

GENETIC DIVERSITY STUDIES FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza sativa* L.)

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B.Sc. (Ag.)

**MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)**



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GENETIC DIVERSITY STUDIES FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza sativa* L.)

BY

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B.Sc. (Ag.)

**THESIS SUBMITTED TO THE PROF. JAYASHANKAR
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UNIVERSITY
2015**

DECLARATION

I, **N. SURESH KUMAR** hereby declare that the thesis entitled “**GENETIC DIVERSITY STUDIES FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza sativa* L.)**” submitted to the **Prof. Jayashankar Telangana State Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place: Jagtial

(N.SURESH KUMAR)

Date:

I.D. No. JAM/2013-06

CERTIFICATE

Mr. N.SURESH KUMAR has satisfactorily prosecuted the course of research and that the thesis entitled “**GENETIC DIVERSITY STUDIES FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza sativa* L.)**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him for a degree of any University.

(Dr. V. RAM REDDY)

Chairman

Date:

CERTIFICATE

This is to certify that the thesis entitled “**GENETIC DIVERSITY STUDIES FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza sativa* L.)**” submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture of the **Prof.Jayashankar Telangana State Agricultural University, Hyderabad** is a record of the bonafide original research work carried out by **Mr. N. SURESH KUMAR** under our guidance and supervision.

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

(Dr. V. RAM REDDY)

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SYMBOLS AND ABBREVIATIONS

%	Per cent
σ^2_p	Phenotypic variance
σ^2_g	Genotypic variance
ANOVA	Analysis of variance
Cm	Centimeter
CD	Critical difference
D ²	Genetic distance
<i>et al.</i>	And others
Fig.	Figure
g	Gram
GA	Genetic advance
GAM	Genetic advance as per cent of mean
GCV	Genotypic coefficient of variation
h ²	heritability in broad sense
ha	Hectare
i.e.,	that is
m.ha	million hectare
mm	Millimeter
m.t	million tones
No.	Number
PCV	Phenotypic coefficient of variation
RBD	Randomized Block Design
viz.,	Namely

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ABSTRACT

The present investigation, “Genetic diversity studies for yield and quality traits in rice (*Oryza sativa* L.)” was under taken with 70 genotypes of rice to study the genetic diversity present in the experimental material for selection of the diverse parents, to estimate the genetic parameters among the genotypes for yield and quality traits and the extent of association between the yield and its component characters including the direct and indirect effects. The experiment was laid out in a Randomized Block Design with three replications at Regional Agricultural Research Station, Polasa, Jagtial, Karimnagar district during *Kharif* , 2014.

The data was collected on days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000-grain weight, grain yield per plant, hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth and L/B ratio.

Analysis of variance indicated the existence of significant differences among the genotypes for all the traits under study. Based on the relative magnitude of D^2 values, the genotypes were grouped into seven clusters. Cluster I was the largest comprising of forty genotypes followed by cluster II with twenty genotypes, cluster V with six genotypes and cluster III, IV, VI and VII were represented by single genotype indicating high degree of heterogeneity among the genotypes. The pattern of group constellations indicated significant variability among the genotypes.

Maximum inter cluster distance was exhibited between cluster V and VII (1949.04) followed by cluster II and VII (1619.25), cluster II and III (1458.41), cluster V and VI (1282.97) and cluster III and VII (1268.29). The greater the distance between two clusters, the wider the genetic diversity among the genotypes of these clusters. Hence, hybridization between the genotypes from these clusters would produce high heterotic recombinants.

The kernel length, kernel breadth, days to 50 per cent flowering, L/B ratio, 1000-grain weight and number of filled grains per panicle together contributed 95.15% towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations.

The cluster I is having highest mean value for grain yield per plant, cluster II for number of filled grains per panicle, head rice recovery percentage and cluster III for 1000-grain weight, kernel breadth, cluster IV for number of productive tillers per plant, hulling percentage, milling percentage, cluster VI for plant height, panicle length, kernel length and cluster VII for days to 50 per cent flowering, days to maturity and L/B ratio. The promising genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

High GCV and PCV values were observed for number of filled grains per panicle, grain yield per plant, 1000-grain weight. High heritability coupled with high genetic advance as per cent of mean was observed for number of filled grains per panicle, kernel length, kernel breadth, L/B ratio, grain yield per plant and 1000-grain weight indicated that these traits were controlled by additive type of gene action. The remaining traits were mostly under the influence of non-additive gene effects as they recorded low to moderate estimates of genetic advance.

Character association studies revealed that the characters grain yield per plant showed significant positive association with plant height, number of productive tillers per plant, panicle length, no. of filled grains per panicle, kernel breadth and 1000-grain weight. This indicated that simultaneous selection of all these characters was important for yield improvement.

A critical analysis of the results by path analysis revealed that 1000-grain weight exerted the highest positive direct effect on grain yield per plant followed by number of filled grains per panicle, number of productive tillers per plant, days to 50 per cent flowering, plant height, panicle length, L/B ratio and milling percentage, indicating that the selection for these characters was likely to bring about an overall improvement in grain yield per plant directly.

Therefore, it is suggested that preference should be given to these characters in the selection programme to isolate superior lines with genetic potentiality for higher yield in rice genotypes.

Chapter I

INTRODUCTION

Rice (*Oryza sativa* L.) is a popular cereal crop commonly used as human food. It is actually a type of grass and belongs to family of Poaceae that includes other cereals such as wheat and corn. Rice is rich in nutrients and contains a number of vitamins and minerals. It is an excellent source of complex carbohydrates the best source of energy. It is the most important staple food crop for more than 60 per cent of the global population and forms the cheapest source of food energy and protein. It provides 43 per cent of calorie of an average human diet in India and rice contributes 20-25 per cent of agricultural income due to its intensive cultivation. In Asia as a whole, much of the population consumes rice in every meal. In many countries, rice accounts for more than 70 per cent of human caloric intake.

In India, rice is one of the most important food crop in terms of area, production and consumer preference. India is the second largest producer and consumer of rice in the world. Rice is the premier food crop in India occupying nearly 43.97 million hectares area with annual production of 104.40 million tonnes and productivity of 2372 kg ha⁻¹ (INDIASTAT, 2012-2013).

To meet the food demands of the growing population, the present production levels need to be increased by 2 million tones every year. It is estimated that 120 million tonnes of rice is required to feed the increased population by 2020. This is possible, when the yield potentiality of the presently grown varieties is further increased by 20-25 per cent by changing the genetic architecture. Success of any breeding programme depends upon the amount of genetic variability available in the crop species, besides the efficiency of selection technique adapted by plant breeder.

Yield is a complex character which is influenced by several quantitative traits, these are governed by polygenes. Application of biometrical techniques in plant breeding has led to the greater understanding of genetics of quantitative characters and proved to be extremely useful to the plant breeder for systematic genetic analysis.

Genetic diversity in a crop species is essential to sustain high level of productivity. The importance of information about the extent and magnitude of genetic divergence in rice and its utilization for the selection of desirable parents/ donors either for exploitation of hybrid vigor or to get desirable recombinants has been stressed by

many workers (Anand and Murthy, 1968). Arunachalam (1981) reported that the greater chance of getting heterotic hybrids and enhanced variation in the segregating population of varietal improvement programmes mainly depended on genetic divergence. Germplasm is the core of any breeding work. The variability and novel characters existing in the germplasm can be exploited during crossing programme to develop need based varieties and hybrids. Before using the germplasm it has to be characterized and also the genetic diversity has to be studied to use effectively in the crossing programme.

A thorough knowledge of nature and magnitude of genetic variability and association of characters in a crop species is a pre-requisite for a successful breeding programme. Information on direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process.

In addition to the above information, quantification of degree of divergence in a given experimental material is of immense value in identification of divergent genotypes for further use in hybridization to create new variability. Mahalanobis D^2 statistic has proved to be a powerful tool for quantifying genetic divergence in a given population. Divergent genotypes could be obtained by collection from different eco-geographical regions or it could be induced by combination breeding.

Yield is the most noticeable characteristic to farmers while the crop is in the ground, but when the product of the crop, the milled rice, reaches the market, quality becomes the key determinant of its sale-ability. Thus breeders are mandated to develop varieties of high quality that suits the particular needs of the market. There are several defined classes of rice, based on the physical appearance of the milled rice, the cooking properties and the aroma of the rice. Thus, quality evaluation programs should go hand-in-hand with breeding programs and all quality evaluation programs should have the capacity to measure atleast the basic traits.

With the importance of human nutritional requirement, equal emphasis needs to be given for grain quality and nutritional value in developing the potential rice varieties, beside higher yield.

Keeping in view the importance of aforesaid aspects, the present investigation is focused at developing high yielding rice varieties with good quality with the following objectives:

- 1) To estimate the extent of genetic diversity for yield and grain quality characters in the available germplasm through D^2 analysis.
- 2) To study the correlation and the direct and indirect effects of yield component characters on grain yield.
- 3) To estimate variability, heritability, genetic advance, phenotypic coefficient of variation and genotypic coefficient of variation for yield and yield components.

Chapter II

REVIEW OF LITERATURE

Rice is one of the most intensively studied crops and hence, a wealth of information is available on genetics of several hereditary parameters, The literature available on genetic analysis of yield and its components in rice (*Oryza sativa* L.) and reviewed under the following sub heads.

2.1 Genetic parameters

2.2 Genetic divergence

2.3 Correlation studies

2.4 Path coefficient analysis

2.1 Genetic Parameters

2.1.1 Variability

Variability refers to the presence of differences among the individuals of plant population. Variability results due to differences either in the genetic constitution of the individuals of a population or in the environment in which they have grown. The existence of variability is essential for resistance to biotic and abiotic factors as well as for wider adoptability. Variance is the amount of variation present among the member of a population.

Fisher (1918) partitioned the total phenotypic variance into genotypic variance and environmental variance. He further divided the genotypic variance in to additive, dominance and epistatic effects.

However, it is the only genetic variation which is heritable. Selection is also effective when there is significant amount of generic variability among the individuals in a population. Hence, insight into the magnitude of generic variability present in a population is of paramount importance to plant breeder for starting a breeding programme in any crop including rice. The quantitative measurement of individual character provides the basis for an interpretation of analysis of variance.

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

A brief review of studies on genotypic and phenotypic coefficients of variation in rice is presented hereunder in tabular form.

S.No.	Character	Range	Reference
1.	Days to 50 per cent flowering	High	Awasthi and Pandey (2000) Rita Bisne <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012).
		Low	Patil <i>et al.</i> (2003) Sinha <i>et al.</i> (2004) Vijayalakshmi <i>et al.</i> (2008) Manoj Kumar Prajapati (2011) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
2.	Plant height	High	Sinha <i>et al.</i> (2004) Akhtar <i>et al.</i> (2011) Selvaraj <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012).
		Moderate	Tara Satyavathi <i>et al.</i> (2001) Nayak <i>et al.</i> (2002) Krishna <i>et al.</i> (2008) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Low	Chikkalingaiah <i>et al.</i> (1999) Patil <i>et al.</i> (2003) Kole <i>et al.</i> (2008).

S.No.	Character	Range	Reference
3.	Number of productive tillers per plant	High	Akhtar <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Selvaraj <i>et al.</i> (2011) Pratap <i>et al.</i> (2012).
		Moderate	Vange and Ojo (1997) Nagajyothi (2001) Krishna <i>et al.</i> (2008)
		Low	Niranjana Murthy <i>et al.</i> (1999) Tara Satyavathi <i>et al.</i> (2001) Surender Raju (2002) Pankaj Garg <i>et al.</i> (2010).
4.	Panicle length (cm)	High	Tripathi <i>et al.</i> (1999) Nayudu <i>et al.</i> (2007)
		Low	Tara Satyavathi <i>et al.</i> (2001) Patil <i>et al.</i> (2003) Kole <i>et al.</i> (2008) Manoj Kumar Prajapati (2011) Ganapati <i>et al.</i> (2014).
5.	Number of filled grains per panicle.	High	Nayudu <i>et al.</i> (2007) Pankaj Garg <i>et al.</i> (2010) Mulugeta Seyoum <i>et al.</i> (2012) Pratap <i>et al.</i> (2012)
		Moderate	Tara Satyavathi <i>et al.</i> (2001) Kole and Hasib (2008) Sanghera <i>et al.</i> (2013) Ganapati <i>et al.</i> (2014).
		Low	Nath and Talukdar (1997)
6.	Days to maturity	Low	Chanbeni <i>et al.</i> (2012)

S.No.	Character	Range	Reference
7.	1000-grain weight (g)	High	Nayudu <i>et al.</i> (2007) Chandra <i>et al.</i> (2007) Mulugeta Seyoum <i>et al.</i> (2012)
		Low	Chikkalingaiah <i>et al.</i> (1999) Vange <i>et al.</i> (1999) Tara Satyavathi <i>et al.</i> (2001)
8.	Grain yield per plant (g)	High	Pankaj Garg <i>et al.</i> (2010) Selvaraj <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012) Sanghera <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Moderate	Chauhan <i>et al.</i> (1993) Pradyumna Rao <i>et al.</i> (1996) Nagajyothi (2001) Tara Satyavathi <i>et al.</i> (2001)
		Low	Supriyo Chakraborty and Hazarika (1994)
9.	Hulling percentage	Moderate	Nayak <i>et al.</i> (2003)
		Low	Nagajyothi (2001) Madhavalatha (2002) Surender Raju (2002)
10.	Milling percentage	High	Chikkalingaiah <i>et al.</i> (1999)
		Low	Nagajyothi (2001) Chaudhary and Motiramani (2003)
11.	Head rice recovery	High	Asish <i>et al.</i> (2010)
		Moderate	Nayak <i>et al.</i> (2003)
		Low	Chaudhary and Motiramani (2003)

S.No.	Character	Range	Reference
			Patil <i>et al.</i> (2003)
12.	Kernel length (mm)	High	Sarawgi <i>et al.</i> (2000) Roy <i>et al.</i> (1995)
		Moderate	Chaudhary and Motiramani (2003) Nayak <i>et al.</i> (2003) Asish <i>et al.</i> (2010)
		Low	De and Suriya Rao (1988) Reddy and De (1996) Umadevi <i>et al.</i> (2009) Dhurai <i>et al.</i> (2014).
13.	Kernel breadth (cm)	High	Pathak and Sharma (1996)
		Moderate	Vivekanandan and Giridharan (1998)
		Low	Chauhan <i>et al.</i> (1991) Reddy and De (1996) Chikkalingaiah <i>et al.</i> (1999) Dhurai <i>et al.</i> (2014).
14.	L/B ratio	High	Sarawgi <i>et al.</i> (2000) Madhavalatha (2002) Saxena <i>et al.</i> (2005)
		Moderate	Nayak <i>et al.</i> (2002) Vanja <i>et al.</i> (2006) Asish <i>et al.</i> (2010) Sanghera <i>et al.</i> (2013)
		Low	Ramesh Kumar (1989) Chikkalingaiah <i>et al.</i> (1999) Tara Satyavathi <i>et al.</i> (2001) Dhurai <i>et al.</i> (2014).

2.1.2 Heritability

Heritability in broad sense refers to the genetic variance present in the population in relation to the total observed variance. Consistency in the selection of succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. Basic information on heritability is a prerequisite for planning any breeding programme. High heritability indicates that it should be easy to conduct effective selection for the trait.

A brief review of studies on heritability in rice is presented hereunder in tabular form.

S.No.	Character	Range	Reference
1.	Days to 50 per cent flowering	High	Nayak <i>et al.</i> (2002) Sankar <i>et al.</i> (2006) Bharadwaj <i>et al.</i> (2007) Kishore <i>et al.</i> (2008) Idris <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Medium	Chauhan <i>et al.</i> (1993) Sahdev Singh <i>et al.</i> (1996) Singh and Choudhary (1985)
2.	Plant height (cm)	High	Akhtar <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Selvaraj <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012) Sanghera <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Moderate	Akinwale <i>et al.</i> (2011)

S.No.	Character	Range	Reference
		Low	Vijayalakshmi <i>et al.</i> (2008) Idris <i>et al.</i> (2013)
3.	Number of productive tillers per plant	High	Anbanandan <i>et al.</i> (2009) Nandan and Sweta Singh (2010) Pratap <i>et al.</i> (2012) Idris <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014).
		Moderate	Venkata Suresh (2001)
		Low	Ramesh Kumar (1989) Niranjana Murthy <i>et al.</i> (1999)
4.	Panicle length (cm)	High	Nayak <i>et al.</i> (2002) Nayudu <i>et al.</i> (2007) Mohan Lal <i>et al.</i> (2011) Idris <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014).
		Moderate	Satya Priya Lalitha and Sreedhar (1996) Venkata Suresh (2001)
		Low	Singh and Chaudhary (1996)
5.	Number of filled grains per panicle.	High	Sankar <i>et al.</i> (2006) Nayudu <i>et al.</i> (2007) Krishna <i>et al.</i> (2008) Pankaj Garg <i>et al.</i> (2010) Pratap <i>et al.</i> (2012) Idris <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Ganapati <i>et al.</i> (2014).
		Moderate	Satya Priya Lalitha and Sreedhar (1996)

S.No.	Character	Range	Reference
			Mulugeta Seyoum <i>et al.</i> (2012)
6.	Days to maturity	High	Chanbeni <i>et al.</i> (2012)
7.	1000-grain weight (g)	High	Bharadwaj <i>et al.</i> (2007) Nandan and Sweta Singh (2010) Abdul Fiyaz <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012) Idris <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014).
		Moderate	Ramesh Kumar (1989) Ganapati <i>et al.</i> (2014).
8.	Grain yield per plant (g)	High	Nayudu <i>et al.</i> (2007) Anbanandan <i>et al.</i> (2009) Pankaj Garg <i>et al.</i> (2010) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Moderate	Satya Priya Lalitha and Sreedhar (1999)
		Low	Bharadwaj <i>et al.</i> (2007) Idris <i>et al.</i> (2013)
9.	Hulling percentage	High	Nayak <i>et al.</i> (2003) Madhavalatha <i>et al.</i> (2005)
		Moderate	Chikkalingaiah <i>et al.</i> (1999)
		Low	Nagajyothi (2001)
10.	Milling percentage	High	Chikkalingaiah <i>et al.</i> (1999) Nayak <i>et al.</i> (2003)
		Moderate	Nagajyothi. (2001)
11.	Head rice recovery	High	Nayak <i>et al.</i> (2003) Patil <i>et al.</i> (2003)

S.No.	Character	Range	Reference
12.	Kernel length (mm)	High	Madhavalatha (2002) Surender Raju (2002) Dhurai <i>et al.</i> (2014)
13.	Kernel breadth (mm)	High	Venkata Suresh (2001) Madhavalatha (2002) Surender Raju (2002) Chaudhary <i>et al.</i> (2004) Dhurai <i>et al.</i> (2014)
14.	L/B ratio	High	Nayak <i>et al.</i> (2003) Bharadwaj <i>et al.</i> (2007) Nandan and Sweta Singh (2010) Mohan Lal <i>et al.</i> (2011) Dhurai <i>et al.</i> (2014)
		Moderate	Sahdev Singh <i>et al.</i> (1996) Chikkalingaiah <i>et al.</i> (1999)

2.1.3 Genetic advance as per cent of mean

Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population. Johnson *et al.* (1955) reported that though the heritable estimates give useful indication of relative values of selection based on phenotypic expression, the genetic gain should also be considered to arrive at a more reliable conclusion.

A brief review of studies on genetic advance as per cent of mean in rice is presented hereunder in tabular form.

S.No.	Character	Range	Reference
1.	Days to 50 per cent flowering	High	Sankar <i>et al.</i> (2006) Bharadwaj <i>et al.</i> (2007) Kishore <i>et al.</i> (2008)
		Medium	Marimuthu <i>et al.</i> (1990) Rao and Shrivastav (1994) Mulugeta Seyoum <i>et al.</i> (2012) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Low	Suman (2003) Madhavalatha <i>et al.</i> (2005) Krishna <i>et al.</i> (2008) Vijayalakshmi <i>et al.</i> (2008)
2.	Plant height (cm)	High	Kishore <i>et al.</i> (2008) Kumar and Ramesh (2008) Mohan Lal <i>et al.</i> (2011) Selvaraj <i>et al.</i> (2011) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Moderate	Marimuthu <i>et al.</i> (1990) Patil <i>et al.</i> (2003) Sinha <i>et al.</i> (2004)
		Low	Vijayalakshmi <i>et al.</i> (2008)
3.	Number of productive tillers per plant	High	Suman (2003) Sankar <i>et al.</i> (2006) Nayudu <i>et al.</i> (2007) Anbanandan <i>et al.</i> (2009) Nandan and Sweta Singh (2010) Selvaraj <i>et al.</i> (2011) Pratap <i>et al.</i> (2012)

S.No.	Character	Range	Reference
			Dhurai <i>et al.</i> (2014).
		Moderate	Venkata Suresh (2001) Patra <i>et al.</i> (2006)
		Low	Sahdev Singh <i>et al.</i> (1996) Niranjana Murthy <i>et al.</i> (1999)
4.	Panicle length (cm)	High	Chikkalingaiah <i>et al.</i> (1999) Nayak <i>et al.</i> (2002) Nayudu <i>et al.</i> (2007) Mohan Lal <i>et al.</i> (2011) Dhurai <i>et al.</i> (2014).
		Moderate	Satya Priya Lalitha and Sreedhar (1996) Venkata Suresh (2001) Patra <i>et al.</i> (2006) Ganapati <i>et al.</i> (2014).
		Low	Borbora and Hazarika (1998) Mokate <i>et al.</i> (1998) Nagajyothi (2001) Suman (2003)
5.	Number of filled grains per panicle	High	Patil <i>et al.</i> (2003) Suman (2003) Sankar <i>et al.</i> (2006) Nayudu <i>et al.</i> (2007) Krishna <i>et al.</i> (2008) Pankaj Garg <i>et al.</i> (2010) Pratap <i>et al.</i> (2012) Ganapati <i>et al.</i> (2014).

S.No.	Character	Range	Reference
		Moderate	Satya Priya Lalitha and Sreedhar (1996)
6.	Days to maturity	Moderate	Chanbeni <i>et al.</i> (2012)
7.	1000- grain weight (g)	High	Bharadwaj <i>et al.</i> (2007) Karad and Pol (2008) Anbanandan <i>et al.</i> (2009) Nandan and Sweta Singh (2010) Abdul Fiyaz <i>et al.</i> (2011) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Moderate	Reddy and De (1996) Reddy <i>et al.</i> (1997) Sinha <i>et al.</i> (2004) Mulugeta Seyoum <i>et al.</i> (2012)
		Low	Chikkalingaiah <i>et al.</i> (1999) Nagajyothi (2001) Suman (2003) Vijayalakshmi <i>et al.</i> (2008)
8.	Grain yield per plant (g)	High	Madhavalatha (2002) Sankar <i>et al.</i> (2006) Nayudu <i>et al.</i> (2007) Kumar and Ramesh (2008) Anbanandan <i>et al.</i> (2009) Pankaj Garg <i>et al.</i> (2010) Dhurai <i>et al.</i> (2014) Ganapati <i>et al.</i> (2014).
		Moderate	Satya Priya Lalitha and Sreedhar (1999) Patra <i>et al.</i> (2006)

S.No.	Character	Range	Reference
		Low	Ramesh Kumar (1989) Suman (2003) Sinha <i>et al.</i> (2004)
9.	Hulling percentage	High	Singh <i>et al.</i> (1998)
		Moderate	Chikkalingaiah <i>et al.</i> (1999) Nayak <i>et al.</i> (2003)
		Low	Nagajyothi (2001) Surender Raju (2002) Madhavalatha <i>et al.</i> (2005) Mall <i>et al.</i> (2011).
10.	Milling percentage	High	Chikkalingaiah <i>et al.</i> (1999)
		Moderate	Nayak <i>et al.</i> (2003)
		Low	Nagajyothi (2001)
11.	Head rice recovery	High	Nayak <i>et al.</i> (2003)
		Low	Patil <i>et al.</i> (2003)
12.	Kernel length (mm)	High	Jaiswal <i>et al.</i> (2007)
		Moderate	Sarawgi <i>et al.</i> (2000) Bharadwaj <i>et al.</i> (2007) Krishna <i>et al.</i> (2008)
		Low	Venkata Suresh (2001) Surender Raju (2002) Nayak <i>et al.</i> (2003) Dhurai <i>et al.</i> (2014).
13.	Kernel breadth (mm)	High	Nayak <i>et al.</i> (2002) Jaiswal <i>et al.</i> (2007)
		Moderate	Vivekanandan and Giridharan (1998) Sarawgi <i>et al.</i> (2000)

S.No.	Character	Range	Reference
14.	Kernel L/B ratio		Dhurai <i>et al.</i> (2014).
		Low	Venkata Suresh (2001) Madhavi latha (2002) Chaudhary and Sarawgi (2004)
		High	Nayak <i>et al.</i> (2003) Bharadwaj <i>et al.</i> (2007) Nandan and Sweta Singh (2010) Mohan Lal <i>et al.</i> (2011)
		Moderate	Satya Priya Lalitha and Sreedhar (1999) Nayak <i>et al.</i> (2003) Patil <i>et al.</i> (2003) Krishna <i>et al.</i> (2008) Dhurai <i>et al.</i> (2014).
		Low	Venkata Suresh (2001) Madhavi latha (2002) Madhavi latha <i>et al.</i> (2005) Vijayalakshmi <i>et al.</i> (2008)

2.2 GENETIC DIVERGENCE

Genetic improvement in any crop mainly depends upon the amount of genetic variability present in the population. The expression “divergence in character” was used by Darwin (1859) for the variation in genera and species. Another term “morphism” was used by Huxley (1955) for genetic diversity implying “genetic polymorphism” which means the coexistence of distant genetic forms in population.

Murthy and Arunachalam (1966) emphasized the importance of genetic diversity in selection of parents for hybridization in different crops and reported that the greatest contributing characters to genetic diversity in grain crops were flowering time, plant height and tiller number per plant.

Sharma and Roy (1993) raised seventeen diverse genotypes of upland rice grouped into five clusters on the basis of D^2 analysis of data on eleven characters. Inter and intra cluster distances are given and their use in the selection of parents for breeding programmes is mentioned.

Surender Raju (2002) assessed the genetic divergence among 42 genotypes by Mahalanobis's D^2 statistic and grouped them into 12 clusters. The characters 100-grain weight, volume expansion ratio, kernel length and days to 50 per cent flowering contributed maximum to the genetic divergence.

Nayak *et al.* (2004) studied nature and magnitude of genetic divergence among two hundred genotypes of scented rice including one non-scented check using Mahalanobis D^2 statistics for 10 quantitative characters. On the basis of D^2 values, the genotypes were grouped into 10 clusters. Grain length and days to 50 per cent flowering played important role in the formation of clusters.

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

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

Suman *et al.* (2005) evaluated one hundred fourteen rice genotypes for 16 quantitative characters to quantify the genetic diversity existing among them using Mahalanobis D^2 statistics. The genotypes fell into 10 clusters. Cluster X had the maximum number of spikelets per panicle, panicle length, filled grains per panicle, plant yield and biological yield. Cluster III exhibited the lowest means for plant height, days to 50 per cent flowering, panicle length. The genotypes from clusters III and X, which had high and low cluster means for majority of the characters, were recommended as parents for hybridization.

Vaithiyalingan (2005) collected twenty nine strains of rice from different geographical regions of world and studied to analyse the extent of genetic divergence. The genotypes were grouped into four clusters. The clustering pattern was independent of the geographical distribution, cluster II included twenty three genotypes and those

can be useful in hybridization to create a wide spectrum of variability. Maximum distance (97.34) was observed between clusters III and IV. Plant height, single plant yield and 1000-seed weight were found to be important contributors for genetic divergence.

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

Naik *et al.* (2006) conducted a study on genetic divergence to estimate the nature and magnitude of diversity in 50 aromatic rice accessions including five improved scented varieties. The D^2 analysis indicated the presence of appreciable amount of genetic diversity in the material. The genotypes were grouped into seven clusters. The cluster VI had the highest mean grain yield per plant and for biological yield per plant. Inter cluster distance was recorded highest between cluster III and cluster IV. The least distance was recorded in between cluster I and cluster V.

Chandra *et al.* (2007) assessed genetic divergence among 49 genotypes of non-scented rice including three checks for seven quantitative characters. The significant varietal difference was observed for all the characters studied on the basis of D^2 values. The genotypes were grouped into eight clusters. Characters like kernel length, kernel breadth, days to 50 per cent flowering and plant height showed more contribution towards total divergence.

Sandhya Kishore *et al.* (2007) studied genetic divergence for different yield attributing traits in 70 rice genotypes. The analysis of variance revealed significant differences among the genotypes for each character. The genotypes were grouped into nine different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity are not related.

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

Ramya and Senthil Kumar (2008) carried out an investigation with 50 genotypes for studying genetic diversity and these genotypes formed into 11 clusters. Number of grains per panicle, number of productive tillers per plant and grain yield per plant showed high per cent contribution towards genetic divergence.

Yogendra Singh *et al.* (2008) analyzed the divergence in 45 genotypes of Basmati rice (*Oryza sativa* L.) representing different regions of India were studied for genetic diversity on the basis of quality characteristics utilizing Mahalanobis D^2 analysis. Among different traits, grain and kernel length, grain breadth and milling recovery had maximum contribution towards total divergence.

Raut *et al.* (2009) grouped 40 rice genotypes into 3 clusters by using Mahalanobis D^2 statistic. Investigation revealed the independence of the genetic diversity from the eco geographic distribution of the genotypes. Length to breadth ratio of grain followed by number of grains per panicle, length of grain and seed yield per plant exhibited the greater contribution to the genetic divergence among genotypes.

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

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

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

good' appearance. Thus, these varieties can be used in breeding programme for improvement of germplasm.

Banumathy *et al.* (2010) evaluated 53 rice genotypes for yield and yield attributing characters using D^2 analysis, based on the analysis the genotypes were grouped into 11 clusters. Among the eight traits studied, grain yield, days to 50 per cent flowering, total grains per panicle and plant height together contributed 86.62 percent towards total divergence. Therefore, these characters may be given importance during hybridization programme.

Baradhan and Thangavel (2010) used Mahalanobis D^2 statistics to study the nature and magnitude of genetic diversity among 45 genotypes of rice. The genotypes were grouped into six clusters. It is suggested that varietal improvement through hybridization should be done among the genotypes having more of divergent clusters.

Dushyantha Kumar and Anand kantti (2010) evaluated 39 rice genotypes using Mahalanobis D^2 statistic. On the basis of genetic distance, these genotypes were grouped into eight clusters. Based on high mean performance of the traits studied are used as parents in future breeding programme to achieve desirable segregants for tall plant stature, number of panicles per plant, panicle length and high grain yield

Hosan *et al.* (2010) evaluated 20 rice landraces to assess the nature and magnitude of genetic divergence among them. Based on 12 characters, the genotypes were grouped into five clusters. Number of filled grains per panicle, number of panicles per plant and grain yield contributed considerably towards total divergence.

Nibedita Mohanty *et al.* (2010) evaluated 40 rice genotypes using Mahalanobis's D^2 analysis. The 40 genotypes were grouped into five clusters. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters *viz.* leaf area at 90 DAS, number of grains per panicle and days to 50 per cent flowering contributed maximum towards genetic divergence among the genotypes.

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

Ubarhande *et al.* (2010) evaluated 44 indica rice cultivars for sixteen quantitative traits to examine the nature and magnitude of variability and genetic divergence. On the basis of D^2 analysis forty four rice genotypes were grouped into nine clusters and three ungrouped clusters.

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

Mall *et al.* (2011) studied the grain quality characteristics of 24 promising genotypes were evaluated under irrigated and drought conditions for studying variability and genetic divergence. Genotypes were grouped into seven clusters, where cluster I was the largest and contained 18 genotypes while, rest of the clusters contained single genotypes. Based on clustering pattern and *per se* performance five genotypes were identified, which may be used in breeding programme to obtain improved genotypes with desirable attributes for stress environments.

Narendra Pratap *et al.* (2011) assessed the genetic divergence in 104 genotypes of rice comprising aromatic as well as non-aromatic germplasm lines by using Non-hierarchical Euclidean cluster analysis. The genotypes were grouped into 11 distinct clusters. Clustering pattern of genotypes showed lack of any relationship between geographic origin and genetic diversity. The crossing between superior genotypes of above diverse cluster pairs may provide desirable transgressive segregants for developing high yielding varieties of aromatic and non-aromatic rice is recommended.

Parikh *et al.* (2011) evaluated the seventy-one rice accessions to study the diversity pattern among the genotypes. The genotypes were grouped into eight clusters. The mode of distribution of genotypes from different geographic regions into various clusters was at random, indicating no association between geographical distribution of genotypes and genetic divergence. The inter cluster distance in most of the cases was higher than the intra-cluster distance, indicating wider genetic diversity among the accessions of different groups.

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

Vennila *et al.* (2011) evaluated 41 rice genotypes to identify diverse genotype for nine yield and yield attributing characters using Mahalanobis D^2 statistics. Based on the genetic distance all the forty one genotypes were grouped under thirteen different clusters. The characters like number of grains per panicle, plant height, grain length and grain breadth contributed maximum towards genetic diversity. Hence these characters could be given due importance for selection of genotypes for further crop improvement programme.

Yadav *et al.* (2011) evaluated nine genotypes for genetic divergence among them based on nine characters grouped and arranged in to 3 non-overlapping clusters by Mahalanobis (1936) D^2 statistics. On the basis of analysis result of genetic divergence and mean performance of four diverse and superior genotypes viz., CSR-27, CSR-36, CSR-839-3 and USAR-3 being exceptionally better for one or more traits and reasonable for other, as compared to checks were selected.

Ovung *et al.* (2012) estimated the nature and magnitude of genetic divergence in seventy rice genotypes using Mahalanobis D^2 statistics by considering 13 quantitative characters. High estimates of GCV and PCV were observed for grain yield per hill followed by tillers per hill and harvest index. High heritability coupled with high genetic advance was recorded for spikelet's per panicle.

Chakravorty *et al.* (2013) analyzed the diversity of phenotypic traits of the landraces of rice. The analysis of variance revealed significant variability in eighteen quantitative traits used in distance analysis. All the traits except ligule length, culm length, number of grains per panicle and number of primary branches per panicle exhibited positive and significant correlation coefficients with kernel weight.

Rashid *et al.* (2013) studied 20 diverse cultivars of rice for variation and correlation. Highly significant differences were presented among the genotypes for all the traits. Among the traits days to heading, days to maturity, number of productive tillers, 1000 grain weight showed highly significant positive correlation with grain yield per plant.

Allam *et al.* (2014) assessed the genetic divergence among 23 genotypes of Basmati rice representing different regions of India on the basis of yield and quality characteristics utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2 values), the rice genotypes were grouped into six clusters. Among different traits, plant height, kernel length, elongation ratio and amylase content had maximum contribution towards total divergence.

2.3 CORRELATION STUDIES

Study of character association helps the breeder in fixing a selection criteria for grain yield in parental lines, so that selections will be effective in isolating the plants with desired combination of characters. Phenotypic correlation is the correlation of phenotypic values and is subjected to changes in the environment. It measures the environment deviation together with non-additive gene action. Genotypic correlation is the correlation of breeding value. Hence, knowledge of association between different characters is highly essential for planning a sound breeding programme.

Several workers have studied the correlation coefficients in rice and contradictory association have been reported for almost all the character pairs which may be due to the different experimental material handled by them.

A brief review of studies on the association of characters in rice is presented here under:

2.3.1 Association of yield component characters with grain yield/plant in rice.

Character	Nature of association	Reference
Days to 50 per cent flowering	Positive significant	Suman (2003) Kuldeep <i>et al.</i> (2004) Sankar <i>et al.</i> (2006) Krishna <i>et al.</i> (2008) Abdul Fiyaz <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
	Positive non-significant	Rao and Shrivastav (1999) Madhavalatha <i>et al.</i> (2005) Satish Chandra <i>et al.</i> (2009) Nandan and Sweta Singh (2010)
	Negative significant	Eradasappa <i>et al.</i> (2007) Pankaj Garg <i>et al.</i> (2010) Ravindra Babu <i>et al.</i> (2012) Augustina <i>et al.</i> (2013) Ganapati <i>et al.</i> (2014) Imad Naseem <i>et al.</i> (2014).
	Negative non-significant	Yolanda and Vijendra (1995) Meenakshi <i>et al.</i> (1999) Mulugeta Seyoum <i>et al.</i> (2012)
	Positive significant	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Eradasappa <i>et al.</i> (2007) Krishna <i>et al.</i> (2008) Abdul Fiyaz <i>et al.</i> (2011) Ganapati <i>et al.</i> (2014)

Character	Nature of association	Reference
Plant height (cm)	Positive non-significant	Suman (2003) Madhavalatha <i>et al.</i> (2005) Karad and Pol (2008) Nandan and Sweta Singh (2010)
	Negative significant	Rao and Shrivastav (1999) Tara Satyavathi <i>et al.</i> (2001) Mahto <i>et al.</i> (2003) Rashid <i>et al.</i> (2013) Imad Naseem <i>et al.</i> (2014).
	Negative non-significant	Gupta <i>et al.</i> (1998) Meenakshi <i>et al.</i> (1999) Satish Chandra <i>et al.</i> (2009) Muluget Seyoum <i>et al.</i> (2012)
Number of productive tillers per plant	Positive significant	Suman (2003) Sankar <i>et al.</i> (2006) Abdul Fiyaz <i>et al.</i> (2011) Kiani <i>et al.</i> (2012) Ravindra Babu <i>et al.</i> (2012) Nagaraju <i>et al.</i> (2013) Rashid <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Imad Naseem <i>et al.</i> (2014).
	Positive non-significant	Reddy <i>et al.</i> (1997) Madhavalatha <i>et al.</i> (2005) Muluget Seyoum <i>et al.</i> (2012)
	Negative non-significant	Haque <i>et al.</i> (1991)

Character	Nature of association	Reference
Panicle length (cm)	Positive significant	Madhavalatha (2002) Sankar <i>et al.</i> (2006) Eradasappa <i>et al.</i> (2007) Satish Chandra <i>et al.</i> (2009) Basavaraja <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013)
	Positive non-significant	Tara Satyavathi <i>et al.</i> (2001) Madhavalatha <i>et al.</i> (2005) Krishna <i>et al.</i> (2008) Mulugeta Seyoum <i>et al.</i> (2012) Ganapati <i>et al.</i> (2014)
	Negative non-significant	Chauhan <i>et al.</i> (1993) Ramesh Babu (1999) Imad Naseem <i>et al.</i> (2014).
Days to maturity	Positive significant	Mareker and Siddiqui (1996)
	Positive non-significant	Ganesan <i>et al.</i> (1997) Reddy <i>et al.</i> (1997) Madhavalatha (2002)
	Negative significant	Krishna <i>et al.</i> (2008) Ganapati <i>et al.</i> (2014) Imad Naseem <i>et al.</i> (2014).
	Negative non-significant	Geeta <i>et al.</i> (1994) Asha Christopher <i>et al.</i> (1999)

Character	Nature of association	Reference
Number of filled grains per panicle	Positive significant	Sankar <i>et al.</i> (2006) Eradasappa <i>et al.</i> (2007) Krishna <i>et al.</i> (2008) Satish Chandra <i>et al.</i> (2009) Pankaj Garg <i>et al.</i> (2010) Padmaja <i>et al.</i> (2011) Kiani <i>et al.</i> (2012) Zulqarnain <i>et al.</i> (2012) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013)
	Positive non-significant	Madhavalatha <i>et al.</i> (2005) Nandan and Sweta Singh (2010) Akinwale <i>et al.</i> (2011) Rashid <i>et al.</i> (2013) Ganapati <i>et al.</i> (2014)
Hulling percentage	Positive non-significant	Roy <i>et al.</i> (1995) Madhavalatha (2002)
Milling percentage	Positive significant	Nagaraju <i>et al.</i> (2013)
Kernel length (mm)	Positive significant	Marekar and Siddiqui (1996) Nagaraju <i>et al.</i> (2013)
	Positive non-significant	Ganesan <i>et al.</i> (1997) Reddy <i>et al.</i> (1997) Madhavalatha (2002)
	Negative significant	Krishna <i>et al.</i> (2008)
	Negative non-significant	Geeta <i>et al.</i> (1994) Asha Christopher <i>et al.</i> (1999)
	Positive significant	Marekar and Siddiqui (1996) Tara Satyavathi <i>et al.</i> (2001) Pankaj Garge <i>et al.</i> (2010)

Character	Nature of association	Reference
Kernel L/B ratio	Positive non-significant	Ramesh Babu (1999) Madhavalatha (2002)
	Negative significant	Sakthivel (2001) Krishna <i>et al.</i> (2008)
	Negative non-significant	Asha Christopher <i>et al.</i> (1999) Satya Priya Lalitha and Sreedhar (1999)
1000-grain weight (g)	Positive significant	Satish Chandra <i>et al.</i> (2009) Basavaraja <i>et al.</i> (2011) Yadav <i>et al.</i> (2011) Zulqarnain <i>et al.</i> (2012) Rashid <i>et al.</i> (2013) Imad Naseem <i>et al.</i> (2014).
	Positive non-significant	Gupta <i>et al.</i> (1998) Vange <i>et al.</i> (1999) Madhavalatha <i>et al.</i> (2005)
	Negative non-significant	Suman (2003)
	Negative non-significant	Wilfred Manuel and Rangaswamy (1993) Geeta <i>et al.</i> (1994) Muluget Seyoum <i>et al.</i> (2012)

2.3.2 Association among the yield component traits in rice, association of days to 50 per cent flowering with

Character	Nature of association	Reference
Plant height(cm)	Positive significant	Kavitha and Sree Rama Reddi (2001) Sakthivel (2001) Madhavalatha (2002) Ravindra Babu <i>et al</i> (2012)
	Positive non-significant	Chauhan <i>et al.</i> (1993) Ramesh Babu (1999) Imad Naseem <i>et al.</i> (2014).
	Negative significant	Satish Chandra <i>et al.</i> (2009)
	Negative non-significant	Debchoudhury and Das (1998) Rao and Shrivastav (1999) Nandan and Sweta Singh (2010)
Number of Productive tillers/plant	Positive significant	Sawant <i>et al.</i> (1995) Sakthivel (2001)
	Positive non-significant	Kavitha and Sree Rama Reddi (2001) Surender Raju (2002) Satish Chandra <i>et al.</i> (2009)
	Negative non-significant	Yolanda and Vijendra (1995) Imad Naseem <i>et al.</i> (2014).
	Negative and significant	Meenakshi <i>et al.</i> (1999) Ravindra Babu <i>et al.</i> (2012)
Panicle length(cm)	Positive significant	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012)
	Positive non-significant	Sarma and Roy (1993) Sawant <i>et al.</i> (1995) Kavitha and Sree Rama Reddi (2001) Imad Naseem <i>et al.</i> (2014).

Character	Nature of association	Reference
	Negative non-significant	Chauhan <i>et al.</i> (1993) Ramesh Babu (1999) Ganapati <i>et al.</i> (2014).
	Negative significant	Nandan and Sweta Singh (2010)
Days to maturity	Positive significant	Ganapati <i>et al.</i> (2014) Imad Naseem <i>et al.</i> (2014).
	Negative significant	Ramesh Babu (1999) Nayak <i>et al.</i> (2001)
	Negative non-significant	Nandan and Sweta Singh (2010)
Number of filled grains/panicle	Positive significant.	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Mulugeta Seyoum <i>et al.</i> (2012)
	Positive non-significant	Satish Chandra <i>et al.</i> (2009) Vange <i>et al.</i> (1999) Nandan and Sweta Singh (2010)
	Negative non-significant	Sawant <i>et al.</i> (1995) Meenakshi <i>et al.</i> (1999) Ganapati <i>et al.</i> (2014)
Hulling percentage	Positive significant	Roy <i>et al.</i> (1995)
Kernel length(mm)	Negative significant	Ramesh Babu (1999) Nayak <i>et al.</i> (2001)
	Negative non-significant	Nandan and Sweta Singh (2010)
Kernel breadth(mm)	Negative non-significant	Nandan and Sweta Singh (2010)
L/B ratio	Positive significant	Deosarkar <i>et al.</i> (1989) Madhavalatha (2002)
	Negative non- significant	Kavitha and Sree Rama Reddi(2001)

Character	Nature of association	Reference
1000-grain weight(g)	Positive significant	Ravindranath <i>et al.</i> (1982) Yadav <i>et al.</i> (2011)
	Positive non-significant	Roy <i>et al.</i> (1995)
	Negative significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001) Sakthivel (2001) Imad Naseem <i>et al.</i> (2014).
	Negative non-significant	Vange <i>et al.</i> (1999) Satish Chandra <i>et al.</i> (2009) Nandan and Sweta Singh (2010) Ganapati <i>et al.</i> (2014)

2.3.3 Association among the yield component traits in rice, association of plant height with

Character	Nature of association	Reference
Number of productive tillers per plant	Positive significant	Janardhanam <i>et al.</i> (2001) Kavitha and Sree Rama Reddi (2001) Surender Raju (2002) Satish Chandra <i>et al.</i> (2009)
	Positive Non-significant	Roy <i>et al.</i> (1995) Yolanda and Vijendra (1995) Pradyumna Rao <i>et al.</i> (1996)
	Negative significant	Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001)
Panicle length (cm)	Positive significant	Tara Satyavathi <i>et al.</i> (2001) Madhavi Latha (2002) Sinha <i>et al.</i> (2004) Satish Chandra <i>et al.</i> (2009) Imad Naseem <i>et al.</i> (2014)

Character	Nature of association	Reference
	Positive non-significant	Chaubey and Singh (1994) Yolanda and Vijendra (1995) Reddy <i>et al.</i> (1997) Rao and Shrivastav (1999) Ganapati <i>et al.</i> (2014)
Number of filled Grains per panicle	Positive significant	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009)
	Positive non-significant	Geeta <i>et al.</i> (1994) Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001) Abdus Salam Khan <i>et al.</i> (2009) Ganapati <i>et al.</i> (2014)
	Negative significant	Debchoudhury and Das (1998) Surender Raju (2002)
	Negative non-significant	Chauhan <i>et al.</i> (1993) Sawant <i>et al.</i> (1995) Reddy <i>et al.</i> (1997)
Days to maturity	Positive non-significant	Ramesh Babu (1999) Imad Naseem <i>et al.</i> (2014)
	Negative significant	Nayak <i>et al.</i> (2001) Ganapati <i>et al.</i> (2014)
	Negative non-significant	De and Suriya Rao (1988) Geeta <i>et al.</i> (1994) Reddy <i>et al.</i> (1997) Nandan and Sweta Singh (2010)
Hulling percentage	Negative non-significant	Roy <i>et al.</i> (1995) Nandan and Sweta Singh (2010)

Character	Nature of association	Reference
Kernel length(mm)	Positive non-significant	Ramesh Babu (1999)
	Negative significant	Nayak <i>et al.</i> (2001)
	Negative non-significant	De and Suriya Rao (1988) Geeta <i>et al.</i> (1994) Reddy <i>et al.</i> (1997) Nandan and Sweta Singh (2010)
Kernel breadth(mm)	Positive significant	Krishna <i>et al.</i> (2008)
L/B ratio(mm)	Positive non-significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddi (2001)
	Negative non-significant	Nayak <i>et al.</i> (2001) Nandan and Sweta Singh (2010)
1000 grain Weight (g)	Positive significant	Reddy <i>et al.</i> (1997) Suman (2003) Yogameenakshi <i>et al.</i> (2004)
	Positive non-significant	Ramesh Babu (1999) Satish Chandra <i>et al.</i> (2009) Ganapati <i>et al.</i> (2014)
	Negative significant	Sukanya Subramanian and Rathinam (1984) Imad Naseem <i>et al.</i> (2014)
	Negative non-significant	Roy <i>et al.</i> (1995) Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001)

2.3.4 Association among the yield component traits in rice association of number of productive tillers per plant with

Character	Nature of association	Reference
Panicle length (cm)	Positive significant	Janardhanam <i>et al.</i> (2001) Sakthivel (2001) Padmaja <i>et al.</i> (2011)
	Positive non-significant	Yolanda and Vijendra (1996) Kavitha and Sree Rama Reddi (2001) Satish Chandra <i>et al.</i> (2009)
	Negative significant	Chaubey and Richharia (1993) Tara Satyavathi <i>et al.</i> (2001) Suman (2003)
	Negative non-significant	Reddy <i>et al.</i> (1997) Abdus Salam Khan <i>et al.</i> (2009) Imad Naseem <i>et al.</i> (2014)
Plant height (cm)	Positive significant	Meenakshi <i>et al.</i> (1999) Janardhanam <i>et al.</i> (2001) Sakthivel (2001)
	Negative non-significant	Imad Naseem <i>et al.</i> (2014)
Number of filled grains per panicle	Positive non-significant	Yolanda and Vijendra (1995) Satya Priya Lalitha and Sreedhar (1996) Abdus Salam Khan <i>et al.</i> (2009)
	Negative significant	Chaubey and Richharia (1993)
	Negative non-significant	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Tara Satyavathi <i>et al.</i> (2001) Satish Chandra <i>et al.</i> (2009)
Days to maturity	Positive significant	Hussain <i>et al.</i> (1989) Chauhan <i>et al.</i> (1994)
	Positive non-significant	Geeta <i>et al.</i> (1994)
	Negative significant	Ramesh Babu (1999)
	Negative non-significant	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001)

Character	Nature of association	Reference
		Imad Naseem <i>et al.</i> (2014)
Hulling percentage	Positive non-significant	Roy <i>et al.</i> (1995)
Kernel length (mm)	Positive significant	Hussain <i>et al.</i> (1989) Chauhan <i>et al.</i> (1994)
	Positive non-significant	Geeta <i>et al.</i> (1994)
	Negative significant	Ramesh Babu (1999)
	Negative non-significant	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001)
Kernel L/B ratio	Positive non-significant	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001)
	Negative significant	Tara Satyavathi <i>et al.</i> (2001)
	Negative non-significant	Ramesh Babu (1999)
1000 grain weight (g)	Positive and significant	Suryanarayana (2000) Sakthivel (2001)
	Positive non-significant	Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001) Tara Satyavathi <i>et al.</i> (2001) Imad Naseem <i>et al.</i> (2014)
	Negative significant	Gopinath <i>et al.</i> (1984) Nayak <i>et al.</i> (2001) Padmaja <i>et al.</i> (2011)
	Negative non-significant	Reddy <i>et al.</i> (1997) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012)

2.3.5 Association among the yield component traits in rice association of panicle length with

Character	Nature of association	Reference
Number of productive tillers per plant	Positive significant	Bala (2001)
	Negative and significant	Ravindra Babu <i>et al.</i> (2012)

Character	Nature of association	Reference
Number of filled grains per panicle	Positive significant	Satish Chandra <i>et al.</i> (2009) Abdus Salam Khan <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011)
	Positive non-significant	Reddy <i>et al.</i> (1997) Debchoudhury and Das (1998) Tara Satyavathi <i>et al.</i> (2001) Ganapati <i>et al.</i> (2014)
	Negative significant	Gopinath <i>et al.</i> (1984)
	Negative non-significant	Sawant <i>et al.</i> (1995) Nandan and Sweta Singh (2010)
Hulling percent	Positive non-significant	Roy <i>et al.</i> (1995)
Kernel length	Positive significant	Reddy <i>et al.</i> (1997) Ramesh Babu (1999)
	Negative non-significant	Nayak <i>et al.</i> (2001)
Kernel L/B ratio	Positive non-significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddi (2001) Nandan and Sweta Singh (2010)
	Negative significant	Nayak <i>et al.</i> (2001)
1000-grain weight (g)	Positive significant	Gopinath <i>et al.</i> (1984) Yogameenakshi <i>et al.</i> (2004) Ravindra Babu <i>et al.</i> (2012)
	Positive non-significant	Kavitha and Sree Rama Reddi (2001) Satish Chandra <i>et al.</i> (2009) Nandan <i>et al.</i> (2010)
	Negative significant	Sukanya Subramanian and Rathinam (1984) Imad Naseem <i>et al.</i> (2014)
	Negative non-significant	Roy <i>et al.</i> (1995) Vange <i>et al.</i> (1999) Nayak <i>et al.</i> (2001) Ganapati <i>et al.</i> (2014)

2.3.6 Association among the yield component traits in rice association of number of filled grains per panicle with

Character	Nature of association	Reference
Hulling percentage	Positive non-significant	Roy <i>et al.</i> (1995) Nandan and Sweta Singh (2010)
Kernel length (mm)	Negative significant	Geeta <i>et al.</i> (1994) Ramesh Babu (1999) Nayak <i>et al.</i> (2001)
	Negative non-significant	Reddy <i>et al.</i> (1997)
Kernel L/B ratio	Positive non-significant	Tara Satyavathi <i>et al.</i> (2001) Ramesh Babu (1999) Nayak <i>et al.</i> (2001)
	Negative significant	Kavitha and Sree Rama Reddi (2001)
1000-grain weight	Positive significant	Ravindranath <i>et al.</i> (1982)
	Positive non-significant	Meenakshi <i>et al.</i> (1999) Satish Chandra <i>et al.</i> (2009) Ganapati <i>et al.</i> (2014)
	Negative significant	Geetha <i>et al.</i> (1994) Nayak <i>et al.</i> (2001)
	Negative non-significant	Kavitha and Sree Rama Reddi (2001) Reddy <i>et al.</i> (1997) Nandan and Sweta Singh (2010)
Days to maturity	Negative significant	Geeta <i>et al.</i> (1994) Ramesh Babu (1999) Nayak <i>et al.</i> (2001)
	Negative non-significant	Reddy <i>et al.</i> (1997) Ganapati <i>et al.</i> (2014)

2.3.7 Association among the yield component traits in rice association of hulling percentage with

Character	Nature of association	Reference
1000 grain weight (g)	Positive and non-significant	Roy <i>et al.</i> (1995)

2.3.8 Association among the yield component traits in rice association of kernel length with

Character	Nature of association	Reference
Kernel L/B ratio	Positive significant	Asha Christopher <i>et al.</i> (1999) Madhavalatha (2002) Nayak <i>et al.</i> (2003) Krishna <i>et al.</i> (2008)
	Positive and non-significant	Sarwar <i>et al.</i> (1999)
Kernel breadth	Positive significant	Krishna <i>et al.</i> (2008)
1000-grain weight (g)	Positive significant	Singh <i>et al.</i> (1998) Nayak <i>et al.</i> (2001) Madhavalatha (2002)
	Positive and non-significant	De and Suriya Rao (1988)
	Negative and non-significant	Madhavalatha (2002)

2.3.9 Association among the yield component traits in rice association of L/B ratio with

Character	Nature of association	Reference
L/B ratio	Negative significant	Subudhi <i>et al.</i> (2007)
1000-grain weight	Positive significant	Nayak <i>et al.</i> (2001) Tara Satyavathi <i>et al.</i> (2001)
	Positive non-significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Sarwar <i>et al.</i> (1999)

2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis, a statistical device developed by Wright (1921) helps in partitioning of the correlation coefficients into direct and indirect effects of independent variable on dependent variable. As grain yield is a complex character influenced by several factors, selection based on simple correlation without taking into consideration between the component characters is not effective. Hence, path analysis is of much importance in any plant breeding programme. Correlation in combination with path analysis would give a better insight into cause and effect relationship between different pairs of characters. Dewey and Lu (1959) demonstrated the utility of path coefficient analysis in plant selection in wheat crop and since then its application has been extended to almost to every crop.

The findings of earlier workers on the relative contribution of different characters to grain yield in rice are furnished hereunder in a tabular form:

2.4.1 Direct effects

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Days to 50 per cent flowering	Khedikar <i>et al.</i> (2004) Sankar <i>et al.</i> (2006) Satish Chandra <i>et al.</i> (2009) Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012) Sanghera <i>et al.</i> (2013)	Deb choudhury and Das (1998) Gupta <i>et al.</i> (1998) Nayak <i>et al.</i> (2001) Pankaj Garg <i>et al.</i> (2010) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)
Plant height (cm)	Madhavalatha (2002) Sankar <i>et al.</i> (2006) Basavaraja <i>et al.</i> (2011) Yadav <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012) Ravindra Babu <i>et al.</i> (2012) Sanghera <i>et al.</i> (2013)	Saravanan <i>et al.</i> (1996) Tara Satyavathi <i>et al.</i> (2001) Suman (2003) Karad and Pol (2008) Satish Chandra <i>et al.</i> (2009) Akhtar <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Number of productive tillers per plant	Sankar <i>et al.</i> (2006) Karad and Pol (2008) Satish Chandra <i>et al.</i> (2009) Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Kiani <i>et al.</i> (2012) Ravindra Babu <i>et al.</i> (2012) Azarpour (2013) Nagaraju <i>et al.</i> (2013) Imad Naseem <i>et al.</i> (2014)	Valarmathi and Leenakumari (1998) Kavitha and Sree Rama Reddi (2001) Mulugeta Seyoum <i>et al.</i> (2012)
Panicle length (cm)	Khedikar <i>et al.</i> (2004) Karad and Pol (2008) Basavaraja <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012) Ravindra Babu <i>et al.</i> (2012)	Ganesan <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Pankaj Garg <i>et al.</i> (2010) Imad Naseem <i>et al.</i> (2014)
Days to maturity	Nagajyothi (2001) Imad Naseem <i>et al.</i> (2014)	Pankaj Garg <i>et al.</i> (2010)
Number of filled grains per panicle	Sankar <i>et al.</i> (2006) Satish Chandra <i>et al.</i> (2009) Nandan and Sweta Singh (2010) Kiani <i>et al.</i> (2012) Mulugeta Seyoum <i>et al.</i> (2012) Azarpour (2013) Nagaraju <i>et al.</i> (2013)	Amirthadevarathinam (1990) Gupta <i>et al.</i> (1998) Akhtar <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
Hulling percentage	Madhavalatha (2002) Nandan and Sweta Singh (2010)	Nagajyothi (2001)

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Kernel length (mm)	Sinha <i>et al.</i> (2004) Nayak <i>et al.</i> (2001) Rajamadhan <i>et al.</i> (2011)	Vivekanandan and Giridharan (1998) Madhavalatha (2002)
Kernel breadth (mm)	Krishna <i>et al.</i> (2008)	Ganesan <i>et al.</i> (1997) Pankaj Garg <i>et al.</i> (2010) Nandan and Sweta Singh (2010)
Kernel L/B ratio	Nagajyothi (2001) Madhavalatha (2002) Chaudhary and Mothiramani (2003) Sabesan <i>et al.</i> (2009)	Pankaj Garg <i>et al.</i> (2010)
1000-grain weight(g)	Suman (2003) Khedikar <i>et al.</i> (2004) Satish Chandra <i>et al.</i> (2009) Akhtar <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Yadav <i>et al.</i> (2011)	Karad and Pol (2008) Pankaj Garg <i>et al.</i> (2010) Basavaraja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Mulugeta Seyoum <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)

2.4.2 Indirect effects

2.4.2.1 Indirect effects of days to 50 per cent flowering on grain yield through

Character	Positive indirect effect	Negative indirect effect
Plant height (cm)	Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011)	Debchoudhury and Das (1998) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)
Number of productive tillers per plant	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)	Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001) Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)
Panicle length (cm)	Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011)	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)
Number of filled grains per panicle	Debchoudhury and Das (1998) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
Days to maturity	Madhavalatha (2002) Imad Naseem <i>et al.</i> (2014)	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001)
Hulling percent	Roy <i>et al.</i> (1995)	Madhavalatha (2002)
Kernel length(mm)	Sinha <i>et al.</i> (2004)	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Rajamadhan <i>et al.</i> (2011)
Kernel L/B ratio	Madhavalatha (2002)	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001)

1000-grain weight(g)	Kavitha and Sree Rama Reddi (2001) Madhavalatha (2002) Basavaraja <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)	Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
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2.4.2.2 Indirect effects of plant height on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Gupta <i>et al.</i> (1998) Madhavalatha (2002) Madhavalatha <i>et al.</i> (2005) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)	Sinha <i>et al.</i> (2004) Kavitha and Sree Rama Reddi (2001) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)
Number of productive tillers per plant	Nagajyothi (2001) Madhavalatha <i>et al.</i> (2005) Satish Chandra <i>et al.</i> (2009) Basavaraja <i>et al.</i> (2011)	Nayak <i>et al.</i> (2001) Tara Satyavathi <i>et al.</i> (2001) Padmaja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)
Panicle length (cm)	Satish Chandra <i>et al.</i> (2009) Basavaraja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Padmaja <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)
Number of grains per panicle	Madhavalatha <i>et al.</i> (2005) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)	Valarmathi and Leenakumari (1998) Suryanarayana (2000)
Days to maturity	Ramesh Babu (1999) Nagajyothi (2001)	Nayak <i>et al.</i> (2001) Madhavalatha (2002)

	Imad Naseem <i>et al.</i> (2014)	
Hulling percentage	----	Nagajyothi (2001) Madhavalatha (2002)
Kernel length (mm)	Ramesh Babu (1999) Sinha <i>et al.</i> (2004) Madhavalatha (2002)	Ganesan <i>et al.</i> (1997) Reddy <i>et al.</i> (1997) Rajamadhan <i>et al.</i> (2011)
Kernel L/B ratio	Ramesh Babu (1999) Nagajyothi (2001)	Nayak <i>et al.</i> (2001) Madhavalatha (2002)
1000-grain weight (g)	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Rajamadhan <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)	Nayak <i>et al.</i> (2001) Padmaja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)

2.4.2.3 Indirect effects of number of productive tillers per plant on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)	Amirthadevarathinam (1983) Kavitha and Sree Rama Reddi (2001) Basavaraja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
Plant height (cm)	Madhavalatha (2002) Basavaraja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)	Reddy <i>et al.</i> (1997) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012)
Panicle length (cm)	Madhavalatha (2002) Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012)

Character	Positive indirect effect	Negative indirect effect
Number of filled grains per panicle	Tara Satyavathi <i>et al.</i> (2001) Satish Chandra <i>et al.</i> (2009) Rajamadhan <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012)	Valarmathi and Leenakumari (1998) Nayak <i>et al.</i> (2001) Madhavalatha (2002) Ravindra Babu <i>et al.</i> (2012)
Hulling percentage	Madhavalatha (2002)	Nagajyothi (2001)
Kernel length (mm)	Ramesh Babu (1999)	Madhavalatha (2002) Rajamadhan <i>et al.</i> (2011)
Kernel L/B ratio	Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Ramesh Babu (1999)
1000-grain weight (g)	Reddy <i>et al.</i> (1997) Nagajyothi (2001) Tara Satyavathi <i>et al.</i> (2001)	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Akhtar <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)

2.4.2.4 Indirect effects of panicle length on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Satish Chandra <i>et al.</i> (2009) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)	Debchoudhury and Das (1998) Padmaja <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)
Plant height (cm)	Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)	Janardhanam <i>et al.</i> (2001) Tara Satyavathi <i>et al.</i> (2001) Imad Naseem <i>et al.</i> (2014)

Character	Positive indirect effect	Negative indirect effect
Number of productive tillers per plant	Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Kiani <i>et al.</i> (2012)	Tara Satyavathi <i>et al.</i> (2001) Madhavalatha (2002) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)
Number of grains per panicle	Nayak <i>et al.</i> (2001) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Mulugeta Seyoum <i>et al.</i> (2012)	Amirthadevarathinam (1983) Satish Chandra <i>et al.</i> (2009)
Hulling percentage	Roy <i>et al.</i> (1995)	Nagajyothi (2001) Madhavalatha (2002)
1000- grain weight (g)	Nagajyothi (2001) Madhavalatha (2002) Basavaraja <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)	Nayak <i>et al.</i> (2001) Satish Chandra <i>et al.</i> (2009)

2.4.2.5 Indirect effects of number of filled grains per panicle on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Gupta <i>et al.</i> (1998) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011)	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001) Rajamadhan <i>et al.</i> (2011)
Plant height (cm)	Madhavalatha (2002) Akhtar <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011)	Reddy <i>et al.</i> (1997) Debchoudhury and Das (1998) Satish Chandra <i>et al.</i> (2009)

Character	Positive indirect effect	Negative indirect effect
Number of productive tillers per plant	Amirthadevarathinam (1990) Valarmathi and Leenakumari 1998) Akhtar <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011)	Ganesan <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011)
Panicle length (cm)	Reddy <i>et al.</i> (1997) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011)	Madhavalatha (2002)
Hulling percent	Roy <i>et al.</i> (1995)	Madhavalatha (2002)
Kernel length	Ganesan <i>et al.</i> (1997) Madhavalatha (2002)	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Rajamadhan <i>et al.</i> (2011)
Kernel L/B ratio	Tara Satyavathi <i>et al.</i> (2001) Madhavi Latha (2002)	----
1000- grain weight (g)	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Akhtar <i>et al.</i> (2011) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011)	Tara Satyavathi <i>et al.</i> (2001)

2.4.2.6 Indirect effects of hulling percentage on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Roy <i>et al.</i> (1995)	Madhavalatha (2002)
Plant height (cm)	Roy <i>et al.</i> (1995) Nagajyothi (2001)	Madhavalatha (2002)
Number of productive tillers per plant	Roy <i>et al.</i> (1995) Nagajyothi (2001) Madhavalatha (2002)	-----

Character	Positive indirect effect	Negative indirect effect
Panicle length (cm)	Roy <i>et al.</i> (1995) Nagajyothi (2001) Madhavalatha (2002)	-----
1000-grain weight (g)	Madhavalatha (2002)	Roy <i>et al.</i> (1995) Nagajyothi (2001)

2.4.2.7 Indirect effects of kernel length on grain yield per plant through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Madhavalatha (2002) Rajamadhan <i>et al.</i> (2011)	Sinha <i>et al.</i> (2004)
Plant height (cm)	Ganesan <i>et al.</i> (1997)	Madhavalatha (2002) Rajamadhan <i>et al.</i> (2011)
Number of productive tillers per plant	Madhavalatha (2002)	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Rajamadhan <i>et al.</i> (2011)
Panicle length (cm)	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001)	Ganesan <i>et al.</i> (1997) Madhavalatha (2002) Rajamadhan <i>et al.</i> (2011)
Number of filled grains per panicle	Ramesh Babu (1999) Rajamadhan <i>et al.</i> (2011)	Nayak <i>et al.</i> (2001) Madhavalatha (2002)
L/B ratio	Vivekanandan <i>et al.</i> (1998) Asha Christopher <i>et al.</i> (1999)	Ramesh Babu (1999)
1000-grain weight (g)	Sinha <i>et al.</i> (2004) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Reddy <i>et al.</i> (1997) Rajamadhan <i>et al.</i> (2011)

2.4.2.8 Indirect effects of 1000-grain weight on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Imad Naseem <i>et al.</i> (2014)	Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
Plant height (cm)	Nagajyothi (2001) Madhavalatha (2002) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012) Imad Naseem <i>et al.</i> (2014)	Ganesan <i>et al.</i> (1997) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011)
Number of productive tillers per plant	Nagajyothi (2001) Tara Satyavathi <i>et al.</i> (2001) Imad Naseem <i>et al.</i> (2014)	Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Ravindra Babu <i>et al.</i> (2012)
Panicle length (cm)	Nayak <i>et al.</i> (2001) Padmaja <i>et al.</i> (2011) Rajamadhan <i>et al.</i> (2011) Imad Naseem <i>et al.</i> (2014)	Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Ravindra Babu <i>et al.</i> (2012)
Number of filled grain per panicle	Tara Satyavathi <i>et al.</i> (2001) Madhavalatha (2002) Satish Chandra <i>et al.</i> (2009) Padmaja <i>et al.</i> (2011)	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Rajamadhan <i>et al.</i> (2011)
Hulling percentage	Nagajyothi (2001) Madhavalatha (2002)	Roy <i>et al.</i> (1995)
Kernel length (mm)	Reddy <i>et al.</i> (1997) Rajamadhan <i>et al.</i> (2011)	Ganesan <i>et al.</i> (1997) Madhavalatha (2002)
L/B ratio	Nagajyothi (2001) Tara Satyavathi <i>et al.</i> (2001)	Madhavalatha (2002)

2.4.2.9 Indirect effects of L/B ratio on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Nayak <i>et al.</i> (2001) Madhaviatha (2002)	Ramesh Babu (1999)
Plant height (cm)	Nagajyothi (2001) Tara Satyavathi <i>et al.</i> (2001)	Nayak <i>et al.</i> (2001) Madhaviatha (2002)
Number of productive tillers per plant	Tara Satyavathi <i>et al.</i> (2001) Madhaviatha (2002)	Nagajyothi (2001) Nayak <i>et al.</i> (2001)
Panicle length (cm)	Nagajyothi (2001) Nayak <i>et al.</i> (2001)	Tara Satyavathi <i>et al.</i> (2001) Madhaviatha (2002)
Number of grain per panicle	Madhaviatha (2002)	Nayak <i>et al.</i> (2001) Tara Satyavathi <i>et al.</i> (2001)
Kernel length (mm)	Ramesh Babu (1999) Nayak <i>et al.</i> (2001)	Asha Christopher <i>et al.</i> (1999) Madhaviatha (2002)
1000 grain weight (g)	Nagajyothi (2001) Nayak <i>et al.</i> (2001)	Tara Satyavathi <i>et al.</i> (2001) Madhaviatha (2002)

Chapter III

MATERIAL AND METHODS

The present experiment was carried out during *Kharif*, 2014-15 at Regional Agricultural Research Station (RARS) Farm, Jagtial Campus, Karimnagar, Telangana State, The material used and methods followed are presented below.

3.1 MATERIAL

The experimental material consists of 70 genotypes obtained from different sources. The information of the genotypes is given in Table 3.1.

3.2 METHODS

All the 70 genotypes were sown separately in the nursery on raised beds. Twenty seven days old seedlings of each genotype were transplanted in two rows each in 4 m length by adopting a spacing of 20cm between rows and 15cm between plants in a Randomized Block Design and replicated thrice. Recommended agronomic practices and plant protection measures for raising a healthy crop were taken up during experiment.

3.3 RECORDING OF OBSERVATIONS

Five plants of each genotype in each replication were selected are used to record data on 14 characters. The mean values were considered for statistical analysis.

3.3.1 YIELD CHARACTERS

3.3.1.1 Days to 50 Per Cent Flowering: The number of days from sowing to the days when primary panicles in 50 per cent plants were in heading was recorded.

3.3.1.2 Plant Height (cm): Plant height is measured in centimeters from ground level to the tip of the tallest panicle in each plant at the time of harvest.

3.3.1.3 Number of Productive Tillers per Plant: Number of ear bearing tillers per plant was counted at the time of harvest.

3.3.1.4 Panicle Length (cm): It was measured in centimeters at the time of plant maturity from the base of panicle to the tip of last spikelet prior to harvesting.

3.3.1.5 Number of Filled Grains per Panicle: Number of filled grains were counted from five panicles in each selected plant.

3.3.1.6 Days to Maturity: The number of days from sowing to the time of harvest was recorded

3.3.1.7 Grain Yield per Plant (g): The weight of filled grains harvested from each plant was recorded in grams after bringing the grains to required moisture content.

3.3.1.8 1000-grain weight (g): One thousand well filled grains were counted at random from each plant and weighed after thorough drying at 12 per cent moisture content and recorded in grams.

3.3.2 GRAIN QUALITY CHARACTERS

3.3.2.1 Hulling Percentage: Hundred grams of rough rice after thorough drying to a moisture level of 12-14 percent were passed through paddy sheller and the weight of the hulled rice taken and hulling percentage was calculated by using the following formula and presented in per cent:

$$\text{Hulling percentage} = \frac{\text{Total weight of hulled rice (g)}}{\text{Total weight of rough rice (g)}} \times 100$$

3.3.2.2 Milling Percentage: Dehusked rice sample of 10g paddy was collected from each genotype and milled in kett type T₂ polisher for 60 seconds and milling recovery was estimated by the formula given below:

$$\text{Milling percentage} = \frac{\text{Weight of milled rice (g)}}{\text{Weight of rough rice (g)}} \times 100$$

3.3.2.3 Head Rice Recovery Percentage: From each milled rice sample brokenes were separated, even $\frac{3}{4}$ of grain is also considered and head rice recovery was calculated by the formula:

$$\text{Head rice recovery (\%)} = \frac{\text{Weight of whole rice (g)}}{\text{Weight of rough rice (g)}} \times 100$$

3.3.2.4 Kernel Length (mm): Ten grains of unbroken milled rice were selected by hand randomly and the length in millimeter was recorded using Dial micrometer.

3.3.2.5 Kernel Breadth (mm): Ten grains of milled rice were selected by hand randomly and the breadth in millimeter was recorded using Dial micrometer.

3.3.2.6 L/B ratio: The L/B ratio was calculated by using the following formula of Murthy and Govindaswamy (1967):

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

Classification of grain length and shape of milled rice (Jennings *et al.*, 1979)

Designation	Length (mm)	Shape	L/B Ratio
Extra long	> 7.50	Slender	> 3.0
Long	6.61 – 7.50	Medium	2.1 – 3.0
Medium	5.51 – 6.60	Bold	1.1 – 2.0
Short	< 5.50	Round	< 1.1

3.4 STATISTICAL PROCEDURE

The data with respect to the above characters was subjected to the following analysis with the help of standard statistical procedures:

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

3.4.1 Analysis of variance

Analysis of variance was computed based on Randomized Block design for each of the character separately as per standard statistical procedure (Panse and Sukhatme, 1978). The significance was tested by referring to the values of 'F' table (Fischer and Yates, 1967).

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

Where,

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

μ = General mean

g_i = True effect of ' i^{th} ' genotype

r_j = True effect of ' j^{th} ' replication

e_{ij} = Random error association with ' i^{th} ' genotype and ' j^{th} ' replication.

The structure of analysis of variance:

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

Where,

r and t = number of replications and treatments, respectively

M'r, M't and M'e = mean sum of squares due to replications, treatments and error respectively.

3.4.2 Variance

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

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

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

$$\text{Where, } (\sigma^2_e) = \text{Error variance}$$

3.4.3 Genotypic and phenotypic coefficients of variance

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

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

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

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

<10% : low

10-20% : moderate

>20% : high

3.4.4 Heritability and genetic advance

Heritability

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

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

Where

h^2 = heritability in broad sense

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance (σ_g^2) + (σ_e^2)

σ_e^2 = environmental variance

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

Low : 0-30%

Medium : 30-60%

High : above 60%

Genetic advance

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

$$GA = K \cdot h^2(b) \cdot \sigma_p$$

Where

GA = expected genetic advance

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

σ_p = phenotypic standard deviation

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

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

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

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

Low : less than 10 %

Moderate : 10-20 %

High : more than 20 %

3.4.5 Estimation of genetic divergence using Mahalanobis's generalized distance (D²)

A measure of group distance based on multiple characters was given by Mahalanobis (1936) using D² statistic. With the help of this, genetic divergence between genotypes was estimated.

D² values between ith and jth genotypes for 'p' characters were calculated as.

$$D_{ij}^2 = \sum_{t=1}^p (Y_{it} - Y_{jt})^2$$

Where

Y_{it} = Uncorrelated mean values of i_{th} genotype for 't' character,

Y_{jt} = Uncorrelated mean values of j_{th} genotype for 't' character,

D_{ij}^2 = D² between i_{th} and j_{th} genotypes

3.4.5.1 Test of significance

After testing the differences between genotypes for each of the characters, a simultaneous test for significance for differences in the mean values of a number of correlated variations with regard to the pooled effect of characters was carried out by using 'V' statistic which in turn utilizes Wilk's 'Λ' criterion. The sum of squares and sum of product of *error* + *genotype* were used for this purpose. The estimation of 'Λ' (Wilk's criterion) was done using the following relationship.

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

Where

$$\text{'}\Lambda\text{' = Wilk's criterion}$$

$$W = \text{determination of error matrix}$$

$$S = \text{determination of error variety matrix}$$

The significance of 'Λ' was tested by:

$$X^2_{pq} = V(\text{stat}) = -m \log_e \text{'}\Lambda\text{' = } - \left[n - \frac{P+Q+1}{2} \right] \log_e \text{'}\Lambda\text{'}$$

Where,

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

$$P = \text{Number of variables or characters}$$

$$Q = \text{Number of variables}-1(\text{or d.f. for population})$$

$$n = \text{Degrees of freedom for error + varieties}$$

$$\text{Log}_e \text{'}\Lambda\text{' = } 2.3026 \log_{10} \text{'}\Lambda\text{'}$$

V (stat) can be approximately considered to be distributed as X^2_{pq} and if the calculated 'V' value from the formula exceeds $X^2_{pq}(K)$, the hypothesis is rejected at K level of significance; otherwise not.

3.4.5.2 Transformation of correlated variables

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

3.4.5.3 Computation of D^2 values

For a given combination of 'i' and 'j' genotype, the mean deviation i.e., $Y_{it} - Y_{jt}$ for $t = 1, 2, \dots, P$ variables were computed and D^2 values were calculated as sum of square deviations:

$$D_{ij}^2 = \sum_{t=1}^P (Y_{it} - Y_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i_{th} genotype for 't' character,

Y_{jt} = Uncorrelated mean values of j_{th} genotype for 't' character,

D_{ij}^2 = D^2 between i_{th} and j_{th} genotype,

3.4.5.4 Testing of significance of D^2 values

The D^2 values obtained for a pair of population is taken as the calculated values of X^2 and is tested against the tabulated value of X^2 for P degrees of freedom, where P is the number of characters considered.

3.4.5.5 Contribution of individual characters towards divergence

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

$$\text{Percentage contribution of characters} = \frac{N \times 100}{M}$$

Where

N = Number of genotype contribution where the character was ranked first

M = All possible combinations of number of genotypes considered

3.4.5.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two varieties belonging to same cluster should at least on an average show a similar D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in an increasing order of magnitude in a tabular form as described by Singh and Chaudhary (1979). To start with two populations having the smallest distance from each other were considered to which a third population having the smallest D^2 value from the first two populations was added. Similarly, next nearest fourth genotype was considered and this procedure was continued. At certain stage where it was felt that after adding a particular population there was abrupt increase in the average D^2 value, that population was not considered for including in that cluster. The group of the first cluster was then omitted and the rest was treated in a similar way. This process was continued till all the genotypes were included into one or other cluster.

3.4.5.7 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D^2_i/n$

Where,

ΣD^2_i = Sum of distances between all possible combinations (n) of the populations included in a cluster

n = Number of clusters

3.4.5.8 Average inter-cluster distance

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

The square root of the average D^2 value gave the genetic distance between the clusters. Based on D^2 values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

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

n_1 and n_2 are number of genotypes of two clusters

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

3.4.5.9 Cluster Diagram

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

3.4.6 Estimation of correlation coefficients

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

$$\text{Genotypic coefficient of correlation } (r_g) = r(x_i, x_j)_g = \frac{\text{Cov. } (x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where

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

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

$V (x_i)_g$ is genotypic variance of i^{th} character

$V (x_j)_g$ is genotypic variance of j^{th} character

$$\text{Phenotypic coefficient of correlation } (r_p) = r (x_i, x_j)_p = \frac{\text{Cov. } (x_i, x_j)_p}{\sqrt{V (x_i)_p \cdot V (x_j)_p}}$$

Where:

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

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

$V (x_i)_p$ is phenotypic variance of i^{th} character

$V (x_j)_p$ is phenotypic variance of j^{th} character

3.4.7 Path coefficient analysis

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

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

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

$$\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot$$

$$: \quad : \quad : \quad : \quad :$$

$$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \dots\dots\dots + P_{ny} r_{nn}$$

Where;

1, 2 n = Independent variables

y = Dependant variable

$r_{1y}, r_{2y} \dots r_{ny}$ = Coefficient of correlation between casual factors `1` to `n` on dependent character Y

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

The above question can be written in matrix form as:

$$\begin{matrix}
 & \text{A} & & \text{C} & & \text{B} \\
 \left(\begin{array}{c} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ \cdot \\ r_{ny} \end{array} \right) & & \left(\begin{array}{cccc} 1 & r_{12} & r_{13} & \dots r_{1n} \\ r_{21} & 1 & r_{23} & \dots r_{2n} \\ \cdot & \cdot & \cdot & \\ \cdot & \cdot & \cdot & \\ \cdot & \cdot & \cdot & \\ r_{n1} & r_{n2} & r_{n3} & \dots 1 \end{array} \right) & & \left(\begin{array}{c} P_{1y} \\ P_{2y} \\ \cdot \\ \cdot \\ \cdot \\ P_{ny} \end{array} \right)
 \end{matrix}$$

Then

$$B = (C)^{-1} A \text{ where } C^{-1} = \left(\begin{array}{cccc} C_{11} & C_{12} & C_{13} \dots & C_{1n} \\ C_{21} & C_{22} & C_{23} \dots & C_{2n} \\ \cdot & \cdot & \cdot & \cdot \\ \vdots & \vdots & \vdots & \vdots \\ \cdot & \cdot & \cdot & \cdot \\ C_{n1} & C_{n2} & C_{n3} \dots & C_{nn} \end{array} \right)$$

Direct effects were as follows:

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

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

$$p_{ny} = \sum_{i=1}^k c_{3i} r_{iy}$$

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

$$P_{ry} = \sqrt{1 - (p_{1y} r_{iy} + p_{2y} r_{iy} + \dots + p_{ny} r_{ny})}$$

Where:

p_{ny} = direct effect of x_n on Y

r_{iy} = correlation coefficient of x_n on Y

Table 3.1.Details of rice genotypes

S.No.	Genotype	Designation	Place of collection
1	IRBL 3-CP4/RL	IRBL 3-CP4/RL	RARS, Jagtial
2	IRBL 7-M/RL	IRBL 7-M/RL	RARS, Jagtial
3	IRBL 9-W/RL	IRBL 9-W/RL	RARS, Jagtial
4	Varalu	Released variety from Warangal	RARS, Jagtial
5	IR 10A234	IR 10A234	RARS, Jagtial
6	IR 11A208	IR 11A208	RARS, Jagtial
7	IR10K148	IR10K148	RARS, Jagtial
8	IR 50	IR 50	RARS, Jagtial
9	IRRI 142	IRRI 142	RARS, Jagtial
10	HANGANGCHAL 1	HANGANGCHAL 1	RARS, Jagtial
11	JINMIBYEO	JINMIBYEO	RARS, Jagtial
12	MTU-3626	Released variety from Maruteru	RARS, Jagtial
13	Shiva	Released variety from Warangal	RARS, Jagtial
14	SAMGANG	SAMGANG	RARS, Jagtial
15	MILYANG 240	MILYANG 240	RARS, Jagtial
16	MILYANG 23	MILYANG 23	RARS, Jagtial
17	HANAREUM	HANAREUM	RARS, Jagtial
18	IR 05K101	IR 05K101	RARS, Jagtial
19	GAYABYEO	GAYABYEO	RARS, Jagtial
20	GP 247	GP 247	RARS, Jagtial
21	HR 20654-39-3-5	HR 20654-39-3-5	RARS, Jagtial
22	IR10K153	IR10K153	RARS, Jagtial
23	IR 58025B	IR 58025B	RARS, Jagtial
24	IR 67684B	IR 67684B	RARS, Jagtial
25	IR 68888B	IR 68888B	RARS, Jagtial
26	IR 68897B	IR 68897B	RARS, Jagtial
27	IR 68895B	IR 68895B	RARS, Jagtial
28	IR 79128B	IR 79128B	RARS, Jagtial
29	IR 79156B	IR 79156B	RARS, Jagtial
30	IR 80151B	IR 80151B	RARS, Jagtial
31	IR 80559B	IR 80559B	RARS, Jagtial
32	IR 59624-34-2-2R	IR 59624-34-2-2R	RARS, Jagtial
33	IR 60819-34-2-1R	IR 60819-34-2-1R	RARS, Jagtial
34	IR 60919-150-3-3-3-2R	IR 60919-150-3-3-3-2R	RARS, Jagtial
35	IR 65483-14-1-1-4-13R	IR 65483-14-1-1-4-13R	RARS, Jagtial
36	IR 65514-5-2-19R	IR 65514-5-2-19R	RARS, Jagtial
37	IR 69502-6 -SRN-3-UBN-2-B	IR 69502-6 -SRN-3-UBN-2-B	RARS, Jagtial
38	JGL 17653	JGL 3828 x OR 1032-5-2	RARS, Jagtial

Table 3.1 cont...

39	JGL 18222	JGL 3855 X JGL 7046	RARS, Jagtial
40	JGL 18629	JGL 7046 x swarna // BPT 5204	RARS, Jagtial
41	JGL 18799	MTU 1001 x JGL 11470	RARS, Jagtial
42	JGL 19607	JGL 11470 X T 1477	RARS, Jagtial
43	JGL 20122	MTU 1010 x JGL 11727	RARS, Jagtial
44	BPT 5204	Released variety from Bapatla	RARS, Jagtial
45	JGL 20776	MTU 1010 x JGL 13595	RARS, Jagtial
46	JGL 20777	MTU 1010 x JGL 13595	RARS, Jagtial
47	JGL 20779	MTU 1010 x JGL 13595	RARS, Jagtial
48	JGL 21002	MTU 1010 x JGL 11727	RARS, Jagtial
49	JGL 21005	MTU 1010 x JGL 11727	RARS, Jagtial
50	JGL 21075	MTU 1010 x JGL 11470	RARS, Jagtial
51	JGL 21078	MTU 1010 x JGL 11470	RARS, Jagtial
52	JGL 21794	MTU 1010 X JGL 11118	RARS, Jagtial
53	JGL 21820	JGL 13595 x JGL 11470	RARS, Jagtial
54	JGL 21828	JGL 13595 x JGL 11470	RARS, Jagtial
55	JGL 21851	JGL 11118 x JGL 11727	RARS, Jagtial
56	JGL 21868	MTU 1010 x JGL 11727	RARS, Jagtial
57	JGL 21883	MTU 1010 x JGL 11470	RARS, Jagtial
58	JGL 23183	JGL 4147 x HMT Sona	RARS, Jagtial
59	JGL 23185	JGL 4147 x HMT Sona	RARS, Jagtial
60	JGL 23666	JGL 17204 x VD 62	RARS, Jagtial
61	JGL 23710	JGL 13595 x VD 62	RARS, Jagtial
62	JGL 23713	JGL 13595 x VD 62	RARS, Jagtial
63	JGL 23745	JGL 11727 x VD 82	RARS, Jagtial
64	JGL 3855	Released variety from Jagtial	RARS, Jagtial
65	JGL 11470	Released variety from Jagtial	RARS, Jagtial
66	JGL 11727	Released variety from Jagtial	RARS, Jagtial
67	MTU 1010	Released variety from Jagtial	RARS, Jagtial
68	JGL 3844	Released variety from Jagtial	RARS, Jagtial
69	JGL 11118	Released variety from Jagtial	RARS, Jagtial
70	JGL 20171	Minikit culture from Jagtial	RARS, Jagtial

Chapter IV

RESULTS AND DISCUSSION

The results of the present investigation on genetic diversity studies for yield and quality traits in rice (*Oryza sativa* L.) are presented under the following heads:

- 4.1 Genetic divergence
- 4.2 Genetic variability, heritability and genetic advance
- 4.3 Correlation studies
- 4.4 Path coefficient analysis

4.1 GENETIC DIVERGENCE

The data collected from 70 genotypes of rice on 14 characters viz., days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000-grain weight, grain yield per plant, hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth, L/B ratio were used to study genetic divergence. The results of the study are presented below under the following heads.

4.1.1 Analysis of Variance

The analysis of variance revealed significant variation for all the traits studied (Table 4.1). Genetic diversity present in the available material has immense value on crop improvement for character of interest. From the point of selecting the parents for hybridization, which are divergent enough for the character of interest, estimation of the genetic distance is most important. The genetic divergence can be estimated by using an effective statistical tool, Mahalanobis D^2 statistics, which gives clear idea about the diverse nature of the population.

4.1.2 MEAN PERFORMANCE

The mean data of fourteen characters of 70 genotypes are presented in Table 4.2.

4.1.2.1 Days to 50 Per Cent Flowering: The number of days to 50 per cent flowering ranged from 79.67 to 113.67 days with a general mean of 94.62. Among all the genotypes, HR 20654-39-3-5 was found to be earliest (79.67 days) while IRBL3-CP4/RL was found to be late (113.67 days).

4.1.2.2 Days to Maturity: For this trait genotypes exhibited a range of 114.67 to 146.00 days with a general mean of 128.24. Among all the genotypes HANAREUM was earliest (114.67 days) while IRBL3-CP4/RL was found to be late (146.00 days).

4.1.2.3 Plant Height (cm): Plant height ranged from 80.80 to 117.20 cm with a general mean of 101.11 cm. The shortest genotype was BPT 5204 (80.80 cm) while the tallest genotype was IR 69502-6-SRN-3-UBN (117.20 cm).

4.1.2.4 Number of Productive Tillers per Plant: The mean productive tillers per plant ranged from 10.10 (JGL 3844) to 17.25 tillers (HANGANGCHAL 1) with a general mean of 11.95 tillers per plant.

4.1.2.5 Panicle Length (cm): The panicle length ranged from 19.00 to 29.20 cm with a general mean of 24.79 cm. The genotype HR 20654-39-3-5 has shorter panicle length 19.00 cm while the genotype JGL 20171 exhibited highest value of 29.20 cm. Which was almost 10.20 cm longer than HR 20654-39-3-5.

4.1.2.6 Number of Filled Grains per Panicle: The mean values for number of filled grains per panicle ranged from 64.50 (IR 79128B) to 281.50 (JGL 21820) with a general mean of 153.55.

4.1.2.7 1000-grain weight (g): The mean value of 1000-grain weight was 20.16 g and the values ranged from 11.17 (JGL 23710) to 28.87 g (JGL 23745). Among the genotypes tested JGL 23745 (28.87g) recorded the highest 1000-grain weight followed by MTU 3626 (27.18g), IRBL 9-W/RL (25.21g), IR 50 (25.19g), IR 10A234 (25.14g) and IRBL 7-M/RL (25.01g).

4.1.2.8 Grain Yield per Plant (g): The general mean for grain yield per plant was 31.92 g and the mean values ranged from 16.64g (IR 79128B) to 48.90g (GP247). The genotype GP247 (48.90g) recorded the highest grain yield per plant followed by JGL 18799 (44.28g), JGL 21075 (43.90g), JGL 21185 (40.81g), JGL 18629 (40.61g) and JGL 20171 (40.40g).

4.1.2.9 Hulling Percentage: The hulling percentage ranged from 77.75 (IR 10A234) to 84.30 per cent (IR 79128B) with general mean of 81.30 per cent.

4.1.2.10 Milling Percentage: The mean values for this character ranged from 67.10 per cent to 76.45 per cent with a general mean of 72.34 per cent. Lowest milling percentage was recorded in the genotype JGL 20171(67.10 per cent) and the genotype JGL 20779 (76.45 per cent) possessed highest milling percentage.

4.1.2.11 Head Rice Recovery Percentage: The head rice recovery percentage ranged from 51.60 per cent (JGL 17653) to 68.50 per cent (IR 50) with a general mean of 60.27 per cent.

4.1.2.12 Kernel Length (mm): The range of variation observed for this character was from 5.11 mm to 7.34 mm with a mean value of 6.33 mm. The genotype JGL 21828 (5.11 mm) had minimum kernel length whereas the genotype IR 79156B (7.34 mm) had maximum kernel length.

4.1.2.13 Kernel Breadth (mm): This trait varied from 1.45 mm to 2.63 mm with a general mean value of 1.91 mm. The genotype IR 67684B (1.45 mm) had minimum kernel breadth while the genotype HR 20654-39-3-5 (2.63 mm) had maximum kernel breadth.

4.1.2.14 L/B ratio: The range of variation observed for this character was from 2.00 to 4.95 with a mean value of 3.35. The genotype HR 20654-39-3-5 (2.00) had minimum length/ breadth ratio while the genotype IR 67684B (4.95) had maximum length/ breadth ratio.

4.1.3 Wilk's 'V' criterion test

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by % at 690 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 70 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.1.4 Mahalanobis's generalized distance D^2 values

In order to assess the genetic diversity among 70 genotypes, D^2 statistic was used following the procedure given by Rao (1952). Since the entire 14 yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method.

4.1.5 Grouping of genotypes into various clusters

Seventy genotypes were grouped into seven clusters based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in Table 4.3 and Fig 4.1. Out of seven clusters, cluster I was the largest comprising of 40 genotypes followed by cluster II with 20 genotypes, cluster V with six genotypes and clusters III, IV, VI, VII, with one genotype each. The clusters III, IV, VI and VII were represented by single genotype indicating high degree of heterogeneity among the genotypes.

4.1.6 Average inter and intra cluster distances

The average intra and inter cluster D^2 values are presented in Table 4.4 among seven clusters. The intra cluster D^2 values ranged from zero (cluster III, IV, VI, VII,) to 282.73 (cluster V). Maximum intra cluster distance was observed in cluster V (282.7) followed by cluster II (176.64), cluster I (155.53), indicating that some genetic divergence

still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding (Fig. 4.2 and 4.3).

From the inter cluster D^2 values of the seven clusters, it can be seen that the highest divergence occurred between cluster V and VII (1949.04) followed by cluster II and VII (1619.25), cluster II and III (1458.41), cluster V and VI (1282.97) and cluster III and VII (1268.29), cluster IV and V (1064.78) suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination. While the lowest was noticed between cluster IV and VI (105.32), followed by cluster VI and VII (223.52), cluster IV and VII (234.88), cluster I and IV (287.78), cluster I and VI (351.14) and cluster I and III (382.37).

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective may not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes (IR 59624-34-2-2R, HR 20654-39-3-5.) of cluster V and cluster VII (IR 67684B), cluster II (JGL 21075, JGL 18629) with cluster VII (IR 67684B), cluster II (JGL 21075, JGL 18629) with cluster III (JGL 23745), cluster V (IR 59624-34-2-2R, HR 20654-39-3-5.) with cluster VI (IR 79156B), cluster III (JGL 23745) with cluster VII (IR 67684B) and cluster IV (IR 58025B) with cluster V (IR 59624-34-2-2R, HR 20654-39-3-5.) would produce encouraging results. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

These findings are in conformity with the findings of Surender Raju (2002), Nayak *et al.* (2004), Bose and Pradhan (2005), Chand *et al.* (2005), Suman *et al.* (2005), Vaithiyalingan (2005), Devi *et al.* (2006), Chandra *et al.* (2007), Kumar and Ramesh (2008), Raut *et al.* (2009), Banumathy *et al.* (2010), Chaturvedi *et al.* (2011), Ovung *et al.* (2012), Chakravorty *et al.* (2013) and Allam *et al.* (2014).

4.1.7 Cluster means of the characters

The cluster means of fourteen characters are presented in Table 4.5. From the data it can be seen that considerable differences existed for all the characters under study. The

data indicated that the cluster mean for days to 50 per cent flowering was highest in cluster VII (97.67) and the lowest in cluster III (86.33). For days to maturity cluster mean was highest in cluster VII (131.67). Plant height was highest in cluster VI (108.10 cm) and lowest in cluster IV (85.30 cm). Cluster IV recorded the highest number of productive tillers per plant (13.00) and the lowest number of productive tillers per plant was in cluster III (10.50). Cluster VI recorded the highest panicle length (27.50 cm) and the lowest was recorded in cluster V (21.98 cm). The number of filled grains per panicle was highest in cluster II (213.53) and the lowest in cluster VII (91.20). Highest 1000 grain weight was recorded in cluster III (28.87 g) and the lowest in cluster II (14.65 g). Cluster I recorded the highest grain yield per plant (32.79 g) while in cluster VII it was low (16.81 g).

Cluster IV and VI recorded high hulling percentage (82.80%) and (80.20%) respectively. High milling percentage was recorded in cluster IV (73.80%) and cluster VI (70.55%). Cluster II recorded the highest head rice recovery percentage (62.55%) and the lowest in cluster III (56.55%). High kernel length was recorded in cluster VI (7.34 mm) whereas it was low in cluster II (5.55 mm). High kernel breadth was recorded in cluster III (2.44 mm) where as low in cluster VII (1.45 mm). High L/B ratio was recorded in cluster VII (4.95) and low in cluster V (2.43). The result indicated that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

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

The cluster I recorded highest mean value for grain yield per plant, cluster II for number of filled grains per panicle, head rice recovery percentage, cluster III for 1000-grain weight and kernel breadth, cluster IV for number of productive tillers per plant, hulling percentage and milling percentage, cluster VI for plant height, panicle length, kernel length and cluster VII for days to 50 per cent flowering, days to maturity and L/B ratio. The promising genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in hybridization programme.

4.1.8 Relative contribution of characters towards genetic divergence

The number of times that each of the fourteen characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.6 and Fig 4.4. The results showed that the contribution of kernel length was highest towards genetic divergence (37.18%) by taking 898 times ranking first, followed by kernel breadth (31.64%) by 764 times, days to 50 per cent flowering (11.76%) by 284 times, L/B ratio (7.45%) by 180 times, 1000-grain weight (3.81%) by 92 times, number of filled grains per panicle (3.31%) by 80 times, plant height (1.41%) by 34 times, milling percentage (1.24%) by 30 times, panicle length (0.87%) by 21 times, head rice recovery percentage (0.70%) by 17 times, grain yield per plant (0.41%) by 10 times, number of productive tillers per plant (0.08%), hulling percentage (0.08%) each by 2 times and days to maturity (0.04%) by 1 time is respectively to the genetic divergence in decreasing order.

Similar results were reported by Surender Raju (2002) for kernel length and days to 50 per cent flowering, Yogendra Singh *et al.* (2008) for grain and kernel length, Venila *et al.* (2011) for number of grains per panicle, plant height, kernel length and kernel L/B ratio, Raut *et al.* (2009) for length to breadth ratio of grain, number of grains per panicle and Allam *et al.* (2014) for plant height, kernel length.

Out of the fourteen characters studied, six characters namely kernel length, kernel breadth, days to 50 per cent flowering, L/B ratio, 1000-grain weight and number of filled grains per panicle together contributed 95.15% towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations.

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

4.2 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for 70 genotypes. Results are furnished in Table 4.7 and Fig 4.5 and 4.6 for PCV, GCV and heritability, genetic advance as per cent of mean respectively. The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values for different traits.

4.2.1 Days to 50 Per Cent Flowering

The genotypic and phenotypic coefficients of variation were low *i.e.*, 8.33 and 8.44, respectively. The observed heritability estimate for this trait was high (97.60 %) while, genetic advance as per cent of mean (16.96) was moderate. These results are in conformity with findings of Manoj Kumar Prajapati (2011), Dhurai *et al.* (2014) and Ganapati *et al.* (2014) for low GCV and PCV. Sanghera *et al.* (2013), Dhurai *et al.* (2014) and Ganapati *et al.* (2014) for high heritability and Mulugeta Seyoum *et al.* (2012) and Ganapati *et al.* (2014) for genetic advance as per cent of mean.

4.2.2 Plant Height (cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were low *i.e.*, 8.64 and 8.95, respectively. The observed heritability estimates for this character was high (93.30 %) with moderate genetic advance as per cent of mean (17.20). The similar results were reported by Patil *et al.* (2003) and Kole *et al.* (2008) for low GCV and PCV, Sanghera *et al.* (2013), Dhurai *et al.* (2014) and Ganapati *et al.* (2014) for high heritability and Patil *et al.* (2003) and Sinha *et al.* (2004) for moderate genetic advance as per cent of mean for plant height.

4.2.3 Number of Productive Tillers per Plant

The genotypic and phenotypic coefficients of variation for this trait were low and moderate *i.e.*, 9.70 and 11.57, respectively. The observed heritability estimate was high (70.20 %) and with moderate genetic advance as per cent of mean (16.74). The similar result were reported by Surender Raju (2002) and Pankaj Garg *et al.* (2010) for low GCV and Nagajyothi (2001), Krishna *et al.* (2008) for moderate PCV, Idris *et al.* (2013) and Dhurai *et al.* (2014) reported high heritability and Venkata Suresh (2001) and

Patra *et al.* (2006) with moderate genetic advance as per cent of mean for number of productive tillers per plant in rice.

4.2.4 Panicle Length (cm)

The GCV and PCV for this trait were low *i.e.*, 8.20 and 8.47, respectively. The heritability observed for this trait was high (93.90 %). This character recorded moderate genetic advance as per cent of mean (16.37). The results agrees with findings of Manoj kumar prajapati *et al.* (2011) and Ganapati *et al.* (2014) for low GCV and PCV. Mohan Lal *et al.* (2011) and Idris *et al.* (2013) for high heritability and Patra *et al.* (2006) for moderate genetic advance as per cent of mean.

4.2.5 Number of Filled Grains per Panicle

The high GCV (31.62) and PCV (32.19) estimates were observed for this trait. The heritability estimate for this trait was very high (94.90 %) with high genetic advance as per cent of mean (62.94). These results are comparable with findings of Pankaj Garg *et al.* (2010) , Mulugeta Seyoum *et al.*(2012) and Pratap *et al.* (2012) for high GCV and PCV, Idris *et al.* (2013) and Sanghera *et al.* (2013) and Ganapati *et al.* (2014) for high heritability and whereas Pratap *et al.* (2012) and Ganapati *et al.* (2014) for high genetic advance as per cent of mean.

4.2.6 Days to Maturity

A low GCV (5.74) and PCV (5.83) estimates were observed for this trait. The heritability estimate for this trait was high (97.00%) with moderate genetic advance as per cent of mean (11.64). The similar results were observed by Chanbeni *et al.* (2012).

4.2.7 1000-grain weight (g)

High genotypic (20.80) and phenotypic (21.03) coefficients of variation were recorded with high heritability estimate of 97.80 and high genetic advance as per cent of mean (42.39). The similar results were reported by Chandra *et al.* (2007) and Mulugeta Seyoum *et al.* (2012) for high GCV and PCV. Idris *et al.* (2013) and Dhurai *et al.* (2014) for high heritability and Abdul Fiyaz *et al.* (2011), Dhurai *et al.* (2014) and Ganapati *et al.* (2014) for high genetic advance as per cent of mean.

4.2.8 Grain Yield per Plant (g)

A high genotypic coefficient of variation (20.56) and phenotypic coefficient of variation (22.73) were observed for this trait. A high heritability estimate (81.80 %) coupled with high genetic advance as per cent of mean (38.31) were observed for this trait. The results are in conformity with findings of Sanghera *et al.* (2013), Dhurai *et al.* (2014) and Ganapati *et al.* (2014) for high GCV and PCV and Pankaj Garg *et al.* (2010), Dhurai *et al.* (2014) and Ganapati *et al.* (2014) for high heritability coupled with high genetic advance as per cent of mean.

4.2.9 Hulling Percentage

A low genotypic (1.68) and phenotypic (1.88) coefficients of variation were observed for this trait. The heritability estimate for this trait was high (80.40) with low genetic advance as per cent of mean (3.10). The similar result were reported by Madhavilatha (2002) and Surender Raju (2002) for low GCV and PCV, Nayak *et al.* (2003) and Madhavilatha *et al.* (2005) for high heritability and whereas for low genetic advance as per cent of mean was reported by Mall *et al.* (2011).

4.2.10 Milling Percentage

The genotypic and phenotypic coefficients of variation were low *i.e.*, 2.95 and 3.30, respectively. The heritability estimate observed was high (79.90) with a low genetic advance as per cent of mean (5.43). These results are agreement with findings of Nagajyothi (2001) and Chaudhary and Motiramani (2003) for low GCV and PCV, Chikkalingaiah *et al.* (1999) and Nayak *et al.* (2003) for high heritability and Nagajyothi (2001) for low genetic advance as per cent of mean.

4.2.11 Head Rice Recovery Percentage

The genotypic and phenotypic coefficients of variation were low *i.e.*, 5.41 and 6.29, respectively. The heritability estimate for this trait was high (74.00 %) with low genetic advance as per cent of mean (9.59). The similar results were reported by Chaudhary and Motiramani (2003) for low GCV and PCV, Patil *et al.* (2003) for high heritability coupled with low genetic advance percent of mean.

4.2.12 Kernel Length(mm)

A moderate genotypic (10.60) and phenotypic (10.63) coefficients of variation were observed for this trait. The heritability estimate was very high (99.40 %) with a high genetic advance as per cent of mean (21.77). The similar result were observed by Nayak *et al.* (2003) and Asish *et al.* (2010) for moderate GCV and PCV, Surender Raju (2002) and Dhurai *et al.* (2014) for high heritability and Jaiswal *et al.* (2007) high genetic advance as per cent of mean.

4.2.13 Kernel Breadth(mm)

A moderate genotypic (13.19) and phenotypic (13.23) coefficients of variation were observed for this trait. The heritability estimate was very high (99.40 %) with a high genetic advance as per cent of mean (27.09). The similar results were reported by Vivekanandan and Giridharan (1998) for moderate GCV and PCV, Chaudhary *et al.* (2004) and Dhurai *et al.* (2014) reported high heritability and Nayak *et al.* (2002) and Jaiswal *et al.* (2007) for high genetic advance for this trait.

4.2.14 L/B ratio

A moderate genotypic (13.19) and phenotypic (13.24) coefficients of variation were observed for this trait. The heritability estimate was very high (99.30 %) with a high genetic advance as per cent of mean (27.09). These results are in accordance with findings of Asish *et al.* (2010) and Sanghera *et al.* (2013) for moderate GCV and PCV, Nandan and Swetha Singh (2010) and Mohan Lal *et al.* (2011) for high heritability coupled with high genetic advance as per cent of mean.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are important selection parameters. Genotypic Coefficient of Variation (GCV) along with heritability estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.* 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Coefficient of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000 grain weight, grain yield per plant, hulling percentage, milling percentage, head rice recovery percentage, kernel length, kernel breadth and kernel L/B ratio indicating that these characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character.

High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection. All quality characters also exhibited high degree of broad-sense heritability, which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values.

The genetic advance as per cent of mean is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The traits which are recorded showed high heritability coupled with high genetic advance. It indicates the control of additive gene and selection may be effective for these characters.

4.3 CORRELATION STUDIES

Crop yield is the end product of the interaction of a number of other, often interrelated attributes. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. Phenotypic and genotypic correlations were worked out among yield and yield contributing characters in 70 genotypes. In general, genotypic

correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between characters studies, its expression is lessened due to influence of environment and considering the importance of phenotypic correlation it was discussed in the results which were presented in table 4.8.

4.3.1 Days to 50 Per Cent Flowering

The days to 50 per cent flowering recorded significant positive phenotypic correlation with days to maturity (0.9868**), positive and non-significant correlation with kernel length (0.0255) kernel breadth (0.0169) and 1000-grain weight (0.0089). While it had negative and non significant association with grain yield per plant (-0.0677), number of filled grains per panicle (-0.0013), L/B ratio (-0.0262) and milling percentage (-0.1044). The characters like plant height (-0.2083**), number of productive tillers per plant (-0.1483*), panicle length (-0.3315*), hulling percentage (-0.2122**) and head rice recovery percent (-0.3032**) showed negative and significant association.

The similar results were reported by Ganapati *et al.* (2014) and Imad Naseem *et al.* (2014) for days to maturity, Roy *et al.* (1995) for 1000 grain weight, Mulugeta Seyoum *et al.* (2012) for plant height, grain yield per plant, 1000 grain weight, kernel breadth, Ganapati *et al.* (2014) for number of filled grains per panicle, Kavitha and Sree Rama Reddi (2001) for L/B ratio, Satish Chandra *et al.* (2009) for plant height, Ravindra Babu *et al.* (2012) for number of productive tillers per plant and Nandan *et al.* (2010) for panicle length.

4.3.2 Days to maturity

Days to maturity showed significant negative association with plant height (-0.2033**), number of productive tillers per plant (-0.1445*), panicle length (-0.3454**), hulling percentage (-0.2063**) and head rice recovery percentage (-0.3008**). While it had non significant positive phenotypic correlation with kernel length(0.0297), kernel breadth (0.0226) and 1000-grain weight (0.0225), whereas it showed negative and non-significant correlation for number of filled grains per panicle (-0.0129), L/B ratio (-0.0245), milling percentage (-0.1013) and grain yield per plant (-0.0743).

The similar results were reported by Reddy *et al.* (1997) and Ganapati *et al.* (2014) for number of filled grains per panicle, Asha Christopher *et al.* (1999) for grain yield per plant, Nayak *et al.* (2001) and Ganapati *et al.* (2014) for plant height and Ramesh Babu (1999) for number of productive tillers per plant.

4.3.3 Plant Height (cm)

The plant height recorded significant positive phenotypic correlation with grain yield per plant (0.4059**), panicle length (0.6120**), number of filled grains per panicle (0.4160**), L/B ratio (0.1643**) and head rice recovery (0.2022**). Whereas it showed negative and non-significant correlation with number of productive tillers per plant (-0.0897), kernel breadth (-0.1724), 1000-grain weight (-0.0709) and hulling per cent (-0.0369) and positive and non-significant association for kernel length (0.0775), while negative and significant for the milling per cent (-0.1810*).

These results are in conformity with the findings of Abdul Fiyaz *et al.* (2011) and Ganapati *et al.* (2014) for grain yield per plant, Imad Naseem *et al.* (2014) for panicle length and 1000-grain weight, Satish Chandra *et al.* (2009) for number of filled grains per panicle and Nandan *et al.* (2010) for hulling percentage.

4.3.4 Number of Productive Tillers per Plant

Number of productive tillers per plant exhibited significant positive phenotypic correlation with grain yield per plant (0.2553**). It also exhibited negatively significant correlation with number of filled grains per panicle (-0.1818**). whereas it had negative and non-significant correlation with kernel breadth (-0.0700), hulling percentage (-0.0223) and milling percentage (-0.0348). The characters, panicle length (0.0755), kernel length (0.0580), L/B ratio (0.0870), 1000-grain weight (0.0230) and head rice recovery (0.0188) showed positive and non-significant correlation with number of productive tillers per plant.

The similar results were reported by Sanghera *et al.* (2013) and Imad Naseem *et al.* (2014) for grain yield per plant, Chaubey and Richharia (1993) for number of filled grains per panicle, Satish Chandra *et al.* (2009) for panicle length, Geeta *et al.* (1994) for kernel length, Nayak *et al.* (2001) for L/B ratio and Imad Naseem *et al.* (2014) for 1000-grain weight.

4.3.5 Panicle Length (cm)

Panicle length revealed significant positive association with grain yield per plant (0.2358**), kernel length (0.3160**), L/B ratio (0.4042**) and head rice recovery (0.1537*). Whereas number of filled grains per panicle (0.1313), 1000-grain weight (0.0329) and hulling per cent (0.0950) showed positive non-significant correlation. While negative and significant correlation with kernel breadth (-0.2098**) and milling per cent (-0.1456*).

The similar results were reported by Nagaraju *et al.* (2013) for grain yield per plant. Ramesh Babu (1999) for kernel length. Tara Satyavathi *et al.* (2001) and Ganapati *et al.* (2014) for number of filled grains per panicle, Nandan and Sweta Singh (2010) for 1000-grain weight and Roy *et al.* (1995) for hulling per cent.

4.3.6 Number of Filled Grains per Panicle

Number of filled grains per panicle exhibited significant positive phenotypic correlation with grain yield per plant (0.3798**) and head rice recovery (0.2705**). Whereas, it showed negative and significant correlation with kernel length (-0.6419**), kernel breadth (-0.4612**) and 1000-grain weight (-0.6757**). While it had negative and non-significant correlation with L/B ratio (-0.0865) and milling per cent (-0.0285) and positive and non-significant correlation shown by the character hulling per cent (0.1280).

The results are in conformity with the findings of Nagaraju *et al.* (2013) and Sanghera *et al.* (2013) for grain yield per plant, Nayak *et al.* (2001) for kernel length and 1000-grain weight, Nandan and Sweta Singh (2010) for hulling per cent.

4.3.7 1000-Grain Weight (g)

This character exhibited significant positive phenotypic correlation with grain yield per plant (0.1876**) while it had negative significant correlation with hulling per cent (-0.3570**) and head rice recovery (-0.2804**). The character milling per cent (-0.1141) showed negatively non-significant correlation with this character. The similar results were obtained by Rashid *et al.* (2013) for grain yield per plant.

4.3.8 Kernel Length (mm)

Kernel length showed significant positive phenotypic correlation with kernel breadth (0.3207**), L/B ratio (0.4563**) and 1000-grain weight (0.6898**) and it was negatively associated with hulling per cent (-0.0867), milling per cent (-0.0928) and grain yield per plant (-0.0694). While it was negatively significant correlation with head rice recovery (-0.2464**).

These results are in accordance with the findings of Krishna *et al.* (2008) for kernel breadth and L/B ratio, Madhavalatha (2002) for 1000-grain weight and Asha Christopher *et al.* (1999) for grain yield per plant.

4.3.9 Kernel Breadth (mm)

The association of kernel breadth was significant and positive with 1000-grain weight (0.8386**) and grain yield per plant (0.2284**). And it was showed significant and negative phenotypic association with L/B ratio (-0.6770**), hulling per cent (-0.3921**) and head rice recovery (-0.2443**). Whereas it showed negative and non significant correlation with milling per cent (-0.0771). The similar results were reported by Subudhi *et al.* (2007) for L/B ratio.

4.3.10 L/B Ratio

L/B ratio showed positive and significant phenotypic correlation with hulling per cent (0.3128**) and it was negatively significant correlation with 1000-grain weight (-0.2527**) and grain yield per plant (-0.3053**). While it showed positive and non significant correlation with milling per cent (0.0207) and head rice recovery (0.0222). These results are in conformity with the findings of Sarwar *et al.* (1999) for 1000-grain weight and Krishna *et al.* (2008) for grain yield per plant.

4.3.11 Hulling Percentage

Hulling percentage revealed significant and positive phenotypic correlation with milling percentage (0.4959**) and head rice recovery (0.3225**). While the character grain yield per plant (-0.2855**) had negatively significant correlation with hulling percentage.

4.3.12 Milling Percentage

Milling percentage showed positively significant phenotypic correlation with head rice recovery (0.3368**) and negatively significant correlation with grain yield per plant (-0.1991**).

4.3.13 Head Rice Recovery percentage

Head rice recovery percentage showed non significant positively phenotypic correlation with grain yield per plant (0.0296).

4.3.14 Grain Yield per Plant

Phenotypic correlations revealed that grain yield per plant had significant positive association with plant height (0.4059**), number of filled grains per panicle (0.3798**), number of productive tillers per plant (0.2553**), panicle length (0.2358**), kernel breadth (0.2284**) and 1000-grain weight (0.1876**). This indicated that all these characters were important for yield improvement. The traits like L/B ratio (-0.3053**), hulling percentage (-0.2855**) and milling percentage (-0.1991**) showed negatively significant association with this character. Whereas, the character head rice recovery percentage (0.0296) showed non-significant positive association with it. While it was showing negative and non-significant association with days to 50 per cent flowering (-0.0677), days to maturity (-0.0743) and kernel length (-0.0694).

Similar kind of association was revealed by Abdul Fiyaz *et al.* (2011) and Ganapati *et al.* (2014) for plant height. Sanghera *et al.* (2013) and Imad Naseem *et al.* (2014) for number of productive tillers per plant. Nagaraju *et al.* (2013) for panicle length. Sanghera *et al.* (2013) for number of filled grains per panicle. Rashid *et al.* (2013) for 1000-grain weight. Krishna *et al.* (2008) for L/B ratio. Muluget Seyoum *et al.* (2012) for days to 50 per cent flowering. Asha Christopher *et al.* (1999) for days to maturity and kernel length.

Hence, these characters could be considered as criteria for selection for higher yield as these were mutually and directly associated with grain yield. The characters like head rice recovery percentage also positively associated with grain yield per plant it indicates that this character also consider for selection for higher yield.

The study of phenotypic correlation studies showed that selection of plants with more plant height, number of filled grains per panicle, more number of productive tillers per plant, panicle length, kernel breadth, 1000- grain weight and head rice recovery percentage would result in improvement of yield.

4.4 PATH COEFFICIENT ANALYSIS

Correlation gives only the relation between two variables whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921). Hence, this objective was undertaken in the present investigation.

Based on the data recorded on the genotypes in the present investigation, the path analysis is done to determine direct and indirect effects of yield and yield attributing characters.

As discussed in correlation studies based on the importance of phenotypic effects the present results of phenotypic path coefficient of yield and yield contributing characters discussed here under which were presented in table 4.9 and Fig 4.7 and 4.8.

4.4.1 Days to 50 Percent Flowering

Days to 50 per cent flowering showed direct phenotypic positive effect (0.3384) on grain yield and the correlation between days to 50 per cent flowering and grain yield per plant was negative and non-significant (-0.0677). The correlation was negative and non significant mainly due to negative indirect effect through days to maturity (-0.3402), plant height (-0.0238), number of productive tillers per plant (-0.0612), panicle length (-0.0074), number of filled grains per panicle (-0.0012), kernel length (-0.0042), kernel breadth (-0.0011), L/B ratio (-0.0003) and milling percentage (-0.0006). Similar results of direct positive effect of days to 50 per cent flowering on grain yield per plant was reported by Padmaja *et al.* (2011), Mulugeta Seyoum *et al.* (2012) and Sanghera *et al.* (2013).

4.4.2 Days to Maturity

Negative direct phenotypic effect (-0.3448) on grain yield per plant was exhibited by days to maturity. The correlation between days to maturity and grain yield per plant was negative and non-significant (-0.0743). The correlation was negative mainly due to negative indirect effect contribution through plant height (-0.0232), number of productive tillers per plant (-0.0596), panicle length (-0.0077), number of filled grains per panicle (-0.0119), kernel length (-0.0049), kernel breadth (-0.0014), L/B ratio (-0.0003) and milling percentage (-0.0006). Similar results of direct negative effect of days to maturity on grain yield per plant was reported by Pankaj Garg *et al.* (2010).

4.4.3 Plant Height

Plant height had phenotypic positive direct effect on grain yield per plant (0.1142) while the correlation of plant height with grain yield was positive and significant (0.4059**). The correlation between plant height and grain yield was positive and significant mainly due to positive indirect effect contribution through days to maturity (0.0701), panicle length (0.0137), number of filled grains per panicle (0.3836), kernel breadth (0.0110), L/B ratio (0.0020) and hulling percentage (0.0035). The similar results were reported by Yadav *et al.* (2011), Mulugeta Seyoum *et al.* (2012), Ravindra Babu *et al.* (2012), Sanghera *et al.* (2013) for positive direct effect of plant height on grain yield per plant.

4.4.4 Number of Productive Tillers per Plant

Number of productive tillers per plant exhibited a phenotypic positive direct effect on grain yield per plant (0.4126) while the correlation with grain yield per plant was also positive and significant (0.2553**). The correlation was positive and significant mainly due to positive indirect effect contribution through days to maturity (0.0498), panicle length (0.0017), kernel breadth (0.0045), L/B ratio (0.0010), 1000- grain weight (0.0218) and hulling percentage (0.0021). The similar results were reported by Ravindra Babu *et al.* (2012), Nagaraju *et al.* (2013), Imad Naseem *et al.* (2014) for positive direct effect of number of productive tillers per plant on grain yield per plant.

4.4.5 Panicle length (cm)

This trait had direct phenotypic positive effect (0.0223) on grain yield per plant. The correlation with grain yield per plant was also positive and significant (0.2358**). The correlation was positive and significant mainly due to positive indirect contribution through days to maturity (0.1191), plant height (0.0699), number of productive tillers per plant (0.0311), number of filled grains per panicle (0.1211), kernel breadth (0.0133), L/B ratio (0.0049) and 1000- grain weight (0.0311).

These results are in accordance with findings of Karad and Pol (2008), Basavaraja *et al.* (2011), Mulugeta Seyoum *et al.* (2012) and Ravindra Babu *et al.* (2012) for positive direct effect of panicle length on grain yield per plant.

4.4.6 Number of Filled Grains per Panicle

Number of filled grains per panicle had direct phenotypic positive effect (0.9221) on grain yield per plant. Its correlation with grain yield per plant was also positive and significant (0.3798**). The correlation between number of filled grains per panicle and grain yield per plant was positive and significant mainly due to positive indirect effect contribution through days to maturity (0.0044), plant height (0.0475), panicle length (0.0029), kernel length (0.1058) and kernel breadth (0.0293). The similar result were reported by Nandan and Sweta Singh (2010), Kiani *et al.* (2012), Mulugeta Seyoum *et al.* (2012), Azarpour, (2013) and Nagaraju *et al.* (2013) for positive direct effect of number of filled grains per panicle on grain yield per plant.

4.4.7 1000-Grain Weight (g)

This trait had direct positive phenotypic effect on grain yield per plant (0.9453) and its correlation with grain yield was also positive and significant (0.1876**). The correlation between 1000 grain weight and grain yield per plant was positive and significant mainly due to positive indirect effect contribution through days to 50 per cent flowering (0.0030), number of productive tillers per plant (0.0095), panicle length (0.0007), hulling percentage (0.0336) and head rice recovery percentage (0.0051). The similar results were reported by Suman (2003), Khedikar *et al.* (2004), Satish Chandra *et al.* (2009), Akhtar *et al.* (2011), Padmaja *et al.* (2011), Yadav *et al.* (2011) for positive direct effect of 1000 grain weight on grain yield per plant.

4.4.8 Kernel Length (mm)

Kernel length had direct negative phenotypic effect on grain yield per plant (-0.1649). The correlation with grain yield was negative and non-significant (-0.0694). The correlation was negative and non-significant mainly due to negative indirect effect contribution through days to maturity (-0.0102), number of filled grains per panicle (-0.5919), kernel breadth (-0.0204) and milling percentage (-0.0006) on grain yield per plant. These results are in accordance with findings of Vivekanandan and Giridharan (1998), Madhavilatha (2002) for negative direct effect of kernel length on grain yield per plant.

4.4.9 Kernel Breadth (mm)

Negative direct phenotypic effect on grain yield per plant (-0.0636) was exhibited by kernel breadth while its correlation with grain yield was positive and significant (0.2284**). The positive correlation between kernel breadth and grain yield per plant mainly due to positive indirect contribution through day to 50 per cent flowering (0.0057), 1000-grain weight (0.7927), hulling percentage (0.0369) and head rice recovery percentage (0.0045). The similar results were reported by Ganesan *et al.* (1997), Pankaj Garg *et al.* (2010) and Nandan and Sweta Singh (2010) for negative direct effect of kernel breadth on grain yield per plant.

4.4.10 Length / Breadth ratio

This trait had direct positive phenotypic effect on grain yield per plant (0.0120) and its correlation to grain yield per plant was negative and significant (-0.3053**). The correlation between L/B ratio and grain yield per plant was negative and significant was mainly due to negative indirect contribution through days to 50 per cent flowering (-0.0089), number of filled grains per panicle (-0.0798), kernel length (-0.0752), 1000 grain weight (-0.2389), hulling percentage (-0.0295) and head rice recovery percentage (-0.0004) on grain yield per plant. The similar result were reported by Nagajyothi (2001), Madhavilatha (2002) and Chaudhary and Mothiramani (2003) and Sabesan *et al.* (2009) were reported positive direct effect of L/B on grain yield per plant.

4.4.11 Hulling Percentage

Hulling percentage had direct negative phenotypic effect on grain yield per plant (-0.0942). The correlation with grain yield was negative and significant (-0.2855**). The correlation was negative and significant mainly due to negative indirect effect contribution through days to 50 per cent flowering (-0.0718), plant height (-0.0042), number of productive tillers per plant (-0.0092), 1000-grain weight (-0.3375) and head rice recovery percentage (-0.0059).

4.4.12 Milling Percentage

This character had direct positive phenotypic effect on grain yield per plant (0.0062). While the correlation with grain yield per plant was negative and significant (-0.1991**). The correlation was negative and significant mainly due to negative indirect contribution through days to 50 per cent flowering (-0.0353), plant height (-0.0207),

number of productive tillers per plant (-0.0143), panicle length (-0.0033), number of filled grains per panicle (-0.0263), 1000 grain weight (-0.1079), hulling percentage (-0.0467) and head rice recovery percentage (-0.0062).

4.4.13 Head Rice Recovery Percentage

Head rice recovery percentage had direct negative phenotypic effect on grain yield per plant (-0.0183). The correlation with grain yield per plant was positive and non-significant (0.0296). The correlation between head rice recovery percentage and grain yield per plant was positive and non-significant mainly due to positive indirect effect contribution through days to maturity (0.1037), plant height (0.0231), number of productive tillers per plant (0.0078), panicle length (0.0034), number of filled grains per panicle (0.2494), kernel length (0.0406), kernel breadth (0.0155), L/B ratio (0.0003) and milling percentage (0.0021).

4.4.14 Residual effect

Residual effect was 0.542 for phenotypic and 0.296 for genotypic path coefficient analysis.

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

Path coefficient analysis revealed that 1000-grain weight exerted the highest positive direct effect on grain yield per plant followed by number of filled grains per panicle, number of productive tillers per plant, days to 50 per cent flowering, plant height, panicle length, L/B ratio and milling percentage, indicating that the selection for these characters was likely to bring about an overall improvement in grain yield per plant directly. Therefore, it is suggested that preference should be given to these characters in the selection programme to isolate superior lines with genetic potentiality for higher yield in rice genotypes.

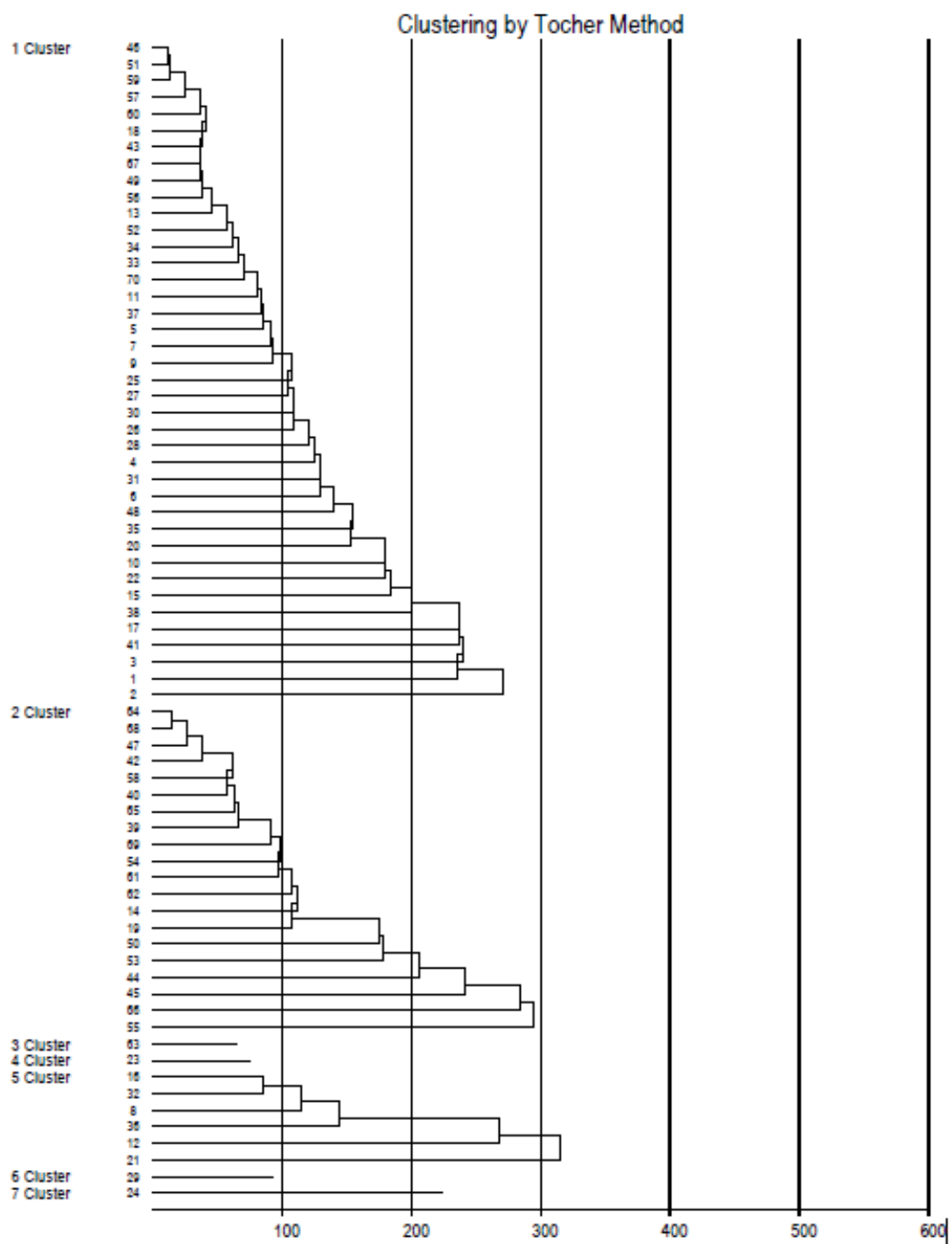


Figure 4.1. Clustering pattern of 70 genotypes in rice by Tocher Method.

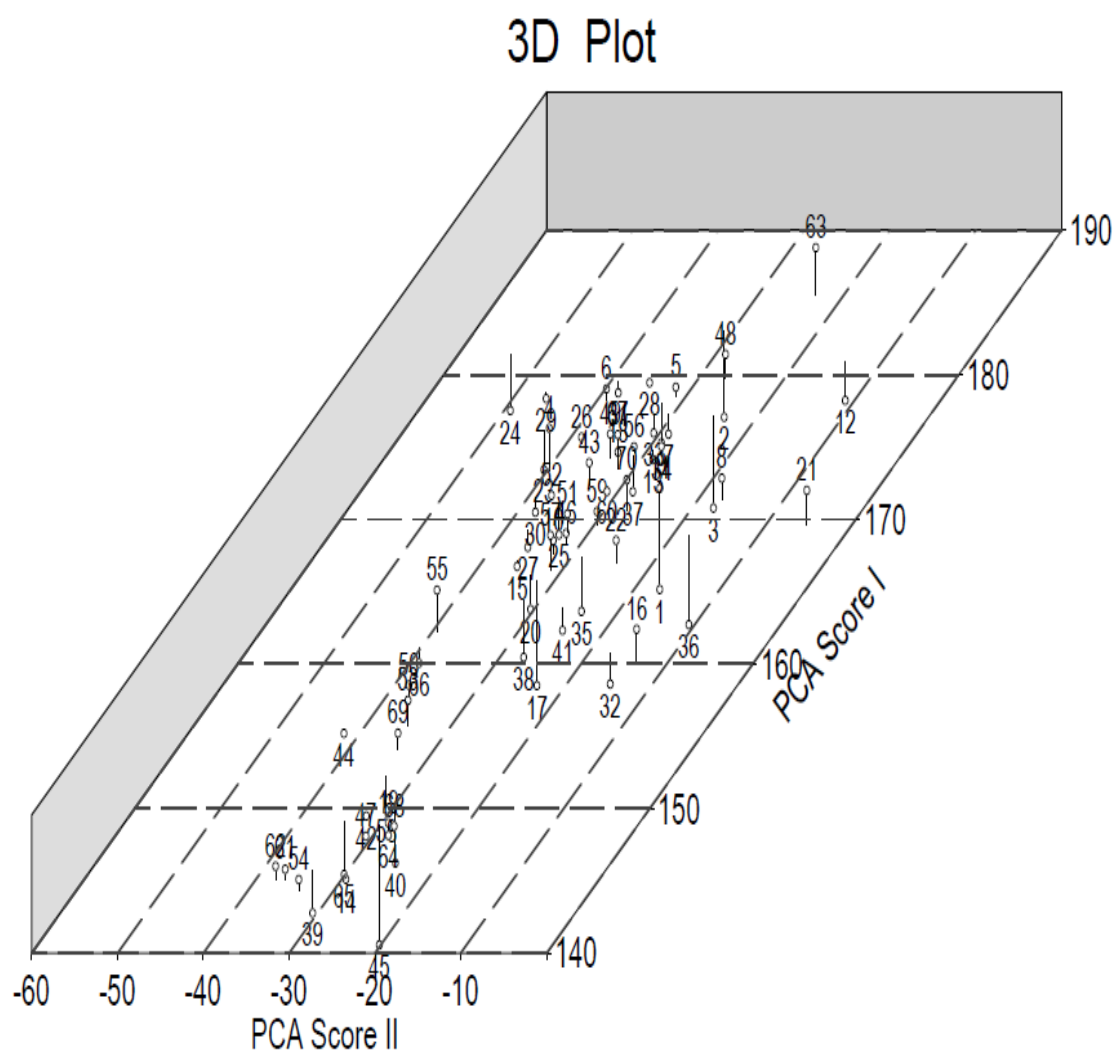


Fig.4.3. Statistical distance among 70 genotypes of rice (3D plot)

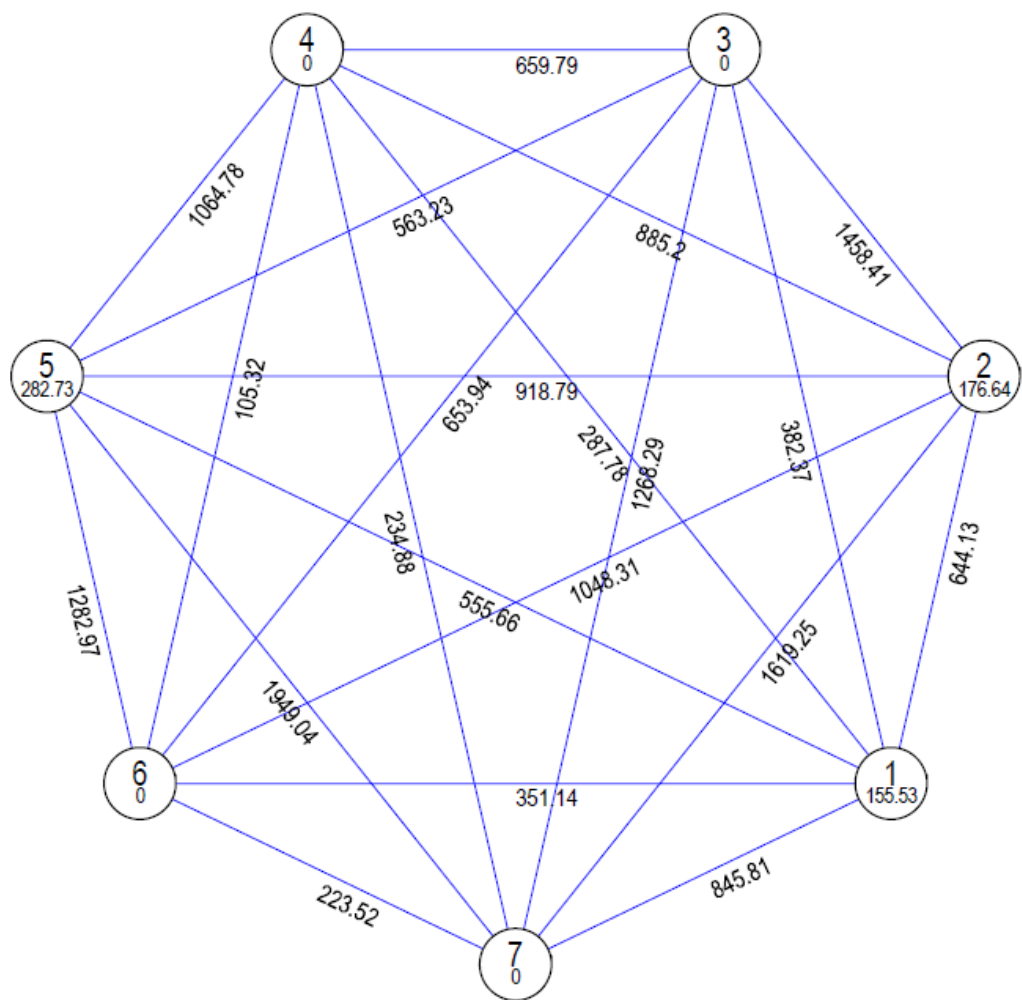


Fig.4.2. Mahalanobis Euclidean Disatnce among 70 genotypes of rice

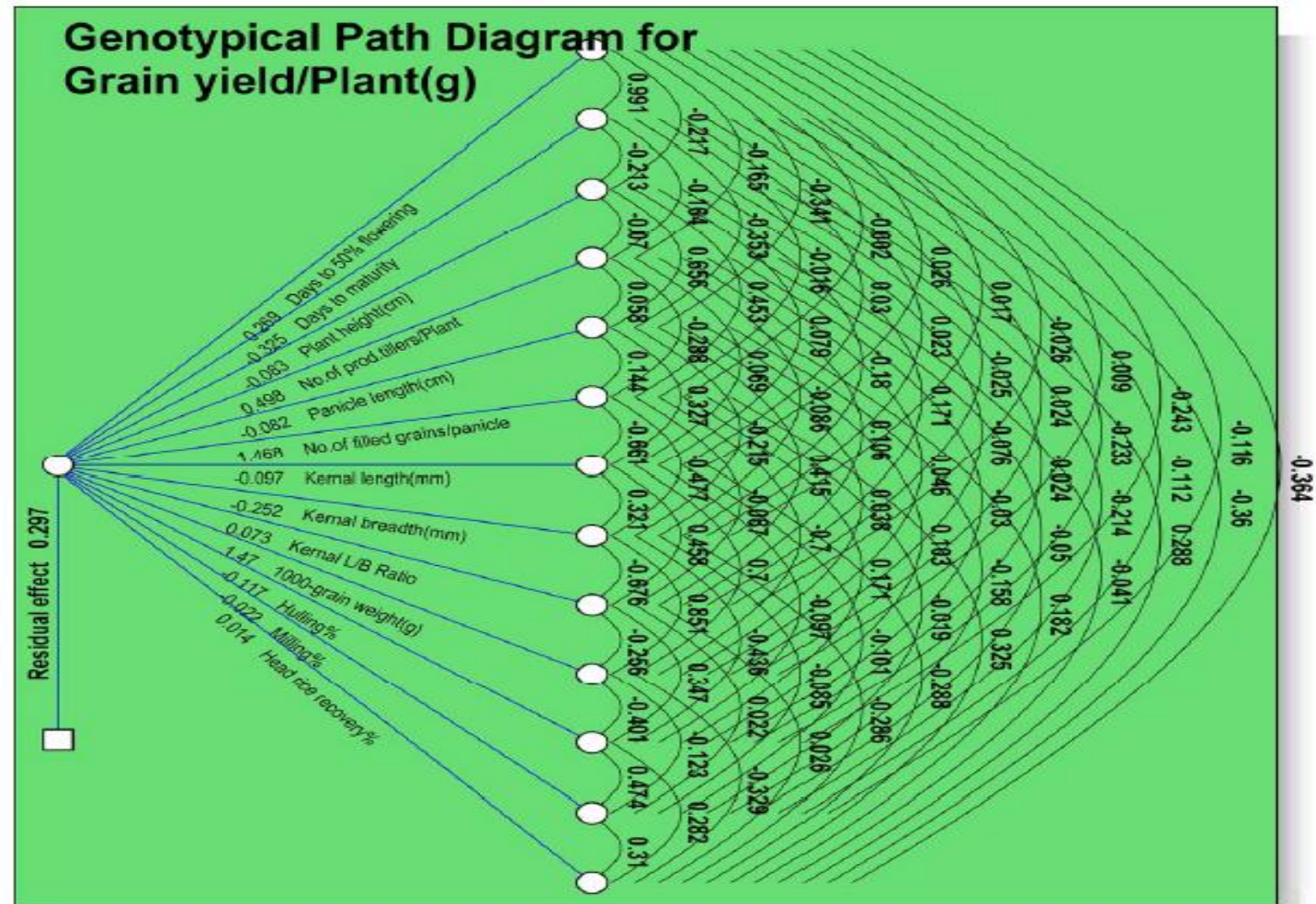


Figure 4.8. Genotypical path diagram for grain yield per plant (g)

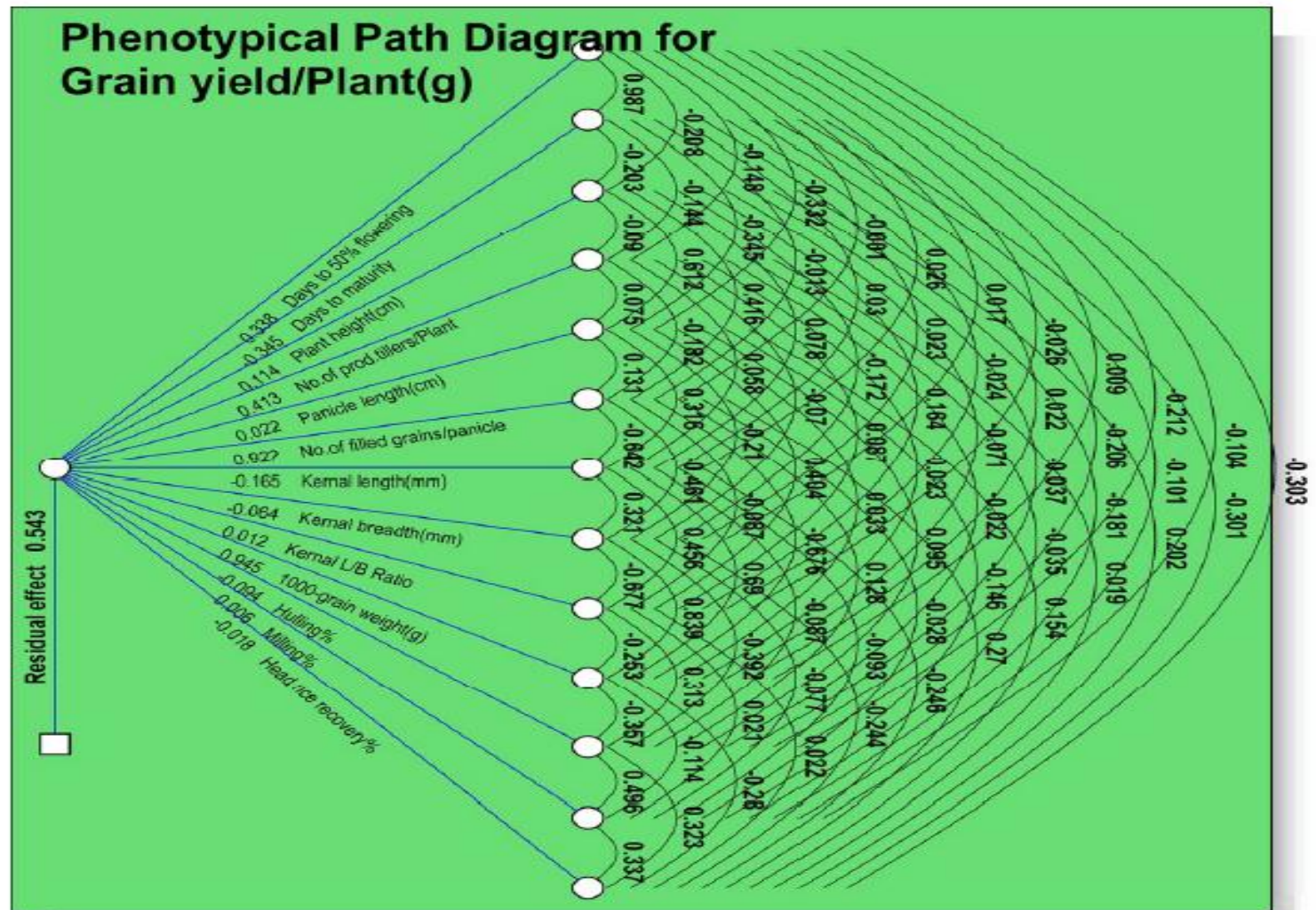


Figure 4.7. Phenotypical path diagram for grain yield per plant (g)

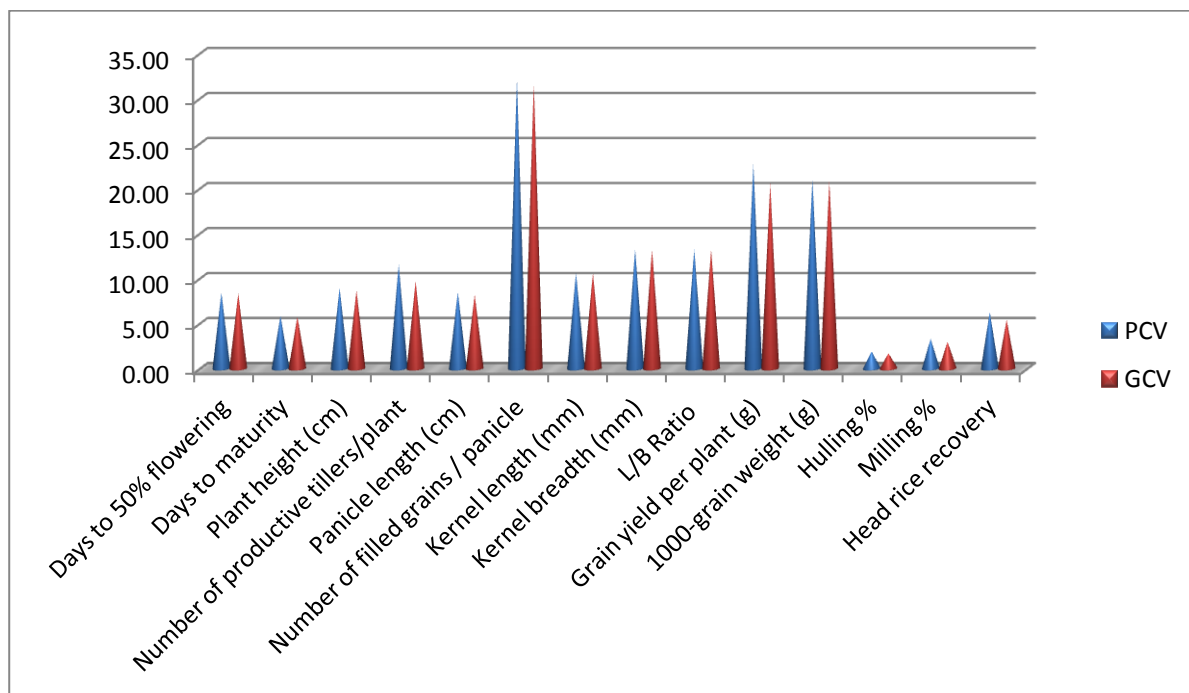


Figure 4.5. Graphical representation of PCV and GCV

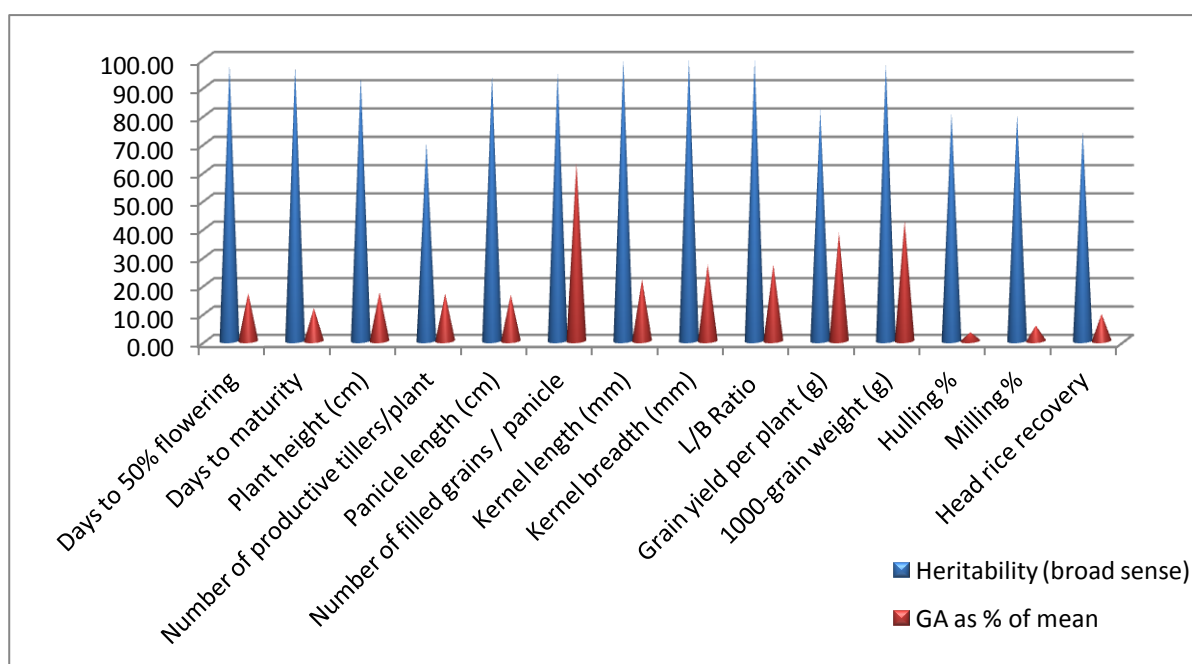


Figure 4.6. Graphical representation of h^2 and Genetic advance (5%)



Plate 3.1. General view of the experimental plot at RARS farm, Jagtial.

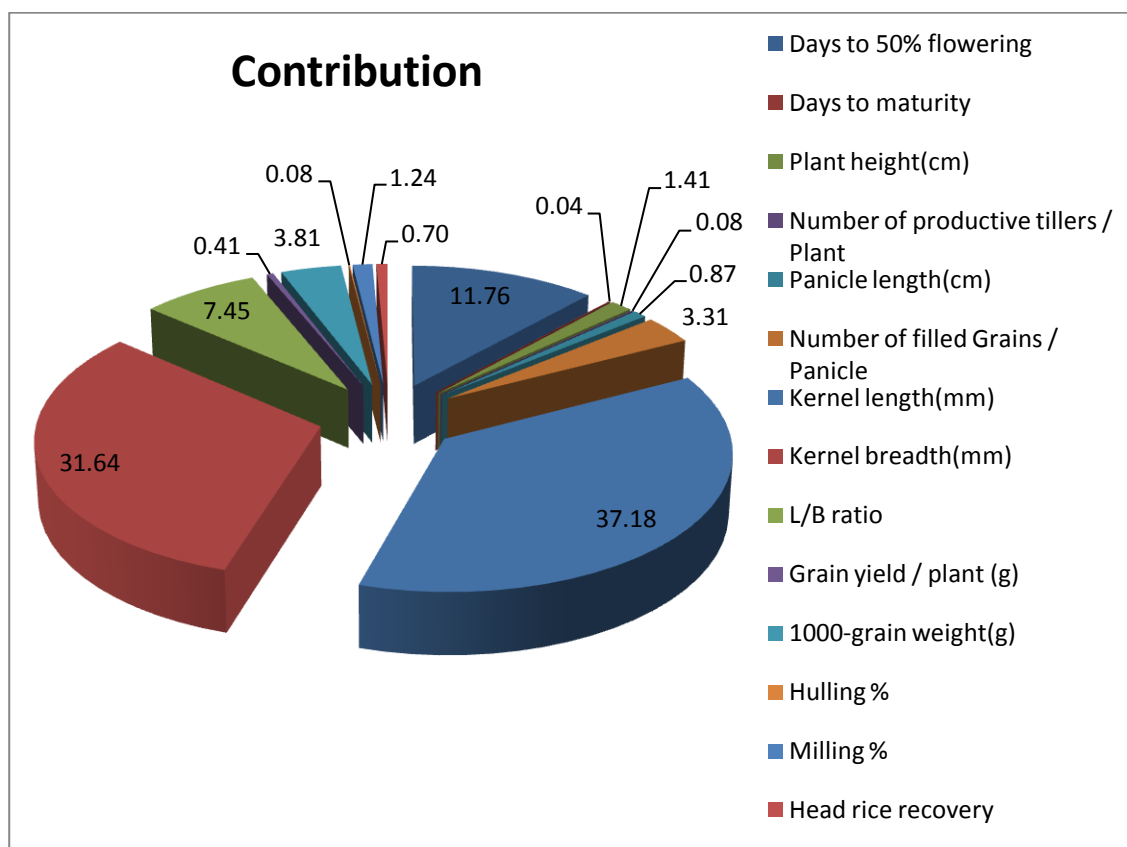


Figure 4.4. Relative contribution of different characters to genetic diversity in 70 rice genotypes.

Table 4.1: Analysis of variance for yield and quality traits in rice (*Oryza sativa* L.)

S.No.	Character	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=69)	Error (d.f.=138)
1	Days to 50% flowering	0.23	188.06 **	1.54
2	Days to maturity	0.13	164.39**	1.69
3	Plant height (cm)	15.36	234.64 **	5.51
4	Number of productive tillers per plant	4.18**	4.59 **	0.57
5	Panicle length(cm)	0.76	12.67 **	0.27
6	Number of filled grains per panicle	3074.33**	7080.98**	123.73
7	Kernel length (mm)	0.00	1.36**	0.00
8	Kernel breadth (mm)	0.00	0.19 **	0.00
9	L/B ratio	0.00	0.59 **	0.00
10	Grain yield per plant (g)	8.75	138.85**	9.59
11	1000-grain weight (g)	0.04	53.18 **	0.39
12	Hulling %	1.15	6.06 **	0.46
13	Milling %	0.21	14.81 **	1.15
14	Head rice recovery	7.69	35.63**	3.74

** Significant at 1 per cent level

Table 4.2: Mean performance of 70 genotypes for yield and quality traits in rice (*Oryza sativa* L.)

S.No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height(cm)	Number of productive tillers/ Plant	Panicle length(cm)	Number of filled grains/panicle	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)	1000-grain weight(g)	Hulling (%)	Milling (%)	Head rice recovery (%)
1	IRBL 3-CP4/RL	113.67	146.00	88.50	13.30	20.90	105.27	6.46	2.08	3.11	31.07	23.37	79.80	74.20	62.55
2	IRBL 7-M/RL	112.00	144.67	93.10	10.80	22.00	89.00	7.29	2.14	3.41	22.92	25.01	79.80	74.60	63.20
3	IRBL 9-W/RL	112.00	145.67	92.70	12.70	21.10	106.27	6.72	2.19	3.08	33.08	25.21	81.10	71.60	57.60
4	Varalu	84.67	117.67	113.50	10.85	27.00	162.80	7.03	1.84	3.83	35.29	21.34	81.75	73.85	58.05
5	IR 10A234	95.33	128.00	115.50	12.55	26.90	112.50	7.04	2.11	3.34	33.11	25.14	77.75	69.85	59.70
6	IR 11A208	95.67	129.00	112.80	10.50	28.60	135.80	7.30	1.94	3.77	28.34	21.78	79.35	71.30	61.65
7	IR 10K48	93.33	126.00	86.90	12.40	25.70	115.77	6.93	2.06	3.37	33.43	24.23	81.73	75.60	58.50
8	IR 50	87.00	122.33	88.00	11.10	23.30	118.00	6.07	2.34	2.59	29.81	25.19	83.30	76.10	68.50
9	IRRI 142	102.67	135.33	95.70	10.80	24.30	123.23	7.08	2.05	3.45	30.06	25.01	82.30	70.40	59.30
10	HANGANGCHAL 1	80.00	115.00	90.70	17.25	23.90	111.20	6.43	1.88	3.43	36.35	19.27	80.05	70.30	59.40
11	JINMIBYEO	91.67	125.67	96.40	12.80	26.40	129.13	6.47	2.16	2.99	35.50	22.86	82.40	74.55	59.95
12	MTU-3626	101.00	133.33	84.70	10.50	22.70	106.23	6.36	2.54	2.51	28.29	27.18	80.10	72.40	54.50
13	Shiva	96.67	129.33	108.80	12.50	24.70	128.70	6.77	2.09	3.24	38.06	24.94	79.25	70.55	60.30
14	SAMGANG	86.33	121.33	96.20	11.30	22.10	182.80	5.13	1.63	3.15	32.42	14.89	81.40	76.15	66.40
15	MILYANG 240	83.67	117.67	89.70	14.60	23.10	95.80	6.42	1.75	3.67	24.65	18.81	81.80	74.10	60.30
16	MILYANG 23	88.67	122.33	98.60	11.10	25.70	146.00	5.29	2.29	2.32	32.59	21.90	79.85	70.90	63.80
17	HANAREUM	112.00	144.67	86.70	11.00	23.00	101.80	6.24	1.82	3.43	18.63	19.17	81.80	72.00	56.30
18	IR 05K 101	88.33	123.33	102.50	13.40	25.90	115.50	6.76	1.99	3.41	35.06	24.31	80.75	68.35	60.30

Table 4.2 cont..

S.No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height(cm)	Number of productive tillers/ Plant	Panicle length(cm)	Number of filled grains/panicle	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)	1000-grain weight(g)	Hulling (%)	Milling (%)	Head rice recovery (%)
19	GAYABYEO	84.67	119.67	97.20	10.90	21.50	182.30	5.32	1.73	3.07	27.10	15.59	80.05	73.00	63.05
20	GP 247	100.33	133.33	98.70	11.80	26.30	194.00	6.39	1.84	3.47	48.90	21.67	79.70	72.05	56.95
21	HR 20654-39-3-5	79.67	114.67	86.10	11.40	19.00	138.50	5.24	2.63	2.00	38.90	24.80	80.50	72.75	57.20
22	IR 10K 153	88.00	122.00	107.70	12.30	25.70	126.30	6.13	2.10	2.92	35.71	23.05	79.50	72.65	59.30
23	IR 58025B	92.67	125.67	85.30	13.00	24.20	110.80	7.08	1.69	4.19	27.02	18.60	82.80	74.80	58.30
24	IR 67684B	97.67	131.67	92.60	11.90	24.40	91.20	7.17	1.45	4.95	16.81	17.61	82.30	73.60	57.65
25	IR 68888B	95.00	127.67	92.50	10.90	24.90	105.00	6.73	1.86	3.63	17.60	18.17	82.50	75.50	56.05
26	IR 68897B	87.67	121.67	95.10	11.20	26.20	80.70	6.96	1.82	3.82	18.63	22.48	83.00	71.80	58.75
27	IR 68895B	93.00	127.00	97.50	13.30	24.20	126.60	6.64	1.79	3.72	30.40	19.35	84.10	75.95	65.10
28	IR 79128B	91.00	125.33	98.90	11.20	24.50	64.50	7.28	2.01	3.63	16.64	21.77	84.30	73.60	59.70
29	IR 79156B	96.00	129.00	108.10	11.00	27.50	145.20	7.34	1.71	4.31	31.94	20.79	80.20	70.55	61.50
30	IR 80151B	94.33	127.33	100.30	12.40	25.90	114.00	6.84	1.79	3.82	26.54	18.95	82.10	68.85	58.25
31	IR 80559B	93.00	126.00	94.40	12.70	26.50	109.70	7.31	1.89	3.87	29.80	22.48	82.85	72.85	59.75
32	IR 59624-34-2-2R	98.00	132.00	97.00	12.50	21.70	157.40	5.55	2.19	2.53	39.25	20.52	79.70	72.60	59.65
33	IR 60819-34-2-1R	97.00	131.00	101.30	12.40	26.40	94.80	6.96	2.02	3.45	27.59	24.03	80.65	72.25	57.85
34	IR 60919-150-3-3-3-2R	95.67	129.33	99.90	13.70	26.00	113.50	6.83	2.07	3.31	33.42	24.31	81.80	74.00	58.50
35	IR 65483-14-1-1-4-13R	103.00	136.00	102.50	11.80	21.90	148.00	6.37	2.01	3.17	31.48	19.42	80.70	75.20	57.50
36	IR 65514-5-2-19R	108.00	141.33	84.10	10.20	19.50	111.73	5.94	2.25	2.65	20.93	22.30	78.30	71.70	53.50

Table 4.2 cont..

S.No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height(cm)	Number of productive tillers/ Plant	Panicle length(cm)	Number of filled grains/panicle	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)	1000-grain weight(g)	Hulling (%)	Milling (%)	Head rice recovery (%)
37	IR 69502-6-SRN-3-UBN	105.00	138.00	117.20	12.50	24.20	132.23	6.82	2.05	3.34	36.13	23.49	81.60	73.80	58.95
38	JGL 17653	103.33	136.00	95.20	12.10	23.00	197.23	6.34	1.90	3.35	39.98	18.39	80.85	67.65	51.60
39	JGL 18222	104.00	137.00	108.90	11.20	24.80	264.40	5.27	1.57	3.37	38.06	13.65	82.60	74.05	56.90
40	JGL 18629	106.33	139.00	103.00	11.60	24.10	234.50	5.43	1.73	3.15	40.61	16.58	81.80	71.05	56.00
41	JGL 18799	104.33	137.00	110.20	10.90	25.20	226.00	6.20	2.08	2.99	44.28	19.66	79.60	68.90	57.60
42	JGL 19607	95.00	129.00	113.40	13.70	25.60	214.50	5.47	1.67	3.28	33.65	14.62	82.05	73.30	61.35
43	JGL 20122	89.33	123.00	109.90	10.90	24.50	132.70	6.84	1.97	3.48	29.89	22.85	81.60	68.10	59.20
44	JGL 20776	88.00	122.00	97.30	11.40	25.20	182.20	5.78	1.46	3.96	23.74	13.43	82.30	74.35	62.80
45	BPT 5204	111.00	143.67	80.80	11.00	19.60	153.23	5.29	1.63	3.25	21.79	13.67	79.70	68.35	55.55
46	JGL 20777	93.00	126.67	106.10	11.60	26.70	165.50	6.50	1.95	3.34	35.22	21.95	80.40	71.75	61.30
47	JGL 20779	91.00	123.67	99.90	12.30	25.70	196.40	5.32	1.68	3.17	27.77	14.28	84.00	76.45	64.20
48	JGL 21002	91.67	126.00	108.90	11.60	25.80	145.70	7.05	2.28	3.09	38.18	25.08	81.45	73.70	60.20
49	JGL 21005	88.67	123.00	110.80	12.60	26.50	135.50	6.86	1.97	3.49	34.70	24.33	80.30	72.40	59.95
50	JGL 21075	93.00	126.00	116.40	11.80	26.00	211.70	6.01	1.68	3.59	43.90	18.29	83.25	72.70	67.25
51	JGL 21078	90.33	123.33	108.70	12.80	27.40	153.50	6.59	1.96	3.37	36.01	20.61	81.35	71.45	57.15
52	JGL 21794	91.67	125.33	104.30	11.20	25.20	159.50	6.83	1.86	3.69	36.42	21.01	81.90	73.45	61.20
53	JGL 21820	92.00	126.00	112.10	10.20	23.50	281.50	6.09	1.82	3.36	32.81	13.92	83.15	72.65	66.25
54	JGL 21828	89.00	124.00	109.00	12.60	25.90	186.20	5.11	1.52	3.38	28.52	13.49	82.60	73.65	65.35

Table 4.2 cont..

S.No.	Genotype	Days to 50 % flowering	Days to maturity	Plant height(cm)	Number of productive tillers/ Plant	Panicle length(cm)	Number of filled grains/panicle	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield per plant (g)	1000-grain weight(g)	Hulling (%)	Milling (%)	Head rice recovery (%)
55	JGL 21851	85.33	122.00	107.70	10.83	27.00	224.00	6.35	1.69	3.76	34.32	17.65	81.35	73.40	64.75
56	JGL 21868	89.67	125.00	107.70	13.80	24.70	126.60	6.81	2.02	3.37	38.49	24.40	80.10	71.60	56.40
57	JGL 21883	87.67	123.00	107.70	10.20	25.60	182.20	6.48	1.98	3.28	36.58	20.71	81.70	71.25	62.60
58	JGL 23183	102.00	136.33	103.50	11.30	25.80	233.77	5.62	1.67	3.37	35.95	15.60	82.70	75.55	60.50
59	JGL 23185	92.00	126.00	103.60	13.00	26.60	144.00	6.54	2.03	3.23	40.81	21.84	80.55	71.65	66.60
60	JGL 23666	93.67	126.67	104.80	13.90	25.30	132.20	6.70	1.99	3.37	37.05	23.26	80.20	68.10	58.10
61	JGL 23710	87.67	123.00	106.00	12.30	25.10	204.70	5.24	1.49	3.52	24.17	11.17	83.70	74.45	62.20
62	JGL 23713	89.33	124.67	105.40	11.50	25.30	216.70	5.29	1.48	3.58	21.63	11.39	83.85	69.70	62.55
63	JGL 23745	86.33	121.67	103.90	10.50	25.70	140.40	7.17	2.44	2.94	30.42	28.87	81.80	73.60	56.55
64	JGL 1798	95.00	125.00	99.10	12.20	24.90	234.70	5.41	1.77	3.05	37.64	14.91	81.55	72.10	62.65
65	JGL 11470	103.67	136.67	97.77	13.90	24.40	205.70	5.43	1.58	3.44	30.82	13.13	81.60	71.75	65.55
66	JGL 11727	101.33	136.00	111.10	11.00	27.90	222.63	6.24	1.64	3.81	32.09	16.60	80.00	69.60	59.40
67	MTU 1010	89.33	125.00	109.60	11.00	25.10	130.60	6.90	2.01	3.44	35.18	23.88	80.80	71.05	62.90
68	JGL 3844	95.67	125.67	105.70	10.10	25.30	236.00	5.39	1.83	2.95	30.74	14.52	80.60	71.70	65.05
69	JGL 11118	88.33	119.00	103.50	11.70	25.10	202.70	5.79	1.70	3.40	29.40	15.54	81.30	73.10	63.15
70	JGL 20171	90.33	124.67	108.00	12.90	29.20	139.10	6.49	2.10	3.10	40.40	23.15	79.25	67.10	58.10
General Mean		94.62	128.24	101.11	11.95	24.79	153.55	6.33	1.91	3.35	31.92	20.16	81.3	72.34	60.27
C.V (%)		1.31	1.01	2.32	6.31	2.10	7.24	0.81	1.05	1.08	9.70	3.09	0.83	1.48	3.21
Range Lowest		79.67	114.67	80.80	10.10	19.00	64.50	5.11	1.45	2.00	16.64	11.17	77.75	67.10	51.60
Range Highest		113.67	146.00	117.20	17.25	29.20	281.50	7.34	2.63	4.95	48.90	28.87	84.30	76.45	68.50
S.E		0.72	0.75	1.35	0.44	0.30	6.42	0.03	0.01	0.02	1.79	0.36	0.39	0.62	1.12
C.D at 5%		2.01	2.10	3.79	1.22	0.84	17.96	0.08	0.03	0.06	5.00	1.00	1.09	1.73	3.12
C.D at 1%		2.65	2.78	5.00	1.61	1.11	23.72	0.11	0.04	0.08	6.60	1.33	1.44	2.28	4.12

Table 4.3. Grouping of 70 genotypes in to different clusters

Cluster No	No.of genotype	Genotype
I	40	JGL 20777, JGL 21078, JGL 23185, JGL 21883, JGL 23666, IR 05K 101, JGL 20122, MTU 1010, JGL 21005, JGL 21868, Shiva, JGL 21794, IR 60919-150-3-3-3-2R, IR 60819-34-2-1R, JGL 20171, JINMIBYEO, IR 69502-6-SRN-3-UBN, IR 10A234, IR 10K48, IRRI 142, IR 68888B, IR 68895B, IR 80151B, IR 68897B, IR 79128B, Varalu, IR 80559B, IR 11A208, JGL 21002, IR 65483-14-1-1-4-13R, GP 247, HANGANGCHAL 1, IR 10K153, MILYANG 240, JGL 17653, HANAREUM, JGL 18799, IRBL 9-W/RL, IRBL 3-CP4/RL, IRBL 7-M/RL.
II	20	JGL 1798, JGL 3844, JGL 20779, JGL 19607, JGL 23183, JGL 18629, JGL 11470, JGL 18222, JGL 11118, JGL 21828, JGL 23710, JGL 23713, SAMGANG, GAYABYEO, JGL 21075, JGL 21820, JGL 20776, BPT 5204, JGL 11727, JGL 21851.
III	1	JGL 23745
IV	1	IR 58025B
V	6	MILYANG 23, IR 59624-34-2-2R, IR 50, IR 65514-5-2-19R, MTU-3626, HR 20654-39-3-5.
VI	1	IR 79156B
V II	1	IR 67684B

Table 4.6: Relative contribution of different characters towards genetic diversity in 70 genotypes of rice (*Oryza sativa* L.)

S.No.	Character	No.of times ranked first	Contribution (%)
1	Days to 50% flowering	284	11.76
2	Days to maturity	1	0.04
3	Plant height (cm)	34	1.41
4	Number of productive tillers per plant	2	0.08
5	Panicle length (cm)	21	0.87
6	Number of filled grains per panicle	80	3.31
7	Kernel length (mm)	898	37.18
8	Kernel breadth (mm)	764	31.64
9	L/B ratio	180	7.45
10	Grain yield per plant (g)	10	0.41
11	1000-grain weight (g)	92	3.81
12	Hulling %	2	0.08
13	Milling %	30	1.24
14	Head rice recovery	17	0.70

Table 4.4: Average intra (Bold values) and inter-cluster D values for fourteen characters in 70 genotypes of rice (*Oryza sativa* L.)

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	12.47 (155.53)	25.38 (644.13)	19.55 (382.37)	16.96 (287.78)	23.57 (555.66)	18.74 (351.14)	29.08 (845.81)
Cluster II		13.29 (176.64)	38.19 (1458.41)	29.75 (885.20)	30.31 (918.79)	32.38 (1048.31)	40.24 (1619.25)
Cluster III			0.00 (0.00)	25.69 (659.79)	23.73 (563.23)	25.57 (653.94)	35.61 (1268.29)
Cluster IV				0.00 (0.00)	32.63 (1064.78)	10.26 (105.32)	15.33 (234.88)
Cluster V					16.81 (282.73)	35.82 (1282.97)	44.15 (1949.04)
Cluster VI						0.00 (0.00)	14.95 (223.52)
Cluster VII							0.00 (0.00)

Values in Paranthesis are D² values

Table 4.5. Cluster means for yield components and quality traits for fourteen characters in 70 genotypes of rice (*Oryza sativa* L.)

Cluster No.	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers / plant	Panicle length (cm)	Number of filled grains / panicle	Kernel length (mm)	Kernel breadth (mm)	L/B ratio	Grain yield / plant (g)	1000-grain weight (g)	Hulling %	Milling %	Head rice recovery
I	94.99	128.58	101.88	12.25	25.18	130.31	6.73	1.98	3.41	32.79	22.27	81.06	71.95	59.42
II	94.33	127.98	103.70	11.64	24.74	213.53	5.55	1.65	3.38	31.36	14.65	81.98	72.85	62.55
III	86.33	121.67	103.90	10.50	25.70	140.40	7.17	2.44	2.94	30.42	28.87	81.80	73.60	56.55
IV	92.67	125.67	85.30	13.00	24.20	100.80	7.08	1.69	4.19	27.02	18.60	82.80	74.80	58.30
V	93.72	127.67	89.75	11.13	21.98	129.64	5.74	2.37	2.43	31.63	23.65	80.29	72.24	59.53
VI	96.00	129.00	108.10	11.00	27.50	145.20	7.34	1.71	4.31	31.94	20.79	80.20	70.55	61.50
VII	97.67	131.67	92.60	11.90	24.40	91.20	7.17	1.45	4.95	16.81	17.61	82.30	73.60	57.65

Table.4.8. Phenotypic (P) and Genotypic (G) correlation coefficients of yield and quality traits in rice (*Oryza sativa* L.)

Character		DFE	DM	PTH	No.PTT	PL	No.FGP	KL	KB	L/B	1000 GW	HUL	MIL	HRR	GYP
DFE	G	1.0000	0.9911**	-0.2172**	-0.1649*	-0.3412**	-0.0017	0.0260	0.0170	-0.0262	0.0091	-0.2426**	-0.1162	-0.3642**	-0.0617
	P	1.0000	0.9868**	-0.2083**	-0.1483*	-0.3315**	-0.0013	0.0255	0.0169	-0.0262	0.0089	-0.2122**	-0.1044	-0.3032**	-0.0677
DM	G		1.0000	-0.2131**	-0.1641*	-0.3533**	-0.0161	0.0303	0.0230	-0.0246	0.0241	-0.2333**	-0.1120	-0.3598**	-0.0680
	P		1.0000	-0.2033**	-0.1445*	-0.3454**	-0.0129	0.0297	0.0226	-0.0245	0.0225	-0.2063**	-0.1013	-0.3008**	-0.0743
PTH	G			1.0000	-0.0696	0.6560**	0.4528**	0.0793	-0.1801**	0.1713*	-0.0757	-0.0243	-0.2140**	0.2880**	0.4544**
	P			1.0000	-0.0897	0.6120**	0.4160**	0.0775	-0.1724	0.1643*	-0.0709	-0.0369	-0.1810**	0.2022**	0.4059**
No.PTT	G				1.0000	0.0577	-0.2877**	0.0686	-0.0858	0.1057	0.0458	-0.0298	-0.0496	-0.0410	0.1799**
	P				1.0000	0.0755	-0.1818**	0.0580	-0.0700	0.0870	0.0230	-0.0223	-0.0348	0.0188	0.2553**
PL	G					1.0000	0.1440*	0.3273**	-0.2147**	0.4153**	0.0384	0.1029	-0.1582*	0.1824**	0.2302**
	P					1.0000	0.1313	0.3160**	-0.2098**	0.4042**	0.0329	0.0950	-0.1456*	0.1537*	0.2358**
No.FGP	G						1.0000	-0.6608**	-0.4771**	-0.0867	-0.7002**	0.1705*	-0.0190	0.3247**	0.4138**
	P						1.0000	-0.6419**	-0.4612**	-0.0865	-0.6757**	0.1280	-0.0285	0.2705**	0.3798**
KL	G							1.0000	0.3211**	0.4582**	0.7002**	-0.0968	-0.1009	-0.2885**	-0.0778
	P							1.0000	0.3207**	0.4563**	0.6898**	-0.0867	-0.0928	-0.2464**	-0.0694
KB	G								1.0000	-0.6760**	0.8510**	-0.4359**	-0.0845	-0.2861**	0.2533**
	P								1.0000	-0.6770**	0.8386**	-0.3921**	-0.0771	-0.2443**	0.2284**
L/B	G									1.0000	-0.2561**	0.3467**	0.0218	0.0260	-0.3397**
	P									1.0000	-0.2527**	0.3128**	0.0207	0.0222	-0.3053**
1000 GW	G										1.0000	-0.4010**	-0.1225	-0.3294**	0.2064**
	P										1.0000	-0.3570**	-0.1141	-0.2804**	0.1876**
HUL	G											1.0000	0.4738**	0.2818**	-0.3283**
	P											1.0000	0.4959**	0.3225**	-0.2855**
MIL	G												1.0000	0.3102**	-0.2372**
	P												1.0000	0.3368**	-0.1991**
HRR	G													1.0000	0.0285
	P													1.0000	0.0296
* Significant at 5 per cent level; ** Significant at 1 per cent level															

DFE:Days to 50% flowering, **DM:**Days to maturity, **PTH:**Plant height(cm), **No.PTT:**Number of productive tillers per plant, **PL:**Panicle length(cm), **No.FGP:**Number of filled grains per panicle, **KL:**Kernel length(mm), **KB:**Kernel breadth(mm), **L/B:**L/B Ratio, **1000 GW:**1000-grain weight, **HUL:**Hulling%, **MIL:**Milling%, **HRR:**Head rice recovery%, **GYP:**Grain yield per plant(g)

Table.4.9. Phenotypic (P) and Genotypic (G) path coefficients of yield and quality traits in rice (*Oryza sativa* L.)

Character		DFF	DM	PTH	No.PTT	PL	No.FGP	KL	KB	L/B	1000 GW	HUL	MIL	HRR	GYP
DFF	G	0.2687	-0.3223	0.0181	-0.0821	0.0279	-0.0024	-0.0025	-0.0043	-0.0019	0.0133	0.0283	0.0026	-0.0050	-0.0617
	P	0.3384	-0.3402	-0.0238	-0.0612	-0.0074	-0.0012	-0.0042	-0.0011	-0.0003	0.0084	0.0200	-0.0006	0.0055	-0.0677
DM	G	0.2663	-0.3252	0.0178	-0.0817	0.0289	-0.0237	-0.0029	-0.0058	-0.0018	0.0354	0.0273	0.0025	-0.0050	-0.0680
	P	0.3339	-0.3448	-0.0232	-0.0596	-0.0077	-0.0119	-0.0049	-0.0014	-0.0003	0.0212	0.0194	-0.0006	0.0055	-0.0743
PTH	G	-0.0584	0.0693	-0.0834	-0.0347	-0.0536	0.6646	-0.0077	0.0455	0.0125	-0.1113	0.0028	0.0047	0.0040	0.4544**
	P	-0.0705	0.0701	0.1142	-0.0370	0.0137	0.3836	-0.0128	0.0110	0.0020	-0.0670	0.0035	-0.0011	-0.0037	0.4059**
No.PTT	G	-0.0443	0.0534	0.0058	0.4980	-0.0047	-0.4223	-0.0066	0.0217	0.0077	0.0673	0.0035	0.0011	-0.0006	0.1799**
	P	-0.0502	0.0498	-0.0103	0.4126	0.0017	-0.1676	-0.0096	0.0045	0.0010	0.0218	0.0021	-0.0002	-0.0003	0.2553**
PL	G	-0.0917	0.1149	-0.0547	0.0287	-0.0817	0.2115	-0.0317	0.0542	0.0303	0.0564	-0.0120	0.0035	0.0025	0.2302**
	P	-0.1122	0.1191	0.0699	0.0311	0.0223	0.1211	-0.0521	0.0133	0.0049	0.0311	-0.0089	-0.0009	-0.0028	0.2358**
No.FGP	G	-0.0004	0.0052	-0.0378	-0.1433	-0.0118	1.4680	0.0639	0.1204	-0.0063	-1.0292	-0.0199	0.0004	0.0045	0.4138**
	P	-0.0004	0.0044	0.0475	-0.0750	0.0029	0.9221	0.1058	0.0293	-0.0010	-0.6387	-0.0121	-0.0002	-0.0049	0.3798**
KL	G	0.0070	-0.0099	-0.0066	0.0342	-0.0268	-0.9701	-0.0968	-0.0811	0.0335	1.0292	0.0113	0.0022	-0.0040	-0.0778
	P	0.0086	-0.0102	0.0089	0.0239	0.0071	-0.5919	-0.1649	-0.0204	0.0055	0.6520	0.0082	-0.0006	0.0045	-0.0694
KB	G	0.0046	-0.0075	0.0150	-0.0427	0.0175	-0.7004	-0.0311	-0.2524	-0.0494	1.2508	0.0509	0.0019	-0.0039	0.2533**
	P	0.0057	-0.0078	-0.0197	-0.0289	-0.0047	-0.4252	-0.0529	-0.0636	-0.0081	0.7927	0.0369	-0.0005	0.0045	0.2284**
L/B	G	-0.0070	0.0080	-0.0143	0.0526	-0.0339	-0.1273	-0.0443	0.1706	0.0730	-0.3764	-0.0405	-0.0005	0.0004	-0.3397**
	P	-0.0089	0.0084	0.0188	0.0359	0.0090	-0.0798	-0.0752	0.0431	0.0120	-0.2389	-0.0295	0.0001	-0.0004	-0.3053**
1000 GW	G	0.0024	-0.0078	0.0063	0.0228	-0.0031	-1.0279	-0.0677	-0.2148	-0.0187	1.4699	0.0469	0.0027	-0.0045	0.2064**
	P	0.0030	-0.0077	-0.0081	0.0095	0.0007	-0.6230	-0.1137	-0.0533	-0.0030	0.9453	0.0336	-0.0007	0.0051	0.1876**
HUL	G	-0.0652	0.0759	0.0020	-0.0148	-0.0084	0.2503	0.0094	0.1100	0.0253	-0.5895	-0.1168	-0.0104	0.0039	-0.3283**
	P	-0.0718	0.0711	-0.0042	-0.0092	0.0021	0.1180	0.0143	0.0249	0.0038	-0.3375	-0.0942	0.0030	-0.0059	-0.2855**
MIL	G	-0.0312	0.0364	0.0178	-0.0247	0.0129	-0.0279	0.0098	0.0213	0.0016	-0.1801	-0.0554	-0.0220	0.0043	-0.2372**
	P	-0.0353	0.0349	-0.0207	-0.0143	-0.0033	-0.0263	0.0153	0.0049	0.0002	-0.1079	-0.0467	0.0062	-0.0062	-0.1991**
HRR	G	-0.0978	0.117	-0.0240	-0.0204	-0.0149	0.4767	0.0279	0.0722	0.0019	-0.4841	-0.0329	-0.0068	0.0138	0.0285
	P	-0.1026	0.1037	0.0231	0.0078	0.0034	0.2494	0.0406	0.0155	0.0003	-0.2651	-0.0304	0.0021	-0.0183	0.0296
Genotypic Residual effect = 0.296 Phenotypic Residual effect = 0.542 Bold values are direct effects															

DFF:Days to 50% flowering, **DM:**Days to maturity, **PTH:**Plant height(cm), **No.PTT:**Number of productive tillers per plant, **PL:**Panicle length(cm), **No.FGP:**Number of filled grains per panicle, **KL:**Kernal length(mm), **KB:**Kernal breadth(mm), **L/B:**L/B Ratio, **1000 GW:**1000-grain weight, **HUL:**Hulling%, **MIL:**Milling%, **HRR:**Head rice recovery%, **GYP:**Grain yield per plant(g)

Table 4.7: Magnitude of variability, heritability and genetic advance for yield and quality traits in rice (*Oryza sativa* L.)

S.no.	Character	General Mean	Range		Phenotypic Coefficient Variation	Genotypic Coefficient Variation	Heritability in broad sense (%)	GA as per cent of mean (%)
			Minimum	Maximum				
1	Days to 50% flowering	94.62	79.67	113.67	8.44	8.33	97.60	16.96
2	Days to maturity	128.24	114.67	146.00	5.83	5.74	97.00	11.65
3	Plant height (cm)	101.11	80.80	117.20	8.95	8.64	93.30	17.20
4	Number of productive tillers/plant	11.95	10.10	17.25	11.57	9.70	70.20	16.74
5	Panicle length (cm)	24.79	19.00	29.20	8.47	8.20	93.90	16.37
6	Number of filled grains / panicle	153.55	64.50	281.50	32.19	31.62	94.90	62.95
7	Kernel length (mm)	6.33	5.11	7.34	10.63	10.60	99.40	21.77
8	Kernel breadth (mm)	1.91	1.45	2.63	13.23	13.19	99.40	27.09
9	L/B Ratio	3.35	2.00	4.95	13.24	13.19	99.30	27.09
10	Grain yield per plant (g)	31.92	16.64	48.90	22.73	20.56	81.80	38.31
11	1000-grain weight (g)	20.16	11.17	28.87	21.03	20.80	97.80	42.39
12	Hulling %	81.30	77.75	84.30	1.88	1.68	80.40	3.10
13	Milling %	72.34	67.10	76.45	3.30	2.95	79.90	5.43
14	Head rice recovery	60.27	51.60	68.50	6.29	5.41	74.00	9.59

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation entitled “Genetic diversity studies for yield and quality traits in rice (*Oryza sativa* L.)” was carried out with 70 rice genotypes in a Randomized Block Design with three replications at Regional Agricultural Research Station, Polasa, Jagtial, Karimnagar district, during *Kharif*, 2014, The objectives of the investigation were to study the genetic diversity present in the experimental material for selection of the diverse parents, for yield and quality traits and the extent of association between the yield and its component characters including the direct and indirect effects.

The observations were recorded on five randomly selected plants per genotype in each replication for fourteen characters viz., days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, panicle length, number of filled grains per panicle, 1000-grain weight, grain yield per plant, hulling percentage, milling percentage, head rice recovery, kernel length, kernel breadth and L/B ratio. The data was subjected to Mahalanobis D^2 statistics.

Analysis of variance revealed highly significant differences among the genotypes for all the traits under study indicating that the existence of genetic variability among the experimental material.

The genetic divergence was high and the 70 genotypes of rice were grouped into seven different clusters. Cluster I was the largest one comprising of forty genotypes followed by cluster II with twenty genotypes, cluster V with six genotypes and cluster III, IV, VI and VII were represented by single genotype indicating high degree of heterogeneity among the genotypes.. The pattern of group constellations indicated significant variability among the genotypes.

Divergence studies through D^2 statistics indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The higher amount of divergence was observed between cluster from the inter cluster D^2 values of seven clusters, it can be seen that the highest divergence occurred between the cluster V and VII (1949.04) followed by cluster II and VII (1619.25), cluster II and III (1458.41), cluster V and VI (1282.97) and cluster III and VII (1268.29) suggesting that the crosses involving genotypes from these clusters would give wider and desirable recombination. Maximum intra cluster distance was observed in cluster V (282.7), followed by cluster II (176.64), cluster I (155.53) indicating that some genetic divergence still existed among the genotypes. This could be made use of in the yield improvement through recombination breeding.

The cluster I is having highest mean value for grain yield per plant. cluster II for number of filled grains per panicle, head rice recovery percentage and cluster III for 1000-grain weight, kernel breadth, cluster IV for number of productive tillers per plant, hulling percentage, milling percentage, cluster VI for plant height, panicle length, kernel length and cluster VII for days to 50 per cent flowering, days to maturity and L/B ratio. The promising genotypes from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

The genotypes belonging to the clusters separated by high statistical distance could be used in hybridization programme for obtaining a wider spectrum of variation among the segregates. In this context, the genotypes (IR 59624-34-2-2R, HR 20654-39-3-5) of cluster V and cluster VII (IR 67684B), cluster II (JGL 21075, JGL 18629) with cluster VII (IR 67684B), cluster II (JGL 21075, JGL 18629) with cluster III (JGL 23745), cluster V (IR 59624-34-2-2R, HR 20654-39-3-5.) with cluster VI (IR 79156B) and cluster III (JGL 23745) with cluster VII (IR 67684B) were selected in future for hybridization programme as they were expected to produce high heterotic crosses.

The results showed that the contribution of kernel length was highest towards genetic divergence (37.18%) followed by kernel breadth (31.64%), days to 50 per cent flowering (11.76%), L/B ratio (7.45%), 1000-grain weight (3.81%), number of filled grains per panicle (3.31%), plant height (1.41%), milling percentage (1.24%), panicle length (0.87%), head rice recovery percentage (0.70%), grain yield per plant (0.41%),

number of productive tillers per plant (0.08%), hulling percentage(0.08%) and days to maturity (0.04%) is respectively to the genetic divergence in decreasing order.

Out of the fourteen characters studied, six characters namely kernel length, kernel breadth, days to 50 per cent flowering, L/B ratio, 1000-grain weight and number of filled grains per panicle together contributed 95.15% towards total divergence. Therefore, these characters should be given importance during hybridization and selection in segregating populations.

A perusal of genetic parameters revealed that phenotypic and genotypic coefficients of variation were high for number of filled grains per panicle followed by grain yield per plant and 1000-grain weight. The values of genotypic and phenotypic coefficients of variation were low for days to 50% flowering, days to maturity, plant height, panicle length, hulling percentage, milling percentage, head rice recovery and only low GCV values for number of productive tillers per plant.

High heritability coupled with high genetic advance as per cent of mean was observed for number of filled grains per panicle, kernel length, kernel breadth, L/B ratio, grain yield per plant and 1000-grain weight. Which indicated that these traits were controlled by additive type of gene action in the inheritance of these characters. These characters can be further improved by following simple selection procedure. The high estimates of heritability coupled with low genetic advance as percent of mean for hulling percentage, milling percentage and head rice recovery indicated the presence of non-additive gene effects, in addition to influence of environment to some extent.

Character association studies revealed that grain yield per plant showed significant positive association with plant height, number of productive tillers per plant, panicle length, no. of filled grains per panicle, kernel breadth and 1000-grain weight. This indicated that simultaneous selection for all these characters was important for yield improvement.

Path coefficient analysis revealed that 1000-grain weight exerted the highest positive direct effect on grain yield followed by number of filled grains per panicle, number of productive tillers per plant, days to 50 per cent flowering, plant height, panicle length, L/B ratio and milling percentage, indicating that the selection for these characters was likely to bring about an overall improvement in grain yield per plant directly.

A critical analysis of correlation and direct and indirect effects indicated that emphasis should be directed towards selection of parents having higher number of productive tillers per plant coupled with higher number of filled grains per panicle, 1000-grain weight, plant height, longer panicle length, kernel breadth, L/B ratio and milling percentage. As the yield component filled grains per panicle is intern dependent on panicle length and plant height, attention should be paid towards increasing the panicle length, maintaining optimum plant height.

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