

GENETIC DIVERGENCE IN RICE **(*Oryza sativa* L.) HYBRIDS**

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B.Sc. (Ag.)

MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)



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GENETIC DIVERGENCE IN RICE **(*Oryza sativa* L.) HYBRIDS**

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B.Sc. (Ag.)

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CHAIRPERSON: Dr. J. DAYAL PRASAD BABU



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2018

DECLARATION

I, **Ms. DEVI MUCHARLA**, hereby declare that the thesis entitled “**GENETIC DIVERGENCE IN RICE (*Oryza sativa* L.) HYBRIDS**”, submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that any material in the thesis has not been published earlier.

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Ms. DEVI MUCHARLA has satisfactorily prosecuted the course of research and that the thesis entitled “**GENETIC DIVERGENCE IN RICE (*Oryza sativa* L.) HYBRIDS**” 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 the thesis or part thereof has not been previously submitted by her for a degree of any university.

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(J. DAYAL PRASAD BABU)

Place:

Chairperson

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This is to certify that thesis entitled “**GENETIC DIVERGENCE IN RICE (*Oryza sativa* L.) HYBRIDS**” submitted in partial fulfillment of the requirements for the degree of Master of Science in Agriculture in the major field of **Genetics and Plant Breeding** of the Acharya N. G. Ranga Agricultural University, Lam, Guntur is a record of the bonafied research work carried out by **Ms. DEVI MUCHARLA** under our guidance and supervision. The subject of the thesis has been approved by the student’s advisory committee.

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

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LIST OF SYMBOLS AND ABBREVIATIONS

ANOVA	:	Analysis of variance
CD	:	Critical Difference
cm	:	Centimeter
CV	:	Coefficient of variation
d f	:	Degrees of freedom
DRR	:	Directorate of Rice Research
<i>et al.</i>	:	And other people
F ₁	:	First filial generation of a cross
g	:	Grams
G	:	Genotypic
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Coefficient of Variation
h ²	:	Heritability
h ² (b)	:	Heritability in broad sense
ha	:	Hectare
HRR	:	Head Rice Recovery
IIRR	:	Indian Institute of Rice Research
Kg	:	Kilogram
KLAC	:	Kernel length after cooking
KLBC	:	Kernel length before cooking
m ²	:	Meter square
ml	:	Milliliter
mm	:	Millimeter
P	:	Phenotypic
PCA	:	Principal Component Analysis
PCV	:	Phenotypic Coefficient of Variation
<i>per se</i>	:	As such with mean
RBD	:	Randomized Block Design

S.No.	:	Serial number
t	:	tonnes
TRVs	:	Traditional Rice Varieties
<i>viz.,</i>	:	Namely
$\overline{X}$	:	Grand mean
°C	:	Degree Celsius
%	:	Percent
/	:	Per
⁻¹	:	Per
3D	:	Three dimensional

ABSTRACT

Name of the Author	: DEVI MUCHARLA
Title of the thesis	: Genetic divergence in rice (<i>Oryza sativa</i> L.) hybrids
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The present investigation was carried out during *kharif*, 2017 at Agricultural College Farm, Bapatla, with 20 genotypes of rice (*Oryza sativa* L.) which consists of 15 hybrids and 5 checks to elicit information on the nature and extent of variability, heritability, genetic advance, character association, the magnitude of direct and indirect effects of yield components on yield and genetic divergence based on the data of the 15 characters viz., days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of total grains per panicle, grain yield per plant, hulling percentage, milling percentage, head rice recovery percentage, L/B ratio, water uptake, kernel elongation ratio, volume expansion ratio and amylose content.

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the presence of sufficient genetic variability for data generated from the above diverse material.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association with the characters at genotypic level. The genetic parameters revealed that moderate to high variability and high heritability coupled with high genetic advance as per cent of mean were for grain yield per plant (g), number of total grains per panicle and water uptake suggesting the predominance of additive type of gene action in controlling these traits with less influence by the environment.

The correlation studies revealed that the traits, plant height and number of total grains per panicle had significant positive association with grain yield at both phenotypic and genotypic levels. So, advancement in grain yield is possible by giving emphasis on these characters in selection scheme. Further, L/B ratio exhibited negative significant correlation with grain yield per plant at genotypic level.

Path coefficient analysis revealed that the characters viz., days to maturity, number of productive tillers per plant, number of total grains per panicle, milling percentage, water uptake and kernel elongation ratio showed positive direct effect and positive correlation with grain yield per plant. Similarly, head rice recovery percentage and L/B ratio showed negative effect and negative correlation with grain yield per plant.

The results of D^2 analysis indicated the presence of considerable genetic divergence among the 20 genotypes studied. The 20 genotypes are grouped into five clusters. Out of five clusters, cluster I was the largest with maximum number of genotypes (9). Cluster II was the second largest with six genotypes followed by cluster IV with three genotypes. Clusters III and V were solitary clusters.

The intra and inter cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values. The maximum inter cluster D^2 values was observed between cluster II and V (444.87) followed by cluster I and V (267.50).

Based on the *per se* performance and cluster mean values of characters, it can be concluded that, the hybrid S-8001 which is present in the cluster II is found to be superior over other hybrids and checks in the present study by having high mean values for the economically important characters viz., number of total grains per panicle, number of productive tillers per plant and yield per plant.

Chapter – I

Introduction

Chapter I

INTRODUCTION

Rice is one of the most important cereal crops in the tropics as well as parts of temperate regions in the world. It is a food crop of world-wide importance and forms the foundation of the diet of over 3 billion people, constituting over half of the world's population. Global rice production for 2015-16 was 472.9 million tonnes over an area of 160.9 million hectares (United States Department of Agriculture, 2015-16). Among the rice growing countries in the world, India has the largest area under rice cultivation and ranks second in production next to China. In India, rice is grown in 44.0 million hectares with the production of 108.50 million tonnes and productivity of 2.4 t/ha. In Andhra Pradesh (Rice Bowl of India) rice is grown in an area of 2.16 million hectares with a production of 7.49 million tonnes and productivity of 3126 kg ha⁻¹ during 2016-17 (Directorate of Economics & Statistics, 2016-17). The state contributes to 12% of total rice production in the country.

Rice offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various qualitative and quantitative characters (Kotaiah, 1983). The conservation of a large amount of genetic variability in rice gene pool provides plant breeder with raw material that can be recommended to produce new improved varieties for yield and quality traits.

For the estimated population of 1.63 billion people by the year 2050 with a per capita rice consumption of 225 to 275 g/day, country would require 133 to 162 mt of rice (Directorate of Rice Research, 2013). At present the rice productivity has reached to a plateau and there is a need to develop the varieties with higher yield potential by breaking the existing yield plateau through utilizing more divergent lines in the breeding programmes.

Hybrid rice technology has proved to be one of the most feasible and readily adoptable approaches to break the yield barrier, as they yield about 15-20 per cent more than the best of the improved or High Yielding Varieties. China ranks first in Hybrid rice production in terms of area and production i.e. about 55 per cent of total rice area and 66 per cent of the total rice output is through hybrid rice. Being convinced of the potential of hybrid rice technology in enhancing the production, India adopted this

technique and has released 93 hybrids till date for commercial cultivation. The estimated area under hybrid rice in India is about 1.32 m ha. Hybrid technology has been widely acclaimed and accepted. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters. Therefore, in addition to studies on mean performance, the evaluation of material for genetic divergence, variability, association among various yield and quality traits and direct and indirect effects contributed by each character towards yield would be more useful to the plant breeders.

The estimation of genotypic variation alone may not provide necessary information on heritable variation. Hence, information on heritability along with genetic advance will be of immense help to the breeder in selecting superior individuals for a desired trait and successfully utilizing them in breeding programme.

Correlation is the measure of mutual relationship between two variables and measures the degree of closeness and the linear relationship between them. To know how the improvement of one character will bring simultaneous improvement in other characters, study of correlations is essential for a plant breeder. Information on the correlation co-efficient between grain yield and yield contributing traits is a prerequisite for improving yield.

Path analysis facilitates the partitioning of correlation coefficients into direct and indirect effects of various characters on yield. Information on association of characters, direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process. Correlation and path analysis establish the extent of association between yield and its components and also bring out relative importance of their direct and indirect effects, thus giving an obvious understanding of their association with grain yield. Ultimately, this kind of analysis could help the breeder to design his selection strategies to improve grain yield (Babu *et al.*, 2012a).

Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of greater importance in breeding programme. Assessment of a large number of germplasm for genetic diversity is of immense importance in selection of diverse genotypes for hybridization programmes. Realising the importance of germplasm in the breeding of

desirable varieties, breeders are now looking for more diverse forms from various sources to further augment the yield potential of the genotypes. Grouping or classification of genotypes based on suitable scale is quite imperative to understand the usable variability existing among them. For the assessment of variation on multivariate scale, Mahalanobis D^2 – statistic has proved to be a powerful technique (Murthy and Arunachalam, 1966).

Grain quality along with crop yield and resistance to pest and disease is one of the important criteria in most rice breeding programmes; it has always been an important consideration in rice variety selection and development. In recent decades as living conditions are being steadily improved, human demand for high quality rice is continuously on increase, which entailed in incorporation of preferred grain quality features as the most important objective next to enhancement in yield.

Hence along with yield, there is also a need to look into the quality aspects to have a better consumer acceptance which determines the profit margin of rice growers which in turn dictates the export quality and foreign exchange in India.

Hence keeping this background in view, the present study was conducted in a set of rice hybrids with the following objectives.

Objectives:

1. To estimate variability, heritability and genetic advance for yield, yield components and quality traits in rice hybrids.
2. To assess the character association among yield, yield components and quality traits in the rice hybrids.
3. To study the direct and indirect effects of yield components and quality traits on grain yield in rice hybrids.
4. To study the genetic divergence among the different rice hybrids.

Chapter – II

Review of Literature

Chapter II

REVIEW OF LITERATURE

Review of literature pertaining to the present investigation in rice is presented under the following headings.

2.1 Variability, heritability and genetic advance as percent of mean

2.2 Correlation studies

2.3 Path analysis

2.4 Genetic divergence

2.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

Knowledge on the nature and magnitude of variability present in any crop species plays a vital role in formulating a successful breeding programme for developing superior cultivars. The magnitude of heritable variation in the traits studied has immense value in understanding the potential of the genotype, assessment of variability for yield and its component characters is absolutely essential in the materials under study which are detected through genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV).

Hanson *et al.* (1956) defined heritability in broad sense as the ratio of genotypic variance to the total variance in the non-segregating populations. Phenotype is the expression of a genotype in a given environment, sometimes when the environmental influence is less; the true heritability becomes much higher. Heritability (h^2) measures the relative amount of the heritable portion of variability, while the genetic advance (GA) helps to measure the amount of progress that could be expected with selection in a character. So, only heritability will not give a true picture of inherited variance and high heritability is not always an indication of true genetic gain. Hence there is need to estimate genetic advance, which is a relative measure and reliable indication of true genetic gain. High heritability estimates together with high genetic advance indicates additive gene effect (Johnson *et al.*, 1955). So, high heritability estimates coupled with high genetic gain could successfully be improved by direct selection. Low genetic advance irrespective of high or low heritability leads to non-additive gene action (Panse, 1957) and improvement of that trait by simple selection may not be rewarding.

Available literature on variability, heritability and genetic advance is reviewed and presented here.

Nandan *et al.* (2010) evaluated 33 rice genotypes to determine the nature and magnitude of variability for 20 yield and quality traits. Low PCV and GCV was observed for traits like kernel elongation ratio and L/B ratio; moderate PCV and GCV was observed for number of productive tillers plant⁻¹ and high PCV and GCV was observed for grain yield per plant. High heritability with high genetic advance as percent of mean was registered for number of productive tillers plant⁻¹, panicle weight, number of total grains panicle⁻¹, number of spikelets panicle⁻¹, 1000 grain weight, kernel length before cooking (KLBC), length breadth(L/B) ratio, water uptake ratio and grain yield plant⁻¹.

Pandey and Anurag (2010a) evaluated 22 genotypes of indigenous rice for yield and quality contributing traits to assess the genetic variability, heritability. They observed maximum value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for head rice recovery. High broad sense heritability was exhibited by test weight followed by grain yield hill⁻¹ and lowest was observed in volume expansion ratio. Highest genetic advance was recorded for milling percentage and lowest was recorded for volume expansion ratio.

Yadav *et al.* (2010) conducted experiment with 40 rice genotypes for genetic variability studies. Analysis of variance revealed that significant amount of genetic variability was present in the entire characters studied. High heritability coupled with high to moderate genetic advance as % of mean was observed on plant height, grain yield plant⁻¹, biological yield, harvest index, test weight and number of spikelets panicle⁻¹.

Akhtar *et al.* (2011) evaluated 10 rice genotypes for variance and heritability for yield and yield contributing traits. The heritability was found to be highest for number of grains panicle⁻¹, days to maturity, plant height and paddy yield while lowest for total number of tillers plant⁻¹.

Prasad *et al.* (2011) evaluated 52 genotypes of rice to study the genetic variability for yield and its component characters. Results showed that characters like spikelet sterility, number of productive tillers, coleoptile length and days to maturity showed high PCV and GCV. High genetic advance was noticed for all the traits except coleoptile length and germination percentage.

Subbaiah *et al.* (2011) conducted studies with 16 parents and 48 hybrids for nine yield components and 25 quality characters. The magnitude of difference between PCV and GCV was relatively low for all the traits. High GCV and PCV were recorded for harvest index, number of productive tillers plant⁻¹ and gelatinization temperature in parents and for total number of productive tillers plant⁻¹, number of total grains panicle⁻¹, gelatinization temperature and amylose content in hybrids. High heritability coupled with high genetic advance as per cent of mean were recorded for gelatinization temperature, harvest index, total number of productive tillers plant⁻¹, number of grains panicle⁻¹, kernel length, kernel L/B ratio and grain yield plant⁻¹ in case of parents and for gelatinization temperature, amylose content, total number of productive tillers plant⁻¹, number of grains panicle⁻¹ and harvest index in case of hybrids.

Tiwari *et al.* (2011) conducted experiment with three CMS lines and 20 diverse genotypes to estimate variability, heritability and genetic advance. The higher magnitude of PCV and GCV was recorded for 100 grain weight, grain yield plant⁻¹, number of fertile spikelets, pollen fertility percent, effective tillers plant⁻¹, panicle length, number of spikelets panicle⁻¹ and harvest index. All the characters showed high broad sense heritability, while narrow sense estimates were higher for biological yield, spikelet fertility percent and number of fertile spikelets; moderate for most of traits except effective tillers per plant and panicle length. High heritability coupled with high genetic advance was recorded for number of fertile spikelets, spikelet fertility percent and pollen fertility percent.

Babu *et al.* (2012b) carried an experiment to study the genetic parameters for yield, yield attributing, quality and nutritional characters in 21 rice hybrids. Analysis of variance revealed significant differences for all the traits under study. The characters viz., number of filled grains panicle⁻¹, number of chaffy grains panicle⁻¹ and iron content exhibited high GCV and PCV. The characters viz., number of filled grains panicle⁻¹ and water uptake exhibited high heritability coupled with high genetic advance.

Bhadru *et al.* (2012b) evaluated 21 rice genotypes for their variability. The highest GCV, PCV, heritability and genetic advance % of mean was reported for number of grains panicle⁻¹, seed yield, 1000 grain weight and plant height.

Ovung *et al.* (2012) conducted experiment using 70 rice genotypes to study variability, heritability and genetic advance. ANOVA revealed the presence of considerable amount of variability among the genotypes. High estimates of genotypic

coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield hill^{-1} followed by tillers hill^{-1} and harvest index. High heritability coupled with high genetic advance was recorded for spikelets panicle $^{-1}$.

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 yield characters, the high percent of GCV and PCV was recorded for the biological yield and lowest was recorded for days to 50% flowering. Among the grain quality characters, highest GCV and PCV was recorded for alkali spreading value, while the character hulling percentage recorded the lowest GCV and PCV values. The highest heritability for grain quality characters was recorded for kernel length. The genetic advance as percentage of mean was highest for biological yield & milling % and lowest for days to 50% flowering and alkali spreading value.

Karuppaiyan *et al.* (2013) evaluated twenty seven rice genotypes for their variability. Analysis of variance revealed significant differences among the genotypes for all the traits studied. Heritability in broad sense was high for all the traits, highest recorded for plant height, grain breadth and length breadth ratio. Number of tillers plant $^{-1}$, grain yield ha^{-1} and length breadth ratio were having high genetic advance coupled with high heritability.

Krishnaveni *et al.* (2013) evaluated seventy rice genotypes for genetic variability between yield, yield components and quality parameters. A wider genetic variability was observed among the genotypes for most of the characters studied. GCV and PCV was found to be highest for water uptake followed by grain yield plant $^{-1}$ and test weight. High heritability coupled with high genetic advance and high GCV were observed for grain yield plant $^{-1}$, water uptake followed by test weight and productive tillers plant $^{-1}$.

Dhurai *et al.* (2014) evaluated thirty two rice genotypes to assess variability, heritability among yield and yield contributing traits. The analysis of variance revealed significant differences among the genotypes for all the nine quantitative and five quality traits in rice indicating enough variability in their study material. The higher magnitude of PCV and GCV was recorded for number of grains panicle $^{-1}$ and grain yield plant $^{-1}$. All the characters showed high broad sense heritability, while high heritability coupled with high genetic advance as per cent mean was recorded for plant

height, number of effective tillers plant⁻¹, panicle length, number of grains panicle⁻¹, kernel elongation ratio, kernel length after cooking, 1000-grain weight, harvest index and grain yield plant⁻¹.

Gokulakrishnan *et al.* (2014) evaluated twenty three genotypes of rice to estimate heritability, genetic advance, phenotypic and genotypic coefficient of variation among yield, quality and its component characters. A high degree of variation was observed for all characters studied. Panicle weight, number of grains panicle⁻¹, grain L/B ratio, plant height, 1000 grain weight and grain breadth recorded moderate phenotypic and genotypic coefficients of variation. High heritability coupled with high genetic advance as percent of mean was observed for grain breadth, grain L/B ratio, plant height, number of grains panicle⁻¹ and grain yield plant⁻¹.

Khare *et al.* (2014) evaluated sixty upland rice germplasm accessions for variability studies. High heritability coupled with high to moderate phenotypic and genotypic coefficient of variation and genetic advance as per cent of mean was recorded for grain yield plant⁻¹, plant height, test weight, fertile spikelet panicle⁻¹, total grains panicle⁻¹ and number of effective tillers plant⁻¹.

Lingaiah *et al.* (2014) carried out an experiment to estimate the variability parameters for quantitative traits in 33 rice cultures. Analysis of variance revealed the existence of significant differences among genotypes for all traits studied. The genotypic and phenotypic coefficients of variations were moderate to high for number of grains panicle⁻¹, test weight and yield. High heritability coupled with high genetic advance as percent of mean was observed for number of grains panicle⁻¹, test weight and yield.

Naseem *et al.* (2014) conducted genetic variability studies on the twenty genotypes of rice 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 twenty one rice varieties for thirteen morphological characters to study variability and heritability. Analysis of variance revealed significant differences among the varieties for all the traits. The phenotypic variance was higher than the corresponding genotypic variance for all the characters. All the characters showed moderate to low phenotypic and genotypic coefficient of variation except for number of ineffective spikelets panicles⁻¹ followed by 1000 grains weight and number of spikelets panicle⁻¹.

Ramanjaneyulu *et al.* (2014) evaluated ten popular low land rice genotypes for variability and heritability under aerobic conditions on alfisols. Results showed low variability in some of the growth and yield attributes like plant height, tillers plant⁻¹, spikelet length and harvest index, whereas high heritability (broad sense) estimates was observed for quantitative characters such as 1000 grain weight and grain yield.

Rao *et al.* (2014) conducted variability analysis among 49 rice cultures for yield and its contributing traits. Analysis of variance revealed the existence of significant differences among genotypes for all characters studied. The magnitude of PCV and GCV was moderate to high for number of grains panicle⁻¹, test weight and grain yield. High heritability coupled with high genetic advance as percent of mean was observed for test weight and grain yield.

Bhati *et al.* (2015) conducted genetic variability studies on 30 elite rice genotypes for grain yield and quantitative traits. Highest GCV and PCV was observed for grain yield hill⁻¹ followed by harvest index. High estimates of heritability coupled with high genetic advance was observed for plant height and spikelets panicle⁻¹.

Devi *et al.* (2015) evaluated ninety two rice genotypes to estimate the genetic variability, heritability and genetic advance for 14 physico-chemical and cooking quality traits. Highly significant differences were observed for all 14 quality characters studied. Among the traits, head rice recovery, water uptake, gel consistency and alkali spreading value exhibited high estimates of GCV and PCV. Highest broad sense heritability and genetic advance was obtained for head rice recovery, milling percentage, water uptake, amylose content and gel consistency. High estimates of heritability in association with medium genetic advance was observed for KLAC, elongation ratio and alkali spreading value.

Ekka *et al.* (2015) evaluated 96 germplasm accessions in rice to estimate variability, heritability, genetic advance for nineteen characters. The highest GCV and PCV was observed for number of effective tillers plant⁻¹, grain yield plant⁻¹ and head rice recovery percentage. Estimates of heritability and genetic advance were high for number of effective tillers plant⁻¹, number of filled grains panicle⁻¹, head rice recovery percentage and grain yield plant⁻¹.

Gampala *et al.* (2015) evaluated 80 rice genotypes for yield and quality contributing traits. Analysis of variance showed highly significant differences among them. Highest PCV was observed for grain yield hill⁻¹ and number of spikelets panicle⁻¹, and highest GCV was observed for number of spikelets panicle⁻¹ and flag leaf length. High estimates of heritability was observed for number of spikelets panicle⁻¹ and test weight. High genetic advance was observed for number of spikelets panicle⁻¹ and plant height.

Sarwar *et al.* (2015) evaluated forty two rice genotypes for variability studies, heritability and genetic advance. The analysis of variance revealed significant deviation for all the characters studied. The PCV values were slightly higher than the respective GCV values for all the characters except unfilled grains panicle⁻¹ indicating that the characters were less influenced by the environment. Total number of tillers plant⁻¹, effective tillers plant⁻¹, filled grains panicle⁻¹, unfilled grains panicle⁻¹ and yield plant⁻¹ showed high heritability coupled with high genetic advance as percentage of mean. High heritability along with low genetic advance as percentage of mean was found for plant height, days to 50% flowering, panicle length, days to maturity and 1000 grains weight.

Tiwari (2015) crossed ten diverse genotypes of rice in a diallel fashion to study variability, heritability and genetic advance for 12 quantitative characters. High estimates of genetic advance was reported for plant height, days to maturity, days to 50% flowering and total biological yield plant⁻¹. However, high heritability estimates with high genetic advance was reported for plant height, days to maturity, days to 50% flowering and number of spikelets panicle⁻¹. The estimates of PCV was higher than those of GCV for all the traits except for plant height. High estimates of heritability and genetic advance was obtained for plant height, number of spikelets panicle⁻¹, days to 50% flowering and days to maturity.

Umesh *et al.* (2015) carried out the investigation on 24 rice genotypes to study different genetic parameters viz., coefficient of variation, heritability and genetic advance 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; genetic advance was highest for spikelets panicle⁻¹ and lowest for spikelet fertility among yield traits and for quality traits it was highest for alkali spread value.

Bhatt *et al.* (2016) conducted experiment with eight local germplasm of rice to study variability, heritability and genetic advance under irrigated condition. Wide range of variation was observed for all the quantitative traits under study. PCV was highest for grain yield plant⁻¹ followed by number of fertile grains panicle⁻¹. High heritability values were also recorded for test weight, plant height at maturity and vegetative plant height. Estimates of genetic advance was highest for number of grains panicle⁻¹, followed by plant height. Genetic advance as percent of mean was highest for number of grains panicle⁻¹ followed by grain yield plant⁻¹.

Chandramohan *et al.* (2016) studied variability among 44 genotypes of rice. The analysis of variance revealed presence of significant variability among the 44 genotypes of rice for all the traits except for number of effective tillers plant⁻¹. Higher magnitude of PCV and GCV were recorded for all the characters studied. Additive gene action was predominant for the traits, number of grains panicle⁻¹ and 1000 grain weight.

Chowdhury *et al.* (2016) evaluated 65 rice genotypes and analysis of variance was conducted to determine GCV, PCV, heritability and GA of the genotypes with respect to important quality parameters and yield per plant. Significant variation was observed among the genotypes. Highest GCV and PCV were observed for gel consistency followed by elongation ratio. In the study, heritability was high for all the quality parameters; but high heritability along with high genetic advance was observed for amylose content and yield per plant.

Devi *et al.* (2016) evaluated 27 rice genotypes for variability studies. Analysis of variance revealed highly significant differences among all genotypes for all the yield components and most of the kernel quality traits except hulling percent, volume expansion ratio and water uptake. Higher estimates of PCV and GCV observed for yield plant⁻¹ and filled seeds panicle⁻¹, while hulling percent, milling percent, kernel elongation ratio, days to 50% flowering, panicle length, kernel length and kernel width showed low PCV and GCV values. High heritability in broad sense and high genetic advance as percent of mean was exhibited by effective tillers per hill, plant height, flag leaf length, filled seeds panicle⁻¹, test weight, yield plant⁻¹, head rice recovery and length/breadth ratio.

Kumar and Verma (2016) carried out an experiment with three testers and 15 salinity tolerant varieties to estimate genetic variability, heritability and genetic advance and for some yield and its contributing characters. Highest GCV was recorded

for 1000 grain weight followed by grain yield plant⁻¹, biological yield plant⁻¹, spikelets panicle⁻¹, ear bearing tillers plant⁻¹, plant height, harvest index, panicle length, and lowest for spikelet fertility. High estimates of heritability in narrow sense were recorded for days to maturity, days to 50% flowering and plant height. High heritability coupled with high genetic advance was observed for 1000 grain weight, grain yield plant⁻¹, days to 50% flowering, spikelets panicle⁻¹, days to maturity and L/B ratio.

Sameera *et al.* (2016) evaluated 25 rice genotypes for their variability with regard to yield and yield components. Results revealed that high variability, heritability and genetic advance as per cent mean was exhibited by productive tillers plant⁻¹, number of 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 percent of mean.

Tejaswini *et al.* (2016) evaluated one hundred and fourteen F₅ families of rice belonging to six crosses along with seven parents to study variability, heritability, genetic advance as percent of mean. High PCV and GCV were observed for grain yield plant⁻¹ and test weight. High heritability coupled with high genetic advance as percent of mean was observed for number of grains panicle⁻¹, grain yield plant⁻¹ and test weight.

Ajmera *et al.* (2017) studied thirty seven rice genotypes for their variability with regard to yield and yield components. Estimates of heritability and genetic advance as percent of mean were also obtained for the above traits. All the characters except days to 50% flowering exhibited high heritability coupled with high genetic advance as percent of mean.

Bhinda *et al.* (2017) carried out the experiment with 42 rice genotypes to obtain information on genetic variability, heritability and genetic advance for yield contributing and quality traits in advance breeding lines of rice. The analysis of variance revealed significant differences among all the genotypes for all the 15 characters studied. High values of PCV were observed than GCV for all the characters. Alkali spreading value exhibited highest GCV and PCV followed by filled grains panicle⁻¹. The highest broad sense heritability was estimated for gel consistency followed by alkali spreading value. Whereas the highest value of genetic advance was recorded for characters namely filled grains panicle⁻¹ and number of grains panicle⁻¹. High heritability coupled with high genetic advance was reported for gel consistency, plant height, filled grains panicle⁻¹, number of grains panicle⁻¹ and days to 50% flowering.

Devi *et al.* (2017) evaluated 27 rice genotypes for variability, heritability and genetic advance for yield and quality traits and observed higher estimates of PCV and GCV for yield plant⁻¹ and filled grains panicle⁻¹. High heritability in broad sense coupled with high genetic advance as percent of mean was exhibited by effective tillers, plant height, flag leaf length, filled grains panicle⁻¹, test weight, yield plant⁻¹, head rice recovery and length/breadth ratio.

Gunasekaran *et al.* (2017) evaluated nine rice genotypes for genetic variability parameters for eleven agronomic and quality traits. The results showed that, PCV was higher than GCV for all the characters studied. The grain yield plant⁻¹ recorded highest GCV, high heritability coupled with high genetic advance.

Jan *et al.* (2017) studied fourteen agro-morphological traits among 35 rice genotypes and observed that harvest index had the highest values of GCV and PCV. Lowest GCV and PCV was recorded by 1000 grain weight. High broad sense heritability coupled with high genetic advance was observed for biological yield, number of spikelets panicle⁻¹, number of filled grains panicle⁻¹.

Lakshmi *et al.* (2017) evaluated the fifty five F₇ generation aromatic rice genotypes for yield and component characters to study the genetic variability, heritability and genetic advance. Studies revealed that number of filled grains panicle⁻¹, 1000 grain weight, grain yield plant⁻¹, kernel length, L/B ratio recorded high GCV. High heritability coupled with high genetic advance as percent of mean was registered for plant height, number of productive tillers plant⁻¹, panicle length, number of filled grains panicle⁻¹, 1000 grain weight, grain yield plant⁻¹, kernel length and L/B ratio.

Limbani *et al.* (2017) conducted a field experiment with 72 genotypes of upland rice to investigate the magnitude of genetic variability in rice. Higher estimates of genotypic and phenotypic coefficient of variation were obtained for number of non-effective tillers plot⁻¹, number of unfilled grains panicle⁻¹, harvest index and grain yield plot⁻¹. Number of effective tillers plot⁻¹ showed high heritability coupled with high genetic advance.

Nandini *et al.* (2017) evaluated three hundred and twenty four traditional rice varieties (TRVs) for grain yield and its attributes in two seasons. Substantial variability among the accessions for quantitative traits was recorded. High heritability coupled with high genetic advance indicated the effectiveness of selection for days to 50% flowering, grain length, grain breadth, L/B ratio and straw yield plant⁻¹.

Prasad *et al.* (2017) evaluated fifty boro rice genotypes for variability, heritability and genetic advance in yield and yield contributing characters. High GCV and PCV values were observed for number of filled grains panicle⁻¹, number of unfilled grains panicle⁻¹ and grain yield plant⁻¹. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of tillers plant⁻¹, number of productive tillers plant⁻¹, number of filled grains panicle⁻¹, number of unfilled grains panicle⁻¹, 1000 grain weight and grain yield plant⁻¹.

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

Mamata *et al.* (2018) evaluated the two F₂ populations of rice viz., 'Rajamudi × BR-2655' and 'Rathnachoodi × BR-2655' to estimate the variability, heritability, genetic advance and genetic advance as percentage of mean. High PCV and GCV values was obtained for grain yield plant⁻¹. Low PCV and GCV was observed for 1000 grain weight and panicle length. Plant height, spikelet fertility, harvest index and grain yield plant⁻¹ had high heritability along with high genetic advance as per cent of mean.

2.2 CORRELATION

Correlation coefficient is a measure of the degree of closeness and the linear relationship between two variables. Studies on correlation between yield and its components in population helps the breeder in understanding the shifts associated with different components to yield. The study of association between different characters may help the plant breeder to know how the improvement of one character will bring simultaneous changes in other characters. Character association studies indicate the magnitude of association between pairs of characters and are useful for selecting genotypes with desirable combination of characters thereby aiding the plant breeder in the improvement of the concerned trait. If the correlation is strong between a set of desirable traits then if we make selection for one character, the other character will be taken care of automatically. If unfavourable association exists between desirable and undesirable traits, selection may result in genetic slippage and limit genetic advance.

Literature on the scientific studies made by several workers on correlation in rice is presented here.

Kumar *et al.* (2010) conducted experiment with five lines and six testers to study correlation coefficient among grain quality components in rice in thirty crosses. In correlation studies, hulling percentage, paddy length, head rice recovery, milling percentage, brown rice length exhibited a positive interrelation among themselves.

Nandan *et al.* (2010) evaluated 33 rice genotypes to study the degree of association between yield and its component characters. The correlation studies revealed strong positive association of yield with days to 50% flowering, plant height, number of grains panicle⁻¹, number of spikelets panicle⁻¹ and spikelet fertility.

Yadav *et al.* (2010) evaluated forty rice genotypes for character association studies to establish the extent of association between yield and yield components and other characters in rice. The correlation coefficient between seed yield plant⁻¹ and other quantitative characters attributing to yield showed that grain yield was significantly and positively associated with harvest index, number of tillers hill⁻¹, number of panicles plant⁻¹, panicle length, number of spikelets panicle⁻¹ and test weight at both genotypic and phenotypic levels.

Akhtar *et al.* (2011) evaluated ten rice genotypes for character association studies. Results revealed significant positive genetic association of yield per plant with number of grains panicle⁻¹, days to maturity and 1000 grain weight. Plant height was found negatively correlated with number of grains panicle⁻¹, number of tillers plant⁻¹ and yield per plant.

Prasad *et al.* (2011) evaluated 52 genotypes of rice to study the character association for yield and its component characters. Correlation coefficient studies revealed that days to 50% flowering had positive and significant correlation with coleoptile length, seedling growth and seed vigor. Plant height exhibited a positive and non-significant association with number of tillers plant⁻¹ and days to 50% flowering. Panicle exertion exhibited positive and significant association with radicle length. Test weight had positive and significant correlation with coleoptile length, seedling growth, radical length and seed vigor. Days to maturity exhibited positive and significant correlation with plant height, days to 50% flowering, coleoptile length, seedling growth and seedling vigor.

Babu *et al.* (2012a) carried out correlation analysis in twenty one popular hybrids of rice. Results revealed significant positive association of grain yield plant⁻¹ with number of productive tillers plant⁻¹.

Bhadru *et al.* (2012a) conducted experiment with 68 hybrids, 21 parents and four checks to study the association among yield components with grain yield. The characters viz., plant height, panicle length, productive tillers plant⁻¹ and filled grains panicle⁻¹ exhibited significant positive association with grain yield plant⁻¹, and indirect association among themselves at both genotypic and phenotypic levels.

Krishnaveni *et al.* (2013) evaluated seventy rice genotypes to study character association between yield and yield components and quality parameters. Days to 50% flowering, productive tillers plant⁻¹, panicle length, head rice recovery and volume expansion ratio manifested significant positive association with grain yield indicating that simultaneous improvement of all the characters is possible.

Raju *et al.* (2013) conducted experiment with six parents and their 15 F₁ crosses for eleven component characters including grain yield to establish the nature of relation between grain yield and yield components by using simple correlation analysis. The results obtained indicated that number of grains panicle⁻¹, total number of productive tillers plant⁻¹, harvest index, kernel L/B ratio, milling percentage and panicle length showed highly significant positive association with grain yield plant⁻¹.

Dhurai *et al.* (2014) conducted field experiment using 32 rice genotypes by adopting RBD with three replications to estimate character association among yield and yield contributing traits. They observed high genotypic and phenotypic correlation indicating strong inherent association between the characters. Grain yield had positive and significant association with yield components.

Khare *et al.* (2014) observed in 60 upland rice germplasm accessions, positive and significant association of days to 50% flowering, days to maturity, plant height, panicle length, fertile spikelets panicle⁻¹, total grains panicle⁻¹ and spikelet fertility with grain yield plant⁻¹ at both genotypic and phenotypic level.

Lakshmi *et al.* (2014) evaluated seventy genotypes of rice to study the nature and extent of correlation among yield and yield attributing characters. The results revealed the grain yield plant⁻¹ to be positively and significantly associated with days to maturity, number of productive tillers plant⁻¹, plant height and kernel length.

Naseem *et al.* (2014) conducted correlation studies on the twenty genotypes of rice for yield and yield related traits. Results showed that number of productive tillers plant⁻¹, number of spikelets panicle⁻¹, number of grains panicle⁻¹ and 1000 grain weight had a highly positive significant genotypic and phenotypic correlation with grain yield plant⁻¹.

Rahman *et al.* (2014) studied character association in twenty one rice varieties for thirteen morphological characters. Significant positive genotypic and phenotypic correlation was found between plant height and straw yield, tiller mortality and panicle length, panicle length and number of spikelets panicle⁻¹, panicle length and number of ineffective spikelets panicle⁻¹, number of maximum tillers m⁻² and number of effective tillers m⁻², number of spikelets panicle⁻¹ and number of effective spikelets panicle⁻¹, and between number of spikelets panicle⁻¹ and number of ineffective spikelets panicle⁻¹.

Ramanjaneyulu *et al.* (2014) observed significant and positive correlation of grain yield with number of tillers plant⁻¹, number of productive tillers plant⁻¹, number of grains spikelet⁻¹ and spikelet length among ten popular low land rice genotypes under aerobic conditions (on alfisols).

In character association studies by Rao *et al.* (2014) among 49 rice cultures, grain yield was found to have significant positive correlation with number of grains panicle⁻¹, panicle length and test weight.

Bhati *et al.* (2015) conducted correlation studies on 30 elite rice genotypes for grain yield and quantitative traits. The results revealed that grain yield hill⁻¹ had positive, significant correlation with harvest index, biological yield hill⁻¹, test weight and plant height at both genotypic and phenotypic level.

Devi *et al.* (2015) evaluated ninety two rice genotypes for character association of 14 physicochemical and cooking quality traits. Significant positive correlation of kernel length after cooking with elongation ratio and L/B ratio; ASV with water uptake; hulling % with milling % and HRR % were observed.

Ekka *et al.* (2015) evaluated 96 germplasm accessions in rice to carry out character association studies for nineteen characters. Correlation studies indicated that grain yield plant⁻¹ had positive significant correlation with leaf width, days to 50% flowering, plant height, panicle length, number of filled grains panicle⁻¹, 100 seed

weight and paddy length. A positive and significant correlation of head rice recovery percentage was also observed with leaf length, leaf width, days to 50% flowering, number of filled grains panicle⁻¹ and milling percentage.

Ramadoss *et al.* (2015) carried out an experiment to assess the association among grain quality parameters in 24 *indica* rice genotypes. The results showed highly positive significant correlation between kernel length after cooking and length wise elongation ratio. Similarly, kernel breadth after cooking showed highly significant correlation with breadth wise elongation ratio. Moderate significant correlation was found between volume expansion ratio and length wise elongation ratio.

Abdala *et al.* (2016) conducted an experiment for correlation coefficient analysis on eleven F₁'s derived from crosses between aromatic and non-aromatic landraces. The results showed positive and highly significant correlation between brown rice length and paddy grain width; paddy grain length and brown grain length; head rice recovery and milling recovery; and brown rice shape and grain rice length. While correlation between brown rice shape and brown rice length was negative. These highly correlated characters could be used for indirect selection and improvement of rice grain quality.

Anis *et al.* (2016) evaluated eleven hybrid combinations developed by three line systems with two standard check varieties in two rice growing seasons to find out interrelationships of yield and yield components. The study showed positive and significant correlations in most of the cases. The highest value was found between flag leaf area and panicle length. Grain yield showed positive significant correlation with number of panicles plant⁻¹.

Bhatt *et al.* (2016) conducted experiment with eight local germplasm of rice to study the association between yield and yield attributing characters under irrigated condition. Number of tillers exhibited positive and significant association with test weight, positive and non significant association with length breadth ratio and grain yield plant⁻¹. It showed negative and non significant association with vegetative plant height, plant height at maturity, panicle length, number of grains panicle⁻¹, fertile grains panicle⁻¹. The direction and magnitude of association indicated that the grain yield of rice in irrigated conditions can be improved by selecting germplasms having higher performances for yield attributing traits.

In studies of Chowdhury *et al.* (2016) milling % showed a positive correlation with respect to HRR in 65 rice genotypes. Yield plant⁻¹ had non-significant association with all the quality parameters reflecting less influence of all these traits upon the final yield.

Ernawati *et al.* (2016) evaluated local brown rice varieties to study association among the characters. There was a significant correlation among the grain yield and the total number of productive tillers hill⁻¹, panicle length and total number of grains panicle⁻¹, weight of 100 grains and grain weight panicle⁻¹.

Ratna *et al.* (2016) studied the correlation for twelve grain characters before cooking and eight characters after cooking on six distinct lines viz., S1, S2, S5, 42(i), 42(ii) and 44(i) of Basmati rice. Hulling per cent had highly significant positive relationship with milling per cent, HRR per cent and kernel breadth of milled rice. HRR per cent showed highly significant positive correlation with kernel breadth of milled rice and insignificant negative association with L/B ratio of rough rice, milled rice and cooked rice. The kernel breadth of cooked rice showed a significant positive relationship with alkali spreading value at genotypic level. Water uptake % exhibited a significant negative relationship with alkali spreading value but an insignificant negative relationship with volume expansion per cent and elongation ratio.

Sameera *et al.* (2016) conducted character association studies on 25 rice genotypes and found that yield was positively associated with number of tillers plant⁻¹, productive tillers plant⁻¹, number of grains panicle⁻¹ and number of filled grains panicle⁻¹.

Devi *et al.* (2017) did correlation analysis on 27 rice genotypes for yield and quality traits. Grain yield plant⁻¹ had highest significant positive association with filled seeds panicle⁻¹, plant height, flag leaf length, effective tillers per plant, flag leaf width and panicle length indicating importance of these characters for yield improvement, while head rice recovery was found to be significantly and positively correlated with milling percent and hulling percent.

Gunasekaran *et al.* (2017) evaluated nine rice genotypes for eleven agronomic and quality traits. The results revealed that number of productive tillers plant⁻¹ and 1000 grain weight showed positive significant correlation with grain yield plant⁻¹.

Jan *et al.* (2017) studied association among fourteen agro-morphological traits in 35 rice genotypes. At both genotypic and phenotypic levels, the harvest index showed significantly positive correlation with grain yield hill^{-1} followed by plant height, while days to 50% flowering showed significant negative correlation with grain yield hill^{-1} .

In fifty five F_7 generation aromatic rice genotypes, Lakshmi *et al.* (2017) found that grain yield plant^{-1} had significant positive association with panicle length, number of filled grains panicle^{-1} , 1000 grain weight, kernel length and L/B ratio both at phenotypic and genotypic level. Days to 50% flowering had recorded significant negative correlation with grain yield plant^{-1} at both genotypic and phenotypic levels.

Limbani *et al.* (2017) conducted a field experiment with 72 genotypes of upland rice. Grain yield plot^{-1} showed positive and highly significant association with harvest index, number of effective tillers plot^{-1} , milling percentage, number of filled grains panicle^{-1} and plant height while it showed highly significant but negative correlation with number of non-effective tillers plot^{-1} and days to 50% flowering at genotypic as well as phenotypic levels.

Priya *et al.* (2017) evaluated forty rice genotypes to carry out character association studies. Character association studies revealed that, traits like productive tillers plant^{-1} , number of grains panicle^{-1} , test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50% flowering and kernel length showed significant positive association with grain yield plant^{-1} at phenotypic level.

Sowmiya and Venkatesan (2017a) conducted experiment with 48 rice genotypes. The genotypic correlation coefficients showed higher magnitude than phenotypic correlation coefficients. The genetic correlation revealed that grain yield plant^{-1} had strong negative and significant association with days to first flower at both genotypic and phenotypic levels.

2.3 PATH COEFFICIENT ANALYSIS

Yield is complex polygenic character and highly influenced by environmental factors. Hence direct selection for yield cannot be exercised. Therefore, it becomes essential to identify the component characters through which yield improvement could be attained.

Path coefficient analysis as devised by Wright (1921) is standardized as partial regression coefficient. It is an important tool for partitioning the correlation coefficient into direct and indirect effects of an independent variable and dependent variable. Though correlation gives information about the component traits associated with the characters, they could not provide an exact picture of relative importance of the direct and indirect contribution of the component characters. Thus, correlation in combination with path analysis would give a better insight into the cause and effect relationship between different pairs of characters.

The review of literature on direct and indirect effects of various yield components on plant yield are presented here.

Kumar *et al.* (2010) conducted experiment with five lines and six testers to study path coefficient among grain quality components in rice in thirty crosses. Path analysis of head rice recovery showed that brown rice length, milling percentage, hulling percentage and water uptake were most important contributing characters towards the head rice recovery based on their high positive direct effects.

Nandan *et al.* (2010) observed that the number of grains panicle⁻¹ had maximum direct effect on grain yield plant⁻¹ followed by kernel length after cooking, days to 50 % flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking.

Yadav *et al.* (2010) observed that path coefficient at genotypic level showed that harvest index, biological yield, number of tillers hill⁻¹, panicle length, number of spikelets panicle⁻¹, plant height and test weight had direct positive effect on seed yield hill⁻¹.

Akhtar *et al.* (2011) evaluated 10 rice genotypes for path coefficient analysis for yield and yield contributing traits. Path coefficient analysis revealed that 1000 grain weight has highest positive direct effect, followed by days to maturity on grain yield per plant.

Prasad *et al.* (2011) revealed that seedling growth exerted highest direct positive effect on grain yield followed by panicle length, days to 50% flowering, early seedling vigor and seed vigor. Panicle exertion showed the highest negative direct effect on grain yield followed by radicle length, seedling maturity, number of tillers plant⁻¹ and days to maturity.

Babu *et al.* (2012a) observed that panicle length and number of productive tillers plant⁻¹ exhibiting positive direct effect on yield.

Bhadru *et al.* (2012a) observed that characters viz., plant height, panicle length, productive tillers plant⁻¹ and filled grains panicle⁻¹ exhibiting direct positive effect with grain yield plant⁻¹, at both genotypic and phenotypic levels.

Krishnaveni *et al.* (2013) revealed that productive tillers, panicle length, kernel breadth and L/B ratio showing positive direct effect on grain yield plant⁻¹.

Raju *et al.* (2013) conducted experiment with six parents and their 15 F₁ crosses for 11 component characters including grain yield to carry out path coefficient analysis. In the path coefficient analysis, number of grains panicle⁻¹ and total number of productive tillers plant⁻¹ should be considered as the main yield components because these traits showed the highest positive direct effects towards increasing grain yield.

Khare *et al.* (2014) observed that highest positive direct effect on grain yield was recorded by fertile spikelets panicle⁻¹, total number of grains panicle⁻¹, plant height and days to 50% flowering.

Naseem *et al.* (2014) conducted path coefficient analysis on the 20 genotypes of rice for yield and yield related traits. Number of productive tillers plant⁻¹, number of spikelets panicle⁻¹, number of grains panicle⁻¹ and days to maturity had positive direct effect on grain yield plant⁻¹.

Rahman *et al.* (2014) studied 21 rice varieties for 13 morphological characters to carry out path coefficient analysis. Path coefficient analysis revealed that number of effective spikelets panicle⁻¹ had maximum direct positive effect on yield where as spikelet fertility showed the highest direct negative effect on yield.

Rao *et al.* (2014) conducted path analysis among 49 rice cultures between yield and its contributing traits. Path coefficient analysis showed that number of grains panicle⁻¹, test weight and productive tillers m⁻² had highest direct positive effect on grain yield.

Bhati *et al.* (2015) conducted path coefficient analysis studies on 30 elite rice genotypes for grain yield and quantitative traits. Path coefficient analysis showed that the traits harvest index, biological yield hill⁻¹, number of spikelets panicle⁻¹, number of tillers hill⁻¹ and plant height had high positive direct effect on grain yield at both genotypic and phenotypic level.

Ekka *et al.* (2015) evaluated 96 germplasm accessions in rice to carry out path coefficient analysis for 19 characters. Path coefficient analysis revealed that brown rice breadth expressed highest positive direct effect on grain yield plant⁻¹ followed by 100 grain weight, leaf width, number of effective tillers plant⁻¹, paddy length, days to 50 per cent flowering, leaf length, milling percentage, panicle length and head rice recovery percentage.

Abdala *et al.* (2016) conducted an experiment for path co-efficient analysis on 11 F₁'s derived from crosses between aromatic and non-aromatic parental landraces genotype. The path coefficient analysis revealed a low direct and positive effect for paddy grain length on brown grain length. The direct effect of brown rice width and brown grain shape on brown rice grain length was high and positive showing that these characters have a direct effect and influence on brown grain length.

Sameera *et al.* (2016) evaluated the 25 rice genotypes with regard for yield and yield components to assess the direct and indirect effects among themselves. Number of tillers plant⁻¹, productive tillers plant⁻¹ and number of filled grains panicle⁻¹ showed high direct effects on grain yield plant⁻¹. High indirect effects of most of the traits were observed mostly through productive tillers plant⁻¹.

Devi *et al.* (2017) evaluated 27 rice genotypes for path analysis for yield and quality traits which reveals that test weight, effective tillers, and filled grains panicle⁻¹ had positive direct effect on grain yield plant⁻¹. Among the quality traits kernel length followed by milling percent and kernel elongation ratio had direct effect on head rice recovery.

Gunasekaran *et al.* (2017) evaluated nine rice genotypes for path coefficient analysis for eleven agronomic and quality traits. The results revealed that number of productive tillers plant⁻¹ and thousand grain weight showed direct effects on grain yield plant⁻¹.

Jan *et al.* (2017) studied the direct and indirect effects of 14 agro-morphological traits on yield among 35 rice genotypes. Studies revealed that at genotypic level flag leaf length showed high direct positive effect with grain yield hill⁻¹ followed by flag leaf width while at phenotypic level flag leaf area showed maximum positive direct effect with grain yield hill⁻¹ followed by harvest index. Days to maturity and flag leaf width showed highest negative direct effect on grain yield hill⁻¹. Lowest negative direct

effect was shown by flag leaf length, panicle length and number of filled grains. At both genotypic and phenotypic levels, highest indirect effect on grain yield was observed through harvest index.

Lakshmi *et al.* (2017) evaluated the 55 F₇ generation aromatic rice genotypes to study the direct and indirect effects of yield contributing characters on yield. Path coefficient analysis revealed that kernel length exerted the highest direct effect on grain yield followed by number of filled grains per panicle, 1000 grain weight, number of productive tillers hill⁻¹ and plant height.

Priya *et al.* (2017) evaluated 40 rice genotypes to determine the magnitude of direct and indirect effects of yield component traits on grain yield of rice. Path coefficient analysis revealed that kernel breadth, L/B ratio, productive tillers plant⁻¹, grains panicle⁻¹, test weight, days to maturity and days to 50% flowering showed true relationship with grain yield plant⁻¹ by establishing significant positive association and high positive direct effect.

Sowmiya and Venkatesan (2017a) conducted experiment to carry out path coefficient analysis in 48 rice genotypes for nine characters. The results revealed that maximum direct effect on grain yield was exhibited by number of panicles plant⁻¹.

2.4 GENETIC DIVERGENCE

Knowledge on the nature and magnitude of genetic diversity present in the hybrids plays an important role in undertaking the cause for heterosis. It has been well established that genetically diverse parents are likely to yield desirable gene recombinants and to produce high heterotic effect. Mahalanobis' D² statistic has proved to be powerful tool for quantifying genetic divergence in a given population.

Earlier studies indicated that the geographical distribution of the genotypes was not related to genetic diversity. Some of the available literature on the above aspects in rice is reviewed hereunder.

Banumathy *et al.* (2010) evaluated fifty three rice genotypes for eight yield and yield attributing characters using D² analysis, to study the diversity pattern among the genotypes. Based on the analysis, the genotypes were grouped into 11 clusters. Maximum number of genotypes (16) were grouped under cluster XI followed by cluster I with 15 genotypes, while clusters II, IV, V, VI, VIII, IX and X had only two genotypes each and clusters III and VII consisting of three and five genotypes

respectively. Maximum inter cluster D^2 value was observed between cluster I and X followed by cluster I and IV. The intra cluster distance was maximum in cluster VII followed by cluster XI. Among the eight traits studied, maximum contribution was made by grain yield followed by days to 50% flowering and total grains panicle⁻¹ towards total divergence.

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

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

Garg *et al.* (2011) evaluated forty eight genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. The forty eight genotypes were grouped into five clusters based on Euclidean cluster analysis with cluster I containing the maximum of 18 genotypes. Maximum intra cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. Days to maturity, gel consistency and days to 50% flowering contributed towards total divergence. Maximum inter cluster distance was observed between clusters II and III followed by clusters III and IV indicating wide genetic diversity.

Vennila *et al.* (2011) evaluated 41 rice genotypes for genetic divergence for different yield and quality traits. Based on the genetic distance, all the 41 genotypes were grouped under thirteen different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The maximum inter-cluster distance was recorded between clusters III and XIII and the maximum intra-cluster distance was found in cluster XI followed by VI. The characters like number of grains panicle⁻¹, plant height, grain length and grain breadth contributed maximum towards genetic diversity.

Bhadru *et al.* (2012b) evaluated 21 rice genotypes for genetic divergence which were grouped into six clusters. Most of the genotypes with same pedigree either male or female parent involved cross combination came under the same cluster and few genotypes in different cluster and genotypes of quite different pedigree grouped into the same cluster. For getting desirable transgressive segregants, for the development of early duration (Genotypes from the clusters II and Cluster VI) and medium duration (from the clusters I and IV), coarse and medium slender high yielding, gall midge and BPH resistant varieties, it was concluded that these genotypes could be utilized in the hybridization programme.

Chakma *et al.* (2012) conducted an experiment with 39 rice genotypes to determine the genetic diversity among them. The genotypes were grouped into six clusters based on Mahalanobis D^2 statistics and Canonical Variate Analysis. Cluster I consisted of highest number (11) of genotypes, whereas cluster IV consisted of lowest number (3) of genotypes. Maximum inter cluster distance was recorded between cluster II and cluster III. Cluster III had the highest mean values for grain yield, harvest index, 1000-grain weight and number of effective tillers hill⁻¹; 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 genetic divergence.

Chakravorty and Ghosh (2012) studied genetic divergence 51 land races of rice and grouped them into 11 clusters. The grouping showed six multigenotypic, three digenotypic and 2 monogenotypic clusters. The maximum intra cluster D^2 value was shown by cluster X followed by cluster IX, III and I, while the inter cluster value was maximum between cluster IX and X. Among the genotypes, maximum contribution towards genetic divergence came from the characters culm length, culm diameter and grain length. Cluster VII recorded highest mean value for plant height, ligule length, culm length, culm diameter, culm number, panicle length and maturity. Hybridization among the genotypes from the cluster I, III, IX and X which had maximum inter cluster distances and desirable values for flag leaf angle, grain breadth, grain weight, number of primary branches panicle⁻¹ and number of grains panicle⁻¹ was recommended.

Eswaran (2012) studied genetic divergence among 34 rice genotypes by using Mahalanobis D^2 statistics and grouped into seven clusters. Cluster II was the largest, consisting of 14 genotypes, followed by cluster I with nine genotypes and cluster VII with three genotypes, while clusters III, IV, V and VI contained two genotypes each.

Among the different characters studied, grain yield plant⁻¹, number of grains panicle⁻¹, days to 50% flowering and grain length contributed significantly for the genetic diversity.

Ovung *et al.* (2012) studied the nature and magnitude of genetic divergence in 70 rice genotypes using Mahalanobis D² statistics by considering 13 quantitative characters. Mahalanobis D² analysis revealed considerable amount of diversity in the material. The genotypes were grouped into nine clusters. Cluster I and cluster III constituted a maximum of 12 genotypes each. The genotypes falling in cluster VII had the 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. Traits like spikelets panicle⁻¹, plant height and biological yield were the major contributors to genetic divergence.

Singh *et al.* (2012) studied thirty aromatic rice genotypes and grouped them into six clusters by both Tocher's and Euclidian methods of divergence. The most diverse parent combination for the component characters of grain yield improvement have been identified on the basis of 3D diagram of PCA scores and Euclidian distance matrix, which were JGL 15336 x Taroari Basmati for effective tillers plant⁻¹, Badsabhog x Rajendra Kasturi for filled grains panicle⁻¹, JGL 15336 x Birsamati for grain weight panicle⁻¹ and Gandhasala x Pusa Sugandha-3 for leaf area index.

Karuppaiyan *et al.* (2013) studied twenty seven genotypes of lowland rice under organic conditions in the mid-hills of Sikkim during the wet season for 11 quantitative traits to estimate the genetic divergence among the genotypes through Mahalanobis D² statistics and grouped them into four clusters. Yield ha⁻¹ contributed maximum towards divergence followed by plant height, grain breadth and grain length.

Manohara and Singh (2013) had studied 24 genotypes of rice comprising landraces of Goa and improved cultivars and grouped them into six clusters by using D² statistics. Cluster I consisted maximum of 13 genotypes followed by Cluster III with six genotypes. Among different traits, days to 50% flowering, 1000 grain weight, grain breadth and plant height had maximum contribution towards the total divergence.

Allam *et al.* (2014) studied genetic divergence among 23 genotypes of basmati rice representing different regions of India on the basis of yield and quality characteristics using Mahalanobis D² analysis. Based on the genetic distance (D²

values), the rice genotypes were grouped into six clusters. Of the six clusters formed cluster VI consisted of maximum eight genotypes followed by cluster V accommodating six genotypes, cluster I with four genotypes, cluster III and IV with three genotypes each and cluster II with one genotype. The results indicated that there was some degree of similarity of genotypes clustered together on the basis of their origin. The maximum intra cluster distance was observed for the cluster III. The highest genetic divergence was observed between the clusters IV and I exhibiting wide diversity. The genotypes representing cluster VI were more yielding combined with excellent cooking quality. Among different traits, plant height, kernel length, elongation ratio and amylose content had maximum contribution towards total divergence.

Bhadra and Roy (2014) estimated the nature and magnitude of genetic diversity in 40 rice genotypes under aluminium toxic environment using Mahalanobis D^2 statistics. The genotypes were grouped into five clusters. Highest inter cluster distance was recorded between cluster IV and V followed by clusters III and IV. Germination speed was found to be major contributing characters towards the total genetic divergence.

Khare *et al.* (2014) evaluated sixty upland rice germplasm accessions for divergence studies. Based on ten quantitative traits, the accessions were clustered into seven groups, the cluster III contained the highest of 14 accessions, followed by cluster I (11 accessions) and cluster VI, VII, V, IV and II with 9, 8, 7, 6 and 5 accessions, respectively. The first four principal components accounted for 77.13% of total variation of all the traits.

Kumar *et al.* (2014) evaluated 29 rice genotypes to study the nature and magnitude of genetic divergence using D^2 statistics. Twenty nine genotypes were grouped into six clusters based on Euclidean cluster analysis with cluster-I containing maximum of 13 genotypes. Maximum intra-cluster distance was observed in cluster-V indicating greater genetic divergence among genotypes belonging to this cluster. Number of spikelets panicle⁻¹, plant height and days to 50% flowering contributed maximum towards genetic divergence. Maximum inter-cluster distance was observed between cluster-IV and VI followed by cluster-II and VI, cluster-I and VI and cluster-III and VI.

Niteshkumaret *al.* (2014) estimated the nature and magnitude of genetic divergence in 134 rice germplasm accessions using Mahalanobis D^2 statistics. The genotypes were grouped into five clusters based on Euclidean cluster analysis. The highest intra cluster distance was observed among the genotypes in cluster IV followed by cluster III and cluster V indicating existence of wide genetic divergence among genotypes. Number of filled grains panicle⁻¹ contributed highest towards divergence. Highest inter cluster distance was observed between cluster IV and V followed by clusters II and V.

Rai *et al.* (2014) assessed genetic divergence of forty rice genotypes. Seven clusters here formed based on Tocher cluster analysis. Cluster III contained the maximum of 10 genotypes followed by nine genotypes in cluster II, seven genotypes in cluster I, six genotypes in cluster IV, four genotypes in cluster VI and two each in cluster V & VII. The highest inter cluster distance was observed between cluster IV and VII followed by cluster III and VII, cluster III and VI. The intra cluster distance was maximum in cluster III followed by II and I. Among the thirteen traits studied, maximum divergence was observed by number of spikelets panicle⁻¹ followed by grain yield, plant height and flag leaf length.

Ramanjaneyulu *et al.* (2014) evaluated ten popular low land rice genotypes for genetic divergence under aerobic conditions. The maximum intra-cluster distance was observed in cluster III. The trait 1000 grain weight exhibited the maximum contribution to total genetic divergence, followed by grain yield, number of grains spikelet⁻¹, straw yield and spikelet length. On the other hand, the traits such as tillers plant⁻¹ and harvest index failed to contribute towards genetic divergence.

Beevi and Venkatesan (2015) studied genetic diversity among 60 rice genotypes which were grouped into six clusters. Cluster I was found to be largest with 50 genotypes followed by cluster II with four genotypes and clusters IV and V with two genotypes each while cluster III and VI are monogenotypic in nature. The characters grain yield plant⁻¹, number of grains panicle⁻¹ and plant height contributed maximum towards genetic divergence among the genotypes. Cluster III recorded highest mean value for grain yield plant⁻¹ and lowest mean value for days to first flower. Highest inter cluster distance was recorded between cluster III and VI.

Kumar *et al.* (2015) studied genetic divergence among 40 genotypes of rice for 12 quantitative characters and grouped them into eight clusters by using D^2 statistics. Cluster I was very large comprising 24 genotypes followed by cluster II with 10 genotypes, while clusters III to VIII were solitary clusters. The maximum inter cluster distance was observed between cluster VI and VII followed by those between cluster VII and VIII which served as potential source to select parents for hybridization. Cluster VIII recorded high grain yield plant⁻¹ showing its potential for yield improvement.

Bharathi *et al.* (2016) studied genetic divergence among 32 rice genotypes using D^2 statistics for 10 characters and grouped into nine clusters containing 1 to 12 genotypes. The random distribution of genotypes indicated the absence of parallelism between geographical diversity and genetic diversity. Filled grains panicle⁻¹ followed by ear bearing tillers panicle⁻¹ and days to 50% flowering contributed maximum for the divergence. The inter cluster distance was maximum between clusters V and IX and between clusters V and VII.

Chandramohan *et al.* (2016) studied genetic divergence among 44 genotypes of rice using D^2 statistics and grouped them into 11 clusters. On the basis of inter cluster distance, genotypes from clusters IV and V followed by V and IX could be used as parents for future hybridization programme. Cluster mean analysis revealed that the genotypes, JGL 21820 and JGL 21849 could be used in breeding programme for obtaining high yielding super fine grain segregants. Days to 50% flowering and 1000 grain weight contributed maximum towards total divergence, thus, these traits could be given due importance for further crop improvement.

Ashok *et al.* (2017) conducted experiment with 64 rice genotypes to study genetic divergence using Mahalanobis D^2 statistics and grouped into nine clusters. Maximum number of genotypes were in cluster I (30). Cluster III was the second largest with 11 genotypes followed by cluster II and V each with nine genotypes. Cluster IV, VI, VII, VIII and IX possessed one genotype each. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. Characters viz., head rice recovery, test weight, volume expansion ratio, milling percentage, number of total grains panicle⁻¹, and protein percent together contributed 80% towards total divergence indicating that these characters should be taken into consideration while selecting parents for hybridization.

Nandini *et al.* (2017) evaluated 324 traditional rice varieties (TRVs) for grain yield and its attributes in two seasons for genetic divergence studies. The pattern of genetic diversity was estimated using model based K means clustering approach statistics. Four distinct clusters were formed. The quantitative trait means and variances differed significantly among the clusters. Cluster I comprised of the maximum number of TRVs (137) and cluster IV consisted of 21 TRVs. The cluster II contributed maximum mean values for many traits.

Sowmiya and Venkatesan (2017b) conducted an experiment to explore the extent of divergence in 48 rice genotypes for nine characters. Using D^2 analysis, the 48 genotypes were grouped into nine clusters. The clustering pattern indicated that there was no parallelism between genetic diversity and geographical origin as the genotypes from different origins were included in same clusters and *vice versa*. The maximum intra cluster distance was registered in cluster VIII. The maximum inter cluster distance was found between Cluster VI and Cluster VIII followed by Cluster VIII and IX. Grain yield plant⁻¹ and 1000 grain weight were the major contributors towards the total genetic divergence among the genotypes studied.

Chapter – III

Material and Methods

Chapter III

MATERIAL AND METHODS

The present investigation on “Genetic divergence in rice (*Oryza sativa* L.) hybrids” was carried out during *kharif*, 2017 in the Southern block of Agricultural College Farm, Bapatla, Andhra Pradesh. The site of experiment is situated at 15° 54' North and 80° 3' East longitude at an altitude of 5.49 m above mean sea level.

3.1 MATERIAL

The experimental material consisted of twenty rice genotypes (15 Hybrids + 5 Checks) obtained from Indian Institute of Rice Research (IIRR), Rajendranagar, Hyderabad, Telangana.

The list of genotypes used in the genetic diversity study is given in Table 3.1. As all were private sector hybrids, their parentage is not revealed.

3.2 METHODS

3.2.1 Nursery

All the genotypes were sown separately in the nursery beds. Thirty days old seedlings were transplanted in the main field.

3.2.2 Experimental design in main field

The main field was laid out in randomized block design with three replications. One month old seedlings were transplanted in thoroughly puddled main field. Each experimental unit consisted of 10 m² and the spacing adopted was 15 cm between rows and 15 cm between plants.

The layout of the experiment is given in the Fig 3.1.

The fertilizers were applied at the rate of 32 kg N, 16 kg P₂O₅, and 16 kg K₂O per acre. Half of the dose of nitrogen, entire dose of P₂O₅ and ¾ th dose of K₂O were applied as basal dose. The remaining nitrogen was applied in two equal split doses one at 30 days after planting and another at panicle initiation stage (PI) along with remaining ¼ th dose of K₂O. The intercultural operations were done at regular intervals and necessary plant protection measures were adopted during the growth of crop.

The detailed experimental technique for the present investigation is furnished in Table 3.2.

Table 3.1. List of genotypes used in the present study

S.No.	Name	Nominating Agency
1	RRX-135	Rasi Seeds, Hyderabad
2	NS-6816	Namdhari Seeds, Bangalore
3	NPH-2899	Nuziveedu Seeds, Hyderabad
4	NK-23831	Syngenta, Hyderabad
5	HRI-195	Bayer Bioscience, Hyderabad
6	S-8001	Syngenta, Hyderabad
7	Indam-200-043	Indo-American Seeds, Hyderabad
8	PHI-17108	Pioneer Overseas, Hyderabad
9	US-308	Seed Works, Hyderabad
10	MEPH-143	Mahyco, Hyderabad
11	CRHR-115	NRRI, Cuttack
12	CRHR-119	NRRI, Cuttack
13	CRHR-116	NRRI, Cuttack
14	RTNRH-11	Ratnagiri
15	CRHR-118	NRRI, Cuttack
16	JKRH-3333 (NCH-1)	National Check Hybrid-1
17	27P63 (NCH-2)	National Check Hybrid-2
18	WGL-14(NCV-1)	National Check Variety-1
19	BPT-5204 (NCV-2)	National Check Variety-2
20	ADT-49 (ZCV)	Zonal Check Variety-1

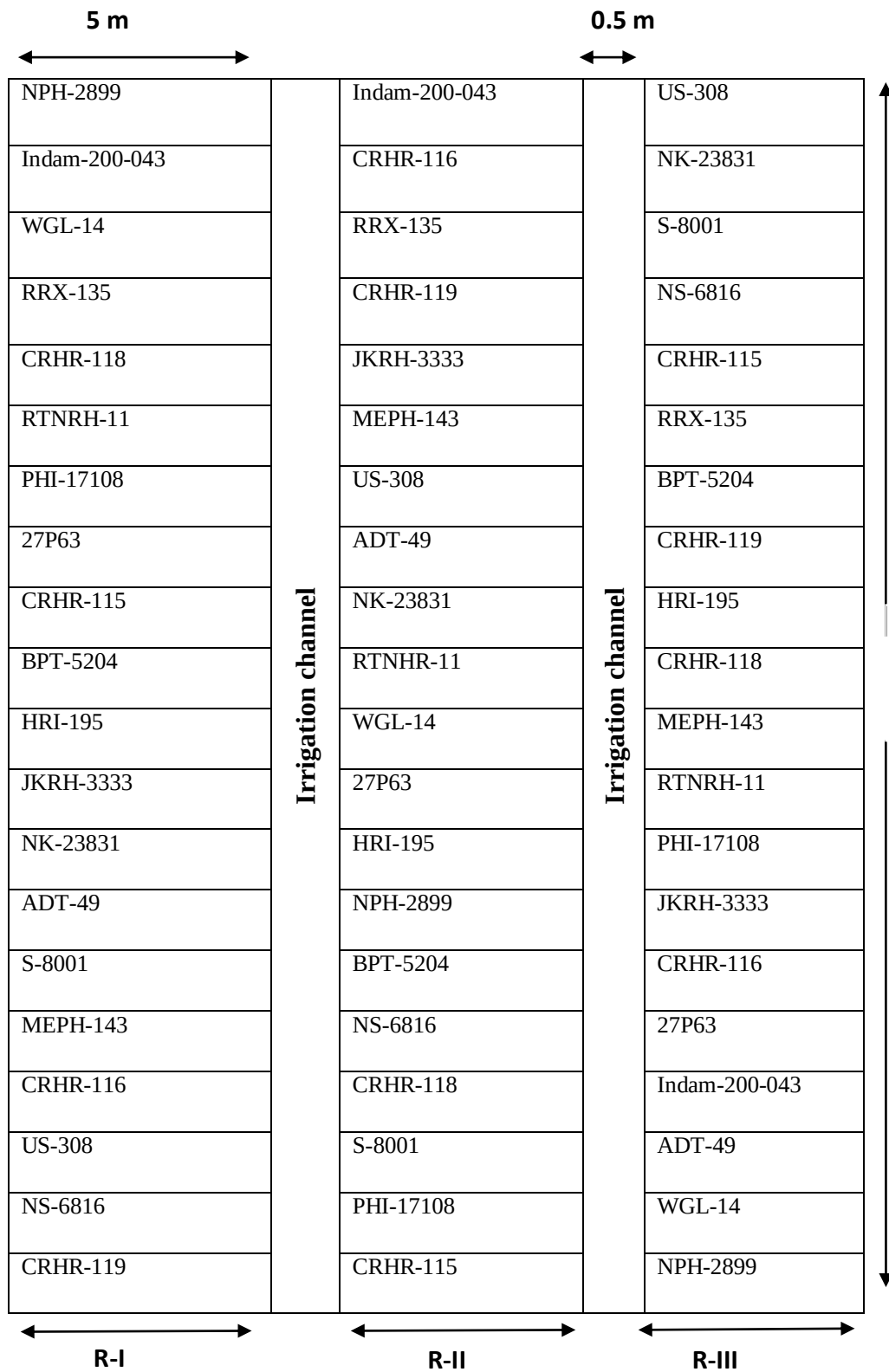


Fig. 3.1. Layout plan of Experimental design.

Table 3.2. Experimental details of evaluation of rice (*Oryza sativa* L.) genotypes

Location	Agricultural College Farm, Bapatla, Andhra Pradesh
Season	<i>Kharif</i> , 2017
Entries	20
Design	Randomised Block Design (RBD)
Replications	Three
Net plot area	15 x 40 = 600 m ²
Gross plot area	17 x 48.6 = 826.2 m ²
Spacing	15 x 15 cm
Row length	5 m
No. of rows	Thirteen
Individual plot size	10 m ²
Fertilizers	32 kg N, 16 kg P ₂ O ₅ , and 16 kg K ₂ O per acre

3.2.3 Data recorded

Single plant observations were recorded on five plants selected at random per genotype per replication and their means were used for statistical analysis. However, observations on days to 50% flowering, days to maturity were recorded on plot basis and all grain quality parameters were done as per DRR laboratory manual on rice grain quality procedures.

The detailed method of recording of observations is given below character wise.

3.2.3.1 Yield component characters

3.2.3.1.1 Days to 50% flowering

The number of days taken from the day of sowing to opening of glumes in panicles in 50% of the plants in a plot was taken as days to 50% flowering.

3.2.3.1.2 Days to maturity

The number of days taken from the day of sowing to complete maturity of grains in the plants in a plot was taken as days to maturity.

3.2.3.1.3 Plant height (cm)

The plant height was measured in centimeters from ground level to the tip of the panicle of the mother tiller excluding awns at the time of harvest.

3.2.3.1.4 Number of productive tillers per plant

Total number of ear bearing tillers in each plant was counted at maturity.

3.2.3.1.5 Panicle length (cm)

Length of panicle was measured from the neck of panicle to the top most spikelet excluding awns.

3.2.3.1.6 Number of total grains per panicle

Number of total grains per each panicle was counted in randomly chosen panicles.

3.2.3.1.7 Grain yield per plant (g)

After thorough cleaning and sun drying to 12% moisture level, grain yield per plant was weighed.

3.2.3.2 Grain quality parameters

3.2.3.2.1 Hulling percentage

200 g of grains after sufficient drying to moisture content of 13-15% were put in the paddy sheller and weight of the hulled rice was taken and the hulling percentage was calculated by using the following formula:

$$\text{Hulling percentage} = \frac{\text{Weight of the dehusked kernel (g)}}{\text{Weight of paddy (g)}} \times 100$$

3.2.3.2.2 Milling percentage

The hulled brown rice was put in a miller / standard polisher and subjected to milling for 90 seconds i.e., 5% of milling (Chauhan *et al.*, 1994) and weight of the polished kernels/white rice was recorded. The milling per cent was calculated by using the formula:

$$\text{Milling percentage} = \frac{\text{Weight of the polished kernel (g)}}{\text{Weight of the paddy (g)}} \times 100$$

3.2.3.2.3 Head rice recovery percentage

Full grains and $\frac{3}{4}$ size grains are considered as head rice. The percentage of the head rice recovery is calculated as per the following formula:

$$\text{Head rice recovery} = \frac{\text{Weight of head rice (g)}}{\text{Weight of paddy (g)}} \times 100$$

3.2.3.2.4 L/B ratio

The length and breadth of the ten kernels from each sample were measured with dial micro meter and the ratio was estimated by using the following formula.

$$\text{L/B ratio} = \frac{\text{Mean of the kernel length (mm)}}{\text{Mean of the kernel breadth (mm)}}$$

Based on the ratio, the following categories were made for grain shape. (Jennings *et al.*, 1979)

Shape	L/B ratio
Slender	>3.0
Medium	2.1-3.0
Bold	1.1-2.0
Round	<1.1

3.2.3.2.5 Water uptake

Two grams of the milled rice was soaked for thirty minutes in a test tube by putting 10 ml of water. Then it was boiled for 45 minutes at 77°C – 80°C in a constant temperature water bath. Two test tubes were kept with 10 ml of water as a control along with the samples in the water bath. Immediately the tubes were placed in a beaker containing cold water for cooling. The supernatant water in the test tube was poured into graduated cylinder after cooling and the volume is measured. (Directorate of Rice Research, 2006).

$$\text{Water uptake} = \frac{100}{2} \times \text{Actual water absorbed}$$

3.2.3.2.6 Kernel elongation ratio

The length of the ten rice grains of each sample was measured before and after cooking and elongation ratio was calculated by using the following formula.

$$\text{Kernel elongation ratio} = \frac{\text{Mean Kernel length after cooking (mm)}}{\text{Mean Kernel length before cooking (mm)}}$$

3.2.3.2.7 Volume Expansion Ratio

Five grams of rice sample was soaked in 15 ml of water for 5 minutes in 50 ml graduated centrifuge tube. The volume of water was recorded after adding rice samples (Y-15). Rice cooked for 20 minutes in water bath was dipped in 100 ml measuring cylinder (X) containing 50 ml water. The volume raised was recorded (X - 50) and was computed by using formula:

Volume expansion ratio was determined as per the formula suggested by Verghese (1950).

$$\text{Volume Expansion} = \frac{\text{Increase in volume after cooking (X-50)}}{\text{Increase in volume before cooking (Y-50)}}$$

3.2.3.2.8 Amylose content (%)

Simplified procedure of Juliano (1971) was used for the estimation of amylose content.

Whole grain milled rice samples were ground separately to pass through a 100 mesh sieve. 100 mg of each sample was weighed accurately in to 50 ml tubes to which 1 ml of 95 % ethanol and 9 ml of 1 N NaOH were added. The contents of the tubes were heated on an electric heater for 10 minutes to gelatinize the starch and then cooled and transferred to a 100 ml volumetric flask, with several distilled water washings. The volume was made up to 100 ml and the contents were shaken vigorously. 5 ml of aliquot was pipetted in to a 100 ml volumetric flask to which 1 ml of 1 N acetic acid iodine solution containing 0.2 g of iodine and 20 g of KI in 100 ml of aqueous solution was added. Volume was again made up to 100 ml adding distilled water. The flask was thoroughly shaken and left for 20 minutes in dark for colour development. Absorbance of solutions at 620 nm was measured with spectrophotometer.

Amylose content was determined by reference to a standard curve and expressed on dry weight basis. For preparing the standard curve, 40 mg of potato amylose (sigma) was taken and wet with 1 ml ethyl alcohol and 9 ml 1 N NaOH, heated for 10 minutes in beakers containing water on an electric heater. Then the content was cooled and volume was made up to 100 ml with several distilled water washings. From this solution 1, 2, 3, 4 and 5 ml portion were placed with a pipette in 100 ml volumetric flask and then these are acidified with 1 N acetic acid (0.2, 0.4, 0.6, 0.8 and 1.0 ml of acetic acid to 1, 2, 3, 4 and 5 ml amylose solutions respectively) and then 2 ml of iodine solution was added. After 20 minutes, absorbance values at 620 nm were recorded on spectrophotometer and were plotted against the concentrations of anhydrous amylose (mg) to determine the conversion factor. The dilution factor of 20 for the sample was included in the conversion factor.

After estimating the amylose content, the samples were classified as low (amylose content 8 - 19%), intermediate (amylose content 20 - 25%) and high (amylose content- above 25%).

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 Block Design

Source of variation	d.f.	SS	MSS	Expected MSS	'F' calculated
Replications	(r-1)	RSS	r	$\sigma^2 e + t \sigma^2 r$	M_r/M_e
Treatments	(t-1)	TrSS	t	$\sigma^2 e + r \sigma^2 g$	M_t/M_e
Error	(r-1) (t-1)	ESS	e	$\sigma^2 e$	
Total	(rt-1)	TSS			

Where,

r	=	Number of replications
g	=	Number of genotypes
M_r	=	Mean sum of square of replication
M_t	=	Mean sum of square of treatment
M_e	=	Mean sum of square of error

$$\begin{aligned}\sigma_e^2 &= \text{Environmental variance} \\ \sigma_r^2 &= \text{Variance due to replications} \\ \sigma_g^2 &= \text{Variance due to genotypes}\end{aligned}$$

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

3.2.4.2.1 Phenotypic and genotypic variance

This was estimated according to the method given by Lush (1940).

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

$$\text{Phenotypic variance } (\sigma_p^2) = \sigma_g^2 + M_e = \frac{M_t - M_e}{r} + M_e$$

3.2.4.2.2 Coefficient of Variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

$$\text{Phenotypic standard deviation } (\sigma_p) = \sqrt{\sigma_p^2} = \sqrt{\sigma_g^2 + \sigma_e^2}$$

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

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

As suggested by Subramanian and Menon (1973), GCV and PCV were categorized into

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

3.2.4.2.3 Heritability in broad sense [h^2 (b)]

Heritability in broad sense was estimated as per Allard (1960).

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

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

Low	0 – 30 %
Moderate	31-60 %
High	61 % and above

3.2.4.2.4 Genetic advance as per cent of mean (GAM)

Genetic advance was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

$$\text{Genetic Advance (GA)} = K \times \sigma_p \times h^2 (b)$$

Where,

K = Selection differential at 5% selection intensity which accounts to a constant value of 2.06.

h^2 (b) = heritability in broad sense.

σ_p = phenotypic standard deviation.

$$GAM = \frac{GA}{\text{Grand mean } (\bar{X})} \times 100$$

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

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

3.2.4.2.5 Correlations

Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

Phenotypic coefficient of correlation (r_p)

$$r(x_i, x_j)_p = \frac{Cov(x_i, x_j)_p}{\sqrt{V(x_i)_p \cdot V(x_j)_p}}$$

Where,

$r(x_i, x_j)_p$ = Phenotypic correlation between i^{th} and j^{th} character

$Cov(x_i, x_j)_p$ = Phenotypic covariance between i^{th} and j^{th} character

$V(x_i)_p$ = Phenotypic variance of i^{th} character

$V(x_j)_p$ = Phenotypic variance of j^{th} character

Genotypic coefficient of correlation (r_g)

$$r(x_i, x_j)_g = \frac{Cov(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(x_i, x_j)_g$ = Genotypic correlation between i^{th} and j^{th} character

$Cov(x_i, x_j)_g$ = Genotypic covariance between i^{th} and j^{th} character

$V(x_i)_g$ = Genotypic variance of i^{th} character

$V(x_j)_g$ = Genotypic variance of j^{th} character

Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where 'n' denotes the number of paired observations used in the calculation.

3.2.4.2.6 Path Coefficient Analysis

Path coefficient analysis suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contribution of various traits to yield.

For estimation of various direct and indirect effects, a set of simultaneous equations were formed:

$$\begin{aligned} r_{1y} &= P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1k} P_{ky} \\ r_{2y} &= r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2k} P_{ky} \\ r_{iy} &= r_{i1} P_{1y} + r_{i2} P_{2y} + r_{i3} P_{3y} + \dots + r_{ik} P_{ky} \\ r_{ky} &= r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \dots + r_{kk} P_{ky} \end{aligned}$$

Where,

r_{1y} to r_{ky} = Coefficient of correlations between causal factors 1 to k and dependent character y.

r_{12} to $r_{k-1,k}$ = Coefficient of correlations among causal factors.

P_{1y} to P_{ky} = Direct effects of characters 1 to k on character y

The above equations were written in a matrix form as under:

$$\begin{matrix} & \text{A} & & \text{C} & & \text{B} \\ \begin{pmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ r_{iy} \end{pmatrix} & = & \begin{pmatrix} 1 & r_{12} & r_{i1} \\ r_{21} & 1 & r_{i2} \\ \vdots & \vdots & \vdots \\ r_{i1} & r_{i2} & i \end{pmatrix} & \begin{pmatrix} p_{1y} \\ p_{2y} \\ \vdots \\ p_{iy} \end{pmatrix} \end{matrix}$$

Then $B = [C]^{-1} A$

$$\text{Where, } [C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & \cdot & \cdot & C_{1i} \\ C_{21} & C_{22} & C_{23} & \cdot & \cdot & C_{2i} \\ C_{i1} & C_{i2} & C_{i3} & \cdot & \cdot & C_{ii} \end{bmatrix}$$

The direct effects were calculated as follows

$$\begin{aligned} P_{1Y} &= \sum_{i=1}^k C_{1i} r_{iY} \\ P_{2Y} &= \sum_{i=1}^k C_{2i} r_{iY} \\ P_{iy} &= \sum_{i=1}^k C_{ii} r_{iy} \end{aligned}$$

Residual effect

The residual effect was estimated with the help of direct effects and simple correlation coefficients using following formula.

$$I = P^2 R_y + \sum P_{iy} r_{iy}$$

Where, $P^2 R_y$ is the square of the residual effect.

3.2.4.2.7 Genetic Divergence

Mahalanobis' D^2 analysis

The data collected on different characters was analyzed using Mahalanobis' D^2 analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1928).

3.2.4.2.7.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and 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 and covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship:

$$\Lambda = \frac{(E)}{(E+V)} = \frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}$$

Where,

$$\begin{aligned} \hat{\Lambda} &= \text{Wilk's criterion} \\ (E) &= \text{Determinant of error matrix and} \\ (E+V) &= \text{Determinant of error + variety sum of squares and sum of product} \\ &\quad \text{matrix.} \\ V(\text{Stat}) &= -m \log_e \hat{\Lambda} = -[n-(p+q+1)/2] \log_e \hat{\Lambda} \end{aligned}$$

Where,

$$\begin{aligned} m &= n-(P+Q+1)/2 \\ n &= \text{Degrees of freedom for error + varieties} \\ \log_e \hat{\Lambda} &= 2.3026 \log_{10} \hat{\Lambda} \\ P &= \text{Number of variables or characters (15)} \\ Q &= \text{Number of variables} - 1(\text{or d.f.}) / (\text{or}) \text{ populations} \end{aligned}$$

V (Stat) is distributed as χ^2 with PQ (15 x 19 = 285) degrees of freedom.

3.2.4.2.7.2 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. $\sum d^2$. 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.

3.2.4.2.7.3 Computation of D^2 values

For the given combination of i and j genotype, the mean deviation i.e., $Y_i^t - Y_j^t$ for $t = 1, 2, \dots, p$ variables are computed and the D^2 values were calculated as

$$D_{ij}^2 = \sum_{t=1}^p (Y_i^t - Y_j^t)^2$$

Where,

Y_i^t is uncorrelated mean value of i^{th} genotype for 't' characters

Y_j^t is uncorrelated mean value of j^{th} genotype for 't' characters

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

The various steps involved in estimation of D^2 values are given below.

3.2.4.2.7.4 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. In the present study P is 15.

3.2.4.2.7.5 Contribution of individual characters towards divergence

In all combinations, each character was ranked on the basis of its contribution towards divergence between two entries ($d_i = Y_i^t - Y_j^t$). Rank 1 is given to the highest mean difference and the rank P to the lowest difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

$$\text{Percentage contribution of the character} = X = \frac{N \times 100}{M}$$

Where,

N= Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

3.2.4.2.7.6 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). 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 (1977). 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.

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.

Average inter- cluster distance

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the members of the other clusters divided by the product of number of genotypes in both the clusters under consideration.

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

Where,

n_1 and n_2 are number of genotypes of two clusters.

D^2 = Difference in mean value between two populations when all the characters are considered simultaneously.

Chapter – IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

The data collected on 20 rice genotypes for characters pertaining to yield, yield contributing traits and quality traits was statistically analysed. The results obtained from the statistical analysis of the data for 15 characters viz., days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of total grains per panicle, grain yield per plant (g), hulling percentage, milling percentage, head rice recovery percentage, volume expansion ratio, water uptake, L/B ratio, kernel elongation ratio and amylose content (%) are presented and under the following heads.

4.1 Mean, variability, heritability and genetic advance as per cent of mean

4.2 Correlation

4.3 Path coefficient analysis

4.4 Genetic divergence

ANALYSIS OF VARIANCE

The analysis of variance revealed significant differences among the genotypes for all the 15 characters studied, indicating the sufficient variability in the material (Table 4.1).

4.1 MEAN, VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PERCENT OF MEAN

The mean performance of genotypes is presented in Table 4.2. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2 broad sense) and genetic advance as percent of mean (GAM) are presented in Table 4.3 and described character wise here under.

Table 4.1. Analysis of variance for yield and yield components among 20 genotypes of rice (*Oryza sativa* L.)

S. No	Source	Replications	Treatments	Error
	Degree of freedom	2	19	38
	MEAN SUM OF SQUARES			
1	Days to 50% flowering	2.5167	90.5649**	1.3939
2	Days to maturity	0.4500	82.2280**	1.6781
3	Plant height (cm)	2.6047	411.9068**	7.8124
4	Number of productive tillers per plant	1.2167	18.8236**	2.3395
5	Panicle length (cm)	0.1499	7.0572**	0.6626
6	Number of total grains/ Panicle	206.8167	9886.7675**	292.6412
7	Grain Yield/ Plant (g)	0.4167	317.0131**	10.1711
8	Hulling %	4.5167	28.3122**	3.9728
9	Milling %	10.5167	27.0973**	5.2711
10	Head Rice Recovery %	9.2167	110.2315**	8.2868
11	Volume Expansion Ratio	0.0072	0.0419**	0.0123
12	Water Uptake	117.9100	13463.4648**	157.8289
13	L/B Ratio	0.0048	0.1850**	0.0120
14	Kernel Elongation Ratio	0.0026	0.0227**	0.0022
15	Amylose Content (%)	3.4042	4.0552**	1.2982

*significant at 5% level,

**significant at 1% level

4.1.1 Yield component characters

4.1.1.1 Days to 50% flowering

Days to 50% flowering ranged from 84 days (HRI-195) to 105 days (NPH-2899) with an overall mean of 97.43. Low phenotypic (5.73) and genotypic (5.60) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The difference between PCV and GCV was low indicating that influence of environment on this character is low. The results were in accordance with results of Devi *et al.* (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Bhinda *et al.* (2017), Devi *et al.* (2017), Gunasekaran *et al.* (2017), Jan *et al.* (2017), Lakshmi *et al.* (2017), Limbani *et al.* (2017), Nandini *et al.* (2017), Prasad *et al.* (2017) and Mamata *et al.* (2018).

High heritability (96.40) coupled with moderate genetic advance as percent of mean (11.27) was recorded for this trait indicating the presence of both additive and non-additive gene actions and desired results may not be obtained by simple selection. Similar result was also reported by Subbaiah *et al.* (2011), Ovung *et al.* (2012), Dhanwani *et al.* (2013), Dhurai *et al.* (2014), Bhinda *et al.* (2017), Devi *et al.* (2017), Gunasekaran *et al.* (2017), Jan *et al.* (2017), Nandini *et al.* (2017), Prasad *et al.* (2017) and Mamata *et al.* (2018).

4.1.1.2 Days to maturity

Days to maturity ranged from 114 days (HRI-195) to 134 days (NPH-2899) with an overall mean of 126.50. Low phenotypic (4.22) and genotypic (4.10) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The difference between PCV and GCV was low indicating that influence of environment on this character is low. The results are in agreement with results of Akhtar *et al.* (2011), Subbaiah *et al.* (2011), Ovung *et al.* (2012), Dhurai *et al.* (2014), Khare *et al.* (2014), Bhati *et al.* (2015), Gampala *et al.* (2015), Umesh *et al.* (2015), Kumar and Verma (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Bhinda *et al.* (2017), Jan *et al.* (2017), Limbani *et al.* (2017) and Prasad *et al.* (2017).

High heritability (94.50) and low genetic advance as per cent of mean (8.19) were recorded for this trait indicating the role of both additive and non-additive gene actions in governing the inheritance of days to maturity and the trait is unsuitable for improvement through selection. These results were in accordance with results of Sarwar *et al.* (2015), Sameera *et al.* (2016), Tejaswini *et al.* (2016) and Limbani *et al.* (2017).

Table 4.2. Mean performance among 20 genotypes of rice (*Oryza sativa* L.) for 15 characters.

S. No.	Character		Days to 50% flowering	Days to maturity	Plant height (cm)	No. of productive tillers/ Plant	Panicle length (cm)	No. of total grains/ Panicle	Hulling %	Milling %	HRR%	Volume expansion ratio	Water uptake	L/B ratio	Kernel elongation ratio	Amylose content (%)	Yield per plant (g)
1	RRX-135		102	130	114	15.33	23.36	244.66	87.33	77.00	73.66	3.70	103.33	2.53	1.87	24.60	28.66
2	NS-6816		89	118	146.20	21.66	23.63	419.33	86.00	75.00	51.33	4.00	118.33	2.32	1.70	22.16	52.33
3	NPH-2899		105	134	127.73	21.33	23.11	410.33	89.33	81.33	70.00	3.62	126.66	2.60	1.66	23.66	61.66
4	NK-23831		101	130	131.86	19.33	21.86	357.00	88.00	75.66	69.00	3.56	85.00	2.72	1.67	23.50	44.33
5	HRI-195		84	114	124.00	19.00	23.86	334.00	81.00	71.33	61.33	3.52	255.00	2.97	1.68	24.53	41.00
6	S-8001		94	124	122.80	22.00	22.03	428.00	83.33	71.66	61.66	3.74	275.00	2.72	1.85	21.73	63.66
7	Indam-200-043		104	132	110.40	15.66	21.03	286.66	81.33	70.00	56.66	3.75	255.00	2.83	1.68	24.66	45.33
8	PHI-17108		97	124	141.33	14.33	21.68	362.00	90.33	76.00	67.33	3.68	261.66	2.88	1.90	22.73	52.33
9	US-308		95	124	132.46	20.66	22.06	307.00	81.33	73.33	61.33	3.57	90.00	2.54	1.90	23.50	56.00
10	MEPH-143		95	125	141.20	18.66	24.46	308.33	85.33	73.00	57.66	3.57	113.33	3.15	1.80	24.26	41.66
11	CRHR-115		101	130	137.26	18.66	24.00	278.00	84.66	74.33	62.00	3.64	116.66	3.12	1.78	23.40	43.66
12	CRHR-119		99	129	135.66	17.00	22.22	384.00	80.66	71.33	54.00	3.55	215.00	2.84	1.88	24.03	60.66
13	CRHR-116		100	129	129.73	12.66	24.26	268.00	80.33	69.66	53.00	3.50	161.66	2.70	1.68	23.43	53.33
14	RTNRH-11		91	121	137.86	17.00	23.43	297.66	80.66	70.00	56.33	3.58	223.33	3.06	1.66	21.63	29.66
15	CRHR-118		102	130	122.13	16.66	26.25	364.66	82.00	71.66	59.66	3.64	115.00	3.24	1.81	24.30	51.33
16	JKRH-3333 (NCH-1)		102	132	132.80	20.00	25.56	345.33	82.66	74.00	62.00	3.62	216.66	3.01	1.66	20.23	42.33
17	27P63 (NCH-2)		96	126	133.80	18.66	25.00	282.00	81.66	70.66	54.00	3.62	93.33	3.15	1.81	23.40	46.33
18	WGL-14(NCV-1)		96	125	123.13	16.66	26.11	327.66	82.33	70.00	59.33	3.65	100.00	3.07	1.75	22.80	46.33
19	BPT-5204 (NCV-2)		97	127	133.26	20.00	25.36	307.00	82.00	71.66	61.00	3.86	133.33	3.07	1.80	22.03	38.66
20	ADT-49 (ZCV)		89	119	96.66	18.33	22.76	220.00	82.33	70.00	54.00	3.64	115.00	2.90	1.80	23.10	29.00
	Mean		97.43	126.50	128.74	18.18	23.60	326.58	83.63	72.88	60.26	3.65	158.66	2.87	1.77	23.18	46.41
	C.V.		1.21	1.02	2.17	8.41	3.44	5.23	2.38	3.15	4.77	3.03	7.91	3.80	2.66	4.91	6.87
	C.D. 5%		1.95	2.14	4.62	2.52	1.34	28.27	3.29	3.79	4.75	0.18	20.76	0.18	0.07	1.88	5.27
	C.D. 1%		2.61	2.86	6.18	3.38	1.80	37.87	4.41	5.08	6.37	0.24	27.81	0.24	0.10	2.52	7.06
	Range	Lowest	84.00	114.00	96.66	12.66	21.03	220.00	80.33	69.66	51.33	3.50	85.00	2.32	1.66	20.23	28.66
		Highest	105.00	134.00	146.20	22.00	26.25	428.00	90.33	81.33	73.66	4.00	275.00	3.24	1.90	24.66	63.66

C.V % = Coefficient of Variation percent

C.D. = Critical Difference

Note: Bold figures are maximum and minimum mean values for each character.

Table 4.3. Mean, variability, heritability and genetic advance as per cent of mean for yield, yield components and grain quality parameters in rice (*Oryza sativa* L.)

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as percent of mean (5% level)
			Maximum	Minimum	PCV %	GCV %		
1	Days to 50% Flowering	97.43	105.00	84.00	5.73	5.60	96.40	11.27
2	Days to Maturity	126.50	134.00	114.00	4.22	4.10	94.50	8.19
3	Plant Height (cm)	128.74	146.20	96.66	9.27	9.01	95.10	18.05
4	Number of productive tillers/ Plant	18.18	22.00	12.66	15.39	12.89	70.80	22.24
5	Panicle Length (cm)	23.60	26.25	21.03	7.08	6.18	76.20	11.13
6	Number of total grains/ Panicle	326.58	428.00	220.00	18.09	17.32	92.10	34.14
7	Hulling %	83.63	90.33	80.33	4.16	3.41	67.50	5.75
8	Milling %	72.88	81.33	69.66	4.86	3.70	58.30	5.81
9	Head Rice Recovery (%)	60.26	73.66	51.33	10.79	9.67	80.70	17.87
10	Volume Expansion Ratio	3.65	4.00	3.50	4.08	2.72	45.30	3.75
11	Water Uptake	158.66	275.00	85.00	42.71	41.97	97.70	84.97
12	L/B Ratio	2.87	3.24	2.32	9.18	8.36	83.90	15.66
13	Kernel Elongation Ratio	1.77	1.90	1.66	5.38	4.67	75.90	8.37
14	Amylose Content (%)	23.18	24.66	20.23	6.42	4.13	41.30	5.48
15	Yield per plant (g)	46.41	63.66	28.66	22.85	21.79	91.40	42.81

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

4.1.1.3 Plant height (cm)

Plant height exhibited a wide range of variation from 96.66 cm (ADT-49) to 146.2 cm (NS-6816) with an overall mean of 128.74 cm. Low phenotypic (9.27) and genotypic (9.01) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. Similar results are also recorded by Akhtar *et al.* (2011), Subbaiah *et al.* (2011), Sarwar *et al.* (2015), Chandramohan *et al.* (2016), Kumar and verma (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Jan *et al.* (2017) and Nandini *et al.* (2017).

High heritability (95.10) coupled with moderate genetic advance as percent of mean (18.05) was recorded for this trait indicating the presence of both additive and non-additive gene actions in the hybrids for this trait. Similar result was also reported by Subbaiah *et al.* (2011), Kumar and verma (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Jan *et al.* (2017) and Nandini *et al.* (2017).

4.1.1.4 Number of productive tillers per plant

The trait, number of productive tillers per plant showed variation ranging from 12.66 (CRHR-116) to 22 (S-8001) with mean of 18.18. Moderate phenotypic (15.39) and genotypic (12.89) coefficients of variation were observed for this trait. The more difference between GCV and PCV indicated the effect of environment on the expression of this trait. Similar results are also obtained by Nandan *et al.* (2010), Tiwari *et al.* (2011), Dhanwani *et al.* (2013), Dhurai *et al.* (2014), Gokulakrishnan *et al.* (2014), Ramanjaneyulu *et al.* (2014), Kumar and Verma (2016), Jan *et al.* (2017) and Nandini *et al.* (2017).

High heritability (70.80) coupled with high genetic advance as percent of mean (22.24) was recorded for this trait indicating the operation of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Nandan *et al.* (2010), Tiwari *et al.* (2011), Krishnaveni *et al.* (2013), Dhurai *et al.* (2014), Ekka *et al.* (2015), Sarwar *et al.* (2015), Umesh *et al.* (2015), Devi *et al.* (2016), Sameera *et al.* (2016), Ajmera *et al.* (2017), Devi *et al.* (2017), Gunasekaran *et al.* (2017), Limbani *et al.* (2017), Nandini *et al.* (2017), Prasad *et al.* (2017) and Mamata *et al.* (2018).

4.1.1.5 Panicle length (cm)

Panicle length among all the genotypes varied from 21.03 cm (Indam-200-043) to 26.25 cm (CRHR-118) with an overall mean of 23.60 cm for this trait. Low phenotypic (7.08) and genotypic (6.18) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The more difference between GCV and PCV indicated the effect of environment on the expression of this trait. The results were in accordance with reports of Yadav *et al.* (2010), Subbaiah *et al.* (2011), Krishnaveni *et al.* (2013), Gokulakrishnan *et al.* (2014), Lingaiah *et al.* (2014), Rao *et al.* (2014), Sarwar *et al.* (2015), Tiwari (2015), Umesh *et al.* (2015), Bhatt *et al.* (2016), Chandramohan *et al.* (2016), Kumar and Verma (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Gunasekaran *et al.* (2017) and Prasad *et al.* (2017).

High heritability (76.20) coupled with moderate genetic advance as percent of mean (11.13) was recorded for this trait indicating the presence of both additive and non-additive gene actions and desired results may not be obtained by simple selection. Similar result was also reported by Rao *et al.* (2014), Ekka *et al.* (2015), Chandramohan *et al.* (2016), Devi *et al.* (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Devi *et al.* (2017) and Mamata *et al.* (2018).

4.1.1.6 Number of grains per panicle

This trait recorded a wide range of variation from 220.00 (ADT-49) to 428.00 (S-8001) with a mean value of 326.58. Moderate phenotypic (18.09) and genotypic (17.32) coefficients of variation were observed for this trait. The results were in accordance with results of Gokulakrishnan *et al.* (2014).

High heritability (92.10) coupled with high genetic advance as percent of mean (34.14) was recorded for this trait indicating the operation of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Nandan *et al.* (2010), Dhurai *et al.* (2014), Gokulakrishnan *et al.* (2014), Lingaiah *et al.* (2014), Bhatt *et al.* (2016), Chandramohan *et al.* (2016), Sameera *et al.* (2016) and Ajmera *et al.* (2017).

4.1.1.7 Grain yield per plant (g)

Grain yield per plant exhibited variation from 28.66 g (RRX-135) to 63.66 g (S-8001) and a mean value of 46.41 g was observed for this trait. High phenotypic (22.85) and genotypic (21.79) coefficients of variation were observed for this trait indicating the existence of high variation among the genotypes studied. The results are in

agreement with results of Ovung *et al.* (2012), Dhanwani *et al.* (2013), Dhurai *et al.* (2014), Ekka *et al.* (2015), Sarwar *et al.* (2015), Umesh *et al.* (2015), Bhatt *et al.* (2016), Devi *et al.* (2016), Tejaswini *et al.* (2016), Ajmera *et al.* (2017), Devi *et al.* (2017), Gunasekaran *et al.* (2017), Lakshmi *et al.* (2017), Prasad *et al.* (2017) and Mamata *et al.* (2018).

High heritability (91.40) and high genetic advance as per cent of mean (42.81) were recorded for this trait. This indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for this character. These results are in agreement with results of Nandan *et al.* (2010), Tiwari *et al.* (2011), Dhanwani *et al.* (2013), Dhurai *et al.* (2014), Kumar and Verma (2016), Sameera *et al.* (2016), Tejaswini *et al.* (2016), Ajmera *et al.* (2017), Devi *et al.* (2017), Gunasekaran *et al.* (2017), Jan *et al.* (2017), Lakshmi *et al.* (2017), Prasad *et al.* (2017) and Mamata *et al.* (2018).

4.1.2 Grain quality parameters

4.1.2.1 Hulling percentage

Hulling percentage varied from 80.33 (CRHR-116) to 90.33 (PH-17108) with a mean of 83.63. Low phenotypic (4.16) and genotypic (3.41) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The difference between PCV and GCV was low indicating that influence of environment on this character is low. The results were in accordance with findings of Subbaiah *et al.* (2011), Devi *et al.* (2015), Ekka *et al.* (2015), Chowdhury *et al.* (2016), Devi *et al.* (2016), Devi *et al.* (2017) and Sahu *et al.* (2017).

High heritability (67.50) coupled with low genetic advance as percent of mean (5.75) indicated the involvement of both additive and non additive gene actions for this trait and selection for such traits may not be rewarding. Similar result was also reported by Subbaiah *et al.* (2011), Dhanwani *et al.* (2013), Devi *et al.* (2015) and Chowdhury *et al.* (2016).

4.1.2.2 Milling percentage

Among 20 genotypes studied the values of milling % ranged from 69.66 (CRHR-116) to 81.33 (NPH-2899) with an overall mean of 72.88 was observed. Low phenotypic (4.86) and genotypic (3.70) coefficients of variation were observed for this

trait indicating less variation among the genotypes studied. The difference between GCV and PCV indicated less influence of environment on milling percentage. Similar results were also reported by Subbaiah *et al.* (2011), Dhanwani *et al.* (2013), Devi *et al.* (2015), Ekka *et al.* (2015), Chowdhury *et al.* (2016), Devi *et al.* (2016), Devi *et al.* (2017) and Sahu *et al.* (2017).

Moderate heritability (58.3) coupled with low genetic advance as percent of mean (5.81) was recorded for this trait indicating the presence of both additive and non additive gene action. These results are in agreement with findings of Subbaiah *et al.* (2011).

4.1.2.3 Head rice recovery percentage (HRR %)

Head rice recovery percentage varied from 51.33 (NS-6816) to 73.66 (RRX-135) with an overall mean of 60.26. Moderate phenotypic (10.79) and low genotypic (9.67) coefficients of variation were observed for this trait. The difference between PCV and GCV was low indicating that influence of environment on this character is low. The results were in accordance with results of Subbaiah *et al.* (2011), Krishnaveni *et al.* (2013) and Devi *et al.* (2017).

High heritability (80.70) coupled with moderate genetic advance as percent of mean (17.87) was recorded for this trait indicating the presence of both additive and non-additive gene actions and desired results may not be obtained by simple selection. Similar result was also reported by Dhanwani *et al.* (2013) and Krishnaveni *et al.* (2013).

4.1.2.4 Volume expansion ratio

Volume expansion ratio in the genotypes studied ranged from 3.50 (CRHR-116) to 4.00 (NS-6816) with an overall mean of 3.65. Low phenotypic (4.08) and genotypic (2.72) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The results were in agreement with results of Subbaiah *et al.* (2011), and Devi *et al.* (2015).

Moderate heritability (45.30) coupled with low genetic advance as percent of mean (3.75) was recorded for this trait indicating the presence of both additive and non additive gene action. The results were in agreement with the results of Subbaiah *et al.* (2011).

4.1.2.5 Water uptake

Water uptake exhibited variation ranging from 85.00 (NK-23831) to 275.00 (S-8001) with an overall mean of 158.66 for this trait. High phenotypic (42.71) and genotypic (41.97) coefficients of variation were observed for this trait indicating more variation among the genotypes studied. The results were in accordance with findings of Dhanwani *et al.* (2013) and Devi *et al.* (2015).

High heritability (97.70) and high genetic advance as percent of mean (84.97) were observed for this trait indicating the presence of additive gene action in the inheritance of this trait and direct selection will be highly rewarding. These results are in accordance with results of Nandan *et al.* (2010), Dhanwani *et al.* (2013) and Devi *et al.* (2015).

4.1.2.6 L/B ratio

L/B ratio in the genotypes studied ranged from 2.32 (NS-6816) to 3.24 (CRHR-118) with a mean of 2.87 for this trait. Low phenotypic (9.18) and genotypic (8.36) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The difference between PCV and GCV was low indicating that influence of environment on this character is low. The results were in accordance with results of Nandan *et al.* (2010), Subbaiah *et al.* (2011), Dhurai *et al.* (2014) and Gunasekaran *et al.* (2017).

High heritability (83.90) coupled with moderate genetic advance as percent of mean (15.66) was recorded for this trait indicating the presence of both additive and non-additive gene actions and desired results may not be obtained by direct selection. Similar result was also reported by Dhurai *et al.* (2014), Tejaswini *et al.* (2016) and Sahu *et al.* (2017).

4.1.2.7 Kernel elongation ratio

This trait exhibited variation ranging from 1.66 (NPH-2899, RTNRH-11, JKRH-3333) to 1.90 (PH-17108, US-308) with a mean value of 1.77. Low phenotypic (5.38) and genotypic (4.67) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The difference between GCV and PCV indicated less influence of environment on kernel elongation ratio. Similar results also reported by Nandan *et al.* (2010), Devi *et al.* (2016) and Devi *et al.* (2017).

High heritability (73.90) and low genetic advance as percent of mean (8.37) were observed for this trait indicating the role of both additive and non-additive gene actions in governing the inheritance of this trait and this trait is unsuitable for direct selection. Similar results were also reported by Chowdhury *et al.* (2016).

4.1.2.8 Amylose content (%)

Amylose content showed variation ranging from 20.23 (JKRH-3333) to 24.66 (Indam-200-043) with an overall mean of 23.18. Low phenotypic (6.42) and genotypic (4.13) coefficients of variation were observed for this trait indicating less variation among the genotypes studied. The results were in accordance with results of Subbaiah *et al.* (2011), Krishnaveni *et al.* (2013), Devi *et al.* (2015), Umesh *et al.* (2015) and Limbani *et al.* (2017).

Moderate heritability (41.30) coupled with low genetic advance as per cent of mean (5.48) was recorded for this trait indicating the presence of both additive and non additive gene action. The results are in accordance with findings of Krishnaveni *et al.* (2013).

4.2 CORRELATIONS

Direct selection for yield and quality traits is not effective as they are complex quantitative characters and highly influenced by environment. High genotype and environment interaction will restrict improvement, if selection is based on yield *per se*. The effective improvement in yield may be brought about through selection of yield component characters. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because any particular trait may bring about changes in other associated characters.

Yield component characters show associations among themselves and also with yield. Unfavorable associations between the desired attributes under selection may limit genetic advance. Hence, knowledge of associations between the yield and yield components and also among the yield components is essential for planning a sound selection programme (Falconer, 1964).

In general, the results revealed that the genotypic correlation coefficients were higher than the phenotypic correlation coefficients for almost all the characters under study. This may be due to the relative stability of genotypes as majority of them were

subjected to certain amount of selection (Johnson *et al.*, 1955). The phenotypic and genotypic correlation coefficients for different grain yield components and quality parameters are presented in Tables 4.4 and 4.5 and discussed hereunder.

4.3.1 Yield component characters

4.3.1.1 Days to 50% flowering

Days to 50% flowering showed significant positive correlation with days to maturity (0.9645** and 0.9920**), hulling percentage (0.2588* and 0.2900*), milling percentage (0.3171*, 0.4378**) and head rice recovery percentage (0.3803** and 0.4322**) at both phenotypic and genotypic levels respectively. It also showed significant negative genotypic association with number of productive tillers per plant (-0.2734*).

This trait recorded positive non-significant association at phenotypic (0.2407) and genotypic levels (0.2480) with grain yield per plant. These results were in accordance with the results of Nandan *et al.* (2010), Raju *et al.* (2013), Lakshmi *et al.* (2014), Rao *et al.* (2014) and Bhati *et al.* (2015).

Above results revealed that increase in days to 50% flowering would lead to increase in days to maturity, hulling percentage, milling percentage and head rice recovery percentage as these showed significant positive association with days to 50% flowering at both phenotypic and genotypic levels. This trait showed significant negative association with number of productive tillers per plant at genotypic level which indicated that increase in days to 50% flowering would lead to decrease in number of productive tillers per plant.

4.3.1.2 Days to maturity

Days to maturity exhibited significant positive correlation with days to 50% flowering (0.9645 and 0.9920**) milling percentage (0.2653* and 0.3993**) and head rice recovery (0.3674** and 0.3837**) at both phenotypic and genotypic levels.

This trait showed non-significant positive phenotypic (0.2344) and genotypic (0.2532) association with grain yield per plant. Similar results were also recorded by Nandan *et al.* (2010), Raju *et al.* (2013) and Bhati *et al.* (2015).

Above results indicating that, increase in days to maturity would lead to increase in milling percentage and head rice recovery as these showed significant positive association with days to maturity both phenotypically and genotypically. Increase in days to maturity may lead to increase in grain yield per plant as this trait shows positive non significant association with grain yield per plant at both phenotypic and genotypic levels.

4.3.1.3 Plant height

Plant height showed significant positive phenotypic correlation with number of grains per panicle (0.4212**). Similarly it also showed significant positive genotypic association with number of total grains per panicle (0.4487**), milling percentage (0.2797*) and significant negative genotypic association with amylose content (-0.3831**).

This trait showed significant positive phenotypic (0.2969*) and significant positive genotypic (0.3311**) association with grain yield per plant. The results are in agreement with results of Dhurai *et al.* (2014), Khare *et al.* (2014), Lakshmi *et al.* (2014), Ramanjaneyulu *et al.* (2014), Bhati *et al.* (2015), Ekka *et al.* (2015), Devi *et al.* (2017), Gunasekaran *et al.* (2017), Jan *et al.* (2017) and Priya *et al.* (2017).

These results are indicating that increase in plant height would lead to increase in number of grains per panicle as this trait had significant positive association with number of grains per panicle at both phenotypic and genotypic levels which leads to increase in yield ultimately. Plant height showed positive significant genotypic association with milling percentage which indicates that increase in plant height leads to increase in milling percentage. This trait showed significant negative genotypic association with amylose content, which results in decrease in amylose content with the increase in the plant height. It also would lead to increase in grain yield per plant, as this trait showed significant positive association with grain yield per plant at both phenotypic and genotypic levels.

4.3.1.4 Number of productive tillers per plant

This trait showed significant positive phenotypic association with number of total grains per panicle (0.4154**). Similarly this trait showed significant positive genotypic correlation with milling percentage (0.3609**), and volume expansion ratio (0.4181**). It also showed negative significant genotypic correlation with days to 50% flowering (-0.2734*) and amylose content (-0.4866**).

Table 4.4. Estimates of phenotypic correlation coefficients among yield and yield components in rice (*Oryza sativa* L.)

Character	Days to 50% flowering	Days to maturity	Plant height	Number of productive tillers/ plant	Panicle length	No. of total grains/ panicle	Hulling %	Milling %	Head rice recovery	Volume expansion ratio	Water uptake	L/B ratio	Kernel elongation ratio	Amylose content	Grain yield/plant
Days to 50% flowering	1.0000	0.9645**	-0.0438	-0.2088	-0.0421	0.0143	0.2588*	0.3171*	0.3803**	-0.0466	-0.1480	-0.0225	-0.0439	0.1367	0.2407
Days to maturity		1.0000	-0.0321	-0.1803	0.0516	0.0076	0.1683	0.2653*	0.3674**	-0.1079	-0.1682	0.0679	-0.0588	0.0845	0.2344
Plant height			1.0000	0.1496	0.1264	0.4212**	0.1724	0.2033	-0.0469	0.0282	-0.0102	0.0126	-0.0270	-0.2137	0.2969*
Number of productive tillers/ plant				1.0000	-0.0057	0.4154**	0.0950	0.2437	0.0235	0.2356	-0.1316	-0.1718	-0.1147	-0.2204	0.2104
Panicle length					1.0000	-0.0952	-0.2887*	-0.1949	-0.1415	0.0409	-0.3213*	0.4818**	-0.1371	-0.1799	-0.2194
No. of total grains/ panicle						1.0000	0.2994*	0.3297*	0.0997	0.2130	0.2640*	-0.2622*	-0.0760	-0.2349	0.6814**
Hulling %							1.0000	0.8044**	0.5748**	0.1793	-0.1470	-0.3031	0.0438*	0.0513	0.0989
Milling %								1.0000	0.6114**	0.0814	-0.1729	-0.3891**	-0.0412	0.0859	0.2019
Head rice recovery %									1.0000	-0.0678	-0.0504	-0.1431	0.0680	0.1175	-0.0567
Volume expansion ratio										1.0000	-0.0236	-0.2847*	0.0840	-0.1875	0.0017
Water uptake											1.0000	0.0572	-0.0903	-0.1558	0.1665
L/B ratio												1.0000	0.0027	-0.0608	-0.2771
Kernel elongation ratio													1.0000	0.0962	0.1447
Amylose content														1.0000	0.0126
Grain yield per plant															1.0000

*significant at 5% level, ** significant at 1% level

Table 4.5. Estimates of genotypic correlation coefficients among yield and yield components in rice (*Oryza sativa* L.)

Character	Days to 50% flowering	Days to maturity	Plant height	Number of productive tillers/ plant	Panicle length	No. of total grains/ panicle	Hulling %	Milling %	Head rice recovery%	Volume expansion ratio	Water uptake	L/B ratio	Kernal elongation ratio	Amylose content	Grain yield/ plant
Days to 50% flowering	1.0000	0.9920**	-0.0328	-0.2734*	-0.0066	0.0211	0.2900*	0.4378**	0.4322**	-0.1384	-0.1490	-0.0059	-0.0226	0.1911	0.248
Days to maturity		1.0000	-0.0192	-0.1963	0.0562	0.0245	0.2335	0.3993**	0.3837**	-0.1957	-0.1784	0.0543	-0.0689	0.1721	0.2532
Plant height			1.0000	0.1965	0.1409	0.4487**	0.2422	0.2797*	-0.0870	0.0977	-0.0074	-0.0022	-0.0008	-0.3831**	0.3311**
Productive tillers/ plant				1.0000	-0.0006	0.5285	0.1293	0.3609**	0.0808	0.4181**	-0.1631	-0.2151	-0.0617	-0.4886**	0.2402
Panicle length					1.0000	-0.1146	-0.2647*	-0.2054	-0.1978	-0.0191	-0.4077**	0.5938**	-0.1539	-0.2420	-0.2054
No. of total grains/ panicle						1.0000	0.3260*	0.4181**	0.1244	0.2988*	0.3001*	-0.2761*	-0.0750	-0.2774*	0.7630**
Hulling %							1.0000	0.9141**	0.7660**	0.2661*	-0.1740	-0.3906**	0.0859	0.0411	0.1025
Milling %								1.0000	0.8345**	0.1888	-0.2484	-0.5299**	-0.0009	0.0095	0.2220
Head rice recovery%									1.0000	-0.1053	-0.0732	-0.2171	0.1391	0.1267	-0.0448
Volume expansion ratio										1.0000	-0.0311	-0.3440**	0.0383	-0.4437**	-0.0126
Water uptake											1.0000	0.0490	-0.0994	-0.2831*	0.184
L/B ratio												1.0000	0.0266	-0.0074	-0.3225*
Kernal elongation ratio													1.0000	0.2702*	0.1742
Amylose content														1.0000	0.0221
Grain yield/ plant															1.0000

*significant at 5% level, ** significant at 1% level

This trait showed non-significant positive phenotypic (0.2104) and genotypic (0.2402) association with grain yield per plant. These results are in accordance with the results of Raju *et al.* (2013), Ramanjaneyulu *et al.* (2014), Ekka *et al.* (2015) and Lakshmi *et al.* (2017).

This trait showed significant positive phenotypic association with number of grains per panicle which indicates that increase in number of productive tillers per plant would lead to increase in number of total grains per panicle and results in increase in yield. This trait showed significant positive genotypic association with milling percentage and volume expansion ratio at genotypic level which suggests that increase in number of productive tillers per plant would lead to increase in above characters. This trait showed significant negative genotypic association with amylose content indicating that increase in number of productive tillers per plant would lead to decrease in amylose content.

4.3.1.5 Panicle length

Panicle length showed significant positive association with L/B ratio (0.4818** and 0.5938**) at both phenotypic and genotypic levels respectively. Similarly this trait showed significant negative association with hulling percentage (-0.2887* and -0.2647*) and water uptake (-0.3213* and -0.4077**) at phenotypic and genotypic levels.

This trait showed non-significant negative association with number of total grains per panicle (-0.0952 and -0.1146), grain yield per plant (-0.2194 and -0.2054), milling percentage (-0.1949 and -0.2054), HRR percentage (-0.1415 and -0.1978), kernel elongation ratio (-0.1371 and -0.1539) and amylose content (-0.1799 and -0.2420) at phenotypic and genotypic levels respectively. These results are agreed with the results given by Nandan *et al.* (2010), Lakshmi *et al.* (2014), Naseem *et al.* (2014), Anis *et al.* (2016) and Jan *et al.* (2017).

This trait showed significant positive association with L/B ratio at both phenotypic and genotypic levels indicating that increase in panicle length would lead to increase in L/B ratio. This trait showed significant negative phenotypic and genotypic association with hulling percentage and water uptake indicating that increase in panicle length results in decrease in hulling percentage and water uptake. Panicle length shows

non-significant negative association with number of total grains per panicle and grain yield at both phenotypic and genotypic levels indicates that increase in panicle length leads to decrease in number of total grains per panicle and ultimately the yield per plant.

4.3.1.6 Number of total grains per panicle

This trait showed significant positive phenotypic association with plant height(0.4212**), number of productive tillers per plant (0.4154**), hulling percentage (0.2994*), milling percentage (0.3297*) and water uptake (0.2640*) and significant negative phenotypic association with L/B ratio (-0.2622*). Similarly this trait showed significant positive genotypic association with plant height (0.4487**), hulling percentage (0.3260*), milling percentage (0.4181**), volume expansion ratio (0.2988*) and water uptake (0.3001*). It also showed significant negative genotypic association with L/B ratio (-0.2761*) and amylose content (-0.2774*).

This trait showed significant positive phenotypic (0.6814**) and genotypic (0.7630**) association with grain yield per plant. These results are in accordance with the results of Akhtar *et al.* (2011), Raju *et al.* (2013), Dhurai *et al.* (2014), Rao *et al.* (2014), Sameera *et al.* (2016) and Priya *et al.* (2017).

This trait showed significant positive association with hulling percentage, milling percentage and water uptake at both phenotypic and genotypic level. This trait showed significant negative association with L/B ratio at both phenotypic and genotypic level. These results indicated that increase in number of total grains per panicle would lead to increased hulling percentage, milling percentage, and water uptake and decrease in L/B ratio. This trait showed significant positive genotypic association with volume expansion ratio and significant negative genotypic association with amylose content indicating that increase in number of total grains per panicle leads to increase in volume expansion ratio and decrease in amylose content. Number of total grains per panicle showed significant positive association with grain yield per plant suggesting that increase in number of total grains per panicle leads to increase in yield per plant.

4.3.2 Grain quality parameters

4.3.2.1 Hulling percentage

Hulling percentage showed significant positive phenotypic association with days to 50% flowering (0.2588*), number of total grains per panicle (0.2994*), milling percentage (0.8044**), head rice recovery percentage (0.5748**) and kernel elongation ratio (0.0438*) and significant negative phenotypic association with panicle length (-0.2887*). This trait showed significant positive genotypic association with days to 50% flowering (0.2900*), number of total grains per panicle (0.3260*), milling percentage (0.9141**), head rice recovery percentage (0.7660**) and volume expansion ratio (0.2661*) and significant negative genotypic association with panicle length (-0.2647*) and L/B ratio (-0.3906**).

This trait showed non-significant positive association (0.0989 and 0.1025) with yield per plant at phenotypic and genotypic levels respectively. Chowdhury *et al.* (2016) reported that hulling percentage showed non-significant positive association with grain yield per plant.

These results are indicating that increase in hulling percentage would lead to increase in milling percentage, head rice recovery percentage and kernel elongation ratio as it showed significant positive phenotypic association with the above characters. It also showed significant positive genotypic association with milling percentage, head rice recovery percentage and volume expansion ratio indicating that increase in hulling percentage leads to increase in above characters.

4.3.2.2 Milling percentage

This character showed significant positive phenotypic association with days to 50% flowering (0.3171*), days to maturity (0.2653*), number of total grains per panicle (0.3297*), hulling percentage (0.8044**) and head rice recovery percentage (0.6114**). This trait also showed significant positive genotypic association with days to 50% flowering (0.4378**), days to maturity (0.3993**), plant height (0.2797*), number of productive tillers per plant (0.3609**), number of total grains per panicle (0.4181**), hulling percentage (0.9141**) and head rice recovery percentage (0.8345**). Milling percentage showed significant negative association with L/B ratio (-0.3891** and 0.5299**) at phenotypic and genotypic levels respectively.

This trait showed non-significant positive association (0.2019 and 0.2220) with yield per plant at both phenotypic and genotypic levels respectively. These results are in accordance with results of Raju *et al.* (2013), Ekka *et al.* (2015) and Chowdhury *et al.* (2016).

This trait showed significant positive association with head rice recovery percentage and also showed significant negative association with L/B ratio at both phenotypic and genotypic levels. These results indicated that increase in milling percentage of grains would lead to increase in head rice recovery and decrease in L/B ratio.

4.3.2.3 Head rice recovery percentage

Head rice recovery percentage showed significant positive association with days to 50% flowering (0.3803** and 0.4322**), days to maturity (0.3674** and 0.3837**), milling percentage (0.5748** and 0.7660**) and hulling percentage (0.6114** and 0.8345**) at phenotypic and genotypic levels, respectively.

This trait showed non-significant negative phenotypic association (-0.0448) and non-significant negative genotypic association (-0.0567) with grain yield per plant. The results are in contrast to results shown by Krishnaveni *et al.* (2013), who reported that head rice recovery percentage showed significant positive genotypic correlation with grain yield per plant.

4.3.2.4 Volume expansion ratio

Volume expansion ratio showed significant positive genotypic correlation with number of productive tillers per plant (0.4181**), number of total grains per panicle (0.2988*) and hulling percentage (0.2661*). It also showed significant negative phenotypic correlation with L/B ratio (-0.2847*) and significant negative genotypic association with L/B ratio (-0.3440**) and amylose content (-0.4437**).

This trait showed non-significant positive phenotypic association (0.0017) and non-significant negative genotypic association (-0.0126) with grain yield per plant. This revealed that the association between these traits might be independent and could be improved independently. Volume expansion ratio showed negative and significant phenotypic correlation with L/B ratio and negative significant genotypic correlation

with L/B ratio and amylose content indicating that increase in volume expansion ratio results in decrease in above characters. The results are contrasting to the results shown by Krishnaveni *et al.* (2013).

4.3.2.5 Water uptake

This character showed significant positive association with number of grains per panicle (0.2640* and 0.3001*) at phenotypic and genotypic levels respectively. This trait also shows significant negative phenotypic association with panicle length (-0.3213*) and significant negative genotypic association with panicle length (-0.4077**) and amylose content (-0.2831*).

Water uptake showed non-significant positive association (0.1665 and 0.184) with grain yield per plant at both phenotypic and genotypic levels respectively. This revealed that the association between these traits might be independent and could be improved independently. Results are in accordance with results of Krishnaveni *et al.* (2013).

This trait had significant negative genotypic association with amylose content indicating that increase in water uptake would lead to decrease in amylose content.

4.3.2.6 L/B ratio

L/B ratio showed significant positive correlation with panicle length (0.4818** and 0.5938**) at both phenotypic and genotypic levels. This trait showed significant negative phenotypic correlation with number of total grains per panicle (-0.2622*), milling percentage (-0.3891**) and volume expansion ratio (-0.2847*). It also showed significant negative genotypic correlation with number of total grains per panicle (-0.2761*), hulling percentage (-0.3906**), milling percentage (-0.5299**) and volume expansion ratio (-0.3440**).

This trait showed non-significant negative phenotypic association (-0.2771) and significant negative genotypic association (-0.3225*) with grain yield per plant. These results are in accordance with the results given by Gunasekaran *et al.* (2017).

4.3.2.7 Kernel elongation ratio

Kernel elongation ratio showed significant positive phenotypic association with hulling percentage (0.0438*) and significant positive genotypic association with amylose content (0.2702*).

This trait showed non-significant positive phenotypic association (0.1447) and non-significant positive genotypic association (0.1742) with grain yield per plant. This revealed that the association between these traits might be independent and could be improved independently. These results were in accordance with results reported by Nandan *et al.* (2010) and Chowdhury *et al.* (2016). As this trait showed significant positive genotypic association with amylose content, increase in kernel elongation ratio results in increase in kernel elongation ratio.

4.3.2.8 Amylose content

This trait showed significant positive genotypic association with kernel elongation ratio (0.2702*) and significant negative genotypic association with plant height (-0.3831**), number of productive tillers per plant (-0.4886**), number of total grains per panicle (-0.2774*), volume expansion ratio (-0.4437**) and water uptake (-0.2831*).

This trait showed non-significant positive phenotypic and genotypic association with (0.0126 and 0.0221) with grain yield per plant. Chowdhury *et al.* (2016) reported the non-significant positive association with grain yield per plant at both phenotypic and genotypic levels. This revealed that the association between these traits might be independent and could be improved independently.

The study revealed positive significant correlation of plant height and number of total grains per panicle at both phenotypic and genotypic level with grain yield per plant. It was also observed that the association of days to 50% flowering, days to maturity, number of productive tillers per plant, hulling percentage, milling percentage, water uptake, kernel elongation ratio and amylose content showed non-significant positive association at phenotypic and genotypic levels with grain yield per plant. Panicle length and head rice recovery showed non-significant negative correlation with grain yield per plant. L/B ratio showed non-significant and significant negative association with grain yield per plant at phenotypic and genotypic levels respectively. Volume expansion ratio showed non-significant positive and negative association with grain yield per plant at phenotypic and genotypic levels respectively.

4.3 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and its component character is the net result of the direct and indirect effects of the component character through other yield attributes. The correlation between grain yield and its component characters may sometimes be misleading. Since, it may be over or under estimate because of its association with other characters. Hence, direct selection on correlation may not be worthwhile. The correlation coefficient needs to be split into direct and indirect effects, using path coefficient analysis for critical evaluation. Thus, the correlation and path analysis in combination, can give a better insight, into cause and effect relationship between different pairs of characters.

In the present investigation, path analysis is carried out with 16 traits as independent variables and grain yield per plant as a dependent variable. The direct and indirect effects of different components on yield at phenotypic and genotypic levels are presented in Tables 4.6 and 4.7 and path diagrams are presented in Fig. 4.1 and Fig. 4.2, respectively.

4.2.1 Yield component characters

4.2.1.1 Days to 50% flowering

At phenotypic level, this trait exhibited non-significant positive correlation (0.2407) with grain yield per plant and positive direct effect (0.0793) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* days to maturity (0.2766), milling percentage (0.0315), amylose content (0.0175) and number of total grains per panicle (0.0100). Predominant negative indirect effects was restricted *via* head rice recovery (-0.1198), hulling percentage (-0.0367), number of productive tillers per plant (-0.0113) and kernel elongation ratio (-0.0111), While other positive and negative indirect effects are negligible.

This trait exhibited significant positive genotypic correlation (0.2480) with grain yield per plant and negative direct effect (-0.5412) on grain yield per plant at genotypic level. Apart from direct effect, it also exhibited prominent positive indirect effects *via* days to maturity (0.9313), milling percentage (0.1400), hulling percentage (0.1125), volume expansion ratio (0.0795) and number of total grains per panicle

(0.0162) and prominent negative indirect effects *via* number of head rice recovery (-0.4334), water uptake (-0.0336) amylose content (-0.0190) and kernel elongation ratio (-0.0114) while other positive and negative indirect effects are negligible.

This trait exhibited negative direct effect at both phenotypic and genotypic levels and non-significant positive association with grain yield at both phenotypic and genotypic levels. Results indicated the weak association between grain yield per plant and days to 50% flowering. Results indicated negative effects were nullified by the positive indirect effects through the characters like number of days to maturity, panicle length, number of total grains per panicle, hulling percentage, milling percentage, volume expansion ratio, L/B ratio and amylose content. Even though the direct effect is negative, the positive association of this trait with grain yield per plant may be attributed to the positive indirect effects of these characters. Hence, indirect selection for the above traits should be practiced for attaining improvement in this character. These results are in accordance with reports of Rao *et al.* (2014), Bhati *et al.* (2015) and Devi *et al.* (2017).

4.2.1.2 Days to maturity

Days to maturity exhibited non-significant positive phenotypic correlation (0.2344) with grain yield per plant and positive direct phenotypic effect (0.2868) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* days to 50% flowering (0.0765), milling percentage (0.0263), volume expansion ratio (0.0182) and amylose content (0.0108) and prominent negative indirect effects *via* head rice recovery (-0.1158), hulling percentage (-0.0238), kernel elongation ratio (-0.0149) and L/B ratio (-0.0108), while other positive and negative indirect effects are negligible.

This trait exhibited non-significant positive genotypic correlation (0.2532) with grain yield per plant and positive direct genotypic effect (0.9298) on grain yield per plant. Apart from direct effect, it also exhibited prominent positive indirect effects *via* milling percentage (0.1277), volume expansion ratio (0.1125), hulling percentage (0.0906), number of grains per panicle (0.0188) and panicle length (0.0122) and prominent negative indirect effects *via* days to 50% flowering (-0.5421), head rice recovery percentage (-0.3848), water uptake (-0.0402), kernel elongation ratio (-0.0349), L/B ratio (-0.0223) and amylose content (-0.0171) while other positive and negative indirect effects are negligible.

This trait showed positive direct effect on grain yield per plant with non-significant positive association at both phenotypic and genotypic levels respectively. The non-significant positive and high direct effect indicates that simultaneous selection of indirect causal factor along with direct causal factor would lead to improvement in yield level. These results are contrasting to the results given by Priya *et al.* (2017).

4.2.1.3 Plant height (cm)

Plant height exhibited significant positive phenotypic association (0.2968*) with grain yield per plant and positive direct phenotypic effect (0.0480) on grain yield per plant. It has shown prominent indirect positive effect *via* number of total grains per panicle (0.2944), milling percentage (0.0202) and head rice recovery percentage (0.0148) and negative indirect effects *via* amylose content (-0.0274), hulling percentage (-0.0244) and panicle length (-0.0099).

This trait exhibited significant positive genotypic association (0.3311**) with grain yield per plant and negative direct genotypic effect (-0.2987) on grain yield per plant. It showed prominent indirect positive effects *via* number of total grains per panicle (0.3451), hulling percentage (0.0940), milling percentage (0.0895), head rice recovery percentage (0.0872), amylose content (0.0380), panicle length (0.0306) and days to 50% flowering (0.0178) and prominent indirect negative effects *via* volume expansion ratio (-0.0562) and days to maturity (-0.0178). The remaining indirect effects are negligible. The negative effects are encountered by the positive direct and indirect effects which resulted in positive genotypic correlation with grain yield per plant.

This trait showed significant positive phenotypic association with grain yield per plant and positive direct phenotypic effect on grain yield per plant. At genotypic level, this trait exhibited significant positive association and negative direct effect on grain yield per plant. These results indicated that negative effects were nullified by the positive indirect effects through the characters like days to 50% flowering, number of productive tillers per plant, panicle length, number of total grains per panicle, L/B ratio, milling percentage, hulling percentage, head rice recovery percentage and amylose content. Even though the direct effect is negative at genotypic level, the positive association of this trait with grain yield per plant may be attributed to the positive indirect effects of these characters. These results are similar to results reported by Krishnaveni *et al.* (2013), Khare *et al.* (2014) and Priya *et al.* (2017).

Table 4.6. Direct and indirect effects (phenotypic) of yield components on yield among 20 genotypes of rice (*Oryza sativa* L.)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers/ plant	Panicle length (cm)	Number of total grains/ panicle	Hulling %	Milling %	Head rice recovery (%)	Volume expansion ratio	Water uptake	L/B ratio	Kernel elongation ratio	Amylose content (%)
Days to 50% flowering	0.0793	0.0765	-0.0035	-0.0166	-0.0033	0.0011	0.0205	0.0252	0.0302	-0.0037	-0.0117	-0.0018	-0.0035	0.0108
Days to maturity	0.2766	0.2868	-0.0092	-0.0517	0.0148	0.0022	0.0483	0.0761	0.1054	-0.0309	-0.0482	0.0195	-0.0169	0.0242
Plant height (cm)	-0.0021	-0.0015	0.0480	0.0072	0.0061	0.0202	0.0083	0.0098	-0.0023	0.0014	-0.0005	0.0006	-0.0013	-0.0103
Number of productive tillers/ plant	-0.0113	-0.0098	0.0081	0.0542	-0.0003	0.0225	0.0052	0.0132	0.0013	0.0128	-0.0071	-0.0093	-0.0062	-0.0120
Panicle length (cm)	0.0033	-0.0040	-0.0099	0.0004	-0.0781	0.0074	0.0226	0.0152	0.0111	-0.0032	0.0251	-0.0376	0.0107	0.0141
Number of total grains/ panicle	0.0100	0.0053	0.2944	0.2903	-0.0665	0.6988	0.2093	0.2304	0.0697	0.1488	0.1845	-0.1832	-0.0531	-0.1641
Hulling %	-0.0367	-0.0238	-0.0244	-0.0135	0.0409	-0.0424	-0.1416	-0.1140	-0.0814	-0.0254	0.0208	0.0429	-0.0062	-0.0073
Milling %	0.0315	0.0263	0.0202	0.0242	-0.0193	0.0327	0.0798	0.0992	0.0607	0.0081	-0.0172	-0.0386	-0.0041	0.0085
Head rice recovery (%)	-0.1198	-0.1158	0.0148	-0.0074	0.0446	-0.0314	-0.1811	-0.1926	-0.3150	0.0214	0.0159	0.0451	-0.0214	-0.0370
Volume expansion ratio	0.0079	0.0182	-0.0047	-0.0397	-0.0069	-0.0359	-0.0302	-0.0137	0.0114	-0.1686	0.0040	0.0480	-0.0142	0.0316
Water uptake	-0.0078	-0.0089	-0.0005	-0.0070	-0.0170	0.0140	-0.0078	-0.0091	-0.0027	-0.0012	0.0529	0.0030	-0.0048	-0.0082
L/B ratio	0.0036	-0.0108	-0.0020	0.0272	-0.0764	0.0416	0.0480	0.0617	0.0227	0.0451	-0.0091	-0.1585	-0.0004	0.0096
Kernel elongation ratio	-0.0111	-0.0149	-0.0068	-0.0291	-0.0348	-0.0193	0.0111	-0.0104	0.0172	0.0213	-0.0229	0.0007	0.2537	0.0244
Amylose content (%)	0.0175	0.0108	-0.0274	-0.0282	-0.0231	-0.0301	0.0066	0.0110	0.0151	-0.0240	-0.0200	-0.0078	0.0123	0.1281
Grain yield/ plant	0.2407	0.2344	0.2968*	0.2104	-0.2194	0.6813**	0.0989	0.2019	-0.0567	0.0017	0.1665	-0.2771*	0.1447	0.0126

*significant at 5% level, ** significant at 1% level

Residual effect = 0.5292

Diagonal bold letters indicate direct effect

Table 4.7. Direct and indirect effects (genotypic) of yield components on yield among 20 genotypes of rice (*Oryza sativa* L.)

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of Productive tillers/ plant	Panicle length (cm)	Number of total grains/ panicle	Hulling %	Milling %	Head rice recovery (%)	Volume expansion ratio	Water uptake	L/B ratio	Kernel elongation ratio	Amylose content (%)
Days to 50% flowering	-0.5412	-0.5421	0.0178	0.1480	0.0036	-0.0114	-0.1570	-0.2369	-0.2339	0.0749	0.0806	0.0032	0.0122	-0.1034
Days to maturity	0.9313	0.9298	-0.0178	-0.1825	0.0523	0.0227	0.2171	0.3713	0.3569	-0.1819	-0.1659	0.0505	-0.0640	0.1600
Plant height (cm)	0.0098	0.0057	-0.2987	-0.0587	-0.0421	-0.1340	-0.0724	-0.0836	0.0260	-0.0292	0.0022	0.0007	0.0002	0.1144
Number of productive tillers/ plant	-0.0039	-0.0028	0.0028	0.0142	0.0001	0.0075	0.0018	0.0051	0.0011	0.0059	-0.0023	-0.0030	-0.0009	-0.0069
Panicle length (cm)	-0.0014	0.0122	0.0306	-0.0001	0.2173	-0.0249	-0.0575	-0.0446	-0.0430	-0.0042	-0.0886	0.1290	-0.0334	-0.0526
Number of total grains/ panicle	0.0162	0.0188	0.3451	0.4064	-0.0881	0.7689	0.2507	0.3215	0.0956	0.2298	0.2308	-0.2123	-0.0576	-0.2134
Hulling %	0.1125	0.0906	0.0940	0.0502	-0.1027	0.1265	0.3880	0.3547	0.2972	0.1033	-0.0675	-0.1516	0.0333	0.0159
Milling %	0.1400	0.1277	0.0895	0.1154	-0.0657	0.1337	0.2924	0.3198	0.2669	0.0604	-0.0795	-0.1695	-0.0003	0.0030
Head rice recovery %	-0.4334	-0.3848	0.0872	-0.0810	0.1983	-0.1247	-0.7680	-0.8368	-1.0026	0.1056	0.0734	0.2177	-0.1395	-0.1270
Volume expansion ratio	0.0795	0.1125	-0.0562	-0.2403	0.0110	-0.1718	-0.1530	-0.1085	0.0605	-0.5747	0.0178	0.1978	-0.0220	0.2550
Water uptake	-0.0336	-0.0402	-0.0017	-0.0368	-0.0919	0.0676	-0.0392	-0.0560	-0.0165	-0.0070	0.2253	0.0110	-0.0224	-0.0638
L/B ratio	0.0024	-0.0223	0.0009	0.0882	-0.2435	0.1132	0.1602	0.2173	0.0890	0.1411	-0.0201	-0.4100	-0.0109	0.0030
Kernel elongation ratio	-0.0114	-0.0349	-0.0004	-0.0312	-0.0779	-0.0380	0.0435	-0.0005	0.0705	0.0194	-0.0503	0.0135	0.5064	0.1369
Amylose content (%)	-0.0190	-0.0171	0.0380	0.0485	0.0240	0.0275	-0.0041	-0.0009	-0.0126	0.0441	0.0281	0.0007	-0.0268	-0.0993
Grain yield/ plant	0.2480	0.2532	0.3311**	0.2402	-0.2054	0.7629**	0.1025	0.2220	-0.0448	-0.0126	0.1840	-0.3224*	0.1742	0.0221

*significant at 5% level, ** significant at 1% level Residual Effect = 0.1719 Diagonal bold letters indicate direct effects

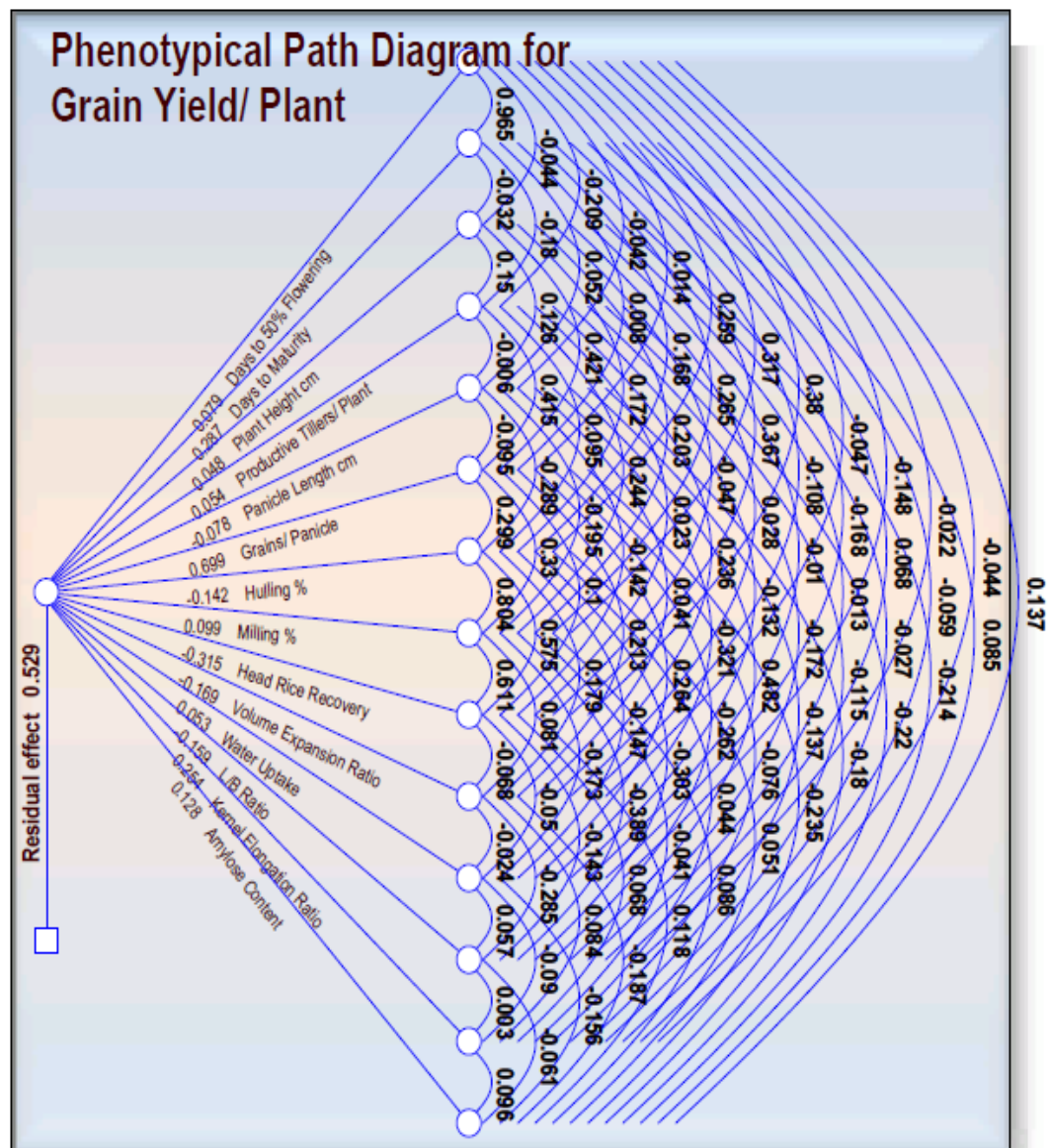


Fig. 4.1. Phenotypic path diagram showing cause-effect relationship in rice (*Oryza sativa* L.)

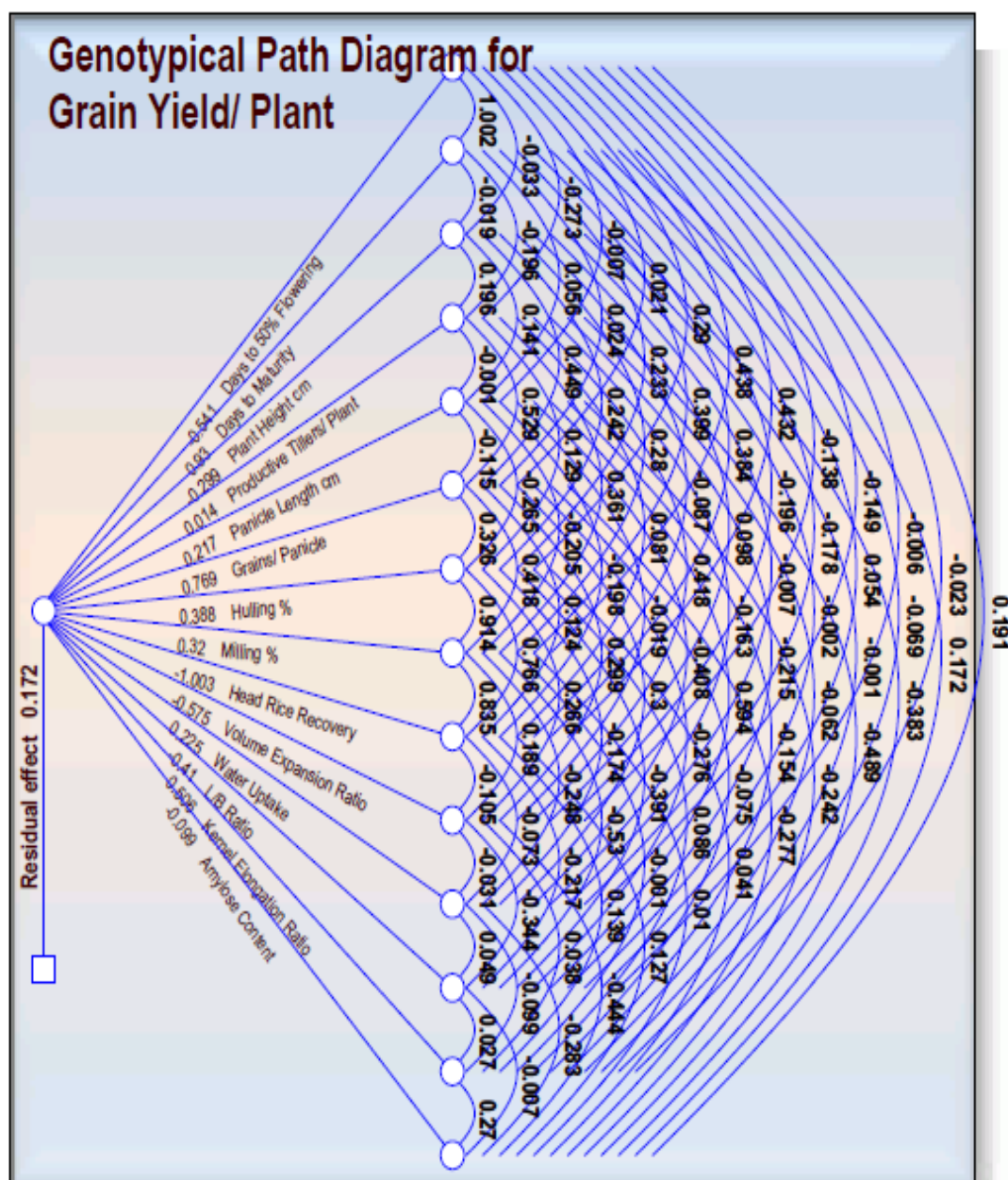


Fig. 4.2. Genotypic path diagram showing cause-effect relationship in rice (*Oryza sativa* L.)

4.2.1.4 Number of productive tillers per plant

This trait exhibited non-significant positive phenotypic association (0.2104) with grain yield per plant and positive direct phenotypic effect (0.0542) on grain yield per plant. This trait has exhibited prominent indirect positive effects *via* total number of grains per panicle (0.2903), L/B ratio (0.0272) and milling percentage (0.0242) and negative indirect effects *via* days to maturity (-0.0517), volume expansion ratio (-0.0397), kernel elongation ratio (-0.0291), amylose content (-0.0282), days to 50% flowering (-0.0166) and hulling percentage (-0.0135). The negative effects were encountered by the positive direct and indirect effects which resulted in positive phenotypic correlation with grain yield per plant.

This trait exhibited non-significant positive genotypic association (0.2402) with grain yield per plant and positive direct genotypic effect (0.0142) on grain yield per plant. It showed prominent indirect positive effects *via* number of total grains per panicle (0.4064), milling percentage (0.1154), days to 50% flowering (0.1480), L/B ratio (0.0882), hulling percentage (0.0502) and amylose content (0.0485) and negative indirect effects *via* days to maturity (-0.1825), volume expansion ratio (-0.2403), head rice recovery percentage (-0.0810), plant height (-0.0587), water uptake (-0.0368) and kernel elongation ratio (-0.0312). The remaining indirect negative effects are negligible. The negative effects were encountered by the positive direct and indirect effects which resulted in positive genotypic correlation with grain yield per plant.

This trait was recorded with non-significant positive association and positive direct effect on grain yield at both phenotypic and genotypic levels. The non-significant positive correlations and low direct positive effects indicated its weak association between number of productive tillers per plant and grain yield per plant. Similar results are also reported by Raju *et al.* (2013), Ekka *et al.* (2015), Gunasekaran *et al.* (2017) and Lakshmi *et al.* (2017).

4.2.1.5 Panicle length (cm)

Panicle length exhibited non-significant negative phenotypic association (-0.2194) with grain yield per plant and negative direct phenotypic effect (-0.0781) on grain yield per plant. This exhibited prominent indirect positive effects *via* head rice recovery percentage (0.0446), hulling percentage (0.0409) and days to maturity

(0.0148) and negative indirect effects *via* L/B ratio (-0.0764), number of total grains per panicle (-0.0665), kernel elongation ratio (-0.0348), amylose content (-0.0231), milling per cent (-0.0055) and water uptake (-0.0170). The remaining indirect effects are negligible.

This trait exhibited non-significant negative genotypic association (-0.2054) with grain yield per plant and positive direct genotypic effect (0.2173) on grain yield per plant. This exhibited prominent indirect positive effects *via* head rice recovery per cent (0.1983), days to maturity (0.0523), amylose content (0.0240) and volume expansion ratio (0.0110) and negative indirect effects *via*, L/B ratio (-0.2435), hulling percentage (-0.1027), water uptake (-0.0919), number of total grains per panicle (-0.0881), kernel elongation ratio (-0.0779), milling percent (-0.0657) and plant height (-0.0421). The remaining indirect effects are negligible.

Non-significant negative association and negative direct effect on grain yield per plant at phenotypic level and non-significant negative association and positive direct effect at genotypic level was exhibited by this trait. These negative associations and low direct effects indicated that selection based on this direct causal factor would not lead to improvement in the grain yield. Similar results were also reported by Krishnaveni *et al.* (2013).

4.2.1.6 Total number of grains per panicle

The direct contribution of this trait was positive (0.6988) and the association was positively significant (0.6813**) at phenotypic level with grain yield per plant. Apart from that, this trait showed prominent indirect effects on grain yield *via* L/B ratio (0.0416), milling percentage (0.0327), number of productive tillers per plant (0.0225), plant height (0.0202) and water uptake (0.0140) and negative indirect effects *via* hulling percentage (-0.0424), volume expansion ratio (-0.0193), head rice recovery percentage (-0.0314), amylose content (-0.0301) and kernel elongation ratio (-0.0193). While other positive indirect genotypic effects were negligible.

This character showed significant genotypic positive (0.7629**) correlation and contributed positive direct genotypic effect (0.7689) on grain yield per plant. This trait also showed predominant indirect positive effects through milling percentage (0.1337), hulling percentage (0.1265), L/B ratio (0.1132), water uptake (0.0676), amylose content

(0.0275) and days to maturity (0.0227) and negative indirect effects *via* volume expansion ratio (-0.1718), plant height (-0.1340), head rice recovery percentage (-0.1247), kernel elongation ratio (-0.0380), panicle length (-0.0249) and days to 50% flowering (-0.0114) on yield per plant. Rest of positive indirect genotypic effects were negligible.

This trait had positive direct effect and significant positive correlation with grain yield per plant at phenotypic level and genotypic level. However, the magnitude of correlation coefficient and direct effect were almost equal, that indicate the true relationship and influence of this trait on grain yield. These results are showed similarity with experimental results of Raju *et al.* (2013) and Priya *et al.* (2017) at genotypic level.

4.2.2 Grain quality parameters

4.2.2.1 Hulling percentage

Hulling percentage showed non-significant positive phenotypic correlation (0.0989) and negative direct phenotypic effect (-0.1416) on grain yield per plant. It had predominant positive phenotypic effects through number of total grains per panicle (0.2093), milling percentage (0.0798), days to maturity (0.0483), L/B ratio(0.0480), panicle length (0.0226), days to 50 % flowering (0.0205)and kernel elongation ratio (0.0111) and predominant negative effects through head rice recovery per cent (-0.1811)and volume expansion ratio (-0.0302). Other indirect positive and negative effects showed negligible influence on grain yield per plant.

This trait showed non-significant positive genotypic correlation (0.1025) and positive direct genotypic effect (0.3880) on grain yield per plant. It had predominant positive genotypic indirect effects through milling percentage (0.2924),number of total grains per panicle (0.2507), days to maturity (0.2171), L/B ratio (0.1602) and kernel elongation ration ratio (0.0435) and predominant negative effects through head rice recovery percentage (-0.7680), days to 50% flowering (-0.1570), volume expansion ratio (-0.1530), plant height (-0.0724), panicle length (-0.0575) and water uptake(-0.0392). Other indirect positive and negative effects were showed negligible influence on grain yield per plant.

This trait exhibited non-significant positive association and negative direct effect on grain yield per plant at both phenotypic level and non-significant positive association and positive direct effect on grain yield per plant at genotypic level. The negative effects were encountered by the positive direct and indirect effects which resulted in positive phenotypic correlation with grain yield per plant. These results are in contrast to the results given by Nandan *et al.* (2010).

4.2.2.2 Milling percentage

Milling per cent exhibited non-significant positive phenotypic association (0.2019) with grain yield and positive direct phenotypic effect (0.0992) on grain yield per plant. Apart from direct effect, this trait showed prominent indirect positive effects through number of grains per panicle (0.2304), days to maturity (0.0761), L/B ratio (0.0617), days to 50% flowering (0.0252), panicle length (0.0152), number of productive tillers per plant (0.0132) and amylose content (0.0110). It had prominent negative effects *via* head rice recovery (-0.1926), hulling percentage (-0.1140), volume expansion ratio (-0.0137) and kernel elongation ratio (-0.0104).

It showed positive direct genotypic effect (0.3198) on grain yield per plant and non-significant positive genotypic (0.2220) association with it. It had predominant genotypic positive indirect effects through days to maturity (0.3713), hulling percentage (0.3547), number of total grains per panicle (0.3215), and L/B ratio (0.2173) and prominent negative effects *via* head rice recovery per cent (-0.8368), days to 50% flowering (-0.2369), volume expansion ratio (-0.1085), plant height (-0.0836), water uptake (-0.0560) and panicle length (-0.0446). Other positive and negative effects were negligible at both phenotypic and genotypic levels.

This character exhibited direct positive effect and non-significant positive correlation at both phenotypic and genotypic levels with grain yield per plant. The non-significant positive correlations and low direct positive effects indicated its weak association between milling percentage and grain yield per plant. Positive direct effect of milling per cent on grain yield at genotypic level was reported by Kumar *et al.* (2010) and Ekka *et al.* (2015).

4.2.2.3 Head rice recovery percentage

Head rice recovery exhibited non-significant negative (-0.0567) association and negative direct phenotypic effect (-0.3150) on grain yield at phenotypic level. It showed prominent indirect phenotypic positive effects *via* days to maturity (0.1054), number of total grains per panicle (0.0697), milling percentage (0.0607), days to 50% flowering (0.0302), L/B ratio (0.0227), kernel elongation ratio (0.0172), amylose content (0.0151), volume expansion ratio (0.0114) and panicle length (0.0111) and negatively prominent *via* hulling percentage (-0.0814). The positive effects are encountered by the negative direct and indirect effects which resulted in negative phenotypic correlation with grain yield per plant.

This character showed non-significant negative (-0.0448) association and negative direct effect (-1.0026) on grain yield at genotypic level. This showed predominant positive genotypic indirect effects *via* number of days to maturity (0.3569), hulling percentage (0.2972), milling percentage (0.2669), number of total grains per panicle (0.0956), L/B ratio (0.0890), kernel elongation ratio (0.0705), volume expansion ratio (0.0605) and plant height (0.0260) and predominant negative effects *via* days to 50% flowering (-0.02339), panicle length (-0.0430), water uptake (-0.0165) and amylose content (-0.0126). Other positive and negative effects were negligible at both phenotypic and genotypic levels. The positive effects were encountered by the negative indirect effects which resulted in negative genotypic correlation with grain yield per plant

This trait showed significant negative correlations and negative direct effects at both phenotypic and genotypic levels that indicated selection based on direct causal factors would not lead to improvement in grain yield and restricted selection of this trait would aid in improvement of grain yield per plant. The results are contrasting to the results given by Krishnaveni *et al.* (2013).

4.2.2.4 Volume expansion ratio

This trait exhibited non-significant positive phenotypic correlation (0.0017) with grain yield per plant and negative direct phenotypic effect (-0.1686). This trait showed prominent phenotypic indirect positive effects *via* total number of total grains per panicle (0.1488), L/B ratio (0.0451), head rice recovery percentage (0.0214), kernel

elongation ratio (0.0213) and number of productive tillers per plant (0.0128) and it showed prominent indirect negative effects through days to maturity (-0.0309), hulling percentage (-0.0254) and amylose content (-0.0240). While other positive and negative effects were negligible.

It had non-significant negative genotypic correlation (-0.0126) with grain yield per plant and negative direct genotypic effect (-0.5747). This trait showed prominent genotypic positive indirect effects *via* number of total grains per panicle (0.2298), L/B ratio (0.1411), head rice recovery percentage (0.1056), hulling percentage (0.1033), days to 50% flowering (0.0749), milling percentage (0.0604), amylose content (0.0441) and kernel elongation ratio (0.0194) and showed prominent indirect negative effects through days to maturity (-0.1819) and plant height (-0.0292).

It had positive non-significant association and positive direct effect on grain yield per plant at both phenotypic and genotypic levels. Crop Improvement in the grain yield might be rewarded by more emphasis on improvement of other causal factors. The results are in contrasting to the results given by Krishnaveni *et al.* (2013).

4.2.2.5 Water uptake

Water uptake was recorded positive phenotypic direct effect (0.0529) on grain yield per plant and showed non-significant phenotypic correlation on it positively (0.1665). This trait showed prominent positive indirect effects grain yield *via* number of total grains per panicle (0.1845), panicle length (0.0251), hulling percentage (0.0208) and head rice recovery percentage (0.0159) and indirect effects negatively *via* days to maturity (-0.0482), kernel elongation ratio (-0.0229), amylose content (-0.0200), milling percentage (-0.0172) and days to 50% flowering (-0.0117) as prominent. Other indirect positive and negative effects were negligible.

This trait recorded positive genotypic direct effect (0.2253) on grain yield per plant and showed non-significant genotypic correlation on it positively (0.1840). This trait showed dominant positive indirect effect grain yield *via* number of total grains per panicle (0.2308), days to 50% flowering (0.0806), head rice recovery percentage (0.0734), amylose content (0.0281) and volume expansion ratio (0.0178) and indirect effects negatively *via* days to maturity (-0.1659), panicle length (-0.0886), hulling percentage (-0.0675), kernel elongation ratio (-0.0503) and L/B ratio (-0.0201) as prominent. Other indirect positive and negative effects were negligible.

This character showed positive non-significant association and positive direct effect on grain yield at both phenotypic and genotypic levels. These results are in agreement with the reports given by Kumar *et al.* (2010) and Krishnaveni *et al.* (2013).

4.2.2.6 L/B ratio

L/B ratio had significant negative phenotypic correlation (-0.2771*) with grain yield per plant and negative direct phenotypic effect (-0.1585). This trait showed prominent phenotypic indirect effects *via* volume expansion ratio (0.0480), head rice recovery percentage (0.0451), hulling percentage (0.0429) and days to maturity (0.0195). This trait exhibited prominent negative indirect effects through number of grains per panicle (-0.1832), milling percentage (-0.0386) and panicle length (-0.0376). Other indirect positive and negative effects were negligible.

It had significant negative genotypic correlation (-0.3224*) with grain yield per plant and negative direct genotypic effect (-0.4100). This trait showed prominent genotypic indirect effects *via* head rice recovery percentage (0.2177), volume expansion ratio (0.1978), panicle length (0.1290), days to maturity (0.0505), kernel elongation ratio (0.0135) and water uptake (0.0110) and indirect negative effect through number of total grains per panicle (-0.2123), milling percentage (-0.1695) and hulling percentage (-0.1516). Other indirect positive and negative effects were negligible.

This trait showed significant negative correlations and negative direct effects at both phenotypic and genotypic levels that indicated selection based on direct causal factors would not lead to improvement in grain yield and restricted selection of this trait would aid in improvement of grain yield per plant. These results are in agreement with the reports given by Nandan *et al.* (2010).

4.2.2.7 Kernel elongation ratio

It showed non-significant positive phenotypic correlation (0.1447) with grain yield per plant and positive direct phenotypic effect (0.2537). This trait showed prominent phenotypic positive indirect effects *via* amylose content (0.0123) and panicle length (0.0107). This trait exhibited prominent negative indirect effects through number of total grains per panicle (-0.0531), head rice recovery percentage (-0.0214), days to maturity (-0.0169) and volume expansion ratio (-0.0142). Rest of indirect negative effects were negligible.

It had non-significant positive genotypic correlation (0.1742) with grain yield per plant and positive direct genotypic effect (0.5064). This trait showed prominent genotypic indirect positive effects *via* hulling percentage (0.0333) and days to 50% flowering (0.0122) and prominent indirect negative effects through head rice recovery percentage (-0.1395), days to maturity (-0.0640), number of total grains per panicle (-0.0576), panicle length (-0.0334), amylose content (-0.0268), water uptake (-0.0224), volume expansion ratio (-0.0220), and L/B ratio (-0.0109). Rest of indirect positive and negative effects were negligible.

This character showed positive non-significant association and positive direct effect on grain yield at both phenotypic and genotypic levels. These results are in contrasting to the reports given by Krishnaveni *et al.* (2013).

4.2.2.8 Amylose content (%)

This trait exhibited non-significant positive phenotypic correlation (0.0126) with grain yield per plant and positive direct phenotypic effect (0.1218) on it. This trait showed prominent phenotypic indirect positive effects *via* volume expansion ratio (0.0316), kernel elongation ratio (0.0244), days to maturity (0.0242), number of productive tillers per plant (0.0141) and days to 50% flowering (0.0108) and it showed indirect negative phenotypic effects *via* number of grains per panicle (-0.1641), head rice recovery percentage (-0.0370), number of productive tillers per plant (-0.0120) and plant height (-0.0103).

This trait exhibited non-significant positive genotypic correlation (0.0221) with grain yield per plant and negative direct genotypic effect (-0.0993) on it. This trait showed prominent positive genotypic indirect effects *via* volume expansion ratio (0.2550), days to maturity (0.1600), kernel elongation ratio (0.1369), plant height (0.1144) and hulling percentage (0.0159) and it showed indirect negative genotypic effect *via* number of total grains per panicle (-0.2134), head rice recovery percentage (-0.1270), days to 50% flowering (-0.1034), water uptake (-0.0638) and panicle length (-0.0526). Other indirect positive and negative effects were negligible at both phenotypic and genotypic level.

Amylose content showed positive non-significant correlation and direct effect at phenotypic level with grain yield. It showed non-significant positive correlation and negative direct effect at genotypic level with grain yield. Results contrasting to these results are recorded by Krishnaveni *et al.* (2013).

Therefore, based on above results of path coefficient analysis it could be concluded that simple selection based on character with direct positive effect towards grain yield per plant and positive correlation with grain yield per plant viz., number of total grains per panicle, number of productive tillers per plant and days to maturity *i.e.*, profuse tillering plants having more number of grains per panicle and more days to maturity might be resulted in higher yield in rice genotypes studied. Days to 50% flowering, plant height, volume expansion ratio and amylose content are the characters with negative direct effect and positive association with grain yield per plant at genotypic level. The negative direct effects and positive associations explained the indirect effects seem to be the cause of positive correlation and the indirect causal factors are to be considered simultaneously for selection. Grain quality parameters like milling percentage, head rice recovery percentage, water uptake and kernel elongation ratio of grain might be improved independent of the yield.

The residual effect determines how best the causal factors account for the variability of the dependent factor. In present investigation residual effect is high, indicating that some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

4.4 GENETIC DIVERGENCE

The multivariate analysis using Mahalanobis' D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. (Singh and Chaudhary, 1977).

The quantitative and quality assessment of genetic divergence was made by adopting Mahalanobis' D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for 15 characters of 20 rice hybrids and the results obtained from the study are discussed below.

Mahalanobis' D^2 analysis

Test with Wilk's criterion

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by percent (%) at 285 degrees of freedom. The 'V' statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of 20 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

Mahalanobis' D^2 values

In order to assess the genetic diversity among 20 genotypes, D^2 statistic was used following the procedure given by Rao (1952). Since the entire 15 yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. The statistical distance (D^2) between the pairs of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated values of any two genotypes considered at one time.

4.4.1 Relative contribution of individual characters towards divergence

The per cent contribution towards genetic divergence by all the 15 characters is presented in Table 4.8. The trait water uptake (42.11) showed maximum contribution towards genetic divergence followed by days to 50% flowering (13.68), plant height (13.16), grain yield per plant (10.00), L/B ratio (6.84), kernel elongation ratio (5.26), number of grains per panicle (4.74), head rice recovery (2.63), number of productive tillers per plant, hulling percentage and amylose content (0.53).

4.4.2 Grouping of genotypes into various clusters

The 20 genotypes were grouped into five clusters using the Tocher's method with the criterion that the intra cluster average D^2 values should be less than the inter cluster D^2 values. The distribution of 20 genotypes into five clusters is presented in Table 4.9.

The distribution of 20 genotypes into five clusters was at random with maximum number of nine genotypes in cluster I. Cluster II is the second largest with six genotypes followed by cluster IV with three genotypes.

Table 4.8. Contribution of different characters towards genetic divergence among 20 genotypes of rice (*Oryza sativa* L.)

Character	Percent contribution towards divergence
Days to 50% Flowering	13.68
Days to Maturity	0.00
Plant Height (cm)	13.16
Number of productive tillers/ Plant	0.53
Panicle Length (cm)	0.00
Number of total grains/ Panicle	4.74
Hulling %	0.53
Milling %	0.00
Head Rice Recovery (%)	2.63
Volume Expansion Ratio	0.00
Water Uptake	42.11
L/B Ratio	6.84
Kernel Elongation Ratio	5.26
Amylose Content (%)	0.53
Grain Yield/ Plant (g)	10.00

Table 4.9. Clustering pattern of 20 genotypes of rice (*Oryza sativa* L.) by Tocher's method

Cluster No.	No. of genotypes	Name of the genotypes
I	9	MEPH-143, 27P63 (NCH-2), BPT-5204(NCV-2), CRHR-115, NK-23831, WGL-14(NCV-1), US-308, CRHR-116, CRHR-118
II	6	PHI-17108, CRHR-119, JKRH-3333 (NCH-1), S-8001, Indam-200-043, NPH-2899
III	1	RRX-135
IV	3	HRI-195, RTNRH-11, NS-6816
V	1	ADT-49 (ZCV)

As could be seen from the results that cluster III and V were solitary clusters. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity. These results were in accordance with reports given by Dutta *et al.* (2011), Vennila *et al.* (2011), Chakravorty and Ghosh (2012), Singh *et al.* (2012), Karuppaiyan *et al.* (2013), Manohara and Singh (2013), Allam *et al.* (2014), Bhadra and Roy (2014), Ramanjaneyulu *et al.* (2014), Beevi and Venkatesan (2015), Kumar *et al.* (2015), Bharathi *et al.* (2016), Chandramohan *et al.* (2016) and Ashok *et al.* (2017).

4.4.3 Average intra and inter cluster D^2 values

The average intra and inter cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977) and presented in Table 4.10. Intra and inter cluster distance of 20 rice genotypes showed in Fig. 4.3. Dendrogram represented relationship among 20 rice genotypes in five clusters based on Mahalanobis' D^2 values are presented in Fig. 4.4.

Table 4.10. Average intra and inter cluster D² values among five clusters in 20 rice (*Oryza sativa* L.) genotypes

Cluster No.	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	41.08	127.17	88.74	152.36	267.50
Cluster II		90.27	229.30	176.61	444.87
Cluster III			0.00	227.43	168.70
Cluster IV				95.18	226.74
Cluster V					0.00

Diagonal bold values indicate intra cluster distances

The maximum intra cluster D² value was 95.18 for cluster IV followed by 90.27 for cluster II, 41.08 for cluster I, while it was zero for clusters III and V. The high intra cluster distance in cluster IV indicated the presence of wide genetic diversity among the genotypes viz., HRI-195, RTNRH-11 and NS-6816. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

Cluster I comprised of nine genotypes and was closest to cluster III (88.74) followed by cluster II (127.17) and it was farthest from cluster V (267.50) followed by cluster IV (152.36).

Cluster II comprised of six genotypes and was closest to cluster I (127.17) followed by cluster IV (176.61) and it was farthest from cluster V (444.87) followed by cluster III (229.30).

Cluster III comprised of one genotype and was closest to cluster I (88.74) followed by cluster V (168.70). It was almost equidistant from two clusters viz., cluster II (229.30) and cluster IV (227.43).

Cluster IV comprised of three genotypes and was closest to cluster I (152.36) followed by cluster II (176.61). It was almost equidistant from two clusters viz., cluster III (227.43) and cluster V (226.74).

Cluster V comprised of one genotype and was closest to cluster III (168.70) followed by cluster IV (226.74), cluster I (267.50) and cluster II (444.87).

The intra and inter cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values. The maximum inter cluster D^2 values was observed between cluster II and V (444.87) followed by cluster I and V (267.50).

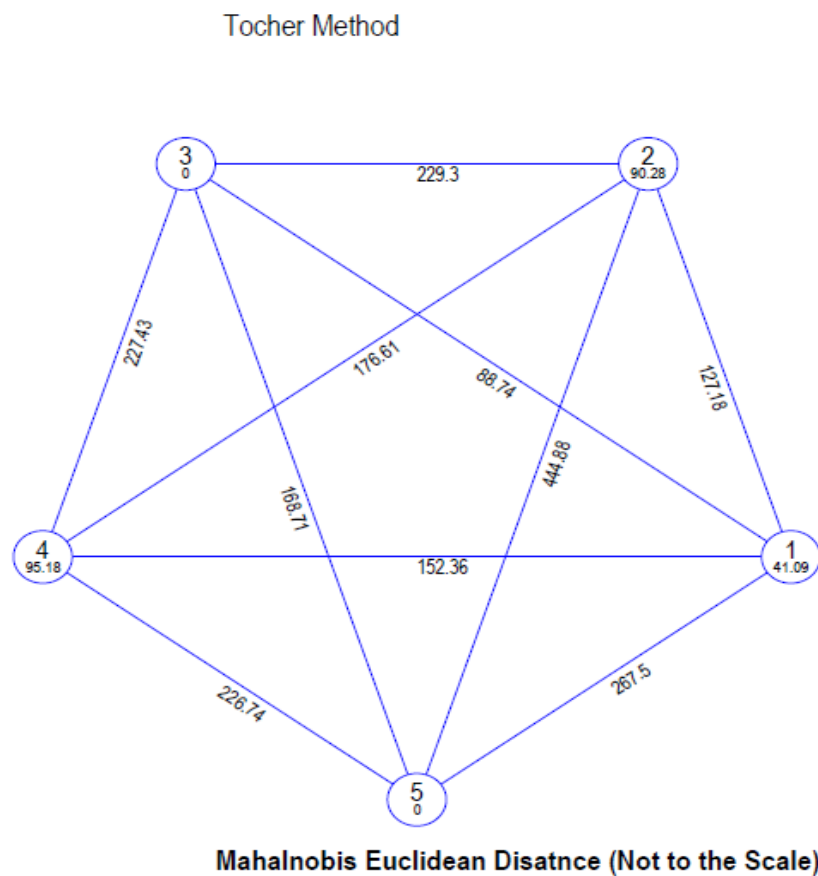


Fig. 4.3. Intra and Inter cluster distances of 20 rice (*Oryza sativa* L.) genotypes in five clusters based on Tocher method.

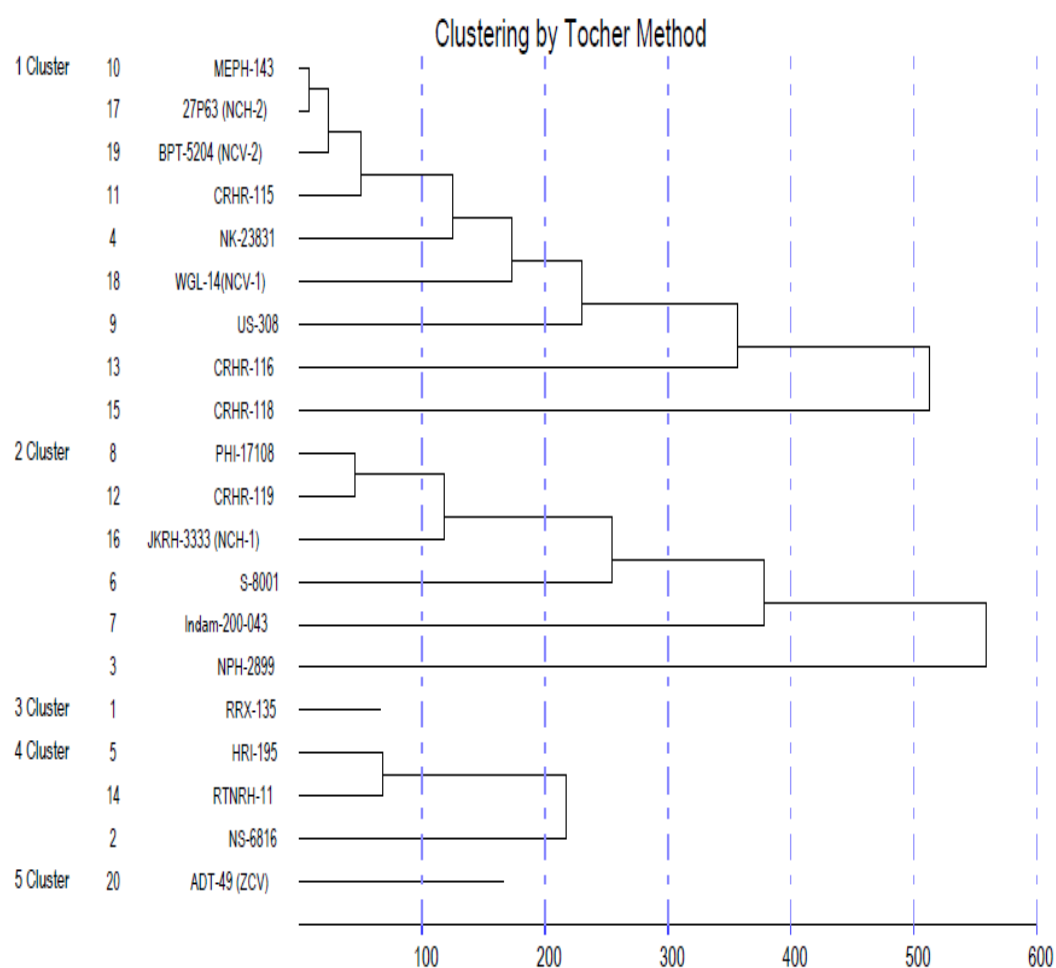


Fig. 4.4. Dendrogram showing relationship among 20 rice (*Oryza sativa* L.) genotypes in five clusters based on Mahalanobis' D^2 values.

4.4.4 Cluster mean values of characters

The cluster mean values for 15 characters are presented in Table 4.11. The data indicated a wide range of mean values between the characters. Days to 50% flowering had a range of 102 days for cluster III to 88 days for cluster IV; days to maturity had a range of 130 days for cluster III to 117 days for cluster IV; plant height (cm) varied from 136.02 cm for cluster IV to 96.66 cm for cluster V; number of productive tillers per plant had a range of 19.22 for cluster IV to 15.33 for cluster III; panicle length (cm) varied from 24.37 for cluster I to 22.60 for cluster II; total number of total grains per panicle had a range of 369.38 for cluster II to 220 for cluster V; grain yield per plant (g) varied as high as 54.33 for cluster II to as low as 28.66 for cluster III; hulling percentage had a range of 87.33 for cluster III to 82.33 for cluster V; milling percentage varied from 77.00 for cluster III to 70.00 for cluster V; head rice recovery percentage had a range of 73.66 for cluster III to 54.00 for cluster V; volume expansion ratio varied from 3.703 for cluster IV to 3.625 for cluster I; water uptake had a range as high as 225.00 for cluster II to as low as 103.33 for cluster III; L/B ratio had a range of 2.97 for cluster I to 2.53 for cluster III; kernel elongation ratio varied from 1.87 for cluster III to 1.68 for cluster IV; amylose content (%) varied from 24.60 for cluster III to 22.77 for cluster IV. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

Based on the *per se* performance and cluster mean values of characters, it can be concluded that, the hybrid S-8001 which is grouped in the cluster II is found to be superior over other hybrids and checks in the present study by having high mean values for the economically important characters viz., number of total grains per panicle, number of productive tillers per plant and yield per plant.

Table 4.11. Mean values of five clusters by Tocher's method for 20 genotypes of rice (*Oryza sativa* L.)

Character / Cluster number	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	Number of productive tillers/ Plant	Panicle Length (cm)	No. of total grains/ Panicle	Hulling %	Milling %	Head Rice Recovery %	Volume Expansion Ratio	Water Uptake	L/B Ratio	Kernel Elongation Ratio	Amylose Content (%)	Grain yield/ plant (g)
Cluster I	98.55	127.88	131.65	18.00	24.37	311.07	83.07	72.22	59.66	3.625	112.03	2.97	1.78	23.40	46.85
Cluster II	100.66	129.38	128.45	18.38	22.60	369.38	84.61	74.05	61.94	3.661	225.00	2.81	1.77	22.84	54.33
Cluster III	102.00	130.00	114.60	15.33	23.36	244.66	87.33	77.00	73.66	3.707	103.33	2.53	1.87	24.60	28.66
Cluster IV	88.00	117.00	136.02	19.22	23.64	350.33	82.55	72.11	56.33	3.703	198.88	2.78	1.68	22.77	41.00
Cluster V	89.66	119.00	96.66	18.33	22.76	220.00	82.33	70.00	54.00	3.647	115.00	2.90	1.80	23.10	29.00

Bold figures indicate maximum and minimum mean values for each character.

Chapter – V

Summary and Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif*, 2017 at Agricultural College Farm, Bapatla, with 20 genotypes of Rice (*Oryza sativa* L.) which included 15 hybrids and five check varieties. Among the hybrids two were hybrid checks. The mean, variability, heritability, genetic advance as per cent of mean, correlation and the magnitude of direct and indirect effects and genetic divergence of yield component traits and grain yield were studied for 15 characters. viz., days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of total grains per panicle, grain yield per plant (g), hulling percentage, milling percentage, head rice recovery percentage, L/B ratio, water uptake, kernel elongation ratio, volume expansion ratio and amylose content (%).

The analysis of variance showed significant differences among 20 genotypes for all the characters studied. The genetic variability studies indicated that the material used in the present investigation possess considerable variability. The genetic parameters revealed that moderate to high variability and high heritability coupled with high genetic advance as per cent of mean were observed for grain yield per plant (g), number of total grains per panicle and water uptake suggesting the predominance of additive type of gene action in controlling these traits with less influence by the environment. These results indicate the operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through direct phenotypic simple selection. The remaining characters under study viz., days to 50% flowering, plant height (cm), panicle length (cm), head rice recovery percentage, L/B ratio, days to maturity, hulling percentage and kernel elongation ratio showed high heritability coupled with moderate to low genetic advance as percent of mean indicating the operation of both additive and non-additive gene effects in the inheritance of these traits. Hence mass selection, progeny selection or any other suitable modified selection procedure is followed for exploitation of the mixed effects of both non-additive and additive gene actions.

Character association studies indicated significant positive association of plant height and number of total grains per panicle with grain yield at both phenotypic and genotypic levels. Hence, selection of these traits would be more effective to bring simultaneous improvement in grain yield.

Path coefficient analysis revealed that selection based on characters showed direct positive effect towards yield and positive correlation with yield viz., number of productive tillers per plant, number of total grains per panicle, and days to maturity i.e., profuse tillering plants having more number of grains per panicle and more days to maturity have resulted in high yielding hybrids. Grain quality parameters like milling percentage, head rice recovery percentage, water uptake and kernel elongation ratio are independent of the yield.

The genetic divergence was high and the 20 rice genotypes studied were distributed into five clusters. Out of five clusters, cluster I was the largest with maximum number of genotypes (9). Cluster II was the second largest with six genotypes, followed by cluster IV with three genotypes. Clusters III and V were solitary clusters. The pattern of distribution of genotypes into various clusters was at random indicating that geographical and genetic diversity were not related. The pattern of group constellations indicated significant variability among the rice hybrids and varieties.

The maximum intra cluster D^2 value was 95.18 for cluster IV followed by 90.27 for cluster II, 41.08 for cluster I, while it was zero for clusters III and V. The high intra cluster distance in cluster IV indicated the presence of wide genetic diversity among the hybrids viz., HRI-195, RTNRH-11 and NS-6816. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

The intra and inter cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values. The maximum inter cluster D^2 values was observed between cluster II and V (444.87) followed by cluster I and V (267.50).

The cluster I had hybrids with highest mean value for panicle length and L/B ratio; cluster II for number of total grains per panicle, water uptake and grain yield per plant (g); cluster III for days to 50% flowering, days to maturity, hulling percentage,

milling percentage, head rice recovery percentage, kernel elongation ratio and amylose content (%); cluster IV for plant height (cm), number of productive tillers per plant and volume expansion ratio.

Based on the *per se* performance and cluster mean values of characters, the hybrid S-8001 which is present in the cluster II is found to be superior over other hybrids and checks in the present study by having high mean values for the economically important characters *viz.*, number of total grains per panicle, number of productive tillers per plant and yield per plant (g). Hence the hybrid S-8001 may be recommended to release to this agro climatic condition duly following the recommended procedures for its release.

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