CHARACTERIZATION OF RICE GENOTYPES FOR DISTINCTIVENESS UNIFORMITY STABILITY AND NUTRITIONAL PARAMETERS

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B.Sc. (Ag.)

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(GENETICS AND PLANT BREEDING)

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BY

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B.Sc. (Ag.)

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DECLARATION

I, **Mr. NELAVELLI NAGA DURGA RAO,** hereby declare that the thesis entitled **"CHARACTERIZATION OF RICE GENOTYPES FOR DISTINCTIVENESS UNIFORMITY STABILITY AND NUTRITIONAL PARAMETERS"**, submitted to the **Acharya N.G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place: **(NELAVELLI NAGA DURGA RAO)**
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Date:

CERTIFICATE

Mr. NELAVELLI NAGA DURGA RAO has satisfactorily prosecuted the course of research and that the thesis entitled **"CHARACTERIZATION OF RICE GENOTYPES FOR DISTINCTIVENESS UNIFORMITY STABILITY AND NUTRITIONAL PARAMETERS"** 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 him for a degree of any university.

Date: **Chairperson**

CERTIFICATE

This is to certify that the thesis entitled "**CHARACTERIZATION OF RICE GENOTYPES FOR DISTINCTIVENESS UNIFORMITY STABILITY AND NUTRITIONAL PARAMETERS"** submitted in partial fulfillment of the requirements for the degree of **'**Master of Science in Agriculture' of the Acharya N.G. Ranga Agricultural University, Lam, Guntur, is a record of the bonafied original research work carried out by **Mr. NELAVELLI NAGA DURGA RAO** 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 the investigations have been duly acknowledged by the author of the thesis.

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Place:

*Date****:*** ***(Nelavelli Naga Durga Rao)***

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LIST OF SYMBOLS AND ABBREVIATIONS

AAE	:	Ascorbic Acid Equivalent
ANOVA	:	Analysis of Variance
AUC	:	Area Under Hydrolysis Curve
CD	:	Critical Difference
cm	:	Centimeter
COV	:	Covariance
CV	:	Coefficient of Variation
d.f	:	Degrees of freedom
et al.,	:	and other people
Fe	:	Iron
g	:	Gram
GA	:	Genetic Advance
GAE	:	Gallic Acid Equivalent
DPPH	:	2,2-diphenyl-1-picrylhydrazyl
AAS	:	Atomic Absorption Spectrophotometer
NaOH	:	Sodium hydroxide
HCL	:	Hydrochloric acid
OD	:	Optical Density
GOD-POD	:	Glucose Oxidase and Peroxidase
TCA	:	Tri Chloro Acetic acid
PCA	:	Principal Component Analysis
DUS	:	Distinctiveness Uniformity Stability
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Coefficient of Variation
GI	:	Glycemic Index
GL	:	Glycemic Load
h^2 (b)	:	Heritability in broad sense
ha	:	Hectare
K	:	Selection differential
Kg ha^{-1}	:	Kilograms per hectare
KSCN	:	Potassium thiocyanate
l	:	Litre
Max.	:	Maximum
mg	:	Milligram

Min.	:	Minimum
ml	:	Millilitre
mm	:	Millimeter
MSS	:	Mean Sum of Square
nm	:	Nanometers
No.	:	Number
NS	:	Non Significant
PCV	:	Phenotypic Coefficient of Variation
per se	:	As such with mean
ppm	:	Parts Per Million
PPV & FR	:	Protection of Plant Varieties and Farmers' Rights
QE	:	Quercetin Equivalent
RBD	:	Randomized Block Design
RDS	:	Rapidly Digestible Starch
RPM	:	Revolutions per minute
RS	:	Resistant Starch
S	:	Significant
SDS	:	Slowly Digestible Starch
SS	:	Sum of Square
TPC	:	Total Phenol Content
via	:	Through
XRF	:	X ray fluorescence spectrometry
Zn	:	Zinc
$\overline{X}$	:	Grand mean
%	:	Per cent
$^{\circ}$C	:	Degree centigrade

ABSTRACT

Name of the Author	:	**N. NAGA DURGA RAO**
Title of the Thesis	:	**Characterization of rice genotypes for Distinctiveness Uniformity Stability and Nutritional parameters**
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Faculty	:	**Agriculture**
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The present investigation was carried out to characterize 30 rice genotypes for Distinctiveness Uniformity Stability based on 26 morphological descriptors. The nature and extent of variability, heritability, genetic advance and diversity among the germplasm was studied based on yield and nutritional parameters.

Out of twenty six essential morphological DUS descriptors studied, only one character was found to be monomorphic and 12 characters were dimorphic and remaining were polymorphic. The analysis of variance demonstrated significant differences among 30 genotypes for all the traits studied.

High PCV and GCV was recorded for the traits *viz*., number of productive tillers plant^{-1}, yield plant^{-1}, 100 grain weight, kernel length/breadth ratio, zinc content, iron content, amylose content, total antioxidant activity and total soluble phenol content indicating that large amounts of variation was present among the set of germplasm. Whereas, low PCV and GCV was recorded for the characters such as days to 50% flowering, starch content and glycemic index indicating less variation among the germplasm. The coefficient of variability studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters, indicating that the characters were less influenced by the environment.

High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of productive tillers plant^{-1}, panicle length, yield plot^{-1}, 100 grain weight, kernel length/breadth ratio, protein content, Zn content, Fe content, amylose content, total antioxidant activity, total soluble phenol content, phytate content. Thus, these traits are mostly under the control of additive gene action and hence these characters may be improved by phenotypic selection. High heritability with moderate genetic advance was recorded for days to 50% flowering, spikelet fertility, total starch content and glycemic index appear to be under the control of both additive and non-additive gene actions and hence these characters may not be improved by simple selection.

D^2 analysis categorized 30 genotypes into six clusters. The inter-cluster D^2 values ranged from 34.51 (cluster II and III) to 213.16 (clusters IV and V) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance (213.16) was observed between cluster IV and V, followed by cluster I and V (173.93), cluster V and VI (152.79), cluster III and IV (134.84)**,** cluster II and cluster IV (130.26), cluster I and IV (120.26). Genotypes present in the cluster IV recorded highest mean values for the traits *viz.,* number of productive tillers plant^{-1}, panicle length, 100 grain weight, total antioxidant activity, total soluble phenol content and amylose (intermediate). The PCA analysis revealed that, the first five principal components with eigen value more than one contributed 75.56% towards the total variability. The traits that were contributing maximum towards the existing variability were plant height, panicle length, spikelet fertility, yield plot^{-1}, 100 grain weight, iron content, antioxidant activity and phenol content.

Genotypes with highest nutritional content as well as good yield potentiality reported in the present study were Mappillai samba with highest yield (4.29 Kg), protein content (14.13%), high antioxidant (98.37 mg 100g^{-1}) and high phenol contents (128.35 mg 100g^{-1}); Parimala sanna and Tulasi baso with highest Zn and Fe contents (47.45 µg g^{-1}, 61.68 µg g^{-1}) respectively. Pancharatna was a red pericarp coloured genotype recorded high yield along with high antioxidant activity (122.40 mg 100g^{-1}) and high phenol content (139.84 mg 100g^{-1}). Kulakar recorded low glycemic index (52.28), intermediate amylose content (21.07%), high phenol content (121.65 mg 100g^{-1}) and antioxidant activity (114.33 mg 100g^{-1}). Karuppu kavuni also recorded high yield (4.16 Kg), low glycemic index (52.29) and high phenol content (204.26 mg 100g^{-1}).

Hence, the crosses between Mappillai samba (cluster III) x Kalabhatt (cluster IV) with inter cluster distance 134.845 and Mappillai samba (cluster III) x Kulakar (cluster IV) with inter cluster distance 134.845 may be considered for obtaining superior transgressive segregants with respect to yield and nutritional parameters as these genotypes exhibited superior performance and also belonged to the divergent clusters.

Chapter – I

Introduction

Chapter I

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important cereal crop belonging to the family Poaceae. Rice remains as a rich source of nutrients and also contains a number of vitamins and minerals. Rice is the best source of energy as it contains complex carbohydrates. Rice is an important staple food crop for about 60% of the global population and is an economical source of proteins and energy. It constitutes about 43% of calories in an average human's diet in India. It contributes 20-25% of agrarian income due to its intensive cultivation. Majority of the population of Asia consumes rice as a whole in every meal. In many nations, rice accounts for more than 70% of average human calorie intake.

In India, rice is being grown in 44 million hectares area which is accounting for production of 111.00 million tonnes and productivity of 3.78 t ha^{-1} (United States Department of Agriculture. 2018-2019. Area, production and productivity of rice in world) while, in Andhra Pradesh it is grown in an area about 55 lakh acres contributing 126.91 lakh tonnes of production and productivity of 2307 kg $acre^{-1}$ (Directorate of Economics and Statistics, 2017-18).

So as to overcome the constraints in productivity, always a breakthrough is essential to improve the productivity of new cultivars and to enhance the biological efficiency through a series of hybridization programmes. Cultural and varietal diversity in rice is vast and its improvement is a puzzling task. A diverse genetic base in any plant breeding programmes can ensure increase in crop yields, inspite of diverse abiotic and biotic stresses. Therefore, to overcome the increasing aggregate demand for food grains, emphasis should be given on genetic improvement of prevailing germplasm lines.

Improvement in respect of nutritional quality is also equally important along with higher yields. Among all the nutrients, rice contains very less amounts of protein as well as micro nutrients. Hence, improvement of protein content along with other important micronutrients especially Fe and Zn are the need of the hour. Polished rice grains contain a small amounts of iron and only 20% of the daily requirement of zinc.

Besides micronutrients, protein deficiency is also affecting human health (Bouis *et al.*, 2003). Proteins function as enzymes, hormones, antibodies, transport and structural components as well. Proteins are commonly concentrated in the bran fraction of rice but, due to milling most of the protein content is lost (Chowdhury *et al.,* 2016a). Brown rice of popular rice varieties has approximately 6.3-24.4 μg g^{-1} of iron and 13.5-28.4 μg g^{-1} of zinc. The crude protein content ranges between 6.0 and 12.6% in cultivated rice. Milled grains of popular rice varieties have about 2 μg g^{-1} iron and 16 μg g^{-1} zinc concentration (Trijatmiko *et al.,* 2016), while the average protein content is approximately 8% (Babu *et al.,* 2012). The wide range of these micronutrient concentrations among the germplasm lines show the presence of genetic variability, thus provides the opportunities for genetic improvement through various breeding programmes. The awareness related to healthy foods has been increasing and the individuals are looking for a best rice cultivar, especially in perspective of starch digestibility. The amylose content is one of the important quality parameter for predicting the rice processing and cooking quality. Low glycemic index is considered to be one of the beneficial forms in nutritional point of view because of its low carbohydrate level.

Offlate consumers are becoming more conscious about health and more aware of the benefits of functional foods, diets containing bio-active compounds (secondary metabolites) such as antioxidants which have received greater attention. The total antioxidant activity which is positively correlated with the total soluble phenolic compounds (TSPCs) are found in higher concentration in genotypes with red and black pericarp colour when compared to those with a light brown pericarp colour (Tian *et al*., 2004). Owing to several health promoting impacts associated with anthocyanins, such as anti-oxidative, anti-inflammatory and anti-carcinogenic effects, coloured rice is noted as a functional food and food ingredient in many asian countries.

Diversity in rice can be well utilized to resolve the present scenario of food problems. Over several decades, land races of rice were collected to use as parents for creating high yielding varieties with both disease as well as pest resistance. Use of adapted varieties resulted in an exceptional rise in rice yields which led to ‘green revolution’ (Jackson and Huggan, 1993). The successful outcome of any breeding programme mostly depends on exploitation of existing variability and therefore it is always advisable to collect, evaluate and utilize the available diverse germplasm for

crop improvement to suit specific need with regards to specific ecosystem. Arunachalam (1981) stated that chance of getting high variability in segregating population and superior heterotic hybrids mostly depends on genetic divergence of the parents utilized in the hybridization programme. The novel characters and existing variability in the germplasm should be exploited to develop the need based varieties and hybrids using crop improvement programmes. The available germplasm should be characterized and genetic diversity should be studied efficiently prior use to use in the breeding programme.

A thorough knowledge on nature and magnitude in the genetic variability and association of characters of a species is a pre-requisite for an effective breeding programme. Information regarding direct and indirect effects contributed for each character towards crop yield will be an added benefit in assisting the selection process. The quantification of the degree of divergence in a given experimental materials of immense value in the identification of divergent genotypes for future use in hybridization to create new variability. Mahalanobis D^2 statistic has been proven to be a powerful tool for the plant breeder in selecting the right type of parents among the genotypes having wider variability for different traits (Shivani *et al.,* 2018). Therefore, development of improved genotypes is the ultimate goal of any plant breeding programme, which is better than the prevailing genotypes for producing the economic yield. This necessitates genetic improvement through maximum exploitation of allelic resources in developing ideal genotype (Pratap *et al.,* 2012).

Selecting a particular trait requires information regarding heritability and genetic advance. Direct selection which is based on yield is often a paradox in plant breeding programmes because crop yield is a complex and polygenically inherited trait, influenced by the component traits. Therefore breeding programmes should consider character association of different component traits into consideration with crop yield **(**Veni *et al.,* 2013). The breeder should isolate superior genotypes from the information of components of variations. The most essential feature is partitioning of total variation into genotypic, phenotypic and environmental components which determines the magnitude of components for different traits which is an absolute measure of the nature of gene action thus aids in deciding the breeding procedure for genetic enhancement of a trait.

Being signatory to General Agreement on Trade and Tariffs (GAAT), Government of India has legislated *Suigeneris* system, Protection of Plant Varieties and Farmers' Right Act (PPV&FRA) for providing protection to plant varieties based on Distinctiveness, Uniformity and Stability (DUS) test, apart from novelty (Anonymous, 2001).

In this context, there is a necessity to characterize rice varieties according to DUS test guidelines for rice prescribed by PPV and FR Authority (Anonymous, 2007). Plant morphological traits have been recognized as the universally undisputed descriptors in sequential fashion which are useful and appropriate in discriminating various varieties. In view of the above criteria, the present investigation has been taken up with the following objectives.

1. Characterization of rice genotypes for important DUS characters
2. To study the variability for the nutritional, yield and yield attributing components
3. To estimate the grain physical, cooking and nutritional properties of rice genotypes
4. Grouping of genotypes into different clusters based on cluster analysis

Chapter – II

Review of Literature

Chapter II

REVIEW OF LITERATURE

In the present investigation, an attempt has been made to characterize the rice genotypes for Distinctness, Uniformity, Stability , genetic variability and genetic divergence among 30 rice genotypes for yield and nutritional parameters like micronutrients (iron and zinc), protein content, phenols, anti-oxidants, total starch, amylose content and glycemic index. Available literature in consonance with the objectives of present investigation is reviewed in the following headings.

2.1 Characterization of rice genotypes for DUS

2.2 Mean performance of rice genotypes for nutritional parameters

2.3 Variability, heritability and genetic advance

2.4 Genetic divergence studies among rice genotypes

2.1 CHARACTERIZATION OF RICE GENOTYPES FOR DUS

Joshi *et al*. (2011) studied 20 indigenous aromatic rice varieties using morphological DUS descriptors. Out of 60 morphological characters studied, 46 traits were visually assessed and 14 were measurable traits. Among 46 morphological characters, 24 were monomorphic, 17 were dimorphic and five were polymorphic characters indicating, their potential for varietal characterization and distinctiveness.

Chakrabarty *et al.* (2012) characterized 91 farmers' grown varieties of rice collected from southern part of West Bengal and evaluated for 52 plant morphological and grain characteristics. Among them, 44 qualitative traits exhibited maximum variability 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.

Parikh *et al.* (2012) characterized 71 aromatic rice germplasm lines and grouped on the basis of anthocyanin pigmentation, plant habit, and awn. On the basis of pigmentation distribution in 10 plant parts, a total of 12 groups were categorized with group one having no pigmentation and group twelve with pigmentation in nine plant parts. Three groups were categorized on the basis of plant habit and awn.

Chakravorty and Ghosh (2013) characterized 51 rice landraces from West Bengal and reported that 27 landraces showed distinctiveness with respect to 22 essential and 24 additional characters prescribed in DUS guidelines. It was suggested that this study would be useful for breeders, researchers and farmers to identify restoration and conservation of beneficial genes for crop improvement and also to seek protection under PPV & FR Act.

Subbarao *et al*. (2013) characterized 65 landraces of rice based on 43 agro-morphological traits for distinctiveness, uniformity and stability (DUS) test. Out of 65 varieties studied, 32 were found to be distinctive on the basis of 22 essential and 24 additional characters. This study will be useful for breeders, researchers and farmers to identify and choose beneficial genes for crop improvement and also to seek protection under protection of plant varieties and farmer's rights act.

Sarawagi *et al*. (2013) characterized 782 germplasm accessions on the basis of 29 morphological and eight agronomical traits. Among 782 accessions, ten accessions were identified with high yield and ancillary traits on the basis of mean values.

Gupta *et al*. (2014) characterized 53 rice accessions from IGKV, Raipur, Chattisgarh and evaluated for 14 morphological and 17 agronomical characters. The specific genotypes namely, S: 663, K: 1514, J: 311 were identified for agronomical characteristics like total number of grains panicle^{-1}, number of filled grains panicle^{-1} and grain yield plant^{-1}. These genotypes may be used in hybridization programme to achieve desirable segregants for higher yield.

Sinha and Mishra (2015) worked on 55 traditional rice varieties of West Bengal for the grain morphological characters to characterize the genotypes. Wide variation for grain characteristics like grain size and shape, anthocyanin colouration of lemma-palea and kernel, presence or absence of aroma, awning characteristics was observed. Wide variation among the grain morphological characters indicated presence of wide genetic variation among these varieties which, may be utilized for the selection of the parents for the production of new improved varieties.

Umarani *et al*. (2017) characterized 70 landraces of rice based on 14 DUS characters. Among 14 characters, anthocyanin colouration of node was dimorphic for 10 genotypes. Three traits namely spikelet colour of stigma, stem length and panicle exsertion were trimorphic. Basal leaf sheath colour, time of heading (50% plants with

panicles), flag leaf attitude (late observation), panicle length, decorticated grain length and shape were tetramorphic and lemma anthocyanin colouration of apex and amylose content showed five states of expression and based on decorticated grain colour six groups were made.

Mani and Kumar (2018) characterized 49 rice landraces for distinctness and uniformity according to DUS test guidelines of PPV & FR authority. Grain characters *viz*., hulled and non-hulled, grain length and width exhibited distinctness among the genotypes. The grain yield of Bangaarugandu, Bagya jyothi, Ratnachudi, Balaji and Kempudoddi landraces was more than check Jyothi. Rice landraces of hilly zone of karnataka evaluated in this study were found to be distinct and uniform with respect to DUS traits and yield characters and hence may be considered for crop improvement programme for various agronomic and quality traits.

Manjunatha *et al*. (2018) studied 60 landraces of rice, including the aromatic genotypes collected from different parts of wayanad, Kerala and were characterized for both qualitative and quantitative characters. Out of 25 descriptors studied, three characters were found to be monomorphic, seven were dimorphic, six were trimorphic, and seven were tetramorphic. Decorticated grain shape showed five states of expression. Lemma and palea colour recorded six states of expression. This detailed characterization of wayanad rice landraces is very important for rice breeding from the standpoint of selection and conservation of different landraces for further utilization in crop improvement programmes.

2.2 MEAN PERFORMANCE OF GERMPLASM FOR NUTRITIONAL PARAMETERS

Deepa *et al*. (2010) studied *in vitro* starch digestibility and glycemic indices of three rice varieties Navara, Jyothi (pigmented rice varieties) and IR 64 (non-pigmented rice) with similar amylose content. Pigmented rice varieties showed more resistant starch content than un-pigmented variety, IR 64. Highest digestible starch was showed by IR 64. Glycemic Index was highest for Navara (74.8). It was concluded that pigmented whole grain rice Navara and Jyothi is better source of dietary fibre and resistant starch.

Sompong *et al*. (2011) analyzed nine red and three black rice varieties to determine the physicochemical and antioxidant properties and reported that the varieties Niaw Dam pleuak Dam (red) and Sung Yod Patthalung (black) showed highest protein content 10.9% and 10.4% respectively. Red rice varieties BG, LP, SR 11, SR12, SR13 had highest amylose content, black rice varieties Niaw Dam pleuak Dam, Niaw Dam pleuak Khao had lowest amylose content. Red rice varieties showed total phenol content of 79.18 to 691.37 mg $100g^{-1}$. While, black rice varieties had 336.69 to 665.16 mg $100g^{-1}$. Total equivalent antioxidant capacity of red rice was 2.08-12.29 m mol $100g^{-1}$ and black rice was 4.98-12.03 m mol $100g^{-1}$.

Anuradha *et al.* (2012a) studied 126 brown rice accessions including cultivated *indica* and *japonica* rice cultivars, germplasm accessions and wild rice genotypes analyzed for Fe and Zn concentration. Iron concentration ranged from 6.2 ppm to 71.6 ppm and zinc from 26.2 ppm to 67.3 ppm. Both Fe and Zn were high in wild rice genotypes and least in *japonica*.

Anuradha *et al.* (2012b) reported Fe and Zn concentrations in unpolished rice of Madhukar were 17.3 ppm and 53.7 ppm respectively, while in Swarna 22.5 ppm and 27.2 ppm respectively. Fe concentration in 168 RIL populations varied from 0.2 ppm to 224 ppm with the mean value of 30.9 ppm and Zn concentration varied from 0.4 ppm to 104 ppm with the mean value of 48.2 ppm.

Basu *et al*. (2012) conducted a study to evaluate and compare the carbohydrate content, antioxidant parameters in polished and unpolished seeds of three edible rice cultivars *viz*., Swarna (SW), Gobindobhog (GB) and Pusa Basmati (PB) and concluded that carbohydrate content was highest in PB seeds (both polished and unpolished), amylose content was highest in SW polished seeds. SW polished seeds were superior as compared to GB and PB cultivars in terms of antioxidant activity. Total phenol content was highest in unpolished seeds of Swarna and flavonoid content was highest in unpolished seeds of Pusa Basmati.

Chakuton *et al*. (2012) analysed the rice seed extracts of 12 colored and non-colored thai rice cultivars to determine the total phenolic content and antioxidant activity. Their results showed that total phenol content of all cultivars with methanolic extract showed highest value (2.02-4.77 mg GAE$100g^{-1}$). 53 colored cultivar showed the highest TPC (7.40 mg GAE$100g^{-1}$). DPPH scavenging activity of colored rice seed extracts was higher than non-colored rice extract.

Irkali *et al*. (2012) evaluated pigmented rice (red and black rice) and non pigmented rice to assess the total phenol content and flavonoid content. Studies revealed that total phenol content and flavonoid content were found to be more in black rice (87.87 µg g^{-1} and 59.19 µg g^{-1} respectively) than red rice (52.76 µg g^{-1} and 24.71µg g^{-1}) and white rice (30.15 µg g^{-1} and 15.95 µg g^{-1}).

Jain *et al*. (2012) conducted an experiment to find out the most suitable method of cooking rice for diabetic patients and reported amylose content in steam cooked method, traditional method, microwave method and raw method was 17.35, 19.67, 22.98 and 25.99 mg ml^{-1} respectively. The results revealed that, if amylose content is high, glycemic index may be low and the rice grains will show high volume expansion and a high degree of flakiness. If amylose content is low, glycemic index may be high and the rice grains will cook moist and sticky (amylose content was inversely proportional to glycemic index) and concluded that raw method of cooking of rice is the most suitable for diabetic patients as the glycemic index will be lowest.

Lee *et al*. (2012) conducted a study to evaluate the antioxidant potential, flavonoids and polyphenol content in exotic rice germplasm. The results revealed that rice germplasm had tremendous variations with respect to total polyphenols (0.08–0.71 mg g^{-1}) and falvonoid contents (0.091–0.413 mg g^{-1}) and antioxidant activity (18–96%). Rice cultivars with red and black seed coat recorded higher total phenols and flavonoid content and antioxidant activity than cultivars with white seed coat color.

RavindraBabu *et al.* (2013) evaluated 21 popular rice hybrids for the micronutrients content. Mean iron concentration of hybrids (68.4 ppm) was found to be 1.83 times that of zinc (37.3 ppm). Two hybrids with both high iron and zinc concentration are DRRH-2 and sahyadri-4 with 125.8 ppm, 43.8 ppm and 104.8,43.0 ppm respectively.

Pitija *et al*. (2013) evaluated the antioxidant activity and total phenols of bran extracts of glutinous and nonglutinous black rice cultivars revealed that black rice variety 1000-11-2-26 had the highest DPPH scavenging activity and total phenol content. Total phenolic content in bran extracts of the black rice samples ranged from 2.93 to 4.01 mg GAE g^{-1}

Saikia *et al*. (2012) analysed pigmented rice along with two non-pigmented aromatic rice varieties for physico chemical properties, total phenols, flavonoids and antioxidant activity. Non-pigmented rice had high amylose content than pigmented one. Red rice variety Chak-hao-amubi had highest total phenolic content (579.00 mg GAE 100^{-1}g) and flavanoid content (220.5 mg QE 100^{-1}g) than purple colored and non-pigmented rice varieties. Both purple and red colored varieties had good DPPH radical scavenging activity of 94.19%, and 96.43% respectively.

Gunaratne *et al*. (2013) studied antioxidant activity and nutritional quality of eight traditional red rice varieties and three light brown colored varieties and reported that red rice varieties had highest total equivalent antioxidant capacity (8.01-17.88 m mol $100g^{-1}$) and highest total phenol content (590-1710 mg $100g^{-1}$) than light brown varieties. The variety Kalu heenati (red rice) had highest protein content (10.1%), while brown rice variety, BG 300 had lowest protein content (6.15%).

Tamanna *et al*. (2013) studied eight genotypes of rice for different biochemical and nutritional parameters in both paraboiled and un-parboiled group. The mean value of phytic acid content for parboiled and un-parboiled group was found to range between 4.25 to 6.65 mg g^{-1} and 4.05 to 6.35 mg g^{-1}, respectively. Among parboiled samples, both BR-3 (6.65 ± 0.27 mg g^{-1}) and BR-11 (6.65 ± 0.05 mg g^{-1}) showed the highest amount of phytic acid content. The range of iron and zinc content in the parboiled group were 0.017 to 0.044 mg g^{-1}, 0.022 to 0.070 mg g^{-1} and that in the un-parboiled group were 0.020 to 0.044 mg g^{-1}, 0.015 to 0.074 mg g^{-1} respectively.

Walter *et al*. (2013) conducted a study to determine the concentration of total soluble phenolic compounds and antioxidant activity of rice grains with light brown, red and black pericarp colors and reported that genotypes with red and black pericarp color had higher values of total soluble phenolic compounds and antioxidant activity than those with a light brown pericarp color. Parboiling and cooking reduced the concentration of TPSCs especially in brown and polished grains.

Babu *et al*. (2014) conducted experiment for *invivo* GI estimation in ten rice varieties and reported that BPT 5204 was found to be low in GI (51.42), Dhan Rasi as medium GI and remaining varieties as high GI varieties. This study indicated that GI had negative correlation with amylose content and positive correlation with amylopectin.

Moko *et al*. (2014) analyzed two non colored and one colored rice varieties to determine the antioxidant activity and flavanoid content of rice bran. The results revealed that red variety had the highest DPPH scavenging radical activity (88.29%) and highest total phenolic content. Cigeulis had 261.96 mg g^{-1} gallic acid, red variety 258.23 mg g^{-1} gallic acid and the lowest was recorded by Superwin variety 239.04 mg g^{-1} gallic acid. Antioxidant properties of colored rice bran were better than that of non colored rice bran.

Selvakumar *et al*. (2014) conducted biochemical analysis to find out the genetic variability and association of amylose content, protein content and lipid content on resistant starch by using 50 rice accessions and reported that amylose content and protein content have significant positive correlation on resistant starch content in rice. Hence analysis of biochemical association of quality characters on resistant starch content help in the selection process for development of rice varieties with health benefits.

Gangadharaiah *et al*. (2015) evaluated 15 cultivars of rice for physiochemical characters and reported that the highest protein content (14.67%) was recorded in Nagabatha. High zinc (26.09 ppm) content was recorded in Moroda and Basumathi. Among rice cultivars, Kanadathumba and Sannamallige showed highest iron content 81.84 ppm and 81.48 ppm repectively.

Rahman *et al*. (2015) conducted a study to assess the total phenol content, antioxidant activity and flavanoid content of Joha rice and reported that DPPH scavenging activity was 81.45 ± 2.29 µg ml^{-1}, total phenolic content was found 74.86 ± 2.474 mg g^{-1} equivalent of gallic Acid and total flavanoid content was 190.7 ± 15.28 mg g^{-1} equivalent of quercetin.

Pathak *et al*. (2016) assessed chemical and antioxidant properties of 22 pigmented glutinous rice varieties along with one non pigmented variety (Memon bora) and reported that total phenolic content of 22 pigmented glutinous rice cultivars ranged from 53.45 to 80.16 mg GAE $100g^{-1}$ against 29.12 mg GAE $100g^{-1}$ in Memon bora while, the flavonoid content of 22 pigmented glutinous rice cultivars ranged from 45.57 to 60.76 mg QE 100 g^{-1}. Memon bora had recorded flavonoid content of 26.78 mg QE $100g^{-1}$. DPPH radical scavenging activity of 22 pigmented glutinous rice cultivars ranged from 14.54 to 21.73%, whereas, no DPPH activity was detected in Memon bora.

Pongjanta *et al*. (2016) evaluated 12 pigmented varieties of rice grain with low, medium high amylose content and four different pigmented bran colors white, brown, red and purple to determine the correlation among total phenolic compounds and starch digestibility. Red and purple pigmented flours had higher total phenolic compounds and more resistant starch than that of white flours. The TPC and resistant starch content of the flours ranged between 7.83- 47.3 mg l^{-1} and 2.44–10.50% respectively.

Veni *et al*. (2016) conducted an experiment to determine the total phenol content and antioxidant activity in 18 rice genotypes comprising of 2 black, 3 red and 13 brown. Black rice had highest amount of total phenols (576.1 mg $100g^{-1}$) and antioxidant activity (11.14 mg AAE $100g^{-1}$) than red rice and brown rice.

Aiyswaraya *et al.* (2017) evaluated 150 rice accessions to identify protein rich germplasm. The results revealed that total soluble protein content ranged from 7.54 g $100g^{-1}$ to 14.54 g $100g^{-1}$ of sample. Among 150 accessions, eight lines had recorded significantly higher protein content (>10.50 g/100g), 48 lines had registered moderate content (9.01 to 10.50 g $100g^{-1}$) and 94 lines had registered low protein content (< 9.00 g $100g^{-1}$).

Chay *et al*. (2017) conducted a study to determine the total phenolic content and antioxidant activity of waxy pigmented and non-pigmented rice varieties. Waxy pigmented rice exhibited significantly higher total polyphenol content of 2074 µg GAE g^{-1} compared to that of the waxy non-pigmented rice of 134 µg GAE g^{-1} db. The per centage of DPPH inhibition (Antioxidant activity) increased along with the increasing concentration of total phenols. Waxy pigmented rice varieties had highest percentage of inhibition (75.37%) than non pigmented rice varieties (6.72%).

Pathak *et al*. (2017) assessed 14 pigmented hill rice cultivars along with a non-pigmented rice to determine the total phenol content, antioxidant activity and flavonoid content. Total phenolic content of 14 pigmented hill rice cultivars varied from 67.89–89.43 mg GAE $100g^{-1}$ against Vandana (33.23 mg GAE $100g^{-1}$) while, pigmented rice cultivars exhibited flavanoid content of 57.75-78.74 mg QE $100g^{-1}$ whereas Vandana had 24.58 mg QE $100g^{-1}$. DPPH scavenging activity of 14 pigmented hill rice cultivars was 19.56-29.29%, whereas no DPPH activity has been detected in non-pigmented rice cultivar Vandana. Positive correlation between phenol content, antioxidant activity and flavanoid content was reported in this study.

Raghuvanshi *et al*. (2017) conducted a study to evaluate and compare the physical characteristics, nutritional quality, anti oxidant properties and glycemic index among red rice and white rice. Studies revealed that red rice had highest 1000 kernel weight (18.3 g) than white rice. In all the parameters red rice proved to be superior to white rice, red rice had highest crude protein content (10.49%), total phenolic content (143.38 mg GAE $100g^{-1}$), flavonoid content (120 mg R.E. $100g^{-1}$), DPPH scavenging activity (25%). Red rice was found to have a lower glycemic index (63.15) than white rice.

Shao *et al*. (2018) assessed 15 rice genotypes comprising of five non pigmented brown rice, five red rice and five black pigmented rice to determine the total phenolic content (folin ciocalteu method). Colored rice genotypes (red rice: 6.55-51.86 mg $100g^{-1}$ and black rice: 4.31-23.72 mg $100g^{-1}$) had highest total phenolic content than non-colored rice (0.79-3.21 mg $100g^{-1}$) genotypes.

2.3 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The nature and extent of variability forms the basis for all crop improvement programs. 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 as a useful measure of the magnitude of genetic variance present in the population.

Heritability, in broad sense, refers to the genetic variation present in the population in relation to the total observed variance. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. Basic information on heritability is a prerequisite for planning any breeding programme. High heritability indicates that it should be easy to conduct effective selection for the trait. Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population**.** Johnson *et al.* (1955) reported that though the heritability estimates give useful indication of relative values of selection based on phenotypic expression. The genetic gain should also be considered to arrive at a more reliable conclusion.

Habibi (2008) studied protein content in F_2 generation of a cross between BPT 5204 x HPR 14. Crude protein content showed high heritability coupled with high genetic advance. High PCV and GCV was recorded for number of productive tillers plant^{-1}, grain weight plant^{-1}, test weight, phosphorus, copper, potassium, zinc manganese and iron. Low PCV and GCV were recorded for 50% flowering, days to maturity, panicle length, and kernel elongation ratio.

Bekele *et al*. (2013) evaluated 64 rice genotypes to study the variability for grain zinc concentrations and yield related traits and reported that phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were highest for grain zinc concentration, number of tillers plant^{-1}, number of productive tillers plant^{-1} and grain yield plant^{-1}. Low values of PCV and GCV were recorded for days to maturity. High heritability coupled with high genetic advance as per cent mean was recorded for all the traits in this study except days to maturity.

Dhanwani *et al*. (2013) evaluated 21 F_1 crosses to assess the genetic variability, heritability and genetic advance for 13 quantitative and 19 quality traits in rice. Among the characters studied, high per cent of GCV and PCV was recorded for biological yield, alkali spreading value and lowest for days to 50% flowering and hulling percentage. High heritability was exhibited by plant height and kernel length. The genetic advance as percentage of mean was highest for biological yield, alkali spreading value and lowest for days to 50% flowering and milling percentage.

Raja *et al*. (2013) conducted experiment on 100 genotypes of local rice genotypes to study the extent of genetic variability and heritability of 13 characters in yield and yield attributing traits and concluded that maximum genotypic co-efficient of variability and phenotypic co-efficient of variability were observed for test weight, number of productive tillers plant^{-1}, number of spikelet panicle^{-1}, amylose per cent and grain yield plant^{-1} (g). High heritability coupled with high genetic advance as per cent of mean was observed for days to 50% flowering, test weight, number of spikelet panicle^{-1}, spikelet fertility, protein content and grain yield plant^{-1} (g).

Sanghera *et al*. (2013) evaluated 14 red rice genotypes from temperate region to assess the genetic variability for grain yield and component traits.The genotypic and phenotypic coefficients of variation was high for grain yield, secondary branches panicle^{-1} and panicle weight. High heritability coupled with high genetic advance was recorded for traits *viz*., days to 50% flowering, days to maturity, plant height, panicle weight, grain length, grain width and L/B ratio.

Veni *et al*. (2013) conducted genetic variability studies on 70 rice (*Oryza sativa* L.) genotypes for yield, yield components and quality parameters. High GCV was exhibited by water uptake followed by grain yield plant^{-1} and test weight. Highest broad sense heritability was exhibited by days to 50% flowering, volume expansion ratio while, genetic advance as per cent of mean was high for grain yield followed by water uptake and test weight.

Dhurai *et al*. (2014) conducted experiment using 32 rice genotypes to estimate the genetic variability, heritability and genetic advance for grain yield and yield contributing traits in rice and reported that number of grains panicle^{-1} and grain yield plant^{-1} showed relatively high GCV and PCV estimates whereas, high estimates of heritability coupled with high genetic advance as per cent of mean were obtained for number of effective tillers plant^{-1}, plant height, panicle length, number of grains panicle^{-1}, L/B ratio, 1000-grain weight and grain yield plant^{-1}.

Gokulakrishnan *et al*. (2014) assessed the heritability, genetic advance, phenotypic and genotypic coefficient of variation among yield, quality and its component characters in 23 genotypes of rice and concluded that high magnitude of phenotypic and genotypic coefficients of variation was observed for panicle weight. Panicle length and days to 50% flowering exhibited the lowest GCV and PCV. High values for heritability was observed for grain yield plant^{-1} while, high genetic advance was obtained for number of grains panicle^{-1}. High genetic advance coupled with high heritability was exhibited by grain breadth, grain L/B ratio, plant height, number of grains panicle^{-1} and grain yield plant^{-1}.

Naseem *et al*. (2014) conducted genetic variability studies on 20 genotypes of rice (*Oryza sativa* L.) for yield and yield related traits and reported that grain yield plant^{-1} showed the highest GCV and PCV followed by number of spikelets panicle^{-1} and plant height.

Rahman *et al*. (2014) evaluated seven advanced fine grain rice lines *viz*., S-1, S-2, S-5, AL-33 (II), AL-36, AL42 (II) and AL-44 (I) to study the variability parameters. The results revealed that plant height, number of effective tillers hill^{-1}, number of total tillers hill^{-1}, panicle length, number of filled spikelets panicle^{-1}, number of unfilled spikelets panicle^{-1}, grain yield plant^{-1}, and grain yield plot^{-1} exhibited highest PCV than GCV. Number of in effective tillers hill^{-1}, 1000 seeds weight showed same GCV and PCV values. High heritability along with high genetic advance as percentage of mean was exhibited by number of ineffective tillers plant^{-1}.

Bhati *et al*. (2015) conducted genetic variability studies on 30 elite rice (*Oryza sativa* L.) genotypes for grain yield and quantitative traits. Highest genotypic coefficient of variance (GCV) phenotypic coefficient of variance (PCV) was observed for grain yield hill^{-1}. High estimates of heritability coupled with high genetic advance was observed for plant height and spikelets panicle^{-1}.

Devi *et al*. (2015) evaluated 92 rice genotypes to estimate the genetic variability and heritability for 14 physico chemical, cooking and observed that water uptake, gel consistency and alkali spreading value exhibited high estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Highest broad sense heritability and high genetic advance was recorded for water uptake, amylose content and gel consistency.

Ekka *et al*. (2015) evaluated 96 rice germplasm accessions to study the variability among yield attributing and quality traits. Studies revealed that highest genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for number of effective tillers plant^{-1} and grain yield plant^{-1}. High heritability coupled with high genetic advance was noticed for number of effective tillers plant^{-1}, number of filled grains panicle^{-1} and grain yield plant^{-1}.

Gampala *et al*. (2015) evaluated 80 rice genotypes to study the genetic variability, heritability and genetic advance for grain yield and quality traits. The result revealed that highest PCV was observed for grain yield hill^{-1} and number of spikelets panicle^{-1} while, highest GCV was observed for number of spikelets panicle^{-1}. High heritability was observed for number of spikelets panicle^{-1}, test weight, plant height, and days to 50% flowering. Whereas, grain yield hill^{-1} showed lowest heritability. High genetic advance was observed for number of spikelets panicle^{-1} and plant height. High heritability coupled with high genetic advance was observed for plant height, panicle length and grain yield plant^{-1}.

Patil *et al*. (2015) screened 61 rice genotypes to study the variability and heritability. Grain yield plant^{-1} exhibited highest PCV and GCV followed by grain Fe content. Low PCV and GCV was exhibited by panicle length, days to 50% flowering and days to maturity. High heritability and high genetic advance as per cent of mean was manifested by grain yield plant^{-1}. Moderate heritability along with high genetic advance was recorded for grain Zn and Fe content.

Samak *et al*. (2015) conducted an experiment to study the genetic variability among protein, Zn and Fe content in segregating generations of rice from a cross BPT × HPR 14 and reported that total grain protein content showed moderate heritability along with moderate genetic advance as per cent of mean whereas, zinc and iron content showed high heritability coupled with high genetic advance as per cent of mean.

Savitha and Kumari (2015) evaluated four traditional land races and six improved high yielding varieties to study the genetic variability among yield and yield component traits. Moderate values of PCV and GCV were recorded for days to 50% flowering, plant height, number of productive tillers plant^{-1} and single plant yield. High heritability coupled with high genetic advance was observed for days to 50% flowering, plant height and number of productive tillers plant^{-1}.

Umesh *et al*. (2015) assessed 24 rice genotypes to study different genetic parameters for yield attributing and quality characters and reported that spikelets panicle^{-1} and alkali spreading value showed the highest GCV and PCV. High heritability in broad sense was noted for plant height and 100 seed weight while, genetic advance was highest for number of spikelets panicle^{-1} and lowest for spikelet fertility, and for quality traits it was highest for alkali spreading value.

Bitew (2016) carried out an experiment to assess the extent of genetic variability for yield and yield related traits among 22 rice genotypes and concluded that high genotypic and phenotypic coefficients of variation was recorded for the traits grain yield, number of effective tillers plant^{-1} and unfilled grains panicle^{-1}. High heritability coupled with moderate genetic advance as per cent of mean was observed for 1000 grain weight.

Chowdhury *et al*. (2016a) evaluated 65 rice genotypes to study the variability among cooking quality parameters and yield. Gel consistency showed highest GCV and PCV values. High heritability along with high genetic advance was recorded for amylose content and yield plant^{-1}.

Chowdhury *et al*. (2016b) evaluated 65 diverse rice germplasm to study the variability among yield contributing characters and yield. Highest GCV and PCV were observed for 1000 grain weight and lowest for grain yield/plant. Higher estimates of heritability along with genetic advance were observed for all the traits except for zinc, protein content and number of panicles plant^{-1}.

Devi *et al*. (2016) evaluated 27 rice genotypes to assess the genetic variability, heritability and genetic advance for grain yield and quality traits. Among the characters studied, yield plant^{-1} and filled grains panicle^{-1} exhibited higher estimates of PCV and GCV. The estimates of PCV and GCV were low for the characters *viz*., kernel elongation ratio, days to 50% flowering, kernel length, kernel width, panicle length and L/B ratio. High heritability in broad sense and high genetic advance as per cent of mean were exhibited by six traits *viz*., effective tillers, plant height, filled seeds panicle^{-1}, test weight, yield plant^{-1} and length/breadth ratio.

Ernawati *et al*. (2016) assessed the brown rice of local varieties to study the genetic parameters and reported that high heritability estimates were found for grain yield, plant height, number of productive tillers plant^{-1} and number of filled grains panicle^{-1} while, 1000 grain weight exhibited low heritability.

Kumar *et al*. (2016) evaluated 81 rice genotypes for 13 quantitative traits to examine the nature and magnitude of variability, heritability and genetic advance as per cent of mean. Number of tillers hill^{-1} exhibited highest genotypic coefficient of variation and phenotypic coefficient of variation followed by number of panicles hill^{-1} and number of spikelets panicle^{-1} whereas, high heritability coupled with high genetic advance was recorded for number of spikelets panicle^{-1} followed by grain yield and plant height.

Mohan *et al*. (2016) evaluated 44 rice genotypes to study the variability among yield parameters. Days to 50% flowering, plant height and panicle length exhibited low levels of PCV and GCV indicating less variability among the genotypes for these traits. Whereas, number of grains panicle^{-1} and 1000 grain weight recorded high estimates of PCV and GCV indicating the presence of high degree of variation for these traits among the genotypes. High heritability along with high genetic advance was observed for number of grains panicle^{-1} and 1000 grain weight indicating the predominance of additive gene affects in controlling these traits.

Pavan *et al*. (2016) evaluated 22 rice genotypes to study variability among yield and quality traits and reported that high GCV and PCV coupled with high heritability and genetic advance as per cent of mean were exhibited by filled grains panicle^{-1} and alkali spreading value.

Rukminidevi *et al*. (2016) evaluated 50 traditional rice varieties and seven popular rice varieties to study the variability among the biometrical traits along with Fe and Zn content. The studies revealed that highest GCV and PCV was observed for single plant yield while, low heritability was manifested by number of productive tillers plant^{-1}. Single plant yield showed the highest genetic advance followed by Zn content and Fe content.

Sameera *et al*. (2016) evaluated 25 rice genotypes for their variability with regard to yield and yield components and revealed that high variability, heritability and genetic advance as per cent mean were exhibited by productive tillers plant^{-1}, number of grains panicle^{-1} and number of filled grains panicle^{-1} while, days to maturity recorded high heritability coupled with low genetic advance as per cent of mean.

Bhinda *et al*. (2017) carried out an experiment to obtain information on genetic variability, heritability and genetic advance for yield contributing and quality traits in advanced breeding lines of rice. The results revealed that alkali spreading value exhibited highest GCV and PCV followed by filled grains panicle^{-1} whereas, high heritability coupled with high genetic advance was reported for plant height, filled grains panicle^{-1}, number of grains panicle^{-1} and days to 50% flowering.

Jan *et al.* (2017) studied fourteen agro morphological traits among 35 rice genotypes for the assessment of genetic variability and observed that harvest index manifested the highest values of GCV and PCV while, lowest GCV and PCV were exhibited by 1000 grain weight. High broad sense heritability coupled with high genetic advance observed for number of spikelets panicle^{-1} and number of filled grains panicle^{-1}.

Lakshmi *et al*. (2017) evaluated 55 aromatic rice genotypes for yield and component characters to study the genetic variability, heritability and genetic advance. The results revealed that number of filled grains panicle^{-1}, grain yield plant^{-1}, kernel length and L/B ratio recorded high GCV and PCV. Days to 50% flowering and kernel breadth recorded low GCV and PCV. High heritability coupled with high genetic advance as per cent of mean was registered for plant height, number of productive tillers plant^{-1}, panicle length, number of filled grains panicle^{-1}, grain yield plant^{-1}, kernel length and L/B ratio.

Nandini *et al*. (2017) evaluated 324 traditional rice varieties in Karnataka for grain yield and yield attributing characters. High heritability coupled with high genetic advance was observed for days to 50% flowering, grain length, grain breadth and L/B ratio. Days to 50% flowering, productive tillers plant^{-1}, L/B ratio and 1000 grain weight exhibited high genotypic variance, high heritability coupled with high expected genetic gain.

Sahu *et al*. (2017) evaluated 215 indigenous rice landraces of Chhattisgarh, to estimate the components of genetic variability for grain quality traits. High heritability coupled with high genetic advance as per cent mean was observed for all the grain quality traits except for hulling and milling per cent. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed for alkali spreading value and gel consistency.

Shaik *et al*. (2017) conducted experiment to study the genetic parameters for yield and yield attributing characters in forty rice genotypes and reported that high phenotypic and genotypic coefficient of variation was recorded for yield plant^{-1} followed by total number of grains plant^{-1}. Low phenotypic and genotypic coefficient of variation was observed for number of filled grains panicle^{-1}, panicle length and days to 50% flowering. High heritability coupled with high genetic advance as per cent of mean was registered for yield plant^{-1}, effective tillers square meter^{-1}, total number of grains plant^{-1}, effective tillers plant^{-1} and 1000 grain weight.

Supriya *et al*. (2017) evaluated 25 rice germplasm accessions to study the genetic variability among quality, yield and yield related traits and reported that high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) was observed for seeds panicle^{-1} followed by days to 50% flowering, plant height, yield plant^{-1} and number of effective tillers among yield related traits. For quality traits, high GCV and PCV was observed for alkali spread value and L/B ratio. High heritability coupled with genetic advance as per cent of mean was observed for days to 50% flowering, effective tillers plant^{-1}, test weight, number of grains panicle^{-1}, grain yield plant^{-1}, L/B ratio and alkali spreading value.

Behera *et al*. (2018) conducted an experiment to study genetic variability in 49 elite slender grain rice genotypes for yield and yield component characters and concluded that both PCV and GCV were high for grain yield and fertile grains

panicle^{-1}. High heritability estimates were associated with moderate to high genetic gain over mean for days to 50% flowering, plant height, panicle length, fertile grains panicle^{-1} and fertility percentage.

Hari *et al*. (2018) evaluated 36 rice genotypes to study the genetic variability among yield component traits and physical quality traits. Studies revealed that high PCV coupled with GCV was recorded for alkali spreading value whereas, high heritability coupled with high genetic advance as per cent of mean was observed for total number of tillers plant^{-1}, number of grains panicle^{-1}, water uptake, alkali spreading value, amylose content and grain yield plant^{-1}.

Mamata *et al*. (2018) evaluated two F_2 populations of rice *viz*., Rajamudi × BR-2655 and Rathnachoodi × BR-2655 to estimate the variability, heritability, genetic advance and genetic advance as per cent of mean. High PCV and GCV values were observed for grain yield plant^{-1} and low PCV and GCV was observed for 1000 grain weight and panicle length. Plant height, spikelet fertility and grain yield plant^{-1} had high heritability along with high genetic advance as per cent of mean. Both the crosses registered high broad sense heritability coupled with high genetic advance.

2.4 GENETIC DIVERGENCE STUDIES

Yield is a complex polygenic trait governed by a wide range of morphological and physiological characters. The degree of genetic divergence is estimated through multivariate analysis by using biometrical tools like D^2 statistics and principal component analysis.

2.4.1 D^2 Statistic

D^2 statistics is found to be a potential biometrical tool for estimating the degree of genetic divergence in the germplasm collection of various crops (Rao, 1952., Singh and Gupta, 1968). This tool aids in identification of the most divergent genotypes for hybridization based on clustering pattern. The genotypes grouped together are considered to be less divergent than the genotypes of different clusters.

On the other hand, principal component analysis is complementary to D^2 analysis. It is a sort of multivariate analysis that measures the divergence between genotypes in terms of spatial distance, determines the effective number of axes differentiation and also indicates the character(s) most important for divergence at each axis.

Chakma *et al.* (2012) evaluated 39 rice genotypes using D^2 statistics and grouped them into six clusters with highest number of 11 and lowest number of 3 genotypes in cluster I and cluster IV, respectively. Maximum inter cluster distance was recorded between cluster II and cluster III. Similarly, cluster III had the highest mean performance for grain yield, harvest index, 1000 grain weight and number of effective tillers $hill^{-1}$ followed by cluster V for number of primary branches $panicle^{-1}$ and cluster VI for number of filled grains $panicle^{-1}$. Number of unfilled grains $panicle^{-1}$, 1000 grain weight and grain yield showed maximum contribution towards the genetic divergence.

Ovung *et al.* (2012) estimated the genetic divergence among 70 rice genotypes and grouped them into 9 clusters using D^2 statistics by considering 13 quantitative characters. Cluster I and cluster III constituted maximum number of genotypes. The genotypes falling in cluster VII had maximum divergence, which was closely followed by cluster V and cluster I. The inter cluster distance was maximum between cluster VI and VII followed by cluster III and IX. Thus, suggested that the genotypes constituted in these clusters may be used as parents for future hybridization programme and stated that the traits *viz*., spikelets $panicle^{-1}$, plant height and biological yield were found to be the major contributors to genetic divergence.

Pratap *et al.* (2012) evaluated 100 high yielding rice genotypes to determine diversity for grain yield, yield components and quality characters. They showed that clustering pattern of genotypes did not have relationship between geographic origin and genetic diversity and stated that cluster XI exhibited very high inter cluster distances from VI, II, III and I. Thus, hybridization of Swarna of cluster I with promising genotypes of cluster VI (Narendra 118, Vandana, Narendra 1, Akashi and Narendra 97) may results in high yielding varieties.

Ramanjaneyulu *et al.* (2014) studied genetic divergence for productivity traits in ten popular low land rice genotypes and grouped them into four clusters. The maximum intra cluster distance was observed in cluster III. The yield attribute 1000 grain weight exhibited maximum contribution to total genetic divergence (57.78%) followed by grain yield (15.56%), number of spikelets (11.11%), straw yield (6.67%) and spikelet length (4.44%). On the other hand, the traits such as tillers $plant^{-1}$ and harvest index failed to contribute towards genetic divergence.

Beevi and Venkatesan (2015) grouped 60 genotypes of rice into six clusters. Out of which, cluster I was found to be the largest comprising of 50 genotypes followed by cluster II with four genotypes. The clusters IV and V had two genotypes each, while cluster III and VI were mono genotypic in nature. The characters *viz*., grain yield plant^{-1}, number of grains panicle^{-1} and plant height contributed maximum towards the genetic divergence. However, cluster III recorded highest mean value for grain yield plant^{-1} and the lowest for days to 50% flowering. Further, the highest inter-cluster distance was recorded between clusters III and VI.

Mohan *et al.* (2015) analyzed 43 genotypes of rice for genetic divergence using D^2 statistics and revealed that highest inter cluster distance (8.69) was observed between cluster II & V followed by cluster II & III (7.87). Among the traits studied, test weight and days to flowering contributed the maximum. The genotypes grouped in cluster II could be crossed with JGL 21002 and JGL 21005 of cluster III to obtain transgressive segregants for improvement of grain yield, number of grains panicle^{-1} and test weight.

Chamundeswari (2016) assessed genetic divergence among 70 cultivars of low land rice and grouped them into eight clusters and observed that the clustering pattern could not show any relationship between geographic distribution and genotypic diversity. The inter cluster distance was maximum between cluster V and VIII (759.25). Further, cluster V exhibited the highest mean performance for grain yield (4.9 t ha^{-1}), while cluster VI showed the lowest mean for test weight (14.8g). The characters *viz*., test weight (29.5%), grain yield (28.5%) and plant height (19.79%) contributed maximum towards the genetic divergence.

Babu and Sree lakshmi (2017) assessed genetic divergence by Mahalanobis D^2 statistics among 50 genotypes of rice and grouped them into six clusters. Of which, cluster I had maximum number of genotypes (12) followed by cluster II with nine genotypes. Maximum intra cluster distance (746.9) was observed in cluster VI and minimum in cluster III (327.8). Days to 50% flowering, gelatinization temperature score and water uptake together contributed around 72% to total divergence. Maximum inter cluster distance was observed between clusters III and VI (827.45) followed by cluster III and IV. Thus, indicated wider genetic diversity among the genotypes of these clusters.

Meena *et al.* (2017) carried out multivariate analysis using 38 maintainer lines of rice for 11 characters and grouped into five different clusters. The inter cluster distance was maximum between clusters I and V (35.700) followed by cluster I and IV (30.090), cluster I and cluster III (26.530) and cluster II and cluster V (22.800). The minimum inter cluster distance was observed between cluster III and cluster IV (3.600) followed by cluster IV and cluster V (5.920) and cluster V and cluster (9.450). Among the characters studied, number of panicles per m^2, number of grains $panicle^{-1}$, number of effective tillers and grain yield $plot^{-1}$ contributed more for divergence.

Sowmya and Venkatesan (2017) conducted genetic diversity studies among 48 rice genotypes using D^2 statistics and grouped them into nine clusters. Maximum intra cluster distance was registered in cluster VIII (35.87), while maximum inter cluster distance was found between Cluster VI and Cluster VIII (54.23) followed by cluster VIII and IX (51.01), cluster V and VIII (50.26) and cluster III and VIII (45.60). Among the traits studied, grain yield $plant^{-1}$ and 1000 grain weight contributed maximum towards genetic diversity.

Supriya *et al.* (2017) grouped 25 scented rice genotypes into six different clusters. Cluster I consisted of six genotypes followed by cluster II with seven genotypes, clusters III with eight, cluster IV and V had one genotype each and cluster VI consist of two genotypes. The highest intra cluster distance for yield traits were found in cluster VI (301.94) while the lowest in cluster IV and V (0.00). Similarly, maximum inter cluster distance was found between cluster IV and I (4463.46) followed by cluster II and cluster I (3265.73). Length of main panicle had very low contribution (0.33%) towards total divergence whereas, the traits *viz.*, number of seeds $panicle^{-1}$ (39.67%) and kernel length after cooking had very high contribution towards total divergence.

Shivani *et al.* (2018) aimed at ascertaining the nature and magnitude of genetic divergence among 26 genotypes by using D^2 statistics and grouped them into six clusters based on Euclidean cluster analysis. Cluster I containing maximum of 11 genotypes. Maximum intra cluster distance was observed in cluster III. Maximum inter cluster distance was noticed between cluster III and IV followed by cluster I and VI. The maximum contribution of individual trait to the divergence among genotypes was recorded by number of spikelet $panicle^{-1}$.

2.4.2 Principal Component Analysis (PCA)

Latif *et al.* (2011) analyzed 14 blast resistant and susceptible rice genotypes using principal component analysis and reported first five axes with more than one eigen value accounted for 90.57% cumulative variation. The first three principal axes accounted for 78.72% of the total variation for 13 characters. Based on the values of PC I and II, a two dimensional scatter diagram was constructed which distributed the positions of the genotypes into seven groups, thus, indicated that considerable diversity existed among the genotypes studied.

Chakma *et al.* (2012) reported that eigen values and per cent of variation for 12 principal component axes among 39 rice genotypes using principal component analysis and showed that only the first three principal components accounted for 65.79% of cumulative variation The first two principal axes accounted for 52.76% of the total variation.

Ahmed *et al.* (2015) conducted an experiment with 40 genotypes of Balam rice germplasm to study 17 morpho-physicochemical characters using the canonical analysis. The traits *viz.*, grain length, cooking time, straw yield hill^{-1}, days to maturity, plant height and grain yield panicle^{-1} contributed maximum to the genetic divergence.

Anyaoha *et al*. (2018) evaluated 77 upland rice genotypes and grouped them into three clusters, the first three principal components explained about 64.55% of the total variation among the ten characters studied. The results revealed that the characters such as grain yield, days to flowering, leaf area and plant height at maturity were the principal discriminatory traits and suggested that selection in favour of these traits might be effective in that population.

Ravikumar *et al.* (2015) studied 24 released and prereleased cultures using principal component analysis and revealed that, first three principal components contributed 83% of variability existing in the rice genotypes for yield contributing characters. Among nine yield components studied, test weight contributed more than 50% to genetic diversity followed by mother panicle length and tiller panicle length demonstrating the significance of these traits in selection procedures for increasing yield.

Chapter – III

Material and Methods

Chapter III

MATERIAL AND METHODS

The present investigation entitled "Characterization of rice genotypes for Distinctness Uniformity Stability and Nutritional parameters**"** was undertaken to characterize the rice genotypes based on DUS guidelines, variability and diversity among yield, nutritional and quality parameters to identify rice genotypes with high nutritional characteristics. The materials utilized and the methodologies adopted in the present study are described below.

3.1 MATERIALS

The experimental material comprising of 30 rice genotypes collected from farmers of different districts of Telangana. The details pertaining the germplasm utilized in the present study is represented in Table 3.1

3.2 METHODS

3.2.1 Experimental Design

The present investigation was carried out during *kharif* 2018 at Southern block of Agricultural College Farm, Bapatla, Guntur district of Andhra Pradesh, which was located at 15°9' North and 80°4' East longitude at an altitude of 5.49 m above Mean Sea Level.

All the 30 genotypes were sown separately in the raised nursery beds. Thirty days old seedlings of each genotype were transplanted separately in 5 rows of 3m length by adopting a spacing of 20 cm between rows and 15 cm between plants with in a row in Randomized Block Design with three replications. All necessary precautions were taken up to maintain uniform plant population of each genotype per replication. The intercultural operations were done at regular intervals and necessary plant protection measures were adopted during the crop growth. Layout of the experimental design was presented in Fig. 3.1.

Analysis pertaining to nutritional and grain quality parameters were carried out at Dept. of Genetics and Plant breeding and Biochemistry and Food Process Engineering Laboratory, Post-Harvest Engineering and Technology (PHET), Agricultural College campus, Bapatla.

Table 3.1 List of genotypes studied in the present investigation

S.No.	Genotype	Place of collection
1	Ambemohar	Kamanpur (Village), Peddapalli (District), Telangana
2	Araku loya	Ranga Reddy, Hyderabad, Telangana
3	Badsha bhog	Kamanpur (Village), Peddapalli (District), Telangana
4	Bahurupi	Gumma konda (Village), Nagarkurnool (District), Telangana.
5	Burma black	Ranga Reddy, Hyderabad, Telangana
6	Chintaluri sannalu	Kamanpur (Village), Peddapalli (District), Telangana
7	Doddiga	Kamanpur (Village), Peddapalli (District), Telangana
8	Ghani	Gumma konda (Village), Nagarkurnool (District), Telangana
9	Illapaipu samba	Gumma konda (Village), Nagarkurnool (District), Telangana
10	Kalabhatt	Ranga Reddy, Hyderabad, Telangana
11	Kalajira	Kamanpur (Village), Peddapalli (District), Telangana
12	Karuppu kavuni	Ranga Reddy, Hyderabad, Telangana
13	Kulakar	Kamanpur (Village), Peddapalli (District), Telangana
14	Madumurangi	Gumma konda (Village), Nagarkurnool (District), Telangana.
15	Mappillai samba	Ranga Reddy, Hyderabad, Telangana
16	Mysore malliga	Ranga Reddy, Hyderabad, Telangana.
17	Narayana kamini	Kamanpur (Village), Peddapalli (District), Telangana
18	Navara	Ranga Reddy, Hyderabad, Telangana.
19	Pancharatna	Kamanpur (Village), Peddapalli (District), Telangana
20	Parimala sanna	Gumma konda (Village), Nagarkurnool (District), Telangana
21	Pathariya	Gumma konda (Village), Nagarkurnool (District), Telangana.
22	Poongar	Kamanpur (Village), Peddapalli (District), Telangana
23	Ramsri	Gumma konda (Village), Nagarkurnool (District), Telangana
24	Ramyagali	Kamanpur (Village), Peddapalli (District), Telangana
25	Ranikanda	Kamanpur (Village), Peddapalli (District), Telangana.
26	Ratnachudi	Ranga Reddy, Hyderabad, Telangana.
27	Sammel bhog	Gumma konda (Village), Nagarkurnool (District), Telangana
28	Sannajajulu	Kamanpur (Village), Peddapalli (District), Telangana
29	Selam sanna	Kamanpur (Village), Peddapalli (District), Telangana
30	Tulasi baso	Kamanpur (Village), Peddapalli (District), Telangana

Fig. 3.1 Layout of Experimental design

3.2.2 Characterization of Rice Genotypes for DUS

Morphological characterization of 30 rice genotypes was studied for 26 descriptors. Visual observations were recorded on single plant basis on ten randomly selected plants in each genotype at appropriate growth stages according to Shobharani *et al.* (2004) on different morphological characters *viz.,* basal leaf sheath colour, leaf anthocyanin colouration, length of blade, width of leaf blade and grain quality traits including amylose content were recorded as per the standard procedures. Details on DUS characters, states and the stage of observation of the above morphological and grain quality traits were presented in the Table 3.2

3.2.3 Recording of Observations

Observations for grain yield and associated characters were recorded on five randomly selected plants for each entry in each replication. The mean data was estimated for each character per each replication. The data collected was subjected to statistical analysis. The method of recording data for each trait is described below:

3.2.3.1 Plant height (cm)

The height of the plant was measured from the base of the plant to the tip of the main panicle at the time of harvest and expressed in cm.

3.2.2 Days to 50% flowering

The total number of days taken from the date of sowing to complete exertion of 50% of panicles in each genotype was recorded as days to 50% flowering.

3.2.3.3 Number of productive tillers plant^{-1}

The total numbers of ear bearing tillers were counted on each plant at the time of maturity.

3.2.3.4 Panicle length (cm)

The length of panicles from each plant was measured in centimetres from neck node to the tip of the last spikelet.

Table 3.2 Essential characters along with descriptors and stage of observation

S.No.	Characteristics	States	Note	Stage of observation	Type of assessment
1	Basal leaf: Sheath colour	Green Light purple Purple lines Purple	1 2 3 4	Booting (early boot stage)	Visual assessment by observation of individual plant or parts of plants
2	Leaf: Anthocyanin colouration	Absent Present	1 9	Booting (early boot stage)	Visual assessment by observation of individual plant or parts of plants
3	Leaf: Length of blade	Short (<30 cm) Medium (30-45 cm) Long (>45 cm)	3 5 7	Booting (early boot stage)	Measurement of a number of individual plants or parts of plants
4	Leaf: Width of blade	Narrow (<1 cm) Medium (1-2 cm) Broad (>2 cm)	3 5 7	Booting (early boot stage)	Measurement of a number of individual plants or parts of plants
5	Time of heading (50% plants with panicles) in days	Very early (<70) Early (71-90) Medium (91-110) Late (111-130) Very late (>131)	1 3 5 7 9	Half of inflorescence emerged	Visual assessment by a single observation of a group of plants or parts of plants
6	Flag leaf: Attitude of blade (early observation)	Erect Semi-erect Horizontal Drooping	1 3 5 7	Beginning of anthesis	Visual assessment by a single observation of a group of plants or parts of plants
7	Lemma: Anthocyanin colouration of keel	Absent/Very weak Weak Medium Strong Very strong	1 3 5 7 9	Anthesis half-way	Visual assessment by observation of individual plant or parts of plants

Table 3.2 (cont.)

S.No.	Characteristics	States	Note	Stage of observation	Type of assessment
8	Spikelet: Colour of stigma	White Light green Yellow Light purple Purple	1 2 3 4 5	Anthesis half-way	Visual assessment by observation of individual plant or parts of plants
9	Panicle: Length of main axis	Very short (<16cm) Short (16-20 cm) Medium (21-25 cm) Long (26-30 cm) Very long (>30 cm)	1 3 5 7 9	Between milk development & ripening (terminal spikelets ripened)	Measurement of a number of individual plants or parts of plants
10	Panicle: Curvature of main axis	Straight Semi-straight Deflexed Dropping	1 3 5 7	Ripening (terminal spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants
11	Panicle: Number plant^{-1}	Few (<11) Medium (11-20) Many (>20)	3 5 7	Between Dough development & Ripening (terminal spikelets ripened)	Measurement of a number of individual plants or parts of plants
12	Spikelet: Colour of tip of lemma	White Yellowish Brown Red Purple Black	1 2 3 4 5 6	Between dough development & Ripening (terminal spikelets ripened)	Visual assessment by observation of individual plant or parts of plants
13	Panicle: Awns	Absent Present	1 9	Ripening (terminal spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants

Table 3.2 (cont.)

S. No.	Characteristics	States	Note	Stage of observation	Type of assessment
14	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	Ripening (terminal spikelets ripened)	Visual assessment by observation of individual plant or parts of plants
15	Panicle: Distribution of awns	Tip only Upper half only Whole length	1 3 5	Ripening (terminal spikelets ripened)	Visual assessment by observation of individual plant or parts of plants
16	Panicle: Presence of secondary branching	Absent Present	1 9	Ripening (terminal spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants
17.	Panicle: Exertion	Partly exerted Mostly exerted Well exerted	3 5 7	Ripening (terminal spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants
18	Time maturity (days)	Very early (<100) Early (101-120) Medium (121-140) Late (141-160) Very late (>160)	1 3 5 7 9	Ripening (terminal spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants
19	Leaf: Senescence	Early Medium Late	3 5 7	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants
20	Grain: Weight of 1000 fully developed grains	Very low (<15 g) Low (15-20 g) Medium (21-25 g) High (26-30) Very high (>30 g)	1 3 5 7 9	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened	Visual assessment by a single observation of a group of plants or parts of plants

Table 3.2 (cont.)

S.No.	Characteristics	States	Note	Stage of observation	Type of assessment
21	Grain: Length	Very short (<6.0 mm) Short (6.1-8.5 mm) Medium (8.6-10.5 mm) Long (10.6-12.5 mm) Very long (>12.5 mm)	1 3 5 7 9	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Measurement of a number of individual plants or parts of plants
22	Grain: Width	Very narrow (<2.0 mm) Narrow (2.1-2.5 mm) Medium (2.6-3.0 mm) Broad (3.1-3.5 mm) Very broad (>3.5mm)	1 3 5 7 9	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Measurement of a number of individual plants or parts of plants
23	Decorticated grain: Length	Short Medium Long Long* (Long for Basmati type) Extra long	1 3 5 7 9	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Measurement of a number of individual plants or parts of plants
24	Decorticated grain: Width	Narrow (<2.0 mm) Medium (2.0-2.5 mm) Broad (>2.5 mm)	3 5 7	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Measurement of a number of individual plants or parts of plants
25	Decorticated grain: Shape (in lateral view)	Short slender Short bold Medium slender Long bold Long slender Long slender* (For Basmati type) Extra-long slender	1 2 3 4 5 6	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Measurement of a number of individual plants or parts of plants

Table 3.2 (Cont.)

S.No.	Characteristics	States	Note	Stage of observation	Type of assessment
26	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	Caryopsis hard (can no longer be dented by thumbnail and over 90% of spikelets ripened)	Visual assessment by a single observation of a group of plants or parts of plants

3.2.3.5 Spikelet fertility (%)

Spikelet fertility was calculated for five panicles per plant from ten randomly selected plants as a proportion of the total number of filled grains to the total number of grains per panicle and expressed in percentage.

$$\text{Spikelet Fertility \%} = \frac{\text{Number of filled grains per panicle}}{\text{Total number of grains per panicle}} \times 100$$

3.2.3.6 Yield plot^{-1} (Kg)

Panicles from ten plants were harvested individually at maturity. The samples were threshed, cleaned and sun dried to 12% moisture content and the average weight of ten plants was recorded in grams.

3.2.3.7 100 grain weight (g)

The weight of 100 well filled grains was recorded in grams.

3.2.3.8 Kernel Length (mm), Kernel Breadth (mm) and Kernel L/B ratio

Ten rice kernels from each entry were selected randomly and the length and breadth was recorded using a dial micrometer. Average of the length and breadth was taken in millimeter and L/B ratio was calculated. Based on kernel length and kernel L/B ratio, grain type was assigned by following Ramaiah (1969) classification.

Grain type	**Length**	**L/B ratio**
Long Slender (LS)	6 mm and above	3 and above
Short Slender (SS)	Less than 6 mm	3 and above
Medium Slender (MS)	5.5 mm-6 mm	2.5-3.0
Long Bold (LB)	6 mm and above	Less than 3.0
Short Bold (SB)	Less than 6 mm	Less than 2.5

3.2.3.9 Protein content (%)

Protein content was estimated by using Lowry's method (Lowry *et al*. 1951). Rice powder of 0.5 g was taken and extracted with 10 ml of 0.1 N NaOH. The sample was centrifuged at 2,500 RPM for 10 min. Supernatant of 0.1 ml was taken and made to 1 ml with distilled water. Bovine Serum Albumin (BSA) standard solution in an aliquot of 0.1 to 1.0 ml was taken and made upto 1 ml with distilled water. 5 ml of alkaline reagent was added and samples were incubated for 10 min, then Folin-Ciocalteaus (FC) reagent of 0.5 ml was added to the samples and incubated in dark chamber for 30 min. The absorbance at 660 nm was recorded using Spectrophotometer. Protein content was calculated by comparing the O.D values of the standard with test sample and expressed as %.

3.2.3.10 Zinc and Iron content (μg g^{-1})

Seeds of individual rice genotypes were harvested and threshed manually. The seeds were dehusked using clean pestle and mortar. The grains were washed quickly with double distilled water to remove any surface contaminants and dried in hot air oven at 70^{o} C for 72 hours. 12.5 ml of 70% concentrated Nitric acid was added to 0.5 g powdered grain samples and the mixture was incubated overnight. Next day, 10 ml of diacid mixture (Nitric acid: Perchloric acid in the ratio of 10: 4) was added to the incubated sample. The mixture was then placed on the electric hot plate, allowing evaporation of acid in the form of white fumes, until white precipitate was formed at the base of the flask. The digested sample was left to cool for an hour and the volume was made up to 50 ml using double distilled water. Calibration of an instrument for estimation of an element was done using five standard solutions with appropriate dilutions. A suitable blank was run simultaneously to account for contamination from the reagents. Zinc and iron concentrations in the grain samples of rice were estimated using Atomic Absorption Spectrophotometer (AAS) at 213.86 nm for zinc and 248.33 nm for iron and expressed as μg g^{-1} of grain.

3.2.3.11 Total starch content (%)

Total starch content was estimated by using Anthrone method (Hodge, J.E and Hofrieter, B.T. 1962). Rice sample of 0.5 g was taken and extracted with 10 ml of hot 80 % ethanol. The sample was centrifuged at 2,500 RPM for 5 min and retained the residue. The residue was washed with hot 80% ethanol till the supernatant does not

give any color with anthrone reagent. The residue was dried on water bath and then 5 ml of distilled water and 6.5 ml 52% perchloric acid was added to the residue. This was kept at 0°C for 20 min and same was repeated twice and supernatant was pooled up and made up to 100 ml with distilled water. Along with test samples glucose working standard was prepared with concentration of 10 mg $100ml^{-1}$. An aliquot of 0.2 to 1.0 ml of glucose working standard was taken and made up to 1 ml with distilled water. Four ml of anthrone reagent was added to the samples and then heated for 8 min at 80°C and the absorbance was read at 630 nm using Spectrophotometer. Total starch content in the test sample was calculated by comparing the O.D. values of the standards and the test samples and expressed as %.

3.2.3.12 Amylose content (%)

Amylose is the linear fraction of starch, has a major influence on cooking quality and it plays an important role in determining the texture of cooked rice. Amylose content in rice was determined as per the method suggested by Juliano (1971).

A standard solution of amylose was prepared by taking 100 mg of amylose dissolved in 10 ml of 1 N NaOH and made to 100 ml with distilled water. An aliquot of 0.2 to 1.0 ml of amylose solution was taken and neutralized with 0.1N HCL using Phenolphthalein as indicator and 1 ml iodine reagent was added. For the test samples, 100 mg rice sample was taken and 1 ml distilled ethanol and 10 ml of 1N NaOH was added. Samples were incubated overnight at room temperature and then volume was made to 100 ml with distilled water. From this 2.5 ml of extract was taken, 20 ml distilled water was added, neutralized with 0.1N HCL using Phenalphthalein as indicator and1 ml iodine reagent was added. Final volume was made upto 50 ml with distilled water and absorbance recorded at 590 nm using Spectrophotometer. The amylose content of the sample was calculated by using the slope value obtained from standard curve and expressed as percentage. After estimating amylose content, the samples were classified as

Classification	**Amylose %**
Waxy	1-2%
Very low	2-9%
Low	9-20%
Intermediate	20-25%
High	25-33%

3.2.3.13 Total antioxidant activity (mg AAE $100g^{-1}$)

The total antioxidant activity was estimated by using 2, 2-diphenyl-1-picrylhydrazyl (DPPH) free radicle scavenging activity by using method suggested by Pathirana and Shahidi (2005). Sample of 0.5 g was incubated in 5 ml Methanol for 24 hrs in an incubator shaker. Contents were filtered and made the volume upto 5 ml with methanol. 0.1 ml of standard solution of ascorbic acid was taken as standard and 0.1 ml methanol was taken as control. 1.9 ml of DPPH working standard solution was mixed to 0.1 ml of test solution, standard, and control. Samples were kept in dark chamber for 30 min and absorbance was measured at 517 nm. The ability to scavenge free radicles was calculated by the following equation:

$$\text{Total antioxidant activity} = \frac{\text{Abs}_{\text{control}} - \text{Abs}_{\text{sample}}}{\textbf{Abs}_{\textbf{control}}} \times 100$$

Where

$\text{Abs}_{\text{control}}$ is the absorbance of DPPH radical + methanol

$\text{Abs}_{\text{sample}}$ is the absorbance of DPPH radical + sample extract/standard

3.2.3.14 Total soluble phenol content (mg $100g^{-1}$)

Total Phenol Content (TPC) was estimated by using Folin Ciocalteu method (Malik, C.P and Singh, M.B.1980). A powdered sample of 0.5 g was taken and extracted with 10 ml of hot 80% ethanol. The sample was centrifuged at 10,000 RPM for 20 min and the supernatant was collected. Five ml of 80% ethanol was added to the residue and again centrifuged to pool the supernatants. The supernatant was evaporated to dryness and dissolved the residue in 5 ml of distilled water and then filtered. 0.5 ml aliquot was taken. Along with this catechol standard was prepared and aliquot of 0.2 to 1.0 ml was taken and made up to 3 ml with distilled water. 0.5 ml Folin-Ciocalteaus (FC) reagent was added, after 3 min 2 ml of 20 % Na_2CO_3 was added and then vertex the samples, tubes were placed in boiling water for 1 min. Finally tubes were cooled and absorbance was measured at 650 nm using spectrophotometer. TPC was calculated by comparing the O.D. at standard with the test sample and expressed as mg $100g^{-1}$.

3.2.3.15 Glycemic Index *(in vitro)*

Glycemic Index was determined, following rice *in vitro* method suggested by Goni *et al.* (1997) with slight modifications. A ground sample of 100 mg was incubated with 0.2 ml of solution containing 1 g of pepsin in 10 ml HCL-KCL buffer (p^H 1.5) and incubated at 40°C for one hour in a shaking water bath. Volume was made upto 25 ml with tris-maleate buffer (p^H 6.9). 5 ml of α-amylase in tris-maleate buffer containing 2.6 UI were added to the sample and incubated at 37°C in a shaking water bath. An aliquot of 0.5 ml was taken for every 30 min for 0-3 hours. These aliquots were placed in a test tube at 100°C and were vertexed for 5 min to inactivate the enzyme and refrigerated until the end of the incubation time. Then 3 ml of 0.4M Sodium acetate buffer (p^H = 4.75) was added to each aliquot, and 60 µl of amyloglucosidase was added to hydrolyse the digested starch into glucose after 45 min at 60°C in a shaking water bath. Volume was adjusted to one ml with distilled water. Triplicated aliquots of 0.5 ml were incubated with GOD-POD reagent. The areas under hydrolysis curves (AUC, 0-180 min) were calculated, with the equation described below, for all the samples.

$$C=C_{\infty}(1 -e^{-kt})$$

Where C is the concentration at t time, C_{∞} is the equilibrium concentration, k is the kinetic constant and t is the chosen time.

The HI was calculated as the relation between AUC of test sample and the AUC for a reference food, white bread, expressed as a percentage. Glycemic index was calculated using the formula given below.

$$GI = 39.71+ 0549\ HI.$$

3.2.3.16 Phytate content (mg $100g^{-1}$)

Phytate content is estimated by the method suggested by Wheeler, E.L and Ferrel, R.E. (1971). Weigh a finely ground (40 mesh) sample estimated to contain 5 to 30 mg phytate P into a 125 ml Erlenmeyer flask. Extract in 50 ml 3% TCA for 30 min with mechanical shaking or with occasional swirling by hand for 45 min. centrifuge the suspension and transfer a 10 ml aliquot of the supernatant to a 40 ml conical centrifuge tube. Add 4ml of $FeCl_3$ solution to the aliquot by blowing rapidly from the pipette. Heat the contents in boiling water for 45 min. If the supernatant is not clear after 30

min, add one or two drops of 3% sodium sulphate in 3% TCA and continue heating. Centrifuge (10-15 min) and carefully decant the clear supernatant. Wash the precipitate twice by dispersing well in 20-25ml 3% TCA, heat in boiling water for 5- 10 min and centrifuge. Repeat washing with water. Disperse the precipitate in few ml of water and add 3 ml of 1.5N NaOH with mixing. Bring volume to approximately 30 ml with water and heat in boiling water for 30 min. Filter hot (quantitatively) through a moderately retentive paper Whatman No. 2. Wash the precipitate with 60-70 ml hot water and discard the filtrate. Dissolve the precipitate from the paper with 40 ml hot 3.2N HNO_3 into a 100 ml volumetric flask. Wash paper with several portions of water, collecting the washings in the same flask. Cool flask and contents to room temperature and dilute to volume with water. Transfer a 5 ml aliquot to another 100 ml volumetric flask and dilute to approximately 70 ml, add 20 ml of 1.5M KSCN, dilute to volume and read colour immediately (within 1 min) at 480 nm. Run a reagent blank with each set of samples. Standard preparation is by weighing accurately 433 mg $Fe(NO_3)_3$ and dissolve in 100 ml distilled water in a volumetric flask. Dilute 2.5 ml of this stock standard and make up to 250 ml in a volumetric flask. Pipette out 2.5, 5, 10, 15, and 20 ml of this working standard into a series of 100 ml volumetric flasks.

3.2.4 Statistical Analysis

The mean data in respect of various characters were subjected to the following statistical techniques.

3.2.4.1 Analysis of variance

The analysis of variance for each character was calculated as per the standard statistical procedure given by Panse and Sukhatme (1967).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij} = Performance of the j^{th} genotype in the i^{th} block

μ = General mean

b_i = True effect of i^{th} block

t_j = True effect of j^{th} genotype

e_{ij} = Random error associates with j^{th} genotype and i^{th} block

The structure of analysis of variance was as follows**.**

ANOVA Table for Randomized Complete Block Design

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	Expected Mean Sum of Squares	'F' calculated Value
Replications	(r-1)	RSS	M_r	$\sigma^2e + t\,\sigma^2r$	M_r/M_e
Treatments	(t-1)	TrSS	M_t	$\sigma^2e + r\,\sigma^2g$	M_t/M_e
Error	(r-1) (t-1)	ESS	M_e	σ^2e	
Total	(rt-1)	TSS			

Where,

r = Number of replications

t = Number of treatments

M_r = Mean sum of square of replication

M_t = Mean sum of square of treatment

M_e = Mean sum of square of error

σ^2_e = Environmental variance

σ^2_r = Variance due to replications

σ^2_g = Variance due to genotypes

Test of significance for each character was carried out against the corresponding error degrees of freedom using 'F' table values given by Fisher and Yates (1963).

3.2.4.2 Estimation of Genetic Parameters

Phenotypic and genotypic variance

Phenotypic and genotypic variances were estimated using the following formula

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + M_e = \frac{M_t - M_e}{r} + M_e$$

Coefficient of Variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton and Devane. (1953).

a. Genotypic coefficient of variation (GCV)

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

b. Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{X})} \times 100$$

The GCV and PCV values were classified as described by Subramanian and Menon (1973).

Classification	GCV/ PCV
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

Heritability

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability in broad sense } (h^2_{bs}) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

Heritability in broad sense was categorized as per the classification given by Johnson *et al.* (1955).

Classification	Heritability
Low	Less than 30%
Moderate	30 – 60%
High	More than 60%

Expected genetic advance

Genetic advance was calculated based on formula given by Johnson *et al.* (1955).

Expected genetic advance (GA) = $K \times \sigma_p \times h^2$

Where,

K = Selection differential at 5% selection intensity (2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\overline{X}} \times 100$$

Where,

GA = Genetic advance

$\overline{X}$ = Grand mean of the character

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

Classification	GAM
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.2.5 Genetic Divergence

3.2.5.1 Mahalanobis' D^2 analysis

The data collected on different yield contributing characters was analysed using Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1936).

3.2.5.2 Test of significance

Variances were calculated for all the characters studied and test of significance was done. For the character pairs analysis of covariance was estimated on the basis of mean values (Panse & Sukhatme, 1967). After testing the difference between genotypes

for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of 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 Wilk's criterion was done using the following relationship.

$$\wedge = \frac{|E|}{|E+V|}$$

Where,

$\wedge$ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E+V|$ = Determinant of error + variety matrix

$$V_{(stat.)} = - m \log_e \wedge \qquad \text{(at pq degrees of freedom)}$$

Where,

$m = n - (p + q + 1)/2$

n = degree of freedom for error + varieties

p = number of variables /characters

q = number of varieties –1 (or degrees of freedom)

$V_{(stat.)}$ is distributed as χ^2 with pq degrees of freedom.

Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation of the differences in the mean values of various characters of the two genotypes *i.e.*, Σd^2_i. Therefore transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.2.5.3 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.,* Y_{it} -Y_{jt} for t=1, 2…p variables are computed and the D^2 values were calculated as,

$$D^2_{ij} = \sum_{t=1}(y_i^t - y_j^t)^2$$

Where,

y_i^t is uncorrelated mean value of i^{th} genotype for character 't'

y_j^t is uncorrelated mean value of j^{th} genotype for character 't'

D^2_{ij} is D^2 between i^{th} and j^{th} genotypes.

3.2.5.4 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for p degrees of freedom, where p is the number of characters considered *i.e.* 17 in the present study.

3.2.5.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using Agglomerative hierarchial clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1979).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.2.5.6 Average intra-cluster distance

For the measurement of intra-cluster distances, the formula used was $\Sigma D^2_i/n$ where, ΣD^2_i was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.2.5.7 Average inter-cluster distance

Clusters were taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the numbers of one cluster to each of the number 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 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.

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

Where,

D^2 = difference in the mean values between two populations when all the character are considered simultaneously.

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

3.2.6 Principal Component Analysis

Principal component analysis was carried according to procedure described by Banfield (1978). PCA can be performed on two types of data matrices *viz.*, variance-covariance matrix and correlation matrix. With characters of different scale, a correlation matrix standardizing the original data set is preferred. If the characters are of same scale, a variance-covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

3.2.6.1 Eigen values and eigen vectors

The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal components. The proportion of variation accounted for each principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

$$\text{Per cent variance explained for } PC_1 = \frac{\text{eigen value } (PC_1)}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components. The principal components were identified by following procedure. The j^{th}principal component (Y_j) of the observations X is the linear combination given as follows:

$$Y_j = A_{1j}X_1 + \ldots\ldots\ldots + A_{pj}X_p$$

Where,

Aij are found such that Y_j is uncorrelated Y_1, Y_2,……..Y_{j-1} the j^{th} largest variance. The Aij are the elements of the normalized eigen vector associated with largest j^{th}eigen value. The variance of the j^{th} principal component of the λj and the total system variance trace (S) = $\lambda_1+\lambda_2+\ldots+\lambda p$.

The importance of the j^{th} principal component is given by,

$$\frac{\lambda_j}{\text{Trace (S)}}$$

This is informative about the proportion of total variation that can be accounted for the i^{th} principal component. The correlation between the i^{th} original variable X_i and the j^{th} principal component Y_j is given by,

$$\rho(X_i, Y_j) = \frac{A_{ij}.\sqrt{\lambda_j}}{\sqrt{S_i}}$$

Where,

S_i is the standard deviation of X_i.

Thus, a principal component is linear function of the test variables given as follows,

$$\text{Principal component} = ax_1+bx_2+\ldots\ldots\ldots+ hx_8$$

Where,

a, b,…. are coefficients and x_1, x_2….. etc., are the variables in such a way that the principal component has a unit variance as reported by Ehrenberg (1985).

PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D or 3D (dimensional) scatter plot of individuals.

Chapter – IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

Rice is a traditional staple food crop consumed by majority of the world's population. Effectiveness of any breeding programme is determined by the amount of genetic variability present in the genotypes. The wild and local cultivated landraces, cultivars and genotypes are the ultimate and ancient source of naturally existing genetic variability which is required to be thoroughly studied to identify desirable traits for the improvement of cultivated rice. These genetically distant land races could also be potential valuable source for enriching the gene pool of improved cultivars. Hence, genetic variability ensures the breeding potential and scope of improvement. Characterization of germplasm comprising of recording of highly heritable characters expressed in all environments and should easily be recognised by the naked eyes. Characterization of germplasm provides information on agro morphological characters, which are essential for gene bank management.

The present study was carried out with 30 genotypes during *Kharif* 2018-19 at College farm, Agricultural College, Bapatla with a prime objective of characterizing the germplasm for DUS (Distinctness, Uniformity and Stability) based on different agro-morphological characters and grain physical quality traits and also to study the magnitude of variability and diversity present in the germplasm based on yield and nutritional parameters. The data collected on these 30 genotypes for yield, yield attributing characters and nutritional parameters was subjected to standard statistical analysis for drawing valid conclusions. The results obtained from the above investigation are discussed character wise and discussed under the following headings.

4.1 Characterization of rice genotypes for important DUS characters

4.2 Mean, genetic variability, heritability and genetic advance

4.3 Genetic divergence

4.1 CHARACTERIZATION OF THE RICE GENOTYPES FOR IMPORTANT DUS CHARACTERS

Characterization of germplasm is useful in conformation of the identity and avoiding duplicates. Characterization of germplasm eventually lead to a system of recording and storing useful information that can be easily retrieved by the breeders

and also made available to others for further utilization in plant breeding programmes. Qualitative traits are more stable over generations and hence reliable for characterization of the available germplam lines.

In the present study, characterization of rice germplasm was done for 26 DUS characters including qualitative and quantitative characters such as basal leaf sheath colour, leaf anthocyanin colouration, length of leaf blade, width of leaf blade, time of heading, attitude of flag leaf, anthocyanin colouration of keel, colour of stigma, length of main axis (panicle), curvature of main axis, number of panicles plant^{-1}, colour of tip of lemma, presence of awns, colour of awns, distribution of awns, presence of secondary branching, panicle exertion, time of maturity, senescence of leaf , 100 grain weight, length of grain, width of grain, decorticated grain length and grain width, shape of decorticated grain and colour of decorticated grain. The characterization of genotypes as per DUS guidelines were presented in the Table 4.1

4.1.1 Basal Leaf Sheath Colour

This character was found to be trimorphic and exhibited three variations among 30 genotypes studied. Green basal leaf sheath colour was exhibited by 24 genotypes, four genotypes exhibited purple colour and two genotypes exhibited purple lines. Variation with respect to the basal leaf sheath colour present in the germplasm lines is represented in Plate 4.3.

4.1.2 Leaf Anthocyanin Colouration

Among the 30 genotypes studied, only three genotypes exhibited anthocyanin colouration in leaf. The remaining 27 genotypes did not exhibit any colouration. Variation in leaf anthocyanin colouration observed in the germplasm is represented in Plate 4.1.

4.1.3 Length of Leaf Blade

Length of leaf blade was long in 19 genotypes, medium in case of nine genotypes, and the remaining two genotypes had short leaf blade. Variation in length of leaf blade observed in the germplasm is presented in Plate 4.1.

Table 4.1. Characterization of 30 rice genotypes as per DUS guidelines

S.No.	Name	BLSC	LAC	LLB	LWB	TH	FLAB	LACK	SCS	PLMA	PCMA	PNPP	SCTL	PA
1	Narayana kamini	Green	Absent	Long	Medium	Medium	Erect	Absent	White	Short	Drooping	Medium	Yellowish	Absent
2	Ranikanda	Green	Absent	Long	Narrow	Medium	Semi-erect	Absent	White	Long	Drooping	Few	Yellowish	Absent
3	Sammel bhog	Green	Absent	Long	Narrow	Early	Erect	Absent	White	Very long	Drooping	Few	Black	Absent
4	Chintaluri sannalu	Green	Absent	Medium	Medium	Early	Semi-erect	Absent	White	Medium	Drooping	Few	Yellowish	Absent
5	Selam sanna	Green	Absent	Medium	Narrow	Early	Semi-erect	Weak	White	Medium	Deflexed	Few	Red	Absent
6	Araku loya	Green	Absent	Medium	Medium	Early	Semi-erect	Absent	White	Short	Drooping	Few	Yellowish	Absent
7	Ambemohar	Green	Absent	Medium	Narrow	Early	Semi-erect	Medium	White	Long	Deflexed	Few	Black	Absent
8	Pancharatna	Purple	Present	Long	Medium	Early	Semi-erect	Medium	Purple	Medium	Deflexed	Few	Brown	Absent
9	Kalajira	Green	Present	Long	Medium	Early	Semi-erect	Very strong	White	Long	Drooping	Medium	Black	Absent
10	Kalabhatt	Purple	Present	Long	Medium	Medium	Semi-erect	Absent	White	Medium	Drooping	Few	Black	Absent
11	Badsha bhog	Green	Absent	Long	Narrow	Medium	Erect	Absent	White	Long	Semi straight	Few	Brown	Absent
12	Poongar	Green	Absent	Medium	Narrow	Early	Erect	Medium	Purple	Medium	drooping	Medium	Yellowish	Absent
13	Ghani	Green	Absent	Medium	Medium	Early	Semi-erect	Absent	White	Medium	drooping	Few	Yellowish	Absent
14	Parimala sanna	Green	Absent	Long	Medium	Medium	Semi-erect	Absent	White	Long	drooping	Medium	Yellowish	Absent
15	Tulasi baso	Green	Absent	Long	Narrow	Medium	Semi-erect	Absent	White	Long	drooping	Medium	Black	Absent

BLSC: Basal leaf: sheath colour**, LAC**: Leaf: anthocyanin colouration, **LLB**: Leaf: length of blade, **LWB**: Leaf: width of blade,**TH**: Time of heading (50% plants with panicles) (days), **FLAB:** Flag leaf: attitude of blade (early observation)**, LACK:** Lemma: anthocyanin colouration of keel**, SCS:** Spikelet: colour of stigma**, PLMA:** Panicle: length of main axis**, PCMA:** Panicle: curvature of main axis**, PNPP:** Panicle: number plant^{-1}**, SCTL:** Spikelet: colour of tip of lemma**, PA:** Panicle: awns

Table 4.1. (cont.)

S.No.	Name	BLSC	LAC	LLB	LWB	TH	FLAB	LACK	SCS	PLMA	PCMA	PNPP	SCTL	PA
16	Ramsri	Green	Absent	Short	Narrow	Early	Semi-erect	Absent	White	Short	Deflexed	Medium	Red	Absent
17	Doddiga	Green	Absent	Long	Medium	Early	Semi-erect	Absent	White	Long	Drooping	Few	Yellowish	Present
18	Mappillai samba	Purple	Absent	Long	Medium	Early	Semi-erect	Strong	Purple	Long	Drooping	Few	Brown	Absent
19	Sannajajulu	Green	Absent	Long	Medium	Medium	Erect	Absent	White	Very long	Deflexed	Few	Yellowish	Absent
20	Illapaipu samba	Green	Absent	Long	Medium	Medium	Semi-erect	Absent	White	Long	Drooping	Few	Black	Absent
21	Burma black	Purple lines	Absent	Long	Broad	Medium	Semi-erect	Strong	Purple	Long	Drooping	Few	Black	Absent
22	Ramyagali	Green	Absent	Short	Medium	Early	Semi-erect	Medium	Purple	Short	Deflexed	Few	Brown	Absent
23	Karuppu kavuni	Purple	Absent	Long	Medium	Medium	Semi-erect	Strong	White	Long	Drooping	Medium	Black	Absent
24	Kulakar	Purple lines	Absent	Medium	Narrow	Early	Semi-erect	Absent	White	Short	Drooping	Medium	Brown	Absent
25	Bahurupi	Green	Absent	Long	Medium	Early	Semi-erect	Absent	White	Medium	Deflexed	Medium	Brown	Absent
26	Ratnachudi	Green	Absent	Long	Medium	Medium	Semi-erect	Absent	White	Medium	Drooping	Medium	Brown	Absent
27	Madumurangi	Green	Absent	Long	Medium	Early	Erect	Medium	White	Very long	Drooping	Medium	Yellowish	Present
28	Navara	Green	Absent	Medium	Narrow	Early	Semi-erect	Absent	White	Medium	Drooping	Medium	Black	Absent
29	Mysore malliga	Green	Absent	Long	Medium	Medium	Semi-erect	Absent	White	Long	Drooping	Medium	Yellowish	Absent
30	Pathariya	Green	Absent	Medium	Narrow	Early	Semi-erect	Absent	White	Medium	Drooping	Medium	Black	Absent

BLSC: Basal leaf: sheath colour**, LAC**: Leaf: anthocyanin colouration, **LLB**: Leaf: length of blade, **LWB**: Leaf: width of blade,**TH**: Time of heading (50% plants with panicles) (days), **FLAB:** Flag leaf: attitude of blade (early observation)**, LACK:** Lemma: anthocyanin colouration of keel**, SCS:** Spikelet: colour of stigma**, PLMA:** Panicle: length of main axis**, PCMA:** Panicle: curvature of main axis**, PNPP:** Panicle: number plant^{-1}**, SCTL:** Spikelet: colour of tip of lemma**, PA:** Panicle: awns

Table 4.1. (cont.)

S. No.	Name	PCA	PDA	PPSB	PE	TM	LS	Gr.W	GL	GW	DGL	DGW	DGS	DGC
1	Narayana kamini	-	-	Present	Well exserted	Medium	Late	Low	Medium	Narrow	Medium	Medium	Long slender	White
2	Ranikanda	-	-	Present	Well exserted	Medium	Late	Low	Medium	Narrow	Medium	Narrow	Long slender	Light brown
3	Sammel bhog	-	-	Present	Well exserted	Early	Medium	Very low	Short	Narrow	Short	Medium	Short bold	White
4	Chintaluri sannalu	-	-	Present	Well exserted	Early	Late	Very low	Short	Very narrow	Short	Narrow	Short slender	White
5	Selam sanna	-	-	Present	Well exserted	Early	Late	Very low	Short	Narrow	Short	Narrow	Short slender	Light brown
6	Arakuloya	-	-	Present	Well exserted	Early	Medium	Low	Medium	Medium	Medium	Medium	Long bold	White
7	Ambemohar	-	-	Present	Well exserted	Early	Late	Very low	Short	Narrow	Short	Narrow	Short bold	White
8	Pancharatna	-	-	Present	Well exserted	Early	Late	Medium	Medium	Medium	Medium	Medium	Long bold	Red
9	Kalajira	-	-	Present	Well exserted	Early	Late	Low	Short	Narrow	Medium	Narrow	Long slender	White
10	Kalabhatt	-	-	Present	Well exserted	Medium	Late	Medium	Medium	Broad	Medium	Broad	Long bold	Dark purple
11	Badsha bhog	-	-	Present	Well exserted	Medium	Late	Very low	Very short	Narrow	Short	Medium	Short bold	White
12	Poongar	-	-	Present	Well exserted	Early	Early	High	Short	Medium	Short	Broad	Short bold	Red
13	Ghani	-	-	Present	Well exserted	Early	Late	Low	Short	Medium	Short	Broad	Short bold	White
14	Parimala sanna	-	-	Present	Well exserted	Medium	Late	Very low	Short	Narrow	Short	Medium	Short bold	White
15	Tulasi baso	-	-	Present	Well exserted	Medium	Medium	Very low	Very short	Narrow	Short	Narrow	Short bold	White

PCA: Panicle: colour of awns (late observation), **PDA:** Panicle: distribution of awns, **PPSB:** Panicle: presence of secondary branching, **PE:** Panicle: exsertion, **TM:** Time maturity (days), **LS:** Leaf:senescence,**Gr.W:** Grain: weight of 1000 fully developed grains, **GL:** Grain: length**, GW:** Grain: width**, DGL:** Decorticated grain: length**, DGW:** Decorticated grain: width**, DGS:** Decorticated grain: shape (in lateral view), **DGC:** Decorticated grain: colour **Table 4.1. (cont.)**

S.No.	Name	PCA	PDA	PPSB	PE	TM	LS	Gr.W	GL	GW	DGL	DGW	DGS	DGC
16	Ramsri	-	-	Present	Well exserted	Early	Early	Low	Short	Medium	Short	Medium	Medium slender	White
17	Doddiga	Yellowish white	Whole length	Present	Mostly exserted	Early	Early	High	Short	Broad	Short	Broad	Short bold	White
18	Mappillai samba	-	-	Present	Well exserted	Early	Medium	Very high	Short	Broad	Short	Broad	Short bold	Light red
19	Sannajajulu	-	-	Present	Well exserted	Medium	Late	Low	Medium	Narrow	medium	Narrow	Long slender	White
20	Illapaipu samba	-	-	Present	Well exserted	Early	Late	Very low	Short	Narrow	Short	Medium	Medium slender	Light brown
21	Burma black	-		Present	Well exserted	Medium	Late	High	Medium	Very broad	Medium	Broad	Long bold	Dark purple
22	Ramyagali	-	-	Present	Well exserted	Early	Medium	High	Short	Medium	Medium	Medium	Long bold	White
23	Karuppu kavuni	-	-	Present	Well exserted	Medium	Late	High	Medium	Broad	Medium	Medium	Long bold	Dark purple
24	Kulakar	-	-	Present	Well exserted	Early	Late	Low	Short	Medium	Short	medium	Short bold	Red
25	Bahurupi	-	-	Present	Well exserted	Early	Late	Medium	Short	Medium	Short	Medium	Short bold	White
26	Ratnachudi	-	-	Present	Well exserted	Early	Late	Low	Short	Narrow	Short	Medium	Medium slender	White
27	Madumurangi	Yellowish white	Whole length	Present	Well exserted	Early	Late	High	Medium	Broad	Medium	Broad	Long bold	Light red
28	Navara	-	-	Present	Well exserted	Early	Early	Low	Short	Medium	Short	Medium	Short bold	Red
29	Mysore malliga	-	-	Present	Well exserted	Medium	Late	Very low	Short	Very narrow	Short	Narrow	Short slender	White
30	Pathariya	-	-	Present	Well exserted	Early	Medium	High	Short	Medium	Short	Broad	Short bold	Red

PCA: Panicle: colour of awns (late observation), **PDA:** Panicle: distribution of awns, **PPSB:** Panicle: presence of secondary branching, **PE:** Panicle: exsertion, **TM:** Time maturity (days), **LS:** Leaf:senescence,**Gr.W:** Grain: weight of 1000 fully developed grains, **GL:** Grain: length**, GW:** Grain: width**, DGL:** Decorticated grain: length**, DGW:** Decorticated grain: width**, DGS:** Decorticated grain: shape (in lateral view), **DGC:** Decorticated grain: colour.

4.1.4 Width of Leaf Blade

Based on the width of leaf blade 30genotypes were grouped into three classes, 18 genotypes possessed medium width, 11 genotypes exhibited narrow leaf blade and one genotype exhibited broad leaf blade. Variation in width of leaf blade observed in the germplasm is represented in Plate 4.1.

4.1.5 Time of Heading (50% plants with panicles) (days)

The experimental material categorized into two classes with respect to time of heading. A total of 18 genotypes were categorized as early heading (71-90 days) and remaining 12 genotypes were categorized as medium heading (91-110 days).

4.1.6 Flag Leaf: Attitude of Blade (early observation)

This character was found to be dimorphic. Among the 30 genotypes studied, 24 genotypes showed semi-erect attitude and six genotypes exhibited erect flag leaf. Variation in attitude of leaf blade observed in the germplasm is represented in Plate 4.2.

4.1.7 Lemma: Anthocyanin Colouration of Keel

This character exhibited polymorphic expression. Out of 30 genotypes studied, 20 genotypes exhibited no colouration, five genotypes exhibited medium colouration, three genotypes exhibited strong colouration, one genotype exhibited very strong colouration and remaining one genotype exhibited weak colouration. Variation in anthocyanin colouration of keel observed in the germplasm is represented in Plate 4.2.

4.1.8 Spikelet: Colour of Stigma

This character is dimorphic in state of expression. Out of 30 genotypes studied, 25 genotypes possessed white stigma and five genotypes possessed purple stigma. Variation in colour of stigma observed in the germplasm is represented in Plate 4.4.

4.1.9 Panicle: Length of Main Axis

According to length of panicle main axis, the germplasm has been categorized into four groups, dominated by 12 genotypes with long panicle, three genotypes had very long panicles, 10 genotypes had medium sized panicle and five genotypes had short panicles. Variation in length of main axis observed in the germplasm is represented in Plate 4.3.

4.1.10 Panicle: Curvature of Main Axis

This character was found to be trimorphic with respect to its expression.Out of30 genotypes studied, one genotype possessed semi-straight panicle, seven genotypes possessed deflexed and the remaining 22 genotypes possessed drooping panicles.

4.1.11 Panicle: Number of Panicles Plant^{-1}

The experimental material in the present study is dimorphic for this character. Out of 30 genotypes, 16 genotypes possessed fewer panicles per plant (<11) and 14 genotypes possessed medium number (11-20) of panicles.

4.1.12 Spikelet: Colour of Tip of Lemma

This is character is found to be tetramorphic in state of expression. Out of 30 genotypes, 10 genotypes exhibited black coloured tip of lemma, 11 exhibited yellowish tips, seven genotypes exhibited brown tip and the remaining two genotypes exhibited red colour tips.

4.1.13 Panicle: Awns

Among the 30 genotypes, only two genotypes possessed awns (Doddiga and Madumurangi) and remaining 28 genotypes were awn less. Plate 4.2.

4.1.14 Panicle: Colour of Awns (late observation)

Only two genotypes (Doddiga and Madumurangi) had awns and colour is yellowish white.

4.1.15 Panicle: Distribution of Awns

Out of 30 genotypes, only two genotypes (Doddiga and Madumurangi) possessed whole length distribution of awns. Plate 4.3.

4.1.16 Panicle: Presence of Secondary Branching

There is no variability in the germplasm with respect to this character. All genotypes showed secondary branching in panicle.

4.1.17 Panicle: Exsertion

The 29 genotypes possessed well exerted panicle and only one genotype exhibited mostly exerted panicle.

4.1.18 Time of Maturity (days)

Out of 30 genotypes, 20 genotypes were of early duration (101-120 days) and 10 were of medium duration (121-140 days) genotypes.

4.1.19 Leaf: Senescence

This character was found to be trimorpic. Among 30 genotypes studied, four genotypes belonged to early senescence type, six genotypes were intermediate and 20 genotypes were late senescencegenotypes.

4.1.20 Grain: Weight of 1000 Fully Developed Grains

The genotypes in the present study were categorized into five classes. Nine genotypes recorded very low weight, 10 genotypes recorded low weight, three were of medium weight, seven genotypes were of high weight and only one genotype had recorded very high test weight.

4.1.21 Grain: Length

This character was observed to be trimorphic. Out of 30 genotypes, two genotypes had very short grains, 19 genotypes had short grains and nine genotypes had medium sized grains. Variation in grain length observed in the germplasm is represented in Plate 4.5.

4.1.22 Grain: Width

The genotypes in the present study were categorized into five classes with respect to width of the grain. Two genotypes were very narrow, 12 genotypes had narrow grains, 10 had medium, five had broad type and one genotype had very broad grains.

4.1.23 Decorticated Grain: Length

Out of 30 genotypes, studied, 19 genotypes had short grain length and 11 genotypes had medium grain length.

4.1.24 Decorticated Grain: Width

The expression of this character was tetramorphic among the 30 genotypes. Eight genotypes possessed narrow grain width, 14 genotypes possessed medium and remaining eight genotypes had broad grain width.

4.1.25 Decorticated Grain: Shape (in lateral view)

Out of 30 genotypes studied, three genotypes possessed short slender grain type, 13 genotypes were short bold type, three genotypes were of medium slender, seven genotypes were long bold grain type and remaining four genotypes were long slender grain type. Plate 4.5.

4.1.26 Decorticated Grain: Colour

The 30 genotypes in the present study were characterized into five groups. white colour group comprising of 18 genotypes, light brown colour group consisting of three genotypes, light red colour group comprising of two genotypes, red colour group comprising of four genotypes and dark purple colour group comprising of three genotypes. Plate 4.6

Out of twenty six essential morphological visually assessed DUS descriptors studied, only one character *i.e.,* presence of secondary branching is monomorphic and 12 characters *viz.,* leaf-anthocyanin colouration, time of heading, flag leaf-attitude of blade, spikelet- colour of stigma, number of panicles plant^{-1}, awns, colour of awns (late observation), decorticated grain length, decorticated grain width, panicle distribution of

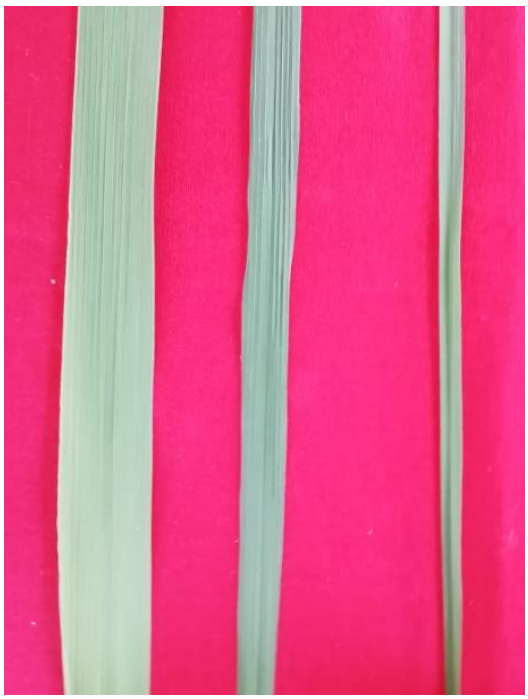
awns, panicle exertion, time maturity (days) were dimorphic and remaining characters *viz*., basal leaf sheath colour, length of leaf blade, width of leaf blade, panicle curvature of main axis, panicle length of main axis, leaf senescence, spikelet colour of tip of lemma, grain width, grain weight of 1000 fully developed grains, decorticated grain shape, and decorticated grain colour were polymorphic.

Absent **Present**

Anthocyanin colouration

Short **Medium** **Long**

Length of Leaf Blade



Broad **Medium** **Narrow**

Width of Leaf Blade

Plate 4.1 Characterization of morphological traits related to leaf

Present **Absent**

Lemma: Anthocyanin colouration of Keel

Present **Absent**

Awns

Semi erect **Erect**

Attitude of blade

Plate 4.2 Characterization of morphological traits related to panicle

Whole length

Panicle: Distribution of awns

Short Medium Long Very long

Length of main axis

Green Purple

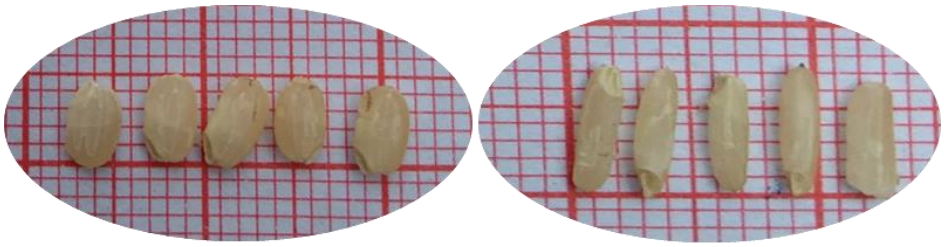
Basal leaf: Sheath colour

Plate 4.3 Characterization of morphological traits related to panicle and stem

White

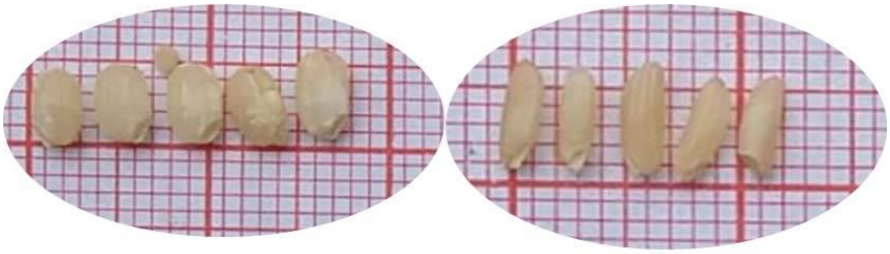
Purple

Plate 4.4 Photograph representing variation in spikelet colouration of stigma



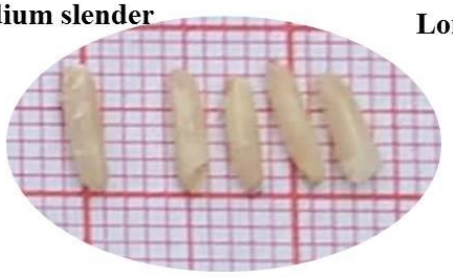
Short Medium

Decorticated grain: length



Short bold Short slender

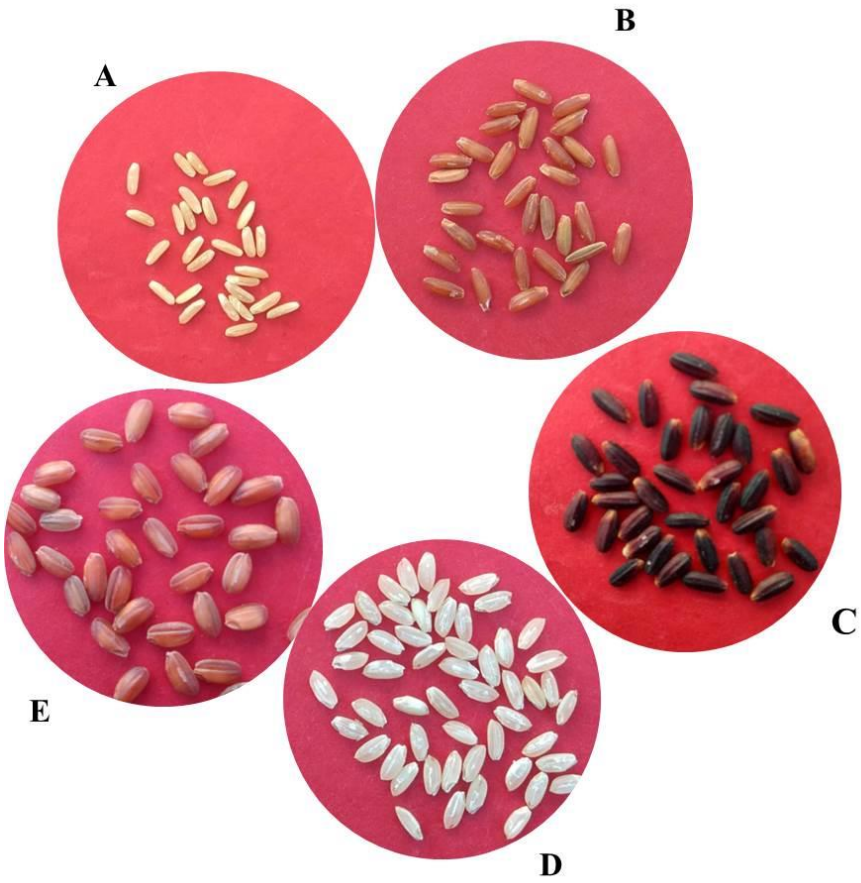
Medium slender Long bold



Long slender

Decorticated grain: shape

Plate 4.5 Characterization of grain quality parameters in rice



A. Light brown B. Light red C. Dark purple D. White E. Red

Plate 4.6 Photograph representing variation in decorticated grain colour

4.2 ANALYSIS OF VARIANCE AND GENETIC VARIABILITY STUDIES

4.2.1 Analysis of Variance (ANOVA)

Analysis of variance was carried out for 17 characters *viz*., Plant height (cm),days to 50% flowering**,** number of productive tillers plant $^{-1}$**,** panicle length (cm), spikelet fertility (%), yield plot^{-1} (Kg), 100 grain weight (g), kernal length/breadth ratio, protein content (%), Zn content (µg g^{-1}), Fe content (µg g^{-1})**,** total starch content (%)**,** amylose content (%)**,** total antioxidant activity (mg AAE 100g^{-1})**,** total soluble phenol content (mg 100g^{-1}), glycemic indexand phytate content (mg 100g^{-1})revealed significant differences among the genotypes for all the above characters under study indicating presence of greater variability among the genotypes. The details pertaining to ANOVA are furnished in Table 4.2.

4.2.2 Mean, Variability, Heritability and Genetic Advance as Per cent of Mean

The mean performance of 30 genotypes for eight quantitative and nine nutritional characters are presented in Table 4.3. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2 broad sense) and genetic advance as per cent of mean (GAM) are represented in Table 4.4 and described character wise here under.

4.2.2.1 Plant height (cm)

Plant height ranged from 81.4 cm (Chintaluri sannalu) to 184.27 cm (Madumurangi) with a mean value of 138.60 cm. The estimates of GCV (15.65%) and PCV (14.90%) recorded for this trait was moderate. The difference between the estimates of PCV and GCV was very narrow indicating, that environmental influence was less in the expression of this trait. Therefore, selection would be effective based on this character.These findings are in agreement with the results reported by Nayak *et al*. (2002), Krishna *et al*. (2008), Padmaja *et al*.(2008), Vanisree *et al*. (2013), Dhurai *et al*. (2014), and Sravan *et al*. (2014).

High heritability (95.2%) combined with high genetic advance as per cent of mean (31.89) was recorded for this trait shows the role of additive gene action in expression of this character. Hence, selection is effective when this character is considered. Similar results were reported by Patel *et al*. (2014), Rahman *et al*. (2014), Dhurai *et al*. (2014) and Supriya *et al*. (2017).

4.2.2.2 Days to 50% flowering

Days to 50% flowering ranged from 76 days (Ramsri and Bahurupi) to 105 days (Karuppu kavuni) with a mean value of 88 days. Genotypic (8.40%) and phenotypic (8.38%) coefficient of variation observed for this trait was low indicating, presence of less variability among the genotypes. These results are in agreement with Devi *et al*. (2017), Jan *et al*. (2017), Lakshmi *et al*. (2017), Nandini *et al*. (2017) and Mamata *et al*. (2018).

High heritability (99.4%) coupled with moderate genetic advance as per cent of mean (17.21) was recorded for this trait. These results are in accordance with the findings by Ekka *et al*. (2015), Gampala *et al*. (2015), Patil *et al*. (2015), Umesh *et al*. (2015), Devi *et al*. (2016), Sameera *et al*. (2016), Devi *et al*. (2017), Nandini *et al*. (2017) and Mamata *et al*. (2018).

4.2.2.3 Number of productive tillers plant^{-1}

The number of productive tillers plant^{-1} ranged from 7.73 (Doddiga) to 20.8 (Araku loya), with a mean value of 12.38. The GCV (23.06%) and PCV (24.54%) observed for this trait were high indicating large variation among genotypes studied. The estimate of PCV was slightly higher than corresponding GCV indicating that the character was less influenced by the environment. Therefore, Selection on the basis of phenotype may be effective for the improvement of this trait. These results are in accordance with the results reported by Gangashetty *et al*. (2013), Vanisree *et al*. (2013) and Bekele *et al*. (2013).

High heritability (93.9%) along with high genetic advance as per cent of mean (44.66) was observed for this trait. It indicates that predominance of additive gene action in expression of this trait, there by direct selection will be effective to obtain the desired results. These results are in agreement with Dhurai *et al*. (2014) and Gangashetty *et al*. (2013).

4.2.2.4 Panicle Length (cm)

The average length of panicle recorded for the genotypes in the present study was 24.51 cm with a range of 16 cm (Kulakar) to 33.9 cm (Madumurangi). The genotypes that recorded high panicle length were Sammel bhog (32.33 cm), Sannajajulu (31 cm) and Ambemohar (27.46 cm). The genotypes that recorded highest and lowest panicle lengths were Kulakar and Madumurangi, which were red coloured genotypes.

Table 4.2 Analysis of variance for yield, yield components and quality characters in 30 genotypes of rice (*Oryza sativa* L.)

	Source	Mean sum of squares		
		Replications	Treatments	Error
	Degree of freedom	2	29	58
1	Plant height (cm)	15.175	1402.364**	5.3602
2	Days to 50% flowering	0.8111	163.6077**	0.3054
3	Number of productive tillers plant^{-1}	2.574	25.569**	1.07605
4	Panicle length (cm)	0.506	55.8669**	0.4211
5	Spikelet fertility (%)	16.526	189.7612**	25.718
6	Yield plot^{-1} (Kg)	0.045	2.0217**	0.0157
7	100 grain weight (g)	0.000502	1.1219**	0.00019
8	Kernal length/breadth ratio	0.001023	1.1017**	0.00854
9	Protein content (%)	0.0362	13.5387**	0.01234
10	Zn content (µg g^{-1})	3.957	138.0167**	1.5314
11	Fe content (µg g^{-1})	15.148	333.6802**	6.5261
12	Total starch content (%)	0.0487	92.094**	0.0828
13	Amylose content (%)	0.0823	147.4006**	0.0331
14	Total antioxidant activity (mg AAE 100g^{-1})	0.0429	3194.148**	0.0669
15	Total soluble phenol content (mg 100g^{-1})	0.169	9827.0916**	0.0547
16	Glycemic Index	1.777	64.573**	0.5797
17	Phytate content (mg 100g^{-1})	4.549	12637.314**	1.5164

* Significant at 5% level; ** Significant at 1% level.

The phenotypic coefficient of variation (17.73%) and genotypic coefficient of variation (17.54%) were moderate for this character. Moderate GCV and PCV reported in this study with respect to the character, panicle length was also reported by Dhurai *et al*. (2014).

The heritability estimate recorded for this trait was high (97.8%) combined with moderate genetic advance as per cent of mean (35.72), showing operation of non-additive gene actions in the inheritance of this trait. These results are deviating from the findings reported by Prasad *et al*. (2011), Sanghera *et al*. (2013), Bhati *et al*. (2015), Ekka *et al*. (2015), Patil *et al*. (2015), Devi *et al*. (2016), Mohan *et al*. (2016) and Devi *et al*. (2017).

4.2.2.5 Spikelet fertility (%)

Spikelet fertility ranged from 55.36% (Ranikanda) to 96.52% (Navara), with a general mean of 84.23%. A low GCV (8.77%) and moderate PCV (10.64%) were recorded for this trait. More PCV was recorded for this trait than GCV indicating, less influence of environment on the expression of this character.

High heritability (68%) and moderate GA as per cent of mean (14.91) was recorded for this trait. It indicates the operation of non-additive gene interaction in expression of this character. Direct selection may not yield desirable results. Similar results of high heritability coupled with moderate GA was reported by Umesh *et al*. (2015) and Nandini *et al*. (2017).

4.2.2.6 Yield plot^{-1} (Kg)

Yield plot^{-1} ranged from 1.19 Kg (Ambemohar) to 4.30 Kg (Mappillai samba) with a general mean of 2.28 Kg. Mappillai samba a red coloured genotype with short bold and broad kernel type recorded highest test weight. The other genotypes with high yield plot^{-1} were Karuppu kavuni (4.16 Kg), Madumurangi (3.62 Kg) and Burma black (3.56 Kg). High GCV (32.7%) and PCV (36.14%) were recorded for this trait. It indicates that high variability is present within the genotypes with respect to yield/plot. Similar results were observed by Vanisree *et al*. (2013), Patel *et al*. (2014) and Suresh *et al*. (2014).

High heritability (90.5%) combined with high GA as per cent of mean (72.755) was recorded for this character indicating that this character is controlled by additive gene interaction. Hence, direct selection may be effective for the improvement of this character. The above results were in conformity with the results reported by Devi *et al*. (2016), Sameera *et al*. (2016), Devi *et al*. (2017), Jan *et al*. (2017), Lakshmi *et al*. (2017) and Mamata *et al*. (2018).

4.2.2.7 100 Grain weight (g)

The weight of 100 grains ranged from 1.10 g (Parimala sanna) to 3.41 g (Mappillai samba) with a mean value of 1.95 g. The genotypes recorded high 100 grain weight were Karuppu kavuni (2.95 g), Ramyagali (2.75 g) and Poongar (2.81 g). The other genotypes with less weight were Tulasi baso (1.25 g), Chintaluri sannalu (1.30 g) and Badsha bhog (1.40 g).

High GCV (29.38%) and high PCV (31.28%) were recorded for this trait indicating presence of high variability in the germplasm. The PCV recorded for this character is slightly higher than GCV which, indicates influence of environment is less on the expression of this trait. Selecting a genotype based on this character may be effective for improvement of this character.

The heritability estimate was high (93.5%) coupled with high GA as per cent of mean (64.42) was recorded for this character. It indicates that, this character is governed by additive gene interaction. Hence, direct selection will be highly rewarding for improvement of this character. These findings are in accordance with the results reported by Yadav *et al*. (2010), Prasad *et al*. (2011), Rahman *et al*. (2014) and Bhuvaneswari *et al*. (2015).

4.2.2.8 Kernal Length / Breadth ratio

The average Kernal Length/Breadth ratio recorded was 2.58, with a range of 1.62 (Doddiga) to 4.5 for (Sannajajulu). Doddiga is a short bold genotype and other short bold genotypes were Badsha bhog (1.90), Sammel bhog (2.00), Tulasi baso (2.09) and Ambemohar (2.69). Sannajajulu, Kalajira (3.3), Narayana kamini (3.27) and Ranikanda (3.05) were long slender types. The GCV (23.37%) and PCV (23.64 %) recorded for this trait was high indicating presence of more variability in the genotypes under study.

High heritability (97.7%) and high GA as per cent of mean (47.6) was recorded for this trait. It shows that, the above character is controlled by additive gene interaction and simple selection is effective for improvement of this character. Similar results were reported by Supriya *et al.* (2017).

4.2.2.9 Protein content (%)

The Protein content ranged from 4.74% to 14.13% with a mean value of 10.11%. The protein content was high in Mappillai samba (14.13%) while, the lowest protein content was present in Poongar (4.74%). Highest protein content is a desirable trait, and the varieties with high protein content identified from this study include Ambemohar (12.30), Ghani (12.07%), Ramyagali (12.39%), and Kulakar (11.58%). The protein content range of 8.46% to 14.67% in traditional rice cultivars were also reported by Gangadharaiah *et al.* (2015) which is on par with the findings of present study. Similarly Aiyswaraya *et al.* (2017) also reported protein content of range 7.54% to 14.54 in traditional rice cultivars.

The GCV and PCV recorded for this trait were moderate (19.03%) and high (21.05%) respectively. This indicates that variation among the genotypes is medium. Phenotypic coefficient of variation is slightly higher than genotypic coefficient of variation which indicates less influence of environment on the expression of this character. Selecting a genotype based on this character may be effective for improvement.

High heritability (90.4%) was observed for this trait combined with high GA as per cent of mean (43.21%). Hence for improvement of this character based on direct selection would be effective. Similar results were reported by Chakraborty *et al*. (2010) and Raja *et al*. (2013).

Table 4.3 Mean performance of 30 rice genotypes (*Oryza sativa* L.) for yield components, nutritional and biochemical quality parameters

S.No.	Character	Plant height (cm)	Days to 50% flowering	Number of productive tillers plant^{-1}	Panicle length (cm)	Spikelet fertility (%)	Yield plot^{-1} (Kg)	100 grain weight (g)	Kernal Length / Breadth ratio	Protein content (%)	Zn content (µg g^{-1})
1	Narayanakamini	139.26	96.00	12.63	19.86	80.71	2.16	1.60	3.27	10.13	30.54
2	Ranikanda	147.50	98.00	10.43	26.56	**55.35**	1.68	1.81	3.05	11.02	31.45
3	Sammel bhog	145.10	86.00	11.43	32.33	84.46	1.89	1.44	2.00	11.98	**11.51**
4	Chintalurisannalu	**81.40**	85.00	18.56	22.76	94.81	1.62	1.30	3.60	8.18	20.23
5	Selamsanna	145.13	89.00	10.40	22.53	88.39	1.86	1.35	3.03	6.45	20.83
6	Arakuloya	145.46	79.00	**20.80**	19.46	76.63	2.18	2.01	2.62	11.44	21.11
7	Ambemohar	143.63	85.00	10.46	27.46	85.99	**1.19**	1.30	2.69	12.30	25.62
8	Pancharatna	134.60	81.00	8.96	20.66	92.63	2.53	2.13	2.75	10.40	22.54
9	Kalajira	143.63	85.00	10.96	25.26	80.48	2.05	1.85	3.30	10.33	34.32
10	Kalabhatt	147.50	94.00	12.80	23.76	85.35	2.31	2.04	2.28	8.80	23.00
11	Badsha bhog	124.86	95.00	11.30	26.86	73.21	1.72	1.40	1.90	7.92	35.45
12	Poongar	121.86	82.00	12.50	24.00	87.89	2.72	2.81	2.31	**4.74**	20.22
13	Ghani	119.40	80.00	11.76	23.83	90.69	2.04	1.85	1.81	12.07	19.73
14	Parimalasanna	159.40	97.00	13.90	27.46	79.30	1.23	**1.10**	1.96	11.84	**47.45**
15	Tulasi baso	146.00	93.00	12.86	27.00	87.34	1.73	1.25	2.09	11.93	24.10
16	Ramsri	102.43	76.00	11.83	17.20	80.62	1.53	1.70	2.56	6.39	21.31
17	Doddiga	155.40	87.00	**7.73**	26.96	90.09	3.30	2.55	**1.62**	11.13	19.68
18	Mappillai samba	170.50	86.00	9.26	26.46	87.97	**4.29**	**3.41**	2.01	**14.13**	20.92
19	Sannajajulu	121.06	93.00	10.03	31.00	82.87	1.94	1.65	**4.50**	7.53	21.50
20	Illapaipu samba	118.10	90.00	10.40	26.00	82.68	1.43	1.35	2.80	10.01	23.10
21	Burma black	157.53	95.00	9.63	27.33	87.06	3.56	2.75	2.42	10.18	20.49

Table 4.3 (cont.)

S.No.	Character	Plant height (cm)	Days to 50% flowering	Number of productive tillers plant^{-1}	Panicle length (cm)	Spikelet fertility (%)	Yield plot^{-1} (Kg)	100 grain weight (g)	Kernal Length / Breadth ratio	Protein content (%)	Zn content (µg g^{-1})
22	Ramyagali	131.93	80.00	10.30	16.40	92.17	2.68	2.75	2.50	12.39	27.74
23	Karuppukavuni	172.23	**105.00**	14.83	25.33	87.93	4.16	2.95	2.53	9.06	29.13
24	Kulakar	117.76	77.00	12.60	**16.00**	81.38	1.38	1.74	2.21	11.58	21.13
25	Bahurupi	164.13	**76.00**	12.10	23.23	71.95	2.33	2.05	2.37	11.33	17.58
26	Ratnachudi	145.46	89	17.2	24.26	84.47	2.43	1.80	2.64	7.58	22.26
27	Madumurangi	**184.26**	90.00	11.76	**33.90**	81.40	3.62	2.66	2.50	11.02	18.16
28	Navara	135.73	85.00	12.30	22.26	**96.51**	2.15	1.90	2.34	9.35	28.83
29	Mysore malliga	125.33	96.00	16.13	28.10	88.48	1.88	1.31	3.38	11.32	20.56
30	Pathariya	134.86	83.00	15.60	20.96	88.11	2.98	2.75	2.33	10.63	26.46
	Range Maximum	184.26	105.00	20.80	33.90	96.51	4.29	3.41	4.50	14.13	47.45
	Range Minimum	81.40	76.00	7.73	16.00	55.35	1.19	1.10	1.62	4.74	11.51
	Mean	**138.60**	**88.00**	**12.38**	**24.51**	**84.23**	**2.28**	**1.95**	**2.58**	**10.10**	**24.23**
	C.D (þ=0.05)	3.78	0.90	1.69	1.06	8.28	0.20	0.02	0.15	0.18	2.02
	C.V (%)	1.67	0.62	8.37	2.64	6.02	5.48	0.69	3.57	1.09	5.10

Table 4.3 (cont.)

S.No.	Character	Fe content (µg g^{-1})	Total starch content (%)	Amylose content (%)	Total antioxidant activity (mg AAE $100g^{-1}$)	Total soluble phenol content (mg $100g^{-1}$)	Glycemic Index	Phytate content (mg $100g^{-1}$)
1	Narayanakamini	32.43	68.61	24.58	33.49	74.10	57.80	432.63
2	Ranikanda	29.76	69.03	24.81	35.19	86.95	60.31	406.20
3	Sammel bhog	27.31	62.42	15.15	30.88	130.45	69.62	457.06
4	Chintalurisannalu	18.15	62.67	27.28	35.38	54.40	56.76	466.53
5	Selamsanna	40.79	71.26	11.84	50.58	70.67	60.58	468.38
6	Arakuloya	24.66	61.40	27.08	40.21	88.23	57.65	407.80
7	Ambemohar	29.90	74.79	23.65	33.30	90.18	65.78	452.49
8	Pancharatna	38.73	68.68	25.26	**122.40**	139.84	59.88	548.89
9	Kalajira	19.30	65.63	24.32	48.64	74.77	55.08	545.10
10	Kalabhatt	22.50	70.73	**4.73**	109.43	**252.99**	68.75	571.92
11	Badsha bhog	15.66	57.12	20.50	49.36	102.39	54.19	**308.96**
12	Poongar	32.95	**74.93**	25.34	112.12	124.10	59.93	403.68
13	Ghani	15.63	63.27	24.29	32.70	80.22	60.21	436.30
14	Parimalasanna	15.65	64.07	25.14	57.4	63.19	60.69	446.35
15	Tulasi baso	**61.68**	61.64	26.11	34.57	81.12	59.13	487.32
16	Ramsri	**13.33**	73.51	28.36	42.32	76.72	56.96	454.79
17	Doddiga	17.47	74.56	17.02	43.39	74.37	57.58	361.74
18	Mappillai samba	17.2733	60.58	24.81	98.37	g128.35	68.75	389.08
19	Sannajajulu	23.58	66.61	29.58	32.52	102.35	59.34	403.13
20	Illapaipu samba	32.73	55.67	15.75	26.60	88.36	56.80	466.94
21	Burma black	15.52	69.67	7.90	96.39	243.59	68.73	413.45

Table 4.3 (cont.)

S.No.	Character	Fe content (µg g^{-1})	Total starch content (%)	Amylose content (%)	Total antioxidant activity (mg AAE $100g^{-1}$)	Total soluble phenol content (mg $100g^{-1}$)	Glycemic Index	Phytate content (mg $100g^{-1}$)
22	Ramyagali	21.90	68.19	20.07	26.51	**52.62**	57.74	495.21
23	Karuppukavuni	28.47	69.57	19.59	75.21	204.26	52.29	512.02
24	Kulakar	19.02	67.69	21.07	114.33	121.65	**52.28**	475.56
25	Bahurupi	15.85	**55.66**	17.11	25.50	64.31	57.04	414.13
26	Ratnachudi	35.29	65.75	12.62	**20.09**	73.45	55.72	447.87
27	Madumurangi	34.35	62.75	14.43	103.14	90.33	61.29	341.73
28	Navara	16.41	68.40	33.73	87.64	230.56	62.84	**572.87**
29	Mysore malliga	15.21	60.39	23.74	58.24	57.51	60.41	417.19
30	Pathariya	21.06	58.51	**34.60**	95.67	187.50	59.03	545.83
	Range Maximum	61.68	74.93	34.60	122.40	252.99	69.62	572.87
	Range Minimum	13.33	55.66	4.73	20.09	52.62	52.28	308.96
	Mean	**25.08**	**65.78**	**21.68**	**59.05**	**110.32**	**59.77**	**451.71**
	C.D (þ=0.05)	4.17	0.47	0.29	0.42	0.38	1.24	0.71
	C.V (%)	10.18	0.43	0.83	0.43	0.21	1.27	0.27

Table 4.4 Estimates of variability, heritability and genetic advance as per cent of mean for yield, quality and nutritional parameters in rice (*Oryza sativa* L.)

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5% level)
			Minimum	Maximum	PCV %	GCV %		
1	Plant height (cm)	138.60	81.40	184.26	15.65	14.90	95.20	31.89
2	Days to 50% flowering	88.00	76.00	105.00	8.40	8.38	99.40	17.21
3	Number of productive tillers plant^{-1}	12.38	7.73	20.80	24.54	23.06	93.90	44.66
4	Panicle length (cm)	24.51	16.00	33.90	17.73	17.54	97.80	35.72
5	Spikelet fertility (%)	84.23	55.35	96.51	10.64	8.77	68.00	14.91
6	Yield plot^{-1} (Kg)	2.28	1.19	4.29	36.14	32.7	90.50	72.75
7	100 grain weight (g)	1.95	1.10	3.41	31.28	29.38	93.50	64.42
8	Kernal Length / Breadth ratio	2.58	1.62	4.50	23.64	23.37	97.70	47.60
9	Protein content (%)	10.10	4.74	14.13	21.05	19.03	90.40	43.21
10	Zn content (µg g^{-1})	24.23	11.51	47.45	28.29	27.83	96.70	56.39
11	Fe content (µg g^{-1})	25.08	13.33	61.68	42.85	41.62	94.40	83.28
12	Total starch content (%)	65.78	55.66	74.93	8.43	8.21	97.30	17.31
13	Amylose content (%)	21.68	4.733	34.60	32.33	31.30	96.80	66.55
14	Total antioxidant activity (mg AAE 100g^{-1})	59.05	20.09	122.40	55.25	50.83	92.00	62.82
15	Total soluble phenol content (mg 100g^{-1})	110.32	52.62	252.99	51.87	50.28	96.00	45.87
16	Glycemic Index	59.77	52.28	69.62	7.83	7.72	97.40	15.70
17	Phytate content (mg 100g^{-1})	451.71	308.96	572.87	14.37	13.75	95.60	29.59

4.2.2.10 Zn content (μg g^{-1})

The range of Zn content varied from 11.5 μg g^{-1} (Sammel bhog) to 47.46 μg g^{-1} (Parimala sanna) with mean of 24.23 μg g^{-1}. High Zn content range of 26.2 μg g^{-1} to 67.3 μg $g^{-1}$was observed in traditional rice genotypes by Anuradha *et al.* (2012a) and Anuradha *et al.* (2012b).

High GCV (27.83%) and PCV (28.29%) were recorded for this trait indicating that variation among the genotypes is high. High heritability (96.7%) coupled with high GA as per cent of mean (56.39) was observed for this trait hence, it may be concluded that this trait is under the control of additive gene effects and direct selection may be practiced for improvement of Zn content in rice. The results are in conformity with the findings of Devi *et al*. (2016), Patil *et al*. (2015), Sala *et al*. (2015) and Samak *et al*. (2015).

4.2.2.11 Fe content (μg g^{-1})

Iron content ranged from 13.33 μg g^{-1} to 61.68 μg g^{-1} with a general mean of 25.08 μg g^{-1}. The genotype Tulasi baso (61.68 μg g^{-1}) recorded highest Fe content while, Ramsri (13.33 μg g^{-1}) recorded lowest Fe content. Selam sanna (40.79 μg g^{-1}) and Ratnachudi (35.29 μg g^{-1}) are brown genotypes which also recorded high Fe content. Laenoia *et al*. (2015) reported that brown rice had higher amount of iron content than white rice. Similarly Anuradha *et al.* (2012a) and Anuradha *et al.* (2012b) also reported that traditional brown rice genotypes had high iron content.

The estimates of GCV (41.62%) and PCV (42.85%) were high, indicating that variation among the genotypes is high. These findings are in agreement with Devi *et al*. (2016). High heritability (94.4%) coupled with high genetic advance as per cent of mean (83.28) was observed for this trait. It indicates that most likely the heritability is due to additive gene effects and selection may be effective in improvement of this character. These findings are in agreement with Devi *et al*. (2016) Patil *et al*. (2015), Sala *et al*. (2015) and Samak *et al*. (2015).

4.2.2.12 Total starch content (%)

The Total starch content ranged from 74.93% to 55.66% with a general mean of 65.78%. The genotype Poongar is red pericarp coloured rice recorded highest (74.93%) total starch content while, Bahurupi and Illapaipu samba recorded lowest (55.67%) starch content.

The estimates of GCV and PCV observed for this trait were 8.21% and 8.43% respectively. The low GCV and PCV indicating less variation among the genotypes for this character. High heritability (97.3%) coupled with moderate genetic advance as per cent of mean (17.3) was observed for this trait indicating that this trait is under the control of non-additive gene interaction. Hence, selection based on this character may not be rewarding.

4.2.2.13 Amylose content (%)

The Amylose was ranged from 4.73% (Kalabhatt) to Pathariya (34.60%) with a mean value of 21.68%. Amylose content plays a key role in determining the texture of cooked rice. The rice varieties with amylose content between 20-25% are considered as intermediate which cook as fluffy and flaky. In milled rice amylose content had positive association with hardness of cooked rice and negative association with stickiness. In the present study the genotypes that recorded medium amylose content were Ambemohar (23.65%), Kalajira (24.32%), Mappillai samba (24.81).

A high GCV (31.30%) and PCV (32.33%) were recorded for this trait indicating presence of high variability among the germplasm. High heritability (96.8%) coupled with high GA as per cent of mean (66.55) was recorded for this trait.The high heritability of this character is due to additive gene effects and selection based on this character is effective for improvement. Similar results are reported by Sunayana *et al*. (2010), Veni *et al*. (2013), Devi *et al*. (2015) and Savitha and Kumari (2015).

4.2.2.14 Total antioxidant activity (mg AAE $100g^{-1}$)

The total antioxidant activity was ranged from 20.09 mg (Ratnachudi) to 122.40 mg (Pancharatna) with a mean value of 59.05 mg. The results were in accordance with findings of Sompong *et al*. (2011). The range of the antioxidant activity observed was 19.4 to 140.8 mg $100g^{-1}$. Pancharatna is a red pericarp coloured genotype exhibited highest antioxidant activity. The total antioxidant activity is high in genotypes with red and black pericarp colour when compared to those with a light brown pericarp colour (Tian *et al.*, 2004).

This character recorded high GCV (50.83%) and PCV (55.25%) indicating variation among the genotypes. High heritability (92.0%) combined with high genetic advance as per cent of mean (62.82) was observed for this trait suggesting the role of

additive gene effects in expression of this trait. Thus direct selection based on this trait will help in improvement of this trait. The results were deviating from the result reported by Raghuvanshi *et al*. (2017).

4.2.2.15 Total soluble phenol content (mg $100g^{-1}$)

Total Soluble Phenol content (TSPC) exhibited wide range of variation among the genotypes under study. The total soluble phenol content ranged from 52.62 mg (Ramyagali) to 252.99 mg (Kalabhatt) with a mean value of 110.32 mg. Highest total soluble phenol content was observed in kalabhatt which is a black coloured genotype. The phenolic compounds are mainly associated with the pericarp in rice and the grains with darker pericarp colour such as red and black contain higher amount of polyphenols (Itani and Ogawa, 2004).

The concentration of total phenolics in the grain has been positively associated with antioxidant activity (Itani *et al.*, 2002) with potential beneficial effects on health, such as reduction of oxidative stress (Hu *et al.*, 2003). Hence highest amount of phenolic compounds is a desirable trait and the colored rice genotypes (black and red) in the present study (Burma black (243.59 mg), Karuppu kavuni (204.26 mg), Poongar (124.10 mg), Mappillai samba (128.35 mg), Pancharatna (139.84 mg) etc.) recorded high amount of phenolic compounds than brown pericarp colored genotypes (Narayana kamini, Ranikanda and Ratnachudi). Irkali *et al*. (2012) also reported that total phenol content was more in black and red rice than non-pigmented rice. Pathak *et al*. (2017), Chakuton *et al*. (2012) Saikia *et al*. (2012) also reported that pigmented rice had higher amount of total phenol content (79.88 mg GAE $100g^{-1}$) than non-pigmented rice (33.23) in their study. Chmiel *et al*. (2017) reported that brown rice had higher amount of total phenol content than white rice.

This trait manifested high estimates of genotypic (50.28%) and phenotypic (51.87%) coefficient of variation indicating that presence of high variation among the genotypes. High heritability (96.0%) coupled with high genetic advance as per cent of mean (45.87) was observed for this trait suggesting that this trait is under the control of additive gene action and direct selection may be employed for improvement of this trait.

4.2.2.16 Glycemic Index (%)

In the present study the glycemic index ranged from of 52.28% (Kulakar) to 69.72% (Sammel bhog) with a mean value of 59.77%. Low glycemic index was observed in Kulakar which is red pericarp coloured genotype. The genotypes that recorded low GI were Kulakar (red pericarp) showed 52.28%, Karuppu kavuni (black coloured genotype) showed 52.29% and Badsha bhog (brown pericarp) with 54.19%.

This trait manifested low estimates for both genotypic (7.72%) as well as phenotypic (7.83%) coefficient of variation, indicating less variation present among the genotypes. High heritability (97.4%) coupled with moderate genetic advance as per cent of mean (15.70) was observed for this trait. suggesting non-additive gene effects in controlling this character.

Glycemic index is the classification of food based on the blood glucose response to a food relative to the standard glucose solution and is considered as the therapeutic principle for Diabetes mellitus. Foods with GI lower than 55 are called as low GI foods. Low GI foods are safe for diabetic patients, as they result in a gradual and steady rise in blood sugar. Foods with GI between 46 and 69 are low to medium GI foods. These help in slower and smooth rise in blood sugar, hence they are healthy diet options for diabetic diet. Foods with GI above 70 are high GI foods and should be restricted in diabetic diet.

4.2.2.17 Phytate content (mg $100g^{-1}$)

The phytate content ranged from 308.96 mg to 572.88 mg with a general mean of 451.71 mg was recorded in the present study. The genotype Navara exhibited highest phytate content while, Badsha bhog recorded lowest phytate content. The range of phytate content reported in the present study is in accordance with the findings of Tamanna *et al.* (2013). Phytic acid is an anti-nutritional factor which bounds to micronutrients like Fe and Zn and prevent their absorption. This results in nutritional deficiencies. Hence, the genotypes with low phytate content are desirable because of its anti-nutritional property.

Moderate estimates of GCV (13.75%) and PCV (14.37%) were recorded for this trait. High heritability (95.6%) combined with high genetic advance as per cent of mean (29.59) was recorded for this trait. It signifies that the above trait is under the control of additive gene effects and direct selection may be practiced for improvement of this character.

The estimates of heritability play a significant role in predicting the reliability of phenotypic value. Therefore, the trait manifested with high heritability along with high genetic advance helps in effective selection for improvement of a particular character. In the present study all quantitative characters showed high heritability (broad sense). High heritability combined with high genetic advance as per cent of mean was observed for plant height, number of productive tillers plant^{-1}, panicle length, yield plot^{-1}, 100 grain weight, kernel length / breadth ratio, protein content, Zn content, Fe content, amylose content, total antioxidant activity, total soluble phenol content, phytate content. Thus, these traits are mainly under the control of additive gene action and hence these characters may be improved by following simple selection.

High heritability with moderate genetic advance was recorded for days to 50% flowering, spikelet fertility, total starch content and glycemic index appear to be under the control of non-additive gene actions.

Coefficients of variation studies indicated that the estimates of phenotypic coefficients of variation (PCV) were slightly higher than the corresponding genotypic coefficients of variation (GCV) for all the characters, indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype may be effective for the improvement of these traits.

4.3. GENETIC DIVERGENCE

The 30 rice genotypes were assessed for genetic divergence by adopting Mahalanobis D^2 statistic for yield and nutritional parameters.

4.3.1 Wilk`s 'V' Criterion Test

Wilk`s 'V' (Statistical) criterion was used to test the significant differences between the groups based on the pooled effects for all the characters in the present study. The $\chi 2$ test at 493 degrees of freedom was conducted to study the significance of 'V' (Statistical) value. Highly significant 'V' statistic value indicating, that there was significant difference among the genotypes when all the characters were considered simultaneously.

The 30 traditional rice varieties in the analysis of variance of dispersion clearly indicated the significant pooled effect for all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.3.2 Mahalanobis Generalized Distance D^2 Values

Pivotal condensation method was used to transform correlated unstandardized means of 17 quantitative characters to standardized uncorrelated set of variables. The statistical distance (Mahalanobis D^2 values) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes. These values were considered at a time and these were used in final grouping of genotypes.

4.3.3 Grouping of Genotypes into Various Clusters

The 30 genotypes were categorized into six clusters based on D^2 values using agglomerative hierarchial clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). 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 furnished in Table 4.5 and Fig 4.1. Cluster I was largest out of the six clusters which is comprising of nine genotypes (Narayana kamini, Chintaluri sannalu, Selam sanna, Ambemohar, Pancharatna, Kalajira, Ramsri, Ramyagali, Ratanachudi) followed by cluster III with seven genotypes (Sammel bhog, Ghani, Parimala sanna, Mappilllai samba, Bahurupi, Madumurangi, Mysore malliga), cluster IV with six genotypes (Araku loya, Kalabhatt, Burma black, Kulakar, Navara, Pathariya), four genotypes (Tulasi baso, Doddiga, Illapaipu samba, Karuppu kavuni) in cluster VI, three genotypes (Ranikanda, Poongar, Sannajajulu) in cluster II and cluster V with one genotype (Badsha bhog). The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster.

4.3.4 Average Inter and Intra Cluster Distances

Intra cluster D^2 values ranged from 0.000 (cluster V) to 95.017 (cluster IV). Maximum intra cluster distance was observed in cluster IV (95.017) followed by cluster VI (79.535). (Table 4.6). It reveals that genotypes present in the same cluster have low level of diversity and selection of parents with in the cluster for hybridization programme may not be considered promising.

The inter-cluster D^2 values ranged from 34.51 (cluster II and III) to 213.16 (clusters IV and V) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster IV and V (213.16), followed by cluster I and V (173.93), cluster V and VI (152.79), cluster III and IV (134.84), cluster II and cluster IV (130.26), cluster I and IV (120.26). The higher inter cluster distances than intra cluster distances indicating presence of wider genetic diversity between the clusters than within the clusters.The higher amount of heterosis can be expected from the crosses involving parents belonging to the most divergent clusters. Hence, it is desirable to select the genotypes from the cluster showing high inter cluster distance in breeding programme. The nearest and the farthest cluster from each cluster based on D^2 values were given in Table. 4.7.

Cluster I comprises nine genotypes (Narayana kamini, Chintaluri sannalu, Selam sanna, Ambemohar, Pancharatna, Kalajira, Ramsri, Ramyagali, Ratanachudi). It was nearest to cluster VI (47.133) followed by cluster III (72.449) and was farthest from the cluster V (173.931) followed by clusterIV (120.261). Pancharatna in this cluster is with highest anti-oxidant activity (122.40 mg $100g^{-1}$).

Cluster II comprises three genotypes (Ranikanda, Poongar, Sannajajulu). It was nearest to cluster III (35.514) followed by cluster VI (60.399) and was farthest from the cluster IV (130.323) followed by cluster V (98.961). Poongar in this cluster has recorded highest total starch content (74.93%).

Cluster III comprises seven genotypes (Sammel bhog, Ghani, Parimala sanna, Mappilllai samba, Bahurupi, Madumurangi, Mysore malliga). It was nearest to cluster VI (54.094) followed by cluster I (72.449) and was farthest from the cluster IV (134.845) followed by cluster V (112.563). Genotypes Parimala sanna recorded highest Zn content (47.45 μg g^{-1}). Mappillai samba recorded highest protein (14.133%) content and highest yield $plot^{-1}$ (4.29 Kg).

Table 4.5 Clustering pattern of 30 rice (*Oryza sativa* L.) genotypes by agglomerative hierarchial clustering based on Mahalanobis distance

S. No.	Clusters	No.	Genotypes
1	Cluster I	9	Narayana kamini, Chintaluri sannalu, Selam sanna, Ambemohar, Pancharatna, Kalajira, Ramsri, Ramyagali, Ratanachudi
2	Cluster II	3	Ranikanda, Poongar, Sannajajulu
3	Cluster III	7	Sammel bhog, Ghani, Parimala sanna, Mappilllai samba, Bahurupi, Madumurangi, Mysore malliga
4	Cluster IV	6	Araku loya, Kalabhatt, Burma black, Kulakar, Navara, Pathariya
5	Cluster V	1	Badsha bhog
6	Cluster VI	4	Tulasi baso, Doddiga, Illapaipu samba, Karuppu kavuni

Table 4.6 Average intra and inter cluster D^2 values among six clusters with 30 rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	**54.476**	81.826	72.449	120.261	173.931	47.133
Cluster II	81.826	**43.992**	34.514	130.323	98.961	60.399
Cluster III	72.449	34.514	**59.385**	134.845	112.563	54.094
Cluster IV	120.261	130.323	134.845	**95.017**	213.162	99.343
Cluster V	173.931	98.961	112.563	213.162	**0.000**	152.790
Cluster VI	47.133	60.399	54.094	99.343	152.790	**79.535**

Bold: Diagonal values indicate intra cluster distance.

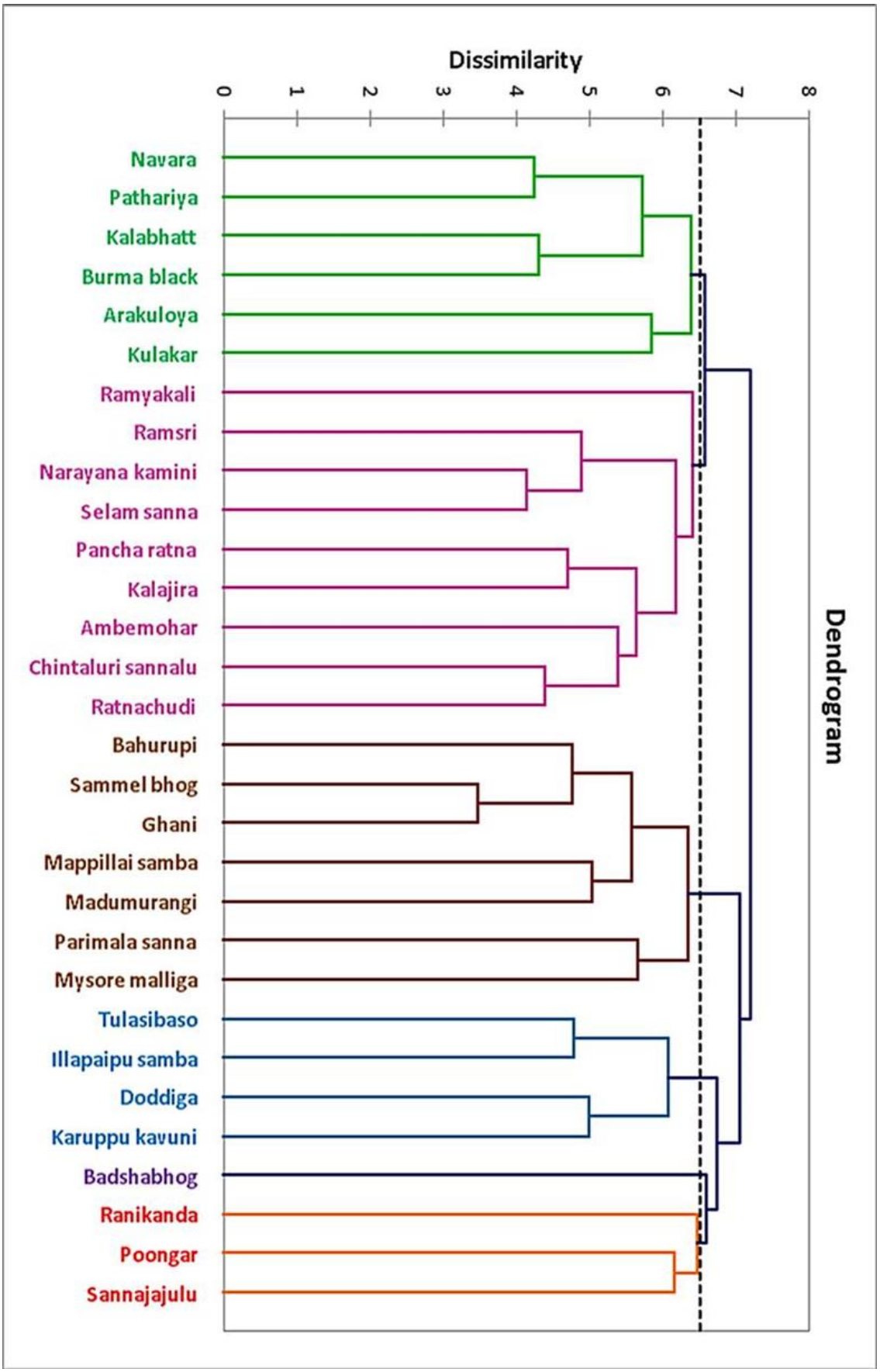


Fig. 4.1. Dendrogram showing relationship among 30 rice genotypes in six clusters based on Mahalanobis distance

Table 4.7 The nearest and the farthest cluster from each cluster based on D^2 value in 30 rice (*Oryza sativa* L.) genotypes

S. No.	Clusters	Farthest cluster	Nearest cluster
1	**Cluster I** (54.476)	**Cluster V** (173.931)	**Cluster VI** (47.133)
2	**Cluster II** (43.992)	**Cluster IV** (130.323)	**Cluster III** (34.514)
3	**Cluster III** (59.385)	**Cluster IV** (134.845)	**Cluster VI** (54.094)
4	**Cluster IV** (95.017)	**Cluster V** (213.162)	**Cluster VI** (99.343)
5	**Cluster V** (0.000)	**Cluster IV** (213.162)	**Cluster II** (98.961)
6	**Cluster VI** (79.535)	**Cluster V** (152.790)	**Cluster II** (60.399)

Cluster IV comprising of six genotypes (Arakuloya, Kalabhatt, Burma black, Kulakar, Navara, Pathariya). It was nearest to cluster VI (99.343) followed by cluster I (120.261) and was farthest from the cluster V (213.162) followed by cluster III (134.845). Majority of the genotypes in this cluster are coloured. Arakuloya in this cluster recorded highest number of productive tillers plant^{-1}. Kulakar a red pericarp coloured genotype in this cluster recorded lowest glycemic index (52.28), which can be recommended for diabetic patients. Kalabhatt a black coloured genotype recorded highest total soluble phenol content (252.99 mg 100g^{-1}).

Cluster V comprises only one genotype Badsha bhog. It was nearest to cluster II (98.961) followed by cluster III (112.563) and was farthest from the cluster IV (213.162) followed by cluster I (173.931). This genotype has recorded low glycemic index of 54.19.

Cluster VI comprises of four genotypes (Tulasi baso, Doddiga, Illapaipu samba, Karuppu kavuni). It was nearest to cluster II (60.399) followed by cluster IV (99.343) and was farthest from the cluster V (152.790) followed by cluster I (47.133). Tulasi baso recorded highest Fe content (61.68 μg g^{-1}). Karuppu kavuni recorded low glycemic index (52.93).

4.1.5 Cluster Mean Values

The cluster means values for all the 17 characters are presented in Table 4.8. Cluster mean values for plant height ranged from 152.59 cm (cluster III) to 124.87 cm (cluster V).

Number of productive tillers plant^{-1} ranged from 13.9 in cluster IV to 10.9 in cluster II. Days to 50% flowering was ranged from 95.00 days in cluster V to 85.33days in cluster I. Panicle length was ranged from 27.90 cm in cluster III to 21.63 cm in cluster IV. Spikelet fertility was ranged from 87.01% in cluster VI to 73.20% in cluster V. Yield plot^{-1} ranged from 2.66 kg in cluster VI to 1.72 kg in cluster V. 100 seed weight ranged from 2.20g in cluster IV to 1.40g in cluster V. Kernel length/ breadth ranged from 3.28 in cluster II to 1.90 in in cluster V. Protein content was ranged from 11.95% in cluster III to 7.76% in cluster II. Zinc content ranged from 35.45 μg g^{-1}in cluster V to 22.27 μg g^{-1} in cluster III. Iron content was ranged from 35.09 μg g^{-1}in cluster VI to 15.66 μg g^{-1} in cluster V. Total starch content was ranged from 70.12% in

cluster II to 57.12% in cluster V. Amylose content was ranged from 26.58%) in cluster II to 19.62% in cluster VI. Total antioxidant activity was ranged from 90.61 mg $100g^{-1}$ in cluster IV to 44.95 mg $100g^{-1}$ in cluster VI. Total phenol content ranged from 187.42 in cluster IV to 78.52 in cluster I. Glycemic Index was ranged from 62.58 in cluster III to 54.19 in cluster V. Phytate content was ranged from 497.91 mg in cluster IV to 308.96 mg in cluster V.

Genotypes present in the cluster IV recorded highest mean values for the traits *viz.*, number of productive tillers $plant^{-1}$, panicle length, 100 grain weight, total antioxidant activity, total soluble phenol content and intermediate amylose content. Whereas, the genotypes present in the cluster VI recorded highest mean value for spikelet fertility, yield $plot^{-1}$ and iron content. Lowest mean value for glycemic index and high mean value for zinc content and low phytate content was recorded for the cluster V. Hence, hybridization between the selected genotypes from the above divergent clusters may be carried out to obtain desirable segregants with good nutritional properties coupled with high yield potential.

Table 4.8. Character wise cluster mean values estimated by agglomerative hierarchial clustering based on Mahalanobis distance

S. No.	Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Plant height (cm)	127.111	130.144	**152.59**	139.811	**124.867**	147.933
2	Days to 50% flowering	**85.333**	91.444	87.476	85.778	**95**	94.083
3	Number of productive tillers plant^{-1}	12.378	**10.989**	12.338	**13.956**	11.3	11.458
4	Panicle length (cm)	21.826	27.189	**27.905**	**21.633**	26.867	26.325
5	Spikelet fertility (%)	86.701	75.374	83.468	85.845	**73.208**	**87.015**
6	Yield plot^{-1} (Kg)	2.008	2.116	2.472	2.431	**1.726**	**2.66**
7	100 grain weight (g)	1.758	2.095	1.977	**2.202**	**1.408**	2.029
8	Kernal Length / Breadth ratio	2.931	**3.289**	2.292	2.372	**1.9**	2.262
9	Protein content (%)	9.354	**7.767**	**11.957**	10.332	7.927	10.536
10	Zn content (μg g^{-1})	25.045	24.392	**22.277**	23.506	**35.453**	24.005
11	Fe content (μg g^{-1})	27.762	28.764	20.186	19.866	**15.66**	**35.091**
12	Total starch content (%)	68.791	**70.123**	61.309	66.069	**57.125**	65.36
13	Amylose content (%)	22.001	**26.581**	20.669	21.522	20.499	**19.624**
14	Total antioxidant activity (mg AAE 100g-1)	45.858	59.945	58.035	**90.615**	49.366	**44.945**
15	Total soluble phenol content (mg 100g-1)	**78.529**	104.472	87.768	**187.422**	102.392	112.032
16	Glycemic Index	58.481	59.861	**62.589**	61.551	**54.193**	56.454
17	Phytate content (mg 100g^{-1})	479.105	404.341	414.554	**497.911**	**308.964**	457.01

4.3.2 Principal Component Analysis

Results obtained from principal component analysis on the correlation matrix of the traits reduce the dimensionality of the data group by generating five significant canonical roots having eigen value more than one. The mean value of canonical vectors for each genotype was used for grouping the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are described here under. Canonical roots (eigen value greater than one), eigen values, per cent of variation, cumulative variation and vectors loading of different characters are presented in Table 4.9.

The PCA scores of thirty genotypes for the first three components compute and considered as three axes x, y, z and squared distances of each genotype from these three axes were calculated and represented in Table 4.10. It is important to study variance as the relative contribution than the signs (indicative of directions) in PCA.

In the present study, the first five principal components with eigen value more than one contributed 75.56% towards the total variability. It was therefore the essential features of data set had been represented the first five principal components.

The first principal component (PC_1) contributed maximum towards the variability (31.74%). The characters *viz*., plant height (0.28), days to 50 % flowering (0.06), no of productive tillers plant^{-1} (0.05), panicle length (0.14), spikelet fertility (0.10), yield plot^{-1} (0.37), 100 grain weight (0.37), protein content (0.01), iron content (0.31), antioxidants (0.28), phenols (0.29) were loaded positively, while l/b ratio (-0.28), zinc content (-0.22), starch content (-0.09), amylose content (-0.09), glycemic index (-0.31), phytate content (-0.28) were negatively loaded.

The second principal component (PC_2) described 16.4% variability of total variance and it reflected through the positive loading of the characters *viz*., plant height (0.06), no of productive tillers plant^{-1} (0.43), panicle length (0.06), yield plot^{-1} (0.03), 100 grain weight (0.16), amylose content (0.07), protein content (0.22), glycemic index (0.19) and phytate content (0.16), were loaded positively, while days to 50 % flowering (-0.43), spikelet fertility (-0.35), l/b ratio (-0.25), zinc content (-0.35), iron content (-0.07), antioxidants (0.11), phenols (-0.23) and starch content (-0.26) were negatively loaded.

Table 4.9 Eigen values, proportion of total variance represented by the first five principal components, cumulative per cent variance and component loading of different characters in rice (*Oryza sativa* L.)

S. No.		PC I	PC II	PC III	PC IV	PC V
	Eigen Value (Root)	5.39	2.79	2.30	1.26	1.08
	% var. Exp	31.74	16.46	13.54	7.45	6.35
	Cum. Var. Exp.	31.74	48.20	61.75	69.21	75.56
1	Plant height	0.28	0.06	0.36	0.021	0.05
2	50% flowering	0.06	-0.43	0.36	0.19	0.02
3	Productive tillers plant^{-1}	0.05	0.43	-0.11	-0.06	-0.03
4	Panicle length	0.14	0.06	0.48	-0.19	-0.20
5	Spikelet fertility	0.10	-0.35	-0.01	0.44	0.09
6	Yield plot^{-1}	0.37	0.03	0.22	0.08	0.18
7	100 grain weight	0.37	0.16	-0.08	0.07	0.26
8	l/b ratio	-0.28	-0.25	0.24	-0.03	-0.17
9	Protein content	0.01	0.22	0.19	0.55	-0.36
10	Zn content	-0.22	-0.35	0.02	-0.009	0.11
11	Fe content	0.31	-0.07	0.01	0.04	0.52
12	Starch content	-0.09	-0.26	-0.25	-0.15	0.23
13	Amylose content	-0.09	0.07	-0.23	0.48	0.14
14	Anti-oxidant activity	0.28	-0.11	-0.27	0.003	-0.28
15	phenols content	0.29	-0.23	-0.19	-0.019	-0.34
16	Glycemic Index	-0.31	0.19	0.30	-0.04	0.32
17	Phytate content	-0.28	0.16	-0.04	0.36	0.07

Table 4.10 PCA scores of divergence in 30 rice (*Oryza sativa* L.) genotypes

S. No.	Genotype	PC I	PC II	PC III
		X Vector	Y Vector	Z Vector
1	Narayana kamini	69.786	-96.524	-70.635
2	Ranikanda	98.251	-109.254	-76.554
3	Sammel bhog	147.290	-137.009	-99.767
4	Chintaluri sannalu	24.739	-69.194	-66.505
5	Selam sanna	80.218	-108.784	-77.669
6	Araku loya	108.041	-86.828	-90.266
7	Ambemohar	84.130	-110.869	-89.688
8	Pancharatna	217.779	-159.653	-200.768
9	Kalajira	68.773	-80.439	-84.144
10	Kalabhatt	364.586	-284.085	-261.100
11	Badsha bhog	136.563	-137.518	-92.153
12	Poongar	228.370	-161.210	-182.505
13	Ghani	84.668	-81.331	-80.826
14	Parimala sanna	60.424	-89.406	-70.041
15	Tulasi baso	67.899	-89.201	-71.455
16	Ramsri	73.989	-94.933	-102.562
17	Doddiga	127.286	-96.518	-78.580
18	Mappillai samba	242.439	-127.708	-152.472
19	Sannajajulu	104.418	-126.360	-86.894
20	Illapaipu samba	77.176	-100.009	-67.439
21	Burma black	384.587	-273.791	-236.320
22	Ramyagali	56.193	-45.470	-60.714
23	Karuppu kavuni	297.785	-218.352	-195.857
24	Kulakar	195.159	-149.539	-187.251
25	Bahurupi	75.270	-58.602	-48.074
26	Ratnachudi	74.464	-90.519	-53.254
27	Madumurangi	201.619	-121.723	-114.167
28	Navara	289.865	-233.628	-244.976
29	Mysore malliga	62.309	-83.505	-67.486
30	Pathariya	261.996	-174.410	-214.509

The third principal component analysis (PC_3) was characterized by 13.54% contribution towards the total variability through the characters *viz*., plant height (0.36), days to 50% flowering (0.36), panicle length (0.48), yield plot^{-1} (0.22), l/b ratio (0.24), protein content (0.19), zinc content (0.02), iron content (0.01), glycemic index (0.30) were loaded positively, while number of productive tillers plant^{-1} (-0.11), spikelet fertility (-0.01), 100 gram weight, (-0.08), starch content(-0.25), amylose content (-0.23), antioxidants content (-0.27), phenols content (-0.19), phytate content (-0.04) were negatively loaded.

The fourth principal component analysis (PC_4) amounted for 7.45% contribution towards the total variability through the characters *viz*., plant height (0.02), days to 50% flowering (0.19),yield plot^{-1} (0.08), 100 grain weight (0.07),spikelet fertility (0.44),protein content (0.55), iron content (0.04), amylose content (0.48), antioxidants (0.003), phytate content (0.36) were loaded positively while no of productive tillers plant^{-1} (-0.06), panicle length (-0.19), l/b ratio (-0.03), zinc content (-0.009), starch content (-0.15), phenols (-0.01), glycemic index (-0.04), were loaded negatively.

The fifth principal component analysis (PC_5) contributed 6.35 % towards the total variability through the characters *viz*., plant height (0.05), days to 50% flowering (0.02), spikelet fertility (0.09), yield plot^{-1} (0.18), 100 grain weight (0.26), zinc content (0.11), iron content (0.52), starch content (0.23), amylose content (0.14), glycemic index (0.32) and phytate content (0.07) were loaded positively while, the characters number of productive tillers plant^{-1} (-0.03), panicle length (-0.20), l/b ratio (-0.17), protein content (-0.36), antioxidants content (-0.28), phenols content (-0.34) were loaded negatively.

The PCA analysis identified that maximum contributing traits towards the existing variability are plant height, panicle length, spikelet fertility, yield per plot, 100 grain weight, iron content, antioxidant activity and phenol content. In PCA analysis magnitude of relative contribution of a particular trait towards total variability is important rather than the sign (+/-) which only indicate the direction of variability. The PCA scores for thirty germplasm lines were plotted in graph to obtain three dimensional scattered diagram. (Fig. 4.2) PCA revealed diversity among the 30 germplasm lines which can be exploited for generating transgressive segregants through crop improvement programmes.

Genotypes with highest nutritional values as well as good yield potential reported in the present study are Mappillai samba with highest yield (4.29 Kg), protein content (14.13%), high antioxidant (98.37 mg $100g^{-1}$) and high phenol contents (128.35 mg $100g^{-1}$); Parimala sanna and Tulasi baso with highest Zn and Fe contents (47.45µg g^{-1}, 61.68 µg g^{-1}) respectively. Pancharatna is a red pericarp coloured genotype also recorded high yield along with high antioxidant activity (122.40 mg $100g^{-1}$) and high phenol content (139.84 mg $100g^{-1}$). Kulakar recorded low glycemic index (52.28), intermediate amylose content (21.07%), high phenol content (121.65 mg $100g^{-1}$) and antioxidant activity (114.33 mg $100g^{-1}$). Karuppu kavuni also recorded high yield (4.16 Kg), low glycemic index (52.29) and high phenol content (204.26 mg $100g^{-1}$).

While choosing genotypes for hybridization programme, the genotypes exhibiting superior performance with high inter-cluster distance has to be considered. Hence, the crosses between Mappillai samba (cluster III) x Kalabhatt (cluster IV) with inter cluster distance 134.845 and Mappillai samba (cluster III) x Kulakar (cluster IV) with inter cluster distance 134.845 may be considered for obtaining superior transgressive segregants.

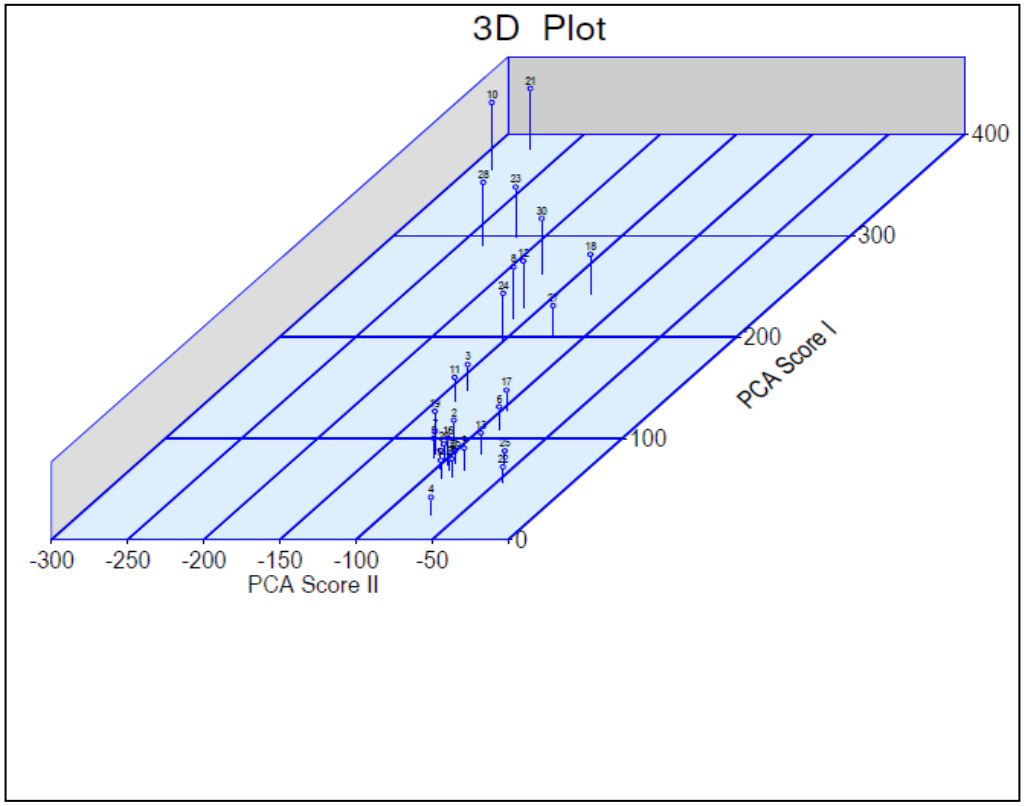


Fig. 4.2 Three dimensional graph showing relative position of 30 rice genotypes based on PCA score

Chapter – V

Summary and Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

In the present investigation, an attempt has been made to characterize the 30 genotypes for Distinctiveness Uniformity and Stability based on 26 morphological characters. The nature and extent of variability, heritability, genetic advance and diversity present among the germplasm based on yield and nutritional parameters was studied to identify potential parents/donors for the hybridization programme.

Out of 26 essential morphological visually assessed DUS descriptors studied, only one character presence of secondary branching is monomorphic and 12 characters *viz.*,leaf-anthocyanin colouration, time of heading, flag leaf-attitude of blade, spikelet-colour of stigma, number of panicles plant^{-1}, awns, colour of awns (late observation), decorticated grain length, decorticated grain width, distribution of awns on panicle, panicle exertion, time maturity (days) were dimorphic and remaining characters *viz*., basal leaf sheath colour, length of leaf blade, width of leaf blade, panicle curvature of main axis, panicle length of main axis, leaf senescence, spikelet colour of tip of lemma, grain width, grain weight of 1000 fully developed grains, decorticated grain shape, and decorticated grain colour were found to be polymorphic.

The analysis of variance revealed significant differences among 30 genotypes for 17 characters studied *viz*., plant height (cm), days to 50% flowering**,** number of productive tillers plant $^{-1}$**,** panicle length (cm), spikelet fertility (%), yield plot^{-1} (kg), 100 grain weight (g), kernel length/breadth ratio, protein content (%), Zn content (µg g^{-1}), Fe content (µg g^{-1})**,** total starch content (%)**,** amylose content (%)**,** total antioxidant activity (mg AAE 100g^{-1})**,** total soluble phenol content (mg 100g^{-1}), glycemic index and phytate content (mg 100g^{-1}) indicating high variation present in the germplasm.

High PCV and GCV was recorded for the traits viz., number of productive tillers plant^{-1}, yield plant^{-1}, 100 grain weight, kernel length/breadth ratio, zinc content, iron content, amylose content, total antioxidant activity and total soluble phenol content indicating that large amount of variation is present among the germplasm. Whereas, low PCV and GCV was recorded for the characters days to 50% flowering, starch

content and glycemic index indicating less variation among the germplasm. The coefficient of variability studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters, indicating that these characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

High heritability combined with high genetic advance as per cent of mean was observed for plant height, number of productive tillers plant^{-1}, panicle length, yield plot^{-1}, 100 grain weight, kernel length/breadth ratio, protein content, Zn content, Fe content, amylose content, total antioxidant activity, total soluble phenol content, phytate content. Thus, these traits are mostly under the control of additive gene interaction and hence these traits can be improved by selection. High heritability with moderate genetic advance was recorded for days to 50% flowering, spikelet fertility, total starch content and glycemic index appear to be under the control of both additive and non-additive gene actions and hence these characters may not be improved by simple selection.

The 30 genotypes were grouped into six clusters based on D^2 values. Cluster I comprising of nine genotypes. Cluster II comprising of three genotypes. Cluster III consisting of seven genotypes. Cluster IV consisting of six genotypes. Cluster V comprising only one genotype and cluster VI comprising of 4 genotypes. The inter-cluster D^2 values ranged from 34.51 (cluster II and III) to 213.16 (clusters IV and V) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance (213.16) was observed between cluster IV and V, followed by cluster I and V (173.93), cluster V and VI (152.79), cluster III and IV (134.84)**,** cluster II and cluster IV (130.26), cluster I and IV (120.26).

Genotypes present in the cluster IV recorded highest mean values for the traits *viz.*, number of productive tillers plant^{-1}, panicle length, 100 grain weight, total antioxidant activity, total soluble phenol content and amylose (intermediate). Whereas, the genotypes present in the cluster VI recorded highest mean value for spikelet fertility, yield plot^{-1} and iron content. Lowest mean value for glycemic index and high mean value for zinc content and low phytate content was recorded for the cluster V.

The PCA analysis revealed that, the first five principal components with eigen value more than one contributed 75.56% towards the total variability. The maximum

contributing traits towards the existing variability are plant height, panicle length, spikelet fertility, yield plot^{-1}, 100 grain weight, iron content, antioxidant activity and phenol content.

Genotypes with highest nutritional content as well as good yield potential reported in the present study are Mappillai samba with highest yield (4.29 Kg), protein content (14.13%), high antioxidant (98.37 mg 100g^{-1}) and high phenol contents (128.35 mg 100g^{-1}); Parimala sanna and Tulasi baso with highest Zn and Fe contents (47.45µg g^{-1}, 61.68 µg g^{-1}) respectively. Pancharatna is a red pericarp coloured genotype also recorded high yield along with high antioxidant activity (122.40 mg 100g^{-1}) and high phenol content (139.84 mg 100g^{-1}). Kulakar recorded low glycemic index (52.28), intermediate amylose content (21.07%), high phenol content (121.65 mg 100g^{-1}) and antioxidant activity (114.33 mg 100g^{-1}). Karuppu kavuni also recorded high yield (4.16 Kg), low glycemic index (52.29) and high phenol content (204.26 mg 100g^{-1}).

While choosing genotypes for hybridization programme, the genotypes exhibiting superior performance with high inter-cluster distance has to be considered. Hence, the crosses between Mappillai samba (cluster III) x Kalabhatt (cluster IV) with inter cluster distance 134.845 and Mappillai samba (cluster III) x Kulakar (cluster IV) with inter cluster distance 134.845 may be considered for obtaining superior transgressive segregants.

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*Original not seen

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