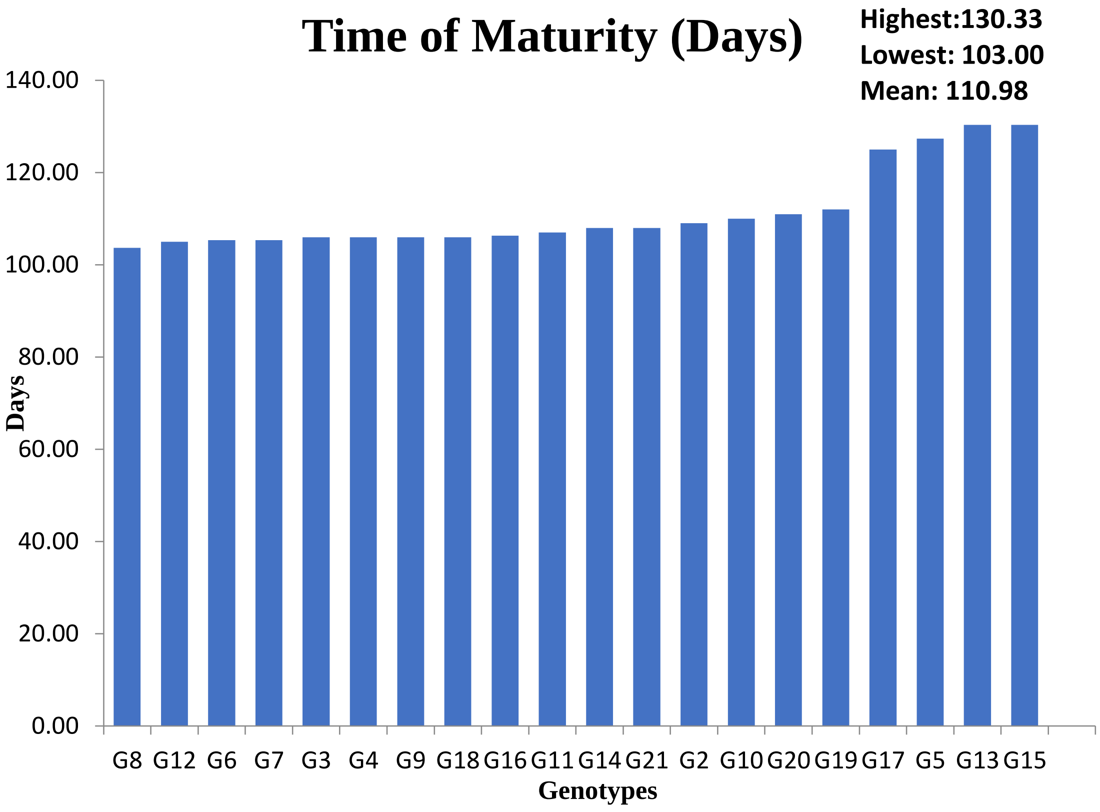

Figure 11. Grouping based on time of maturity.

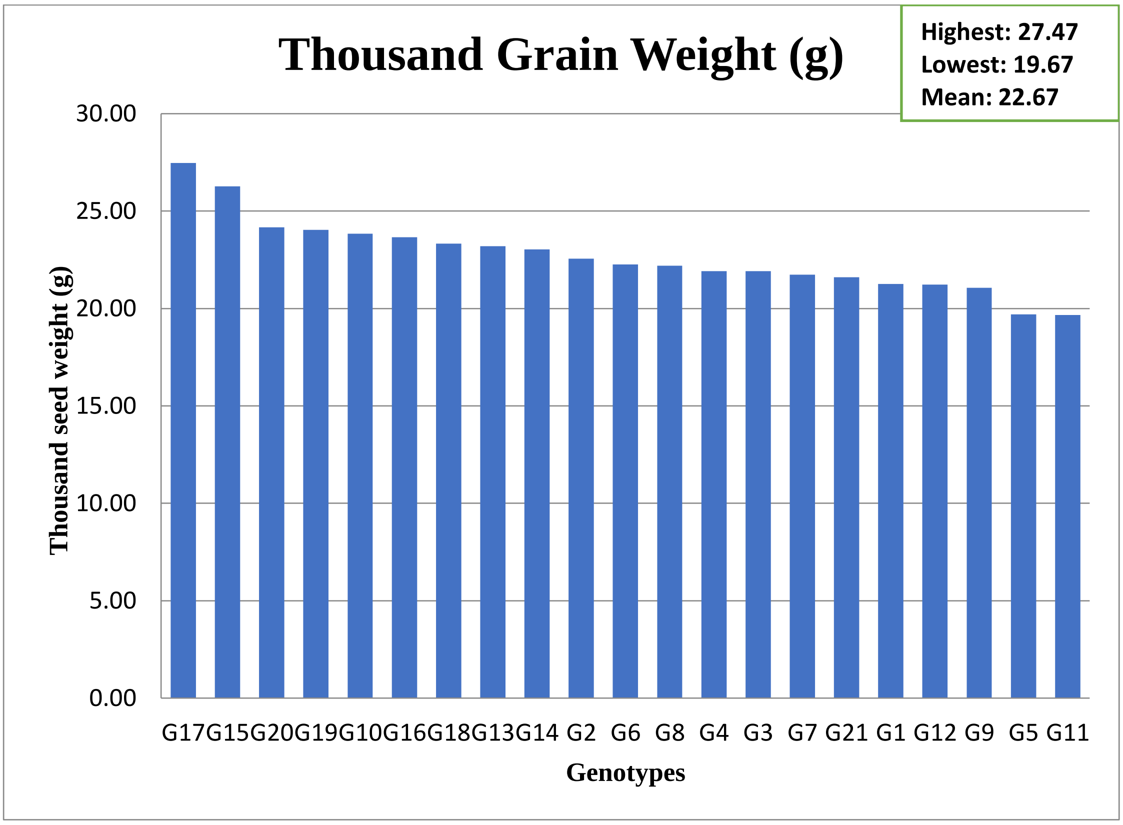

Figure 12. Grouping based on thousand grain weight.

Plate 20. Measurement of grain length (without dehulling).

Plate 21. Measurement of decorticated grain length.

Plate 22. Very long type grain length.

Plate 23. Long type grain length.

Plate 24. Medium type grain length

4.2.9 Sterile Lemma Length: Measure at postharvest stage

Sterile lemma length was measured in mm and a digital caliper was used for clear visualization. Ten grains from every genotypes were measured and the mean value was recorded. Sterile lemma length of 21 rice genotypes ranged from 2.66 mm to 1.71 mm with a mean value of 1.89 mm (Appendix-V). On the basis of sterile lemma length, the observed genotypes were grouped as short (<1.5 mm), medium (1.5-2.5 mm), long (2.6-3.0 mm) and very Long (>3.0 mm). Twenty genotypes (G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19 and G21) were recorded as medium and rest one genotype (G20) as long (Table 40). No genotypes were found as short and very long type.

4.2.10 Decorticated Grain: Length (After dehulling, before milling)

Decorticated grain length was measured in mm and a digital caliper was used for clear visualization. Ten grains from every genotypes were measured and the mean value was recorded. Decorticated grain length of 21 rice genotypes ranged from 8.19 mm to 6.05 mm with a mean value of 6.43 mm (Appendix-V). On the basis of decorticated grain length, the observed genotypes were grouped as short (<5.5 mm), medium (5.6-6.5 mm), long (6.6-7.5 mm) and very long (>7.5 mm). Fifteen genotypes (G1, G2, G3, G4, G6, G7, G8, G9, G10, G11, G12, G14, G16, G18, G19 and G21) were recorded as medium, four genotypes (G5, G13, G15 and G17) as long and rest one genotype (G20) as very long (Table 41). No genotypes were found as short type.

Table 40. Categorization and grouping based on sterile lemma length

Groups	Scale	Code	Genotypes
Short	<1.5 mm	1	Nil
Medium	1.5-2.5 mm	3	G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19 and G21
Long	2.6-3.0 mm	5	G20
Very long	>3.0 mm	7	Nil
Range	(G20) 2.66 mm - (G4) 1.71 mm		
Average	1.89 mm		

Table 41. Categorization and grouping based on decorticated grain length

Groups	Scale	Code	Genotypes
Short	<5.5 mm	1	Nil
Medium	5.5-6.5 mm	3	G1, G2, G3, G4, G6, G7, G8, G9, G10, G11,G12, G14, G16, G18, G19 and G21
Long	6.6-7.5 mm	5	G5, G13, G15 and G17
Very long	>7.5 mm	7	G20
Range	(G20) 8.19 mm- (G6) 6.05 mm		
Average	6.43 mm		

CHAPTER V

SUMMARY AND CONCLUSION

A study was carried out at Sher-e-Bangla Agricultural University, Dhaka, Bangladesh on “Characterization of 18 F_5 lines of Aus Rice” during the period of aus seasons in 2015. The experiment was designed to characterize rice genotypes on the basis of morphological and quality traits. Eighteen rice genotypes were evaluated for thirty one qualitative and ten quantitative traits of morphological characters.

All the genotypes scored exactly same for eleven qualitative characters viz. anthocyanin coloration of leaf sheath (scored as 1), penultimate leaf ligule shape (scored as 3), male sterility (scored as 1), microscopic observation of pollen with I_2-KI solution (scored as 7), anthocyanin coloration of lemma and palea (scored as 1), anthocyanin coloration of area below lemma apex (scored as 1), anthocyanin coloration of lemma apex (scored as 1), anthocyanin coloration of nodes (scored as 1), anthocyanin coloration of internodes (scored as 1), color of stigma (scored as 1), awns in the spikelet (scored as 1), and decorticated grain aroma (scored as 1). Such result revealed that there were no variation for these traits among the observed genotypes. Differences were found in the genotypes studied for rest of the aforesaid characteristics. The rice germplasms were classified based on qualitative and quantitative traits of morphological characters developed by Biodiversity International, IRRI and WARDA-2007 for DUS test of inbred rice. All the genotypes were grouped and classified as well as described based on qualitative and quantitative characters as per descriptors so that all the observed genotypes containing described characters could be easily evaluated and identified at a glance.

A wide range of variation was observed in all the genotypes for 14 qualitative and all the quantitative character. The following characters such as leaf color, attitude of the flag leaf blade, number of effective tillers per plant, panicle length, panicle curvature, panicle attitude of branches, panicle exertion, time of maturity, thousand grain weight, culm length, culm diameter, decorticated grain length, decorticated grain shape, decorticated grain aroma are important for selection of better rice genotypes. There are three types of flag leaf blade attitude such as erect, semi-erect and horizontal were observed in all genotypes among them 15 genotypes (G1, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G17, G19 and G20) showed erect type flag leaf. In case of number of effective tillers per plant genotypes G1, G2, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G15, G16, G17, G19, G20 and G21 showed variable types of effective tillers per plant (>10 tillers per plant). Panicle length is the most yield contributing character of rice. Panicle length of observed genotypes ranged from (G9) 26.40 cm to (G11) 20.21 cm with a mean value of 24.33 cm where G1, G2, G3, G6, G7, G8, G9 and G18 genotypes showed long panicle length (>26-30cm). In case of panicle curvature of main axis, G11 genotype showed semi-upright and G2, G4, G6, G7, G9, G10, G18 and G20 genotypes showed slightly drooping pattern between panicle and main axis. Panicle attitude of branches are three types such as erect, semi-erect and sprading where G1, G3, G4, G5, G6, G7, G8, G9, G10, G11, G12, G13, G14, G15, G16, G17, G18, G19, G20 and G21 genotypes showed semi-erect panicle attitude.

Culm length of observed genotypes ranged from 99.46 (G17) cm to 57.43 (G11) cm with a mean value of 79.57 cm. A single genotype G11 (57.43cm) was short type and G1, G2, G3, G4, G6, G7, G8, G9, G10, G12, G14, G16, G18, G19, G20 genotypes were medium type (61-80 cm). In case of days of maturity G1, G2, G3, G4, G6, G7, G8, G9, G10, G11, G12, G14, G16, G18, G19, G20 and G21 genotypes showed early in maturity (101-115 days) with an average of 111 days including 130 days of maturity time (G15). Thousand grain weight character results in better agronomic performance in which G10, G15, G16, G17, G19 and G20 genotypes showed high grain weight (24-27 gm/1000 grains). Thousand grain weight of observed genotypes ranged from (G17) 26.27 gm to (G11) 19.67 gm with a mean value of 22.67 gm. Decorticated grain length of observed genotypes ranged from (G20) 8.19 mm to (G6) 6.05 mm with a mean value of 6.43 mm. Asingle genotype G20 was very long type (>7.5 mm) and G5, G13, G15 and G17 genotypes were long type (6.6-7.5 mm) of decorticated grain length. The most promising lines such as G1, G3, G6, G8, G9, G10, G12, G16 and G18 were selected in respect of yield and quality for further study.

CHAPTER VII

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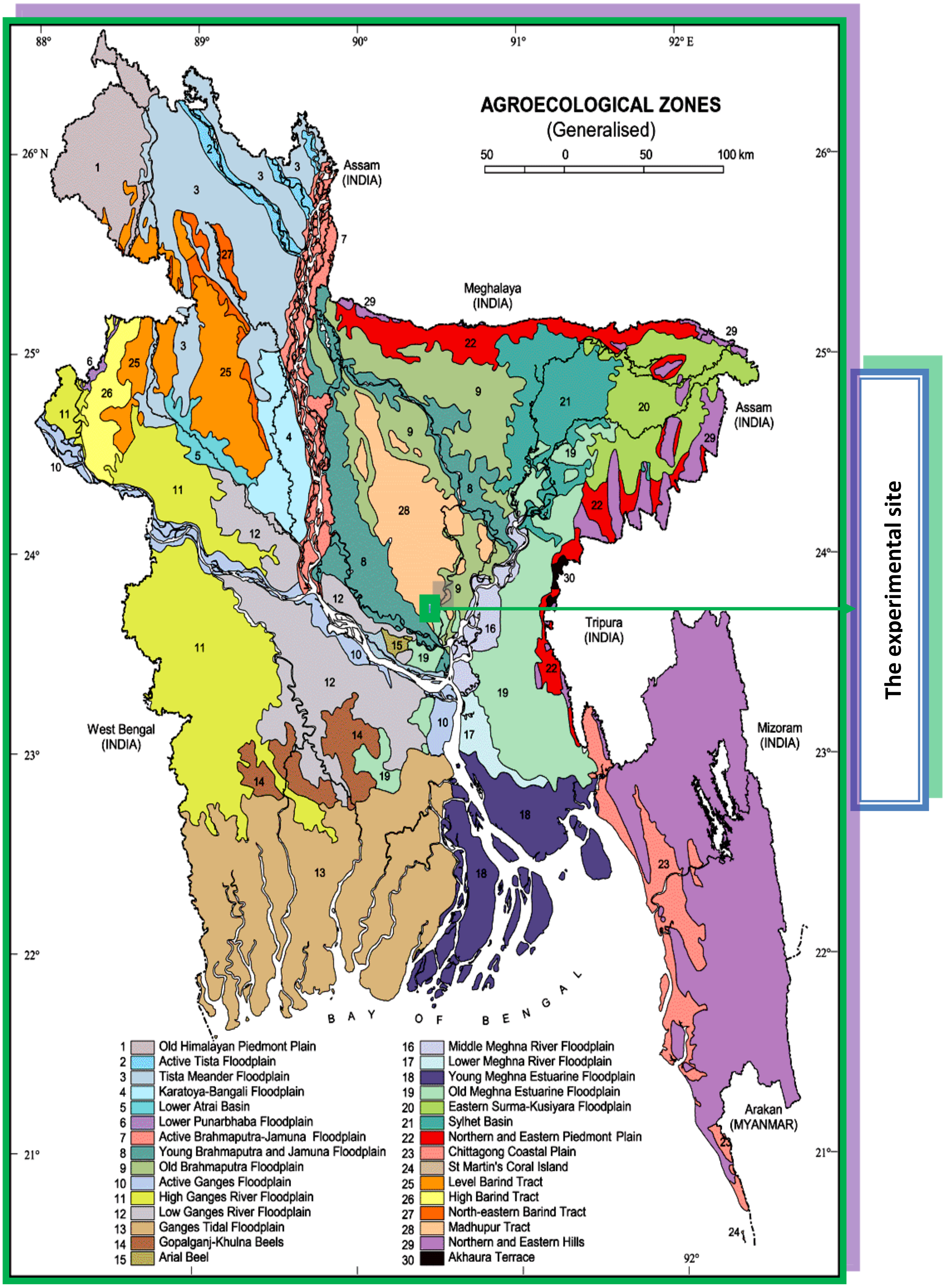
CHAPTER VIII

APPENDICES

Appendix I. Map showing the experimental site under study



Appendix II. Descriptors with codes for qualitative characteristics

SL. No.	Characteristics	Descriptors with Codes
1	Leaf sheath: anthocyanin color	Absent-1, Present-9.
2	Leaf color	Pale green-1, Green-2, Dark green-3, Purple tip-4, Purple margins-5, Purple blotch-6, Purple-7.
3	Penultimate leaf pubescence	Absent or very weak-1, Weak or only on the margins-3, Medium hairs on the medium portion of the leaf-5, Strong hairs on the leaf blade-7, Very strong-9.
4	Penultimate leaf: anthocyanin coloration of auricles and collar	Absent-1, Present-9.
5	Penultimate leaf: ligule	Absent-1, Present-9.
6	Penultimate leaf: shape of the ligule	Truncate-1, Acute-2, Split or two-cleft-3.
7	Flag leaf: attitude of the blade	Erect ($<30^0$)-1, Intermediate or Semi-erect (30^0-45^0)-3, Horizontal (46^0-90^0)-5, Reflexed or descending ($>90^0$)-7.
8	Male sterility	Absent-1, CMS-3, TGMS-5, PGMS-7, P (T) GMS-9.
9	Microscopic observation of pollen with I_2-KI solution	Completely sterile with TA pollen-1, Completely sterile with 80% TA pollen-2, Completely sterile with 50% TA pollen-3, Sterile (91-99%)-4, Partial sterile(31-70%)-5, Partial fertile (31-70%)-6, Fertile (21-30%)-7 and Fully fertile (0-20%)-8.
10	Lemma and Palea: anthocyanin coloration	Absent or very weak-1, Weak-3, Medium-5, Strong-7, Very strong-9.
11	Lemma: anthocyanin coloration of area below apex	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
12	Lemma: anthocyanin coloration of apex	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
13	Color of stigma	White-1, Light green-2, Yellow-3, Light purple-4, Purple-5.
14	Stigma exertion	No or a few (>5%)-1, Low (5-20%)-3, Medium (21-40%), High (41-60%)-7, Very high (>61%)-9.
15	Stem: anthocyanin coloration of nodes	Absent-1, Present-9.
16	Stem: intensity of anthocyanin coloration of nodes	Weak-3, Medium-5, Strong-7 and Very strong-9.

Appendix II. Descriptors with codes for qualitative characteristics(cont'd)

17	Stem: anthocyanin coloration of internodes	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
18	Panicle: curvature of main axis (i.e. recurved main axis)	Absent or very weak -1, Weak-3, Medium-5, Strong- 7.
19	Spikelet: pubescence of lemma and palea	Absent or very weak -1, Weak-3, Medium-5, Strong- 7, Very strong-9.
20	Spikelet: color of the tip of lemma	White-1, Yellowish-2, Brownish-3, Red-4, Purple-5, Black-6.
21	Spikelet: awns in the spikelet	Absent-1, Present-9.
22	Spikelet: Length of the longest awn	Very short (<2 mm)-1, Short (2-5 mm)-3, Medium (5-10 mm)-5, Long (11-20 mm)-7 and Very long (>20 mm)-9.
23	Panicle: Distribution of awns	Tip only-1, Upper half only-3 and Whole length-5.
24	Panicle: Color of awns	Yellow white-1, Brown-3, Reddish-5, Purple-7 and Black-9.
25	Panicle: attitude of branches	Erect-1, Semi-erect-3, Spreading-5.
26	Panicle: exertion	Enclosed-1, Partly exerted-3, Just exerted-5, Moderately exerted-7, Well exerted-9.
27	Leaf senescence: Penultimate leaves are observed at the time of harvest.	Late and slow (2 or more leaves retain green color at maturity)-1, Intermediate-5 and Early and fast (leaves are dead at maturity)-9.
28	Decorticated grain: shape (length-width ratio of de-hulled grain)	Round (L:W<1.5)-1, Bold (L:W=1.5-2.0)-3, Medium (L:W=2.1-2.5)-5, Medium slender (L:W=2.6-3.0)-7 and Slender (L:W>3.0)-9.
29	Decorticated grain (bran): color	White-1, Light brown-2, Variegated brown-3, Dark brown-4, Red-5, Variegated purple-6 and Purple-7.
30	Polished grain: size of white core or chalkiness (% of kernel area)	Absent or very small-1, Small (<10%)-3, Medium (11-20%)-5 and Large (11-20%)-7.
31	Decorticated grain: aroma	Absent-1, Lightly present-5 and Strongly present-9.
32	Other distinct special character (if any)	

Source: BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007. Descriptors for wild and cultivated rice (*Oryza spp*.).

Appendix III. Descriptors with codes for quantitative characteristics

SL. No.	Characteristics	Descriptors with Codes
1	Time of heading (50% of plants with heads)	Very early (< 70 days)-1, Early (70-85 days)-3, Medium (86-105 days)-5, Late (106-120 days)-7, Very late (>120 days)-9.
2	Stem: culm diameter (from 5 mother tillers in the lowest internode)	Small (<5.0 mm)-1, Medium (5.1-6.0 mm)-3, Large (6.1-7.0 mm)-5, Very Large (>7.0 mm)-7.
3	Stem length (culm length): Measure from the base of the plants to the neck of the panicles	Very short (<40 cm)-1, Short (41–60 cm)-3, Medium (61–80 cm)-5, Long (81-110 cm)-7, Very long (>110 cm)-9.
4	Panicle length: measured from the neck to the tip of the panicle of main tillers without awns	Short (<20 cm)-3, Medium (21-25 cm)-5, Long (26-30 cm)-7 and Very long (>30 cm)-9.
5	Panicle: number of the effective tillers per plant	Few (>6)-3, Medium (6-10)-5, Many (>10)-7.
6	Time of maturity	Very early (>100 days)-1, Early (101-115 days)-3, Medium (116-135 days)-5, Late (136-150 days)-7, Very late (>150 days)-9.
7	Grain: weight of 1000 fully developed grains (adjusted of 12% of moisture)	Very low (<15 gm)-1, Low (16-19 gm)-3, Medium (20-23 gm)-5, High (24-27 gm)-7, Very high (>27 gm)- 9.
8	Grain: length (without dehulling)	Very short (<6.0 mm)-1, Short (6.1-7.0 mm)-3, Medium (7.1-8.0 mm)-5, Long (8.1-9.0 mm)-7 and Very Long (>9.0 mm)-9.
9	Sterile lemma length: Measure at postharvest stage	Short (<1.5 mm)-1, Medium (1.5-2.5 mm)-3, Long (2.6-3.0 mm)-5 and Very Long (>3.0 mm)-7.
10	Decorticated grain: length (After dehulling, before milling)	Short (<5.5 mm)-1, Medium (5.6-6.5 mm)-3, Long (6.6-7.5 mm)-5 and Very Long (>7.5 mm)-7.

Source: BIOVERSITY INTERNATIONAL, IRRI and WARDA-2007. Descriptors for wild and cultivated rice (*Oryza spp*.).

Appendix IV. Mean performance of qualitative characters of twenty one genotypes

Genotypes	LSAC	LC	PLP	PLACAC	PLL	PLSL	FLAB	MS	MOP	LPAC	LACBA	LACA	CS	SE
G1	1	7	7	2	9	3	1	1	7	1	1	1	1	7
G2	1	2	7	2	9	3	3	1	7	1	1	1	1	3
G3	1	3	7	2	9	3	3	1	7	1	1	1	1	5
G4	1	2	7	2	9	3	3	1	7	1	1	1	1	3
G5	1	3	7	2	9	3	1	1	7	1	1	1	1	3
G6	1	2	7	2	9	3	1	1	7	1	1	1	1	1
G7	1	2	7	2	9	3	1	1	7	1	1	1	1	1
G8	1	3	9	2	9	3	1	1	7	1	1	1	1	5
G9	1	1	7	2	9	3	1	1	7	1	1	1	1	1
G10	1	2	7	2	9	3	1	1	7	1	1	1	1	7
G11	1	2	9	2	9	3	1	1	7	1	1	1	1	7
G12	1	2	7	2	9	3	1	1	7	1	1	1	1	3
G13	1	1	7	2	9	3	1	1	7	1	1	1	1	7
G14	1	2	7	2	9	3	1	1	7	1	1	1	1	1
G15	1	2	7	2	9	3	1	1	7	1	1	1	1	5
G16	1	2	7	1	9	3	3	1	7	1	1	1	1	1
G17	1	2	7	2	9	3	1	1	7	1	1	1	1	5
G18	1	2	7	2	9	3	3	1	7	1	1	1	1	1
G19	1	2	7	2	9	3	1	1	7	1	1	1	1	5
G20	1	3	7	2	9	3	1	1	7	1	1	1	1	5
G21	1	2	7	2	9	3	5	1	7	1	1	1	1	7

LSAC: Leaf Sheath Anthocyanin Color, **LC:** Leaf Color, **PLP:** PenultimateLeaf Pubescence, **PLACAC:** Penultimate Leaf Anthocyanin Coloration of Auricles and Collor, **PLL:** Penultimate Leaf Ligule, **PLSL:** Penultimate Leaf Shape of the Ligule, **FLAB:** Flag Leaf Attitude of the Blade, **MS:** Male Sterility, **MOP:** Microscopic observation of pollen with I_2-KI solution, **LPAC:** Lemma and Palea Anthocyanin Coloration, **LACBA**: Lemma Anthocyanin Coloration of area below Apex, **LACA:** Lemma Anthocyanin Coloration of Apex, **CS:** Color of Stigma, **SE:** Stigma Exertion.

Appendix IV. Mean performance of qualitative characters of twenty one genotypes (cont’d)

Genotypes	**SACN**	**SACI**	**PCMA**	**SPLP**	**SCL**	**SAS**	**PAB**	**PE**	**LS**	**DGS**	**DGC**	**PGC**	**DGA**
G1	1	1	7	5	2	1	3	7	1	9	2	1	1
G2	1	1	5	5	2	1	5	9	1	9	2	1	1
G3	1	1	7	5	1	1	3	7	1	7	1	1	1
G4	1	1	5	5	2	1	3	5	1	9	1	1	1
G5	1	1	7	5	2	1	3	9	1	9	2	1	1
G6	1	1	5	5	3	1	3	5	5	7	2	1	1
G7	1	1	5	5	2	1	3	9	1	9	1	3	1
G8	1	1	7	5	2	1	3	5	5	9	1	1	1
G9	1	1	5	5	2	1	3	3	1	9	1	1	1
G10	1	1	5	5	3	1	3	9	1	7	2	1	1
G11	1	1	3	5	2	1	3	9	1	9	2	1	1
G12	1	1	7	5	2	1	3	5	1	7	2	1	1
G13	1	1	7	5	3	1	3	5	1	9	1	1	1
G14	1	1	7	5	2	1	3	7	1	7	2	1	1
G15	1	1	7	5	2	1	3	9	1	9	2	3	1
G16	1	1	7	5	3	1	3	5	1	9	2	1	1
G17	1	1	7	5	2	1	3	9	1	9	1	1	1
G18	1	1	5	5	2	1	3	5	5	9	2	1	1
G19	1	1	7	7	3	1	3	9	5	9	1	1	1
G20	1	1	5	5	1	1	3	7	1	9	1	1	1
G21	1	1	7	5	3	1	3	9	5	9	1	1	1

SACN: Stem Anthocyanin Coloration of Nodes**, SACI:** Stem Anthocyanin Coloration of Internodes, **PCMA:** Panicle Curvature of Main Axis (i.e. recurved main axis), **SPLP:** Spikelet Pubescence of Lemma and Palea, **SCL:** Spikelet Color of the tip of Lemma, **SAS:** Spikelet: Awns in the Spikelet, **PAB:** Panicle Attitude of the Branches, **PE:** Panicle Exertion, **LS:** Leaf senescence: Penultimate leaves are observed at the time of harvest, **DGS:** Decorticated grain: shape (length-width ratio of de-hulled grain), **DGC:** Decorticated grain (bran): color, **PGC:** Polished grain: size of white core or chalkiness (% of kernel area), **DGA:** Decorticated grain: aroma.

Appendix V. Mean performance of quantitative characters of twenty one genotypes

Genotype	TH(Days)	CD(mm)	CL(cm)	PL(cm)	NET/P
G1	73.33	6.28	78.52	25.51	12.23
G2	73.33	5.95	77.64	25.57	12.90
G3	73.33	6.12	78.08	25.52	12.57
G4	73.33	6.12	78.08	22.03	12.57
G5	93.33	7.93	92.89	23.58	12.77
G6	73.33	6.89	75.79	25.73	14.80
G7	73.33	6.66	78.35	25.44	12.13
G8	71.66	6.32	78.35	25.85	12.20
G9	71.67	6.72	69.00	26.40	13.73
G10	76.67	5.18	78.79	24.67	13.27
G11	75.00	5.84	57.43	20.21	15.03
G12	70.67	5.86	75.88	22.91	11.63
G13	96.67	5.71	92.50	24.66	13.43
G14	75.00	6.17	78.66	23.90	9.83
G15	96.67	6.95	95.81	24.45	12.77
G16	70.67	6.26	69.15	24.30	10.27
G17	93.33	7.03	99.46	24.12	11.63
G18	75.33	5.67	78.55	25.25	9.80
G19	87.00	6.90	78.61	23.95	13.53
G20	80.00	6.66	73.51	24.95	13.97
G21	76.00	6.75	85.96	22.43	12.39
Mean	78.56	6.38	79.57	24.33	12.55
Maximum	96.67	7.93	99.46	26.40	15.03
Minimum	70.67	5.18	57.43	20.21	9.80

TH=Time of Heading**, CD**=Stem**:** Culm Diameter, **CL**=Stem**:** Culm Length, **PL**= Panicle Length, **NET/P**=Number of Effective Tillers per Plant,

Appendix V. Mean performance of quantitative characters of twenty one genotypes (cont'd)

Genotype	TM(Days)	TGW(gm)	GL(mm)	SLL(mm)	DGL(mm)
G1	103.00	21.27	8.28	1.73	6.16
G2	109.00	22.57	8.11	1.88	6.33
G3	106.00	21.92	8.33	1.91	6.24
G4	106.00	21.92	8.25	1.71	6.11
G5	127.33	19.70	8.92	1.76	6.77
G6	105.33	22.27	8.07	1.75	6.05
G7	105.33	21.73	8.01	1.73	6.1
G8	103.67	22.20	8.58	1.82	6.5
G9	106.00	21.07	8.41	1.86	6.16
G10	110.00	23.83	8.13	1.75	6.08
G11	107.00	19.67	8.14	1.92	6.3
G12	105.00	21.23	7.81	1.87	6.16
G13	130.33	23.20	8.51	1.73	6.58
G14	108.00	23.03	8.21	1.86	6.08
G15	130.33	26.27	9.02	2.13	7.42
G16	106.33	23.67	8.2	1.74	6.15
G17	125.00	27.47	9.49	2.3	6.88
G18	106.00	23.33	8.46	2.02	6.24
G19	112.00	24.03	8.54	1.97	6.37
G20	111.00	24.17	10.63	2.66	8.19
G21	108.00	21.60	8.39	1.74	6.26
Mean	110.98	22.67	8.499	1.897	6.434
Maximum	130.33	27.47	10.63	2.66	8.19
Minimum	103.00	19.67	7.81	1.71	6.05

TM=Time of Maturity, **TGW**= Thousand Grain Weight, **GL**=Grain: length (without dehulling), **SLL**=Sterile lemma length: Measure at postharvest stage, **DGL**=Decorticated grain: length (After dehulling, before milling).

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

A. Physical composition of the soil

Soil separates	Percent (%)	Methods employed
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

B. Chemical composition of the soil

Sl. No.	Soil characteristics	Analytical data	Methods 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	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka.

Appendix VII. Monthly average Temperature, Relative Humidity and Total Rainfall of the experimental site during the period from April, 2015 to September, 2015

Month	Air temperature (ºc)		Relative humidity (%)	Rainfall (mm) (total)
	Maximm	Minimum		
April, 2015	38.0	28.0	79.80	293
May, 2015	37.5	27.0	80.20	307
June, 2015	37.70	27.80	81.08	315
July, 2015	35.45	26.50	83.43	327
August, 2015	34.50	26.00	85.82	338
September, 2015	34.60	25.80	78.08	251

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