MORPHOLOGICAL CHARACTERIZATION AND STUDIES ON GENETIC DIVERGENCE OF SOFT RICE (*Oryza sativa* L.) GENOTYPES

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B.Sc. (Ag.)

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(GENETICS AND PLANT BREEDING)

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BY

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2014

DECLARATION

I, **Ms. K. PRAGNYA,** hereby declare that the thesis entitled **"MORPHOLOGICAL CHARACTERIZATION AND STUDIES ON GENETIC DIVERGENCE OF SOFT RICE (*Oryza sativa* L.) GENOTYPES"** submitted to the **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of the original research work done by me. I also declare that no material contained in this thesis has been published earlier in any manner.

Place: Hyderabad **(K. PRAGNYA)**

Date: **I. D. No. RAM/2011-30.**

CERTIFICATE

Ms. **K. PRAGNYA** has satisfactorily prosecuted the course of research and that the thesis entitled **"MORPHOLOGICAL CHARACTERIZATION AND STUDIES ON GENETIC DIVERGENCE OF SOFT RICE (*Oryza sativa* L.) GENOTYPES"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any University.

Date: **Chairperson**

(Dr. K. V. RADHA KRISHNA)

CERTIFICATE

This is to certify that the thesis entitled **"MORPHOLOGICAL CHARACTERIZATION AND STUDIES ON GENETIC DIVERGENCE OF SOFT RICE (*Oryza sativa* L.) GENOTYPES"** submitted in partial fulfilment of requirements for the degree of '**Master of Science in Agriculture'** of the Acharya N. G. Ranga Agricultural University, Hyderabad is a record of the bonafide original research work carried out by **Ms. K. PRAGNYA** under our guidance and supervision.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of investigations have been duly acknowledged by the author of the thesis.

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LIST OF SYMBOLS AND ABBREVIATIONS

%	per cent
σ^2_p	Phenotypic variance
σ^2_g	Genotypic variance
ANOVA	Analysis of variance
^oC	Degee centigrade
cm	Centimeter
CD	Critical difference
D^2	Genetic distance
DUS	Distinctivity, uniformity and stability
et al.	and others
Fig.	Figure
g	Gram
GA	Genetic advance
GT	Grain type
GCV	Genotypic coefficient of variation
h^2	heritability in broad sense
ha	hectare
i.e.,	that is
Kg ha^{-1}	kilograms per hectare
KI	potassium iodide
KOH	potassium hydroxide
mg	milli gram
m.ha	million hectare
ml	milli litre
mm	millimeter
m.t	million tonnes
1N	one normal
NaOH	sodium hydroxide

nm	nano metre
No.	Number
PBR	Plant breeders rights
PCV	Phenotypic coefficient of variation
per se	In accordence with
PPV&FRA	Protection of Plant Varieties & Farmers' Rights Act
RCV	Reference collection varieties
SE	Standard error
SR	Soft rice
sui generis	Of their own kind (self generation)
UPOV	*Union internationale pour la protection des obtentions vegetales*
viz.	namely

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ABSTRACT

In the present investigation, seventy five speciality rices called soft rice genotypes collected from different parts of north-east Assam were characterized for 62 agro-morphological traits using DUS discriptors and the same set of genotypes were evaluated to study the genetic diversity present in the experimental material for selection of the diverse parents, to estimate the genetic parameters among the genotypes for yield and component traits, and the extent of association between the yield and its component characters including the direct and indirect effects. The experiment was laid out in a randomized block design with three replications at Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad, India, during *kharif* 2013.

Among the 75 genotypes, some genotypes wer monomorphic for coleoptile colour, presence of leaf auricles, presence of leaf collor, presence of leaf ligule, shape of the ligule, width of the leaf blade, absence of male sterility, presence of secondary branching, phenol reaction of lemma and decorticated grain width, some were bimorphic, some were trimorphic and the remaining genotypes exhibited large variation for some traits. On the whole, significant variations were noticed for plant morphological characters, which is usful for each genotype to establish its diagnostic features.

The presence of purple basal leaf sheath colour, purple auricles, purple leaf ligule, deflexed flag leaf, very strong lemma anthocyanin colouration of apex, light green and purple stigma, deflexed panicle curvature of main axis, well exserted panicles, higher test weight and presence of very low and low amylose content, constitute the distinct features of soft rice genotypes.

Analysis of variance indicated the existence of significant genotypic differences among the genotypes for the yield and its components traits for all the characters. High GCV and PCV values were observed for seed yield per plant, number of tillars per plant and number of productive tillars per plant, moderate for plant height, panicle length, per cent filled grains per panicle and test weight. The values were low for days to 50% flowering and days to maturity.

High heritability coupled with high genetic advance as percent of mean was observed for plant height, number of tillars per plant, number of productive tillers per plant, per cent filled grains per panicle, seed yield per plant and test weight, which indicated that these traits were controlled by additive type of gene action. The remaining traits were mostly under the influence of non additive gene effects as they recorded low to moderate estimates of genetic advance.

Based on the relative magnitude of D^2 values, the genotypes were grouped into seven clusters. Cluster I was the largest comprising of 62 genotypes followed by cluster II with eight genotypes, cluster III, IV, V, VI and VII with one genotype each. The highest divergence occurred between cluster IV and cluster VII (1817.85) followed by cluster III and cluster VII (1795.23), cluster I and cluster VII (1425.51) and cluster III and cluster VI (1286.81).

The data on character means for seven clusters indicated that, The clusters III is having highest mean value for per cent filled grains per panicle, cluster V for seed yield per plant and cluster I for test weight (1000-grain weight) and cluster II for number of productive tillers per plant and cluster IV for panicle length.

The characters per cent filled grains per panicle (5181.98%), plant height (2237.84%), seed yield per plant (1441.44%), days to maturity (403.6%), test weight (371.17%), number of tillars per plant (252.25%), days to 50% flowering (50.45%), panicle length (46.85%) and number of productive tillars per plant (14.41%) contributed maximum to the genetic divergence.

Based on the inter-cluster distances, crossing between the genotypes (SR-12) of cluster IV and cluster VII (SR-38), cluster III (SR-55) and cluster VII (SR-38), cluster I with cluster VII (SR-38) and cluster III (SR-55) and cluster VI (SR-68) is suggested to generate diversified breeding material.

Character association studies revealed that the grain yield per plant showed positive association with days to 50% flowering, plant height, number of tillars per plant, per cent filled grains per panicle, days to maturity and test weight (1000-grain weight) at both genotypic and phenotypic levels. This indicated that a simultaneous selection for these characters would be more advantageous for yield improvement in rice.

Critical analysis of the results by path analysis revealed that the traits like number of tillars per plant, days to maturity, test weight and per cent filled grains per panicle were directly influencing the grain yield per plant. Hence, these traits were considered as important attributes in formulating selection criterion for achieving desired targets.

Chapter I

INTRODUCTION

Rice is the world's second most important cereal crop and staple food for more than 60 per cent of the global population. It is the major food crop in India occupying nearly 42.86 million hectares with annual production and productivity levels of 95.97 million tonnes and 2023 kg ha^{-1} respectively. While in Andhra pradesh it is grown in 43.75 millon hectares with production and productivity levels of 14.41 million tonnes and 3003 kg ha^{-1} (INDIASTAT, 2012). Over two billion people in Asia alone derive 80% of their energy needs form rice which contains 80% carbohydrates, 7-8% protein and also fat and dietary fibre (Juliano, 1985). The outstanding genetic diversity that exists for rice in the Indian sub continent has been brought forth not only by natural processes, the conscious human selection due to socio-economic compulsions, socio-economic traditions also played a dominant role in adding variations to morphological features especially to the grain characters, aroma, endosperm properties for specialty preparations, rice based products and even medicinal use.

The north-east region of India is a veritable natural gene bank representing wide spectrum of rice genetic resources. Among the different classes of rice available in Assam, glutinous / waxy rice is an important class. It is called glutinous (Latin *glutinosus*) in the sense of being glue-like or sticky. The waxy rice of Assam has been classified in two groups *viz., Bora* (glutinous) and *Chokuwa* (Semi-glutinous) based on amylose content (Shaptadvipa and Sarma, 2009).Waxy rice of Assam has significance in social and religious ceremonies and forms a popular daily breakfast diet in rural Assam. Milled rice is also used in the preparation of snacks, flat rice, puffed rice, bamboo rice, sweet rice beer and other dishes. The parboiled polished chokuwa rice swells on soaking and becomes soft and is used by the people of Assam as a fast food with curd. The multiplicities of uses make the glutinous rice very popular among farmers, in spite of the advent of modern high yielding rice varieties. These rices are also considered as “soft rice (komal chawl)” because of its soft cooking consistency (Rathi and R N Sarma, 2012). These soft rices being mostly landraces are highly valuable and possess traits that are most prefered by farmers. Further, they can be utilized to produce high yielding cultivars with specific quality if properly characterized, conserved as well as documented the inherent potential characteristics. In the present study, efforts were made to collect the Bora and Chakua rices to undertake detailed morphological, DUS characterization, agronomic performance for yield and yield components.

Until now, these cultivars have not grown outside the north-east, but the scientists at Central Rice Research Institute, Cuttak, have managed to develop a high yielding hybrid of a traditional soft rice variety called "Aghunibora". The field trials of the new hybrid were already positive, suggesting that it could be grown in different climates across India. As such there is no technical barrier in cultivating it in any part of the country. Therefore the plant breeders should focus their attention towards the improvement of both quality and high yield potential of these soft rices to fetch high premium price in the market.

The global dependence on rice has led to the development of thousands of varieties with large genetic and morphological diversity. Therefore, the documentation of distinguishing characters is very essential to carry out the scientific study. Characterizing the genetic basis of variation in plants and linking it to the observable traits will provide an important framework for significantly increasing the efficiency of selections made in plant breeding programmes. The need for a detailed examination of diagnostic characteristics thus has become imperative to maintain identity of released and notified varieties. Characterization of variety is useful to identify and avoid duplication. Qualitative traits being more stable over generations (Raut, 2003) hence are reliable for characterization of varieties.

Until recently, worldwide the germplasm was considered as the heritage of mankind to be shared and used by all but after the 1992 Convention on Biological diversity, there was a paradigm shift from the heritage of mankind to the sovereign rights of the state. Government of India has developed a '*Sui generis'* system to provide a frame work for Plant Variety Protection. In order to implement the *sui generis* system for plant variety protection for granting PBR to a breeder or farmer or institution, DUS testing is compulsory. DUS testing involves the comparison between new candidate varieties with selected RCVs (Reference Collection Varieties) for a range of phenotypic characters, which are predominantly morphological traits. Initially, 62 agro-morphological traits based to some extent on UPOV test guidelines were incorporated in the Indian National guidelines for the conduct of DUS tests in Rice.

India has a rich source of genetic diversity for rice. Rice contains significant diversity in plant architecture and growing habits and in grain phenotypes such as width, weight, cooking properties, aroma and texture. The extensive phenotypic and genotypic variation within the *Oryza sativa* makes these varieties a powerful tool to study rice genetic diversity, such that methods can be developed to enhance health promoting qualities of rice grain. Hence, to study the nature and magnitude of genetic divergence and characters contributing to it should be based on sound scientific procedures such as D^2 analysis to measure the genetic divergence among the test entries and their grouping into different clusters.

In addition to studies on mean performance, the evaluation of material for genetic divergence and variability and also association among various yield and quality would be more useful to the plant breeders. Parents identified on the basis of divergence for any breeding programme would be more promising (Arunachalam, 1981). Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. Similarly, heritability is the measure of transmission of characters from generation to generation and the estimates of heritability will be of immense help to the breeder in selecting superior individuals for a desired trait and successfully utilizing them in breeding programme.

Correlation is the measure of the mutual relationship between two variables. It is a measure of the degree of closeness and the linear relationship between two variables. The study of correlations may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters. Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable upon the other. Direct selection for yield is not a reliable approach since it is influenced by the environment. Therefore, it is essential to identify the component characters through which yield can be improved. Selection would be more effective for the trait, which has got high genetic advance and high correlation with grain yield.

Research in this direction on soft rice has been initiated and efforts are made by the Directorate of Rice Research for collection of these soft rice germplasm and land races. At present some of the lines of this soft rice are available at Directorate of Rice Research. So far no work has been done on characterisation and diversity of these soft rice genotypes. The systemic characterisation and study of genetic analysis in the material is meagre. Hence, keeping in view the importance of soft rices and scanty literature on these aspects, the present investigation was undertaken as a first attempt in the state of Andhra Pradesh with the following objectives:

1. Morphological characterization in soft rices of north-east region using DUS discriptors.
2. To study the genetic divergence among the soft rices through D^2 analysis.
3. To estimate the correlation and path analysis for yield and yield components of soft rice genotypes.

Chapter II

REVIEW OF LITERATURE

2.1 Morphological Characterization

Plant breeders always look for the traits which contribute towards either yield enhancement or providing tolerance/resistance to different stress for sustained production harnessing full genetic yield potential. Most of the times, the descriptive morphological characters have been overlooked as they usually do not contribute towards crop improvement. However with the enactment of Protection of Plant Varieties & Farmers' Rights Act (PPV&FRA) in 2001 and with the establishment of (PPV&FRA) in 2005, many of the morphological features which were ignored earlier, have now become important in Distinctness, Uniformity, Stability Testing for registration of plant varieties. Due to this development, a set of DUS descriptors have been developed in each crop for full characterization.

Olesan (1974) reported that seed colour which is a heritable character has been used by several workers to distinguish crop genotypes.

Rosta (1975) reported large variation in plant height and suggested that plant height can contribute to genetic diversity.

Chakrabarthy and Agarwal (1989) and Agarwal and Pawar (1990) noted that seed colour which is a heritable character has been used by several workers to distinguish crop genotypes.

Sharma *et al*. (1990) and Gupta (1990) identified similar variation in seed length and breadth in rice by looking in to area it can be concluded that most of the genotypes either come under medium or large genotype category.

Chaudhury and Sahai (1993) found high variability for stigma colour while evaluating 1270 Cambodian rice genotype.

Ganesan and Subramanian (1994) suggested that panicle length and days to 50% flowering was influenced by both additive and non-additive gene expression.

Katsuta *et al*. (1996) tested eight rice genotypes and found that days to flowering and time of heading are very important traits in classification of rice cultivars.

Ong and Blanshard (1998) studied the constituent starches from eleven cultivars of non-waxy rice with different amylopectin structures and this explains why rices that possess similar amylose contents can have different textural properties and degrees of cooking hardness.

Sawar *et al.* (1999) studied the morphological characters of 20 rice varieties viz., length, width, thickness, ratios of length to width, length to thickness and width to thickness and found significant differences for all the parameters except for grain thickness.

Shah *et al*. (1999) and Santhy (1999) tested eight rice genotypes and found that days to flowering is a very important trait in classification of rice cultivars.

Aidy *et al.* (2000) studied 23 rice cultivars belonging to *japonica, indica and japonica /indica* groups and suggested that each group can be differentiated from others by different characters such as 50 per cent flowering, leaf, plant height, 1000 grain weight, grain length and width, phenol test.

RohiniDevi's (2000) study show that morphological characterization though influenced by environment, are simple and useful traits for broad classification of rice genotypes.

Thimmanna *et al.* (2000) studied the morphological characteristics of the parents of Karnataka rice hybrids and opined that the leaf length, leaf width, pubescence, colour, flag leaf angle, ligule length, ligule colour, shape, auricle colour, inter node colour, panicle type, secondary branching, exersion percentage awning, seed length, width, L/T ratio, L/W ratio, and 100 seed weight could be used to differentiate the parental lines.

Bond and Crofton (2001) given successful reports on plant characters for varietal identification in crops like *Vida laba.*

Dhanaraj (2001) used stigma colour and panicle awns to characterize seven genotypes.

Rao *et al.* (2001) studied 123 native cultivars and land races which were characterized using morpho agronomic discriptors to estimate variability. Based on frequency distribution for eleven morphological characters, a majority of cultivars were found to possess green basal leaf sheath, green corolla and white stigma.

Selvaraju and Sivasubramaniam (2001) characterized 19 sorghum varieties based on the seed characters like length, breadth, length / breadth ratio and colour.

Anitalakshmi (2002) worked on characterizing the 18 rice genotypes by using morphological and chemical characters of seed, seedling and plant of rice. And categorized in different groups and her finding revealed that coleoptile and stigma colour were found useful for identification of genotypes.

Gomez calderin *et al*. (2002) developed the key for the identification of 16 cultivars of *Vigna radiata and V.anguiculata*. The key is mainly based on the seed colour, pubescence and size.

Evera (2003) used leaf ligule trait to characterize twenty six paddy cultivars.

Kumar (2003) had given uccessful reports on plant characters for varietal identification in lucerne.

Nethra (2003) studied the morphological, biochemical and molecular characterization of 24 genotypes of rice, her study revealed that the morphological characterization of seed, seedling and plant were found useful for varietal characterization. Seed colour, seed size served greater tool in categorizing the genotypes, morphological characters like flag leaf length, width, curvature, number of tillers, panicle type, length and number of panicle, days to 50 per cent flowering were most differentiating characters.

Patra and Dhua (2003) collected and characterized 120 upland rice germplasm accessions and the characterization data revealed enormous morphological as well as agronomical variability among the land races.

Suman (2003) studied on genetic diversity and agro-morphological characterization of rice *(Oryza sativa L.)* germplasm.

Thangavel (2003) had given uccessful reports on plant characters for varietal identification in sorghum.

Kumar (2004) had given successful reports on plant characters for varietal identification in pearl millet.

Sharma *et al.* (2004) characterized the *ahu* rices of Assam using 21 morphoagronomic traits and showed that the co-efficient of variation for spikelet per panicle, grain yield, panicle weight, 100 grain weight were relatively higher among the traits observed.

George *et al.* (2005) evaluated the grain quality characteristics of aromatic rice varieties in Waynad and Kerala for their suitability for cultivation in that area.

Reddy (2005) characterized the cotton hybrid based on morphological, chemical and electrophoresis of cotton hybrids and their parents. He said leaf characters *viz.*, leaf size leaf shape, leaf colour, leaf hairiness were useful in differentiating the cotton genotypes.

Yong-Sham *et al.* (2005) studied the potential of SSR markers for variety identification by comparing twenty-seven SSR markers and morphological traits in tests of distinctiveness, uniformity, and stability (DUS) of 66 pepper varieties (*Capsicum annuum* L.). SSR markers could be used to complement a DUS test of a candidate variety and to select complimentary varieties by pre-screening existing varieties in the context of protecting new varieties of pepper.

Suhasini (2006) characterized the 22 sesame genotypes based on morphological, chemical and molecular markers and opinioned that the morphological characters served a great tool in differentiating the genotypes.

Chakrabarthy *et al*. (2007) characterized 49 varieties of rice based on variations in phenol colour test and classified the varieties as colour positive and colour negative.

Joseph *et al.* (2007) characterized Navara - a traditional medicinal rice cultivar of Kerala based on morphological features. Detailed characterization of navara germplasm reveals that there are many different morphotypes exist with respect to qualitative traits. Different groups could be identified based on vegetative, panicle and grain characters.

Joshi *et al.* (2007) studied 19 rice varieties of non-basmati and basmati for 12 morphological descriptors at different stages of plant growth. These descriptors showed variability and heritability coupled with moderate to high genetic advance for most of morphological traits, signifying their utility in varietal characterization.

Monika *et al*. (2007) reported that at booting stage of rice plant, leaf and leaf sheath characters like anthocyanin colouration, its distribution and intensity along with the presence or absence of auricles, collar, ligules and attitude of culms can be used for varietal characterization.

Siddiqui *et al.* (2007) evaluated the rice grain quality characters pertaining to morphology within Pakistan local rice germplasm and suggested that a wide variation present in grain size, shape and weight with respect to altitude of collection site.

Sumathi (2007) had given successful reports on plant characters for varietal identification in oats.

Bisne and Sarawgi (2008) carried out studies to characterize thirty two aromatic rice accessions of Badshah bhog group. These germplasm accessions were evaluated for twenty-two morphological, six agronomical and eight quality characters. The specific genotypes B: 1340, B: 2039, B: 2495, B: 2816, B: 16930 B: 2354, B: 1639, B: 2094 were identified for quality and agronomical characteristics. These may be used in hybridization programme to achieve desired segregants for good grain quality with higher yield.

Bora *et al.* (2008)(a) characterized rice varieties on the basis of hulled and unhulled grain characters like grain length, grain colour, grain width, decorticated grain length, decorticated grain width, decorticated grain colour, L/B ratio and 1000 grain weight.

Bora *et al.* (2008)(b) characterized eleven local and popular rice varieties of Assam based on the colour developed after 4 hours by placing the seeds in petri plates on two layers of filter paper soaked in one per cent phenol solution.

Chandrashekhar (2008) reported that Morphological characterization of French bean genotypes based on seed coat colour, shape, test weight, seed length, phenological, seedling characters was found to be more reliable for varietal identification.

Patra *et.al.*, (2008) studied 483 accessions of wild rice germplasm for various morpho agronomic descriptors like leaf pubescence, blade colour, ligule colour, ligule shape, collar colour, leaf angle, days to 50% flowering, culm angle, internode colour, flag leaf angle, stigma colour, awning, sterile lemma colour etc. Irrespective of species diversity, leaves were pubescent, shape of ligule cleft, panicle axis straight, straw sterile lemma, long and fully awned. The leaf blade colour mostly green, collar and auricle light green, panicle type mostly open and well exserted.

Singh and Singh (2008) studied the consumer point of view paddy were length, kernel length, cooked kernel length, elongation ratio, gelatinizing temperature, gel consistency, amylase concentration and aroma are important characteristics.

Veasey *et al.* (2008) used several morpho-agronomic traits to characterize the genetic variability among the species and populations of South American wild rice.

Ameena (2009) and Macha (2010) had given successful reports on plant characters for varietal identification in cotton.

Reddy *et al.* (2009) evaluated 29 sorghum (*Sorghum bicolor* L. Moench) cultivars for 39 agro-morphological traits used in DUS testing guidelines. Large variation among cultivars was found for the traits, time of panicle emergence (65-87 days), plant total height (120-272 cm), leaf length (57-87 cm), panicle length (22-35 cm), 1000 -grain weight (23-46 g).

Bhonsle and Sellappan (2010) observed the physicochemical characteristics such as physical (hulling, head rice recovery (HR), broken rice (BR), grain classification,chalkiness), chemical (alkali spreading value, amylose content (AC), gel consistency (GC), aroma) and cooking characteristics (volume expansion, elongation ratio, water uptake) for 22 traditionally cultivated rice varieties, in comparison with high yielding rice varieties Jaya, Jyoti and IR8. They reported that some of traditionally cultivated rice varieties are with excellent grain quality characteristics.

Chavan (2010) given Successful reports on plant characters for varietal identification in soyabean.

Das and Ghosh (2010) studied four hundred thirty one traditional rice cultivars to improve yield, its components and grain size and shape. Characterization had been done on thirty one traits. Among the qualitative traits, considerable variability was recorded for basal leaf sheath colour, awning and auricle colour.

Kosina (2010) had given successful reports on plant characters for varietal identification in wheat.

Macha (2010) and Singh *et al*. (2010) reported that seed colour which is a heritable character has been used by several workers to distinguish crop genotypes.

Mageshwaran (2010) repoted that morphological, chemical and bio-chemical characters were also found to be useful inaugmenting the taxonomic approach for cultivar identification and discrimination.

NaimaGhalmi *et al*. (2010) collected twenty landraces of cowpea (*Vigna unguiculata* L. Walp.)Scattered throughout Algeria were compared through morphological and genetic characterization.

Patra *et al*. (2010) characterized eighteen basmati rice varieties using morphological descriptors adopted from the DUS guidelines of PPV & FR Authority and subsequently examined for their Distinctiveness, Uniformity and Stability. Among the 46 visually assessed characters 26 characters were monomorphic, 11 characters were dimorphic and 7 characters were polymorphic indicating their potential for varietal characterization and distinctivenes.

Begum and Kumar (2011) characterized thirty two jute (Corchorus olitorius and C. capsularis) varieties through distinctness, uniformity and stability (DUS) testing trials using 17 heritable morphological traits to enable identification of these varieties and for unambiguous ascertainment of distinctness. Out of 17 traits, 8 were found to be monomorphic, 7 dimorphic and only 2 polymorphic in C. capsularis, while 8 traits were dimorphic and 9 polymorphic among C. olitorius varieties, indicating their potential for varietal characterization.

Gowda *et al.* (2011) studied 45 colored rice accessions, which had been earlier collected from peninsular India. The accessions were evaluated at two diverse locations for 12 morpho-agronomic traits and genotypes using 50 simple sequence repeat (SSR) markers. The most discriminatory traits were number of seeds per panicle, biomass yield, and days to flowering and maturity.

Joshi *et al.* (2011*)* conducted experiment on twenty indigenous rice varieties and characterized them using morphological descriptors adopted from the DUS guidelines and subsequently examined for their distinctiveness, uniformity and stability.

Mathure *et al.* (2011) studied eighty-eight aromatic cultivars for determinants of kernel quality (kernel size-shape, test weight and aroma) and grain morphology such as awning, lemma and palea characters, pubescence, colour of sterile lemma and apiculus colour. They reported that increase the yield, improvement in length of panicle and increasing number of productive tillers in medium or mild scented cultivars would be the best strategy.

Moukoumbi (2011) characterized 60 lowland NERICA varieties and 18 promising lines of their genetic inheritance 23 morphological characters and found significant variation for all the characters evaluated.

Nascimento *et al.* (2011) characterized 146 accessions of upland rice (*Oryza sativa* L.), based on qualitative and quantitative agro-morphological descriptors. Polymorphism was observed among 12 of 14 qualitative characters evaluated, whereas significant differences were observed for 11 of the 14 analysed quantitative traits.

Sarawgi *et al.* (2011) carried out studies to characterize seven hundred eighty-two rice germplasm accessions on the basis of twenty-nine morphological and eight agronomical traits. After evaluation of 782 accessions for eight quantitative characters, on the basis of mean values, top ten accessions were identified for the yield ancillary traits. These can be used to identify phenotypically divergent sources for traits of interest in breeding programmes.

Chakrabarthy *et al.* (2012) collected ninety one farmers grown rice varieties and evaluated for 52 plant morphological and grain characteristics. Of the 44 qualitative traits studied in, maximum variability was recorded with respect to density of pubescence of lemma, curvature of main axis of panicle, attitude of branches of panicle, anthocyanin colour of keel in lemma, colour of tip of lemma and lemma and palea colour.

Chakravorty and Ghosh (2012) studied characterization of fifty one landraces of rice was done using 46 agro-morphological traits following Distinctiveness, Uniformity and Stability test (DUS). Out of fifty one varieties studied, twenty seven were found to be distinctive on the basis of twenty two essential and twenty four additional characters.

Parikh *et al.* (2012) characterized seventy-one aromatic rice germplasm. These germplasm were grouped on the basis of anthocyanin pigmentation, plant habit, and awning character.

Sarawgi *et al.* (2012) characterized forty six aromatic rice accessions of Dubraj group. These germplasm accessions were evaluated for twenty morphological, six agronomical and eight quality characters. The specific accessions D: 1137, D: 812, D: 950, D: 959, D: 925, D: 1008, D: 939, D: 666I and D: 1090 were identified for quality and agronomical characteristics.

Subudhi *et al.* (2012) reported that analysis of variance for 16 quantitative morpho-agronomic characters showed very significant results. These landraces can be popularized among the farmers and can be used as donor in varietal development programme.

Ekka *et al.* (2013) indicated that out of the eighteen qualitative characters, the absolute frequency was very high for intermediate type of leaf pubescence, white ligule colour, cleft type of ligule shape, pale green auricle colour, green internode colour, absent type of awning and straw sterile lemma colour. There is good scope to bring about improvement through hybridization and selection.

Mallick *et al.* (2013) have discribed morpho-agronomic characteristics of a newly released variety BNKR – 1 (Dhiren) in detail through DUS test data.

Selvi *et al.* (2013) stated that as per DUS guidelines maize inbreds vary widely in their characters. The study revealed that among the 17 inbreds, UMI 1200 and UMI 1230 were distinct from other inbreds and UMI 551 had the distinguishable character of tassel anthocyanin colouration at glume base. Dendrograms were constructed based on the morphological characters that established differences among the individuals indicating reportable variation among the 17 maize inbreds which would aid in selection of inbreds with desirable characters for further breeding programme.

Sinha and Mishra (2013) indicated that morphological traits were useful for preliminary evaluation for crop improvement program and can be used for assessing genetic diversity among morphologically distinguishable rice landraces.

SubbaRao *et al.* (2013) characterized sixty-five landraces of rice using forty three agro-morphological traits following Distinctiveness, Uniformity and Stability test. Out of Sixty-five varieties studied, thirty-two were found to be distinctive on the basis of twenty two essential and twenty four additional characters.

2.2 Genetic Variability

The nature and extent of variability forms the basis for all crop improvement programmes. According to Allard (1960), yield is polygenically controlled quantitative character and is highly influenced by environment. Partitioning of observed variability into heritable and non-heritable components is very much essential to get a true indication of the genetic coefficient of variability.

Gomatinayagam *et al.* (1990) reported that genotypic and phenotypic coefficients of variation were low for days to 50% flowering and days to maturity.

Sawant *et al.* (1994) observed significant differences for all the traits, with high genotypic and phenotypic coefficients of variation for grains/panicle, plant height, ear bearing tillers/plant, 100-grain weight and grain yield/plant. Heritability and genetic advance were high for plant height, graina per panicle and grain weight. Grain yield had low heritability with moderate genetic advance.

Ganesan *et al*. (1995) noted moderate amount of variability (10-20%) for days to panicle emergence, plant height and days to 50% flowering.

Mishra *et al.* (1996) identified that PCV and GCV estimates were high for grains per panicle whereas PCV was high for number of chaffs per panicle, 100-grain weight and yield. Heritability estimates were high for all characters except number of tillers per hill, panicle length and number of chaffs per panicle indicating better scope for selection. However, genetic advance was low for most of the traits

Datke *et al.* (1997) evaluated 24 F_6 lines of paddy rice. All lines showed significant differences for all the characters studied, except number of effective tillers/plant and straw yield/plant. GCV was high for grain yield/plant and low to moderate for the remaining traits. High heritability values were associated with high genetic advance with respect to days to 50% flowering, plant height, number of spikelets/panicle and grain yield/plant, indicating the presence of additive genes.

Vange and Ojo (1997) reported moderate GCV and PCV values observed for test weight and number of productive tillars.

Chaudhary and Das (1998) observed high genotypic coefficient of variation for grain yield followed by grains per panicle. High heritability with high genetic advance was found for grains per panicle followed by grain yield.

Balan *et al.* (1999) noted that genotypic and phenotypic coefficients of variation were low for days to 50% flowering and days to maturity.

Lalitha and Sreedhar (1999) estimated high heritability for amylose content, length/breadth ratio of grain and alkali value while they were moderate for grain yield per plant and volume expansion ratio and low for protein content and gel consistency.

Shridhara *et al.* (1999) studied high heritability and genetic advance coupled with large genetic variability for amylose content, milling recovery, kernel elongation ratio, total number of tillers and number of effective tillers.

Singh *et al.* (1999) observed range, phenotypic coefficient of variation and genotypic coefficient of variation were higher for all characters in F_5 of Pankaj x Janki, except days to 50% flowering and 1000-grain weight. Heritability for all the characters were high, the highest (99.81) for days to 50% flowering (*Oryza longistaminata* x Jagannath) and the lowest for panicles/plant (Pankaj x Janaki). Heritability was comparatively higher in cross *Oryza longistaminata* x Jagannath for most of the characters studied. All crosses recorded high genetic advance for panicles/plant, grains/panicle and grain yield/plant, the highest values (47.18%) for grain yield/plant in cross *Oryza longistaminata* x Jagannath.

Sadhukhan and Chattopadhyay (2000) recorded high GCV and PCV values for grain yield per plant and number of grains per panicle. Graian test weight, plant height, length and length-width ratio of grain and grain length after cooking had moderate to high GCV and PCV values. Broad-sense heritability estimates were moderate to high for all the characters studied. Yield per plant, test grain weight, plant height, number of grains per panicle, length-width ratio of grain, grain length after cooking and amylose content had high genetic gain as a percentage of the population mean.

Yadav (2000) studied genetic variability for yield and its components in 15 genotypes of rice. Appreciable amount of genotypic coefficient of variation, heritability and genetic advance were observed for total grains per panicle, total grains per plant and grain yield per plant. This indicated the role of additive genetic component controlling these traits and scope for selections.

Bidhan *et al*. (2001) observed high phenotypic and genotypic variances for grain yield, followed by number of filled grains per panicle. They recorded heritability which ranged from 50% (grain yield per hill) to 90% (grain breadth). Genetic advance as percent of mean was highest for number of filled grains per panicle (70.34), followed by grain yield (68.72). Number of filled grains per panicle, 1000-grain weight, grain length and breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance.

Zen and Bahar (2001) reported high heritability of all plant characters and yield (76.98%-97.96%), heritability of filled spikelets per panicle was medium (37.29 percent). Plant height, productive tillers, spikelets per ear, and yield had a wide genetic variability. Selection for those characters could be done at early generation.

Nayak *et al*. (2002) studied genetic variability, heritability and genetic advance for grain yield and yield contributing characters in 2000 scented rice genotypes and high estimates of GCV and PCV were observed for number of panicles/plant and grain yield/plant.

Singh *et al*. (2002) noted high genotypic and phenotypic variances for grain yield per plant, panicle weight, number of grains per panicle and number of branches per panicle, medium for panicle length, 1000-seed weight and low for panicle length and milling percent. High heritability with high genetic advance was recorded for number of grains per panicle followed by panicle weight and grain yield per plant.

Chaudhary and Motiramani (2003) observed a wide range of variation for most of the characters. Heritability in broad sense was very high for all the characters exhibited high heritability coupled with high genetic advance except harvest index.

Nayak *et al*. (2003) recorded moderate to high genetic variability for all characters.

Patil *et al*. (2003) suggested high heritability associated with high genetic advance for alkali spreading value, unfilled grain percentage, 1000-grain weight, grain yield per plant, brown rice length: breadth ratio, ear-bearing tillers, filled grains per panicle, kernel length:breadth ratio, paddy length:breadth ratio, kernel length:breadth ratio of cooked rice, brown rice length and paddy length.

Satish *et al*. (2003) observed high GCV and PCV values for spikelets/panicle, number of grains/panicle and grain yield/plant. High heritability along with high genetic advance was observed for number of spikelets/panicle, number of grains/panicle, grain yield/plant followed by other characters. Emphasis should be given on these characters while selecting scented rice varieties to improve grain yield.

Singharia *et al.* (2003) recorded larger PCV and GCV values for number of secondary branches, panicle and grains borne on primary branch and low for days to 50% flowering, panicle length, kernel length and kernel breadth. High heritability coupled with high genetic advance was recorded for 1000-seed weight, seeds per panicle and primary branch length indicating greater scope for yield improvement through selection.

Hasib *et al*. (2004) evaluated mean performance, variability, heritability and genetic advance for four selected lines in the F_6 generation. The difference between the value of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was low in all the 8 quantitative characters studied indicating the effect of the genetic factor in controlling these traits. High heritability, and moderate to low PCV, GCV and genetic advance were observed for all the traits.

Sarma and Bhuyan (2004) identified higher GCV and PCV values for the number of grains per panicle, followed by grain yield per plant and number of effective panicles per plant. Broad-sense heritability was highest for plant height followed by days to 50% flowering and number of effective panicles per plant. The highest genetic advance was observed for number of grains per panicle, followed by grain yield per plant and number of effective panicles per plant. Grains per panicle and the number of effective panicles per plant showed high heritability and genetic advance.

Sinha *et al.* (2004) observed high GCV for grain yield followed by test weight and panicles per plant. High heritability with high genetic advance was found for grain yield followed by test weight and panicles per plant.

Vivek *et al*. (2004) revealed a wide range of variation for all the characters among the genotypes. Grain yield per plant, biological yield per plant, number of tillers and panicles per plant had high values of genetic coefficient of variation and phenotypic coefficient of variation. They reported high heritability with high genetic advance for grain yield per plant and biological yield per plant.

Bose and Pradhan (2005) reported that traits like plant yield, test weight, days to 50% flowering, and plant height were the major contributors to genetic divergence.

Elayaraja *et al*. (2005) observed high heritability associated with moderate to high genetic advance as a percent of mean for number of productive tillers, panicle length, number of grains per panicle, 100- grain weight and grain yield per plant in M2 generation.

Madhavilatha *et al*. (2005a) revealed high variability, heritability and genetic advance for number of grains per panicle, grain yield per plant, harvest index and kernel L/B ratio, while days to maturity, fertility percentage, hulling recovery and kernel elongation ratio had high heritability coupled with low genetic advance.

Nayak and Reddy (2005) noted maximum GCV and PCV values for grain yield followed by alkali spreading in the rabi seasons and vice versa for the kharif seasons. Broad sense heritability was high for all the studied characters in both rabi and kharif seasons. High genetic advance was also observed for alkali spreading value and grain yield in both seasons, while moderate genetic advance values were observed for head rice recovery, kernel length, length/breadth ratio and amylose content in both seasons indicating non-additive gene action.

Panwar (2005) observed high heritability and genetic advance for grain yield per panicle, chaffy grains per panicle, grain yield per plant, filled grains per panicle and secondary branch number per panicle, indicating the effectiveness of selection for these characters.

Patil and Sarawgi (2005) reported the genetic and phenotypic coefficients of variation were high for number of unfilled grains per panicle, unfilled grain percentage, grain yield per plant, 1000-grain weight, number of ear-bearing tillers per plant, and number of filled grains per panicle. 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.

Sarkar *et al.* (2005) studied high GCV and PCV values for number of panicles per plant, number of tillers per plant, and grain yield per plant. The highest heritability value was registered for 1000-grain weight, followed by brown kernel length and grain length. The number of spikelets per panicle and number of grains per panicle showed high heritability along with high genetic advance.

Satyanarayana *et al*. (2005) reported high variability, heritability and genetic advance for number of grains per panicle, spikelet fertility, days to 50% flowering and plant height, while test weight recorded high variability and heritability, coupled with low genetic advance. The number of effective tillers per plant and panicle length recorded low heritability.

Saxena *et al*. (2005) observed high PCV and GCV values for number of unfilled spikelets, seed yield per plant, biological yield per plant, number of filled spikelets, total number of spikelets, and length:breadth ratio of rough rice. Broad-sense heritability was also very high for number of filled spikelets, 100-seed weight, plant height, total number of spikelets and panicle length, indicating the possibility of improving such traits through selection. Seed yield per plant and number of unfilled spikelets showed high genetic advance.

Singh *et al*. (2006) recorded a wide range of variation for all the traits. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability and high genetic advance were recorded for plant height, indicating the predominance of additive gene action for this trait.

Karim *et al.* (2007) noted high genotypic coefficient of variation (GCV) value was observed for 1000-grain weight followed by spikelet sterility (%), grain yield per hill and number of filled grains per panicle, whereas days to maturity showed very low GCV. High heritability with high genetic advance in percent of mean (GAPM) was observed for 1000-grain weight followed by spikelet sterility (%) and number of filled grains per panicle.

Kumar *et al*. (2007) recorded high PCV, GCV coupled with high heritability estimates and high genetic advance as percentage of mean for number of filled grains per panicle, 100-grain weight, biomass per plant and grain yield per plant in the F_2 populations of the cross P1 P3. Similarly, the F3 population of the cross P2 P1 exhibited high genetic parameters for number of productive tillers per plant and grain yield per plant.

Mustafa and Elsheikh (2007) observed a wide range of genetic variability among the genotypes for most of the characters. The highest genotypic coefficient of variation was recorded for grain yield, percent unfilled grains per panicle, number of grains per panicle and number of filled grains per panicle.

Nayudu *et al.* (2007) reported high GCV and PCV and high heritability coupled with high genetic advance for number of productive tillars per plant.

Karad and Pol (2008) observed high GCV values for number of mature and immature panicles m.sq.$^{-1}$, 1000 grain weight and plant height. The estimate of heritability together with genetic advance was high for 1000 grain weight, number of mature and immature panicles and plant height.

Kole *et al*. (2008) recorded high PCV and GCV values 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.

Anbanandan *et al.* (2009) suggested high PCV and GCV values for grain yield per plant for cross 1 followed by cross 2 in both F_3 and F_4 generations. Also, cross 1 and cross 2 recorded high heritability and genetic advance for number of productive tillers per plant, 1000-grain weight and grain yield per plant in both F_3 and F_4 generations.

Chandra *et al*. (2009) observed high PCV and GCV values for number of productive tillers per plant, number of grains per panicle, 1000-grain weight and grain yield per plant. High heritability along with high genetic advance was observed for plant height, number of grains/panicle and 1000-grain weight.

Khan *et al*. (2009) reported highly significant differences among 25 genotypes for all the morphological traits and six genotypes used for the grain quality studies also showed significant differences among grain quality traits except volume expansion ratio and grain elongation ratio. Broad sense heritability estimates were higher for morphological traits ranging from 67.37 to 98.24.

Sabesan *et al*. (2009) noted high values of heritability along with genetic advance for grain yield per plant, 100 grain weight, productive tillers per plant, grains per panicle, grain length, grain breadth, kernel length, panicle length and plant height.

Jayasudha and Sharma (2010) studied high PCV and GCV values for grain yield per plant, harvest index, pollen fertility (%) and spikelet fertility (%). Characters like pollen fertility (%), spikelet fertility (%), days to 50% flowering and grain yield per plant showed high value of heritability coupled with high genetic advance.

Nandan *et al*. (2010) observed high heritability along with high genetic advance as percent of mean for number of effective tillers per plant, panicle weight, number of grains per panicle, number of spikelets per panicle, 1000 grain weight, kernel length before cooking (KLBC), length breadth(L/B) ratio, water uptake ratio and grain yield per plant.

Babu *et al*. (2011) worked on high genotypic coefficient of variation for number of panicles/hill and high phenotypic coefficient of variation for number of panicles/hill and number of tillers/hill whereas plant height, number of tillers/hill, panicle length, flag leaf length and test weight showed high estimates of heritability. Number of panicles/hill and number of tillers/hill showed high genetic advance as percent of mean.

Fiyaz *et al.* (2011) noted significant differences among the genotypes for all the traits. High values of heritability and genetic advance were observed for total spikelet per panicle, 1000- grain weight and total biomass.

Pandey and Singh (2011) observed high PCV and GCV values for grains/panicle, grain yield/plant and gel consistency. Total tillers/plant and effective tillers/plant at maturity had moderate PCV, GCV and genetic advance coupled with moderate heritability. High heritability coupled with high genetic advance was observed for grains/panicle, grain yield/plant.

Singh and Pandey (2011) reported high heritability and high genetic advance for the traits plant height, effective tillers per plant, spikelets per panicle, filled grains per panicle, grain weight per panicle, specific leaf weight, test weight, kernel length cooked kernel length, leaf area index, grain length, L/B ratio and gelatinization temperature.

Tiwari *et al.* (2011) identified high GCV and PCV were observed for grain yield per plant.

Yadav *et al*. (2011) recorted high PCV and GCV values for seed yield, harvest index, biological yield, number of spikelets per panicle, flag leaf length, plant height and number of tillers. High heritability coupled with high genetic advance as percent of mean was registered for seed yield, harvest index, number of spikelets per panicle, biological yield and flag leaf length.

Chakravorty *et al*. (2013) identified the existence of inherent variability in the landraces of rice that could be used to exploit the variability directly or through crop improvement programmes.

2.3 Genetic Divergence

Vairavan *et al*. (1973) evaluated representative group of 190 rice types collected from North-East India along with four standard varieties to understand the nature of genetic divergence. Preliminary grouping was done by canonical analysis and the resultant 42 groups were further classified using the D^2 statistic.

Singh *et al*. (1996) assessed the nature and magnitude of genetic divergence in 40 scented and fine genotypes of rice and grouped them into six clusters. It was observed that grain yield and plant height had contributed greatly to the divergence.

Kumary and Rangasamy (1997) estimated genetic divergence by using Mahalanobis's D^2 statistics in 62 early rice genotypes and grouped them into six clusters. They found that there was no relationship between geographical distribution and genetic diversity. Characters like grain yield per plant, panicle exertion and plant height made largest contribution to total divergence.

Sarawgi *et al.* (1998) studied the genetic divergence in 132 rice genotypes by using the D^2 technique and grouped them into 10 clusters and the maximum intra-cluster distance was observed in cluster VIII. Clusters VI and VIII were identified as genetically divergent. Considering the cluster means and cluster distances, Bakal-B and Jondhera Dhan of cluster VI, Gonda Jhul of cluster VIII, Poorva and IR-36 of cluster VII, Kranchi, X-12, Moti Bakiya and Assam Chudi of cluster V and Kranti of cluster X were the most promising varieties.

Shanthi and Singh (2001) studied the genetic divergence by using Mahalanobis's D^2 statistic and Tocher's method and grouped them into four clusters. The first cluster contained nine genotypes, the second containing six while third (MM-72) and fourth (MM-71) clusters were monogenic. The genotypes belonging to clusters II and III having greater cluster distance were recommended for inclusion in a hybridization programme as they were expected to produce good segregants.

Yadav *et al*. (2002) assessed the genetic divergence of 100 aromatic rice genotypes and grouped them into 9 clusters. The pattern of distribution of genotypes within various clusters was random and independent of geographical isolation. Based on mean performance, genetic distance and clustering pattern, inter-crossing of genotypes Gam Poon, Khao Jao Hawam, Basmati Sufaid 187, KCN 80152, Abor Bora and Hara may be useful in creating wider variability for important agronomic and quality traits with high yielding segregants.

Chauhan and Singh (2003) studied genetic divergence in 45 genotypes and grouped into 11 clusters. Cluster II was the largest and consisted of 10 genotypes followed by cluster I with 9 genotypes. Clusters III and V had 7 genotypes each, similarly clusters VI and VII contained 3 genotypes each. Clusters VIII to XI were monogenetic. Hybridization among genotypes included in the diverse clusters (I, IV, VIII, X and XI) and the clusters having high means for quality traits such as high elongation (cluster IV), intermediate alkali value (cluster VIII and IX) and high milling recovery (cluster IX and X) would give high heterotic combinations and produce large variability, better segregants in the segregating generations.

Mani (2003) assessed the degree and nature of genetic divergence among a set of 61 elite basmati rice genotypes and grouped into four clusters. Maximum number of genotypes (43) were included in cluster I, followed by cluster II (13), cluster III (4) and cluster IV (1). Cluster III and II showed the maximum and minimum intra cluster distance, respectively. Cluster III showed the maximum genetic distance from cluster IV, while cluster II and III had the minimum genetic distance. Plant height contributed the maximum towards genetic divergence followed by days to 50% flowering and grain yield per plant.

Mishra *et al.* (2003) evaluated the nature and magnitude of the genetic diversity in 16 rice cultivars and their 72 F_1 hybrids. The genotypes were grouped in to 12 clusters based on the relative magnitude of multivariate D^2 values. The highest number of genotypes were in cluster XII. The highest genetic distance was observed between clusters III and VIII and lowest between cluster VII and VIII. No close correspondence was evidenced between geographical distribution and genetic divergence.

Das *et al*. (2004) studied genetic divergence in 50 landrace collections of rice and grouped them into 10 clusters. Days to 50% flowering, grain yield per plant, grain length, kernel breadth and 100-kernel weight were identified as potential characters that can be used as parameters while selecting diverse parents in the hybridization programme for yield and quality improvement.

Nayak *et al*. (2004) grouped 200 rice genotypes in to 10 clusters based on grain weight and days to 50% flowering.

Souroush *et al*. (2004) estimated the genetic diversity of quantitative and qualitative traits of 36 lines and cultivars of rice. Cluster analysis with Ward's method classified all of the genotypes into 5 clusters. Genotypes of the third cluster including four pure lines (Nos. 4, 21, 22 and 24) had high yield, high number of panicle and filled grains per panicle, intermediate amylose and lower plant height, therefore, these suitable traits can be transferred through hybridization programmes. Genotypes of the first and fifth clusters can also be used to improve yield and grain cooking quality, respectively.

Awasthi *et al*. (2005) studied the genetic divergence of 21 Indian aromatic rice genotypes and grouped into six clusters for different characters. The inter-cluster distance ranged from 0.00 for clusters IV, V and VI to 40.21 for cluster III. The inter-cluster distance was observed to be highest between clusters II and III, indicating that the genotypes of these 2 clusters were genetically more diverse. The number of grains per panicle, grain yield per plant, days to 50% flowering, leaf length and leaf width showed high percent contribution towards total genetic divergence.

Bhutia *et al*. (2005) carried out genetic divergence studies in 41 high yielding and local rice genotypes and grouped them into six clusters. Cluster I had the highest number of genotypes (27) followed by cluster II with eight, and cluster III with three genotypes, respectively. Clusters IV, V and VI were mono genotypic. Cluster IV showed the maximum genetic distance from cluster VI followed by its distance from cluster V. The genotypes included in clusters III and IV may be used as parents in hybridization programme to improve yield and cooking quality.

Bose and Pradhan (2005) assessed the nature and magnitude of genetic divergence among 35 deep water rice genotypes and grouped them into 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Traits such as plant yield, days to 50% flowering, and plant height were the major contributors to genetic divergence.

Chand *et al*. (2005) studied 19 genotypes of Aman rice for their genetic divergence by using Mahalanobis D^2 statistics and grouped them into six clusters. Cluster I was the largest with eight genotypes followed by cluster II with four genotypes. The maximum inter-cluster distance was found between these groups.

Chaturvedi and Maurya (2005) worked on genetic divergence analysis in 26 rice genotypes which were grouped into eight clusters. The maximum inter-cluster D^2 value was obtained between cluster III and VI and III and VIII. It is suggested that for developing better cultivar, the genotypes of cluster III could be utilized in hybridization programme with the genotypes of cluster VI and VIII.

Kandamoorthy and Govindarasu (2005) studied genetic diversity in 30 extra-early rice genotypes. Cluster I had the highest number of genotypes. The highest inter-cluster distance was observed between cluster I and III followed by cluster II in direct sown condition. Under transplanted condition, cluster II showed the highest inter-cluster distance with cluster V followed by cluster II and IV. Plant height and days to flowering contributed to genetic diversity in transplanted conditions.

Madhavilatha *et al*. (2005b) assesed the genetic diversity in 44 elite rice germplasm lines classified them into nine clusters based on Mahalanobis D^2 statistic. Results on inter-cluster distances revealed maximum diversity between genotypes of clusters IV and VIII. Intra-cluster distance was maximum for cluster V, indicating the existence of variability within the cluster. Plant height and days to 50% flowering accounted for 82.04% of the total genetic divergence, indicating their importance in the choice of parents for hybridization programmes.

Pradhan and Mani (2005) studied the genetic divergence in 38 elite basmati rice genotypes and grouped them into ten clusters. Cluster means indicated that none of the clusters were superior with respect to all the characters studied. All the minimum and maximum cluster mean values were distributed in relatively distant clusters.

Sankar *et al*. (2005) assessed the nature and magnitude of genetic divergence among 34 genotypes for eight characters using Mahalanobis D^2 statistics. The genotypes were grouped into seven clusters. Days to 50% flowering, single plant yield and grains per panicle were the major characters contributing towards divergence.

Senapati and Sarkar (2005) studied the genetic divergence in 40 tall indica rice genotypes and clustered them into five groups. Majority of the genotypes (30) were included in cluster I. Cluster II was second with six genotypes, while cluster III had only two genotypes. Cluster IV and V were the mono genotypic clusters. Cluster IV showed maximum genetic distance from cluster V suggested wide diversity between these groups. Panicle number per hill, panicle length, sterility percentage, yield per plot and 1000-grain weight was the chief contributors towards genetic divergence.

Sood *et al.* (2005) studied genetic divergence in 43 rice genotypes and grouped them into nine clusters. Cluster IV showed highest intra-cluster distance. Based on the mean performance, genetic distance and clustering pattern, hybridization involving genotypes HPR 824 and KC 1 (Achhoo) are likely to give desirable segregants for yield and its component traits.

Suman *et al.* (2005) grouped 114 rice genotypes into 10 clusters by using Mahalanobis D^2 statistic. The maximum inter-cluster distance was observed between clusters V and X. Harvest index gave the highest contribution towards divergence followed by seed density and total number of tillers per plant. Geographical diversity did not relate to genetic diversity.

Vaithiyalingan (2005) studied 29 strains of rice collected from different geographical regions of world to analyze the extent of genetic divergence and grouped them into four clusters. The clustering pattern was independent of the geographical distribution, cluster II included 23 genotypes and those can be useful in hybridization to create a wide spectrum of variability. Maximum distance was observed between clusters III and IV. Plant height, single plant yield and 1000-seed weight were found to be important contributors to genetic divergence.

Devi *et al*. (2006) evaluated genetic diversity in 54 rice cultivars for yield and yield components. The genotypes were grouped into nine clusters. Cluster VI recorded high mean values for plant height (140.33 cm), flag leaf length (48.11 cm) and flag leaf width (2.10 cm). Plant height contributed the most to genetic divergence (40.16%), followed by flag leaf width (20.12%), yield per plant (15.79%).

Mundhe *et al*. (2006) studied genetic diversity in 39 rice genotypes and grouped them into seven clusters. Intra-cluster distance was maximum in cluster III followed by cluster II and cluster I. Inter-cluster distance was maximum between cluster V and VII followed by cluster III and V, and cluster II and V.

Naik *et al*. (2006) studied genetic divergence to estimate the nature and magnitude of diversity in 50 aromatic rice accessions and grouped them into 7 clusters. The cluster VI had the highest mean for grain yield per plant and for biological yield per plant. Inter-cluster distance was recorded highest between cluster III and cluster IV. The conclusion drawn by the cluster analysis is that in the studied population high variability observed between the genotypes in different clusters for different characters.

Ravinder *et al.* (2006) studied genetic divergence in 50 unscented rice genotypes for yield and grouped them in 3 and 4 clusters in normal and late-sown conditions, respectively. There was no relationship between clustering pattern and geographical distribution. Based on the high cluster mean and wide genetic distance, hybridization between superior genotypes of clusters Individuals (IR 36, Palman 579, BR 827, HKR 117, HKR 126, HKR 86-105, IR 64 and RP 2151-21-22) and cluster III (Govind and NDR 84) had been advocated to achieve high heterosis and high yielding segregants.

Reddy *et al*. (2006) assessed the genetic divergence in 64 early rice genotypes and the genotypes were grouped into 13 clusters. There was no relationship observed between geographical distribution and genetic diversity. Per cent contribution of characters, i.e. 1000-grain weight, plant height, grain yield per plant and number of spikelets per panicle was highest towards genetic divergence indicating that due consideration should be given to these characters while selecting parents from distant clusters for hybridization.

Sarkar *et al.* (2006) assessed the genetic divergence among 46 rice genotypes and grouped them into seven clusters. Cluster IV showed highest inter-cluster distance from Cluster VI which was immediately followed by Cluster III and Cluster VII. Highest intra-cluster distance was observed in Cluster V and lowest in Cluster I. The desirable yield and its contributing traits were distributed mainly in Cluster III followed by Cluster VII and Cluster I. The genotypes within Cluster III, VII and I may be used as parents in hybridization programme to develop high yielding line.

Singh *et al*. (2006) studied the genetic divergence in 52 traditional lowland rice genotypes by using Mahalanobis D^2 statistics and grouped into six clusters. Clusters II, III, and IV exhibited high values for most of the characters. Plant height, followed by leaf angle and leaf area, highly contributed to the formation of clusters. Clusters II, IV, and V showed maximum inter-cluster distances and high values of plant height, days to 50% flowering, panicle length, grain yield/plant and milling percent, may be used for initiating a hybridization programme.

Chandra *et al.* (2007) assessed the nature and magnitude of genetic divergence in 57 upland rice genotypes and grouped them into five clusters. The most divergent clusters were III and IV (D^2=3387.9) followed by III and V (D^2=2808.2) and clusters II and III (D^2=1908.7). The clustering patterns of the genotypes were quite at random indicating that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were 1000-grain weight, grain yield and biological yield.

Sandhyakishore *et al*. (2007) studied genetic divergence for different yield attributing traits in 70 rice genotypes and grouped them into nine different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related.

Sarawgi and Bisne (2007) worked on genetic divergence in 81 scented rice genotypes. Based on D^2 statistics genotypes were grouped into nine clusters. The genotypes from cluster II having desired mean for characters like hulling %, milling % and head rice recovery and panicle length; cluster VII having high value for kernel length and L/B ratio and cluster V low value for days to 50% flowering but highest value for grain yield Kg ha^1.

Kumar *et al*. (2008) estimated genetic divergence in 30 genetically diverse genotypes of rice by using Mahalanobis D^2 statistic and grouped them into eight clusters. The inter-cluster distance was highest between clusters V and VI. This indicates that the genotypes could be used in hybridization programme and are likely to exhibit high heterosis and possibility of throwing transgressive segregants in subsequent generations.

Ramya and kumar (2008) studied the genetic divergence in 50 genotypes of rice and formed them in to 11 clusters. Cluster I was the largest with 35 genotypes. The inter cluster distances were greater than intra cluster distances. The inter cluster distance between clusters IV and VIII recorded maximum distance (37.58), which indicates that the divergence among these clusters was the highest. Number of grains per panicle, number of productive tillers per plant and grain yield per plant showed high per cent contribution towards genetic divergence.

Arivoli *et al.* (2009) evaluated a total of 23 rice genotypes, which were grouped into 11 clusters based on D^2 analysis. Results revealed the presence of morphological differences between the genotypes.The characters like total number of grains per panicle, number of filled grain per panicle and plant height contributed maximum towards total genetic divergence.

Raut *et al*. (2009) grouped 40 rice genotypes into three clusters by using Mahalanobis D^2 statistic. Cluster I emerged as the largest with 36 genotypes. Cluster II had three genotypes while cluster III was mono genotypic. Investigation revealed the independence of the genetic diversity from the eco geographic distribution of the genotypes. Length to breadth ratio of grain followed by number of grains per panicle, length of grain and seed yield per plant exhibited the greater contribution to the genetic divergence among genotypes.

Rouf *et al*. (2009) used D^2 analysis to measure the genetic distance in 75 genotypes and grouped them into 11 clusters. Cluster VI, IX and X among themselves showed greater genetic separation. Though Cluster II and Cluster I had more strength which would help in achieving high genetic gain.

Sabesan *et al*. (2009) studied the genetic diversity in rice genotypes by using Mahalanobis D2 statistic and grouped them into 13 clusters. Cluster I with seven genotypes was the largest cluster followed by Cluster V with four genotypes. Clusters IV, VII, VIII, X, XI, XII and XIII were mono genotypic clusters. The maximum inter cluster distance (D^2 = 8235.56) was recorded between clusters II and III. 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 (42.71%) followed by days to first flower (25.62%) contributed maximum to total divergence.

Shahidullah *et al*. (2009) assessed the genetic divergence in 40 aromatic rices for grain quality and nutrition aspects. In multivariate analysis, genotypes were grouped into six clusters. The inter-cluster D^2 value was maximum (26.53) between I and VI followed by 21.28 (between I and V). Majority of the local aromatic rice varieties with smaller kernels were included in the cluster I. The cluster III contains Elai, sarwati and sugandha-1 with long-slender kernel and 'very good' appearance. Thus, these varieties can be used in breeding programme for improvement of germplasm.

Banumathi *et al.* (2010) found that genetic divergence is an efficient tool for the selection of parents used in hybridization programme. In the present study, fifty three rice genotypes consisting of high yielding rice varieties and IRRI germplasm lines were raised to identify diverse genotypes. They were evaluated for eight yield and yield attributing characters using D^2 analysis, to study the diversity pattern among the genotypes.

Padmaja *et al*. (2010) analysed the genetic divergence in 150 genotypes of rice by using Mahalanobis D^2 statistics revealed the existence of considerable diversity among the genotypes. On the basis of D^2 values, the genotypes were categorized into 13 clusters. Cluster XI was the largest consisting of 28 genotypes, while cluster I contained only two genotypes. Cluster I showed maximum inter-cluster distance with cluster IX indicating that the genotypes from these clusters may be used as potential donors in hybridization programme to obtain desirable recombinants.

Pandey and Anurag (2010) assessed the nature and magnitude of genetic divergence in 40 rice genotypes by using Mahalanobis D^2-statistics and grouped them into seven clusters. Cluster VI was the largest one containing 11 genotypes followed by cluster III with nine genotypes. Plant height, biological yield and test weight contributed considerably, accounting for 86.16% of total divergence. The highest inter-cluster distance was observed between cluster II and VII.

Reddy *et al*. (2010) estimated the genetic divergence in 50 rice genotypes and grouped into 11 clusters. Cluster IV was emerged as largest cluster with 12 genotypes. The highest inter-cluster distance was observed between clusters VIII and XI. The genotypes UPR-1840, PAU-3042-3-3-4, UPR-2554-9-1 and NDR-2062 were identified as genetically diverse parents. These genotypes may be used further as parents in hybridization programme.

Chaturvedi *et al*. (2011) assessed the nature and magnitude of genetic divergence in 35 rice genotypes by using Mahalanobis D^2 and grouped them into eight clusters. The panicle weight followed by effective tillers per plant and yield per plant contributed maximum towards divergence. The genotypes belonging to cluster VII could be utilized as diverse parent in hybridization program with the genotypes of clusters II and VIII respectively, to achieve greater variability in the segregating generations.

Dutta *et al*. (2011) studied the genetic divergence in 62 aromatic rice genotypes by using Mahalanobis D^2 statistics and grouped into eight clusters where, cluster I was largest containing 38 genotypes followed by cluster II with nine genotypes. Based on the inter cluster distance, the entries viz. Pankey, 60-Chali, Dudheswar, Sitabhog, Kalonunia, MTU-7029, Netaisail, Bhutmuri (Kelias) were selected which could be intercrossed to obtain high heterotic effect and also to recover desirable transgressive segregants.

Sharma *et al*. (2011) evaluated the genetic divergence using D^2 statistic in 63 rice genotypes and grouped them into eight different clusters, in which, cluster VII was the largest having 16 genotypes. Based on mean performance, genetic distances and clustering pattern, the genotypes; Pusa Basmati-1 and Taraori Basmati of cluster II, Sarju-52, Narendra Usar-3 and Narendra-80 of cluster IV, Badshah Bhog, MTU-7029 and BPT-5204 of cluster VI and Malviya-36, Kanakjeer and Super Basmati of cluster VIII proved to be promising for use in hybridization programme.

Vennila *et al*. (2011) carried out investigation with 41 rice genotypes to identify diverse genotypes. They were evaluated for nine yield and yield attributing characters using Mahalanobis D^2 statistics. The analysis of variance revealed significant differences among the genotypes for all the characters studied.

2.4 Character Association

Yield of paddy is a complex quantitative character controlled by many genes interacting with the environment and is the product of many factors called yield components. Selection of parents based on yield alone often misleading. Hence, the knowledge about relationship between yield and its contributing characters is needed for an efficient selection strategy for the plant breeders to evolve an economic variety. The information about phenotypic and genotypic interactions of various economic traits is the immense importance to a plant breeder for the selection and breeding of different genotypes with increasing yield potential.

NeWall and Eberhart (1961) reported that when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety.

Ravindranath *et al.* (1982) reported positive significant association of nunber of grains per panicle with 1000-grain weight.

Amirthadevarathinam (1983) studied correlation coefficients between grain yield and its component characters in some rice genotypes and reported significant negative correlation between grain yield and plant height.

Chauhan *et al.* (1986) reported significant positive relationship between yield and panicle length.

Suarez *et al.* (1989) reported that 1000-grain weight was highly correlated to grain yield.

Haque *et al.* (1991) reported negative non-significant association of grain yield per plant with number of productive tillars per plant.

Mirza *et al*. (1992) reported positive significant correlation between plant height and panicle length.

Chauhan *et al.* (1993) observed positive non-significant association of days to 50% flowering with plant height and panicle length and negative non-significant association of seed yield per plant with panicle length.

The association between plant height and panicle length was found significantly positive at genotypic level, indicating that higher panicle length could be found while selction is made in favour of higher plant height, which is in full support with the findings of Chaubey and Singh (1994).

Reddy *et al.* (1995) observed negative non-significant association of number of productive tillars per plant with 1000 grain weight and positive non-significant association of number of grains per panicle with 1000-grain weight.

Yolanda and Das (1995) reported positive non-significant association of number of productive tillars per plant with number of filled grains per panicle in rice.

Reddy *et al.* (1997) negative non-significant association of number of productive tillars per plant with 1000 grain weight and number of grains per panicle with 1000-grain weight and positive but non–significant association of panicle length with test weight.

Bhatti *et al.* (1998) reported significant positive association of grain yield with panicle length and 1000-grain weight in rice.

Chaudhary and Das (1998) reported negative non-significant direct correlation between grain yield with days to 50% flowering and plant height at both level but flag leaf width with only genotypic level.

Gupta *et al.* (1998) reported positive non-significant association of grain yield per plant with 1000-grain weight.

Kennedy and Rangasamy (1998) reported significant positive association of grain yield with harvest index and 1000-grain weight in rice.

Samonte *et al.* (1998) reported significant positive association of grain yield with number of filled grains per panicle in rice.

Babu (1999) observed positive non-significant association of days to 50% flowering with plant height and panicle length and negative non-significant association of seed yield per plant with panicle length.

Rao and Shrivastav (1999) observed positive and non-significant association of plant height with number of productive tillars per plant.

Vange *et al.* (1999) reported positive non-significant association of grain yield per plant with 1000-grain weight.

Sadhukhan and Chattopadhyay (2000) reported very strong genotypic correlation of yield per plant with test grain weight followed by grain length but negatively correlated with grain breadth. Grain length and grain width were negatively correlated. Elongation ratio had very strong positive correlation with grain length after cooking, grain length and test grain weight at both the genotypic and phenotypic level.

Kavitha and Reddi (2001) reported positive non-significant association of number of productive tillars with panicle length, 1000 grain weight and panicle length with 1000 grain weight.

Nayak *et al.* (2001) reported significant negative association of days to 50% flowering with 1000-grain weight, kernel length and L/B ratio, significant positive correlation of plant height with panicle length at both genotypic and phenotypic levels, significant positive correlation of grain yield with plant height, panicle number per plant, panicle length, total number of spikelets/panicle and total number of grain/panicle, kernel length with kernel breadth at both genotypic and phenotypic levels.

Prasad *et al.* (2001) revealed that paddy yield exhibited significant positive genetic association with number of grains panicle^{-1}, days to maturity, number of productive tillers per plant and 1000-grain weight.

Shanthi and Singh (2001) reported negative non-significant direct correlation was observed between grain yield with days to 50% flowering and plant height at both level but flag leaf width with only genotypic level.

Iftekharuddaula *et al.* (2002) reported positive and significant association of panicle length and 1000-grain weight with grain yield per plant both at genetic and phenotypic levels.

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

Suman (2003) reported that pflant height exhibited positive but non-significant association at both genotypic and phenotypic levels with seed yield per plant.

Surek & Beser (2003) observed significant positive association of grain yield with number of productive tillers per square meter and number of filled grains per panicle; negative significant association of grain yield with days to 50% flowering.

De *et al.* (2005) observed positive and significant association of number of number of productive tillers with number of filled grains per panicle in aromatic rice.

Madhavilatha *et al.* (2005a) reported the yield was positively associated with days to 50% flowering, plant height, number of effective tillers per plant, panicle length, number of grains per panicle, harvest index and 1000-grain weight. Non-significant associations were observed for yield and the quality parameters, indicating the ineffectiveness of simultaneous selection for improvement of yield and quality.

Nayak and Reddy (2005) reported positive significant correlation of kernel length with length/breadth ratio and cooked kernel length in both seasons but had negative significant correlation with elongation ratio during the kharif seasons. The elongation ratio had negative significant correlation with volume expansion and grain yield in both seasons.

Patil and Sarawgi (2005) observed positive and significant correlation of grain yield 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.

Qamar *et al.* (2005) reported highly significant negative genetic association of days-to-50% flowering and days-to-maturity with grain yield per plant.

Sarkar *et al.* (2005) observed positive association of grain yield per plant for all the characters except panicle length, 1000-grain weight, grain breadth, brown kernel breadth and brown kernel L/B ratio.

DeepaSankar *et al*. (2006) reported positive and significant correlation of single plant yield with days to 50 per cent flowering, productive tillers/plant, panicle length and grains/panicle and negative significant correlation of days to 50 per cent flowering with 1000-grain weight and its positive non-significant association with plant height.

Ramakrishnan *et al*. (2006) revealed positive and significant association of panicle length with 1000 grain weight and kernel length, significant negative association of days to 50% flowering with 1000-grain weight at both genotypic and phenotypic levels.

Tayeng and Singh (2006) observed a significant positive correlation of grain yield with all the characters at both the genotypic and phenotypic levels. Panicle length, followed by number of spikelets per panicle showed the highest positive correlation with yield. The number of days to 50% flowering had high positive correlation with the number of spikelets per panicle, panicle length and 1000-seed weight.

Zahid *et al.* (2006) revealed that paddy yield exhibited significant positive genetic association with number of grains panicle^{-1}, days to maturity and 1000-grain weight.

Agahi *et al.* (2007) observed that grain yield was significantly correlated with days to heading, total tillers, number of productive tillers , days to maturity , number of grain per panicle , flag leaf length , flag leaf width and plant height.

Mustafa and Elsheikh (2007) observed phenotypic correlations between grain yield and number of filled grains per panicle, number of panicles/m^2 and 1000-grain weight were 0.52, 0.36 and 0.27, respectively. These results suggested that improvement in yield could be attained by selecting rice plants for higher number of filled grains per panicle, number of panicles/m^2 and 1000-grain weight.

Anbumalarmathi and Nadarajan (2008) reported grain yield plant^{-1} had positive and significant association with productive tillers plant^{-1}, grains panicle^{-1}, 100 grain weight, root length, root dry weight, root:shoot ratio and harvest index and negative significant association of days to 50% flowering with grain yield and 1000-grain weight.

Karad and Pol (2008) reported the grain yield was positively correlated with almost all the characters except 1000-grain weight at both genotypic and phenotypic levels. Genotypic correlation estimates were higher than phenotypic correlation with grain yield plot^{-1}.

Kole *et al*. (2008) reported positive and significant correlation of grain yield with plant height, panicle number per plant, straw weight and harvest index but negative and significant correlation with days to 50% flowering at both genotypic and phenotypic levels. Plant height was significantly and positively correlated with panicle length.

Khan *et al*. (2009) reported positive and significant association of plant height with panicle length.

Sabesan *et al*. (2009) reported positive significant association of grain yield per plant with panicle length and productive tillers per plant at both genotypic and phenotypic levels. The 100 grain weight was positively significantly correlated with plant height, grains per panicle and grain breadth. Days to 50% flowering was positively significantly correlated with number of productive tillers while plant height was positively and significantly correlated with panicle length and kernel breadth.

Saravanan and Sabesan (2009) revealed that grain yield per plant had significant positive association with total number of tillers per plant, number of productive tillers per plant and grain breadth.

Satishchandra *et al*. (2009) revealed significant positive association of grain yield per plant with number of productive tillers per plant, 1000-grain weight, panicle length and number of grains per panicle.

Chakraborty *et al*. (2010) revealed significant positive genotypic correlation of yield/plant with plant height (0.21), panicles/plant (0.53), panicle length (0.53), effective grains/panicle (0.57) and harvest index (0.86). The panicle length was positively and significantly correlated with number of filled grains per panicle.

Nandan *et al*. (2010) identified strong positive association of yield with days to 50% flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility.

Pandey and Singh (2010) revealed that grain yield exhibited significant positive correlation with grains/panicle, spikelets/panicle and effective tillers/plant at maturity at both phenotypic and genotypic levels. Total tillers/plant had correlation with grain yield/plant at phenotypic level only. Significant negative genotypic correlation with days to 50% flowering and days to maturity revealed that early maturing types gave higher yields.

Yadav *et al.* (2010) reported that grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicle per plant, panicle length, number of spikelet's per panicle and test weight, negative significant correlation with days to 50% flowering whereas non-significant correlation with plant height at both genotypic and phenotypic levels.

Akhtar *et al.* (2011) noted negative non-significant association of plant height and positive significant correlation of 1000-grain weight with paddy yield at both phenotypic and genetic levels.

Babu *et al.* (2011) recorded characters like number of tillers/hill, number of spikelets/panicle and number of panicles/hill showed positive significant correlation with grain yield/hill at both genotypic and phenotypic levels.

Bagheri *et al.* (2011) revealed panicle length (r=0.818), the total number of spikelet per panicle, the number of filled grains per panicle, and the panicle number per plant correlated significantly with grain yield.

Fiyaz *et al*. (2011) stated that number of productive tillers, total spikelet per panicle, total biomass, days to 50 percent flowering and plant height had significant positive association with grain yield.

Laxuman *et al*. (2011) reported days to heading, days to 50 per cent flowering, number of productive tiller per plant, and panicle length had significant positive correlation with grain yield at both phenotypic and genotypic level. Days to 50% flowering was positively and non-significantly correlated with number of productive tillers whereas plant height was negatively and significantly correlated with productive tillers per hill.

Pal *et al*. (2011) observed positive and significant correlation of grain yield with test weight and L/B ratio.

Sadeghi (2011) suggested positive and significant correlation of grain yield with grains per panicle, days to maturity, panicle weight, the number of productive tillers per plant, days to flowering, plant height, panicle length, flag leaf width and flag leaf length. Plant height was positively and significantly correlated with panicle length, kernel length was negatively and significantly correlated with kernel breadth.

Singh *et al.* (2011) reported grain yield/plant was positively and significantly associated with panicle bearing tillers/plant, harvest-index, biological yield/plant, L/B ratio and significant positive correlation with 1000-grain weight in all environments and pooled level.

Yadav *et al.* (2011) studied the extent of genetic association between yield and its components. Grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicles per plant, panicle length, number of spikelet's per panicle and test weight at both genotypic and phenotypic levels and negative correlation with days to 50% flowering and plant height.

Babu *et al.* (2012) revealed significantly positive association of grain yield per plant with number of productive tillers per plant, negative significant correlation with days to 50% flowering. Plant height was significantly and positively correlated with panicle length and negatively with productive tillers per hill.

Haider *et al.* (2012) recorded positive and significant association of root length, root shoot, thousand grain weight, grains per panicle, spikelet fertility and drought response index with yield per plant under drought stress at genotypic level.

Rangare *et al.* (2012) noted grain yield was significantly and positively associated with biological yield per plant, number of fertile tillers per plant, number of spikelets per panicle, test weight, panicle length and days to maturity but non significantly associated with days to 50% flowering, days to initial flowering, harvest index and plant height.

Seyoum *et al.* (2012) reported days to 50% flowering, days to 85% maturity, plant height and 1000-grain weight had negative and non-significant correlation with grain yield both at genotypic and phenotypic levels.

2.5 Path Coefficient Analysis

Gomathinayagam *et al.* (1988) reported highest direct effect of plant height on grain yield in rice.

Chaudhary and Das (1998) for negative indirect effect of days to 50% flowering on grain yield through plant height.

Luzikihupi (1998) reported positive direct effect of 1000-grain weight on grain yield at both genotypic and phenotypic levels.

Samonte *et al.* (1998) noted high positive direct effect (0.407) of number of filled grain per panicle on yield. Its indirect effect via panicle length, the total number of spikelets per panicle and the number of panicle per plant was very high, whereas its effect via number of secondary branches per panicle was negative.

Kavitha and Reddi (2001) observed positive indirect effect of days to 50% flowering on grain yield through panicle length, plant height through days to 50% flowering and negative direct effect of number of productive tillers on grain yield.

Nagajyothi (2001) identified positive indirect effect of plant height on grain yield through panicle length and positive direct effect of panicle length on grain yield.

Nayak *et al.* (2001) reported highest positive direct effect of plant height, number of productive tillers, 1000-grain weight, grain number and kernel length on grain yield per plant and also reported negative direct effect of days to 50% flowering and panicle length on grain yield.

Prasad *et al.* (2001) revealed that the number of fertile grains/panicle had the highest positive direct effect on grain yield followed by days to maturity, 1000-grain weight and panicle length and also observed negative direct effect of days to 50% flowering on grain yield.

Babu *et al.* (2002) recorded highest positive direct effect of plant height on single plant yield via positive indirect effect of panicle length, number of grains/panicle and spikelet fertility. Selection based on these characters would be efficient.

Madhavilatha (2002) reported positive indirect effect of days to 50% flowering on grain yield through plant height and 1000-grain weight.

Chaudhary and Motiramani (2003) observed a greater contribution of effective tillers per plant, spikelet density and biological yield per plant towards grain yield.

Khedikar *et al*. (2004) noted positive direct effect of number of productive tillers and days to 50% flowering on grain yield.

Madhavilatha *et al*. (2005a) identified the number of effective tillers per plant, plant height and harvest index exhibited high positive direct effects while negative direct effect of panicle length on grain yield. High indirect effects of the different yield component and quality traits were also noticed through plant height and harvest index.

Patil and Sarawgi (2005) reported positive direct effect of 1000-grain weight on grain yield, followed by number of ear-bearing tillers per plant, number of filled grains per panicle, and number of days to 50% flowering. However, 1000-grain 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 panicle and plant height.

Qamar *et al.* (2005) suggested that productive tillers per hill, days to maturity and days to 50% flowering may be considered important for the improvement of grain yield in the non-aromatic group whereas productive tillers per hill, spikelets per panicle, fertility per cent and plant height may be considered as the selection criteria for the direct improvement of grain yield in the aromatic group.

Sarkar *et al.* (2005) observed the greatest direct effect of number of panicles per plant on grain yield per plant, followed by number of grains per panicle; however, the number of panicles per plant was negatively associated with number of grains per panicle.

DeepaSankar *et al*. (2006) recorded that correlated traits except panicle length exhibited high positive direct effects towards single plant yield.

Ramakrishnan *et al*. (2006) revealed highest positive direct effect of number of filled grains per panicle, kernel length, L/B ratio and 1000-grain weight but negative direct effect of panicle length on grain yield.

Tayeng and Singh (2006) observed direct effects for the number of grains per panicle, harvest index and panicle length on grain yield. Panicle weight, number of spikelets per panicle and number of effective tillers had negative direct effects on grain yield.

Zahid *et al*. (2006) reported highest positive direct effect of number of filled grains per panicle and negative direct effect of number of productive tillers per plant on grain yield.

Agahi *et al.* (2007) noticed that the number of productive tillers had the highest positive direct effect on grain yield (p_p=1.034, p_g=1.196). The second and third traits were the number of grain per panicle (p_p=0.665, p_g=0.813) and 100-grain weight (p_p=0.440, p_g=0.425) respectively.

Ashwani *et al.* (2007) recorded that the grain yield per panicle, days to 50% flowering, number of effective tillers per plant had the highest positive direct effect on grain yield.

Mustafa and Elsheikh (2007) assessed that number of filled grains per panicle had direct positive (0.87) contribution to the grain yield/ha and positive (0.33) indirect effect on grain yield/ha through days to 50% maturity and number of grains per panicle (0.089), while the number of filled grains per panicle had negative (-0.30) and (-0.21) indirect effect on grain yield/ha through number of tillers per plant and number of panicles/m^2, respectively.

Anbumalarmathi and Nadarajan (2008) reported positive direct of number of productive tillers and 1000-grain weight on grain yield, negative direct effect of days to 50% flowering on grain yield.

Chaturvedi *et al.* (2008) noted positive direct effect of 1000-grain weight on grain yield at both genotypic and phenotypic levels.

Karad and Pol (2008) identified that length of panicle had the highest positive direct effect followed by number of panicles, number of tillers plant^{-1} and number of mature panicles whereas the characters plant height, number of immature panicles and 1000 grain weight had the negative direct effect via indirect effect on grain yield plot^{-1}.

Kole *et al.* (2008) revealed that panicle number had the highest positive direct effect followed by grain number, test weight, plant height, days to flower and straw weight on grain yield. Panicle length had negative direct effect on grain yield.

Rokonuzzman *et al.* (2008) reported positive direct effect of number of productive tillers per hill on grain yield.

Khan *et al.* (2009) observed highest positive direct effect of number of filled grains per panicle and negative direct effect of number of productive tillers per plant on grain yield.

Krishnappa *et al.* (2009) observed poor direct effect (0.224) of plant height. Tillers per plant showed negative direct effects (-0.1492), panicle length showed high direct effects (0.4124), grain number per panicle showed direct effect (0.0788) and 100-grain weight showed positive low direct effects (0.0355) on grain yield.

Saravanan and Sabesan (2009) revealed that grain breadth, grain L/B ratio and total number of tillers per plant had the highest direct effect on grain yield per plant, suggesting that the improvement in grain yield could be efficient if the selection is based on these component traits.

Satishchandra *et al.* (2009) noticed that number of grains per panicle, days to 50% flowering, 1000-grain weight and number of productive tillers per plant have shown high positive direct effects and panicle length had negative direct effect on grain yield.

Chakraborty *et al.* (2010) reported positive direct effect of plant height, 1000-grain weight and panicle length on grain yield.

Hairmansis *et al*. (2010) revealed highest positive direct effect of number of filled grains per panicle on grain yield.

Nandan *et al.* (2010) recorded that the number of grains per panicle had maximum direct effect on grain yield per plant followed by kernel length after cooking (KLAC), days to 50% flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking (KBAC).

Pandey and Singh (2010) studied highest positive direct effect of grain length on grain yield, followed by effective tillers/plant at maturity, grains/panicle, protein content, plant height at maturity, amylose content and days to maturity at genotypic level was observed whereas length:breadth ratio had a negative direct effect.

Yadav *et al.* (2010) revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of spikelets per panicle, plant height and test weight had direct positive effect on seed yield per hill, whereas days to 50% flowering had negative direct effect on grain yield.

Akinwale *et al.* (2011) reported significant positive correlation of grain yield with the number of tillers per plant (r = 0.58**), panicle weight (r =0.60*) and number of grains per panicle (r=0.52*). Therefore, the results suggest that these traits can be used for grain yield selection.

Babu *et al.* (2011) noted number of tillers/hill and number of spikelets/panicle had maximum direct effect on grain yield/hill at both genotypic and phenotypic levels.

Bagheri *et al.* (2011) observed that panicle length had the highest positive direct effect (0.510) on grain yield. Grain yield linearly correlated with panicle length, the number of panicles per plant, and the number of filled grains per panicle. Therefore, these traits may be used in the selection for grain yield in rice.

Laxuman *et al*. (2011) revealed that number of tillers per plant (2.559), panicle weight (0.882), days to 50% flowering (0.856), shoot length at 21 days (0.378) and spikelet fertility (0.088), had high direct effect on seed yield.

Pal *et al*. (2011) reported test weight, L:B ratio, harvest index spikelets per panicle, panicle length, panicle bearing tillers per plant and days to 50% flowering had direct effect on grain yield per plant.

Sadeghi *et al*. (2011) recorded that the number of productive tillers had the highest positive direct effect followed by days to maturity, plant height, grains per panicle and 1000-grain weight.

Singh *et al*. (2011) reported harvest index had the highest positive direct effect followed by biological yield/plant and kernel length on grain yield/plant in all environments and pooled level.

Yadav *et al*. (2011) revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of spikelets per panicle, plant height and test weight had direct positive effect on seed yield while days to 50% flowering had negative direct effect on grain yield.

Haider *et al.* (2012) noticed positive direct effect of 1000-grain weight and its positive significant genetic correlation with grain yield per plant.

Rangare *et al*. (2012) reported that biological yield per plant (1.0284 and 1.0216), harvest index (0.6381 and 0.6291), number of fertile tiller per plant (0.1058 and 0.1048), days to 50% flowering (0.0806 and 0.0756), test weight (0.0353 and 0.0338), days to maturity (0.0022 and 0.0076) and panicle length (0.0007 and 0.0002) had high direct effect on grain yield per plant while days to initial flowering (-0.0644 and -0.0676), number of spikelets per panicle (-0.0483 and -0.0359), plant height (-0.0106 and -0.0170) had negative direct effect on grain yield per plant on genotypic and phenotypic level.

Chapter III

MATERIAL AND METHODS

3.1 Experimental Site, Design and Layout

Present investigations were conducted at the Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad, India. Seventy five soft rice genotypes were characterized for 62 agro-morphological parameters and the same set of genotypes were used for genetic diversity study. They were evaluated during *kharif* 2013. The experiment site is geographically situated at 17.5°N latitude and 78.27°E longitude with an altitude of 545 metres above the sea level. The experiment was laid out in a Randomized Block Design with three replications during the season. Thirty days old seedlings were transplanted at the rate of one seedling per hill in three rows of five metre length with plant to plant distance of 15 cm and row to row distance of 20 cm. The standard cultivation practices prescribed for rice under irrigated conditions were followed precisely. The layout of the experiment was shown in figure 3.2.

3.2 Recording of Observations

Five random plants were selected from central rows and the data was recorded in each replication on these five plants for characterization as well as diversity studies. The 62 agro-morphological characters studied were those given in DUS characterization of rice varieties (Subbarao *et al*. 2013) as per the national test guidelines, and the details of each character studied are presented in table 3.3. Nine yield components were recorded for genetic diversity analysis and the mean values were considered for statistical analysis.

3.3 Details of the Experimental Material

The experimental material consist of seventy five soft rice genotypes obtained from the germplasm collections maintained at Directorate of Rice Research, Rajendranagar, Hyderabad and these genotypes were primarily collected from the north eastern region of Assam. The soft rice lines were given the notation as SR and the names of these soft rices were mentioned in table 3.1 and some of the lines were shown in figure 3.1.

Table 3.1. Details of soft rice genotypes used in the study

S.No.	Soft rice line number	Local name of the genotype during collection
1	SR-1	Joha bora
2	SR-2	Ranga bora
3	SR-3	Sungal bora
4	SR-4	Noldong bora
5	SR-5	Tegori bora
6	SR-6	Bongari bora
7	SR-7	Kola ampaki bora
8	SR-8	Bora-1
9	SR-9	Dadhora bora
10	SR-10	Chokura bora
11	SR-11	Sakoibhanu bora
12	SR-12	Kola bora
13	SR-13	Misiri chakua
14	SR-14	Boka chakua
15	SR-15	Ch-5 bora chakua
16	SR-16	Kagori chakura
17	SR-17	Kola boka chakura
18	SR-18	Haru chakua
19	SR-19	Boga chakua
20	SR-20	Lahi chakua
21	SR-21	Sam chakua
22	SR-22	Maju chakua
23	SR-23	Ham chakua
24	SR-24	Hampori chakua
25	SR-25	Malbhog
26	SR-26	Helochi
27	SR-27	Kalamdani
28	SR-28	Dadhora
29	SR-29	Aghoni bora
30	SR-30	Bhogali bora
31	SR-31	Abor bora
32	SR-32	Beji bora1
33	SR-33	Begun bora
34	SR-34	Boga bora1
35	SR-35	Boga bora 3

Table 3.1 (cont.).

36	SR-36	Bhat bora
37	SR-37	Bora 1
38	SR-38	Bora 3
39	SR-39	Bora 5
40	SR-40	Botia bora
41	SR-41	Bor malbhog
42	SR-42	Chakkua bora 1
43	SR-43	Chansep bora
44	SR-44	Chandra bora
45	SR-45	Danbori bora
46	SR-46	Fakkai bora
47	SR-47	Gela bora
48	SR- 48	Ghew bora 1
49	SR-49	Garu chakua bora 2
50	SR-50	Gomiri bora
51	SR-51	Naldang bora
52	SR-52	Helochi bora 1
53	SR-53	Helochi bora 2
54	SR-54	Aghoni
55	SR-55	Bhogali
56	SR-56	KMJ bora 56
57	SR-57	KMJ bora 53
58	SR-58	KMJ bora 51
59	SR-59	KMJ bora 41
60	SR-60	KMJ bora 36
61	SR-61	KMJ bora49
62	SR-62	KMJ bora 74
63	SR-63	KMJ bora 5
64	SR-64	KMJ bora 13
65	SR-65	KMJ bora 21
66	SR-66	KMJ bora 25
67	SR-67	Boka chakua 1
68	SR-68	Boka chakua 2
69	SR-69	Kajoli chakua
70	SR-70	Kalamdani chakua
71	SR-71	Lahi chakua1
72	SR-72	Maju chakua 1
73	SR-73	Maju chakua 2
74	SR-74	Misiri chakua
75	SR-75	Sam chakura

3.4 Collection of Experimental Data for Characterization:

The total of 62 agro-morphological and quality traits were studied as per the DUS testing guidelines of rice (Subbarao *et.al.*, 2013) based on UPOV guidelines and data was collected on 62 DUS testing traits for each replication at different growth stages of the crop (Table 3.2). The characters which were evaluated and the notes for each character were given in (Table 3.3).

Table 3.2. Decimal code for growth stages

Decimal code		Growth stage
10	:	After germination, emergence of first leaf through coleoptile / second leaf visible (less than 1 cm)
40	:	Booting : the increase in the size of the young panicle and its inward extension inside the upper leaf sheaths detectable as a bulge in the rapidly elongating Culm
50	:	1st spikelet of inflorescence just visible
55	:	½ of inflorescence emerged
60	:	Beginning of anthesis : it begins with the protrusion of the first dehiscing anthers in the terminal spikelets on the panicle branches
65	:	Anthesis half way
70	:	Milk development stage – formation of white milky sap within the spikelets.
80	:	Dough development (spikelets become hard)
90	:	Ripening (terminal spikelets ripened)
92	:	Caryopsis hard (can be no longer be dented by thumb nail and over 90% spikelets ripened)

Type of assessment of characteristics may be:

MG : Measurement by a single observation of a group of plants or parts of plants

MS : Measurement of a number of individual plants or parts of plants

VG : Visual assessment by a single observation of a group of plants or parts of plants

VS : Visual assessment by observation of individual plants or parts of plants

Table 3.3. Table of DUS characteristics

S.No.	Characteristics	States	Note	Stage of observation	Type of assessment
1.	Coleoptile: colour	colourless green purple	1 2 3	10	VS
2. (*)	Basal leaf: sheath colour	green light purple purple lines purple	1 2 3 4	40	VS
3.	Leaf: intensity of green colour	light medium dark	3 5 7	40	VG
4.	Leaf: anthocyanin colouration	absent present	1 9	40	VG
5.	Leaf : distribution of anthocyanin colouration	on tips only on margins only in blotches only uniform	1 2 3 4	40	VG
6.	Leaf sheath: anthocyanin colouration	absent present	1 9	40	VG
7.	Leaf sheath : intensity of anthocyanin colouration	very weak weak medium strong very strong	1 3 5 7 9	40	VG
8. (*)	Leaf: pubescence of blade surface	absent weak medium strong very strong	1 3 5 7 9	40	VS
9. (*)	Leaf : auricles	absent present	1 9	40	VS
10. (*)	Leaf: anthocyanin colouration of auricles	colourless light purple purple	1 2 3	40	VS
11.	Leaf: collar	absent present	1 9	40	VS

Table 3.3 (cont.).

12.	Leaf: anthocyanin colouration of collar	absent present	1 9	40	VS
13.	Leaf: ligule	absent present	1 9	40	VS
14. (*)	Leaf: shape of ligule	truncate acute split	1 2 3	40	VS
15 (*).	Leaf: colour of ligule	green light purple purple	1 2 3	40	VS
16.	Leaf: length of blade	short medium long	3 5 7	40	MS
17.	Leaf: width of blade	narrow medium broad	3 5 7	40	MS
18.	Culm: attitude (for floating rice only)	non procumbent procumbent	1 9	40	VS
19.	Culm: attitude	erect semi-erect open spreading	1 3 5 7	40	VS
20. (*)	Time of heading (50% of plants with panicles)	very early (<71 days) early (71-90 days) medium (91-110 days) late (111-130 days) very late (>130 days)	1 3 5 7 9	55	VG
21. (*)	Flag leaf: attitude of blade (early observation)	erect semi-erect horizontal deflexed	1 3 5 7	60	VG
22. (*)	Spikelet: density of pubescence of lemma	absent weak medium strong very strong	1 3 5 7 9	60-80	VS
23.	Male sterility	absent present	1 9	65	VG

Table 3.3 (cont.).

24.	Lemma: anthocyanin colouration of keel	absent or very weak weak medium strong very strong	1 3 5 7 9	65	VS
25.	Lemma: anthocyanin colouration of area below apex	absent weak medium strong very strong	1 3 5 7 9	65	VS
26. (*)	Lemma: anthocyanin colouration of apex	absent weak medium strong very strong	1 3 5 7 9	65	VS
27. (*)	Spikelet: colour of stigma	white light green yellow light purple purple	1 2 3 4 5	65	VS
28.	Stem: thickness	thin medium thick	3 5 7	70	VS
29. (*)	Stem: length (excluding panicle; excluding floating rice)	very short (<91 cm) short (91-110 cm) medium (111-130 cm) long (131-150 cm) very long (>150 cm)	1 3 5 7 9	70	VS
30. (*)	Stem: anthocyanin colouration of nodes	absent present	1 9	70	VS
31.	Stem : intensity of anthocyanin colouration of nodes	weak medium strong	3 5 7	70	VS
32.	Stem: anthocyanin colouration of internodes	absent present	1 9	70	VS

Table 3.3 (cont.).

33. (*)	Panicle: length of main axis	very short (<16 cm) short (16-20 cm) medium (21-25 cm) long (26-30 cm) very long (>30 cm)	1 3 5 7 9	70-90	MS
34. (*)	Flag leaf: attitude of blade (late observation)	erect semi-erect horizontal deflexed	1 3 5 7	90	VG
35. (*)	Panicle: curvature of main axis	straight semi-straight drooping deflexed	1 3 5 7	90	VG
36.	Panicle: number per plant	few (<11) medium (11-20) many (>20)	3 5 7	80-90	MS
37. (*)	Spikelet : colour of tip of lemma	white yellowish brown red purple black	1 2 3 4 5 6	80-90	VS
38.	Lemma and Palea: colour	straw gold and gold furrows on straw background brown spots on straw brown furrows on straw brown (tawny) reddish to light purple purple spots on straw purple furrows on straw purple black	1 2 3 4 5 6 7 8 9 10	80-90	VG

Table 3.3 (cont.).

39. (*)	Panicle : awns	absent present	1 9	90	VG
40. (*)	Panicle: colour of awns (late observation)	yellowish white yellowish brown brown reddish brown light red red light purple purple black	1 2 3 4 5 6 7 8 9	90	VS
41.	Panicle: length of longest awn	very short short medium long very long	1 3 5 7 9	90	VG-MS
42. (*)	Panicle: distribution of awns	tip only upper half only whole length	1 3 5	90	VS
43.	Panicle: presence of secondary branching	absent present	1 9	90	VG
44.	Panicle: secondary branching	weak strong clustered	1 2 3	90	VG
45. (*)	Panicle: attitude of branches	erect erect to semi-erect semi-erect semi-erect to spreading spreading	1 3 5 7 9	90	VG
46. (*)	Panicle: exsertion	partly exserted exserted well exserted	3 5 7	90	VG
47.	Time of maturity	very early early medium late very late	1 3 5 7 9	90	VG
48.	Leaf: senscence	early medium late	3 5 7	92	VG

Table 3.3 (cont.).

49. (*)	Sterile lemma: colour	straw gold red purple	1 2 3 4	92	VS
50.	Grain: weight of 1000 fully developed grains	very low low medium high very high	1 3 5 7 9	92	MG
51.	Grain: length	very short short medium long very long	1 3 5 7 9	92	MS
52.	Grain: width	very narrow narrow medium broad very broad	1 3 5 7 9	92	MS
53.	Grain: phenol reaction of lemma	absent present	1 9	92	VG
54. (*)	Decorticated grain: length	very short short medium long very long	1 3 5 7 9	92	MS
55. (*)	Decorticated grain: width	narrow (<2.0 mm) medium (2.0-2.5 mm) broad (>2.5 mm)	3 5 7	92	MS
56. (*)	Decorticated grain: shape (in lateral view)	short slender short bold medium slender long slender long bold extra long slender	1 2 3 4 5 6	92	MS

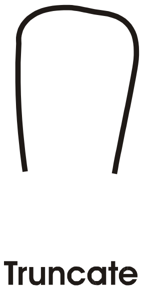
57. (*)	Decorticated grain: colour	white light brown variegated brown dark brown light red red variegated purple purple dark purple	1 2 3 4 5 6 7 8 9	92	VG
58.	Endosperm: presence of amylose	absent present	1 9	92	MG
59. (*)	Endosperm: content of amylose	very low (<10%) low(10-19%) medium(20-25%) high(26-30%) very high (>30%)	1 3 5 7 9	92	MG
60.	Varieties with endosperm of amylose absent only Polished grain : expression of white core	absent or very small smal medium large	1 3 5 7	90	MG
61.	Gelatinization temperature through alkali spreading value.	low medium high medium high	1 3 5 7	92	MG
62. (*)	Decorticated grain: aroma	absent present	1 9	92	MG

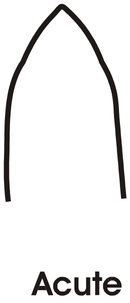
Note: (*) indicates that Characteristics should be used on all varieties in every growing season over which examinations are made and always be included in the variety descriptions, except when the state of expression of a preceding characteristic or regional conditions render this impossible.

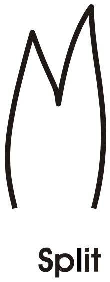
3.4.1 Discription of some essential characters

3.4.1.1 Leaf shape of ligule

It is the joint between the leaf sheath and blade. The scores of the ligule shape were given as 1 for truncate, 2 for acute and 3 as split.







3.4.1.2 Flag leaf attitude of blade (early observation)

It is the observation of flag leaf (i.e. penultimate leaf from top) bending in relation to panicle base at booting stage. If the angle of bending is 0-30^0 at full blooming is rated as erect, 31-60^0 as semi erect, 61-90^0 as horizontal and 91^0 or more as deflexed and it is observed at beginning of anthesis stage.

3.4.1.3 Panicle length of main axis

Length of panicles from each plant was measured in centimeters from neck to the tip of the panicle and the mean was computed. The scores were given as 1 for very short (< 16 cms), 3 for short (16-20 cms), 5 for medium (21-25 cms), 7 for long (26-30 cms) and 9 for very long (> 30 cms) and is observed at milk development stage to ripening stage.

3.4.1.4 Panicle number per plant

The number of panicles was counted at the time of physiological maturity and is categorized as few (which measures less than 10), medium (which measures between 11-20) and high (which measures more than 20) and is observed at dough development to ripening stage.

3.4.1.5 Panicle awns

It is a filiform extension of varying lengths from the keel (middle nerve) of the lemma and is observed at ripening stage.

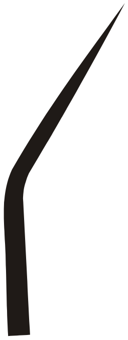
3.4.1.6 Sterile lemma colour

It is the two flowerless bracts at the base of the spikelet. The two sterile lemma may differ in length shape and colour and observed at caryopsis hard stage.

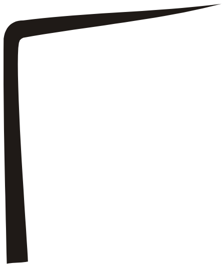
3.4.1.7 Flag leaf attitude of blade (late observation)

It is the observation of flag leaf (i.e. penultimate leaf from top) bending in relation to panicle base at booting stage. If the angle of bending is 0-30^0 at full blooming is rated as erect, 31-60^0 as semi erect, 61-90^0 as horizontal and 91^0 or more as deflexed and is observed at ripening stage.

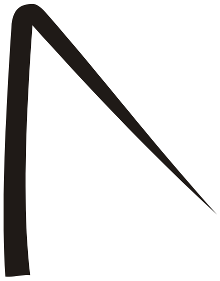
Erect



Semi-erect



Horizontal



Deflexed

3.4.1.8 Panicle attitude of branches

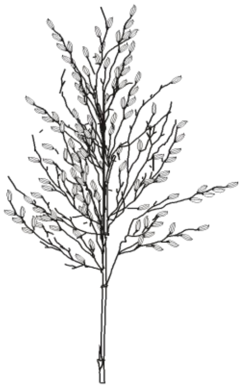
It is observed as bending of the branches from panicle base at ripening stage.

Erect

Erect to semi-erect

Semi -erect

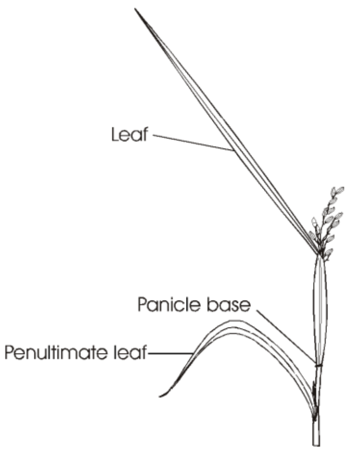
semi-erect to spreading



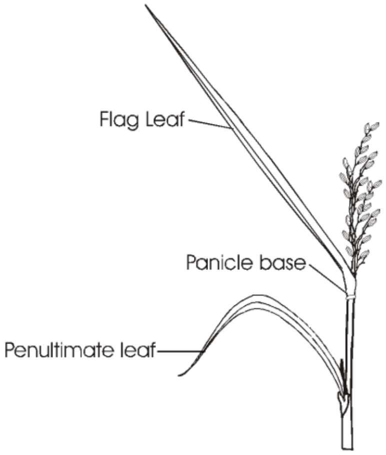
Spreading

3.4.1.9 Panicle exsertion

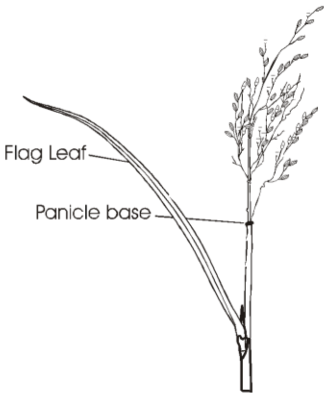
It is the exsertion of panicle from the panicle base. If the panicle is less than 80% exserted from base, it is treated as partly exserted, and if the panicle is exserted between 81-99%, then it is treated as mostly exserted and if the panicle is exserted 100%, it is treated as well exserted observed at ripening stage.



Partly exserted



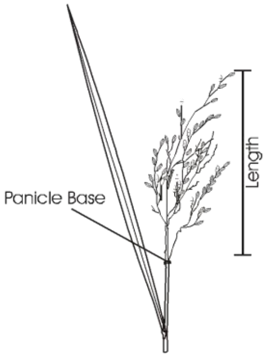
Mostly exserted



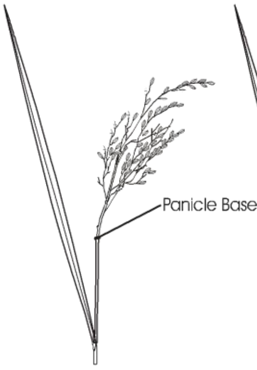
Well exserted

3.4.1.10 Panicle curvature of main axis

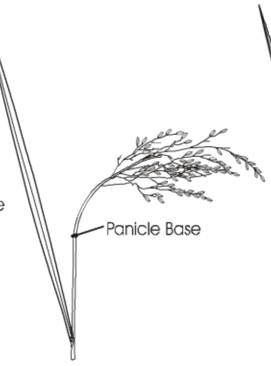
It is the bending of panicle base to the last spikelet. It is noted as straight, semi straight, horizontal and deflexed and is observed at ripening stage.



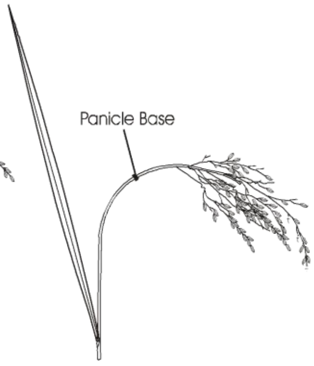
Straight



Semi-straight



Deflexed



Drooping

3.4.1.11 Amylose content (%)

Amylose is the linear fraction of starch in the non-glutinous genotypes. Amylopectin, the branch fraction makes up the remainder of the starch. Amylose content has a major influence on the texture of cooked milled rice.

For standard curve, 40mg of potato amylase was wetted with 1ml ethyl alcohol and 9ml of 1N NaOH heated for 5-10 minutes in a boiling water bath, cooled and made upto 100ml with distilled water. 1,2,3,4, and 5ml solution was taken followed by 0.2, 0.4, 0.6, 0.8 and 1.0ml of 1N acetic acid and 2ml Iodine solution + KI and factor was derived as per Juliano, 1971. for amylase estimation of the rice sample, 100mg rice flour passed through 100mm sieve was taken in a test tube (2×19.5 cm), 1ml rectified spirit and 9ml of 1N NaOH was added to it and the mixture was shaken well. The tubes were heated over water bath for 15 minutes and the contents were transferred to 100ml volumetric flask and the volume made upto 100ml with distilled water. From this, 5ml of solution was taken in 100ml volumetric flask (in three replications) and 1ml acetic acid and 2ml $KI+I_2$ reagent were added and the final volume was made upto 100ml. These flasks were covered with black cloth for color development and after 20 minutes, the transmission values at 620 nm were recorded. Then the amylose content of the sample was calculated by multiplying the mean of the transmission values of that sample with the factor calculated by using the standard curve and expressed as percentage.

3.4.1.12 Alkali Spreading Value (Gelatinizing temperature)

Time required for cooking is determined by the gelatinization temperature. Gelatinization temperature, a physical property of starch, is the range of temperature within which the starch granules begin to swell irreversibly in hot water. The gelatinization temperature ranges from 55 to 79°C and is divided into three main groups: low (< 70°C), intermediate (70-74°C) and high (75-79°C). Gelatinization temperature is estimated by the extent of alkali spreading and clearing of milled rice soaked in 1.7% KOH for 23 hours at room temperature. Rice with low gelatinization temperature disintegrate completely, whereas, rice with intermediate gelatinization temperature show only partial disintegration. Rice with high gelatinization temperature remains largely unaffected in the alkali solution.

Six whole milled grains per replication were spread evenly in transparent plastic boxes containing 10ml of 1.7 percent potassium hydroxide solution (KOH). These boxes were kept undisturbed in an incubator at 23- 30°C for 23 hours. The alkali spreading of kernals noted on a 7 point scale. Scoring was done as follows

1 - Kernel not affected
2 - Kernel swollen
3 - Kernel swollen, collar incomplete and narrow
4 - Kernel swollen, collar complete and wide
5 - Kernel split or segmented, collar complete wide
6 - Kernel dispersed, merging with collar
7 - Kernel completely dispersed and intermingled

According to alkali spreading score, the gelatinization temperature of the entries was classified as follows:

Alkali spreading value	Rating	GT
1-2	Low	High
3	Low Intermediate	High
4-5	Intermediate	Intermediate
6-7	High	low

3.5 Collection of Experimental Data for Genetic Diversity:

For recording observations on yield components panicles from five labeled plants were harvested separately from each replication.

3.5.1 Yield characters

3.5.1.1 Days to fifty per cent flowering

The total number of days taken from the date of sowing to complete exersion of the panicle in fifty per cent of the total plants in the net plot.

3.5.1.2 Plant height (cm)

Plant height was measured in centimeters from ground level to the tip of the mother panicle in each plant at the time of harvest.

3.5.1.3 Number of tillers per plant

The total number of tillers produced by the plant.

3.5.1.4 Number of productive tillers per plant

Number of panicle bearing tillers per plant was counted at the time of harvest.

3.5.1.5 Panicle length

Length of panicles from each plant was measured in centimeters from neck to the tip of the panicle and the mean was computed.

3.5.1.6 Per cent filled grains per panicle

The ratio of number of filled grains to the total number of grains in the panicle, was counted from five panicles in each selected plant and the mean was taken.

3.5.1.7 Days to maturity

The numbers of days from date of sowing to till complete ripening of the grains in panicle is recorded.

3.5.1.8 Seed yield per plant (g)

The weight of filled grains harvested from each plant was recorded in grams after bringing the grains to required moisture content.

3.5.1.9 Test weight (g)

One thousand well filled grains were counted at random from each plant and weighed, after thorough drying to 15 per cent moisture content.

3.6 Statistical Procedure

The mean values with respect to the above characters were subjected to the following analysis with the help of standard statistical procedures:

1. Analysis of variance
2. Genotypic and phenotypic coefficients of variation
3. Heritability and genetic advance
4. Estimation of genetic divergence using Mahalanobis's generalized distance (D^2)
5. Estimation of correlation coefficients.
6. Direct and indirect effects of characters using path coefficient analysis.

3.6.1 Analysis of Variance

Analysis of variance was computed based on randomized block design for each of the character separately as per standard statistical procedure (Panse and Sukhatme, 1985). The significance was tested by referring to the values of ‘F’ table (Fisher and Yates, 1963).

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where ,

Y_{ij}= phenotypic observation of i^{th} genotype and j^{th} replication

μ=general mean

g_i =effect of i^{th} genotype

r_j =effect of j^{th} replication

e_{ij} = random error associated with i^{th} genotype and j^{th} replication

Analysis of variance:

Source	**Degrees of freedom**	**Mean sum of squares**	**F-ratio**
Replication	(r-1)	M’s	M’s/M’e
Treatment	(t-1)	M’t	M’t/M’e
Error	(r-1)(t-1)	M’e	
Total	(tr-1)	TMSS	

Where,

r and t = Number of replications and treatments, respectively.

M’s, M’t and M’e = Mean sum of squares due to replications, treatments and error respectively.

Variance

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{(Mean sum of squares due to treatments – Mean sum of squares due to error)}}{\text{Number of replications}}$$

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

$(\sigma^2_e) =$ error variance

3.6.2 Genotypic and Phenotypic Coefficients of Variance

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973).

<10%	:	Low
10-20%	:	Moderate
>20%	:	High

3.6.3 Heritability and Genetic Advance

Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

$$h^2_{(bs)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

$h^2_{(bs)}$ = heritability in broad sense

σ^2_g = genotypic variance

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

σ^2_e = environmental variance

As suggested by Johnson *et al.* (1955) (h^2) estimates were categorized as:

Low : 0-30%

Medium : 30-60%

High : above 60%

Genetic advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K.\ h^2_{(bs)}.\ \sigma_p$$

Where,

GA = expected genetic advance

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

σ_p = phenotypic standard deviation

$h^2_{(bs)}$ = heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent for mean was computed.

$$\text{Genetic advance as percent of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al*. (1955)

Low	:	Less than 10 %
Moderate	:	10-20 %
High	:	More than 20 %

3.6.4 Estimation of genetic divergence using Mahalanobis's Generalized Distance (D^2)

Genetic diversity between genotypes can be better estimated using D^2 statistics given by Mahalanobis (1936).

3.6.4.1 Test of significance

Variances were calculated for all the thirteen characters studied and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1985). After testing the difference between genotypes for each of the character, a simultaneous test of significance for differences in the mean values for a number of correlated variables with regard to pooled effect of 13 characters was carried out using 'V' statistic, which in turn utilizes Wilk's Criterion. The sum of squares and sum of products of error and error + variety variance – covariance matrix were used for this purpose. The estimation of 'V' (Wilk's criterion) was done by using the following relationship.

$$\text{'V'} = W/S$$

Where,

'V' = Wilk's criterion

W = Determinant of error matrix and

S = Determinant of error + variety matrix

The significance of ‘V’ was tested by V (stat):

$$\chi^2 pq = V\,(\text{stat}) = -m \log_e \text{‘V’} = -\left[n - \frac{P+Q+1}{2}\right] \log_e \text{‘V’}$$

Where,

m = n-(P + Q + 1)/2

p = number of characters (or) variable observations

q = number of genotypes-1 (or) degrees of freedom for population

n = degrees of freedom for error + genotypes at base of natural log = 2.7183

V (stat) can be approximately considered to be distributed as χ^2pq and if the calculated ‘V’ value from the formulae exceeds χ^2pq’K’, the hypothesis is rejected at ‘K’ level of significance; otherwise not.

3.6.4.2 Transformation of correlated variables

Transformation was done by using pivotal condensation method. Transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values because of computation of D^2 values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., $\sum di^2$.

3.6.4.3 Computation of D^2 values

The D^2 value between i^th and j^th genotypes for ‘p’ character was calculated as:

$$D^2_{ij} = \sum_{t=1}^{P} (\overline{Y}_{it} - \overline{Y}_{jt})^2$$

Where,

$\overline{Y}_{it}$ = uncorrelated mean value of the i^th genotype for t character

$\overline{Y}_{jt}$ = uncorrelated mean value of the j^th genotype for t character

D^2_{ij} = D^2 between i^th and j^th genotype

3.6.4.4 Testing the significance of D^2 values

The D^2 value obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against tabulated χ^2 at p degrees of freedom where, 'p' is the number of characters considered.

3.6.4.5 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done by using Tocher's method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should have a smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all the combinations for each genotype were arranged in the increasing order of their magnitude (Singh and Chaudhary, 1985). To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average D^2 value from the first two genotypes was considered and so on. At certain stage when it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. The process was continued till all the genotypes were included in one or the other clusters.

3.6.4.6 Intra and inter cluster distance

Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D_i^2/n$. where ΣD_i^2 was the sum of distance between all possible combinations and 'n' is the number of genotypes included in a cluster.

Average inter cluster distance

Clusters were taken one by one and their distances from other clusters were calculated. The distance between the two clusters as the sum of D^2 value between the number one cluster to each of the members of other cluster divided by the product of number of genotypes in both the clusters under consideration. The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D^2 values (inter cluster distance), the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average inter cluster distance} = \frac{D^2}{n_1 \times n_2}$$

n_1 and n_2 are number of genotypes of two clusters

Category	**'D' values**
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

3.6.4.7 Cluster Diagram

The clusters and their mutual relationship were presented diagrammatically by using D^2 values.

3.6.4.8 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($di = y_{it} - y_{jt}$). Rank I was given to the highest mean difference and rank 'p' to the lowest difference; p is the total number of characters considered. Percentage contribution of each character (X) towards genetic divergence was calculated using the following formula:

$$\text{Percent contribution of character (X)} = \frac{N \times 100}{M}$$

Where,

X = Percent contribution of character

N = Number of genotype combinations where the characters ranked first.

M = All possible combinations of genotypes considered.

3.6.5 Estimation of Correlation Coefficients

Correlation coefficients were calculated at genotypic and phenotypic level using the formulae suggested by Falconer (1964).

Genotypic coefficient of correlation (r_g) = $r(x_i . x_j)g = \dfrac{\text{Cov.}(x_i . x_j)g}{\sqrt{v(x_i)g \,.\, v(x_j)g}}$

Where,

$r\,(x_i.x_j)_g$ is genotypic correlation between i^{th} and j^{th} characters

Cov. $(x_i.x_j)_g$ is genotypic covariance between i^{th} and j^{th} characters

$v\,(x_i)_g$ is genotypic variance of i^{th} character

$v\,(x_j)_g$ is genotypic variance of j^{th} character

Phenotypic coefficient of correlation (r_p) = $r(x_i . x_j)p = \dfrac{\text{Cov.}(x_i . x_j)p}{\sqrt{v(x_i)p \,.\, v(x_j)p}}$

Where,

$r\,(x_i.x_j)_p$ is phenotypic correlation between i^{th} and j^{th} characters

Cov. $(x_i.x_j)_p$ is phenotypic covariance between i^{th} and j^{th} characters

$v\,(x_i)_p$ is phenotypic variance of i^{th} character

$v\,(x_j)_p$ is phenotypic variance of j^{th} character

3.6.6 Path Coefficient Analysis

The direct and indirect effects both at genotypic and phenotypic levels were estimated by taking seed yield as dependant variable, using path coefficient analysis as suggested by Wright (1921) and Dewey and Lu (1959). The following equations were formed and solved simultaneously for estimating the various direct and indirect effects.

$$r_{1y} = P_{1y}\, r_{11} + P_{2y}\, r_{12} + P_{3y}\, r_{13} \ldots\ldots\ldots\ldots + P_{ny}\, r_{1n}$$

$$r_{2y} = P_{1y}\, r_{21} + P_{2y}\, r_{22} + P_{3y}\, r_{23} \ldots\ldots\ldots\ldots + P_{ny}\, r_{2n}$$

$$\begin{array}{cccccc} . & & . & . & . & . \\ \vdots & & \vdots & \vdots & \vdots & \vdots \end{array}$$

$$r_{ny} = P_{1y}\, r_{n1} + P_{2y}\, r_{n2} + P_{3y}\, r_{n3} \ldots\ldots\ldots\ldots + P_{ny}\, r_{3n}$$

Where;

1, 2 ……………..n = Independent variables

y = Dependant variable

r_{1y}, r_{2y} ……….. r_{ny} = Coefficient of correlation between casual factors `1` to `n` on dependent character 1

P_{1y}, P_{2y} …… P_{ny} = Direct effect of character 1 to n on character Y

The above equations can be written in matrix form as:

$$\begin{array}{ccc} A & C & B \\ \begin{pmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ r_{ny} \end{pmatrix} & \begin{pmatrix} 1 & r_{12} & r_{13} & \ldots\ldots\ldots\, r_{1n} \\ r_{21} & 1 & r_{23} & \ldots\ldots\ldots\, r_{2n} \\ . & . & . & \\ . & . & . & \\ . & . & . & \\ r_{n1} & r_{n2} & r_{n3} & \ldots\ldots\ldots\, 1 \end{pmatrix} & \begin{pmatrix} P_{1y} \\ P_{2y} \\ . \\ . \\ . \\ P_{ny} \end{pmatrix} \end{array}$$

Then,

$$B = (C)^{-1} A \text{ where } C^{-1} = \begin{pmatrix} c_{11} & c_{12} & c_{13}\ldots\ldots\ldots\ldots & c_{1n} \\ c_{21} & c_{22} & c_{23}\ldots\ldots\ldots\ldots & c_{2n} \\ . & . & . & . \\ : & : & : & : \\ : & : & : & : \\ c_{n1} & c_{n2} & c_{n3}\ldots\ldots\ldots\ldots & c_{nn} \end{pmatrix}$$

Direct effects were as follows:

$$P_{1y} = \sum_{i=1}^{k} c_{1i} \; r_{iy}$$

$$P_{2y} = \sum_{i=1}^{k} c_{2i} \; r_{iy}$$

$$P_{ny=} \quad \sum_{i=1}^{k} c_{nj} \; r_{iy}$$

Residual effect, which measures the contribution of characters not considered, was obtained as:

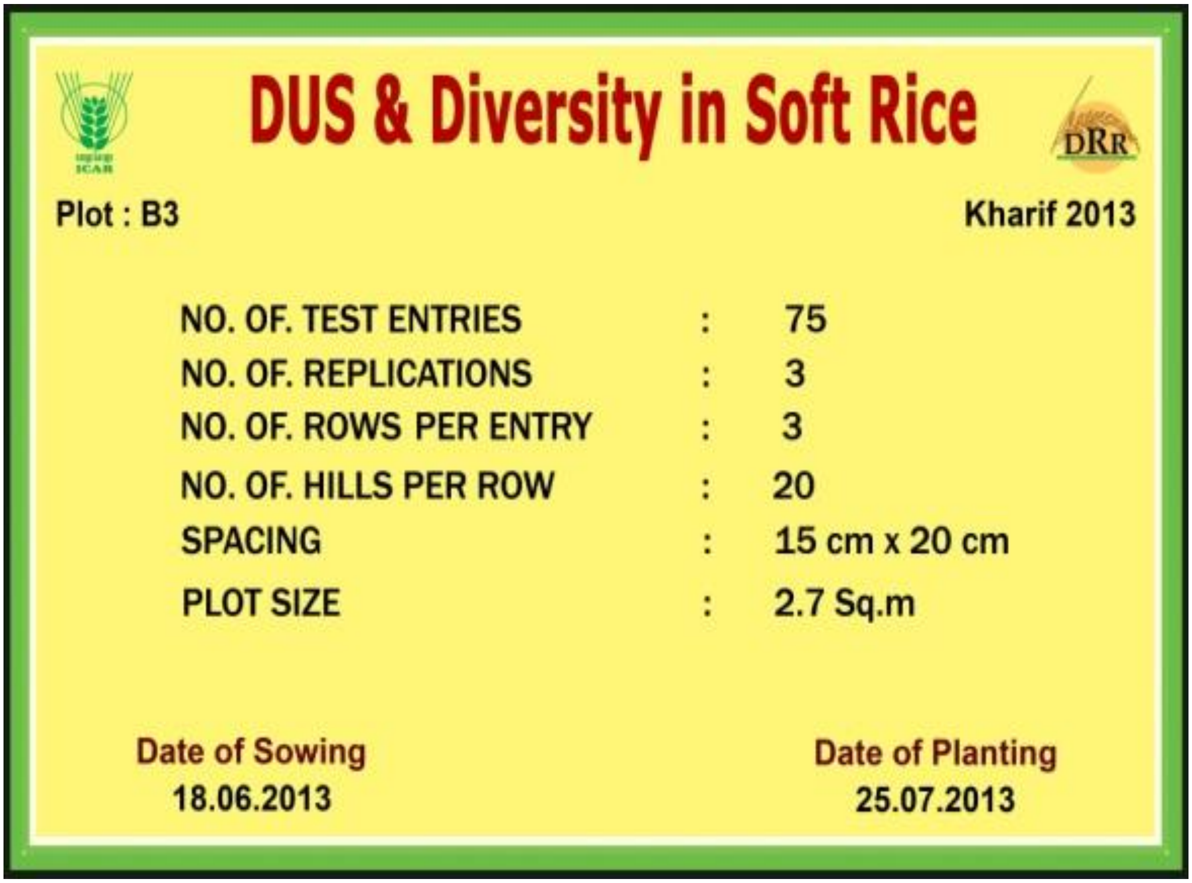
$$p_{ry} = \sqrt{1-(p_{1y}\, r_{iy} + p_{2y}\, r_{iy} + \ldots\ldots + p_{ny}\, r_{ny}}$$

Where,

p_{ny} = Direct effect of x_n on Y

r_{iy} = Correlation coefficient of x_n on y.

Figure 3.1. Soft rice genotypes grown for characterization and genetic diversity.



DUS & Diversity in Soft Rice

Plot : B3

Kharif 2013

NO. OF. TEST ENTRIES : 75
NO. OF. REPLICATIONS : 3
NO. OF. ROWS PER ENTRY : 3
NO. OF. HILLS PER ROW : 20
SPACING : 15 cm x 20 cm
PLOT SIZE : 2.7 Sq.m

Date of Sowing
18.06.2013

Date of Planting
25.07.2013

Figure 3.2. Layout of the experiment.

Chapter IV

RESULTS AND DISCUSSION

4.1 Morphological Characterization of Soft Rice Genotypes

In the present investigation, 75 soft rice genotypes were evaluated in a Randomized Block Design with three replications. The genotypes were characterized for morphological characters using distinctiveness, uniformity and stability (DUS) criteria as per the national guidelines for the conduct of DUS tests. Characterization was done for each genotype, to establish its diagnostic features. The data was collected on 62 agro-morphological characters and nine quantitative characters representing yield parameters during *kharif* 2013 at DRR, Rice Farm, ICRISAT campus, Hyderabad. The results of the observations recorded were presented in detail in table 4.1 and figures 4.1(a) to 4.1(d) and figure 4.2.

4.1.1 Coleoptile colour:

All the 75 genotypes under study had colourless coleoptiles and no variation was observed for this trait among these genotypes (plate 4.1).

4.1.2 Basal leaf: sheath colour:

The anthocyanin pigmentation of the basal leaf sheath varied among the soft rice genotypes as green, light purple, purple lines and purple. Among the 75 genotypes evaluated 39 genotypes showed green basal leaf sheath colour, 14 genotypes showed light purple colour, 11 genotypes showed purple lines and the remaining 11 genotypes showed uniform purple colour (plate 4.2). Similar work was reported by Bisne and Sarawgi (2008) and Moukoumbi (2011).

4.1.3 Leaf: intensity of green colour:

Among the 75 genotypes evaluated, 27 genotypes showed light green leaf colour, 19 genotypes showed medium green colour and 29 genotypes had dark green colour (plate 4.3). The intensity of green colour was found to be a useful trait to characterize the genotypes. Monika *et al.* (2007) also grouped nineteen varieties of rice based on intensity of green colour of leaf.

4.1.4 Leaf: anthocyanin colouration:

Among the 75 genotypes evaluated 40 genotypes are devoid of anthocyanin coloration and 35 genotypes possesed leaf anthocyanin colouration. Similar type of work was carried out by Anitalakshmi (2002), Nethra (2003), Mageshwaran (2010) and Mathure *et al*. (2011).

4.1.5 Leaf distribution of anthocyanin colouration:

Thirty five genotypes had anthocyanin colouration in the leaf. Of the 35 genotypes, anthocyanin is distributed only on tips for 13 genotypes and for 22 genotypes it is present on margins only. Among the 75 genotypes studied there are no genotypes in the category where antocyanin is neither distributed in bloches nor uniform distribution. Similar type of results were reported by Mageshwaran (2010) and Mathure *et al*. (2011).

4.1.6 Leaf sheath: anthocyanin colouration:

Among the 75 genotypes evaluated, anthocyanin colour in leaf sheath is absent for 41 genotypes and is present for 34 genotypes (plate 4.4).

4.1.7 Leaf sheath: intensity of anthocyanin colouration:

Among the 34 genotypes for which leaf sheath had anthocyanin colouration, two genotypes namely SR-34 and SR-35 had very weak intensity of anthocyanin colouration, 11 genotypes showed weak intensity, ten genotypes showed medium intensity, nine genotypes had strong intensity and the genotypes SR-6 and SR-49 had very strong leaf sheath intensity of anthocyanin colouration. Similar work was reported by Bisne and Sarawgi (2008) and Moukoumbi (2011).

4.1.8 Leaf pubescence of blade surface:

Among the 75 genotypes studied, 37 genotypes showed medium pubesence, 19 genotypes showed strong genotypes and the remaining 19 genotypes weak pubesence. Evera (2003) used this trait to characterize twenty six rice cultivars while Monika *et al.* (2007) and Bora *et al.* (2008a) also characterized nineteen and eleven cultivars in rice respectively and Mageshwaran (2010) grouped 10 rice genotypes based on this character.

4.1.9 Leaf auricles:

Auricles are present in all 75 genotypes.

4.1.10 Leaf: anthocyanin colouration of auricles:

Among the 75 genotypes, 35 genotypes had colourless auricles followed by 24 genotypes with light purple auricle and 16 genotypes with purple auricles (plates 4.5 & 4.6). Bisne and Sarawgi (2008) and Moukoumbi (2011) reported similar results on auricles characterization.

4.1.11 Leaf collar:

Leaf collar is present in all the 75 genotypes. Similar results were obtained by Binse and Sarawgi (2008).

4.1.12 Leaf: anthocyanin colouration of collar:

Among the 75 genotypes studied, 40 genotypes had anthocyanin in leaf collar and 35 genotypes had no anthocyanin colouration of collar (plate 4.7 & 4.8). Similar work was reported by Bisne and Sarawgi (2008) and Moukoumbi (2011).

4.1.13 Leaf ligule:

All the 75 genotypes had leaf ligule.

4.1.14 Leaf: shape of ligule:

Of the 75 genotypes evaluated, all the genotypes showed split shaped ligule, and none of the genotypes showed truncate and acute shaped ligule (plate 4.9). Evera (2003) used this trait to characterize twenty six paddy cultivars while Monika *et al.* (2007) and Bora *et al.* (2008a) used the same trait to characterize nineteen and eleven cultivars of rice respectively.

4.1.15 Leaf: colour of ligule:

Among the 75 genotypes evaluated, 48 genotypes showed green ligule and 21 genotypes showed light purple ligule and six genotypes namely SR-10, SR-19, SR-33, SR-51, SR-65 and SR-71 showed purple ligule.

4.1.16 Leaf: length of the blade:

Wide variation was recorded for the length of the leaf blade. It ranged from 26.4 cm to 55.2 cm. Of the 75 genotypes evaluated 56 genotypes are medium length, 10 genotypes are long length and 9 genotypes showed short length of the leaf blade.

4.1.17 Leaf: width of the blade:

All the 75 evaluated genotypes showed medium leaf width of the blade between 1-2 cm. Sililar variations in the length and width of the leaf were observed by Sharma *et al*. (2004).

Rosta (1975) suggested that length and width of blade were quite useful traits in varietal identification. Monika *et al.* (2007) also grouped nineteen rice varieties based on length and width of the blade.

4.1.18 Flag leaf: attitude of blade (early observation):

Fourty genotypes showed semi-erect flag leaf, followed by 19 genotypes showed erect flag leaf and 16 genotypes showed horizontal flag leaf and none of the genotypes showed deflexed flag leaf attitude of blade at early observation among the 75 genotypes evaluated (plate 4.10). Similar work was reported by Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012).

4.1.19 Flag leaf: attitude of blade (late observation):

Evaluation of 75 genotypes for flag leaf attitude of blade as late observation, 39 genotypes showed horizontal flag leaf, followed by 16 genotypes showed erect flag leaf, and 14 genotypes showed semi erect flag leaf and none of the genotypes showed deflexed flag leaf attitude of blade at late observation. Bora *et al.* (2008a) characterized eleven cultivars of rice using this character.

4.1.20 Culm: attitude (for floating rice only):

It is varied as procumbent and non procumbent. This trait is not applicable in the present investigation.

4.1.21 Culm attitude:

Among the 75 genotypes, 53 genotypes had erect attitude of the culm, 14 were semi-erect followed by eight open type of culm attitude (plates 4.11 & 4.12). None of the genotypes had spreading culm attitude.

4.1.22 Time of heading (50% of the plants with panicles):

Most of the genotypes i.e., 58 of the 75 were late duration (111-130 days) type and 17 genotypes took 91-110 days for flowering (medium duration). Similar variation in time of heading was reported by Katsuta *et al.* (1996), Shah *et al.* (1999) and Santhy (1999) tested eight rice genotypes and found that days to flowering is a very important trait in classification of rice cultivars. Similar results were also reported by Ganesan and Subramanian (1994) and in rice.

4.1.23 Male sterility:

It is absent in all 75 genotypes.

4.1.24 Lemma: anthocyanin colouration of keel:

Twenty two genotypes showed lack of anthocyanin colour, ten were weak, 21 genotypes had medium colouration, 19 genotypes with strong anthocyanin and three genotypes namely SR-6, SR-33 and SR-51 had very strong anthocyanin colouration of keel (plates 4.13 & 4.14). Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012) reported similar results.

4.1.25 Lemma: Anthocyanin colouration of area below apex:

About 27 of the 75 genotypes do not have colour below the apex, 14 genotypes are weakly coloured, 14 were medium, 16 were strong and four genotypes namely SR-2, SR-6, SR-8 and SR-51 had very strong anthocyanin colouration of area below apex (plate 4.15). The results were in accordance with the work reported by Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012).

4.1.26 Lemma Anthocyanin colouration of apex:

Among the 75 genotypes evaluated, 34 genotypes do not have anthocyanin colouration at the apex of lemma, one genotype (SR-29) had weak anthocyanin colouration, two genotypes (SR-35, SR-5) had medium colour, 16 genotypes had strong anthocyanin colouration and 22 genotypes with very strong anthocyanin colouration at the apex of lemmae (plate 4.16). Monika *et al.* (2007) in nineteen rice varieties used this parameter for characterization.

4.1.27 Spikelet: colour of stigma:

Of the 75 genotypes, 35 genotypes had white colour stigma, 23 genotypes with light green stigma, three genotypes namely SR-14, SR-27 and SR-75 were yellow, three genotypes (SR-3, SR-35, SR-52) were light purple and 11 genotypes had purple stigma (plate 4.17). Similar type of classification was reported by, Dhanaraj (2001) and Anitalakshmi (2002) in rice. Chaudhury and Sahai (1993) found high variability for stigma colour while evaluating 1270 Cambodian rice genotype.

4.1.28 Stem thickness:

All the genotypes had thin stem girth (<0.40 cm) except SR-66 and SR-73 which had medium thickness.

4.1.29 Stem lengh (excluding panicle):

Thirty nine of the 75 genotypes had medium stem length followed by 22 genotypes with short stems, nine genotypes namely SR-21, SR-23, SR-26, SR-27, SR-28, SR-29, SR-30, SR-54 and SR-55 were very short and five gnotypes (SR-1, SR-12, SR-40, SR-52, SR-58) had long stem length. None of the genotype had very long stem length. A similar variation in plant height was reported by Rosta (1975), Anitalakshmi (2002), Nethra (2003) and Mageshwaran (2010) grouped rice genotypes based on this character.

4.1.30 Stem: anthocyanin colouration of nodes:

Fourty four genotypes showed non pigmented anthocyanin colouration of nodes and 31 genotypes showed anthocyanin colouration of nodes.

4.1.31 Stem: intensity of anthocyanin colouration of nodes:

Of the 31 genotypes which showed anthocyanin colouration of nodes, 16 genotypes showed strong intensity, 12 were medium and three genotypes (SR-20, SR-38, SR-44) had weak intensity of anthocyanin colouration of nodes (plate 4.18).

4.1.32 Stem: anthocyanin colouration of inter nodes:

Of the 75 genotypes evaluated, 38 genotypes had non pigmented inter nodes and 37 genotypes had anthocyanin colouration of inter nodes (plate 4.19). Similar work on nodes and inter nodes was reported by Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012).

4.1.33 Panicle: length of main axis:

Eight genotypes (SR-4, SR-40, SR-41, SR-63, SR-65, SR-69, SR-70, SR-71) showed very long length of panicle, 37 genotypes had long length (26-30 cm), 29 genotypes had medium length (21-25 cm) and only one genotype (SR-73) showed short panicle length (16-20 cm) of main axis (plate 4.20). Similar results were obtained by Sarma *et al*. (2004) where they characterized 142 *ahu* rice genotypes of Assam and found that eight genotypes showed more than 25 cm panicle length and the remaining genotypes recorded lesser panicle length. Similar type of classification was reported by RohiniDevi (2000), Dhanaraj (2001) and Anitalakshmi (2002) in rice.

4.1.34 Panicle: curvature of main axis:

Among the 75 genotypes evaluated, one straight panicle, 29 genotypes with semi straight panicles followed by 29 genotypes with drooping panicles, 16 genotypes had deflexed panicle curvature of main axis and one genotype (SR-29) had straight panicle (plate 4.21). Similar work was reported by Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012).

4.1.35 Panicle: number per plant:

Most of the genotypes, 57 of the 75 had medium number of panicles per plant (11-20), 17 genotypes had few panicles and only one genotype, SR-60 with many panicles (>20), per plant. Monika *et al.* (2007) distinguished nineteen and eleven number of rice cultivars respectively based on panicle number per plant.

4.1.36 Spikelet: density of pubescence of lemma:

Thirty eight genotypes showed strong pubescence of lemma, Medium pubescence of lemma was shown by 22 genotypes, followed by eight genotypes (SR-14, SR-20, SR-32, SR-38, SR-51, SR-52, SR-66 and SR-67) with weak pubescence of lemma and seven (SR-2, SR-23, SR-25, SR-31, SR-47, SR-51 and SR-59) with very strong pubescence, and none of the genotypes were non pubesent (plate 4.22). Bora *et al.* (2008a) suggested that density of pubescence of lemma was a very important character for varietal characterization of rice.

4.1.37 Spikelet: colour of tip of lemma:

About 30 genotypes showed purple lemma tip followed by 21 yellow, 12 had brown tip, 11 showed black lemma tip and one with white lemma tip (plate 4.23).

4.1.38 Lemma and palea colour:

Out of the 75 genotypes, 20 showed brown furrows on straw back ground, 13 had purple furrows on straw back ground, 12 were purple, 11 had brown spots on straw back ground, eight genotypes had brown lemma and palea colour, four (SR-8, SR-10, SR-51 and SR-65) had black colour, three (SR-27, SR-64 and SR-68) with gold furrows on straw back ground, two (SR-29 and SR-61) had reddish to light purple and two (SR-23 and SR-28) showed straw colour lemma and palea. Similar work was reported by Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012).

4.1.39 Panicle awns:

Of the 75 genotypes, 45 are awnless and 30 are awned (plate 4.24).

4.1.40 Panicle: colour of awns (late observation):

Among the 30 genotypes with awns, 12 were purple followed by eight yellowish white, four (SR-23, SR-26, SR-32 and SR-67) were yellowish brown, three (SR-3, SR-10 and SR-72) brown and three genotypes namely SR-24, SR-35 and SR-44 had red colour of awns.

4.1.41 Panicle: length of longest awns:

Thirteen genotypes had medium length awns, nine genotypes showed short awns, three (SR-4, SR-25 and SR-63) were very short, four (SR-26, SR-35, SR-58 and SR-60) long and only one genotype SR-23 had very long length awns (plate 4.26).

4.1.42 Panicle: distribution of awns:

Fourteen genotypes had awns on tips only, nine had awns only on upper half and seven genotypes namely SR-21, SR-23, SR26, SR-27, SR-32, SR-35 and SR-58 showed awns on whole length of the panicle (plate 4.25). Similar type of classification was reported by RohiniDevi (2000), Dhanaraj (2001) and Anitalakshmi (2002) in rice.

4.1.43 Panicle: presence of secondary branching:

All the 75 genotypes had secondary branching of the panicles.

4.1.44 Panicle: secondary branching:

About 54 genotypes had strong secondary branching, 14 genotypes with weak secondary branching and seven genotypes namely SR-2, SR-7, SR-27, SR-35, SR-43, SR-63 and SR-64 showed clustered secondary branching of the panicle (plate 4.27 & 4.28). Similar work was reported by Bisne and Sarawgi (2008), Moukoumbi (2011) and Sarawgi *et al.* (2012).

4.1.45 Panicle: attitude of branches:

About 37 genotypes showed semi erect branches, 19 had semi erect to spreading type, 16 were spreading, ten genotypes namely SR-37 and SR-38 were spreading and only one genotype SR-73 had erect attitude of branches.

4.1.46 Panicle exsertion:

About 38 genotypes with well exerted panicle followed by 23 mostly exerted panicles and 14 genotypes with partly exerted panicles (plate 4.29). The extent of panicle exsertion is important character in achieving successful pollination. This character is not only useful for characterization of genotypes *per se* but also to assess their suitability in hybrid development.

4.1.47 Time of maturity:

Most of the genotypes (60 of the 75) took long time for maturity (140-160 days) and the remaining 15 genotypes took medium time for maturity.

4.1.48 Leaf sensence:

Out of the 75 genotypes evaluated 30 genotypes recorded late leaf sensence, 27 genotypes with intermediate leaf sensence and 18 genotypes showed early leaf sensence.

4.1.49 Sterile lemma colour:

Forty one genotypes with straw sterile lemma colour, followed by 24 genotypes with purple colour and 10 genotypes had golden colour sterile lemma and none of the genotypes showed red coloured sterile lemma (plate 4.30).

4.1.50 Grain: weight of 1000 fully developed grains:

The grain weight of 1000 fully developed grains ranged from 14.5 g to 33.16 g with a mean of 24.40 g. Highest number of the genotypes (51) showed medium grain weight (21-25 g), followed by 17 genotypes with high grain weight (26-30 g), four genotypes (SR-18, SR-20, SR-24 and SR-58) showed very high (> 31 g) grain weight, two genotypes namely SR-59 and SR-60 with low grain weight (15-20 g), only one (SR-1) genotype with very low weight (< 15 g). Thousand grain weight has been used for characterizing rice varieties by several workers, Rosta (1975), Bose and Pradhan (2005), Joshi *et al.* (2007).

4.1.51 Grain length:

Forty genotypes with medium grain length (8.6-10.5), 30 were short length grain and five genotypes namely SR-23, SR-26, SR-27, SR-32 and SR-35 had long grain length. None of the genotypes showed very short or very long grain length (plate 4.31 and plate 4.32).

4.1.52 Grain width:

Of the 75 genotypes evaluated, 61 genotypes showed very narrow grain (<2 mm) and 14 genotypes had narrow grain width (plate 4.33). Similar variations in grain length and width were observed by Gupta (1990) and Sharma *et al.*, (1990).

4.1.53 Grain phenol reaction of lemma:

All the 75 genotypes showed positive response to phenol reaction of lemma (plate 4.34).

4.1.54 Decorticated grain length:

Of the 75 genotypes studied, 45 genotypes have medium decorticated grain length (5.51-6.50 mm) followed by 20 were short length (<5.5 mm) and 10 genotypes were long (6.51-7.5 mm). None of them have extra long length (plate 4.31 and plate 4.32).

4.1.55 Decorticated grain width:

All the 75 evaluated genotypes showed narrow decorticated grain width (<2 mm) (plate 4.33).

4.1.56 Decorticated grain shape:

Forty seven genotypes have short slender shape follwed by 19 with long slender, five were medium slender and four genotypes were in basmati grain shape.

4.1.57 Decorticated grain colour:

Sixty two of the 75 genotypes had white decorticated grain colour and the remaining 13 genotypes had red colour (plate 4.35 & 4.36). None of the genotypes were found with any other colour. Decorticated Seed colour which is a heritable character has been used by several workers to distinguish crop genotypes, Olesan (1974), Chakrabarthy and Agarwal (1989), Agarwal and Pawar (1990), particularly in rice Nehra (2003), in cotton Reddy (2005) and in sesame Suhasini (2006). Similar works are carried out by Gowda *et al.* (2011), Mageshwaran (2010), Macha (2010), Mathure *et al*. (2011) and NaimaGhalmi *et al*. (2010).

4.1.58 Endosperm: presence of amylose:

All the 75 evaluated genotypes had amylose in the endosperm.

4.1.59 Endosperm content of amylose:

About 38 genotypes had very low amylose (3-9%), 27 genotypes with low amylose content, nine genotypes were intermediate and only one genotype (SR-26) with high amylose in the endosperm. None of the genotypes had very high endosperm content of amylose.

4.1.60 Varieties with endosperm of amylose absent: expression of white core:

This is not appicable in the present investigation.

4.1.61 Gelatinization temparature through alkali spreading values:

Of the 75 genotypes 36 had low gelatinization temparature, 36 had medium gelatinization temparature and three genotypes (SR-18, SR-25 and SR-53) showed high medium gelatinization temparature (plate 4.37).

4.1.62 Decorticad grain aroma:

Only two genotypes, SR-23 and SR-26 were aromatic and all the other genotypes were devoid of aroma. Das and Ghosh (2010) studied four hundred thirty one traditional rice cultivars from genotype collection of Rice Research Station, Chinsurah, characterization had been done on thirty one traits.

Successful reports on plant characters for varietal identification was reported in crops like *Vida laba* by Bond and Crofton (2001), sorghum by Thangavel (2003), lucerne by kumar (2003) and pearl millet by Kumar *et al.* (2004), Oat by Sumathi (2007), cotton by

Reddy (2005), Macha (2010) and Ameena (2009), wheat by Kosina (2010), rice by Anitalakshmi (2002), Nethra (2003), Bora *et al*. (2008), Mageshwaran (2010) and Mathure *et al*. (2011), french bean by Chandrashekhar (2008), soybean by Chavan (2010) and cowpea by NaimaGhalmi *et al*. (2010).

The experimental results obtained from the present study on evaluation of 75 soft rice genotypes for the yield characters are presented under the following heads:

1. Mean performance
2. Genetic variability, heritability and genetic advance
3. Genetic divergence
4. Character association
5. Path coefficient analysis

4.2 Mean Performance

The pooled analysis of variance revealed highly significant differences among the 75 genotypes for all the traits indicating presence of considerable genetic variation in the experimental material. The mean values for nine yield components for 75 soft rice genotypes are given in Table 4.2 and the results of analysis of variance are presented in Table 4.3.

4.2.1 Yield Characters

4.2.1.1 Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 107 to 130 with a general mean of 115. The genotypes SR-14 and SR-23 took only 107 days to reach 50 per cent flowering stage while SR-38 was found to be late (130 days) among all the genotypes.

4.2.1.2 Plant height (cm)

Plant height ranged from 70.00 cm to 142.26 cm with a general mean of 111.79 cm. The shortest genotype was SR-55 (70.00 cm) while the tallest genotype was SR-12 (142.26cm). SR-55 was the smallest fallowed by SR-21 (72.56 cm) and SR-29 (75.73 cm).

4.2.1.3 Number of tillers per plant

The mean values for number of tillers per plant ranged from 9 (SR-43) to 26 (SR-8) with a general mean of 16.41 tillers per plant. The genotypes SR-39 (23.66) and SR-60 (23.00) were on par with SR-8.

4.2.1.4 Number of produvtive tillers per plant

The mean values for productive tillers per plant ranged from 8 (SR-43) to 22 (SR-8) tillers with a general mean of 14.32 tillers per plant. SR-40 (20.66) and SR-39 (20.33) was on par with SR-8 having maximum number of productive tillers per plant.

4.2.1.5 Panicle length (cm)

The mean values for panicle length ranged from 18.30 cm to 33.60 cm with a general mean of 27.01 cm. The genotype SR-73 showed lowest value of 18.30 cm and the genotype SR-40 exhibited highest value of 33.60 cm. SR-41 (33.2 cm), SR-63 (32.96cm), SR-69 (32.46cm) and SR-71 (32.20 cm) were on par with SR-40.

4.2.1.6 Per cent filled grains per panicle

The mean values for number of filled grains per panicle ranged from 35.40% (SR-38) to 98.40% (SR-71) grains followed by 98.09% (SR-6), 97.51% (SR-16), 96.56% (SR-75) and 96.31% (SR-11) with a general mean of 83.94%.

4.2.1.7 Days to maturity

The mean values for days to maturity ranged from 136 days in SR-23 to 159 in SR-38 with a general mean of 144 days.

4.2.1.8 Seed yield per plant (g)

The general mean for seed yield per plant was 18.97 g and the mean value ranged from 8.56 g (SR-60) to 29.82 g (SR-29). The genotype SR-29 (29.82 g) recorded highest seed yield per plant followed by SR-9 (29.48), SR-6 (28.99), SR-51 (26.36) and SR-35 (26.32).

4.2.1.9 Test weight (1000-grain weight) (g)

The general mean of 1000-grain weight was 24.50 g and the mean values ranged from 14.50 g in SR-1 to 33.16 g in SR-18. Among the genotypes tested SR-18 recorded the highest grain weight and was superior to all the genotypes tested. SR-20 (32.76 g), SR-24 (32.16 g) and SR-58 (31.00 g) genotypes were on par with SR-18.

4.3 Genetic Variability, Heritability and Genetic Advance

The basic idea in the study of variation is its partitioning into components attributable to different causes. The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Hence total varience should be partitioned in to heritable and non heritable components to assess the true breeding nature of the particular trait under study.

Besides genetic variability, knowledge of heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby helping the breeder to employ a suitable breeding strategy to achieve the objective faster. Heritability and genetic advance are important selection parameters. Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.*, 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone and there by enabling the selection of most potential genotype.

The genotypic and phenotypic coefficients of variation, heritability, genetic advance and genetic advance as per cent of mean were estimated for 75 genotypes and are furnished in Table 4.4 and represented in Figure 4.3.

4.3.1 Yield characters

4.3.1.1 Days to 50 per cent flowering

The genotypic and phenotypic coefficients of variation were low, 3.97 and 4.20, respectively. The observed heritability estimate for this trait was high (89.0) while, genetic advance (8.9) and genetic advance as per cent of mean (7.71) were low.

4.3.1.2 Plant height (cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate *i.e.,* 14.44 and 14.60 respectively. The observed heritability estimates for this character was high (97.9) with a high genetic advance (32.91) and genetic advance as per cent of mean (29.44).

4.3.1.3 Number of tillers per plant

The genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate to high *i.e.,* 19.18 and 20.38, respectively. The observed heritability estimate was high (88.5) with a low genetic advance (6.10) and high genetic advance as per cent of mean (37.18).

4.3.1.4 Number of productive tillers per plant

The genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate to high *i.e.* 18.23 and 20.53, respectively. The observed heritability estimate was high (78.8) with a low genetic advance (4.77) and high genetic advance as per cent of mean (33.36).

4.3.1.5 Panicle length (cm)

The GCV and PCV for this trait were moderate, 10.54 and 12.38, respectively. The heritability for this trait was high (72.5) with a low genetic advance (4.99) and moderate genetic advance as per cent of mean (18.49).

4.3.1.6 Per cent filled grains per panicle

A moderate GCV (13.76) and PCV (13.80) were observed for this trait. The heritability estimate for this trait was highest (99.4) with a high genetic advance (23.72) and genetic advance as per cent of mean (28.26).

4.3.1.7 Days to maturity

The GCV and PCV for this trait were low, 3.19 and 3.29, respectively. The heritability for this trait was high (93.8) with a low genetic advance (9.22) and genetic advance as per cent of mean (6.36).

4.3.1.8 Seed yield per plant (g)

A high genotypic coefficient of variation (26.08) and phenotypic coefficient of variation (26.62) were observed for this trait. A high heritability estimate (96.0) coupled with low genetic advance (9.99) and high genetic advance as per cent of mean (52.65).

4.3.1.9 Test weight (1000-grain weight) (g)

The estimates of genotypic (12.19) and phenotypic (12.89) coefficients of variation were moderate. The heritability observed for this trait was high (89.5). The genetic advance was low (5.82) while, genetic advance as per cent of mean was high (23.76).

In the present investigation, the genotypic and phenotypic coefficients of variation were low for days to 50% flowering and days to maturity. Similar results were reported by Sinha *et al*. (2004), Karim *et al*. (2007), and Kole *et al*. (2008) for days to 50% flowering and Gomatinayagam *et al.* (1990), Balan *et al.* (1999) and Karim *et al*. (2007) for days to maturity.

The moderate GCV and PCV values observed for the traits *viz.,* plant height, panicle length, per cent filled grains per panicle and test weight. Only moderate GCV value observed for number of tillers per plant and number of productive tillers per plant. Only high PCV value observed for number of tillers per plant and number of productive tillers per plant. The results were in confirmity with Vange and Ojo (1997) for test weight and number of productive tillers, Nayak *et al.* (2002) for plant height, panicle length and test weight, patil *et al.* (2003) for plant height and Chaudary and Motiramani (2003) for number of productive tillers per plant.

The high GCV and PCV were observed for seed yield per plant. Similar findings were reported by Patil and Sarawgi (2005) and Mustafa and Elsheikh (2007) for number of filled grains per panicle and grain yield per plant, Jayasudha and Sharma (2010) and Tiwari *et al.* (2011) for grain yield per plant.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population.

The heritability estimates were high for all the traits viz., days to 50% flowering, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, per cent filled grains per panicle, days to maturity, seed yield per plant and test weight (1000- grain weight). These are in conformity with Patil *et al.* (2003) for all the characters, Hasib *et al*. (2004) for all quantitative characters, Saxena *et al*. (2005) for plant height, panicle length, number of filled grains per panicle and 1000- grain weight, Madhavilatha *et al*. (2005a) for number of filled grains per panicle, grain yield per plant, Sarkar *et al*. (2005) for 1000-grain weight, Nayudu *et al.* (2007) for number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000-grain weight and grain yield per plant. High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection.

Genetic advance was high for the traits plant height and per cent filled grains per panicle where as low for the traits days to 50% flowering, number of tillers per plant, number of productive tillers per plant, panicle length, days to maturity, seed yield per plant and test weight (1000-grain weight). Similar results were reported by Satyanarayana *et al*. (2005) for plant height and 1000-grain weight, Sarkar *et al.* (2005) for number of filled grains per panicle, Karad and Pol (2008) for plant height. High heritability with high genetic advance indicates the control of additive gene and selection may be effective for those characters.

Genetic advance as percent of mean was high for plant height, number of tillers per plant, number of productive tillers per plant, per cent filled grains per panicle, seed yield per plant and test weight (1000-grain weight). It was moderate for the trait panicle length and it was low for days to 50% flowering and days to maturity. These results are in conformity with Nayudu *et al*. (2007) for number of productive tillers per plant, panicle length, per cent filled grains per panicle, 1000 -grain weight and grain yield per plant.

4.4 Genetic Divergence

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for 75 soft rice genotypes and the results obtained from the study are presented below.

4.4.1 Wilk’s ‘V’ criterion test

Wilk's 'V’ (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V’ (statistic) value was tested by percent (%) at 666 degrees of freedom. The 'V’ statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of 75 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.4.2 Mahalanobis’s generalized distance D^2 values

In order to assess the genetic diversity among 75 genotypes, D^2 statistic was used following the procedure given by Rao (1952). Since the entire nine yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method.

4.4.3 Composition of D^2 clusters for 75 soft rice genotypes

The seeventy five soft rice genotypes were grouped into nine clusters using Tocher's method (Rao 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is presented in Table 4.5. Out of seven clusters, cluster I was the largest comprising of 62 genotypes followed by cluster II with eight genotypes, and cluster

III, IV, V, VI and VII with only one genotype each. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. The cluster diagram (dendrogram) is given in Figure 4.4.

The clusters III, IV, V, VI and VII were represented by single genotypes namely SR-55, SR-12, SR-29, SR-68 and SR-38 respectively indicating high degree of heterogeneity among the genotypes.

4.4.4 Average inter and intra cluster distances

The average intra and inter cluster D^2 values are presented in Table 4.6. Intra cluster D^2 values ranged from 0.000 (cluster III, IV, V, VI and VII) to 157.08 (cluster II). Maximum intra cluster distance was observed in cluster II (157.08), followed by cluster I (104.95) indicating that some genetic divergence still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding.

From the inter cluster D^2 values of seven clusters, it can be seen that the highest divergence occured between cluster IV and cluster VII (1817.85) followed by cluster III and cluster VII (1795.23), cluster I and cluster VII (1425.51) and cluster III and cluster VI (1286.81), suggesting that the crosses involving lines from these clusters would give wider and desirable recombinations. The lowest divergence was noticed between cluster VI and cluster VII (186.32) followed by cluster I and cluster IV (192.07) and cluster I and cluster III (195.12) and cluster II and V (236.14). Statistical representation of cluster distances was shown in fig 4.5.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes (SR-12) of cluster IV and cluster VII (SR-38), cluster III (SR-55) and cluster VII (SR-38), cluster I with cluster VII (SR-38) and cluster III (SR-55) and cluster VI (SR-68) would produce encouraging results. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

4.4.5 Cluster means of the characters

The cluster means for each of nine characters are presented in Table 4.7. From the data it can be seen that considerable differences exist for all the traits studied. It indicated that the cluster mean for days to 50% flowering was highest in cluster VII (130.33) and the lowest in cluster II (113.88). Plant height was highest in cluster IV (142.27 cm) and lowest in cluster III (70.00 cm). Cluster II recorded the highest number of tillers per plant (17.08) and the lowest number of tillers per plant was in cluster VII (12.33). Cluster II recorded the highest number of productive tillers per plant (15.21) and the lowest number of productive tillers per plant was in cluster VI (11.00).

Cluster IV recorded the highest panicle length (27.53 cm) and the lowest was recorded in cluster III (21.47 cm). The per cent filled grains per panicle was highest in cluster III (95.40) and the lowest in cluster VII (35.40). Days to maturity was highest in cluster VII (159.67) lowest in cluster VI (142.33). Cluster V recorded the highest seed yield per plant (29.83 g) while, in cluster IV it was low (11.00 g). Highest test weight (1000-grain weight) was recorded in cluster I (24.98 g) and the lowest in cluster IV and cluster VII (21.00 g).

It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The cluster III is having highest mean value for per cent filled grains per panicle, cluster V for seed yield per plant and cluster I for test weight (1000-grain weight) and cluster II for number of productive tillers per plant and cluster IV for panicle length. The genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

4.4.6 Relative contribution of characters towards genetic divergence

The number of times that each of the nine characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.8. The results showed that the contribution of per cent filled grains per panicle was highest towards genetic divergence (5181.98%) by ranking 1438 times first, followed by plant height (2237.84%) by 621 times, seed yield per plant (g) (1441.44%) by 400 times, days to maturity (403.6%) by 112 times, test weight (371.17%) by 103 times, number of tillers per plant (252.25%) by 70 times, days to 50% flowering (50.45%) by 14 times, panicle length (cm) (46.85%) by 13 times, number of productive tillers per plant (14.41%) by 4 times respectively to the genetic divergence in decreasing order. The results were in conformity with Mani (2003) for plant height, Nayak *et al*. (2004) for panicle length, Patil and Sarawgi (2005) 1000-grain weight, grain yield per plant and Chandra *et al*. (2007) for plant height.

The traits, per cent filled grains per panicle, plant height and seed yield per plant contributed maximum towards total divergence, these characters should be taken into consideration while selecting parents for hybridization.

The conclusion drawn from the cluster analysis is that in the studied population high variability was observed between the genotypes in different clusters for different traits. Recombination breeding among genotypes belonging to cluster II having maximum intra-cluster distance can improve the yield potential. As maximum inter-cluster distance was noticed between cluster IV and VII, cluster III and VII, crosses involving genotypes from these clusters would give wider and desirable recombinations.

4.5 Character Association

The efficiency of selection for yield in plant breeding mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between traits and helps in selection for the improvement of the character. In general genotypic correlations were higher than the corresponding phenotypic correlations indicating strong inherent associations between the characters genetically. Information on the inter association of yield components showed the nature and extent of their relationship with each other. This will help in the simultaneous improvement of different characters along with yield in breeding programmes.

Correlation studies would provide reliable information in nature, extent and the direction of selection, especially when the breeder needs to combine high yield potentials with desirable agronomic traits and grain quality traits. The genotypic and phenotypic correlation coefficients among yield and its component characters are presented in Table 4.9.

4.5.1 Days to 50% flowering

This trait showed positive but non significant association at both genotypic and phenotypic levels with seed yield per plant (0.0721/0.0701) and plant height (0.1272/0.1219), at genotypic level with days to maturity (0.09605) and at phenotypic level with number of tillers per plant (0.0012). It showed positive and significant association at phenotypic level with days to maturity (0.8824**). Similar results were reported by

Madhavi latha *et al.* (2005) and Satishchandra *et al.* (2009) for seed yield per plant, Chauhan *et al.* (1993) and Babu (1999) for plant height

This trait showed negative non-significant association at both levels with number of productive tillers per plant (-0.0194/-0.0146). It showed negative and non-significant association at genotypic level only, with number of tillers per plant (-0.0132), panicle length (-0.02388), per cent filled grains per panicle (-0.2802) and test weight (-0.2515). The trait expressed significant negative association at phenotypic level with panicle length (-0.1795**), per cent filled grains per panicle (-0.2660**) and test weight (-0.2284**). Similar results were reported by Chauhan *et al.* (1993) and Babu (1999) for panicle length, Nayak *et al.* (2001), Qamar *et al*. (2005), DeepaSankar *et al.* (2006) and Ramakrishnan *et al*. (2006), Anbumalarmathi and Nadarajan (2008) and Satishchandra *et al.* (2009) for 1000-grain weight.

4.5.2 Plant height (cm)

Plant height exhibited positive but non-significant association at both genotypic and phenotypic levels with seed yield per plant (0.0462/0.0449), days to maturity (0.0485/0.0438) and test weight (0.0165/0.0228) and at genotypic level only with panicle length (0.2552). It showed positive significant association at phenotypic level with panicle length (0.2179**). Similar results were reported by Suman (2003), Madhavi Latha *et al.* (2005) and Karad and Pol (2008) for seed yield per plant, Mirza *et al*. (1992), Chaubey and Singh (1994), Nayak *et al.* (2001), Kole *et al.* (2008), Khan *et al*. (2009), Sabesan *et al.* (2009), Sadeghi (2011) and Babu *et al.* (2012) for panicle length and Babu (1999) and Satishchandra *et al.* (2009) for 1000-grain weight.

Negative and non-significant association was observed at genotypic and phenotypic levels with number of tillers per plant (-0.0199/-0.0145), number of productive tillers per plant (-0.0604/-0.0557) and per cent filled grains per panicle (-0.0956/-0.0951). Similar observations were reported by Rao and Shrivastav (1999), Laxuman *et al.* (2011), Babu *et al.* (2012) for number of productive tillers per plant.

4.5.3 Number of tillers per plant

This trait showed positive but non–significant association at both genotypic and phenotypic levels with seed yield per plant (0.0384/0.0348), panicle length (0.0604/0.0377), per cent filled grains per panicle (0.0561/0.0563) and days to maturity (0.0110/0.0112) and with number of productive tillers per plant (0.09100) at genotypic level only. It showed significant positive association at phenotypic level only with number of productive tillers per plant (0.08207**).

This trait showed negative but non–significant association at both genotypic and phenotypic levels with test weight (-0.0502/-0.0545).

4.5.4 Number of productive tillers per hill

This trait exhibited positive but non–significant association at both genotypic and phenotypic levels with panicle length (0.1031/0.0517), per cent filled grains per panicle (0.0581/0.0515) and days to maturity (0.0313/0.0234). Similar results were reported by Kavitha and Reddi (2001) for panicle length and Yolanda and Das (1995) and De *et al.* (2005) for number of filled grains per panicle.

This trait showed negative but non–significant association at both genotypic and phenotypic levels with test weight (-0.0361/-0.0417) and seed yield per plant (-0.0918/ -0.0812). Reddy *et al.* (1995) and Reddy *et al.* (1997) had reported similar results for test weight and Haque *et al.* (1991) for seed yield per plant.

4.5.5 Panicle length (cm)

This trait exhibited positive but non–significant association at both genotypic and phenotypic levels with test weight (0.0592/0.0522). It was in confirmity with the results of Reddy *et al.* (1997) and Kavitha and Reddi (2001).

This trait showed negative but non–significant association at both genotypic and phenotypic levels with per cent filled grains per panicle (-0.0399/-0.0357), seed yield per plant (-0.0115/-0.0038) and at genotypic level only with days to maturity (-0.2151). This trait showed negative significant association at phenotypic level only with days to maturity (-0.1785**). Similar results were in accordance with the work done by Chauhan *et al.* (1993) and Babu (1999) for seed yield per plant.

4.5.6 Per cent filled grains per panicle

This trait exhibited positive but non–significant association at both genotypic and phenotypic levels with seed yield per plant (0.0566/0.0587) and with test weight at genotypic level only (0.1564). At phenotypic level it showed positive and significant association with test weight (0.1463*). Similar results were reported by Madhavi Latha *et al.* (2005) and Samonte *et al.* (1998), Surek and Beser (2003), Chakraborty *et al.* (2010), Bagheri *et al.* (2011) got positive but significant results for grain yield per plant, Ravindranath *et al.* (1982) and Satishchandra *et al.* (2009) for test weight.

This trait showed negative but non–significant association at genotypic level and significant negative association at phenotypic level with days to maturity (-0.2846/ -0.2742**).

4.5.7 Days to maturity

This trait exhibited positive but non–significant association at both genotypic and phenotypic levels with seed yield per plant (0.0650/0.0575).

This trait showed negative but non–significant association at genotypic level and significant negative association at phenotypic level with test weight (-0.3130/-0.2837**).

4.5.8 Test weight

This trait exhibited positive, non–significant association at both genotypic and phenotypic levels with seed yield per plant (0.1831/0.1666). Similar results were reported by Gupta *et al.* (1998), Vange *et al.* (1999) and Madhavi Latha *et al.* (2005) for grain yield per plant. It suggests that yield can be improved in rice genotypes by using this trait as selection criterion in succeeding generations.

4.5.9 Seed yield per plant (g)

Genotypic and phenotypic correlations revealed that seed yield per plant had non-significant positive association with days to 50% flowering (0.0721/0.0701), plant height (0.0462/0.0449), number of tillers per plant (0.0384/0.0348), per cent filled grains per panicle (0.0566/0.0587), days to maturity (0.0650/0.0575) and test weight (0.1831/0.1666), at both genotypic and phenotypic levels.

The trait showed negative non significant association with number of productive tillers per plant (-0.0918/-0.0812) and panicle length (-0.0115/-0.0038) at both genotypic and phenotypic levels. Pleiotropy and / or linkage may also be the genetic reasons for this type of negative association. According to NeWall and Eberhart (1961) when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety. Hence, under such situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters.

Seed yield per plant showed positive association with days to 50% flowering, plant height, number of tillers per plant, per cent filled grains per panicle, days to maturity and test weight (1000 grain weight) at both levels. This indicated that all these characters were important for yield improvement. Similar kind of association was revealed by Madhavilatha *et al*. (2005a) for panicle length and 1000 grain weight, Patil and Sarawgi

(2005) for number of filled grains per panicle, Satishchandra *et al.* (2009) for 1000-grain weight, Fiyaz *et al*. (2011) for number of productive tillers per hill, Singh *et al*. (2011) for number of productive tillers, Yadav *et al*. (2011) for 1000 grain weight. Hence, these characters could be considered as criteria for selection for achieving higher yield as these were mutually and directly associated with grain yield.

4.6 Path Coefficient Analysis

Information obtained from correlation study does not give comprehensive idea about the contributions of each component. Hence, path coefficient analysis, a statistical device developed by Wright (1921) helps in partitioning of the correlation coefficients in to direct and indirect effects of independent and dependent variable and also enables us to compare the causal factors on the genetic basis of their relative contributions.

The direct and indirect effects of different yield components on yield were estimated using genotypic and phenotypic correlation coefficients and are presented in Table 4.10. The cause and effect relationship is diagrammatically represented in Figure 4.6 and Figure 4.7.

4.6.1 Days to 50 percent flowering

The direct contribution of this character to grain yield was negative (-0.3215) at genotypic level and positive at phenotypic level (0.0272). Nayak *et al.* (2001), Prasad *et al.* (2001), Anbumalarmathi and Nadarajan (2008), Yadav *et al.* (2010), Yadav *et al.* (2011) reported negative direct effect of days to 50 % flowering on yield and Kole *et al*. (2008) and Laxuman *et al.* (2011) reported positive direct effect of it on grain yield.

The indirect effect through plant height was negative (-0.0409) at genotypic level and positive (0.0033) at phenotypic level and it is the same with days to maturity (-0.3088/0.0240). It showed indirect positive influence on grain yield at genotypic level through number of tillers per plant (0.0043), number of productive tillers per plant (0.0063), panicle length (0.0768), per cent filled grains per panicle (0.0901) and test weight (0.0809). It showed indirect negative influence on grain yield at phenotypic level through, number of productive tillers per plant (-0.0004), panicle length (-0.0049), per cent filled grains per panicle (-0.0072) and test weight (-0.0062). This trait had positive non-significant association with seed yield per plant (0.0721/0.0701) at both the levels. Similar results were reported by Madhavilatha (2002) and choudary and Das (1998) for plant height, Kavitha and Reddi (2001), khedikar (2004) and Satishchandra *et al.* (2009) for panicle length and Madhavi Latha (2002) and Satishchandra *et al.* (2009) for test weight.

4.6.2 Plant height (cm)

The direct effect of this character on yield was positive (0.0183/0.0212). Gomathinayagam *et al.* (1988), Nayak *et al.* (2001), Madhavilatha *et al.* (2005a), Kole *et al.* (2008), Chakraborty *et al.* (2010), Yadav *et al.* (2010), Sadeghi *et al.* (2011), Yadav *et al.* (2011) had reported positive direct effect of plant height on grain yield per plant.

The indirect positive influence on grain yield through days to 50% flowering (0.0023/0.0026), panicle length (0.0047/0.0046), days to maturity (0.0009/0.0009) and test weight (0.0003/0.0005) at both phenotypic and genotypic levels. Whereas, the number of tillers per plant (-0.0004/-0.0003), number of productive tillers (-0.0012/-0.0012) and per cent filled grains per panicle (-0.0017/-0.0020) showed negative indirect effect at phenotypic and genotypic levels. This trait had non-significant positive association with grain yield per plant (0.0462/0.0449) at genotypic and phenotypic levels respectively. Similar results were reported by Madhavilatha (2002) for days to 50% flowering, Nagajyothi (2001) for panicle length and Madhavilatha (2002) and Satishchandra *et al.* (2009) for test weight and Nayak *et al.* (2001) for number of productive tillers per plant.

This trait had positive direct effect on grain yield, it can be considered as selection criteria for improvement of yield.

4.6.3 Number of tillers per plant

The direct effect of this character on yield was positive (0.7967/0.3199). The indirect positive influence on grain yield through number of productive tillers per plant (0.7250/0.2626), panicle length (0.0481/0.0120), per cent filled grains per panicle (0.0447/0.0180), days to maturity (0.0088/0.0036) at both levels and days to 50% flowering at phenotypic level only. Whereas, the plant height (-0.0158/-0.0046) and test weight (-0.0400/-0.0174) showed negative indirect effect at phenotypic and genotypic levels and days to 50% flowering (-0.0105) at genotypic level only. This trait had non-significant positive association with grain yield per plant (0.0384/0.0348).

4.6.4 Number of productive tillers per plant

The direct effect of this character on yield was negative (-0.8371/-0.3411). The indirect positive influence on grain yield through days to 50% flowering (0.0163/0.0050), plant height (0.0530/0.0190) and test weight (0.0302/0.0142) at both genotypic and phenotypic levels. Kavitha and Reddi (2001), Nayak *et al.* (2001) had reported the same.

Whereas, number of tillers per plant (-0.7618/-0.2799), panicle lenth (-0.0863/ -0.0176), per cent filled grains per panicle (-0.0486/-0.0176) and days to maturity (-0.0262/-0.0080) showed negative indirect effect at phenotypic and genotypic levels. This trait had non-significant negative association with grain yield per plant (-0.0918/ -0.0812).

4.6.5 Panicle length

Panicle length exhibited positive direct effect on yield (0.0409/0.0148) at both genotypic and phenotypic levels. The indirect effects *via* plant height (0.0104/0.0032), number of tillers per pant (0.0025/0.0006), number of productive tillers per plant (0.0042/0.0008) and test weight (0.0024/0.0008) were positive at both levels.

Days to 50% flowering (-0.0098/-0.0027), per cent filled grains per panicle (-0.0016/-0.0005) and days to maturity (-0.0088/-0.0026) showed negative indirect effect at phenotypic and genotypic levels. How ever negative and non-significant correlation was observed with grain yield per plant (-0.0115/-0.0038) at both levels.

Kavitha and Reddi (2001), Nagajyothi (2001), Suman (2003), Khedikar *et al.* (2004) and Karad and Pol (2008) reported positive direct effect of panicle length on grain yield.

4.6.6 Per cent filled grains per panicle

Positive direct effect (0.0765/0.0707) at genotypic and phenotypic levels was exhibited and it was reported by Ramakrishman *et al.* (2006), Zahid *et al*. (2006), Mustafa and Elsheikh (2007), Kole *et al*. (2008), Hairmansis *et al*. (2010), Bagheri *et al.* (2011).

The indirect negative effects through days to 50% flowering (-0.0214/-0.0188) and plant height (-0.0073/0.0067), panicle length (-0.0031/-0.0025) and days to maturity (-0.0218/-0.0194) were expressed by this trait at both the levels. Number of tillers per plant (0.0043/0.0040), number of productive tillers per plant (0.0044/0.0036) and test weight (0.0120/0.0103) showed negative indirect effects at genotypic and phenotypic levels. This trait had non-significant positive association with grain yield per plant (0.0566/0.0587) at both levels.

4.6.7 Days to maturity

Positive direct effect (0.5005/0.1149) at genotypic and phenotypic levels was exhibited by this trait. The indirect positive effects through days to 50% flowering

(0.4807/0.1014), plant height (0.0243/0.0050), number of tillers per plant (0.0055/0.0013), number of productive tillers per plant (0.0157/0.0027) at both levels.

Panicle length (-0.1077/-0.0205), per cent filled grains per panicle (-0.1424/ -0.0315) and test weight (-0.1567/-0.0326) showed negative indirect effects at genotypic and phenotypic levels. This trait had non-significant positive association with grain yield per plant (0.0650/0.0575) at both levels.

4.6.8 Test weight

Positive direct effect (0.2540/0.1970) at genotypic and phenotypic levels was exhibited by this trait on grain yield. The indirect positive effects through plant height (0.0042/0.0045), panicle length (0.0150/0.0103) and per cent filled grains per panicle (0.0397/0.0288) at both genotypic and phenotypic levels.

Days to 50% flowering (-0.0639/-0.0450), number of tillers per plant (-0.0128/ -0.0107), number of productive tillers per plant (-0.0092/-0.0082) and days to maturity (-0.0795/-0.0559) showed negative indirect effects at genotypic and phenotypic levels. This trait had non-significant positive association with grain yield per plant (0.1831/0.1666) at both levels.

Prasad *et al.* (2001), DeepaSankar *et al.* (2006), Ramakrishnan *et al*. (2006), Anbumalarmathi and Nadarajan (2008), Chaturvedi *et al.* (2008), Kole *et al*. (2008), Satishchandra *et al*. (2009), Chakraborty *et al.* (2010), Yadav *et al.* (2010), Pal *et al.* (2011), Sadeghi *et al*. (2011), Yadav *et al.* (2011), Haider *et al.* (2012) reported positive direct effect of 1000-grain weight. This trait considered as important attribute in formulating selection criterion for achieving desired target due to its positive direct effect and significant genetic correlation with grain yield.

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be some times fruitful. When many characters are affecting a given character, splitting total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria.

Path coefficient analysis revealed that number of tillers per plant exerted the highest direct effect on grain yield followed by days to maturity, test weight (1000-grain weight), per cent filled grains per panicle, panicle length and plant height indicating the selection for these characters is likely to bring about an overall improvement in single plant yield directly.

These findings were in agreement with the reports made by Babu *et al.* (2002) for plant height, Chaudhary and Motiramani *et al.* (2003) for number of productive tillers per plant, Madhavilatha *et al.* (2005a) for plant height and number of productive tillers per plant, Patil and Sarawgi *et al.* (2005) for number of productive tillers per plant, number of filled grains per panicle and 1000-grain weight, Agahi *et al.* (2007) for number of productive tillers per plant and 1000- grain weight, Kole *et al.* (2008) for plant height and 1000-grain weight, Krishnappa *et al.* (2009) for plant height and 1000-grain weight, Nandan *et al.* (2010) for plant height, Pandey and Singh (2010) for number of productive tillers per plant and plant height, Bagheri *et al.* (2011) for number of filled grains per panicle.

The results of path analysis suggested that preference should be given to these characters in the selection programme to isolate superior lines with genetic potentiality for higher yields.

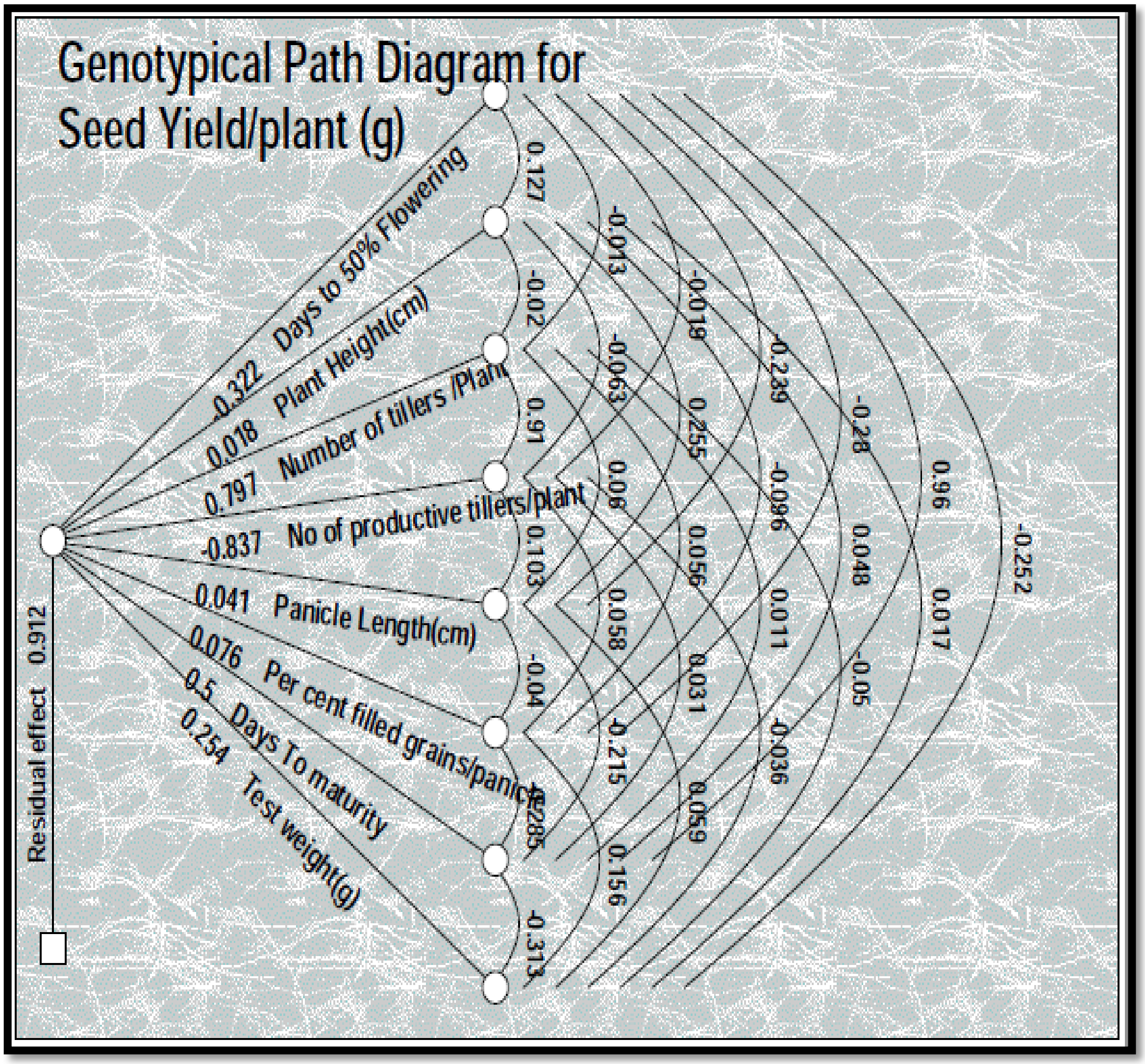


Figure 4.6. Genotypical path diagram for grain yield per plant (g).

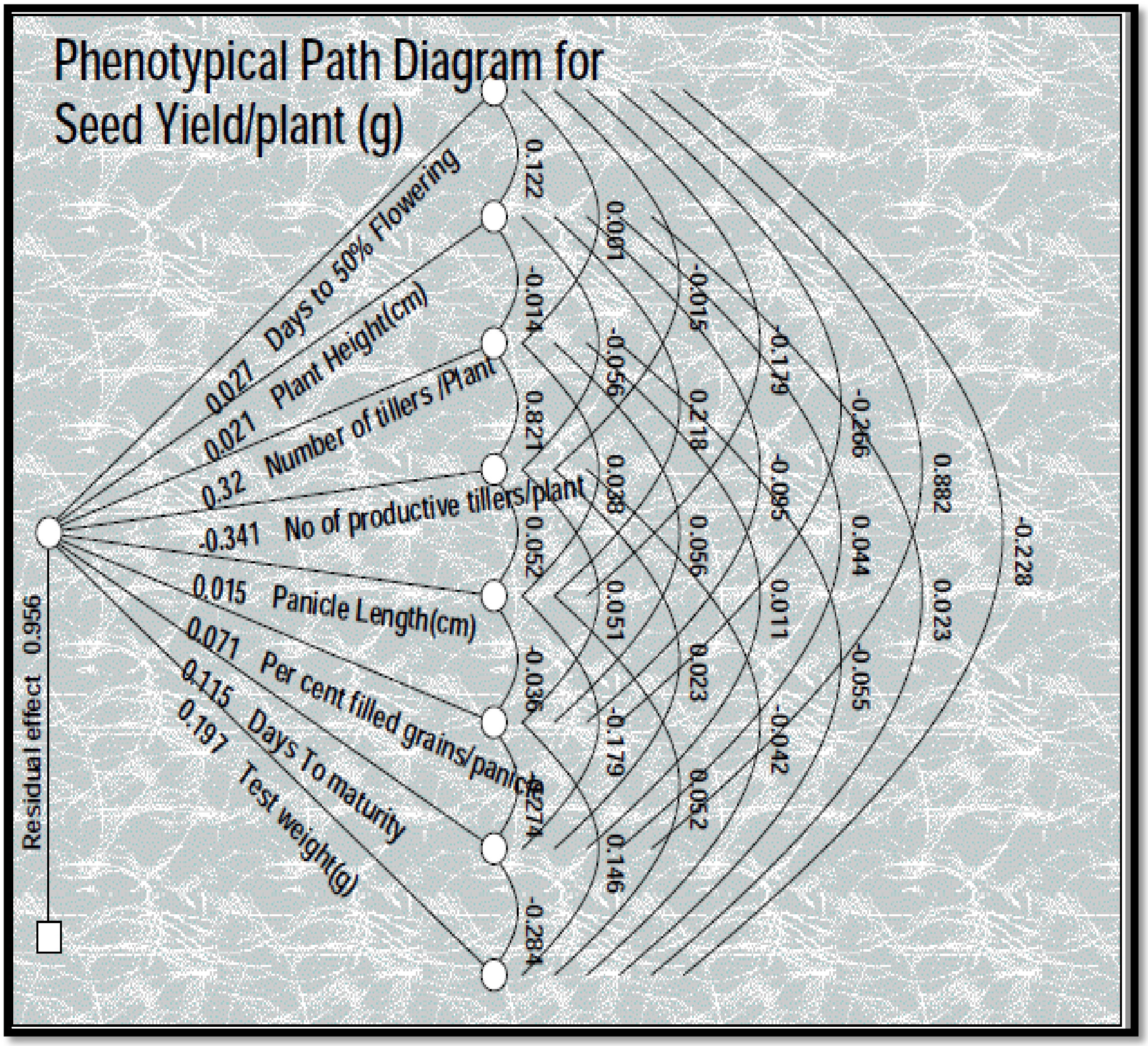
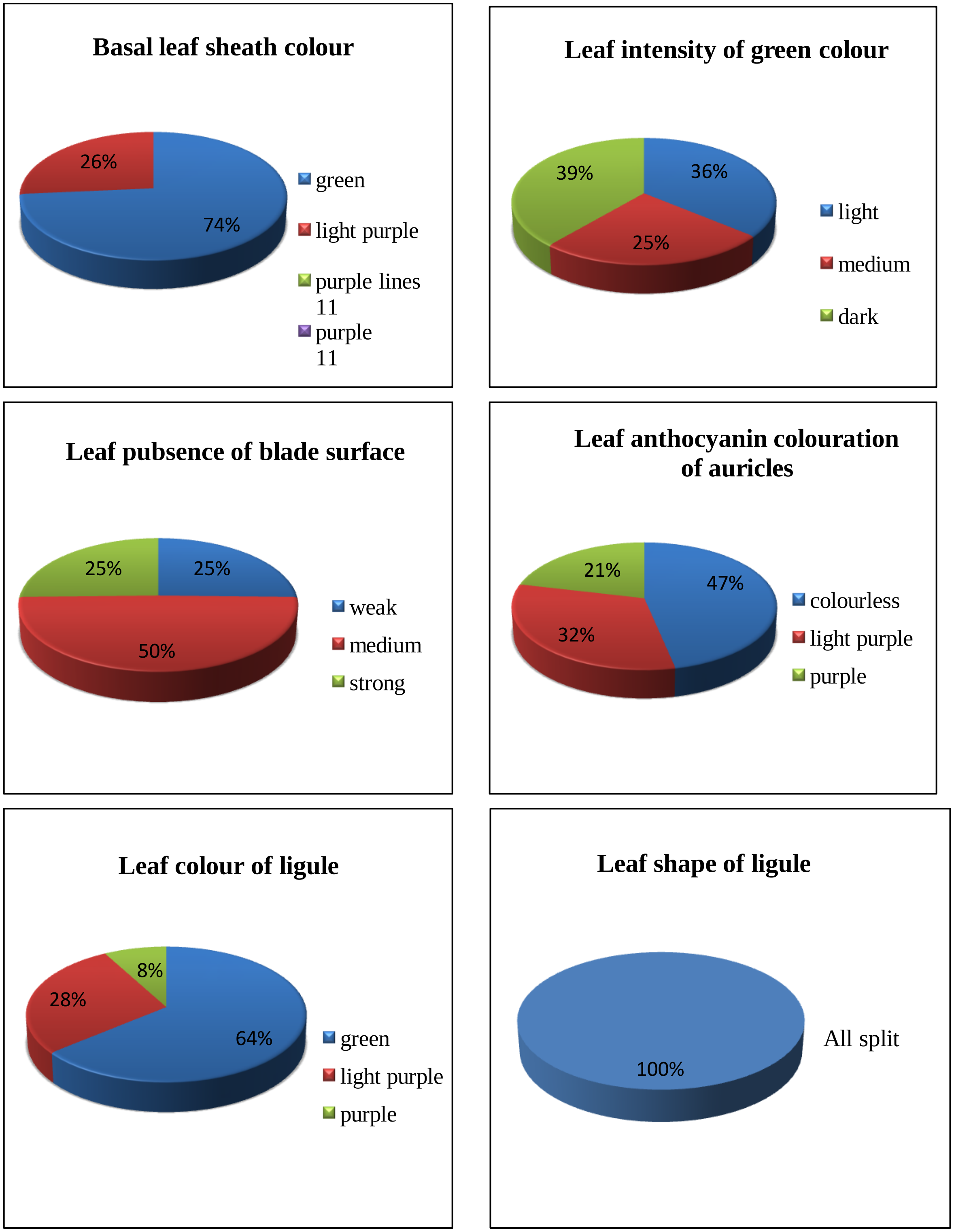


Figure 4.7. Phenotypical path diagram for grain yield per plant (g).



Basal leaf sheath colour

Leaf intensity of green colour

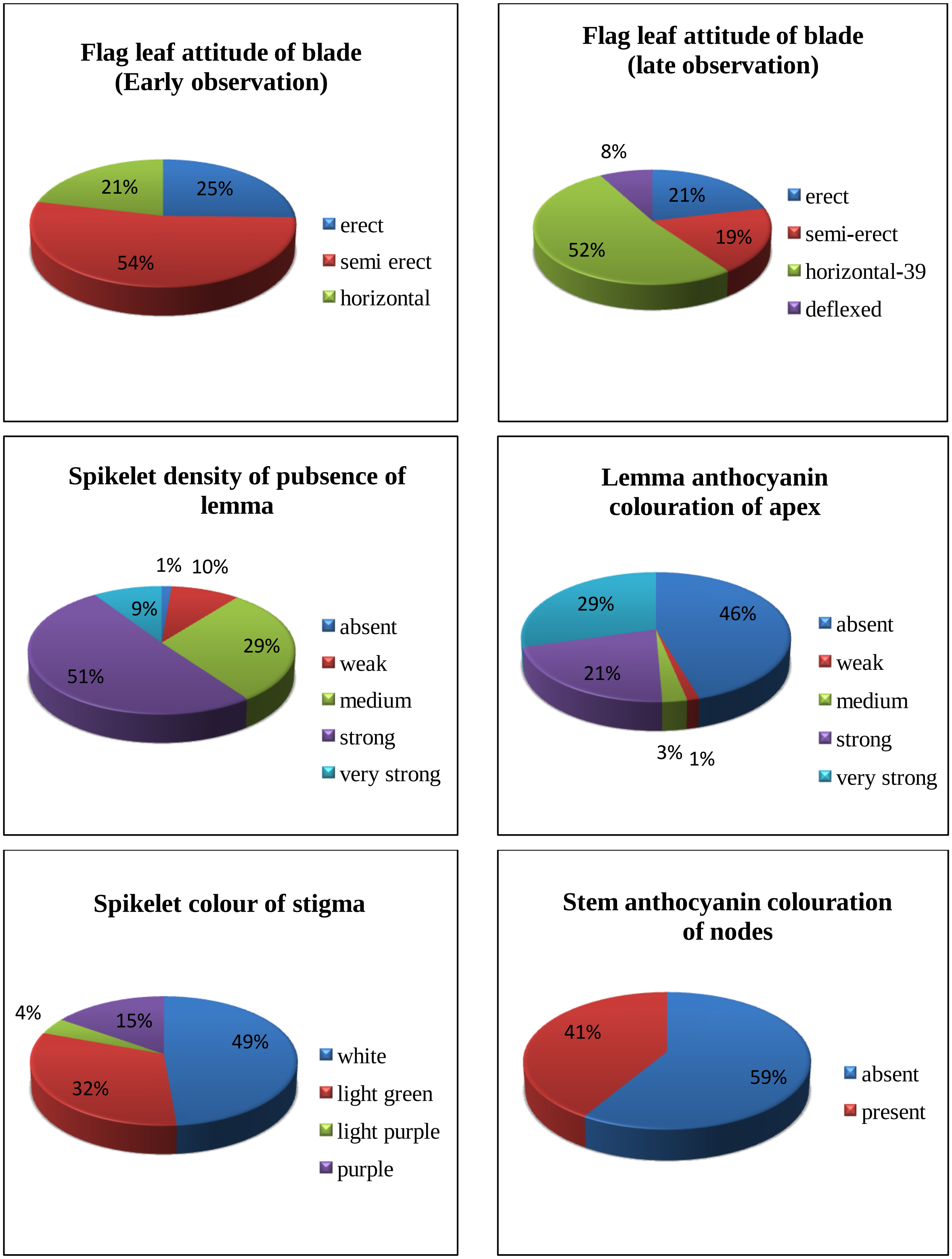
Leaf pubsence of blade surface

Leaf anthocyanin colouration of auricles

Leaf colour of ligule

Leaf shape of ligule

Figure 4.1(a). Frequency distribution charts of some important morphological traits.



Flag leaf attitude of blade (Early observation)

Flag leaf attitude of blade (late observation)

Spikelet density of pubsence of lemma

Lemma anthocyanin colouration of apex

Spikelet colour of stigma

Stem anthocyanin colouration of nodes

Figure 4.1(b). Frequency distribution charts of some important morphological traits.

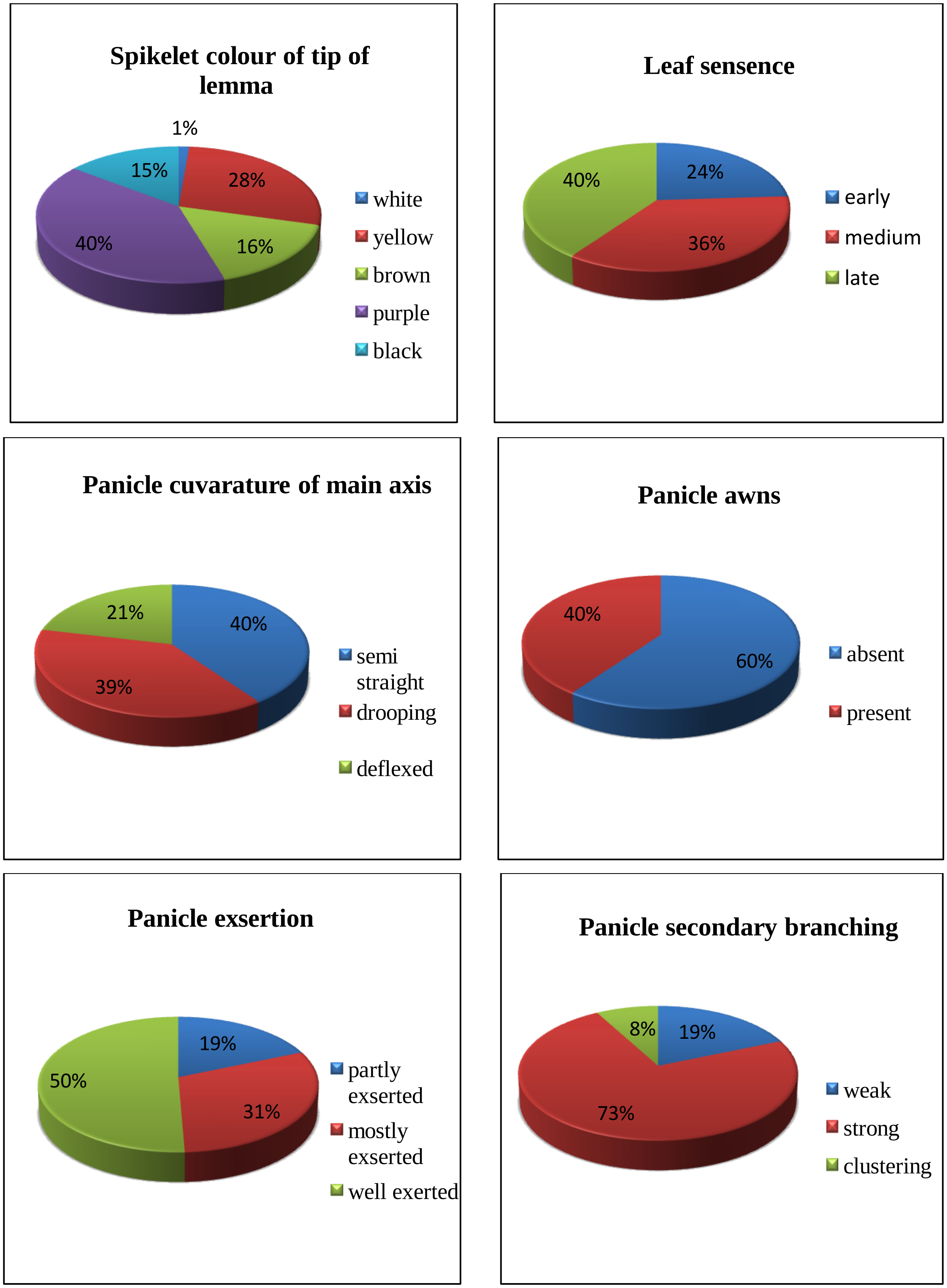


Figure 4.1(c). Frequency distribution charts of some important morphological traits.

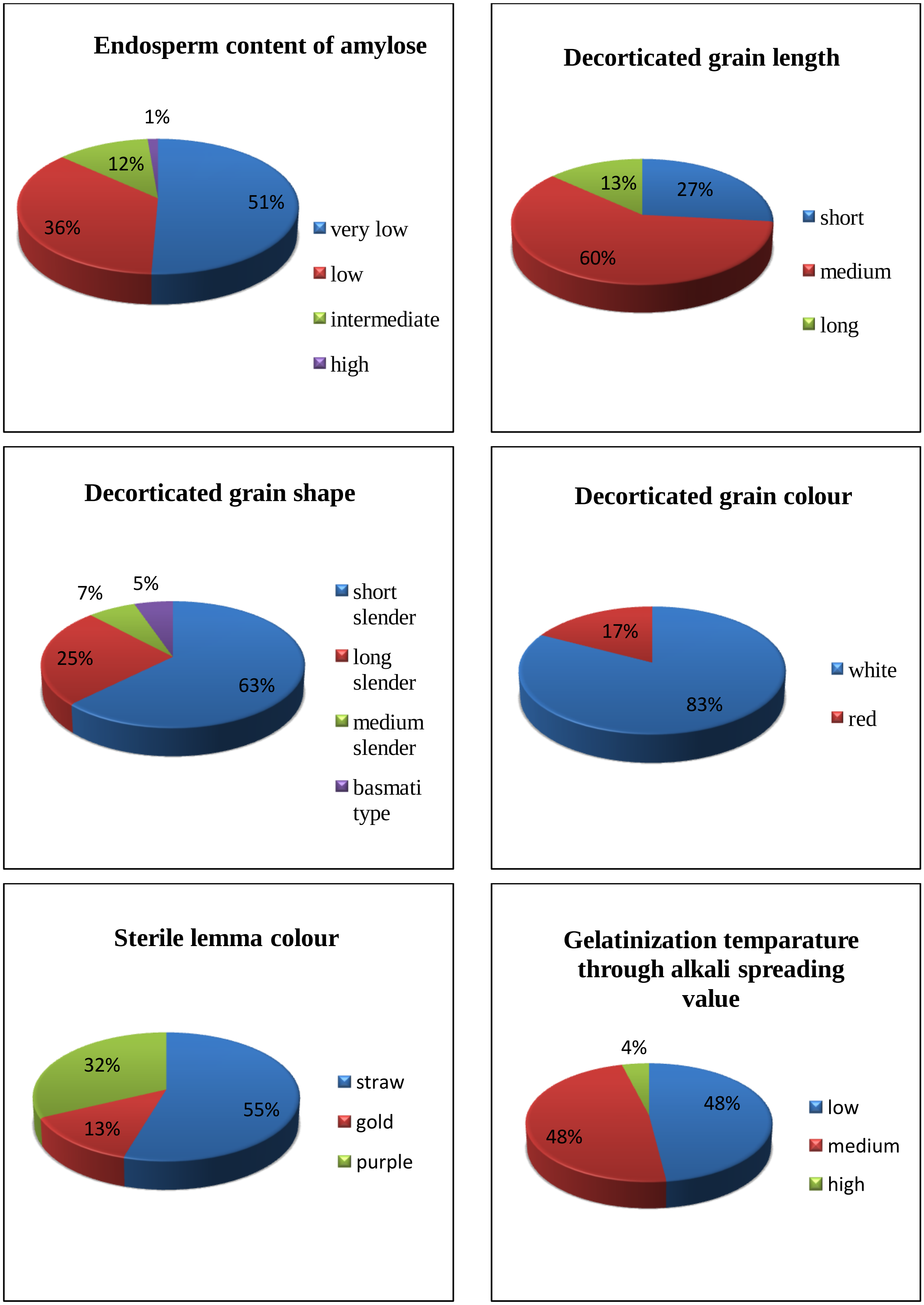


Figure 4.1(d). Frequency distribution charts of some important morphological traits.

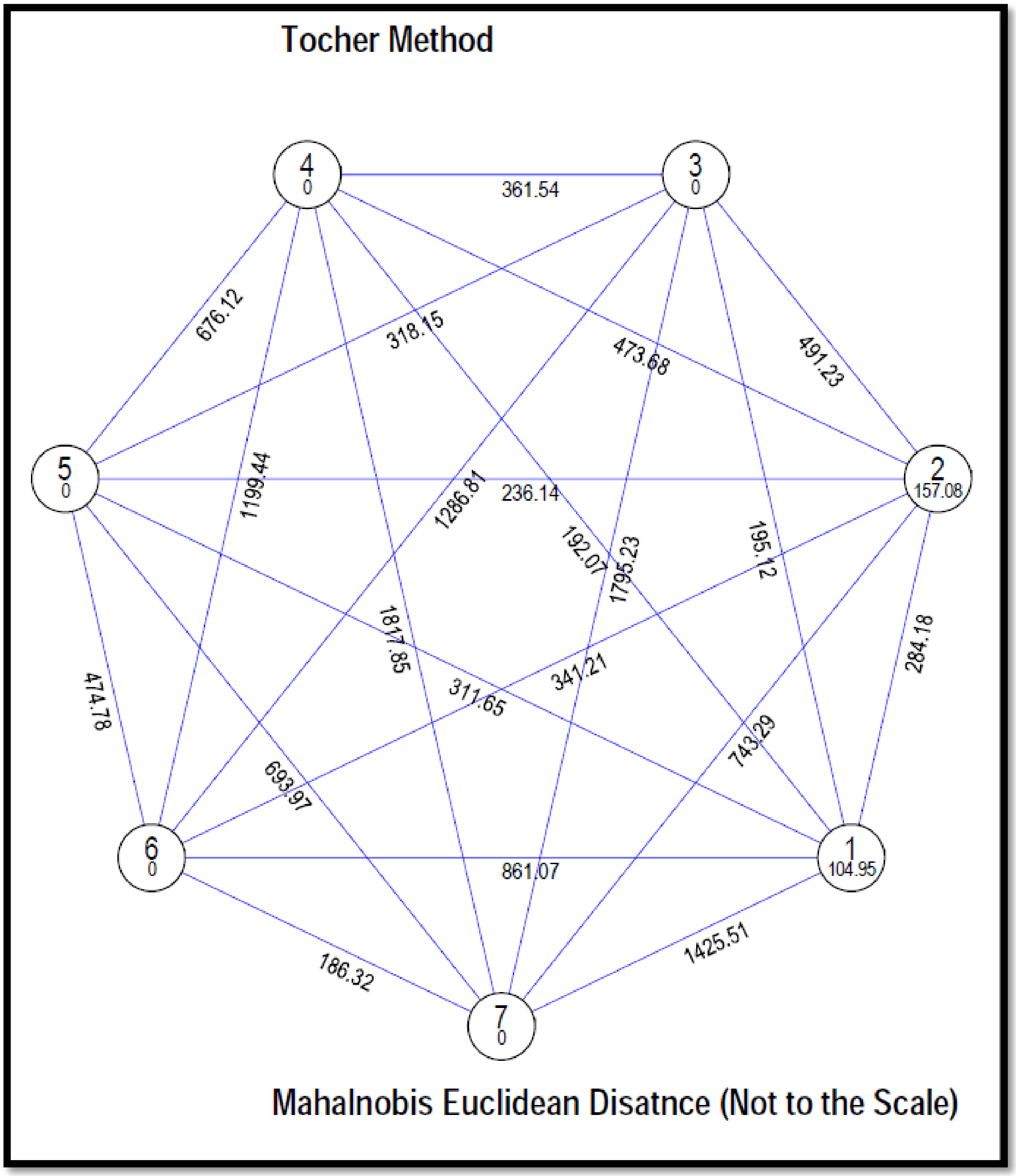


Figure 4.5. Intra and inter cluster statistical distances of various clusters.

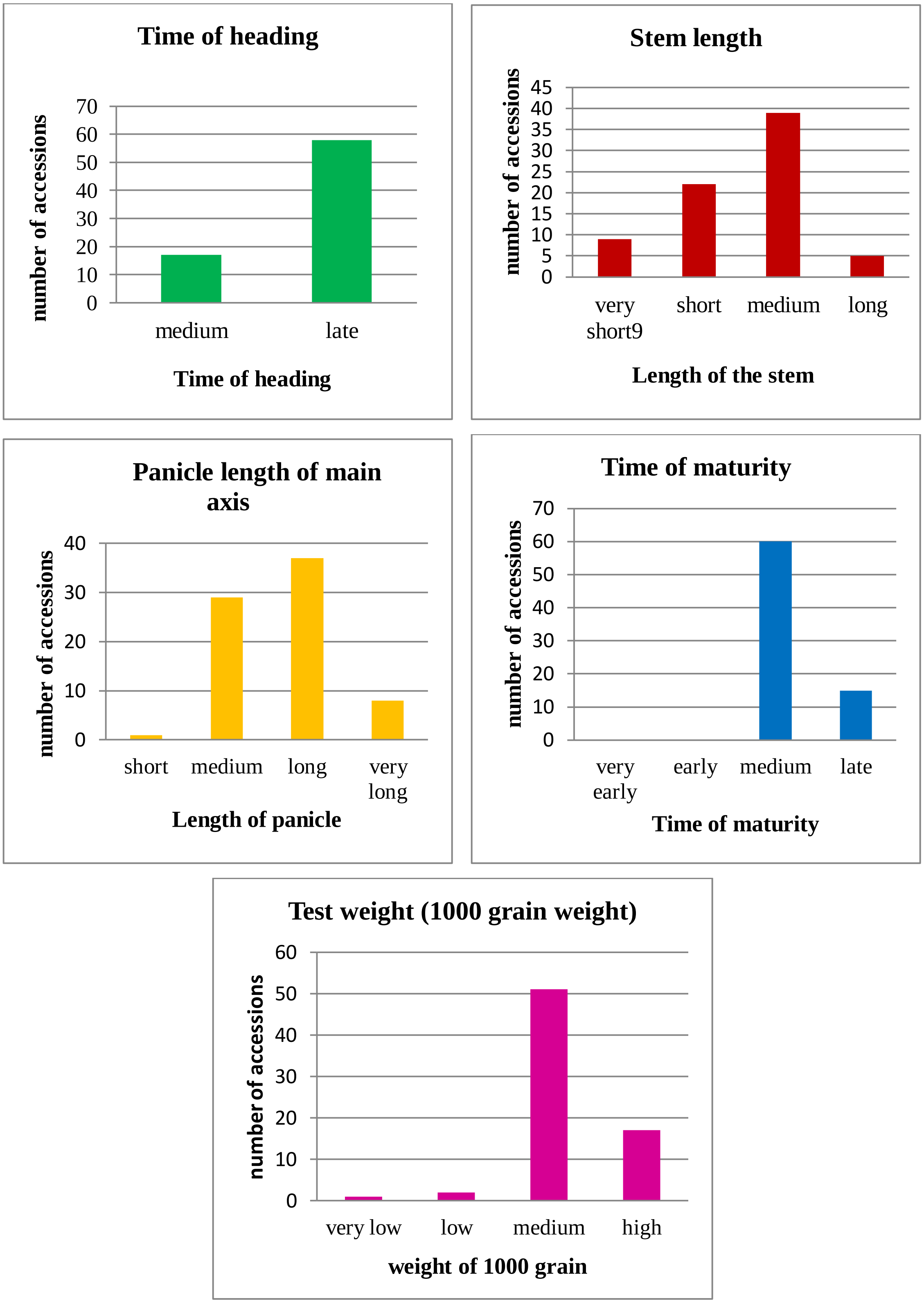


Figure: 4.2. Frequency distribution charts of some important quantitative traits.

Table 4.1. Morphological characterization of soft rice genotypes

1.	**Coleoptile colour:** SR-1 to SR-75 have colourless coleoptiles.
2.	**Basal leaf sheath colour**
	Green- 39 genotypes- SR-3, SR-7, SR-11, SR-12, SR-13, SR-15, SR-15, SR-16, SR-18, SR-21, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-32, SR-34, SR-36, SR-37, SR-38, SR-39, SR-40, SR-42, SR-46, SR-48, SR-53, SR-54, SR-55, SR-60, SR-62, SR-64, SR-66, SR-67, SR-68, SR-69, SR-70 and SR-74. **Light Purple - 14 genotypes** SR-1, SR-5, SR-17, SR-19, SR-20, SR-22, SR-25, SR-47, SR-50, SR-52, SR-65, SR-71, SR-72 and SR-73. **Purple lines – 11 genotype** SR-2, SR-33, SR-35, SR-44, SR-45, SR-51, SR-56, SR-57, SR-58, SR-59 and SR-61. **Uniform purple – 11 genotypes** SRR-4, SR-6, SR-8, SR-9, SR-10, SR-31, SR-41, SR-43, SR-49, SR-63 and SR-75.
3.	**Leaf: Intensity of green colour**
	Light-27 genotypes SR-1, SR-3, SR-5, SR-8, SR-12, SR-13, SR-17, SR-19, SR-24, SR-35, SR-36, SR-37, SR-39, SR-42, SR-44, SR-45, SR-52, SR-57, SR-62, SR-63, SR-64, SR-65, SR-67, SR-69, SR-70, SR-71 and SR-74. **Medium-19 genotypes** SR-2, SR-9, SR-10, SR-14, SR-18, SR-22, SR-25, SR-29, SR-32, SR-33, SR-40, SR-43, SR-46, SR-47, SR-51, SR-53, SR-56, SR-61 and SR-73. **Dark-29 genotypes** SR-4, SR-6, SR-7, SR-11, SR-15, SR-16, SR-20, SR-21, SR-23, SR-26, SR-27, SR-28, SR-30, SR-31, SR-34, SR-38, SR-41, SR-48, SR-49, SR-50, SR-54, SR-55, SR-58, SR-59, SR-60, SR-66, SR-68, SR-72 and SR-75.
4.	**Leaf: anthocyanin colouration**
	Absent-40 genotypes SR-2, SR-3, SR-5, SR-11, SR-12, SR-13, SR-14, SR-15, SR-16, SR-20, SR-23, SR-26, SR-27, SR-28, SR-29, SR-30, SR-31, SR-32, SR-34, SR-36, SR-37, SR-38, SR-39, SR-40, SR-42, SR-43, SR-45, SR-46, SR-51, SR-53, SR-54, SR-60, SR-62, SR-64, SR-66, SR-67, SR-68, SR-69, SR-70 and SR-74. **Present-35 genotypes** SR-1, SR-4, SR-6, SR-7, SR-8, SR-9, SR-10, SR-17, SR-18, SR-19, SR-21, SR-22, SR-24, SR-25, SR-33, SR-35, SR-41, SR-44, SR-47, SR-48, SR-49, SR-49, SR-50, SR-52, SR-55, SR-56, SR-57, SR-58, SR-59, SR-61, SR-63, SR-65, SR-71, SR-72, SR-73 and SR-75.
5.	**Leaf: distribution of anthocyanin colouration**
	On tips only- 13 genotypes SR-7, SR-17, SR-21, SR-24, SR-33, SR-44, SR-47, SR-48, SR-50, SR-55, SR-65, SR-71 and SR-72 **On margins only- 22 genotypes** SR-1, SR-4, SR-6, SR-8, SR-9, SR-10, SR-18, SR-19, SR-22, SR-25, SR-35, SR-41, SR-49, SR-52, SR-56, SR-57, SR-58, SR-61, SR-63, SR-73, SR-75. **In bloches only - nil** **Uniform – nil**

Table 4.1 (cont.).

6.	**Leaf sheath anthocyanin colouration**
	Absent – 41 genotypes SR-1, SR-2, SR-7, SR-11, SR-12, SR-13, SR-14, SR-15, SR-16, SR-18, SR-20, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-32, SR-36, SR-37, SR-39, SR-40, SR-42, SR-46, SR-47, SR-53, SR-54, SR-55, SR-57, SR-59, SR-60, SR-62, SR-64, SR-66, SR-67, SR-68, SR-69, SR-70, SR-71 and SR-74. **Present- 34 genotypes** SR-3, SR-4, SR-5, SR-6, SR-8, SR-9, SR-10, SR-17, SR-19, SR-21, SR-22, SR-25, SR-31, SR-33, SR-34, SR-35, SR-38, SR-41, SR-43, SR-44, SR-45, SR-48, SR-49, SR-50, SR-51, SR-52, SR-56, SR-58, SR-61, SR-63, SR-65, SR-72, SR-73 and SR-75.
7.	**Leaf sheath: intenssity of anthocyanin colouration**
	Very weak- two genotypes SR-34 and SR-35. **weak- 11 genotypes** SR-31, SR-38, SR-45, SR-48, SR-52, SR-56, SR-58, SR-61, SR-72 and SR-73. **Medium-10 genotypes** SR-4, SR-19, SR-21, SR-22, SR-25, SR-41, SR-44, SR-51 and SR-65. **Strong- nine genotypes** SR-5, SR-8, SR-10, SR-17, SR-33, SR-43, SR-50, SR-63 and SR-75. **Very strong- two genotypes** SR-6 and SR- 49.
8.	**Leaf: pubesence of blade surface**
	Absent- nil **Weak-19 genotypes** SR-4, SR-8, SR-9, SR-13, SR-15, SR-29, SR-33, SR-36. SR-37, SR-42, SR-43, SR-44, SR-46, SR-47, SR-48, SR-68, SR-69, SR-70 and SR-73. **Medium- 37 genotypes** SR-1, SR-5, SR-7, SR-10, SR-11, SR-12, SR-16, SR-18, SR-19, SR-20, SR-23, SR-25, SR-26, SR-27, SR-30, SR-31, SR-35, SR-40, SR-41, SR-45, SR-50, SR-51, SR-52, SR-53, SR-55, SR-56, SR-57, SR-58, SR-60, SR-61, SR-62, SR-63, SR-64, SR-65, SR-66, SR-72 and SR-75. **Strong- 19 genotypes** SR-SR-2, SR-3, SR-6, SR-14, SR-17, SR-21, SR-22, SR-24, SR-28, SR-32, SR-34, SR-38, SR-39, SR-49, SR-54, SR-59, SR-67, SR-71 and SR-74. **Very strong- nil**
9.	**Leaf auricles:** present in all genotypes from SR-1 to SR-75.
10.	**Anthocyanin colouration of auricles**
	Colourless- 35 genotypes SR-1, SR-7, SR-11, SR-12, SR-13, SR-14, SR-15, SR-18, SR-23, SR-24, SR-26, SR-27, SR-29, SR-30, SR-32, SR-34, SR-35, SR-36, SR-37, SR-39, SR-42, SR-46, SR-49, SR-56, SR-57, SR-59, SR-60, SR-64, SR-66, SR-67, SR-68, SR-69, SR-70, SR-74 and SR-75. **Light purple-24 genotypes** SR-2, SR-3, SR-5, SR-8, SR-10, SR-16, SR-17, SR-19, SR-20, SR-22, SR-25, SR-31, SR-38, SR-41, SR-44, SR-45, SR-50, SR-53, SR-54, SR-55, SR-58, SR-65, SR-72 and SR-73. **Purple-16 genotypes** SR-4, SR-6, SR-9, SR-21, SR-33, SR-40, SR-43, SR-47, SR-48, SR-49, SR-51, SR-52, SR-61, SR-62, SR-63 and SR-71.

Table 4.1 (cont.).

11.	**Leaf collar:** present in all genotypes from SR-1 to SR-75.
12.	**Leaf: anthocyanin colouration of collar**
	Absent- 35 genotypes SR-1, SR-7, SR-11, SR-12, SR-13, SR-14, SR-15, SR-16, SR-18, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-32, SR-34, SR-36, SR-37, SR-38, SR-42, SR-45, SR-46, SR-53, SR-54, SR-SR-56, SR-59, SR-60, SR-64, SR-66,SR-67, SR-68, SR-69 and SR-74. **Present- 40 genotypes** SR-2, SR-3, SR-4, SR-5, SR-6, SR-9, SR-10, SR-17, SR-19, SR-20, SR-21, SR-22, SR-25, SR-31, SR-33, SR-35, SR-39, SR-SR-40, SR-41, SR-43, SR-44, SR-47, SR-48, SR-49, SR-50, SR-51, SR-52, SR-55, SR-57, SR-58, SR-61, SR-62, SR-63, SR-65, SR-70, SR-71, SR-72, SR-73 and SR-75.
13 & 14	**Leaf ligule and shape of ligule** All the genotypes from SR-1 to SR-75 have split shaped ligule.
15.	**Leaf colour of ligule**
	Green- 48 genotypes SR-1, SR-2, SR-6, SR-7, SR-8, SR-9, SR-11, SR-12, SR-13, SR-15, SR-16, SR-18, SR-20, SR-21, SR-22, SR-23, SR-24, SR-26, SR-28, SR-29, SR-30, SR-31, SR-36, SR-37, SR-38, SR-39, SR-40, SR-42, SR-43, SR-45, SR-46, SR-47, SR-49, SR-53, 54, SR-56, SR-59, SR-60, SR-61, SR-62, SR-63, SR-66, SR-67, SR-68, SR-70, SR-72, SR-73 and SR-75. **Light purple- 21 genotypes** SR-3, SR-4, SR-5, SR-14, SR-17, SR-25, SR-27, SR-32, SR-34, SR-35, SR-41, SR-44, SR-48, SR-50, SR-52, SR-55, SR-57, SR-58, SR-64, SR-69 and SR-74. **purple- 6genotypes** SR-10, SR-19, SR-33, SR-51, SR-65 and SR-71.
16.	**Leaf- length of the blade**
	Short- nine genotypes SR-13, SR-28, SR-29, SR-30, SR-54, SR-55, SR-57, SR-65 and SR-66. **Medium- 56 genotypes** SR-1, SR-2, SR-3, SR-4, SR-5, SR-7, SR-8, SR-9, SR-10, SR-11, SR-12, SR-14, SR-15, SR-17, SR-19, SR-21, SR-22, SR-23, SR-24, SR-25, SR-26, SR-31, SR-33, SR-34, SR-35, SR-36, SR-37, SR-39, SR-40, SR-41, SR-43, SR-44, SR-45, SR-46, SR-47, SR-48, SR-49, SR-51, SR-52, SR-56, SR-58, SR-59, SR-60, SR-61, SR-62, SR-63, SR-64, SR-67, SR-68, SR-69, SR-70, SR-71, SR-72, SR-73, SR-74 and SR-75. **Long- ten genotypes** SR-6, SR-16, SR-18, SR-20, SR-27, SR-32, SR-38, SR-42, SR-50 and SR-53.
17.	**Leaf: width of the blade-** SR-1 to SR-75 have medium leaf width.
18.	**Flag leaf attitude of the blade (early observation)**
	Erect-19 genotypes SR-2, SR-5, SR-11, SR-15, SR-19, SR-20, SR-21, SR-23, SR-26, SR- 28, SR-29, SR-30, SR-36, SR-44, SR-51, SR-55, SR-65, SR-68 and SR-74. **Semi erect-40 genotypes** SR-1, SR-3, SR-4, SR-6, SR-7, SR-8, SR-10, SR-14, SR-16, SR-18, SR-22,, SR-24 SR-27, SR-32, SR-33, SR-34, SR-35, SR-37, SR-38, SR-41, SR-42, SR-43, SR-45, SR-47, SR-48, SR-49, SR-50, SR-52, SR-53, SR-54, SR-58, SR-59, SR-60, SR-62, SR-67, SR-68, SR-70, SR-71, SR-73 and SR-75. **Horizontal- 16 genotypes** SR-7, SR-9, SR-12, SR-13, SR-17, SR-25, SR-31, SR-39, SR-40, SR-46, SR-56, SR-61, SR-63, SR-66, SR-69 and SR-72.

Table 4.1 (cont.).

19.	**Flag leaf attitude of the blade (late observation)**
	Erect-16 genotypes SR-8, SR-20, SR-21, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-38, SR-43, SR-54, SR-55, SR-60 and SR-62. **Semi erect-14 genotypes** SR-5, SR-7, SR-11, SR-22, SR-32, SR-33, SR-34, SR-41, SR-45, SR-49, SR- 50, SR-51, SR-52 and SR-63. **Horizontal- 39 genotypes** SR-1, SR-2, SR-3, SR-4, SR-10, SR-12, SR-13, SR-14, SR- 15, SR-16, SR-18, SR-19, SR-25, SR- 35, SR-36, SR-37, SR-39, SR-40, SR-42, SR-44, SR-46, SR-47, SR-48, SR-53, SR-56, SR-57, SR-58, SR-59, SR-61, SR-65, SR-66, SR-67, SR-68, SR-69, SR-71, SR-72, SR-73, SR-74 and SR-75. **Deflexed- six genotypes** SR-6, SR-9, SR-17, SR-31, SR-64 and SR-70.
20.	**Culm attitude (for floating rice only)-** not applicable here.
21.	**Culm attitude**
	Erect-53 genotypes SR-1, SR-3, SR-6, SR-7, SR-9, SR-10, SR-11, SR-12, SR-13, SR-14, SR-15, 16, SR-17, SR-18, SR-19, SR-20, SR-21, SR-23, SR-24, SR-25, SR-27, SR-27, SR-28, SR-29, SR-30, SR-31, SR-33, SR-36, SR-40, SR-41, SR-42, SR-44, SR-46, SR-48, SR- 49, SR-50, SR-51, SR-52, SR-54, SR-55, SR-56, SR-57, SR-58, SR-59, SR- 61, SR-64, SR-66, SR-67, SR-68, SR-69, SR-71, SR-72, SR-73 and SR-75. **Semi erecct-14 genotypes** SR-4, SR-5, SR-8, SR-22, SR-26, SR-32, SR-38, SR-43, SR-45, SR-53, SR-60, SR-63, SR-65 and SR-74. **Open-eight genotypes** SR-2, SR-34, SR-35, SR-37, SR-39, SR-47, SR-62 and SR-70. **Spreading- nil**
22.	**Time of heading (50% of plants with panicles)**
	Very early- nil **Early- nil** **Medium -17 genotypes** SR-1, SR-6, SR-9, SR-11, SR-14, SR-15, SR-16, SR-18, SR-23, SR-26, SR-31, SR-39, SR-46, SR-49, SR-69, SR-71 and SR-72. **Late- 58 genotypes** SR-2, SR-3, SR-4, SR-5, SR-7, SR-8, SR-10, SR-12, SR-13, SR-17, SR-19, SR-20, SR-21, SR-22, SR-24, SR-25, SR-27, SR-28, SR-29, SR-30, SR-32, SR-33, SR-34, SR-35, SR-36, SR-37, SR-38, SR-40, SR-41, SR-42, SR-43, SR-44, SR-45, SR-47, SR-48, SR-50, SR-51, SR-52, SR-53, SR-54, SR-55, SR-56, SR-57, SR-58, SR-59, SR-60, SR-61, SR-62, SR-63, SR-64, SR-65, SR- 66, SR-67, SR-68, SR-70, SR-73, SR-74 and SR-75. **Very late- nil**
23.	**Male sterility:** Absent in all 75 genotypes

24.	**Lemma : Anthocyanin colouration of keel**
	Absent-22 genotypes SR-12, SR-13, SR-18, SR-20, SR-23, SR-24, SR-26, SR-27, SR-28, SR-32, SR-34, SR-36, SR-41, SR-42, SR-53, SR-54, SR-55, SR-61, SR-66, SR-68, SR-73 and SR-74. **Weak-ten genotypes** SR-5, SR-15, SR-22, SR-35, SR-39, SR-45, SR-46, SR-62, SR-69 and SR-70. **Medium-21 genotypes** SR-1, SR-3, SR-7, SR-11, SR-14, SR-21, SR-29, SR-37, SR-38, SR-40, SR-47, SR-48, SR-50, SR-56, SR-59, SR-60, SR-63, SR-64, SR-70, SR-72 and SR-75. **Strong-19 genotypes** SR-2, SR-4, SR-8, SR- 9, SR-10, SR-16, SR-17, SR-19, SR-25, SR-30, SR-31, SR-43, SR-44, SR-49, SR-52, SR- 58, SR-65, SR-67 and SR-71. **Very strong- three genotypes** SR-6, SR-33 andd SR-51.
25.	**Lemma: anthocyanin colouration of area below apex**
	Absent-27 genotypes SR-3, SR-13, SR-15, SR-18, SR-20, SR-23, SR-26, SR-27, SR-28, SR-30, SR- 32, SR-34, SR-36, SR-37, SR-41, SR-42, SR-47, SR-53, SR-57, SR-58, SR-59, SR-61, SR-64, SR-66, SR-70 and SR-72. **Weak-14 genotypes** SR-7, SR-11, SR-12, SR- 29, SR-35, SR- 39, SR-40, SR-46, SR-48, SR-55, SR-60, SR-62, SR-73 and SR-74. **Medium-14 genotypes** SR-5, SR-9, SR-21, SR-22, SR-25, SR-28, SR-31, SR-38, SR-45, SR-50, SR-54, SR-56, SR-67 and SR-75. **Strong-16 genotypes** SR-1, SR-4, SR-10, SR-14, SR-16, SR-17, SR-19, SR-33, SR-43, SR-44, SR-49, SR-52, SR-63, SR-65, SR-69 and SR-71. **Very strong-4 genotypes** SR-2, SR-6, SR-8 and SR-51.
26.	**Lemma: anthocyanin colouration of apex**
	Absent-34 genotypes SR-7, SR-11, SR-12, SR-13, SR-15, SR-21, SR- 23, SR-26, SR-27, SR-28, SR-30, SR-32, SR-34, SR-36, SR-37, SR-38, SR-42, SR-43, SR-46, SR-47, SR-48, SR-54, SR-57, SR-58, SR-59, SR-60, SR-61, SR-62, SR-64, SR-66, SR-67, SR-68, SR-70 and SR-74. **Weak-1 genotype** SR-29. **Medium-two genotypes** SR-5 and SR-35. **Strong- 16 genotypes** SR-3, SR-4, SR-9, SR-17, SR-18, SR-20, SR-22, SR-24, SR-39, SR-40, SR-41, SR-50, SR-56, SR-72, SR-73 and SR-75. **Very strong- 22 genotypes** SR-1, SR-2, SR-6, SR-8, SR-10, SR-14, SR-16, SR-19, SR-25, SR-31, SR-33, SR-44, SR-45, SR-49, SR-51, SR-52, SR-53, SR-55, SR-63, SR-65, SR-69 and SR-71.

Table 4.1 (cont.).

27.	**Spikelet: Colour of stigma**
	White- 35 genotypes SR-1, SR-4, SR-10, SR-11, SR-12, SR-17, SR-21, SR-25, SR-26, SR-29, SR-30, SR-31, SR-32, SR-33, SR-34, SR-36, SR-37, SR- 38, SR-41, SR-44, SR-45, SR-46, SR-47, SR-48, SR-49, SR-50, SR-51, SR-53, SR-54, SR-56, SR-57, SR-60, SR-64, SR-65 and SR- 67. **Light green- 23 genotypes** SR-5, SR-6, SR-8, SR-9, SR-13, SR-15, SR-16, SR-19, SR-22, SR-23, SR-28, SR-38, SR-42, SR-55, SR-58, SR-59, SR-61, SR-62, SR-66, SR-68, SR-69, SR-70 and SR-72. **Yellow- three genotypes** SR-14, SR-27 and SR-52. **Light purple- three genotypes** SR-3, SR-35 and SR-52. **Purple-11 genotypes** SR-2, SR-18, SR-20, SR-24, SR-39, SR-40, SR-43, SR-63, SR-71, SR-73 and SR-74.
28.	**Stem thickness:** all 75 genotypes have thin stem girth except SR-66 & SR-73 had medium girth.
29.	**Stem length (excleding panicle)**
	Very short- nine genotypes SR-21, SR-23, SR-26, SR-27, SR-28, SR-30, SR-54 and SR-55. **Short- 22 genotypes** SR-3, SR-4, SR-6, SR-7, SR- 8, SR-9, SR-10, SR-19, SR-20, SR-25, SR-31, SR-35, SR-38, SR-41, SR-45, SR-46, SR-57, SR-60, SR-69, SR-70, SR-72 and SR-73. **Medium- 39 genotypes** SR-2, SR-5, SR-11, SR-13, SR-14, SR-15, SR-16, SR-17, SR-18, SR-22, SR-24, SR-32, SR-33, SR-34, SR-36, SR-37, SR-39, SR-42, SR- 43, SR-44, SR-47, SR-48, SR-49, SR-50, SR-51, SR-53, SR-56, SR-59, SR-61, SR-62, SR-63, SR-64, SR-65, SR-66, SR-67, SR-68, SR-71, SR-74 and SR-75. **Long- five genotypes** SR-1, SR-12, SR-40, SR-52 and SR-58. **Very long- nil**
30.	**Stem: anthocyanin colouration of node**
	Absent- 44 genotypes SR-1, SR-3, SR-11, SR-12, SR-13, SR-14, SR-15, SR-17, SR-18, SR-21, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-32, SR-33, SR-34, SR-36, SR-37, SR-39, SR-42, SR- 43, SR- 45, SR-46, SR-47, SR-53, SR-54, SR-55, SR-59, SR-61, SR-62, SR-63, SR-64, SR-66, SR-67, SR-68, SR-69, SR-70, SR-72, SR-73 and SR-74. **Present- 31 genotypes** SR-2, SR-4, SR-5, SR-6, SR-7, SR-8, SR-9, SR-10, SR-16, SR-19, SR-20, SR-22, SR-25, SR-31, SR-35, SR-38, SR-40, SR-41, SR-44, SR-48, SR-49, SR-50, SR-51, SR-52, SR-56, SR-57, SR-58, SR-60, SR-65, SR-71 and SR-75.
31.	**Stem: intensity of anthocyanin colouration**
	Weak- three genotypes SR-20, SR-38 and SR-44 **Medium- 12 genotypes** SR-2, SR-6, SR-8, SR-10, SR-16, SR-22, SR-48, SR-50, SR-52, SR-56, SR-58 and SR-75. **Strong- 16 genotypes** SR-4, SR-5, SR-7, SR-9, SR-19, SR-25, SR-31, SR-40, SR-41, SR-49, SR-51, SR-57, SR-60, SR-65 and SR-71.

Table 4.1 (cont.).

32.	**Stem: anthocyanin colouration of inter nodes**
	Absent- 38 genotypes SR-3, SR-11, SR-12, SR-13, SR-14, SR-15, SR-16, SR-18, SR- 20, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-34, SR-36, SR-37, SR-39, SR-40, SR-42, SR-43, SR-46, SR-53, SR-54, SR-55, SR-61, SR-62, SR-63, SR-64, SR-66, SR-67, SR-68, SR-69, SR-70, SR-72 and SR-74. **Present- 37 genotyps** SR-1, SR-2, SR-4, SR-5, SR-6, SR-7, SR-8, SR-9, SR-10, SR-17, SR-19, SR-21, SR-22, SR-25, SR-31, SR-32, SR-33, SR-35, SR-38, SR- 41, SR-44, SR-45, SR-47, SR-48, SR-49, SR-50, SR-51, SR-52, SR-56, SR-57, SR-58, SR-59, SR-60, SR-65, SR-71, SR-73 and SR-75.
33.	**Panicle: length of main axis**
	Very short – nil **Short-** SR-73 **Medium- 29 genotypes** SR-2, SR-5, SR-7, SR-8, SR-9, SR-11, SR-14, SR-15, SR-20, SR-21, SR-22, SR-27, SR-28, SR-30, SR-36, SR-38, SR- 42, SR-44, SR-46, SR-47, SR-51, SR-54, SR-55, SR-57, SR-61, SR-64, SR-66, SR-68 and SR-74. **Long- 37 genotypes** SR-1, SR-3, SR-6, SR-10, SR-12 , SR-13, SR-16, SR-17, SR-18, SR-19, SR-23, SR-24, SR-25, SR-26, SR-29, SR-31, SR-32, SR-33, SR-34, SR-35, SR-37, SR-39, SR-43, SR-45, SR-48, SR-49, SR-50, SR-52, SR-53, SR-56, SR-58, SR-59, 60, SR-62, SR-67, SR-72 and SR-75. **Very long- eight genotypes** SR-4, 40, SR-41, SR-63, SR-65, SR-69, SR-70 and SR-71.
34.	**Panicle: curvature of main axis**
	Straight- SR-29 **Semi straight- 29 genotypes** SR-5, SR-9, SR-10, SR-11, SR-12, SR-13, SR-15, SR-21, SR-25, SR-28, SR-30, SR-35, SR-39, SR-40, SR-44, SR-48, SR-49, SR-53, SR-56, SR-60, SR-61, SR-62, SR-63, SR-64, SR-65, SR-66, SR-67, SR-73 and SR-75. **Drooping- 29 genotypes** SR-1, SR-2, SR-4, SR-14, SR-16, SR-17, SR-19, SR-20, SR-22, SR-24, SR-26, SR-27, SR-31, SR-34, SR-37, SR-38, SR-41, SR-42, SR-43, SR-45, SR-46, SR-47, SR-50, SR-51, SR-54, SR- 57, SR-58, SR-71 and SR-74. **Deflexed- 16 genotype** SR-3, SR-6, SR-7, SR, 8, SR-18, SR-23, SR-32, SR-33, SR-36, SR-52, SR-55, SR-59, SR-68, SR-69, SR-70 and SR-72.
35.	**Panicle number per plant**
	Few- 17 genotypes SR-5, SR-7, SR-11, SR-16, SR-18, SR-23, SR-24, SR-29, SR-34, SR-37, SR-38, SR-44, SR-51, SR-52, SR-57, SR-58 and SR-66. **Medium- 57 genotypes** SR-1, SR-2, SR-3, SR-4, SR-6, SR-8, SR-9, SR-10, SR-12, SR-13, SR-14, SR-15, SR-17, SR-19, SR-20, SR-21, SR-22, SR-25, SR-26, SR-27, SR-28, SR-30, SR-31, SR-32, SR-33, SR-35, SR-36, SR-39, SR-40, SR-41, SR-42, SR-43, SR-45, SR-46, SR-47, SR-48, SR-49, SR-50, SR-53, SR-54, SR-55, SR-56, SR-59, SR-61, SR-62, SR-63, SR-64, SR-65, SR-67, SR-68, SR-69, SR-70, SR-71, SR-72, SR-73, SR-74 and SR-75. **Many- 1 genotype** SR-60.

Table 4.1 (cont.).

36.	**Spikelet: Density of pubsence of lemma**
	Absent- nil **Weak- eight genotypes** SR-14, SR-20, SR-32, SR-38, SR-51, SR-52, SR-66 and SR-67. **Medium-22 genotypes** SR-3. SR-9, SR-10, SR-12, SR-13, SR-15, SR-22, SR-24, SR-28, SR-29, SR-35, SR-36, SR-38, SR-39, SR-40, SR-46, SR-53, SR-58, SR-60, SR-69, SR-70 and SR-72. **Strong-38 genotypes** SR-1, SR-4, 5, SR-6, SR-7, SR-8, SR-11, SR-16, SR-17, SR-18, SR-19, SR-26, SR-27, SR-30, SR-33, SR-34, SR-37, SR-41, SR-42, SR-43, SR-44, SR-45, SR-48, SR-49, SR-51, SR-54, SR-55, SR-56, SR-57, SR-62, SR-63, SR-64, SR-65, SR-68, SR-71, SR-73, SR-74 and SR-75. **Very strong- seven genotypes** SR-2, SR-23, SR-25, SR-31, SR-47, SR-51 and SR-59.
37.	**Spikelet colour of tip of lemma**
	White- one genotype SR-35. **Yellow- 21 genotypes** SR-11, SR-12, SR-14, SR-15, SR-20, SR-23, SR-26, SR-27, SR-28, SR-30, SR-32, SR-34, SR-37, SR-53, SR-54, SR-60, SR-64, SR-66, SR-67, SR-68 and SR-70. **Brown- 12 genotypes** SR-**4,** SR-9, SR-31, SR-33, SR-38, SR-41, SR-46, SR-62, SR-66, SR-69, SR-71 and SR-74. **Red- nil** **Purple- 30 genotypes** SR-5, SR-7, SR-13, SR-16, SR-18, SR-19, SR-21, SR-22, SR-24, SR-25, SR-29, SR-36, SR-39, SR-40, SR-42, SR-43, SR-44, SR-45, SR-47, SR-48, SR-50, SR-52, SR-55, SR-57, SR-58, SR-61, SR-63, SR-72, SR-73 and SR-75. **Black- 11 genotypes** SR-1, SR-2, SR-3, SR-6, SR-8, SR-10, SR-17, SR-51, SR-56, SR-59 and SR-65.
38.	**Lemma and palea colour**
	Straw- two genotypes SR-23 and SR-28. **Gold furrows on straw back ground- three genotypes** SR-27, SR-64 and SR-68. **Brown spots on straw back ground- 11 genotypes** SR-11, SR-13, SR-14, SR-18, SR-26, SR-30, SR-32, SR-34, SR-42, SR-54 and SR-63. **Brown furrows on straw back ground- 20 genotypes** SR-4, SR-9, SR-12, SR-15, SR-17, SR-24, SR-31, SR-33, SR-35, SR-40, SR-46, SR-49, SR-50, SR-53, SR-59, SR-60, SR-69, SR-70, SR-71 and SR-72. **Brown- eight genotypes** SR-20, SR-36, SR-37, SR-52, SR-56, SR-62, SR-66 and SR- 67. **Reddish to light purple- two genotypes** SR-29 and SR-61. **Purple spots on straw back ground: -** **Purple- 12 genotypes** SR-2, SR-3, SR-19, SR-21, SR-38, SR-44, SR-45, SR-47, SR-48, SR-55, SR-57 and SR-58. **Black- four genotypes** SR-8, SR-10, SR-51 and SR-65.

Table 4.1 (cont.).

39.	**Panicle awns**
	Absent: 45 genotypes SR-1, SR-5, SR-6, SR-7, SR-8, SR-9, SR-11, SR-13, SR-14, SR-15, SR-16, SR-17, SR-18, SR-19, SR-20, SR-22, SR-28, SR-31, SR-33, SR-36, SR-37, SR-38, SR-39, SR-40, SR-42, SR-43, SR-46, SR-49, SR-50, SR-51, SR-52, SR-53, SR-56, SR-57 SR-59, SR-62, SR-64, SR-65, SR-66, SR-68, SR-69, SR-71, SR-73, SR-74 and SR-75. **Present- 30 genotypes** SR-2, SR-3, SR-4, SR-10, SR-12, SR-21, SR-23, SR-24, SR-25, SR-26, SR-27, SR-29, SR-30, SR-32, SR-34, SR-35, SR-41, SR-44, SR-45, SR-47, SR-48, SR-54, SR-55, SR-58, SR-60, SR-61, SR-63, SR-67, SR-70 and SR-72.
40.	**Panicle: colour of awns (late observation)**
	Yellowish white- eight genotypes SR-12, SR-27, SR-29, SR-30, SR-34, SR-54, SR-60 and SR-70. **Purple- 12 genotypes** SR-2, SR-4, SR-21, SR-25, SR-41, SR-45, SR-47, SR-48, SR-55, SR-58, SR-61 and SR-63. **Black- nil**
41.	**Panicle: length of longest awns**
	Very short- three genotypes SR-4, SR-25 and SR-63. **Short- nine genotypes** SR-2, SR-3, SR-12, SR-24, SR-29, SR-41, SR-47, SR-61 and SR-72. **Medium- 13 genotypes** SR-10, SR-21, SR-27, SR-30, SR-32, SR-34, SR-44, SR-45, SR-48, SR-54, SR-55, SR-67 and SR-70. **Long: four genotypes** SR-26, SR-35, SR-58 and SR-60. **Very long- one genotype** SR-23.
42.	**Panicle: distribution of awns**
	Tips only- 14 genotypes SR-2, SR-3, SR-4, SR-12, SR-24, SR-29, SR-34, SR-41, SR-44, SR-47, SR-54, SR-61, SR-67 and SR-72. **Upper half only- nine genotypes** SR-10, SR-25, SR-30, SR-45, SR-48, SR-55, SR-60, SR-63 and SR-70. **Whole length- seven genotypes** SR-21, SR-23, SR26, SR-27, SR-32, SR-35 and SR-58.
43.	**Panicle: presence of secondary branching-** present from SR-1 to SR-75.
44.	**Panicle- secondary branching**
	Weak- 14 genotypes SR-5, SR-6, SR-10, SR-12, SR-19, SR-20, SR-22, SR-24, SR-25, SR-45, SR-50, SR-52, SR-59 and SR-69. **Strong- 54 genotypes** SR-1, SR-3, SR-4, SR-8, SR-9, SR-11, SR-13, SR-14, SR-15, SR-16, SR-17, SR-18, SR-21, SR-23, SR-26, SR-28, SR-29, SR-30, SR-31, SR-32, SR-33, SR-34, SR-36, SR-37, SR-38, SR-39, SR-40, SR-41, SR-42, SR-44, SR-46, SR-47, SR-48, SR-49, SR-51, SR-53, SR-54, SR-55, SR-56, SR-57, SR-58, SR-60, SR-61, SR-62, SR-65, SR-66, SR-67, SR-68, SR-70, SR-71, SR-72, SR-73, SR-74 and SR-75. **Clustering- seven genotypes** SR-2, SR-7, SR-27, SR-35, SR-43, SR-63 and SR-64.

Table 4.1 (cont.).

45.	**Panicle attitude of branches**
	Erect- one genotype SR-73. **Erect to semi erect- two genotypes** SR-37 and SR-38. **Semi erect- 37 genotypes** SR-2, SR-7, SR-11, SR-12, SR-13, SR-14, SR-15, SR-18, SR-21, SR-23, SR-26, SR-27, SR-28, SR-29, SR-30, SR-32, SR-34, SR-35, SR-36, SR-39, SR-40, SR-42, SR-44, SR-46, SR-47, SR-48, SR-49, SR-51, SR-54, SR-56, SR-57, SR-58, SR-60, SR-61, SR-63, SR-64 and SR-72. **Semi erect to spreading- 19 genotypes** SR-1, SR-3, SR-4, SR-9, SR-17, SR-22, SR-24, SR-31, SR-43, SR-52, SR-53, SR-55, SR-59, SR-62, SR-65, SR-66, SR-68, SR-70 and SR-75. **Spreading- 16 genotypes** SR-4, SR-5, SR-6, SR-8, SR-10, SR-16, SR-19, SR-20, SR-25, SR-33, SR-45, SR-50, SR-67, SR-69, SR-71 and SR-74.
46.	**Panicle exertion**
	Partly exerted- 14 geenotypes SR-7, SR-12, SR-13, SR-21, SR-23, SR-26, SR-27, SR-38, SR-41, SR-43, SR-53, SR-60, SR-66 and SR-74. **Mostly exerted- 23 genotypes** SR-2, SR-3, SR-11, SR-18, SR-20, SR-29, SR-30, SR-34, SR-36, SR-37, SR-42, SR-45, SR-46, SR-51, SR-52, SR-54, SR-56, SR-57, SR-63, SR-64, SR-65 and SR-70. **Well exerted- 38 genotypes** SR-1, SR-4, SR-5, SR-6, SR-8, SR-9, SR-10, SR-14, SR-15, SR-16, SR-17, SR-19, SR-22, SR-24, SR-25, SR-31, SR-32, SR-33, SR-35, SR-39, SR-40, SR-44, SR-47, SR-48, SR-49, SR-50, SR-55, SR-58, SR-59, SR-61, SR-62, SR-67, SR-68, SR-69, SR-71, SR-72, SR-73 and SR-75.
47.	**Time of maturity**
	Very early- nil **Early- nil** **Medium- 15 genotypes** SR-1, SR-6, SR-11, SR-14, SR-15, SR-18, SR-23, SR-26, SR-28, SR-46, SR-49, SR-69, SR-70, SR-71 and SR-72. **Late- 60 genotypes** SR-2, SR-3, SR-4, SR-5, SR-7, SR-8, SR-9, SR-10, SR-12, SR-13, SR-16, SR-17, SR-19, SR-20, SR-21, SR-22, SR-24, SR-25, SR-27, SR-29, SR-30, SR-31, SR-32, SR-33, SR-34, SR-35, SR-36, SR-37, SR-38, SR-39, SR-40, SR-41, SR-42, SR-43, SR-44, SR-45, SR-47, SR-48, SR-50, SR-51, SR-52, SR-53, SR-54, SR-55, SR-56, SR-57, SR-58, SR-59, SR-60, SR-61, SR-62, SR-63, SR-64, SR-65, SR-66, SR-67, SR-68, SR-73, SR-74 and SR-75. **Very late- nil**

Table 4.1 (cont.).

48.	**Leaf sensence**
	Early- 18 genotypes SR-8, SR-11, SR-14, SR-15, SR-20, SR-28, SR-35, SR-39, SR-40, SR-43, SR-45, SR-52, SR-54, SR-56, SR-59, SR-62, SR-70 and SR-72. **Intermediate- 27 genotypes** SR-3, SR-4, SR-10, SR-13, SR-16, SR-18, SR-22, SR-23, SR-25, SR-27, SR-29, SR-30, SR-33, SR-34, SR-41, SR-44, SR-46, SR-49, SR-53, SR-57, SR-60, SR-61, SR-63, SR-65, SR-68, SR-73 and SR-74. **Late- 30 genotypes** SR-1, SR-2, SR-5, SR-6, SR-7, SR-9, SR-12, SR-17, SR-19, SR-21, SR-24, SR-26, SR-31, SR-32, SR-36, SR-37, SR-38, SR-42, SR-47, SR-48, SR-50, SR-51, SR-55, SR-58, SR-64, SR-66, SR-67, SR-69, SR-71 and SR-75.
49.	**Sterile lemma colour**
	Straw- 41 genotypes SR-2, SR-3, SR-5, SR-6, SR-11, SR-12, SR-13, SR-14, SR-15, SR-17, SR-18, SR-22, SR-23, SR-24, SR-26, SR-27, SR-28, SR-29, SR-30, SR-32, SR-34, SR-36, SR-37, SR-40, SR-42, SR-43, SR-49, SR-52, SR-53, SR-54, SR-55, SR-57, SR-60, SR-62, SR-63, SR-64, SR-66, SR-67, SR-68, SR-72 and SR-74. **Gold- 10 genotypes** SR-4, SR-8, SR-10, SR-16, SR-19, SR-31, SR-41, SR-46, SR-51 and SR-70. **Red- nil** **Purple-24 genotypes** SR-1, SR-7, SR-9, SR-20, SR-21, SR-25, SR-33, SR-35, SR-38, SR-39, SR-44, SR-45, SR-47, SR-48, SR-50, SR-56, SR-58, SR-59, SR-64, SR-65, SR-69, SR-71, SR-73 and SR-75.
50.	**Grain: weight of 1000 grain**
	Very low- one genotype SR-1. **Low- two genotypes** SR-59 and SR-60. **Medium- 51 genotypes** SR-3, SR-6, SR-7, SR-10, SR-11, SR-12, SR-13, SR-15, SR-16, SR-17, SR-19, SR-21, SR-22, SR-23, SR-25, SR-26, SR-27, SR-29, SR-30, SR-31, SR-32, SR-33, SR-37, SR-38, SR-39, SR-41, SR-42, SR-44, SR-45, SR-46, SR-47, SR-48, SR-49, SR-50, SR-51, SR-53, SR-54, SR-55, SR-56, SR-57, SR-61, SR-62, SR-64, SR-65, SR-66, SR-67, SR-68, SR-69, SR-73, SR-74 and SR-75. **High- 17 genotypes** SR-2, SR-4, SR-5, SR-8, SR-9, SR-14, SR-28, SR-34, SR-35, SR-36, SR-40, SR-43, SR-52, SR-63, SR-70, SR-71 and SR-72. **Very high- four gnotypes** SR-18, SR-20, SR-24 and SR-58.

Table 4.1 (cont.).

51.	**Grain: length**
	Very short- nil **Short- 30 genotypes** SR-1, SR-3, SR-4, SR-5, SR-6, SR-7, SR-11, SR-12, SR-13, SR-22, SR-31, SR-33, SR-37, SR-38, SR-39, SR-40, SR-43, SR-45, SR-49, SR-50, SR-52, SR-53, SR-56, SR-62, SR-65, SR-66, SR-67, SR-68, SR-73 and SR-75. **Medium- 40 genotypes** SR-2, SR-8, SR-9, SR-10, SR-14, SR-15, SR-16, SR-17, SR-18, SR-19, SR-20, SR-21, SR-24, SR-25, SR-28, SR-29, SR-30, SR-34, SR-36, SR-41, SR-42, SR-44, SR-46, SR-47, SR-48, SR-51, SR-54, SR-55, SR-57, SR-58, SR-59, SR-60, SR-61, SR-63, SR-64, SR-69 and SR-70, SR-71, SR-72 and SR-74. **Long- five genotypes** SR-23, SR-26, SR-27, SR-32 and SR-35. **Very long- nil**
52.	**Grain width**
	Narrow- 14 genotypes SR-5, SR-9, SR-15, SR-18, SR-20, SR-22, SR-31, SR-33, SR-34, SR-49, SR-50, SR-72, SR-73 and SR-75. **Very narrow: all other 61 genotypes**
53.	**Grain phenol reaction of lemma:** present in all genotypes from SR-1 to SR-75.
54.	**Decorticated grain: length**
	Short- 20 genotypes SR-3, SR-5, SR-6, SR-7, SR-12, SR-13, SR-22, SR-28, SR-33, SR-38, SR-39, SR-40, SR-52, SR-53, SR-56, SR-57, SR-62, SR-67, SR-73 and SR-74. **Medium- 45 genptypes** SR-1, SR-2, SR-4, SR-8, SR-9, SR-10, SR-11, SR-14, SR-15, SR-16, SR-17, SR-19, SR-21, SR-24, SR-25, SR-29, SR-30, SR-31, SR-34, SR-35, SR-36, SR-37, SR-41, SR-42, SR-43, SR-44, SR-45, SR-46, SR-47, SR-49, SR-50, SR-51, SR-54, SR-55, SR-59, SR-61, SR-63, SR-64, SR-65, SR-66, SR-68, SR-69, SR-71, SR-72 and SR-75. **Long- 10 genotypes** SR-18, SR-20, SR-23, SR-26, SR-27, SR-32, SR-48, SR-58, SR-60 and SR-70.
55.	**Decorticated grain: width-** all genotypes have narrow decorticated grain width.
56.	**Decorticated grain: shape**
	Short slender- 47 genotypes SR-1, SR-3, SR-4, SR-5, SR-6, SR-7, SR-8, SR-9, SR-10, SR-11, SR-12, SR-13, SR-14, SR-15, SR-17, SR-19, SR-21, SR-24, SR-25, SR-29, SR-31, SR-33, SR-34, SR-36, SR-37, SR-38, SR-39, SR-40, SR-41, SR-42, SR-45, SR-46, SR-49, SR-50, SR-51, SR-52, SR-53, SR-56, SR-65, SR-66, SR-67, SR-68, SR-71, SR-72, SR-73, SR-74 and SR-75. **Medium slender- 5 genotypes** SR-22, SR-28, SR-30, SR-61 and SR-62. **Long slender- 19 genotypes** SR-2, SR-16, SR-18, SR-32, SR-35, SR-43, SR-44, SR-47, SR-48, SR-54, SR-55, SR-57, SR-58, SR-59, SR-60, SR-63, SR-64, SR-69 and SR-70. **Basmati type- four genotypes** SR-20, SR-23, SR-26 and SR-27.

Table 4.1 (cont.).

57.	**Decorticated grain colour**
	Red- 13 genotypes SR-12, SR-13, SR-16, SR-39, SR-40, SR-45, SR-53, SR-56, SR-57, SR-60, SR-65, SR-67, and SR-69. **White- other 62 genotypes**
58.	**Endosperm: content of amylose-** present in all genotypes from SR-1 to SR-75.
59.	**Endosperm content of amylose**
	Very low- 38 genotypes SR-2, SR-3, SR-7, SR-8, SR-9, SR-10, SR-11, SR-12, SR-13, SR-21, SR-29, SR-30, SR-35, SR-36, SR-37, SR-38, SR-40, SR-42, SR-43, SR-44, SR-46, SR-47, SR-48, SR-52, SR-53, SR-54, SR-55, SR-57, SR-58, SR-59, SR-60, SR-61, SR-63, SR-64, SR-65, SR-67, SR-70 and SR-74. **Low- 27 genotypes** SR-1, SR-4, SR-5, SR-14, SR-15, SR-17, SR-18, SR-19, SR-20, SR-22, SR-23, SR-24, SR-25, SR-31, SR-32, SR-34, SR-39, SR-41, SR-45, SR-49, SR-50, SR-56, SR-68, SR-71, SR-72, SR-73 and SR-75. **Itermediate- nine genotypes** SR-5, SR-16, SR-27, SR-28, SR-33, SR-51, SR-62, SR-66 and SR-69. **High- one genotype** SR-26. **Very high- nil**
60.	**Varieties with endosperm of amylose absent: expression of white core**
61.	**Gelatinization temparature through alkali spreading value**
	Low- 36 genotypes SR-4, SR-5, SR-6, SR-7, SR-8, SR-11, SR-14, SR-17, SR-21, SR-22, SR-23, SR-27, SR-28, SR-29, SR-30, SR-32, SR-33, SR-34, SR-36, SR-37, SR-38, SR-41, SR-42, SR-45, SR-46, SR-47, SR-48, SR-49, SR-50, SR-54, SR-55, SR-57, SR-58, SR-59, SR-60 and SR-75. **Medium- 36 genotypes** SR-1, SR-2, SR-3, SR-9, SR-10, SR-12, SR-13, SR-15, SR-16, SR-19, SR-20, SR-24, SR-26, SR-31, SR-35, SR-39, SR-40, SR-43, SR-44, SR-51, SR-52, SR-56, SR-61, SR-62, SR-63, SR-64, SR-65, SR-66, SR-67, SR-68, SR-69, SR-70, SR-71, SR-72, SR-73 and SR-74. **High medium- three genotypes** SR-18, SR-25 and SR-53.
62.	**Decorticated grain aroma**
	Present- two genotypes SR-23 and SR-26 **Abent- all other genotpes**

Table 4.2. Mean performance of 75 soft rice genotypes for grain yield and its components traits

S. No	Genotypes	Days to 50% flowering	Plant height (cm)	Number of tillers per plant	Number of Productive tillers per plant	Panicle length (cm)	Per cent filled grains per panicle	Days to maturity	seed yield per plant (g)	Test weight (1000 grain) (g)
1	Joha bora	111.00	136.00	19.00	15.33	27.90	62.72	139.00	17.35	14.50
2	Ranga bora	114.66	119.16	16.00	14.00	24.16	96.79	146.33	14.64	26.73
3	Sungal bora	115.00	103.46	12.33	11.33	28.60	87.54	145.00	23.24	24.33
4	Noldong bora	117.33	103.06	18.00	15.00	31.80	84.86	145.33	23.44	27.06
5	Tegori bora	116.66	112.46	15.33	13.66	24.86	88.63	145.00	25.93	27.00
6	Bongari bora	110.00	96.50	15.00	12.66	26.53	98.09	139.66	28.99	24.45
7	Kola ampakhi bora	119.66	106.66	14.33	9.00	23.86	87.57	147.00	17.90	21.50
8	Bora-1	111.66	108.40	26.33	22.66	25.60	66.41	143.00	25.54	26.40
9	Dadhora bora	110.00	105.00	18.00	12.66	25.23	86.53	141.00	29.48	27.00
10	Chokua bora	116.66	110.60	18.00	15.00	29.80	76.54	144.00	15.97	25.00
11	Sakoibhanu bora	111.00	115.50	18.33	15.33	25.13	96.31	139.66	14.05	22.33
12	Kola bora	123.00	142.26	15.00	14.00	27.53	91.70	152.33	11.00	21.00
13	Misiri chokura	120.66	130.93	15.00	13.33	26.73	83.28	149.66	23.26	23.33
14	Boka chokura 2	107.66	112.06	17.66	17.33	25.33	82.06	139.33	13.33	25.83
15	Ch-5 bora chokura	111.66	116.73	18.00	16.66	24.46	81.73	140.33	12.92	25.50
16	Kajori chokura	110.66	121.46	13.66	12.66	30.66	97.51	141.66	25.92	23.15
17	Kola boka chokua	114.33	118.20	14.66	11.66	27.90	85.42	147.00	16.70	23.53
18	Haru chokua	112.33	114.63	14.33	12.66	26.00	85.48	137.00	16.88	33.16
19	Boga chokura	115.33	108.20	15.00	14.33	30.56	86.87	142.33	12.06	25.00
20	Lahi chokura	114.00	102.46	15.00	11.00	22.33	93.11	141.00	25.97	32.76
21	Sam chokura	117.00	72.56	21.66	20.00	23.80	90.50	149.66	13.85	23.66
22	Maju chokura	116.33	116.20	18.66	12.33	24.93	93.43	143.00	18.35	24.40

Table 4.2 (cont.).

S. No	Genotypes	Days to 50% flowering	Plant height (cm)	Number of tillers per plant	Number of Productive tillers per plant	Panicle length (cm)	Per cent filled grains per panicle	Days to maturity	seed yield per plant (g)	Test weight (1000 grain) (g)
23	Ham chokura	107.66	79.73	11.33	10.00	30.03	75.80	136.00	13.70	21.66
24	Hampori chakua	112.33	117.73	12.33	11.00	30.60	72.19	144.00	21.64	32.16
25	Kasturi	111.00	110.73	15.33	15.33	27.93	93.11	141.33	15.67	25.33
26	Vasumati	110.00	82.26	12.00	13.00	27.73	76.28	139.66	9.54	21.43
27	Vikas	111.00	76.46	11.33	11.00	24.46	94.93	143.66	13.79	24.13
28	Jaya	111.66	75.86	18.66	16.00	23.46	87.68	140.33	17.43	26.40
29	Aghoni bora	119.66	75.73	17.00	14.66	26.26	73.72	151.00	29.82	23.00
30	Bhogali bora	119.66	78.46	19.00	17.00	24.53	84.99	152.33	16.25	25.00
31	Abor bora	113.00	105.00	22.33	16.33	28.40	81.38	142.66	12.88	24.00
32	Beji bora1	115.00	130.26	17.00	13.66	28.46	90.04	145.33	16.96	23.66
33	Begun bora	112.00	115.43	19.66	17.00	27.20	95.14	141.00	21.01	25.66
34	Boga bora-1	114.00	117.66	17.66	15.00	26.56	75.32	141.66	13.71	30.66
35	Boga bora -3	124.00	110.33	17.66	15.66	26.36	90.77	151.66	26.32	28.00
36	Bhat bora	123.66	129.60	17.00	15.00	24.4	76.82	151.00	25.67	24.00
37	Bora 1	122.33	125.93	11.00	10.33	27.73	71.57	149.66	12.05	24.33
38	Bora 3	130.33	105.33	12.33	12.33	25.40	35.40	159.66	25.57	21.00
39	Bora 5	112.00	115.53	23.66	20.33	29.36	81.36	142.00	17.50	23.66
40	Botia bora	113.33	131.06	22.66	20.66	33.60	95.64	142.66	19.86	27.66
41	Bor mulbhog	115.00	101.00	18.66	16.66	33.20	80.82	145.00	23.93	22.66
42	Chakua bora 1	112.33	121.93	19.0	17.66	23.53	92.55	142.66	15.91	24.33
43	Chansep bora	111.00	122.26	9.66	8.66	27.00	78.93	141.33	16.14	27.00
44	Chandra bora	111.66	115.33	17.00	15.00	25.76	85.92	141.66	23.34	23.00
45	Danbori bora	115.00	110.33	19.66	16.66	27.46	76.21	145.00	16.07	21.33

Table 4.2 (cont.).

S. No	**Genotypes**	**Days to 50% flowering**	**Plant height (cm)**	**Number of tillers per plant**	**Number of Productive tillers per plant**	**Panicle length (cm)**	**Per cent filled grains per panicle**	**Days to maturity**	**seed yield per plant (g)**	**Test weight (1000 grain) (g)**
46	Fakial bora	111.00	107.00	18.33	17.33	25.40	97.96	139.33	11.30	23.66
47	Gella bora	120.00	122.40	13.66	11.66	24.46	91.49	147.66	21.52	21.66
48	Ghew bora 1	122.33	128.20	16.00	14.66	29.33	77.45	150.33	15.38	25.66
49	Garu chakua bora 2	112.33	116.80	14.66	13.66	30.60	86.02	139.00	19.75	25.66
50	Gomiri bora	113.66	116.60	11.00	12.00	29.50	90.41	144.00	13.62	25.66
51	Naldang bora	113.66	119.53	15.00	14.33	21.73	90.05	141.00	26.36	25.50
52	Helochi bora 1	113.66	131.73	14.66	15.00	30.26	66.05	143.00	14.63	26.73
53	Helochi bora 2	118.33	125.20	17.66	16.00	27.56	84.46	146.00	17.68	21.00
54	Aghoni bora	122.00	75.73	17.00	15.66	24.86	81.51	151.00	16.60	23.66
55	Bhogali bora	119.66	70.00	16.33	15.00	21.46	95.40	149.00	18.06	23.00
56	KMJ bora 56	119.33	126.96	16.00	12.00	30.53	86.30	149.00	21.86	24.00
57	KMJ bora 53	118.00	108.00	11.00	10.33	24.00	91.43	147.00	14.30	21.00
58	KMJ bora 51	118.33	138.26	16.00	14.00	27.00	86.63	146.00	21.20	31.00
59	KMJ bora 41	120.00	115.33	17.00	15.33	27.80	89.80	149.000	19.20	19.00
60	KMJ bora 36	123.33	106.00	23.00	19.33	26.13	70.60	153.33	8.56	20.66
61	KMJ bora 49	121.33	125.53	13.33	11.33	24.93	86.88	151.33	19.20	23.00
62	KMJ bora 74	111.33	114.33	17.66	13.33	27.06	87.73	141.66	22.49	22.83
63	KMJ bora 5	111.33	129.73	16.33	15.33	32.96	83.33	141.66	24.65	26.16
64	KMJ bora 13	116.33	122.93	13.33	13.66	24.86	80.83	148.00	21.46	24.60
65	KMJ bora 21	116.00	120.06	14.00	13.00	30.33	61.28	149.00	13.61	22.33

Table 4.2 (cont.).

S. No	**Genotypes**	**Days to 50% flowering**	**Plant height (cm)**	**Number of tillers per plant**	**Number of Productive tillers per plant**	**Panicle length (cm)**	**Per cent filled grains per panicle**	**Days to maturity**	**seed yield per plant (g)**	**Test weight (1000 grain) (g)**
66	KMJ bora 25	117.66	121.20	16.33	13.33	22.10	66.41	149.33	17.86	23.00
67	Boka chakua 1	122.00	126.16	19.00	13.66	28.00	77.43	150.66	22.50	23.93
68	Boka chakua 2	115.00	122.60	15.33	11.00	25.06	45.31	142.33	19.90	24.13
69	Kajoli chakua	109.66	109.60	14.66	12.66	32.46	94.58	139.00	21.28	23.00
70	Kalamdani chakua	110.00	101.33	16.00	15.00	30.90	82.08	140.33	18.33	27.00
71	Lahi chakua	110.33	112.66	19.33	15.66	32.20	98.40	139.66	21.20	27.50
72	Maju chakua 1	110.33	103.06	16.33	14.00	29.73	95.70	139.00	21.54	27.60
73	Maju chakua 2	113.66	104.93	12.33	11.66	18.30	89.27	142.33	21.78	25.00
74	Misiri chakua	124.00	121.26	21.00	19.33	25.66	94.71	152.00	21.17	21.00
75	Sam chakua	114.00	114.80	17.33	13.00	27.40	96.56	146.33	24.33	21.00
	Mean	115.37	111.79	16.41	14.32	27.01	83.94	144.76	18.97	24.50
	C.V (%)	1.39	2.11	6.90	9.44	6.48	1.07	0.81	5.31	4.18
	S.E±	0.93	1.36	0.65	0.78	1.01	0.51	0.68	0.58	0.59
	C.D at 5%	2.60	3.82	1.82	2.18	2.82	1.45	1.90	1.62	1.65
	C.D at 1%	3.43	5.04	2.41	2.88	3.73	1.91	2.52	2.14	2.18

Table 4.4. Estimates of variability, heritability (broad sense), genetic advance and genetic advance as per cent of mean for grain yield and its components in soft rice genotypes

S.No.	Character	Range	PCV (%)	GCV (%)	Heritability in Broad sense (h^2_{bs}) (%)	Genetic Advance Per cent (at 5%)	GA as per cent ofmean (at 5%)
1.	Days to 50% flowering	107.66-130.33	4.20	3.97	89.0	8.9	7.71
2.	Plant height (cm)	70.00-142.26	14.60	14.44	97.9	32.91	29.44
3.	Number of tillars per plant	9.66-26.33	20.38	19.18	88.5	6.10	37.18
4.	Number of productive tillers per plant	8.66-22.66	20.53	18.23	78.8	4.77	33.36
5.	Panicle length (cm)	18.30-33.60	12.38	10.54	72.5	4.99	18.49
6.	Per cent filled grains per panicle	35.40-98.40	13.80	13.76	99.4	23.72	28.26
7.	Days to maturity	136.00-159.66	3.29	3.19	93.8	9.22	6.36
8.	Seed yield per plant (g)	8.56-29.82	26.62	26.08	96.0	9.99	52.65
9.	Test weight (g)	14.50-33.16	12.89	12.19	89.5	5.82	23.76

Table 4.6. Intra (diagonal) and Inter cluster average of D^2 values of soft rice genotypes

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**
Cluster I	**104.95**	284.18	195.12	192.07	311.65	861.07	1425.51
Cluster II		**157.08**	491.23	473.68	236.14	341.21	743.29
Cluster III			**0.00**	361.54	318.15	1286.81	1795.23
Cluster IV				**0.00**	676.12	1199.44	1817.85
Cluster V					**0.00**	474.78	693.97
Cluster VI						**0.00**	186.32
Cluster VII							**0.00**

Table 4.7. Cluster means for yield components and quality traits (D^2 analysis) in soft rice genotypes

Cluster No.	Days to 50% flowering	Plant height (cm)	Number of tillers per plant	Number of Productive tillers per plant	Panicle length (cm)	Per cent filled grains per panicle	Days to maturity	seed yield per plant (g)	Test weight (1000 grain) (g)
Cluster I	115.07	112.63	16.42	14.28	27.10	87.24	144.36	19.32	24.98
Cluster II	113.88	110.69	17.08	15.21	27.51	68.20	144.04	15.10	22.09
Cluster III	119.67	70.00	16.33	15.00	21.47	95.40	149.00	18.07	23.00
Cluster IV	123.00	142.27	15.00	14.00	27.53	91.71	152.33	11.00	21.00
Cluster V	119.67	75.73	17.00	14.67	26.27	73.72	151.00	29.83	23.00
Cluster VI	115.00	122.60	15.33	11.00	25.07	45.31	142.33	19.91	24.13
Cluster VII	130.33	105.33	12.33	12.33	25.40	35.40	159.67	25.57	21.00

Table 4.8. Relative contribution of different traits towards total genetic divergence in soft rice

S. No.	Character	No. of times ranked first	Contribution (%)
1	Days to 50% flowering	14	50.45
2	Plant height (cm)	621	2237.84
3	Number of tillars per plant	70	252.25
4	Number of productive tillers per plant	4	14.41
5	Panicle length (cm)	13	46.85
6	Per cent filled grains per panicle	1438	5181.98
7	Days to maturity	112	403.6
8	Seed yield per plant (g)	400	1441.44
9	Test weight (g)	103	371.17

Table.4.9. Estimation of phenotypic and genotypic correlation coefficients between yield and its component characters

Character		Days to 50% flowering	Plant height (cm)	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)	Per cent filled grains per panicle	Days to maturity	Test weight (g)	Seed yield per plant(g)
Days to 50% flowering	**G**	**1.000**	0.1272	-0.0132	-0.0194	-0.2388	-0.2802	0.09605	-0.2515	0.0721
	P	**1.000**	0.1219	0.0012	-0.0146	-0.1795**	-0.2660**	0.8824**	-0.2284**	0.0701
Plant height(cm)	**G**		**1.000**	-0.0199	-0.0634	0.2552	-0.0956	0.0485	0.0165	0.0462
	P		**1.000**	-0.0145	-0.0557	0.2179**	-0.0951	0.0438	0.0228	0.0449
Number of tillers per plant	**G**			**1.000**	0.9100	0.0604	0.0561	0.0110	-0.0502	0.0384
	P			**1.000**	0.8207**	0.0377	0.0563	0.0112	-0.0545	0.0348
Number of productive tillers per plant	**G**				**1.000**	0.1031	0.0581	0.0313	-0.0361	-0.0918
	P				**1.000**	0.0517	0.0515	0.0234	-0.0417	-0.0812
Panicle length (cm)	**G**					**1.000**	-0.0399	-0.2151	0.0592	-0.0115
	P					**1.000**	-0.0357	-0.1785**	0.0522	-0.0038
Per cent filled grains per panicle	**G**						**1.000**	-0.2846	0.1564	0.0566
	P						**1.000**	-0.2742**	0.1463*	0.0587
Days to maturity	**G**							**1.000**	-0.3130	0.0650
	P							**1.000**	-0.2837**	0.0575
Test weight (g)	**G**								**1.000**	0.1831
	P								**1.000**	0.1666

P -represents phenotypic correlation coefficient; **G-** represents genotypic correlation coefficient;

*5% level of significance, **1% level of significance

Table.4.10. Estimation of genotypic and phenotypic direct and indirect effects between yield and yield attributing characters

Character		Days to 50% flowering	Plant height (cm)	Number of tillers per plant	Number of productive tillers per plant	Panicle length (cm)	Per cent filled grains per panicle	Days to maturity	Test weight (g)	Correlation with grain yield per plant (r)
Days to 50% flowering	G	**-0.3215**	-0.0409	0.0043	0.0063	0.0768	0.0901	-0.3088	0.0809	0.0721
	P	**0.0272**	0.0033	0.0000	-0.0004	-0.0049	-0.0072	0.0240	-0.0062	0.0701
Plant height(cm)	G	0.0023	**0.0183**	-0.0004	-0.0012	0.0047	-0.0017	0.0009	0.0003	0.0462
	P	0.0026	**0.0212**	-0.0003	-0.0012	0.0046	-0.0020	0.0009	0.0005	0.0449
Number of tillers per plant	G	-0.0105	-0.0158	**0.7967**	0.7250	0.0481	0.0447	0.0088	-0.0400	0.0384
	P	0.0004	-0.0046	**0.3199**	0.2626	0.0120	0.0180	0.0036	-0.0174	0.0348
Number of productive tillers per plant	G	0.0163	0.0530	-0.7618	**-0.8371**	-0.0863	-0.0486	-0.0262	0.0302	-0.0918
	P	0.0050	0.0190	-0.2799	**-0.3411**	-0.0176	-0.0176	-0.0080	0.0142	-0.0812
Panicle length (cm)	G	-0.0098	0.0104	0.0025	0.0042	**0.0409**	-0.0016	-0.0088	0.0024	-0.0115
	P	-0.0027	0.0032	0.0006	0.0008	**0.0148**	-0.0005	-0.0026	0.0008	-0.0038
Per cent filled grains per panicle	G	-0.0214	-0.0073	0.0043	0.0044	-0.0031	**0.0765**	-0.0218	0.0120	0.0566
	P	-0.0188	-0.0067	0.0040	0.0036	-0.0025	**0.0707**	-0.0194	0.0103	0.0587
Days to maturity	G	0.4807	0.0243	0.0055	0.0157	-0.1077	-0.1424	**0.5005**	-0.1567	0.0650
	P	0.1014	0.0050	0.0013	0.0027	-0.0205	-0.0315	**0.1149**	-0.0326	0.0575
Test weight (g)	G	-0.0639	0.0042	-0.0128	-0.0092	0.0150	0.0397	-0.0795	**0.2540**	0.1831
	P	-0.0450	0.0045	-0.0107	-0.0082	0.0103	0.0288	-0.0559	**0.1970**	0.1666

Phenotypic residual effect = 0.9564

Genotypic residual effect = 0.9121

P- represents phenotypic correlation coefficient;

G- represents genotypic correlation coefficient.

Bold values- direct effects

Normal values- indirect effects

Table 4.3. Analysis of variance for grain yield and its components traits in soft rice genotypes

S.No.	Character	Mean sum of squares		
		Replications (d.f=2)	Treatments (d.f=74)	Error (d.f=148)
1.	Days to 50% flowering	3.29	65.53**	2.6
2.	Plant height (cm)	15.49	788.20**	5.61
3.	Number of tillers per plant	12.41**	31.02**	1.28
4.	Number of productive tillars per plant	19.24**	22.29**	1.83
5.	Panicle length (cm)	5.30	27.40**	3.07
6.	Per cent filled grains per panicle	5.93**	401.25**	0.80
7.	Days to maturity	12.65**	65.43**	1.40
8.	Seed yield per plant	0.15	74.51**	1.01
9.	Test weight (gm)	5.75**	27.84**	1.05

Table 4.5. Clustering pattern among 75 soft rice genotypes (D^2 analysis)

Cluster No	**No. of genotypes**	**Names of the Genotypes**
I	62	SR-2, SR-3, SR-4, SR-5, SR-6, SR-7, SR-9, SR-10, SR-11, SR-13, SR-14, SR-15, SR-16, SR-17, SR-18, SR-19, SR-20, SR-21, SR-22, SR-24, SR-25, SR-27, SR-28, SR-30, SR-31, SR-32, SR-33, SR-34, SR-35, SR-36, SR-37, SR-39, SR-40, SR-41, SR-42, SR-43, SR-44, SR-45, SR-46, SR-47, SR-48, SR-49, SR-50, SR-51, SR-53, SR-54, SR-56, SR-57, SR-58, SR-59, SR-61, SR-62, SR-63, SR-64, SR-67, SR-69, SR-70, SR-71, SR-72, SR-73, SR-74 and SR-75.
II	8	SR-1, SR-8, SR-23, SR-26, SR-52, SR-60, SR-65, SR-66.
III	1	SR-55.
IV	1	SR-12.
V	1	SR-29.
VI	1	SR-68.
VII	1	SR-38.

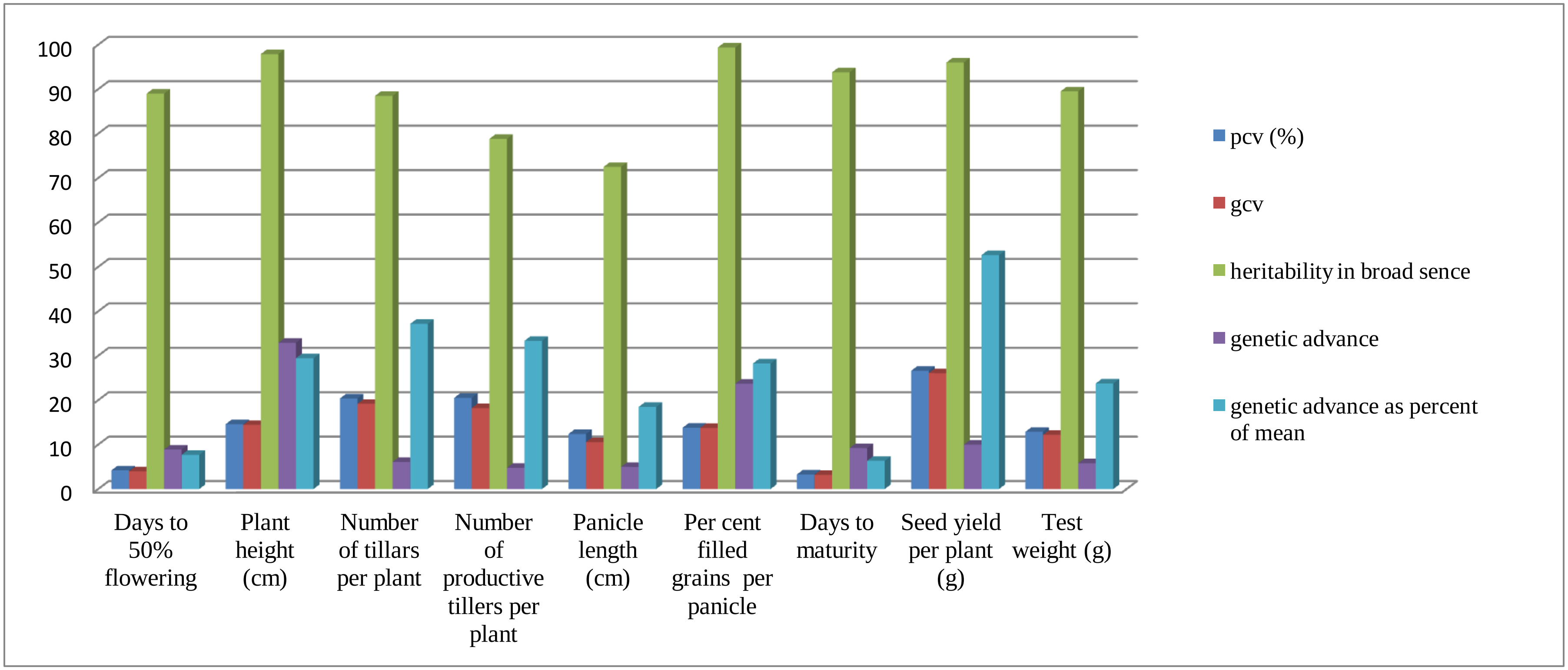


Figure 4.3. Variability, heritability, genetic advance, genetic advance as per cent of mean in soft rice genotypes

Plate 4.1. Colourless coleoptile colour of soft rices.

Plate 4.2. Uniform purple colour of basal leaf sheath.

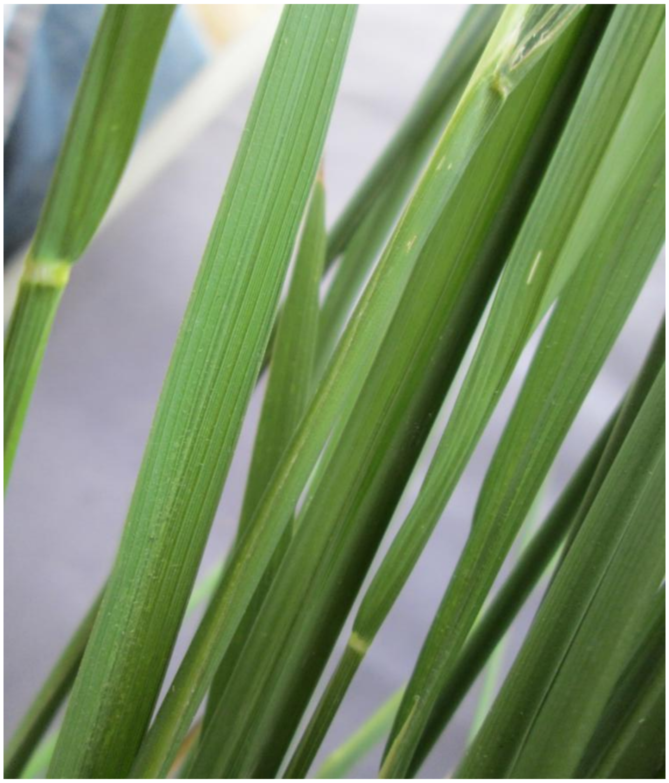


Plate 4.3. Intensity of green colour of leaf- dark green.

Plate 4.4 Green colour of leaf sheath (no anthocyanin colour).

Plate 4.5. Auricles anthocyanin colouration- absent.

Plate 4.6. Auricles anthocyanin colouration- present.

Plate 4.7. Anthocyanin colouration of collar- absent.

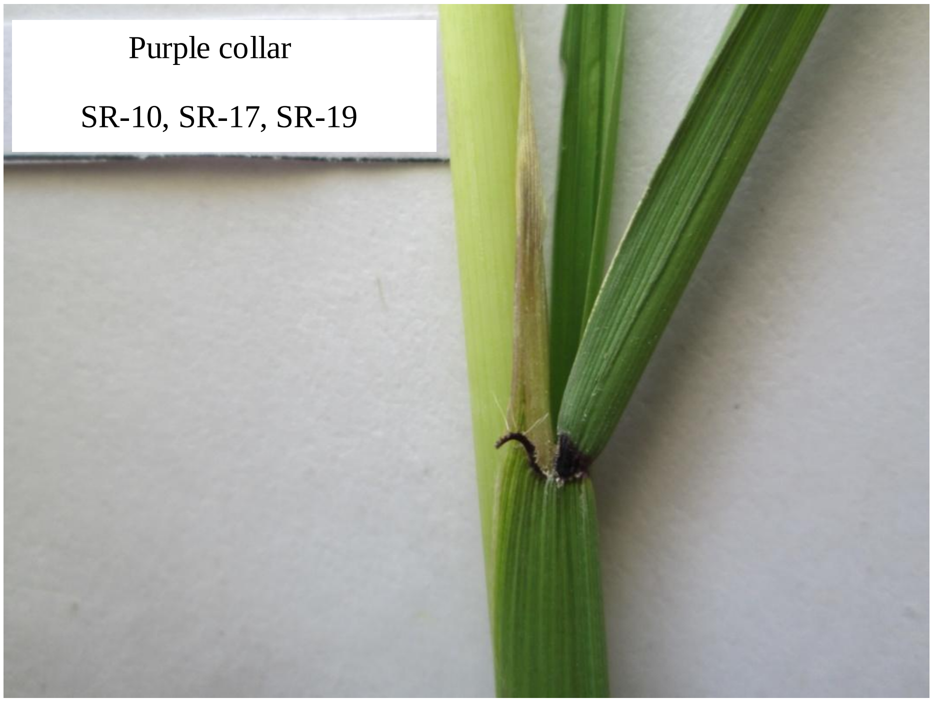


Plate 4.8. Anthocyanin colouration of collar- present.

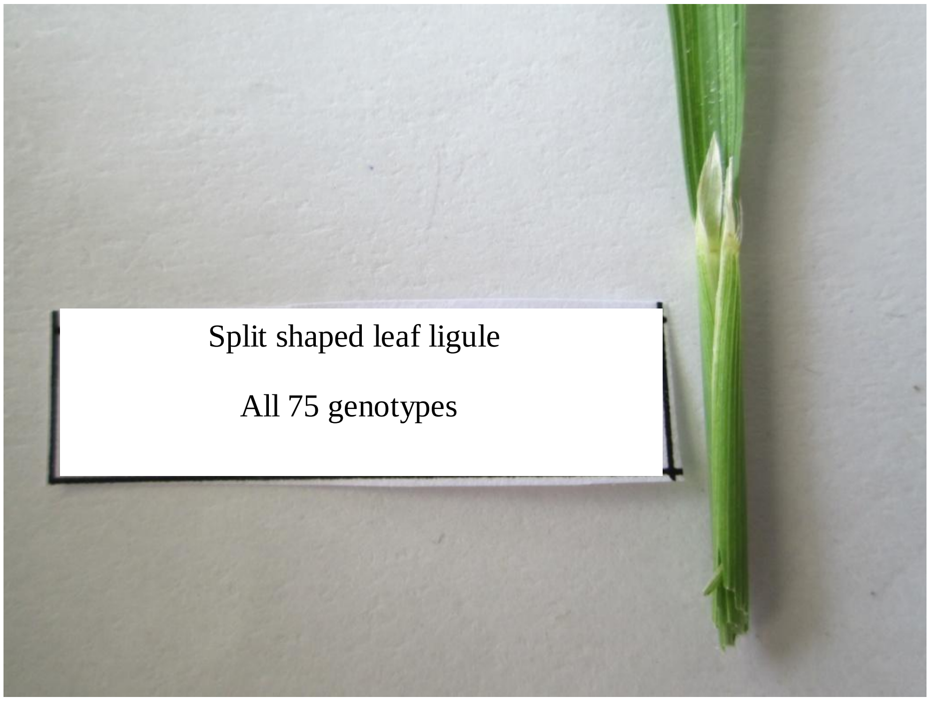


Plate 4.9. shape of the leaf ligule- split.

Plate 4.10. Flag Leaf attitude of blade (early observation).

Plate 4.11. Culm attitude- erect.

Plate 4.12. Culm attitude- open.

Plate 4.13. Lemma: anthocyanin colouration of keel- absent.

Plate 4.14. . Lemma: anthocyanin colouration of keel- present.

Plate 4.15. Lemma: anthocyanin colouration of area below the apex.

Plate 4.16. Lemma: anthocyanin colouration of apex.

Plate 4.17. Colour of stigma- purple.

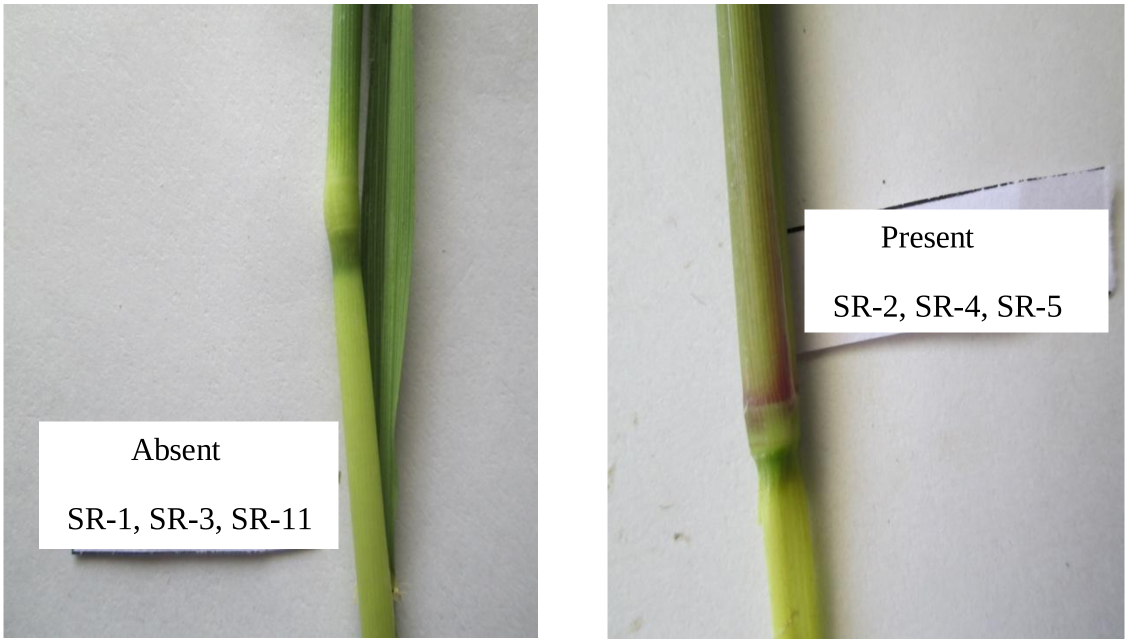


Plate 4.18. Anthocyanin colouration of node.

Plate 4.19. Anthocyanin colouration of inter node.

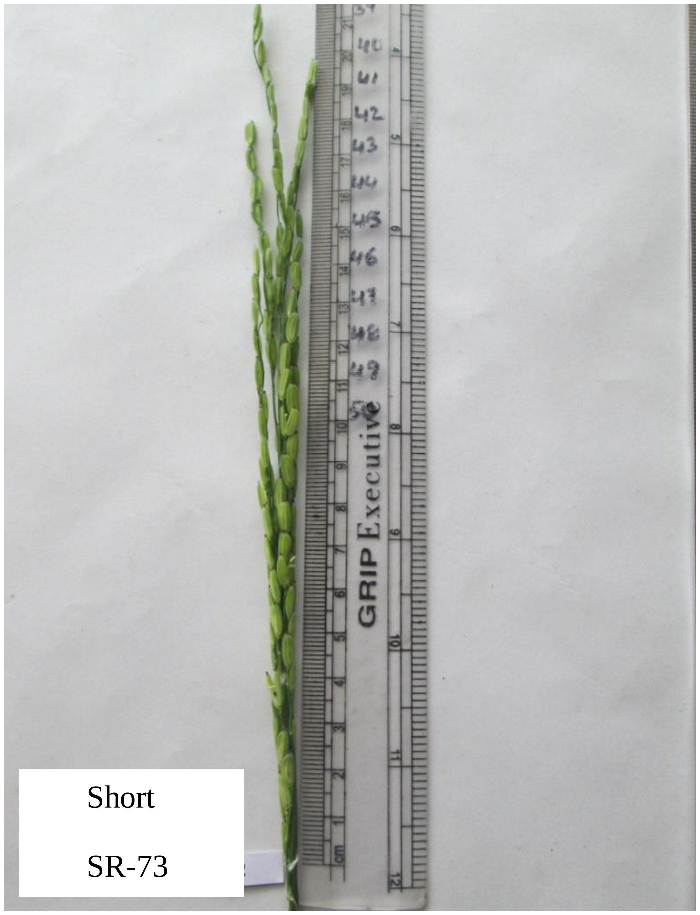


Plate 4.20. Panicle length of main axis.

Plate 4.21. Panicle curvature of main axis.

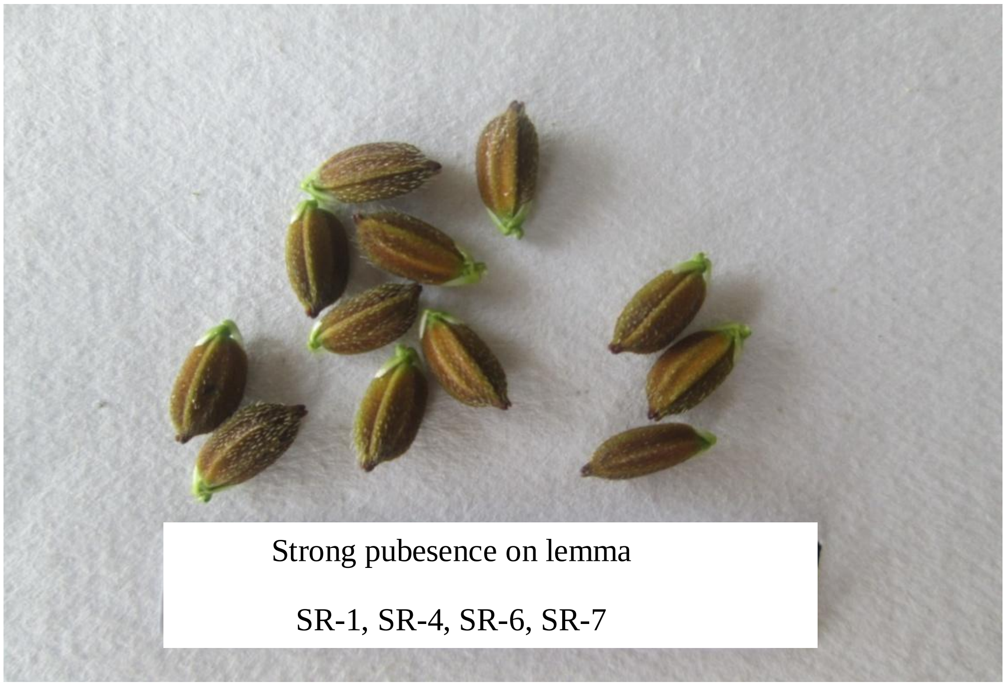


Plate 4.22. Spikelet: density of pubesence of lemma.

Plate 4.23. Spikelet: colour of tip of lemma.

Plate 4.24. Panicle awns.

Plate 4.25. Panicle: distribution of awns.

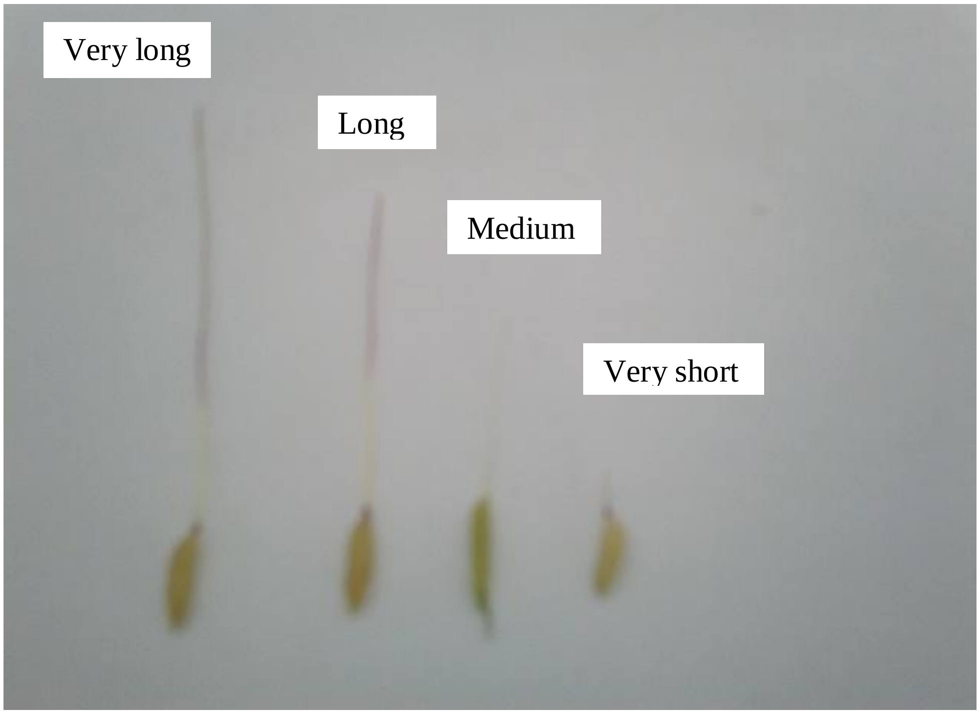


Plate 4.26. Panicle: length of longest awns.

Plate 4.27. Panicle: secondary branching.

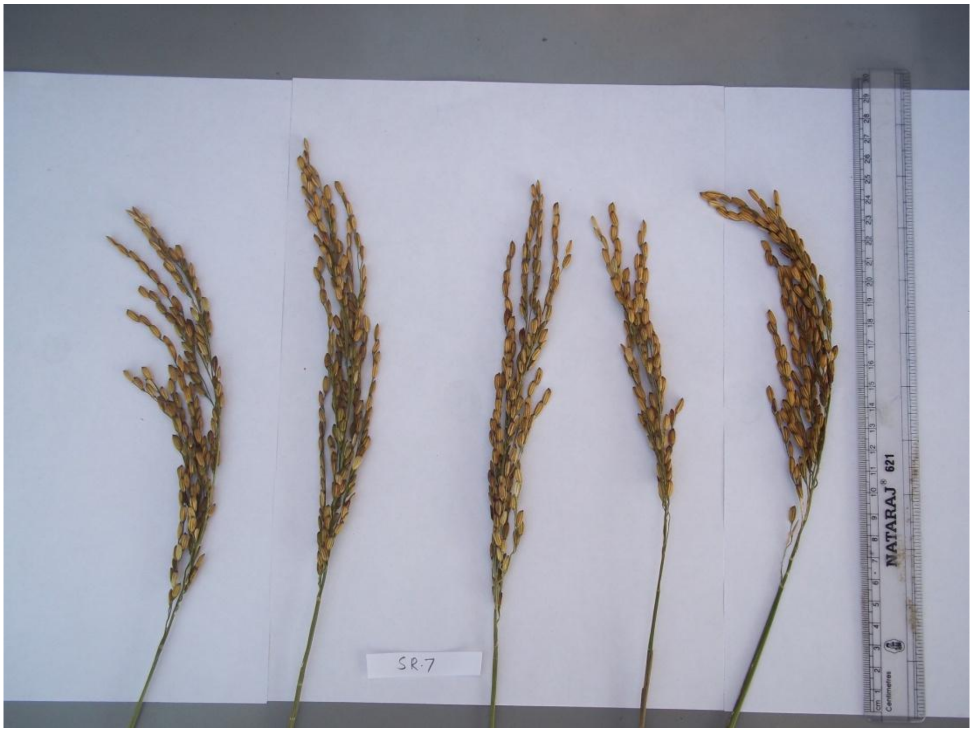


Plate 4.28. Panicle: secondary branching- clustered.

Plate 4.29. panicle exsertion.

Plate 4.30. Sterile lemma colour- straw.

Plate 4.31. Grain and decorticated grain length- medium.

Plate 4.32. Grain and decorticated grain length- long.

Plate 4.33. Grain and decorticated grain width- medium.

Plate 4.34. Grain: phenol reaction of lemma.

Plate 4.35. Decorticated grain colour- red.

Plate 4.36. Decorticated grain colour- white.

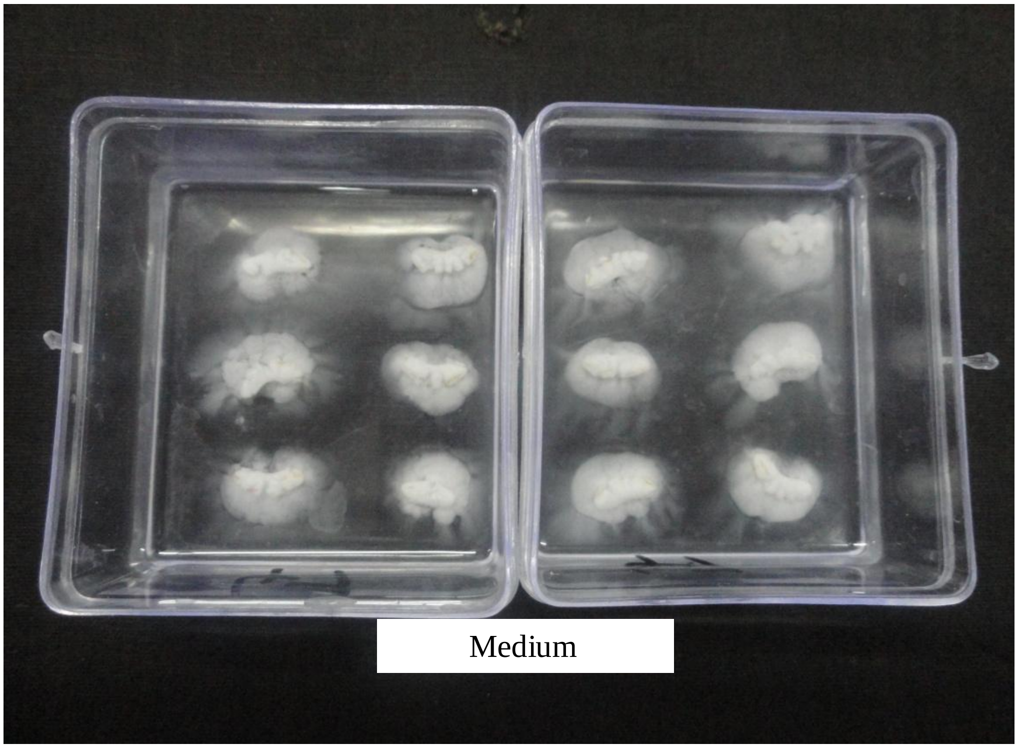


Plate 4.37. Gelatinization temparature through alkali spreading value.

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled **"Morphological characterization and studies on genetic divergence in soft rice (*Oryza sativa L.*) genotypes"** was conducted with 75 genotypes in a Randomized Block Design with three replications at Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad during *kharif*, 2013. The objectives of the research work were to characterize the experimental material through DUS discriptors and to estimate the genetic divergence, to assess the degree of association between yield and its component characters in addition to direct and indirect effects.

The observations were recorded on five randomly selected plants per genotype in each replication for 62 agro-morphological characters as per those given in DUS testing guidelines of Rice and nine yield components *viz,* days to 50 per cent flowering, plant height, number of tillars per plant, number of productive tillers per plant, panicle length, per cent filled grains per panicle, days to maturity, seed yield per plant and test weight (1000-grain weight).

Morphological features play a major role in cultivar identification because they provide easy identification through quick visualization. In present investigation among the 62 agro-morphological characters, most of the characters showed variations in different accessions except colourless coleoptile colour, presence of leaf auricles, presence of leaf collor, presence of leaf ligule, shape of the ligule, width of the leaf blade, absence of male sterility, presence of secondary branching, phenol reaction of lemma and decorticated grain width and endosperm content of amylose were found to be monomorphic. In addition, leaf distribution of anthocyanin colouration, time of heading, stem thickness, time of maturity, grain width, decorticated grain length and decorticated grain colour were reported to be bimorphic. Basal leaf sheath colour, leaf intensity of green colour, leaf pubesence of blade surface, anthocyanin colouration of auricles, colour of the ligule, length of the leaf blade, flag leaf attitude of blade (early observation), culm attitude, intensity of anthocyanin colouration of nodes, panicle curvature of main axis, panicle number per plant, distribution of awns on panicle, secondary branching of the panicle, panicle exsertion, leaf senscence, sterile lemma colour, grain length and gelatinization temparature through alkali spreading value, which were found to be trimorphic.

The remaining characters like leaf sheath intensity of anthocyanin colouration, flag leaf attitude of the blade (late observation), lemma anthocyanin colouration of keel, anthocyanin colouration of area below the apex, stem length, panicle length of main axis, spikelet colour of tip of lemma, lemma and palea colour, panicle colour of awns, length of awn, panicle attitude of branches, weigtht of 1000 grain and decorticated grain shape, were found to exhibit large variations in their characters in different genotypes. The presence of purple basal leaf sheath colour, purple auricles, purple leaf ligule, deflexed flag leaf, very strong lemma anthocyanin colouration of apex, light green and purple stigma, deflexed panicle curvature of main axis, well exserted panicles, higher test weight and presence of very low and low amylose content, constitute the distinct features of soft rice genotypes.

Analysis of variance indicated highly significant differences among the genotypes for all the traits under study. A perusal of genetic variability parameters revealed that phenotypic and genotypic coefficients of variation were high for seed yield per plant, number of tillars per plant and number of productive tillars per plant. The phenotypic and genotypic coefficients of variation were moderate for plant height, panicle length, per cent filled grains per panicle and test weight. The values were low for days to 50% flowering and days to maturity.

High heritability coupled with high genetic advance as percent of mean was observed for plant height, number of tillars per plant, number of productive tillers per plant, per cent filled grains per panicle, seed yield per plant and test weight (1000-grain weight), which indicated that these traits were controlled by additive type of gene action. The high estimates of heritability coupled with low genetic advance as percent of mean for days to 50% flowering and days to maturity indicated the presence of non-additive gene effects, in addition to influence of environment to some extent.

Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The diversity was more for per cent filled grains per panicle, plant height, seed yield per plant, days to maturity and test weight indicating their importance in contribution towards genetic diversity. The multivariate analysis revealed that 75 genotypes were distributed into seven clusters. The clusters III is having highest mean value for per cent filled grains per panicle, cluster V for seed yield per plant and cluster I for test weight (1000-grain weight) and cluster II for number of productive tillers per plant and cluster IV for panicle length and also they were highly divergent from each other. Hence, crosses between genotypes selected from these clusters may be used to generate soft rice varieties with good grain yield and quality traits.

The genetic divergence was high and the 75 genotypes of soft rice were grouped into seven divergent clusters. Cluster I was the largest one comprising of 62 genotypes followed by cluster II with eight genotypes and cluster III, IV, V, VI and VII with one genotype each. This indicated that geographical distribution and genetic diversity were not related. The pattern of group constellations indicated significant variability among the genotypes.

The higher amount of divergence was observed between cluster IV and cluster VII (1817.85) followed by cluster III and cluster VII (1795.23), cluster I and cluster VII (1425.51) and cluster III and cluster VI (1286.81). The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes (SR-12) of cluster IV and cluster VII (SR-38), cluster III (SR-55) and cluster VII (SR-38), cluster I with cluster VII (SR-38) and cluster III (SR-55) and cluster VI (SR-68) would produce encouraging results and promising segregants for grain yield. Inter cluster distances were low between cluster VI and cluster VII (186.32) followed by cluster I and cluster IV (192.07) and cluster I and cluster III (195.12) and cluster II and V (236.14). Maximum intra cluster distance was observed in cluster II (157.08), followed by cluster I (104.95).

The maximum genetic divergence was contributed by per cent filled grains per panicle (5181.98%), plant height (2237.84%), seed yield per plant (1441.44%), days to maturity (403.6%), test weight (371.17%), number of tillars per plant (252.25%), days to 50% flowering (50.45%), panicle length (46.85%) and number of productive tillars per plant (14.41%).

Character association studies revealed that the characters grain yield per plant showed positive association with days to 50% flowering, plant height, number of tillars per plant, per cent filled grains per panicle, days to maturity and test weight (1000-grain weight) at both the levels. This indicated that simultaneous selection of all these characters was important for yield improvement.

Critical analysis of the results by path analysis revealed that the traits like number of tillars per plant, days to maturity, test weight and per cent filled grains per panicle were directly influencing the grain yield per plant. This indicated that direct selection for yield improvement via these traits would rewarding.

A critical analysis of correlation and direct and indirect effects indicated that emphasis should be directed towards selection of parents having higher per cent of filled grains per panicle coupled with higher number of tillars per plant. As the yield component filled grains per panicle is inturn dependent on panicle length and plant height, attention should be paid towards increasing the panicle length, maintaining optimum plant height. Thus a plant with medium height, increased panicle length, higher per cent of filled grains per panicle would be more desirable for soft rice genotypes to realize higher yield with good quality traits. Genotypes identified based on the mean performance, variability, genetic divergence and character association studies could be used for the creation of variability for component traits and selection of superior transgressive segregants.

It may be concluded from the present investigation that the morphological DUS descriptors can be effectively used for identification and grouping of varieties and varieties satisfying the DUS criteria for these morphological descriptors could be registered under the PPV & FR Act for obtaining Plant Breeders and Farmers' rights. Systematic study on characterization and genetic diversity of soft rice germplasm is not only important for utilizing the appropriate attribute based donors, but also essential in the present era for protecting this unique rice.

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