

**GENETIC DIVERGENCE FOR GRAIN
YIELD AND YIELD COMPONENTS IN
RICE [*Oryza sativa* L.]**

BY

CH. SANTHI PRIYA

B.Sc. (Ag.)

**THESIS SUBMITTED TO THE
ACHARYA N. G. RANGA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF**

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

CHAIRPERSON: Dr. Y. SUNEETHA



**DEPARTMENT OF GENETICS AND PLANT BREEDING
AGRICULTURAL COLLEGE, BAPATLA
ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
GUNTUR, ANDHRA PRADESH**

2016

**GENETIC DIVERGENCE FOR
GRAIN YIELD AND YIELD
COMPONENTS IN
RICE [*Oryza sativa* L.]**

CH. SANTHI PRIYA

B.Sc. (Ag.)

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



2016

CERTIFICATE

Ms. CH. SANTHI PRIYA has satisfactorily prosecuted the course of research and that thesis entitled “**GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS 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 her for a degree of any University.

Date:

(Y. SUNEETHA)
Chairperson
Scientist (Plant Breeding)
APRRI & RARS, Maruteru - 534122

CERTIFICATE

This is to certify that the thesis entitled “**GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS IN RICE [*Oryza sativa* L.]**” submitted in partial fulfilment of the requirements for the degree of ‘**Master of Science in Agriculture**’ of the Acharya N. G. Ranga Agricultural University, Guntur is a record of the bonafide original research work carried out by **Ms. CH. SANTHI PRIYA** 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.

Thesis approved by the student’s advisory committee

Chairman : **Dr. Y. SUNEETHA**
Scientist (Plant Breeding)
APRRI & RARS
Maruteru

Member : **Dr. D. RATNA BABU**
Scientist (Plant Breeding)
RARS, Lam farm
Guntur

Member : **Dr. V. SRINIVASA RAO**
Professor & University Head
Department of Statistics and Mathematics
Agricultural College
Bapatla

Date of Final Viva-Voce:

DECLARATION

I, **CH. SANTHI PRIYA**, hereby declare that the thesis entitled “**GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS IN RICE [*Oryza sativa* L.]**” submitted to the **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place: Bapatla

(CH. SANTHI PRIYA)
I.D. No. BAM-14-13

Date:

LIST OF CONTENTS

Chapter No	Title	Page No.
I	INTRODUCTION	
II	REVIEW OF LITERATURE	
III	MATERIAL AND METHODS	
IV	RESULTS AND DISCUSSION	
V	SUMMARY AND CONCLUSIONS	
	LITERATURE CITED	

LIST OF TABLES

S. No.	Title	Page No.
2.1	Review of literature on genetic variability of yield and yield components in rice [<i>Oryza sativa</i> L.]	
2.2	Review of literature on heritability and genetic advance as per cent of mean of yield and yield components in rice [<i>Oryza sativa</i> L.]	
2.3	Review of literature on association of component characters with grain yield per plant in rice [<i>Oryza sativa</i> L.]	
2.4	Review of literature on association of yield components among themselves in rice [<i>Oryza sativa</i> L.]	
2.5	Review of literature on direct effects of component characters on grain yield in rice [<i>Oryza sativa</i> L.]	
2.6	Review of literature on indirect effects of component characters on grain yield in rice [<i>Oryza sativa</i> L.]	
3.1	Name and origin of rice genotypes employed in the present study	
4.1	Mean Performance of 40 Genotypes in rice [<i>Oryza sativa</i> L.] for all the characters under study.	
4.2	Analysis of variance for yield and yield component characters in rice [<i>Oryza sativa</i> L.]	
4.3	Estimates of variability, heritability and genetic advance as per cent of mean for seed yield and yield components in rice [<i>Oryza sativa</i> L.]	
4.4	Phenotypic correlations among grain yield and yield contributing characters rice [<i>Oryza sativa</i> L.]	
4.5	Direct and indirect effects of different traits on grain yield per plant in rice [<i>Oryza sativa</i> L.]	
4.6	Contribution of different characters towards genetic divergence in 40 rice [<i>Oryza sativa</i> L.] genotypes	
4.7	Clustering pattern of 40 rice [<i>Oryza sativa</i> L.] genotypes by Tocher's method	
4.8	Average intra and inter-cluster D^2 values among seven clusters with 40 rice [<i>Oryza sativa</i> L.] genotypes	
4.9	The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 40 rice genotypes	
4.10	Mean values seven clusters estimated by Tocher's method from 40 rice [<i>Oryza sativa</i> L.] genotypes	
4.11	Eigen values, proportion of the total variance represented by first four principal components, cumulative per cent variance and components loading of different characters in rice [<i>Oryza sativa</i> L.].	

S. No.	Title	Page No.
4.12	PCA scores of 40 rice [<i>Oryza sativa</i> L.] genotypes.	
4.13	Clustering pattern of 40 rice [<i>Oryza sativa</i> L.] genotypes by Ward's minimum variance method	
4.14	Average intra and inter-cluster Euclidian ² values among seven clusters in 40 rice [<i>Oryza sativa</i> L.] genotypes	
4.15	Mean values of seven clusters estimated by Ward's minimum variance method from 40 rice [<i>Oryza sativa</i> L.] genotypes	

LIST OF FIGURES

S. No.	Title	Page No.
4.1	Phenotypic path diagram showing direct and indirect effects of yield components on seed yield per plant in rice [<i>Oryza sativa</i> L.]	
4.2	Intra and inter-cluster distance of 40 rice [<i>Oryza sativa</i> L.] genotypes in seven clusters based on Tocher's method	
4.3	Dendrogram showing relationship among 40 rice [<i>Oryza sativa</i> L.] genotypes in seven clusters based on Mahalanobis' D^2 values	
4.4	Two dimensional graph showing relative position of 40 rice [<i>Oryza sativa</i> L.] genotypes based on PCA scores	
4.5	Three dimensional graph showing relative position of 40 rice [<i>Oryza sativa</i> L.] genotypes based on PCA scores	
4.6	Dendrogram showing relationship of 40 rice [<i>Oryza sativa</i> L.] genotypes in seven clusters based on Euclidean ² distance	
4.7	Intra and inter-cluster distance of 40 rice [<i>Oryza sativa</i> L.] genotypes in seven clusters based on Euclidean ² values	

LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
ANOVA	:	Analysis of Variance
ARS	:	Agricultural Research Station
CD	:	Critical Difference
cm	:	Centimeter
CV	:	Coefficient of variation
d.f	:	Degrees of freedom
<i>et al.</i>	:	and others people
g	:	Gram
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Co-efficient of Variation
<i>i.e.,</i>	:	That is
kg	:	Kilogram
kg h ⁻¹	:	Kilograms per hectare
L/B	:	Kernel length to breadth ratio
L ha	:	Lakh hectares
Lt	:	Lakh tonnes
m	:	Meter
Mha	:	Million hectares
mm	:	millimeters
MSL	:	Mean sea level
MSS	:	Mean sum of square
Mt	:	Million tonnes
NS	:	Non-significant
PCA	:	Principal Component Analysis
PCV	:	Phenotypic Co-efficient of Variation
<i>Per se</i>	:	As such with in
RRU	:	Rice research unit
S.E.	:	Standard error
S.Ed	:	Standard Error of difference
sq. m	:	Square metre
SS	:	Sum of square
t ha ⁻¹	:	Tonnes per hectare
via	:	Through
<i>viz.,</i>	:	Namely
2D	:	Two dimensional
3D	:	Three dimensional

ABSTRACT

Name of the Author	: CH. SANTHI PRIYA
Title of the thesis	: GENETIC DIVERGENCE FOR GRAIN YIELD AND YIELD COMPONENTS IN RICE (<i>Oryza sativa</i> L.)
Degree to which it is submitted	: Master of Science in Agriculture
Faculty	: Agriculture
Department	: Genetics and Plant Breeding
Chairperson	: Dr. Y. SUNEETHA
University	: Acharya N.G. Ranga Agricultural University
Year of Submission	: 2016

Present investigation was carried out during *kharif* 2015 at Agricultural College Farm, Bapatla with the prime objective of grouping the 40 genotypes of rice (*Oryza sativa* L.) into distinct classes based on their genetic diversity. Other parameters like mean, genetic variability, heritability, genetic advance as per cent of mean, character association and the magnitude of direct and indirect effects of yield component traits on grain yield were also studied.

The analysis of variance indicated significant differences among 40 genotypes for all the characters studied. High PCV and moderate GCV were recorded for Productive tillers per plant, grains per panicle and grain yield per plant, moderate PCV with GCV were recorded for panicle length and test weight, moderate PCV coupled with low GCV was recorded only for kernel breadth. While low PCV coupled with low GCV were recorded for days to 50% flowering, days to maturity, plant height, kernel length and L/B ratio. These results indicate that there is considerable amount of variability for majority of the characters studied.

The estimates of heritability and genetic advance as per cent of mean were high for Panicle length, grains per panicle, test weight and grain yield per plant indicating the predominance of additive gene action and hence direct selection is useful with respect to these traits. High heritability combined with moderate genetic advance as per cent of mean was recorded for Plant height, kernel length, kernel breadth and L/B ratio indicating the predominance of both additive and non-additive gene actions. Moderate heritability with high genetic advance as per cent of mean was observed for Productive tillers per plant. Moderate heritability with low genetic advance as per cent of mean was observed for 50% flowering. Low heritability and genetic advance as per cent of mean were recorded in case of days to maturity.

The traits, Productive tillers per plant, grains per panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50% flowering and kernel length were found to possess significant positive association with grain yield per plant.

Further, path analysis studies revealed that kernel breadth, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant height showed true relationship with grain yield per plant by establishing significant positive association and high positive direct effect.

Considering the nature and magnitude of character associations and their direct and indirect effects, it can be inferred that kernel breadth, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant height could serve as important traits in any selection programme for selecting high yielding genotypes in rice.

The results of multivariate analysis revealed considerable genetic divergence among the 40 genotypes studied. In principal component analysis, four principal components all together explained 78.913% of the total variability. All the 11 characters were significant and positively loaded in PC₁, maximum divergence was contributed by grain yield per plant followed by grains per panicle, panicle length, test weight and productive tillers per plant.

Both D² analysis (whose group constellations are confirmed by PCA) and Ward's method grouped the 40 rice genotypes into seven clusters. However the clusters are different in different methods with respect to total number of genotypes and the actual genotypes included in each cluster. In D² analysis, cluster III is the largest with 13 genotypes followed by cluster II with 12 genotypes, cluster I with nine genotypes cluster IV with 3 genotypes and cluster V, VI and VII were monogenotypic clusters having only one genotype. In ward's method cluster V was the largest containing 12 genotypes followed by cluster I containing 10 genotypes, cluster III with 7 genotypes, cluster II with 6 genotypes and cluster IV & VII containing two genotypes each.

The pattern of distribution of genotypes into different clusters was at random. Further, the two clustering methods differently and clustering pattern for genotypes is also not same. There was only one solitary cluster in Ward's minimum variance method *i.e.*, cluster VI, where as in D² analysis there were three solitary clusters *viz.*, cluster V, cluster VI and cluster VII. This indicate that genetic diversity was the outcome of several factors along with geographic diversity and the selection for hybridization should be more based on genetic diversity.

According to the Mahalanobis D² analysis the genotypes grouped in cluster IV (NLR 3390, MTU 2195-201-1-3 and MTU 2195-105-1-5) are having maximum genetic distance with the genotypes placed in the cluster VII (BPT 2658). But the genotypes MTU 2195-105-1-5 and MTU 2195-105-1-5 are poor yielders hence, cross between NLR 3390 and BPT 2658 may only produce superior hybrids or transgressive segregants depending on the gene action.

Similarly the clusters obtained using Ward's method indicate that the genotypes grouped in cluster IV (NLR 3385 and BPT 2658) are much divergent from the genotypes present in cluster VII (MTU 2195-201-1-3 and MTU 2195-105-1-5). But both the genotypes in cluster VII are having very less *per se* performance with regard to yield. However the genotype NLR 3385 which is placed in cluster IV of Ward's method was placed in cluster VI of D² analysis which is having an inter cluster distance of 97.62 with cluster IV of D² analysis where NLR 3390 is placed. Hence, it can be concluded that F₁s obtained by crossing BPT 2658 with NLR 3390 and / or NLR 3385 are having a good chance of producing heterotic hybrid varieties in presence of dominance and may result in

good transgressive segregants if additive component of gene action is predominant. So, these genotypes should be tested for their gene action and combining ability using suitable mating design before using them in hybridization programme.

ACKNOWLEDGEMENT

There is a divinity that shapes our ends. The unceasing presence of the god, the blessings and love of my parents, teachers and help of my friends.

*First and foremost, I would like to put on record of my heartfelt gratitude to **Dr. Y. Suneetha**, Scientist, RARS Maruteru, Department of Genetics and Plant Breeding, and the esteemed chairman of my Advisory Committee. I am profoundly thankful to her for constant encouragement, keen interest, constructive suggestions, boundless help and indefatigable guidance which provided me commendable encouragement and shaped my efforts into a successful research work.*

*I deem it a great pleasure to exhibit inexplicable gratitude to **Dr. D. Ratna Babu**, Scientist, RARS Lam, Guntur, Department of Genetics and Plant Breeding, member of my advisory committee, for his encouragement in conducting research, valuable comments, indefatigable patience and meticulous reasoning to refine the dissertation to recon with expeditious co-operation during the whole course of my research work.*

*I express my deep sense of gratitude to **Dr. V. Srinavasa Rao**, Professor & Head, Department of Statistics & Mathematics, Agricultural College, Bapatla member of my advisory committee for his timely and valuable help rendered during the course of investigation.*

*I deem it a great privilege to express my gratitude to **Dr. P. V. Rama Kumar**, Professor & Head, Department of Genetics and Plant Breeding, Agricultural College, Bapatla for his unstinted attention, constant encouragement, valuable suggestions and generous help during my post graduation study and research work.*

*I accord my effusive thanks to **Dr. B. Krishnaveni**, Scientist, Rice Research Unit, Bapatla for her cooperation, valuable help and suggestions during my research work.*

*I sincerely owe my deep sense of gratitude to distinguished faculties of our department **Dr. V. Sathynnarayana**, professor, **Dr. Lal Ahamed M.**, Assistant Professor and **Dr. J. Dayal Prasad Babu**, Assistant Professor for their suggestions and co-operation extended to me during the course of my study.*

*I am very much thankful to **Dr. P. V. N. Prasad**, Principal Scientist (Agronomy)& Head, Agricultural College Farm, Bapatla and **Sri. K. Venkateswar Rao**, Block Manager for their help during my farm operations by providing sufficient labour.*

*I am in dearth of words to express my unboundful gratitude and love to my beloved parents, **Sri. Simhachalam Chappa** and **Smt. Vijaya Lakshmi** and my beloved and dearest sisters **Dr. Hari Priya**, and **Kalyani &** brothers **Dr.Aravind, Ajay, Ashok, Shiv Prasad, Nani** and **My Relatives** for their unbounding love, affection, guidance and dedicated efforts to educate me to this level.*

*I wish to express my unboundful love and fondness to my beloved everlasting friends, **Renuka, Tulasi, Suma, Vasanthi, Sujatha, Sunitha, Keerthi, Sabina Marry, Deekshita, Sudha Rani, Revathi, Ramya** whose encouragement is a constant inspiration to me during the course of my educational career.*

*It gives me immense pleasure to express my profound thanks to my seniors **Shalini, Karuna sree, chinni, Divya, Vijaya durga, Tejaswini, Shiva Devika, Yamini** for the much needed moral support and help during the course of my study.*

*I place my sincere thanks to my colleagues **Bharathi, Krishna Veni, Sudeepthi, Nidhi Mohan, Haritha, Mercy Grace, Vennela** for always being there besides me in difficult times during my course of study and giving constant motivation.*

*It gives me immense pleasure to express my profound thanks to the junior friends **Mounika, Vedha sri, Uma sowjanya, Kusuma, Srilakshmi, Divya, Chaitanya Srilakshmi, Anamika, Jai Sankar babu, Sudheer** for their help and co-operation during the course of this work.*

*I am very much thankful to Record Assistants, **Sri Bhaskara Rao, Sri Srinivasa Reddy**, Office Subordinate **Siva parvathi** and Casual Worker **Ramulamma and Chittamma** for their help during my PG programme in the department.*

I am thankful to Eswar Digitals and Computers for the neat typing and execution of my thesis.

Place:

Date:

(CH. SANTHI PRIYA)

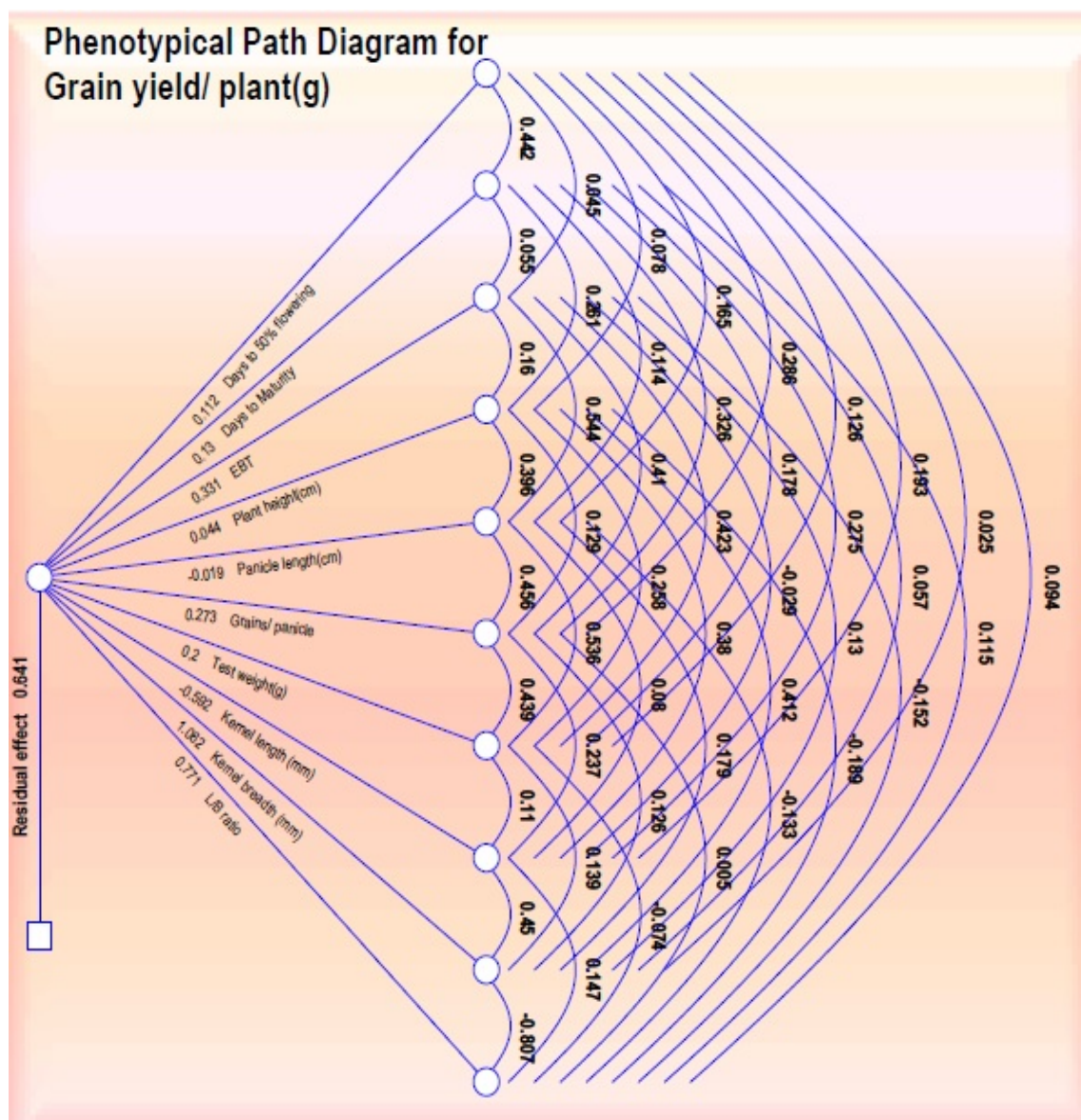
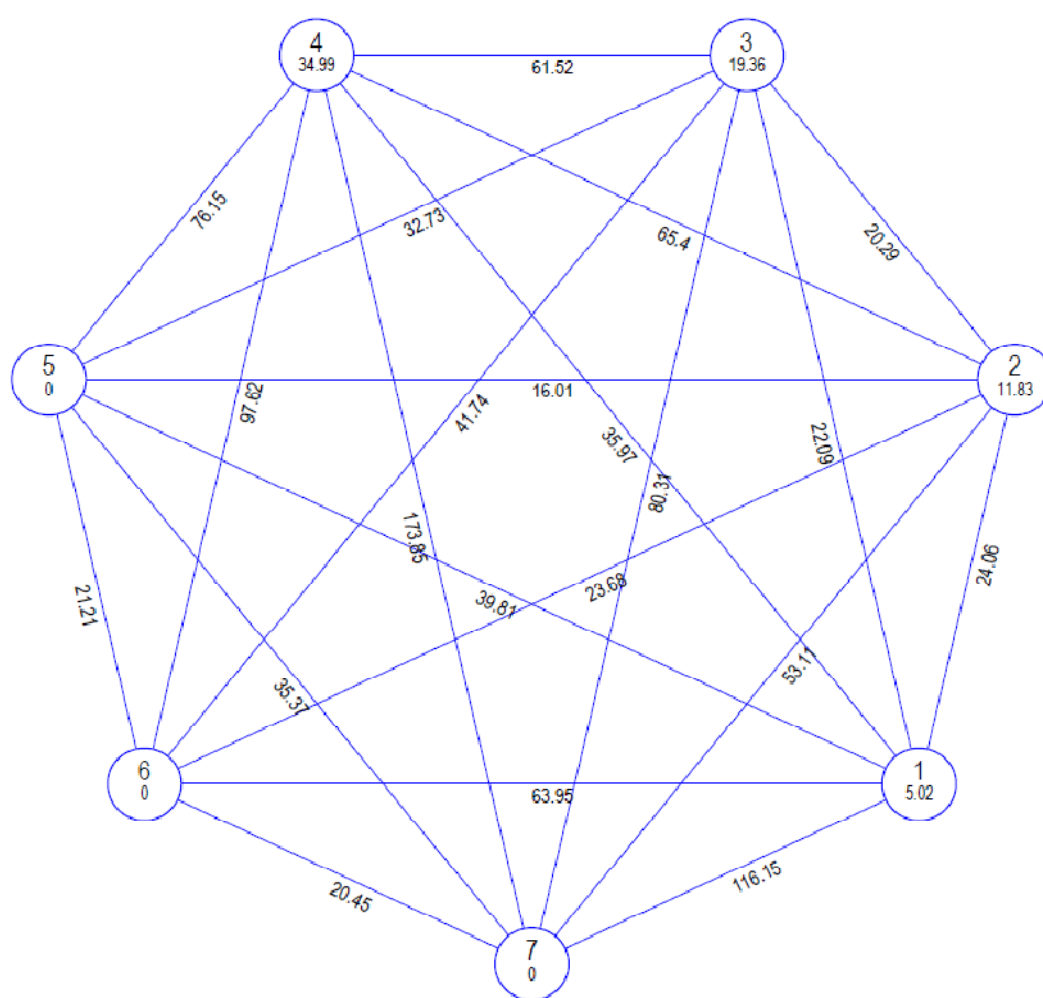


Fig. 4.1. Phenotypic path diagram showing direct and indirect effects of yield components on grain yield per plant in rice (*Oryza sativa* L.)

Tocher Method



Mahalanobis Euclidean Distance (Not to the Scale)

Fig. 4.2. Intra and inter-cluster distance of 40 rice (*Oryza sativa* L.) genotypes in seven clusters based on Tocher's method

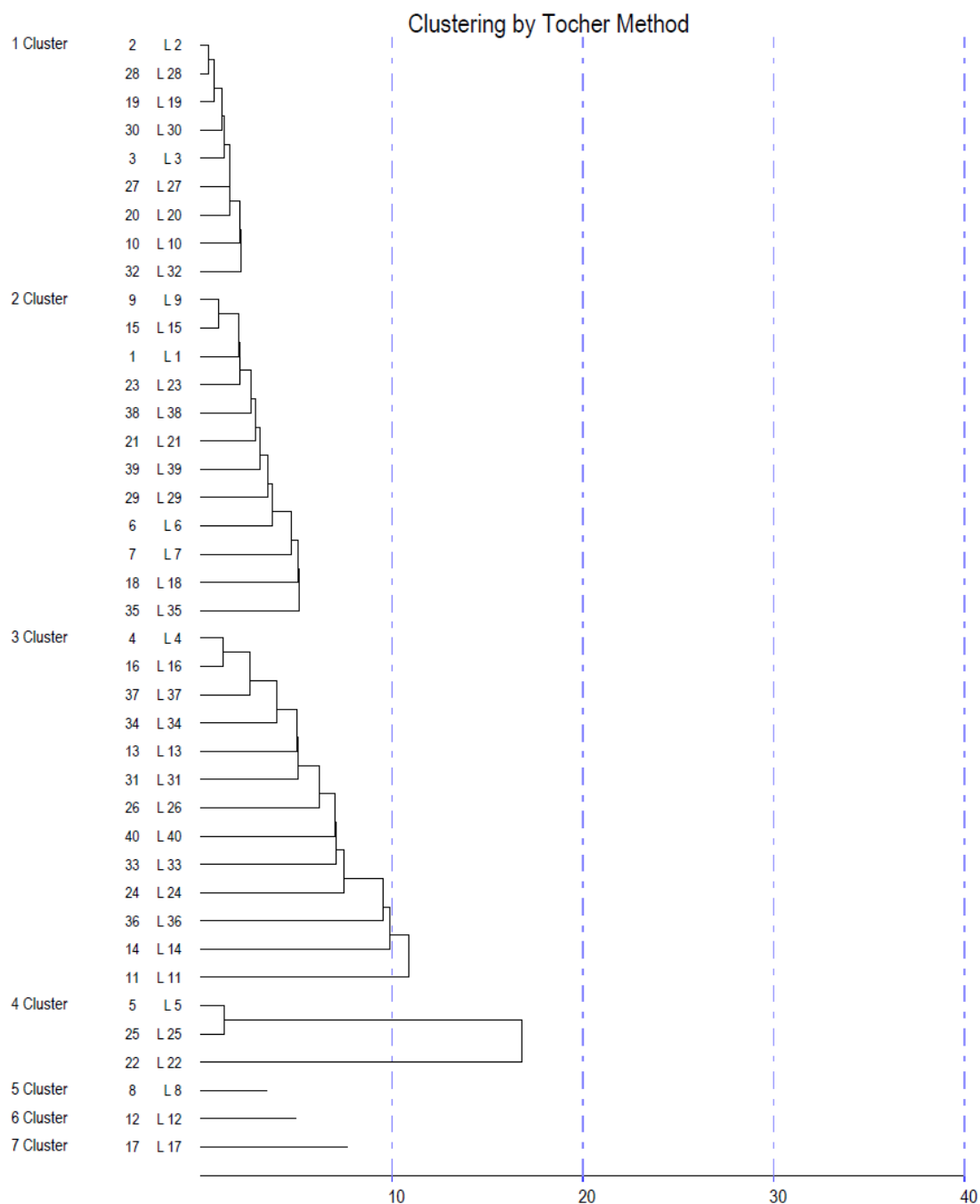


Fig. 4.3. Dendrogram showing relationship among 40 rice (*Oryza sativa* L.) genotypes in seven clusters based on Mahalanobis' D^2 values

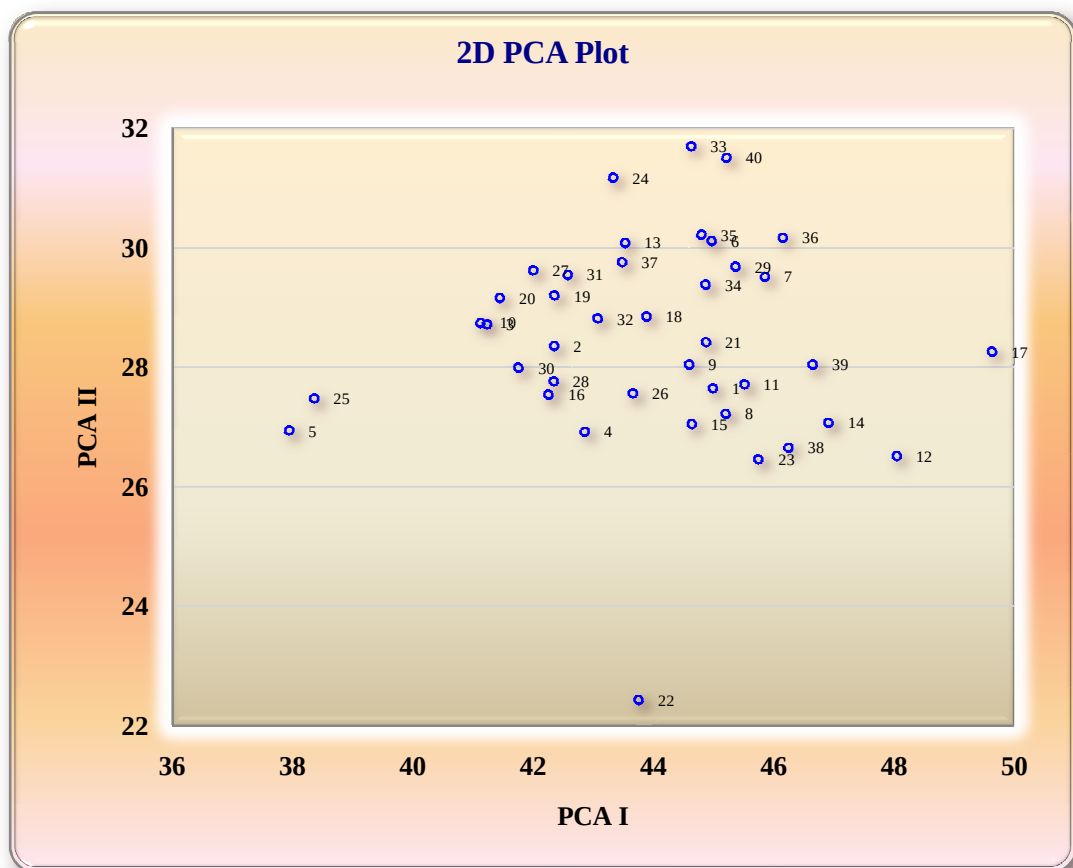


Fig. 4.4. Two dimensional graph showing relative position of 40 rice (*Oryza sativa* L.) genotypes based on PCA scores

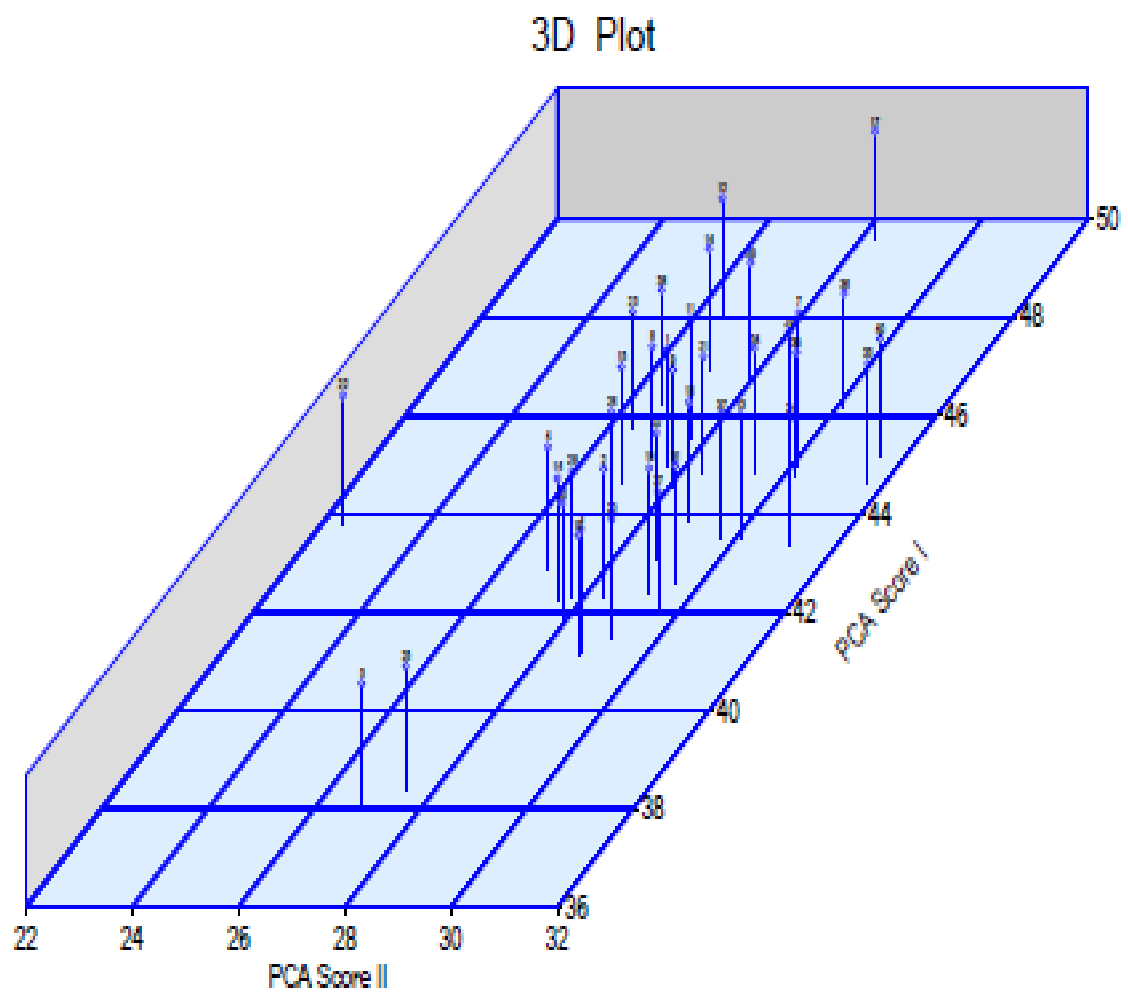


Fig. 4.5. Three dimensional graph showing relative position of 40 rice (*Oryza sativa* L.) genotypes based on PCA scores

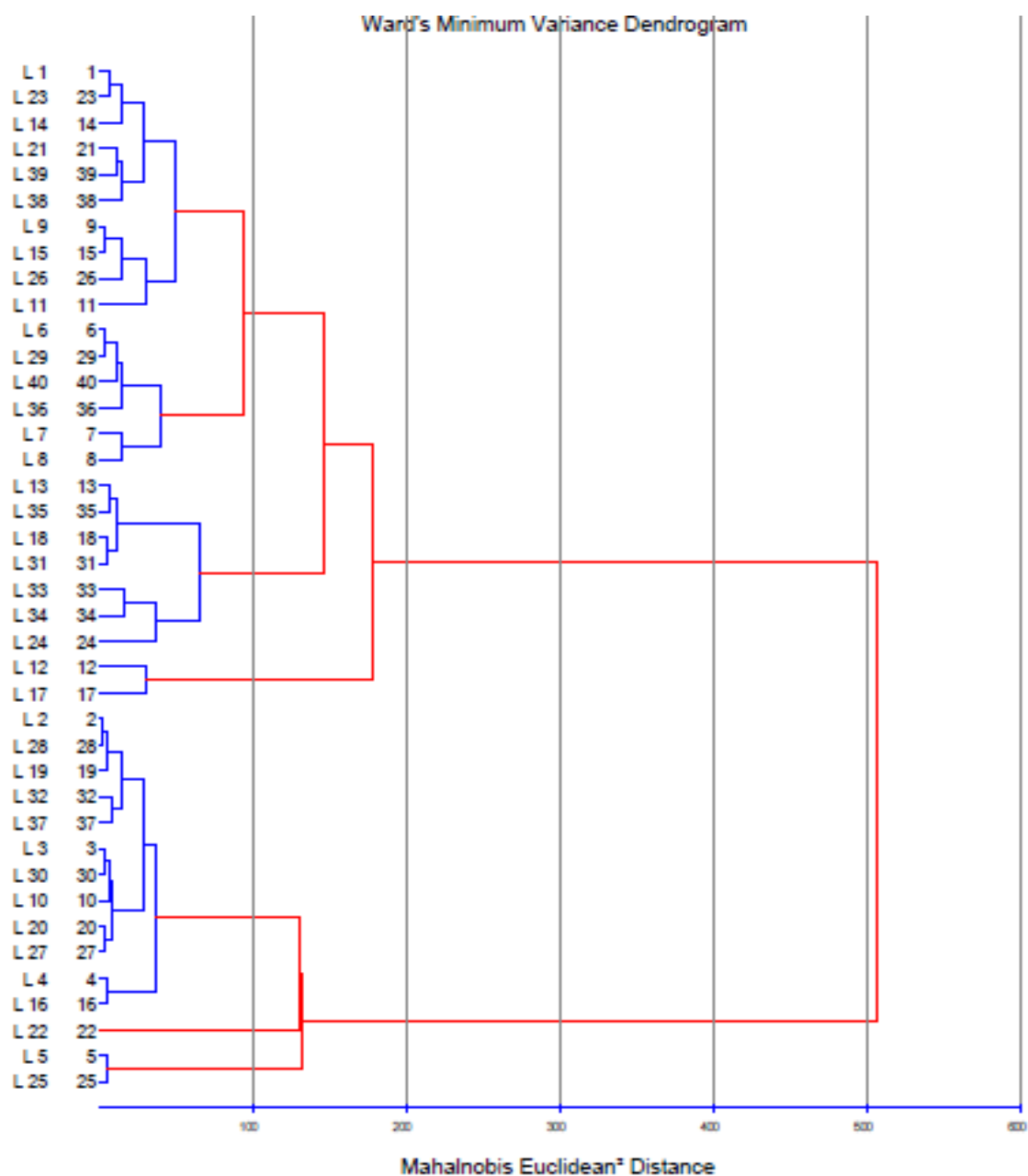
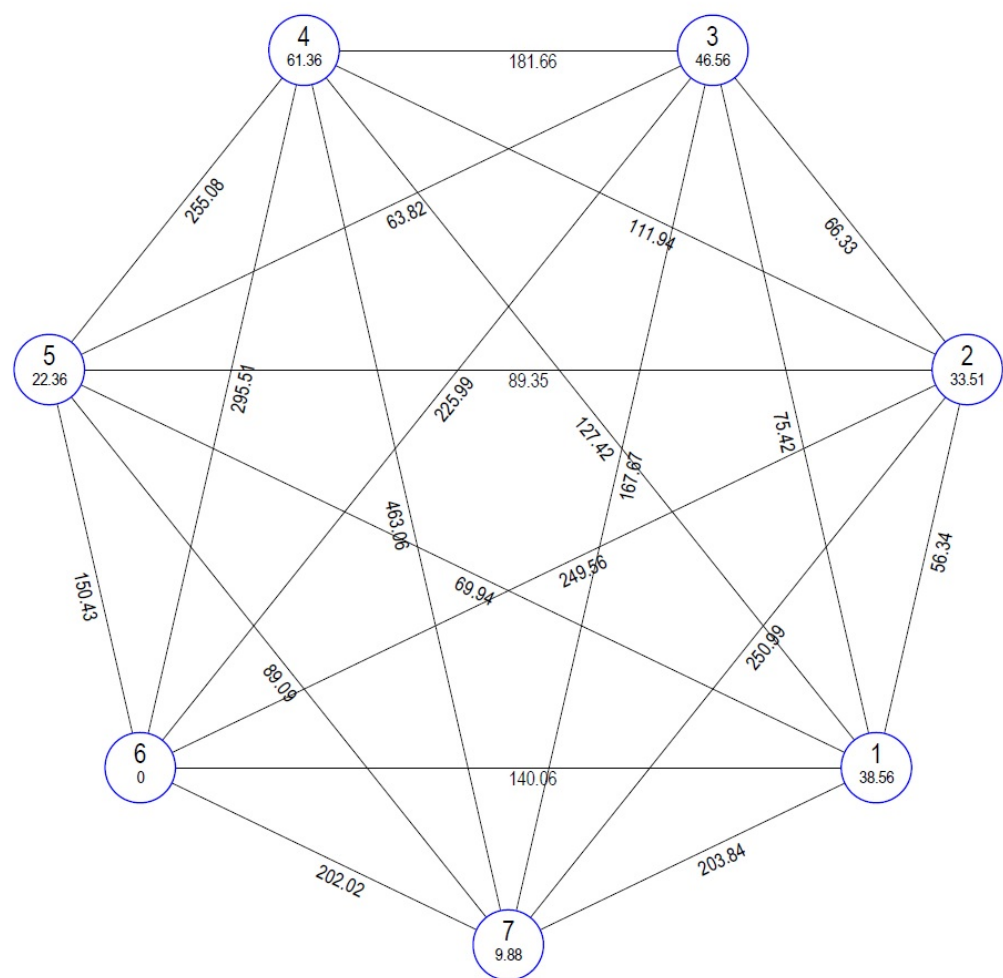


Fig. 4.6. Dendrogram showing relationship of 40 rice (*Oryza sativa* L.) genotypes in seven clusters based on Elucidean² distance



Euclidean² Distance (Not to the Scale)

Fig. 4.7. Intra and inter-cluster distance of 40 rice (*Oryza sativa* L.) genotypes in seven clusters based on Elucidean² distance

Chapter 1

INTRODUCTION

Rice (*Oryza sativa* L., $2n = 2x = 24$) is the principal staple cereal food and source of calories for more than half of the world's population. It offers a wealth of material for genetic studies because of its wide ecological distribution and enormous variation encountered for various qualitative and quantitative characters (Kotaiah, 1983). It is the staple food for 65% of the global population and forms the cheapest source of food energy and protein. In India, rice is grown in an area of 43.86 Mha with a production and productivity of 105.48 Mt and 2424 kg ha^{-1} respectively (WWW.indiastat.com, 2014-15). In Andhra Pradesh, rice is cultivated in an area of 38.09 L ha with a production of 115.65 Lt and productivity of 2856 kg ha^{-1} (WWW.indiastat.com, 2014-15).

To meet the food demands of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 million tonnes every year, which is possible through heterosis breeding and other innovative breeding approaches. Genetic divergence is an efficient tool for an efficient choice of parents for hybridization programme. Such study selects the genetically divergent parents to obtain desirable combinations in the segregating generations (Padmaja *et al.*, 2010).

Assessment of variability present in any crop species is an essential prerequisite for formulating an effective breeding programme. The existing variability can be used to further enhancement of yield level of the cultivars by following an appropriate breeding strategies. As the estimation of genetic variability alone does not give a clear indication of the possible improvement that can be achieved through simple selection it should be used in conjunction with heritability and genetic advance.

Heritability measures relative amount of the heritable portion of variation while the genetic advance helps to measure the amount of progress that could be expected with selection in a character.

Genotypic and phenotypic association reveals the degree of association between different characters and thus, aids in selection to improve the yield and yield attributing characters, simultaneously. Further, path coefficient analysis helps to determine direct and indirect relations among the traits as it is important in order to determine the plant selection criteria (Dewey and Lu, 1959).

Genetic diversity plays an important role in plant breeding either to exploit heterosis or to generate productive recombinants. The choice of parents is of greater importance in breeding programme. Assessment of a large number of germplasm for genetic diversity is of immense importance in selection of diverse genotypes for hybridization programme. Realising the importance of germplasm in the development of desirable varieties, breeders are now looking for more diverse forms from various sources to further augment the yield potential of the genotypes. Mahalanobis's D^2 statistic, Principal component analysis are few powerful tools for quantifying genetic divergence among the available genotypes with respect to characters considered together.

Keeping the above aspects in consideration the present investigation was proposed with the following objectives:

1. To estimate variability, heritability and genetic advance for yield and yield components.
2. To assess the character association among yield and yield components in rice.
3. To study the direct and indirect effects of yield components on grain yield in rice.
4. To study the genetic divergence among 40 genotypes of rice.

LITERATURE CITED

- Abarshahr, M., Rabiei, B and Samizadeh, H.L. 2011. Genetic variability, correlation and path analysis in rice under optimum and stress irrigation regimes. *Notulae Scientia Biologicae*. 3 (4):134-142.
- Aditya J.P and Bhartiya. A. 2013. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of uttarakhand hills. *Journal of Rice Research*. 6 (2): 24-34.
- Akhtar, N., Nazir, M.F., Rabnawaz, A., Mahmood, T., Safdar, M.E., Asif, M and Rehman, A. 2011. Estimation of heritability, correlation and path coefficient analysis in fine grain rice. *The Journal of Animal & Plant Sciences*. 21 (4): 660-664.
- Akinwale, M.G., Gregario, G., Nwilene, F., Akinyele, B.O., Ogunbuyo, S.A and Odiyi, A.C. 2011. Heritability and correlation coefficient analysis for yield and its components in rice (*Oryza sativa* L.). *African Journal of Plant Science*. 5: 207-212.
- Allam, C.R., Jaiswal H.K and Qamar, A. 2015. character association and path analysis studies of yield and quality parameters in basmati rice (*Oryza sativa* L.). *The Bioscan*. 9 (4): 1733-1737.
- Anbanandan, V., Saravanan, K and Sabesan, T. 2009. Variability, heritability and genetic advance and chemical mutagens on certain quantitative characters in rice (*Oryza sativa* L.). *Crop Research*. 30 (2): 309-312.
- *Anderberg, M.R. 1993. *Cluster analysis for application*. Academic Press, New York.
- Anjaneyulu, M., Reddy, D.R and Reddy, K.H.P. 2010. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Research on Crops*. 11 (2): 415-416.
- Arulmozi, R and Muttuswamy, A. 2013. Correlation studies on grain yield and its component traits in rice (*Oryza sativa* L.). *International Journal of Scientific Research*. 2 (11): 13-14.

- Arunachalam, V and Ram, J. 1967. Geographical diversity in relation to genetic divergence in cultivated sorghum. *Indian Journal of Genetics and Plant Breeding*. 27: 369-380.
- Ashfaq, M., Khan., Salam, A., Khan, U., Habib, S., Ahmad and Rashid. (2012). Association of Various Morphological Traits with Yield and Genetic Divergence in Rice (*Oryza sativa* L.). *International Journal of Agriculture & Biology*. 14 (1): 55-62.
- Ashifshirkari, A., Hussain, S.Z., Parry, G.A., Rather, A.G and Wani, A.S. 2008. Physico chemical and cooking properties of non basmati tempatate rice (*Oryza sativa* L.). *Crop improvement*, 35 (2): 109-114.
- Ashim, C and Ghosh, P. D. 2013. Estimation of variability, diversity and correlation studies with respect to different agro-morphological traits in traditional rice of West Bengal. *Oryza*. 50 (2): 127-131.
- Ashisbinodh, Kalaiyarasi and Thiyagarajan. 2007. Genetic parameter studies on quality traits in rice. *Madras Agricultural Journal*. 94 (1-6): 109-113.
- Ashok, S. 2015. Genetic divergence studies for yield components and grain quality parameters in Rice (*Oryza sativa* L.). *M.Sc (Ag.) Thesis*. Acharya N.G. Ranga Agricultural University, Guntur, India.
- Awasthi, L.P., Mishra, C.H and Pandey, V.K. 2005. Genetic divergence in Indian aromatic rice. *Crop Research*. 30 (2): 199-201.
- Babu, G.S., Lavanya, G.R and Singh, A.P. 2011. Genetic variability for grain yield and character association studies in upland rice (*Oryza sativa* L.) germplasm. *Environment and Ecology*. 29 (1): 164-168.
- Babu, R.V., Shrey, K., Dangi. K.S., Usharani, G and Nagesh, P. 2012. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *International Journal of Scientific and Research Publications*. 2: 1-5.
- Balakrishna, B., Satyanarayana, P.V., Rao, S and Rao, V.S. 2015a. Genetic Variability, Heritability and Genetic Advance in Rice (*Oryza sativa* L.) *The Andhra Agricultural Journal*. 62 (2): 313-315.

- Balakrishna, B., Satyanarayana, P.V., Rao, S and Rao V.S. 2015b. Character Association and Path Coefficient analysis in Rice (*Oryza sativa* L.) *The Andhra Agricultural Journal*. 62 (3): 516-564.
- *Banfield, C.F. 1978. Principal component analysis for genstat. *Journal of Statistics and Computer Simulation*. 6: 211-222.
- Baradwaj, C., Mishra, R., Satyavathi, C.T., Rao, S.K and Kumar, K.S. 2007. Genetic variability, heritability and genetic advance in some new plant type crosses in rice. *Indian Journal of Agricultural Research*. 41 (3): 189-194.
- Basavaraja, T., Gangaprasad, S., Mallikarjun K., Vijay Kumar, L and Mahesh, M. 2012. Correlation and path analysis of yield and yield attributes in local rice cultivars (*Oryza sativa* L.). *Journal of Progressive Agriculture*. 3 (1): 47-49.
- Bekele, B. D. A., Rakhia, S., Naveen, G.K., Kundur, P.J and Shashidhara, H.E. 2013. Estimation of genetic variability and correlation studies for grain zinc concentrations and yield related traits in selected rice (*Oryza sativa* L.) genotypes. *Asian Journal of Experimental Biology and Science*. 4 (3) 2013: 391-397.
- Bhabendra, K., Biswas, Alam, N., Jaime, A., Silva, T., Mohammad, M., Haque, Mohammad, A.K., Azad, Mohammad, K and Hossain. 2013. Framework for selecting indicators to improve yield potential in fine rice (*Oryza sativa* L.). *International Journal of Plant Breeding*. 7 (1): 42-49.
- Bhadru, D., Rao, V.T., Mohan, Y.C and Bharathi, D. 2012. Genetic variability and diversity studies in yield and its component traits in rice (*Oryza sativa* L.). *SABRAO Journal of Breeding and Genetics*. 44 (1): 129-137.
- Bhattacharyya, R., Roy, B., Kabi, M.C and Basev, A.K. 2007. Path analysis of seed yield in rice as influenced by *Azotobacter chroococcum* under tropical climate. *Crop Research*. 34 (1,2,3): 160-165.
- Bhavana, P. 2003. Genetic divergence of rice genotypes with regards to seed, growth and yield characters. *M.Sc. (Ag) Thesis*. Acharya N. G. Ranga Agricultural University, Hyderabad, India.
- Binse, R., Motiramani, N.K and Sarwgi, 2006 Association analysis and variability analysis in rice. *Mysore Journal of Agricultural Sciences*. 40 (3): 375-380.

- Borbora, T.K., Hazarika, G.N and Medhi, A.K. 2005 Correlation and path analysis for plant and panicle characters in rice (*Oryza sativa* L.). *Crop Research*. 30 (2): 215-220.
- Borkakati, R.P., Chowdhury, R.K and Kurmi, K. 2005. Studies on genetic variability and correlation in some rice hybrids. *National Journal of Plant Improvement*. 7 (2): 119-121.
- Bornare, S.S., Mitra, S.K and Mehta, A.K. 2014. Genetic, variability correlation and path analysis of floral, yield and its component traits in CMS and restorer lines of rice (*Oryza sativa* L.). *Bangladesh Journal of Botany*. 43 (1): 45-52.
- Bose, L.K. and Pradhan, S.K. 2005. Genetic divergence in deep water rice genotypes. *Journal of Central European Agriculture*. 6 (4): 635-640.
- Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of the 6th International Grassland Congress*, Pennsylvania State College, USA. 277-283.
- Chakravorty, A and Ghosh, P. D. 2012. Genetic divergence in land races of rice of West Bengal. *Journal of Crop and Weed*. 8 (2): 23-28.
- Chamundeswari, N., Raja Reddy, K., Suryanarayana, Y and Satyanarayana, P.V. 2012. Genetic divergence studies in rice (*Oryza sativa* L.). *Crop Research*. 44 (3): 375-379.
- Chand, S.P., Roy, S.K and Senapati, B.K. 2005. Genetic divergence in *Aman* rice under semi- deep rainfed condition. *Crop Research*. 30 (1): 46-49.
- Chandra, S.B., Reddy, D.T and Kumar, S.S. 2009. Variability parameters for yield, its components and quality traits in rice (*Oryza sativa* L.). *Crop Research*. 38: 144-146.
- Chaturvedi, H.P., Talukdar, P and Changkija, S. 2011. Genetic divergence in lowland rice genotypes of Nagaland. *Environment and Ecology*. 29 (1): 27-29.
- Chaudhary, M and Motiramani, N.K. 2003. Variability and association among yield attributes and grain quality in traditional aromatic rice accessions. *Crop Improvement*. 30 (1): 84-90.

- Chaudhary, M., Sarawgi, A.K and Motiramani, N.K. 2004. Genetic variability of quality, yield and yield attributing traits in aromatic rice (*Oryza sativa* L.). *Advances in Plant Sciences*. 17 (2): 485-490.
- Das, P., Kundu, A., Mandal, N and Indrani, D. 2004. Genetic divergence in landrace collections of rice. *Journal of Interacademia*. 8 (4): 488-494.
- Datt, I.B.S., Mehela, B., Goyat and Ramana, K.S. 2012. Variability and correlation of plant height, yield and yield components in rice (*Oryza sativa* L.). *Annals of Biology*. 28 (1): 45-52.
- Devi, L.S., Dass, A., Pandey, M.K and Kole, C.R. 2006. Depiction of genetic diversity in rice. *Crop Research*. 32 (3): 459-461.
- Dewey, D.R and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*. 51 (9): 515-518.
- Dhurai, S.Y., Bhati, P.K and Saroj, S.K. 2014. Studies on genetic variability for yield quality characters in rice (*Oryza sativa* L.) under integrated fertilizer management. *The Bioscan*. 9 (2): 745-748.
- Dwivedi, D.K., Kumar, M.V.K.A and Dwivedi, S. 2012. Phenotypic correlation and path coefficient analysis in rice (*Oryza sativa* L.) introgression lines under drought and controlled conditions. *International Journal of Current Research*. 4 (7): 7-12.
- Ehrenberg, A.S.C. 1985. *Data Reduction Analysis and Interpreting Statistical Data*. John Wiley and Sons Inc., New York. 24 (1): 54-56.
- Elayaraja, K., Prakash, M., Saravanan, K., Kumar, B. S and Ganesan, J. 2005. Effect of physical and chemical mutagens on certain quantitative characters in rice (*Oryza sativa* L.). *Crop Research*. 30 (2): 309-312.
- Eradasappa, E., Nadarajan. N., Ganapathy, K.N., Shanthala, J and Satish, R.G. 2007. Correlation and path analysis for yield and its attributing traits in rice (*Oryza sativa* L.). *Crop Research*. 34 (1,2,3): 156-159.
- Falconer, D.S. 1964. *An Introduction to Quantitative Genetics*. 2nd ed. Oliver and Boyd Publishing Co. Pvt. Ltd. Edinburgh. 312-324.

- Fisher, R.A and Yates, F. 1963. *Statistical Tables for Biological, Agricultural and Medical Research*. Oliver and Boyd, London. 46-63.
- Gangashetty., Prakash, I., Salimath, P.M and Hanamaratti, N.G. 2013. Association analysis in genetically diverse non-basmati local aromatic genotypes of rice. *Molecular Plant Breeding*. 4 (4): 31-37.
- Garg, P., Pandey D.P and Singh, D. 2010. Correlation and path analysis for yield and its components in rice (*Oryza sativa* L.). *Crop Improvement*. 37 (1):46-51.
- Ghosh, S.C and Sharma, D. 2012. Genetic parameters of agro-morpho-physiological traits in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 3 (1): 711-714.
- Gopikannan, M and Ganesh, S.K. 2013. Inter-relationship and path analysis in rice (*Oryza sativa* L.) under sodicity. *Indian Journal of Science and Technology*. 6 (9): 5223-5227.
- Gulzar, S and Parray, G.A. 2010. Variation for drought tolerance in hill rice genotypes. *Crop Improvement*. 37 (1): 21-24.
- Hanson, G.H., Robinson, H.F and Comstock, R.E. 1956. Biochemical studies of yield in segregating populations of Korean Lespedeza. *Agronomy Journal*. 48: 267-272.
- Haque, A., Begum, S.N., Robin A. H. K and Hassan, L. 2015. Partitioning of Rice (*Oryza sativa* L.) Genotypes Based on Morphometric Diversity. *American Journal of Experimental Agriculture*. 7 (4): 242-250.
- Hasan, M. J., Kulsum, M. U., Akter, A., Masuduzzaman A. S. M and Ramesha M. S. 2012. Genetic variability and character association for agronomic traits in hybrid rice (*Oryza sativa* L.). *Bangladesh Journal of Plant Breeding and Genetics*. 24 (1): 45-51.
- Hasib, K.M. 2005. Genetic variability, interrelations and path analysis for panicle characters in scented rice. *Crop Research*. 30 (1): 37-39.
- Hossain, B.R and Hossain, F. 2001. Genetic variability in yield components of rice (*Oryza sativa* L.). *Environment and Ecology*. 19 (1): 186-189.

- Idris, A.E., Justin, F.J., Dagash, Y.M.I and Abuali, A.I. 2012. Genetic variability and inter relationship between yield and yield components in some rice genotypes. *American Journal of Experimental Agriculture*. 2 (2): 233-239.
- Idris, A.E and Mohammed, K.A. 2013. Estimation of genetic variability and correlation for grain yield components in rice (*Oryza sativa* L.). *Global Journal of Plant Ecophysiology*. 3 (1): 1-6.
- Indiastat. 2014-15. <http://www.Indiastat.com>
- Jackson, J.E., 1991. *A User's Guide to Principal Components*. John Wiley and Sons Inc., New York.
- Jaiswal, H.K., Srivastava, A.K and Day, A. 2007. Variability and association studies in indigenous aromatic rice (*Oryza sativa* L.). *Oryza*. 44 (4): 351-353.
- Janardhanam, V., Nandarajan, N and Jebaraj, S. 2001. Correlation and path analysis in rice (*Oryza sativa* L.). *Madras Agricultural Journal*. 88 (10-12): 719-720.
- Jennings, P.R., Coffman, W.R and Kaufman, M.H.E. 1979. Rice improvement. International Rice Research Institute, Philippines Chapter, 6: 101-120.
- Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.
- Kar, A.K., Das, S.R and Bastia, D. 2013. Genetic divergence in selected indigenous aromatic rice of Odisha. *Oryza*. 50: 185-188.
- Karad, S.R and Pol, K.M. 2008. Character association, genetic variability and path-coefficient analysis in rice (*Oryza sativa* L.). *International Journal of Agricultural Sciences*. 4 (2): 663-666.
- Karhikeyan, P., Anbuselvan, Y., Venkatesan, M and Palaniraja, K. 2007. Genetic studies in rice (*Oryza sativa* L.) under saline situation. *Madras Agricultural Journal*. 94 (7-12): 272-276.
- Karim, D., Sarkar, U., Siddique, M. N. A., Miah, M. A. K and Hasnat, M. Z. 2007. Variability and genetic parameter analysis in aromatic rice. *International Journal of Sustainable Crop Production*. 2 (5): 15-18.

- Karuppaiyan, R., Kapoor, C and Gopi, R. 2013. Variability, heritability and genetic divergence in lowland rice genotypes under the mid-hills of Sikkim. *Oryza*. 50: 81-84.
- Khare, R., Singh, A.K., Eram, S and Singh, P.K. 2014. Genetic variability, association and diversity analysis in upland rice (*oryza sativa* L.). *SAARC Journal of Agriculture*. 12 (2): 40-51.
- Kole, P.C., Chakraborty, N.R and Bhat, J.S. 2008. Analysis of variability, correlation and path coefficient in induced mutants of aromatic non-basmati rice. *Tropical Agricultural Research and Extension*. 11: 60-64.
- Kotaiah, K.C. 1983. Genetic divergence in rice (*Oryza sativa* L.). *M.Sc. (Ag) Thesis*. Acharya N. G. Ranga Agricultural University, Hyderabad, India.
- Krishna, J.N.V.V.M., Ahamed, M.L., Vijayalakshmi, B and Ramaih, K.V.S. 2011. Correlation and path coefficient analysis in F₃ generation of rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*. 58 (3): 333-337.
- Krishna, L., Raju, Ch. D and Raju, Ch.S. 2008. Genetic variability and correlation in yield and grain quality characters of rice germplasm. *The Andhra Agricultural Journal*. 55 (3): 276-279.
- Krishnaveni, B and Niveditha, M.S. 2014. Effect of mutagens on quantitative and qualitative characters in M₃ generation of rice variety 'Akshaya' (BPT 2231). *Journal of Rice Research* .7 (1): 16-24.
- Krishnaveni, B and Sobharani, N. 2006. Association of grain yield with quality characteristics and other yield components in rice. *Oryza*. 43 (4):320-322.
- Krishnaveni, B., Ramana J.V and vijayalakshmi B. 2015. Assessment of Genetic diversity for yield components and quality parameters in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*. 62 (1): 71-74.
- Kuchanur, P.H., Dronavalli, N and Vijayakumar, A. G. 2009. Genetic variability and divergence in New Plant Type rice genotypes. *Crop Improvement*. 36 (1): 20-24.
- Kulsum, M.U., Hasan, M.J., Begum, H., Billah, M.M and Rahman, H. 2011. Genetic diversity of some restorer lines for hybrid rice development. *Bangladesh Journal of Agricultural Research*. 36 (1): 21-28.

- Kumar, D.B.M. 2008. Genetic divergence in red rice. *Karnataka Journal of Agricultural Sciences*. 21 (3): 346-348.
- Kumar, P and Ramesh, B. 2008. Genetic variability and character associations in rice. *Progressive Agriculture*. 8 (2): 260-262.
- Kumar, S., Gautam, A.S and Chandel, S. 2006. Estimates of genetic parameters for quality traits in rice (*Oryza sativa* L.) in mid hills of Himachal Pradesh. *Crop Research*. 32 (2): 206-208.
- Kumar, S.P and Bapu, K.J.R. 2005. Character association in inter sub-specific rice hybrids involving wide compatible gene. *Crop Research*. 30 (2): 208-210.
- Kumar, V., Singh, P.K and Verma, O.P. 2013. Correlation and path analysis of yield and its component characters in scented rice. *Oryza*. 4: 317-323.
- Kumari, K.M., Ramaih, K.V.S., Rao, V.S and Sreekanth, B. 2011. Correlation and path analyses in rice. *The Andhra Agricultural Journal*. 58 (4): 434-438.
- Kundu, S and Kundagrami S. 2015. Estimation of path coefficient analysis to identify the yield contributing traits in rice (*Oryza sativa* L.) under saline and non-saline coastal regions of West Bengal. *International Journal of Pure and Applied Biosciences*. 8 (1): 1433-1438.
- Lakshmi, M.V., Suneetha, Y., Yugandhar, G and Venkatalakshmi, N. 2014. Correlation studies in rice (*Oryza sativa* L.). *International Journal of Genetic Engineering and Biotechnology*. 5 (2): 121-126.
- Lal, M and Chauhan, D.K. 2011. Studies of genetic variability, heritability and genetic advance in relation to yield traits in Rice. *Agricultural Science Digest*. 31 (3): 220-222.
- Laxuman, Salimath, P.M., Shashidhar, H.E., Kumar, M.H.D., Patil, S.S., Vamadevaiah, H.M and Janagoudar, B.S. 2011. Analysis of genetic variability in interspecific backcross inbred lines in rice (*Oryza sativa* L.). *Karnataka Journal of Agricultural Sciences*. 23 (4): 563-565.
- *Legendre, L and Legendre, P. 1984. Ecologia Numerique. *Presses de l'Universite du Quebec*. Xv+260p, viii+335p.

- Madhavalatha, L and Suneetha, Y. 2005. Studies on genetic divergence in rice germplasm lines. *Madras Agricultural Journal*. 92 (1-3): 12-16.
- Madhusoodanan, A., Kumar, P.V.R., Krishnaveni, B and Rani, Y.A. 2013. Character association and path analysis of yield components in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*. 60 (3): 535-539.
- *Mahalanobis, P.C. 1928. A statistical study at Chinese head measurement. *Journal of Asiatic Society of Bengal*. 25: 301-307.
- Maji, A. T and Shaibu A. A. 2012. Application of principal component analysis for rice germplasm characterization and evaluation. *Journal of Plant Breeding and Crop Science*. 4 (6): 87-93.
- Mall, A. K., Babu, J. D. P and Babu, G. S. 2005. Estimation of genetic variability in rice. *Journal of Maharashtra Agricultural Universities*. 30 (2): 166-168.
- Manna, M.M.D., Ali, N and Samal, B.G. 2006. Variability, correlation and path coefficient analysis in some important traits of lowland rice. *Crop Research*. 31 (1):153-156.
- Manonmani, S., Malarvizhi, D., Robin, S., Umadevi, M., Ameenul, M and Pushpam, R., Mohanasundaram, K and Thiyagarajan, K. 2010. Breeding three line rice hybrids with good grain quality. *Electronic Journal of Plant Breeding*. 1 (4): 1265- 1269.
- Minnie, M.C., Reddy, D.T and Surenderraju, Ch. 2013. Correlation and path analysis for yield and its components in rice (*Oryza sativa* L.). *Journal of Research ANGRAU*. 41 (1): 132-134.
- Mishra, L.K and Pravin, J. 2004. Variability and genetic diversity in rice (*Oryza sativa* L.). *Mysore Journal of Agricultural Sciences*. 38 (3):367-375.
- Mishra, L.K., Sarawgi, A.K and Mishra, R.K. 2003. Genetic diversity for morphological and quality traits in rice. *Advances in Plant Sciences*. 16 (1): 287-293.
- Mundhe, B.S., Jambhale, N.D and Bendale, V.W. 2006. Genetic divergence in mid-late genotypes of rice. *Journal of Maharashtra Agricultural Universities*. 31 (1): 21-23.

- Murthy, P.S.N and Govindaswamy, S. 1967. Inheritance of grain size and its correlation with the hulling and cooking qualities. *Oryza* 4 (1): 12-21.
- Nagajyothi, B. 2001. Studies on performance and heterosis of rice hybrids for yield, yield components and certain grain quality characters. *M.Sc. (Ag) Thesis*, Acharya N. G. Ranga Agricultural University, Hyderabad, India.
- Nagaraju, C., ReddiSekhar, M., Hariprasad Reddy, K and Sudhakar, P. 2013. Correlation between traits and path analysis coefficient for grain yield and other components in rice (*Oryza sativa* L.) genotypes. *International Journal of Applied Biology and Pharmaceutical Technology*. 4 (3): 137-142.
- Naik, K.R. 2004. Variability and character association in rice (*Oryza sativa* L.) genotypes. *M.Sc. (Ag) Thesis*, Acharya N. G. Ranga Agricultural University, Hyderabad, India.
- Nair, K.R and Mukherjee, H.K.1960. Classification of natural and plantation teak (*Tectona grandis*) grown at different locations of India and Burma with respect to its physical and mechanical properties. *Sankhya*.22: 1-20.
- Nayudu, K.S.R., Vasline, Y.A and Vennila, S. 2007. Studies on variability, heritability and genetic advance for certain yield components in rice (*Oryza sativa* L.) var. Jeeraga Samba. *Crop Improvement*. 34 (2): 142-144.
- Neelima, L., Bhanumurthy, V.B and Ramanjaneyulu, A.V. 2007. Studies on correlation and path coefficient analysis in rice crop as influenced by nitrogen fertilizer and sunhemp green manuring. *Madras Agricultural Journal*. 94 (7-12): 269-272.
- Neha, S., Pathak, S.K., Gampala, S., Singh, V.J., Suresh, B.G and Lavanya, G.R. 2014. Evaluation of exotic upland rice germplasm for grain yield and its component characters in rainfed ecosystem (*Oryza sativa* L.). *International Journal of Food, Agriculture and Veterinary Sciences*. 4: 102-109.
- Niteshkumar., Singh, P.K., Vaishampayan, A., Ram, M., Saini, R., Singh, A and Singh, N.K. 2015. Appraisal of genetic architecture of yield and its contributing traits in rice germplasm. *Annals of Plant and Soil Research*. 17 (2): 125-128.

- Ogunbayo, S.A., Sie, M., Ojo, D.K., Sanni, K.A., Akinwale, M.G., Toulou, B., Shittu, A., Oldhen, E.O., Popoola, A.R., Daniel, I.O and Gregorio, G.B. 2014. Genetic variation heritability of yield and related traits in promising rice genotypes (*Oryza sativa* L.). *Journal of Plant breeding and crop science*. 6 (11): 153-159.
- Osman, K.A., Mustafa, A.M., Ali, F., Zheng, Y.L and Qiu, F.A.Z. 2012. Genetic variability for yield and related attributes of upland rice genotypes in semi arid zone (Sudan). *African Journal of Agricultural Research*. 7 (33): 4613-4619.
- Padmaja, D., Radhika, K., Rao, S.L.V and Padma, V. 2008. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). *Journal of Plant Genetic Resources*. 21 (3): 196-198.
- Padmaja, D., Radhika, K., Rao, S.L.V and Padma, V. 2010. Studies on genetic divergence in rice (*Oryza sativa* L.) germplasm. *Crop Research*. 40 (1&2&3): 117-121.
- Paikhomba, N., Arvind, K., Chaurasia, A.K and Rai, P.K. 2014. Assessment of genetic parameters for yield and yield components in hybrid rice and parents. *Journal of Rice Research*. 2: 1-3.
- Pal, G., Verma O.P, Verma, G.P., Pratap, N., Chaudhary, R K., Kumar, M and Singh, K. 2011. Association studies in rice (*Oryza sativa* L.) under saline alkaline condition. *Plant Archives*. 11 (2): 879-881.
- Panse, V.G and Sukhatme, P.V. 1978. *Statistical Methods for Agricultural Workers*. ICAR, New Delhi. 103-108.
- Panse, V.G. 1957. Genetics of competitive characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding*. 17: 318-328.
- Panwar, L.L. 2006. character association and path analysis in rice (*Oryza sativa* L.). *Annual Agriculture Research New Series*. 27 (3): 257-260.
- Panwar, L.L and Ali, M. 2007. Correlation and path analysis of yield and yield components in transplanted rice. *Oryza*. 44 (2): 115-120.
- Parmhansh. P., Kumar, A and Mishra, S.B. 2010. Correlation and path coefficient study in rice (*Oryza sativa* L.). *Indian Agricultural Journal*. 54 (1&2): 49-52.

- Parvathi, S.P. 2010. Genetic divergence in rice (*Oryza sativa* L.). *M.Sc. (Ag) Thesis*. Acharya N. G. Ranga Agricultural University, Hyderabad, India.
- Parvathi P.S., Rao, S.V., Ahamed, M.L and Kumar, A.P. 2011. Correlation and path analysis of yield and quality attributes in rice. *The Andhra Agricultural Journal*. 58 (3): 310-314.
- Patel, J.R., Saiyad, M.R., Prajapati, K.N., Patel, R.A and Bhavani, R.T. 2014. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 5 (3): 531-537.
- Patil, P.V., Sarawgi, A.K and Shrivastava, M.N. 2003. Genetic analysis of yield and quality traits in traditional aromatic accessions of rice. *Journal of Maharashtra Agricultural Universities*. 28 (3):255-258.
- Prasad, R., Prasad, L.C and Agarwal, R.K. 2009. Genetic diversity in Indian germplasm of aromatic rice. *Oryza*. 46 (3): 197-201.
- Prasad, S.G., Sujatha, M., Chaitanya, U and Rao, L.V.S. 2011. Studies on variability, heritability, genetic advance, correlation and path analysis for quantitative characters in rice (*Oryza sativa* L.). *Journal of Research ANGRAU*. 39 (4): 104-109.
- Premkumar, R., Gnanamalar, R.P and Anandakumar, C.R. 2015. Correlation and path coefficient analysis among grain yield and kernel characters in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 6 (1): 288-291.
- Rajeswari, S., Robin, S., Chandirakala, R., Preamalatha, N and Muthuramu, S. 2010. Genetic analysis of and character association of quality in rice. *Oryza*. 47: 86-90.
- Ramya, K and Senthilkumar. 2008. Genetic divergence in rice (*Oryza sativa* L.). *Crop Improvement*. 35 (2): 119-21.
- Rangare, N.R., Krupakar, A., Ravichandra, K., Shukla, A.K and Mishra, A.K. 2012. Estimation of characters association and direct and indirect effects of yield contributing traits on grain yield in exotic and Indian rice (*Oryza sativa* L.). germplasm. *International Journal of Agri Science*. 2 (1): 54-61.

- Rani, G.M and Reddy, S.N. 2010. Comparison of direct and indirect effects of yield contributing and physiological characters between hybrids and varieties of rice. *The Andhra Agricultural Journal*. 57 (1): 56-61.
- Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and sons. New York. 236-272.
- Rashid, K., Kahliq, I., Farooq, O and Ahsan, M.Z. 2014. Correlation and cluster analysis of some yield and yield related traits in rice (*Oryza sativa* L.). *Journal of Recent Advances in Agriculture*. 2 (6): 271-276.
- Ravikumar, B.N.V.S.R., Kumari, P. N., Rao, P.V.R., Rani, M.G., Satyanarayana, P.V., Chamundeswari, N., Vishnuvardhan, K.M., Suryanarayana, Y., Bharathalakshmi, M and Reddy, A.V. 2015. Principal component analysis and character association for yield components in rice (*Oryza sativa* L.) cultivars suitable for irrigated ecosystem. *Current Biotica*. 9 (1):25-35.
- Role, C.R., Marilyn, C.F., Celia, L., Diaz., Cristina, M., Newingham, V and Gabriel O.R. 2014. Phenotypic diversity of farmers' traditional rice varieties in the Philippines. *Agronomy*. 4: 217-241.
- Rouf, A.B., Singh, S.G and Parray, G.A. 2009. Genetic divergence studies in high altitude temperate rice. *Asian Journal of Experimental Sciences*. 23 (3): 487-490.
- Roy, S., Edpuganti, N., Senapati, B.K and Sarkar, G. 2008. Polygenic variation and character association in M₄ progenies of rice (*Oryza sativa* L.). *Indian Agriculturist*. 52 (3/4): 159-167.
- Sabesan, T., Saravanan, K and Anandan, A. 2009. Genetic divergence analysis for certain yield and quality traits in rice grown in irrigated saline low land of Annamalainagar, South India. *Journal of Central European Agriculture*. 10 (4): 405-410.
- Saiaiah, P., Kumar, S. S and Ramesha, M.S. 2010. Variability for yield and yield component attributes in rice. *Crop Research*. 39 (1,2,3): 91-93.
- Sandhyakishore, N., Babu, V.R., Ansari, N.A and Chandran, R. 2007. Genetic divergenc analysis using yield and quality traits in rice. *Crop Improvement*. 34 (1): 12-15.

- Sanghera, G.S., Kashyap, S.C and Parry, G.A. 2013. Genetic variation for grain yield and related traits in temperate red rice (*Oryza sativa* L.). ecotypes. *Notulae Scientia Biologicae*. 5 (3): 400-406.
- Sankar, P.D., Ibrahim, S.M., Vivekanadan, P., Abumalarmathi, J and Sheeba, A. 2005. Genetic divergence in rice. *Crop Research*. 30 (3): 428-431.
- Sarawgi, A.K and Bisne, R. 2007. Studies on genetic divergence of aromatic rice germplasm for agro-morphological and quality characters. *Oryza*. 44 (1): 74-76.
- Sarawgi, A.K., Rastogi, N.K and Soni, D.K. 2000. Studies on some quality parameters of indigenous rice in Madhya Pradesh. *Annals of Agricultural Research*. 21 (2): 258-261.
- Sarkar, K.K., Bhutia, K.S., Senapathy, B.K and Roy, S.K. 2007. Genetic variability and character association of quality traits in rice (*Oryza sativa* L.). *Oryza*. 44 (1): 64-67.
- Satheeshkumar, P and Saravanan, K. 2012. Genetic variability, correlation and path analysis in rice (*Oryza sativa* L.). *International Journal of Current Research*. 4 (9): 82-85.
- Satish, B. 2000. Heterosis and combining ability analysis for yield and grain quality characteristics in rice (*Oryza sativa* L.). *M.Sc. (Ag) Thesis*, Acharya N. G. Ranga Agricultural University, Hyderabad, India.
- Saxena, R.R., Motiramani, N.K., Nichal, S.S and Sahu, R.K. 2005. Studies on variability, heritability and genetic advance in scented rice germplasm accessions. *Journal of Interacademia*. 9 (4): 487-489.
- Seesang, J., Sripicchitt, P., Somchit, P and Sreewongchan, T. 2013. Genotypic correlation and path coefficient for some agronomic traits of hybrid and inbred rice (*Oryza sativa* L.) cultivars. *Asian Journal of Crop Science*. 5 (3): 319-324.
- Selvaraj, C.I., Nagarajan, P., Thiagarajan, K., Bharathi, M and Rabindran, R. 2011. Genetic parameters of variability, correlation and path-coefficient studies for grain yield and other yield attributes among rice blast disease resistant genotypes of rice (*Oryza sativa* L.). *African Journal of Biotechnology*. 10 (17): 3322-3334.

- Seyoum, M., Alamerew, S and Bantte, K. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). *Journal of Plant Sciences*. 7 (1): 13-22.
- Shanmugasundaram, P., Souframanien, J and Sadasivam, S. 2000. Genetic divergence among rice varieties released from paddy breeding station, Coimbatore, India. *Oryza*. 37 (3): 225-228.
- Shanthi, P and Singh, J. 2001. Genetic divergence for yield and its components in induced mutants of Mahsuri rice. *Research on Crops*. 2 (3): 390-392.
- Sharma, A and Koutu, G.K. 2013. Study of heritability, genetic advance and variability for attributing characters in exotic germplasm of rice. *Oryza*. 4: 404-408.
- Sharma, A.K and Sharma, R.N. 2007. Genetic variability and character association in early maturing rice. *Oryza*. 44(4): 300-303.
- Sharma, S.K., Nandan, R., Singh, S.K., Sharma, A.K., Kumar, S., Sharma, P.K., Singh, M.K and Kumar, V. 2011. Genetic divergence in rice genotypes under irrigated condition. *Progressive Agriculture*. 11 (2): 321-325.
- Shashidhar, H.E., Pasha, F., Janamatti. M., Vinod, M.S and Kanbar, A. 2005. Correlation and path analysis in traditional cultivars and doubled haploid lines of rainfed low land rice (*Oryza sativa* L.). *Oryza*. 42 (2): 156-159.
- Sheet, R.M., Rajanna, M.P., Ramesh, S., Sheshshayee, M.S and Mahadevu, P. 2012. Genetic variability, correlation and path coefficient studies in F₂ generation of aerobic rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 3 (3): 925-931.
- Shejul, M.B., Deosarkar, D.B., Kalpande, H.V., Chavan, S.K., Deshmukh, V.D., Utpal Dey., Anil Kumar, R. D., Bhandhavi and Arbad, S.K. 2013. Variability studies for grain quality characters in upland rice (*Oryza sativa* L.). *African Journal of Agricultural Research*. 8 (38): 4872-4875.
- Shivani, D., Viraktamath, B.C and Shobharani, N. 2007. Correlation among various grain quality characteristics in rice. *Oryza*. 44 (3): 212-215.

- Singh, J., Dey, K., Singh, S and Shahi, J.P. 2005. Variability, heritability, genetic divergence in induced mutants of irrigated basmati rice (*Oryza sativa* L.). *Oryza*. 42(3): 210-213.
- Singh, M., Kuamr, K and Singh, R.P. 2007. Study of coefficient of variation, heritability and genetic advance in hybrid rice. *Oryza*. 44 (1): 160-162.
- Singh, P.K., Dhakad, B.K., Singh, H.B and Singh, A.K. 2012. Genetic variability and association analysis in rice (*Oryza sativa* L.) treated with *Trichoderma harzianum*. *Crop Research*. 44 (1&2): 141-145.
- Singh, P.K., Mishra, M.N., Hore, D.K and Verma, M.R. 2006. Genetic divergence in lowland rice of north eastern region of India. *Communications in Biometry and Crop Science*. 1 (1): 35-40.
- Singh, R.K and Chaudhary, B.D. 1977. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. 215-218.
- Singh, R.K and Singh, O. 2005. Genetic variation for yield and quality characters in mutants of aromatic rice. *Annals of Agricultural Research*. 26 (3): 406-410.
- Singh, S.K., Singh, C.M and Lal, G.M. 2011. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Research in Plant Biology*. 1 (4): 73-76.
- Sivasubramanian, P and Menon, P.M. 1973. Inheritance of short stature in rice. *Madras Agricultural Journal*. 60: 1129-1133.
- Souroush, H.R., Mesbah, M., Hossainzadeh, A and Bozorgipour, R. 2004. Genetic and phenotypic variability and cluster analysis for quantitative and qualitative traits of rice [Persian]. *Seed and Plant*. 20 (2): 167-182.
- Sravan, T., Rangare, N, R., Suresh, B, and Kumar, R.S. 2012. Genetic variability and character association in rainfed upland rice. *Journal of Rice Research*. 5(1- 2).
- Sreeparvathy, P.V., Vashi, R.D and Kodappully, V.C. 2010. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Journal of Ecobiology*. 26 (3/4): 205-210.

- Sudharani, M., Reddy, R.P., Reddy, H.G and Raju, S.Ch. 2013. Correlation and path coefficient analysis for yield and physiological attributes In rice (*Oryza sativa* L.) hybrids under saline soil conditions. *Journal of Research ANGRAU*. 41(1): 105-108.
- Swain, B and Reddy, J.N. 2006. Correlation and path analysis of yield and its components in rainfed lowland rice genotypes under normal and delayed planting conditions. *Oryza*. 43 (1): 58-61.
- Swarup and Chaugle, B.S. 1962. Studies on genetic variability in sorghum; phenotypic variation and heritable component in some quantitative characters contributing towards yield. *Indian Journal of Genetics and Plant Breeding*. 22: 31-36.
- Tejaswini, K.L.Y. 2016. Character association and screening for sheath blight and bacterial leaf blight of F₅ families in rice (*Oryza sativa* L.). *M.Sc (Ag.) Thesis*. Acharya N.G. Ranga Agricultural University, Guntur, India.
- Tushara, M., Rao, V.S., Ahamed, M.L., Krishnaveni, B and Rao, K.L.N. 2013. Correlation of quantitative and qualitative characters with yield in medium and long duration genotypes of rice. *The Andhra Agricultural Journal*. 60 (1): 29-35.
- Vaithiyalingan, M and Nadarajan, N. 2006. Genetic variability and genetic advance in F₂ population of inter sub-specific crosses of rice. *Crop Research*. 31 (3): 476-477.
- Vanaja, T and Babu, L.C. 2006. Variability in grain quality attributes of high yielding rice varieties (*Oryza sativa* L.) of diverse origin. *Journal of Tropical Agriculture*. 44 (1-2): 61-63.
- Venkanna, V., Rao, M.V.B., Raju, CH.S., Rao V.T and Lingaiah N. 2014. Association analysis of F₂ generation in rice (*Oryza sativa* L.). *International Journal of Pure and Applied Biosciences*. 2 (2): 278-283.
- Verma, G.P.O.P., Verma, G.P., Pratap, N., Kumar, M., Chaudhary, R.K and Singh, K. 2011. Genetic variability, heritability and divergence studies in rice (*Oryza sativa* L.) under sodic soil. *Environment and Ecology*. 29 (3b): 1597-1600.
- Vijayalakshmi, B., Vijay, D., Raju, P.R.K and Satyanarayana, P.V. 2008. Genetic divergence of qualitative and quantitative characters in lowland rice germplasm. *Crop Research*. 36 (1, 2, 3): 212-214.

Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*. 20: 557-585.

Yadav, S.K., Suresh, B.G., Pandey, P and Kumar, B. 2010. Assessment of genetic variability, correlation and path association in rice. *Journal of Bio-Sciences*. 18: 1-8.

Zada, A.M. 2002. Genetic variability of different plant and yield characters in rice. *Sarhad Journal of Agriculture*. 18 (2): 207-210.

***Original not seen**

Note : The pattern of Literature Cited presented above is in accordance with the guidelines for thesis presentation, Acharya N. G. Ranga Agricultural University, Guntur, Andhra Pradesh.

Chapter III

MATERIAL AND METHODS

The present investigation was carried out during *kharif* 2015 at Agricultural College Farm, Bapatla, Guntur District, Andhra Pradesh, which is located at an altitude of 5.4 m MSL, 15°54' N latitude and 80°25' E longitude. The material used and the methods followed in the present investigation are described hereunder.

3.1 MATERIAL

The experimental material for this study consisted of forty genotypes of long duration maturity groups obtained from Rice Research Unit (RRU) Bapatla, Guntur district, Andhra Pradesh. The information about the material used in this study is presented in Table 3.1.

Table 3.1 Name and origin of rice (*Oryza sativa* L.) genotypes employed in the present study

S. No.	Genotype	Origin
1.	RGL 7014	Srikakulam
2.	BPT 2675	Guntur
3.	BPT 5204	Guntur
4.	MTU 2035-12-2-4-3	West Godavari
5.	MTU 2195-201-1-3	West Godavari
6.	BPT 2660	Guntur
7.	NLR 3379	Nellore
8.	MTU 2071-13-1-1	West Godavari
9.	MTU 335-19-1-1-1	West Godavari
10.	JMP 43	Guntur
11.	MTU 2111-13-1-2	West Godavari
12.	NLR 3385	Nellore
13.	BPT 2595	Guntur
14.	MTU 2127-35-1-1-1	West Godavari
15.	NLR 3380	Nellore
16.	MTU 2127-48-1-1-1	West Godavari
17.	BPT 2658	Guntur
18.	BPT 2743	Guntur
19.	NLR 5785-12-2-1	Nellore

S. No.	Genotype	Origin
20.	JMP 24	Guntur
21.	MTU 20601-1-1-1-1	West Godavari
22.	NLR 3390	Nellore
23.	BPT 2661	Guntur
24.	MTU 7029	West Godavari
25.	MTU 2195-105-1-5	West Godavari
26.	MTU 2022-8-3-3	West Godavari
27.	BPT 2650	Guntur
28.	MTU 2244-47-15-6-77	West Godavari
29.	BPT 2757	Guntur
30.	MTU PS 257-1-1-1	West Godavari
31.	BPT 2587	Guntur
32.	MTU 2035-18-1-2-7	West Godavari
33.	BPT 2644	Guntur
34.	BPT 2774	Guntur
35.	BPT 2571	Guntur
36.	BPT 2758	Guntur
37.	BPT 2593	Guntur
38.	BPT 2763	Guntur
39.	BPT 2741	Guntur
40.	BPT 2772	Guntur

3.2 METHODS

3.2.1 Experimental technique

The experimental techniques of the present investigation are detailed hereunder.

Location	:	Agricultural College Farm, Bapatla.
Season	:	<i>Kharif</i> , 2015
Design	:	Randomized Complete Block Design
Treatments	:	40 rice long duration genotypes
Replications	:	3
Spacing	:	20 cm × 15 cm
Number of rows	:	5 rows /genotype / replication
Row length	:	4 m
Plot size	:	5 sq. m
Fertilizers	:	100kg: 60kg: 40kg NPK/ ha

3.2.2 Record of observations

Observations were recorded on ten randomly selected plants per treatment per replication and their means were used for statistical analysis. However, days to 50% flowering and days to maturity were recorded on plot basis. The data on the following yield and yield component traits were recorded.

3.2.2.1 Days to 50% flowering

The number of days taken from sowing to the opening of flowers in 50% of population in each genotype were recorded.

3.2.2.2 Days to maturity

The total number of days taken from date of sowing to complete maturity was taken as days to maturity.

3.2.2.3 Number of productive tillers per plant

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

3.2.2.4 Plant height (cm)

The height of the fully matured plant from the base of the plant to the tip of the inflorescence (panicle) was measured in centimeters.

3.2.2.5 Panicle length (cm)

It was measured in centimeters at the time of plant maturity from the base of panicle (neck node) to the tip of last spikelet prior to harvest.

3.2.2.6 Grains per panicle

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

3.2.2.7 Test weight (g)

The weight of 1000 randomly selected seeds was recorded in grams at 12 % moisture level.

3.2.2.8 Grain yield per plant (g)

Ten randomly selected plants were harvested and threshed. The cleaned seed was dried and weighed in grams and the mean yield of ten plants was taken as grain yield per plant.

3.2.2.9 Kernel length (mm)

Ten grains of milled rice were selected randomly and the length in millimeter was recorded using Dial micrometer.

3.2.2.10 kernel breadth (mm)

Ten grains of milled rice were selected randomly and the breadth in millimeter was recorded using Dial micrometer.

3.2.2.11 L/B ratio

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

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

Based on kernel length and L/B ratio classification, the grain type was assigned to the experimental material as per Jennings *et al.* (1979).

Grain type	Length (mm)	Shape	L/B ratio
Extra long	More than 7.50	Slender	More than 3.0
Long	6.61-7.50	Medium	2.1-3.0
Medium	5.51-6.60	Bold	1.1-2.0
Short	Less than 5.50	Round	Less than 1.1

3.3 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to the following statistical analysis.

3.3.1 Analysis of variance

Analysis of variance of the characters was done as per standard statistical procedure for randomized complete block design as given by Panse and Sukhatme (1978).

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

Where,

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

μ = General mean

t_i = i^{th} genotype effect

r_j = j^{th} block effect

e_{ij} = Random error

The structure of analysis of variance was as follows.

ANOVA Table for Randomized Block Design

Source of variation	Degrees of freedom	Mean sum of squares	Expected mean sum of squares	“F” calculated value
Replications	$r-1$	M_r	$\sigma_e^2 + t \sigma_r^2$	M_r / M_e
Treatments	$t-1$	M_t	$\sigma_e^2 + r \sigma_g^2$	M_t / M_e
Error	$(r-1)(t-1)$	M_e	σ_e^2	
Total	$(rt-1)$			

Where,

r = Number of replications

g = Number of genotypes

M_r = Mean sum of square of replication

M_t = Mean sum of square of treatment

M_e = Mean sum of square of error

σ_e^2 = Environmental variance

σ_r^2 = Variance due to replications

σ_g^2 = Variance due to genotypes

3.3.2 Estimation of genetic parameters

3.3.2.1 Estimation of variance components

Phenotypic and genotypic variances were estimated using the following formula,

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

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

The test of significance was carried out using 'F' table value of Fisher and Yates (1963).

3.3.2.2 Coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton (1952).

a) Genotypic coefficient of variation (GCV)

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

b) Phenotypic coefficient of variation (PCV)

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

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

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

3.3.2.3 Heritability

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

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

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

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

3.3.2.4 Expected genetic advance

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

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

Where,

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

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

3.3.2.5 Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

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

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

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

3.3.5 Correlation studies

The phenotypic and genotypic correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components by using covariance technique as per Falconer (1964).

$$\text{Phenotypic coefficients of correlation } (r_p) = r(x_i x_j)_p = \frac{\text{Cov}(x_i x_j)_p}{\left[V(x_i)_p \cdot V(x_j)_p \right]^{1/2}}$$

Where,

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

$\text{Cov}(x_i x_j)_p$ = Phenotypic covariance between i^{th} and j^{th} characters

$V(x_i)_p$ and $V(x_j)_p$ = Phenotypic variance of i^{th} and j^{th} characters respectively

$$\text{Genotypic coefficients of correlation } (r_g) = r(x_i x_j)_g = \frac{\text{Cov}(x_i x_j)_g}{\left[V(x_i)_g \cdot V(x_j)_g \right]^{1/2}}$$

Where,

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

$\text{Cov}(x_i x_j)_g$ = Genotypic covariance between i^{th} and j^{th} characters

$V(x_i)_g$ and $V(x_j)_g$ = Genotypic variance of i^{th} and j^{th} characters respectively

3.3.5.1 Test of significance

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

3.3.6 Path coefficient analysis

Path coefficient analysis was carried out by using the correlation coefficients to know the direct and indirect effects of the component characters on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Path coefficients were obtained by solving the simultaneous equations which express the basic relationship between correlations and path coefficients.

The equations are as follows:

$$\begin{aligned} r_{1,y} &= P_{1,y} + r_{1,2} P_{2,y} + r_{1,3} P_{3,y} + \dots + r_{1,k} P_{k,y} \\ r_{2,y} &= r_{2,1} P_{1,y} + P_{2,y} + r_{2,3} P_{3,y} + \dots + r_{2,k} P_{k,y} \\ &\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot \\ &\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot \\ &\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot \\ r_{k,y} &= r_{k,1} P_{1,y} + r_{k,2} P_{2,y} + r_{k,3} P_{3,y} + \dots + r_{k,k} P_{k,y} \end{aligned}$$

Where,

$r_{1,y}$ to $r_{k,y}$ = Correlation coefficients between independent characters

$r_{1,2}$ to $r_{k-1,k}$ = Correlation coefficients between all possible combinations of independent characters

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

The residual effect was computed by using the formula

$$R = \left[1 - (P_{1,y} r_{1,y} + P_{2,y} r_{2,y} + P_{3,y} r_{3,y} + \dots) \right]^{1/2}$$

Where,

R = Residual effect

$P_{1,y}$ = Direct effect of independent character '1' on dependent character 'y'

$r_{1,y}$ = Correlation coefficient of independent character '1' on dependent character 'y'

3.3.7 Genetic divergence

3.3.7.1 Mahalanobis' D² analysis

The data collected on different yield contributing characters was analysed using Mahalanobis' D² analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1928).

3.3.7.1.1 Test of significance

Variances were calculated for all the characters studied and test of significance was done. For the character pairs analysis of covariance was estimated on the basis of mean values (Panse & Sukhatme, 1978). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion. The sum of squares and sum of products of error and error + variety, variance-covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

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

Where,

Λ = Wilk's criterion

$|E|$ = Determinant of error matrix and

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

$$\log_e \Lambda V_{(stat)} = -m \log_e = -\left(n - \frac{p+q+1}{2}\right) \log_e \hat{\Lambda} \dots\dots\dots (at pq df)$$

Where,

$$m = n - (p + q + 1)/2 = 2.3026 \log 10 \Lambda$$

n = degree of freedom for error + varieties

p = number of variables /characters (11)

q = number of varieties –1 (or d.f.)

$V_{(stat)}$ is distributed as χ^2 with pq (429) degrees of freedom.

Transformation of correlated variables

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

3.3.7.1.2 Computation of D^2 values

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

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

Where,

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

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

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

3.3.7.1.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for p degrees of freedom, where p is the number of characters considered *i.e.*, 11 in the present study.

3.3.7.1.4 Contribution of individual characters towards divergence

In all combinations, each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 is given to the highest mean difference and the rank p to the lowest difference, where p is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

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

Where,

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

M = All possible combinations of number of genotypes considered.

3.3.7.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977).

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

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

3.3.7.1.6 Average intra-cluster distance

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

3.3.7.1.7 Average inter-cluster distance

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

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

Where,

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

n_1 & n_2 = number of genotypes of two clusters.

3.3.7.2 Principal component analysis and cluster analysis

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

3.3.7.2.1 Eigen values and eigen vectors

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

$$\text{Per cent variance explained for PC}_1 = \frac{\text{eigen value (PC}_1\text{)}}{\text{Sum of eigen values}}$$

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

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

Where,

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

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

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

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

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

Where, S_i is the standard deviation of X_i .

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

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

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

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

3.3.7.2.2 Cluster analysis

Agglomerative hierarchical clustering technique was followed as given by Anderberg (1993).

3.3.7.2.2.1 Obtaining data matrix

PCA scores for 40 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

3.3.7.2.2.2 Standardizing the data matrix

To compare the similarities among the genotypes, the data matrix was standardized with a column standardizing function *i.e.*, Q analysis. The data matrix is standardize in cluster analysis to make the characters contribute more equally to the similarities among genotypes and to nullify the arbitrarily affect the units chosen for measuring the attributes among the genotypes.

Column standardizing function CA-Q analysis was carried by the following formula.

$$Z_{ij} = \bar{X}_{ij} - X_j / S_{ij}$$

$$\text{Where, } \bar{X}_j = \sum_{i=1}^n X_{ij} / n$$

$$\text{Where, } S_{ij} = \frac{\sum_{i=1}^n X_{ij} - X_j / n}{n-1}$$

For, i = genotypes *i.e.*, 40

j = total variables *i.e.*, 11

The resulting data after standardization is unit less and have mean zero and variance one.

3.3.7.2.2.3 Computing the resemblance matrix

A resemblance coefficient, which measures the overall resemblance (the degree of similarity or distance) between a pair of genotypes, was computed. Here 40 genotypes were taken in data matrix therefore resemblance coefficient was computed.

The data matrix was transformed to distance matrix (resemblance matrix) based on the dissimilarity coefficients using squared Euclidean distance method.

$$\text{Squared Euclidean distance } [d_{ij}] = \sum_{k=1}^P (X_{ik} - X_{jk})^2$$

Where,

P = Number of genotypes *i.e.*, 40

X_{ik} = Value of i^{th} genotype for k PCA scores

X_{jk} = Value of j^{th} genotype for k PCA scores

3.3.7.2.2.4 Execution of the clustering method

Distance matrix was converted into dendrogram by using Ward's method where the distance between two clusters is the sum of squares between two clusters summed over all variables. At each stage in the clustering procedure within cluster sum of squares is minimized over all partitions obtained by combining two clusters from previous stage.

Chapter IV

RESULTS AND DISCUSSION

Variability in a crop species is of utmost importance as it provides the basis for effective selection. The amount of variability present in a population is generally measured in terms of phenotypic and genotypic coefficients of variation. The information on the nature and magnitude of genetic variability present in a population is a prerequisite to start any crop improvement programme.

Yield is a complex character and dependent on many component traits. Hence it is necessary to have knowledge on the extent of association between yield and yield contributing characters. Expression of various traits often varies with breeding material and environment. Therefore, the information on character association between the traits themselves and with the yield for the specific breeding material being used at a particular location is important for breeding high yielding genotypes. Apart from the information on degree and direction of relationship between two or more traits it is very important to know the cause of association by knowing the direct and indirect effects of independent characters on dependent character.

Mahalanobis' D^2 statistic is an effective tool in quantifying the degree of genetic divergence at genotypic level and provides quantitative measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1928). Principal component analysis was carried out to transform the inter dependent traits into a set of independent traits as well as to reduce the dimensionality of the data structure (Banfield, 1978). It is defined as a method of data reduction to clarify the relationship between two or more characters into limited number of uncorrelated new variables. The reduction is achieved by linear transformation of the original characters into a set of uncorrelated variables known as principal components (PCs).

The data collected on forty rice genotypes for eleven different traits was subjected to standard statistical analysis for drawing valid conclusions. The details of results obtained from the above investigation are discussed character-wise and presented under the following headings.

4.1 Mean, genetic variability, heritability and genetic advance

4.2 Character association

4.3 Path coefficient analysis

4.4 Genetic divergence

4.1 MEAN, GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The success of any breeding programme depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and expected genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance present in the available genetic material.

Genetic variability together with the heritability estimates would give a better idea on the amount of genetic gain expected out of selection (Burton, 1952 and Swarup and Chaugle, 1962). Further, the magnitude of heritable variability is the most important aspect (Panse, 1957), which has close relationship with response to selection. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance (Johnson *et al.*, 1955).

The analysis of variance revealed significant differences among the genotypes for all characters under study, indicating a high degree of variability in the material. The details are presented in Table 4.1, Table 4.2 and Table 4.3.

4.1.1 Days to 50% flowering

The variation for number of days taken to 50% flowering ranged from 102.33 days (JMP 43) to 118 days (NLR 5785-12-2-1) with a mean of 110.79 days. The PCV (4.28) and GCV (2.92) estimates were low indicating less variation for days to 50% flowering among genotypes studied and such estimates of PCV and GCV were earlier reported by Prasad *et al.* (2011), Ghosh and Sharma (2012), Sravan *et al.* (2012), Gangashetty *et al.* (2013), Paikhomba *et al.* (2014), Neha *et al.* (2014), Balakrishna *et al.* (2015a) and Tejaswini (2016).

Moderate heritability (46.43%) combined with low genetic advance as per cent of mean (4.10) was observed for this trait indicating the predominance of non-additive gene action in the inheritance of this trait and the desired results may not be obtained by simple selection. Low genetic advance as percent of mean was in accordance with the results of Sreeparvathy *et al.* (2010) and Osman *et al.* (2012).

4.1.2 Days to maturity

The number of days to maturity ranged from 141.33 days (MTU 2195-201-1-3) to 152.33 days (BPT 2741) with a mean of 145.38 days. The estimates of PCV (2.61) and GCV (1.34) were low indicating less variation for days to maturity among genotypes studied. Low estimates of PCV and GCV were earlier reported by Chaudary and Motiramani (2003), Souroush *et al.* (2004), Naik (2004) and Tejaswini (2016).

Low heritability (26.38%) accompanied with low genetic advance as per cent of mean (1.42) was observed indicating the predominance of non-additive gene action in the inheritance of this trait and desired results may not be obtained by simple selection. Low genetic advance as percent of mean was earlier reported by Madhavalatha and Suneetha (2005), Karim *et al.* (2007) Singh *et al.* (2011), Verma *et al.* (2011) and Osman *et al.* (2012).

4.1.3 Productive tillers per plant

This character possessed variability ranging from 5.00 (MTU 2195-201-1-3) to 11.67 (BPT 2661) with a mean of 8.87. The estimates of PCV (21.14) and GCV (16.27) were high and moderate, respectively. Higher PCV value than GCV revealed that variation is not only due to genotypes but also due to influence of environment and therefore simple selection based on phenotype will be misleading. Similar results were reported by Binse *et al.* (2006), Devi *et al.* (2006), Singh *et al.* (2006), Vijayalakshmi *et al.* (2008), Chandra *et al.* (2009), Saidaiah *et al.* (2010) and Balakrishna *et al.* (2015a).

Moderate heritability (59.23%) combined with high genetic advance as per cent of mean (25.79) was observed for this trait indicating the predominance of non-additive gene action in the inheritance of this trait and the desired results may not be obtained by simple selection. These findings are in accordance with that of Mishra and Pravin (2004) and Krishna *et al.* (2008).

4.1.4 Plant height (cm)

The variation for plant height ranged from 99.00 cm (MTU 2195-201-1-3) to 130.67 cm (NLR 3385) with a mean of 111.97 cm. The PCV (8.83) and GCV (7.24) estimates were low for both indicates less variation for plant height among genotypes. Similar findings were earlier reported by Ogunbayo *et al.* (2014).

High heritability (67.25%) coupled with moderate genetic advance as per cent of mean (12.25) was observed indicating the operation of both additive and non-additive gene action in the inheritance of this trait and the desired results may not be obtained by simple selection. The above findings are in agreement with Chand *et al.* (2005), Vaithiyalingan and Nadarajan (2006), Singh *et al.* (2007), Paikhomba *et al.* (2014) and Tejaswini (2016).

4.1.5 Panicle length (cm)

This character ranged from 16.33 (MTU 2195-201-1-3 and MTU 2195-105-1-5) to 29.67 (BPT 2658) with a mean of 23.66. The PCV (12.67) and GCV (11.83) of this trait were moderate indicating the presence of considerable amount of variability for this character and difference between PCV and GCV is narrow indicating that the phenotypic variability is the direct measure of genetic variability. Similar results were reported by Naik (2004), Hasib (2005), Devi *et al.* (2006), Sharma and Sharma (2007), Vijayalakshmi *et al.* (2008), Saidaiah *et al.* (2010), Prasad *et al.* (2011), Idris and Mohamed (2013) and Gangashetty *et al.* (2013).

High heritability (87.26%) combined with high genetic advance as per cent of mean (22.77) was recorded for this trait which revealed the importance of additive gene action in the inheritance of this character. Further, it indicates that this character can be improved through simple selection. These results are in conformity with the observations of Naik (2004), Elayaraja *et al.* (2005), Vaithiyalingan and Nadarajan (2006), Baradwaj *et al.* (2007), Nayudu *et al.* (2007), Sharma and Sharma (2007), Vijayalakshmi *et al.* (2008), Sateeshkumar and Saravanan (2012), Gangashetty *et al.* (2013) and Dhurai *et al.* (2014).

4.1.6 Grains per panicle

The variation for grains per panicle varied from 91.33 (MTU 2195-201-1-3) to 283 (MTU 2127-35-1-1-1) with a mean of 189.02. The PCV (23.48) and GCV (19.45) estimates were high and moderate respectively. Higher PCV value than GCV revealed that there is enough amount of variation for this character among the genotypes studied. Similar results were reported by Kuchanur *et al.* (2009) and Laxuman *et al.* (2011).

High heritability (68.61%) in conjunction with high genetic advance as per cent of mean (33.18) was recorded. This indicates that the inheritance of grains per panicle is controlled by additive gene action and simple selection may be rewarding in improving

this trait. The above findings are in agreement with Hossain and Hossain (2001), Chaudhary and Motiramani (2003), Patil *et al.* (2003), Binse *et al.* (2006), Devi *et al.* (2006), Panwar (2006), Vaithiyalingan and Nadarajan (2006), Karim *et al.* (2007), Karthikeyan *et al.* (2007), Sharma and Sharma (2007), Kuchanur *et al.* (2009) and Prasad *et al.* (2009).

4.1.7 Test weight (g)

The variation for test weight ranged from 14.52g (MTU 2195-201-1-3) to 29.32g (BPT 2658) with a mean of 18.65g. The PCV (16.79) and GCV (16.06) estimates were moderate and difference between them is narrow indicates that there is a little role environmental component in the observed variation. Similar results were reported by Satish (2000), Naik (2004), Kumar and Bapu (2005), Vaithiyalingan and Nadarajan (2006), Sarkar *et al.* (2007), Sharma and Sharma (2007), Singh *et al.* (2007), Karthikeyan *et al.* (2007), Krishna *et al.* (2008), Chandra *et al.* (2009) and Sharma and Koutu (2013).

High heritability (91.48%) combined with high genetic advance as per cent of mean (31.64) was recorded. This indicates that the inheritance of test weight per plant is controlled by additive gene effects and simple selection methods are sufficient in improving this trait. These results are in conformity with that of Baradwaj *et al.* (2007), Karim *et al.* (2007), Karthikeyan *et al.* (2007), Sharma and Sharma (2007), Karad and Pol (2008), Vijayalakshmi *et al.* (2008), Anbanandan *et al.* (2009), Chandra *et al.* (2009), Saidaiah *et al.* (2010), Lal and Chauhan (2011), Prasad *et al.* (2011), Bhadru *et al.* (2012), Sateeshkumar and Saravanan (2012), Gangashetty *et al.* (2013), Bornare *et al.* (2014) and Tejaswini (2016).

4.1.8 Kernel length (mm)

The variation for kernel length ranged from 5.16mm (BPT 2650) to 6.99mm (NLR 3390) with a mean of 5.67mm. This character possessed low PCV (6.45) and GCV (5.83) indicating less variation for kernel length among the genotypes studied and such low estimates of PCV and GCV were earlier reported by Krishnaveni and Niveditha (2014), Venkanna *et al.* (2014) and Tejaswini (2016).

High heritability (81.77%) combined with moderate genetic advance as per cent of mean (10.87) was noted for this trait which revealed the operation of both additive and non-additive gene actions in the inheritance of this trait indicate that desired results may not be obtained by simple selection. High heritability coupled with moderate genetic advance as per cent of mean for this character were earlier reported by Tejaswini (2016).

4.1.9 Kernel breadth (mm)

Kernel breadth in the genotypes studied ranged from 1.67mm (BPT 2757) to 2.57mm (MTU 2111-13-1-2) with a mean value of 2.04mm. The estimates of PCV (11.09) and GCV (9.85) were moderate and low. Higher PCV value than GCV revealed that variation is not only due genotypes but also due to influence of environment and therefore simple selection based on phenotype will be misleading. Low GCV for this trait was earlier reported by Krishnaveni and Niveditha (2014), Venkanna *et al.* (2014) and Tejaswini (2016).

High heritability (78.92%) combined with moderate genetic advance as per cent of mean (18.02) was noted for this trait which may be due to the predominance of both additive and non-additive gene actions and desired results may not be obtained by simple selection. These findings are in agreement with the results of Krishnaveni and Niveditha (2014) and Tejaswini (2016).

4.1.10 L/B ratio

The variation for this trait ranged from 2.19mm (MTU 2111-13-1-2) to 3.27 (BPT 2757) with a mean of 2.81mm. The PCV (9.32) and GCV (7.82) estimates are low indicating less variation for L/B ratio among genotypes studied and such estimates of PCV and GCV were earlier reported by Krishnaveni and Sobharani (2006) and Krishnaveni and Niveditha (2014).

High heritability (70.49%) combined with moderate genetic advance as per cent of mean (13.53) was noted for this trait indicating the predominance of both additive and non-additive gene actions in the inheritance of this trait. Further, these results indicate that the desired progress may not be obtained by simple selection for this character. Similar results were earlier reported by Krishnaveni and Niveditha (2014).

4.1.11 Grain yield per plant (g)

The range of variation noted for this trait is from 10.20g (MTU 2195-201-1-3) to 24.93g (BPT 2658) with a mean of 17.79g. The PCV (26.04) and GCV (19.63) estimates were high and moderate, respectively. Higher PCV value than GCV revealed that variation is not only due to genotypes but also due to environment and therefore direct selection based on phenotype will be misleading. These findings are in conformity with the results of Nagajyothi (2001), Borkakati *et al.* (2005), Manna *et al.* (2006), Panwar (2006), Kumar and Ramesh (2008) and Laxuman *et al.* (2011).

High heritability (56.81%) combined with high genetic advance as per cent of mean (30.47) was noted for this trait which revealed the importance of additive gene action in the inheritance of this trait. These findings are in agreement with the results of Garg *et al.* (2010), Sreeparvathy *et al.* (2010), Parvathi *et al.* (2011), Singh *et al.* (2011), Bhadru *et al.* (2012), Sateeshkumar and Saravanan (2012), Gangashetty *et al.* (2013), Sharma and Koutu (2013), Paikhomba *et al.* (2014), Neha *et al.* (2014) and Tejaswini (2016).

4.2 CHARACTER ASSOCIATION

Yield is a complex and polygenically inherited character resulting from multiplicative interaction of its component traits. The cumulative effect of such traits determines the yield. The change in one character brings about a series of changes in the other characters, since they are interrelated. Therefore, the correlation studies are of considerable importance in any selection programme as they provide degree and direction of relationship between two or more component traits.

The phenotypic correlation coefficients between grain yield and yield component characters and among themselves were estimated and presented in Table 4.4. The results were discussed character wise hereunder.

4.2.1 Days to 50% flowering

Days to 50% flowering recorded highest significant positive association with days to maturity (0.4418**) followed by grains per panicle (0.2861**), grain yield per plant (0.2719**) and kernel length (0.1929*). These results are in agreement with Khare *et al.* (2014), Ogunbuyo *et al.* (2014), Ashok *et al.* (2015) and Tejaswini (2016) for days

to maturity; Sateeshkumar and Sharma (2012) and Aditya and Bhartiya (2013) for grains per panicle; Chandra *et al.* (2009) and Tushara *et al.* (2013) for grain yield per plant and Sanghera *et al.* (2013) and Ogunbuyo *et al.* (2014) for kernel length.

It also had non-significant positive association with panicle length (0.1650), test weight (0.1263), L/B ratio (0.0938), plant height (0.0785), productive tillers per plant (0.0452) and kernel breadth (0.0246). Similar results were earlier reported by Khare *et al.* (2014) for panicle length and test weight; Sanghera *et al.* (2013) and patel *et al.* (2014) for L/B ratio; Nagaraju *et al.* (2013) and Sanghera *et al.* (2013) for plant height and Tejaswini (2016) for kernel breadth.

4.2.2 Days to maturity

Days to maturity was found to have highest significant positive association with grains per panicle (0.3264**) followed by grain yield per plant (0.3175**), kernel length (0.2745**) and plant height (0.2614**). Similar results were indicated by Panwar (2006) for grains per panicle; Rashid *et al.* (2014) and Bornare *et al.* (2014) for grain yield per plant; Tejaswini (2016) for kernel length and plant height.

It also had highest non-significant positive association with test weight (0.1775) followed by L/B ratio (0.1150), panicle length (0.1141), kernel breadth (0.0566) and productive tillers per plant (0.0550). These results were in agreement with those of Lakshmi *et al.* (2014) for test weight, L/B ratio and kernel breadth; Patel *et al.* (2014) and Tejaswini (2016) for panicle length and Ashok (2015) for productive tillers per plant.

4.2.3 Productive tillers per plant

This trait possessed highest positive association with grain yield per plant (0.5740**) followed by panicle length (0.5445**), test weight (0.4225**) and grains per panicle (0.4105**). Similar results were also reported by Rashid *et al.* (2014), Bornare *et al.* (2014) and Ashok (2015) for grain yield per plant; Rani and Reddy (2010) for panicle length; Lakshmi *et al.* (2014) for test weight and Eradasappa *et al.* (2007) for grains per panicle.

It also had non-significant positive association with plant height (0.1599) and kernel breadth (0.1297) further, it also had negative non-significant association with L/B ratio (-0.1516) and kernel length (-0.0293). These results are in agreement with those of Sateeshkumar and Saravanan (2012) for L/B ratio and kernel length.

4.2.4 Plant height (cm)

Plant height recorded highest significant positive association with kernel breadth (0.4119**) followed by panicle length (0.3961**), kernel length (0.3799**), grain yield per plant (0.2852**) and test weight (0.2583**). Similar results were indicated by Ogunbuyo *et al.* (2014) and Lakshmi *et al.* (2014) for kernel breadth; Tejaswini (2016) for panicle length and kernel length; Idris and Mohammed (2013) and Bekele *et al.* (2013) for grains yield per plant and Minnie *et al.* (2013) for test weight.

Further it also exhibited significant negative association with L/B ratio (-0.1889*). Similar association was earlier indicated by Bekel *et al.* (2013).

4.2.5 Panicle length (cm)

This character exhibited highest significant positive association with test weight (0.5357**) followed by grain yield per plant (0.4826**) and grains per panicle (0.4557**). These results are in accordance with those of Babu *et al.* (2012) and Minnie *et al.* (2013) for test weight; Rashid *et al.* (2014), Bornare *et al.* (2014) and Ashok (2015) for grain yield per plant and Aditya and Bhartiya (2013) for grains per panicle.

It had positive non-significant association with kernel breadth (0.1786) and kernel length (0.0803). Similar findings were also reported by Sateeshkumar and Saravanan (2012). Further it also recorded non-significant negative association with L/B ratio and such result was earlier reported by Nagaraju *et al.* (2013).

4.2.6 Grains per panicle

This character exhibited highest significant positive association with grain yield per plant (0.5644**) followed by test weight (0.4389**) and kernel length (0.2366**). Similar results were reported by Panwar and Ali (2007), Sharma and Sharma (2007) and Ashok (2015) for grain yield per plant and Panwar *et al.* (2006) for test weight.

This character also exhibited non-significant positive association with kernel breadth (0.1257) and L/B ratio (0.0046). Similar results were indicated by Sateeshkumar and Saravanan (2012) for L/B ratio.

4.2.7 Test weight (g)

This character exhibited highest significant positive association with grain yield per plant (0.5233**). Similar results were reported by Sudharani *et al.* (2013), Rashid *et al.* (2014), Bornare *et al.* (2014) and Ashok (2015).

It had also exhibited non-significant positive association with kernel breadth (0.1392) and kernel length (0.1097). Similar findings were earlier reported by Ogunbuyo *et al.* (2014) and Allam *et al.* (2015) for kernel length and Aditya and Bhartiya (2013) and Sanghera *et al.* (2013) for kernel breadth.

4.2.8 Kernel length (mm)

This trait recorded significant positive association with kernel breadth (0.4498**) and grain yield per plant (0.1481*). These findings are in agreement with those of Aditya and Bhartiya (2013) and Sanghera *et al.* (2013) for kernel breadth and Sateeshkumar and Saravanan (2012) and Premkumar *et al.* (2015) for grain yield per plant. It also recorded non-significant positive association with L/B ratio (0.1471).

4.2.9 Kernel breadth (mm)

Kernel breadth had significant positive association with grain yield per plant (0.3025**) and this finding is in conformity with those of Sateeshkumar and Saravanan (2012) and Premkumar *et al.* (2015). Further it also had significant negative correlation with L/B ratio (-0.8072**) and such finding is in conformity with that of Patel *et al.* (2014), Lakshmi *et al.* (2014), Premkumar *et al.* (2015) and Tejaswini (2016).

4.2.10 L/B ratio

This trait recorded negative significant association with grain yield per plant (-0.2167*) and similar result was earlier reported by Krishnaveni and Sobharani (2006).

It can be summarized that nine out of ten characters included in the study recorded significant positive association with the dependent variable *i.e.*, grain yield per plant. The association was strongest with Productive tillers per plant (0.5740**) followed by grains per panicle (0.5644**), test weight (0.5233**), panicle length (0.4826**), days to maturity (0.3175**), kernel breadth (0.3025**), plant height (0.2852**), days to 50% flowering (0.2719**) and kernel length (0.1481**). In case of L/B ratio also the

association was significant but in negative direction. This indicates that almost all the characters which were included in the study are having important role in the process of selection for improvement of the grain yield per plant.

4.3 PATH COEFFICIENT ANALYSIS

Yield being a complex character, is composed of several components some of which affect yield directly while others contribute towards it indirectly. Correlation studies provide information only on the magnitude and direction of association of yield with its components and also among various components. But to know the direct effects of each independent variable on yield and indirect effects through other characters of each variable, path coefficient analysis has to be performed. In the present study, path analysis was used to work out the direct and indirect effects of yield contributing characters on yield using 40 genotypes of rice and the results are presented (Table 4.5.) character wise hereunder. The path diagrams were given in figures 4.1.

4.3.1 Days to 50% flowering

Days to 50% flowering had positive significant association (0.2719**) and positive direct effect (0.1116) on grain yield per plant. Similar results for both correlation and direct effect were recorded by Panwar (2006).

This trait also exhibited positive indirect effects via grains per panicle (0.0780), L/B ratio (0.0724), days to maturity (0.0574), kernel breadth (0.0261), test weight (0.0253), productive tillers per plant (0.0150) and plant height (0.0034). Similar indirect effects were indicated by Panwar (2006) for days to maturity, productive tillers per plant and test weight; Aditya and Bhartiya (2013) for grains per panicle and L/B ratio and Tejaswini (2016) for plant height and kernel breadth.

For improvement of grain yield per plant, along with days to 50% flowering which is showing positive direct effect, other characters which are showing positive indirect effects viz., grains per panicle, L/B ratio, days to maturity, kernel breadth, test weight, productive tillers per plant and plant height are to be considered simultaneously during selection.

4.3.2 Days to maturity

It showed significant positive correlation (0.3175**) and positive direct effect (0.1300) on grain yield per plant. Similar result for direct effect was earlier reported by Aditya and Bhartiya (2013).

This trait also possessed positive casual factors via grains per panicle (0.0890), L/B ratio (0.0887), kernel breadth (0.0601), days to 50% flowering (0.0493), test weight (0.0355), productive tillers per panicle (0.0182) and plant height (0.0034). Similar indirect effects were indicated by Hasan *et al.* (2012) for days to 50% flowering, productive tillers per plant and test weight; Aditya and Bhartiya (2013) for grains per panicle; Allam *et al.* (2015) for plant height and kernel breadth and Tejaswini (2016) for L/B ratio.

For improvement of grain yield per plant, along with days to maturity which is showing positive direct effect, other characters which are showing positive indirect effects viz., grains per panicle, L/B ratio, kernel breadth, days to 50% flowering, test weight, productive tillers per plant and plant height are to be considered simultaneously during selection.

4.3.3 Productive tillers per plant

This character expressed significant positive association (0.5740**) and positive direct effect (0.3307) on grain yield per plant. Similar results for both correlation and direct effect were earlier reported by Eradasappa *et al.* (2007) and Panwar and Ali (2007).

It also possessed positive indirect effects through kernel breadth (0.1377), test weight (0.0845), kernel length (0.0174), grains per panicle (0.1119), days to maturity (0.0071), plant height (0.0070) and days to 50% flowering (0.0050). Similar indirect effects were earlier reported by Sudharani (2013) for test weight and days to 50% flowering; Allam *et al.* (2015) for kernel breadth, days to maturity and plant height; Binse *et al.* (2006) for grains per panicle and Premkumar *et al.* (2015) for kernel length.

Thus this trait showed high positive direct effect coupled with highly significant positive association on grain yield per plant, this indicates direct effect of productive tillers per plant accounted for the major portion in the total correlation between them, hence, for improvement of grain yield per plant, direct selection through productive tillers per plant will be effective.

4.3.4 Plant height (cm)

It showed positive significant correlation (0.2852**) and positive direct effect (0.0436) on grain yield per plant. Similar results for both correlation and direct effect were recorded by Janardanam *et al.* (2001), Nagajyothi (2001), Shasidhar *et al.* (2005) and Bekele *et al.* (2013).

This trait also exhibited positive indirect effects via kernel breadth (0.4372), productive tillers per plant (0.0529), test weight (0.0517), grains per panicle (0.0352), days to maturity (0.0340) and days to 50% flowering (0.0088). Similar indirect effects were indicated by Sateeshkumar and Saravanan (2012) for kernel breadth; Aditya and Bhartiya (2013) for days to maturity and grains per panicle; Premkumar *et al.* (2015) for days to 50% flowering and productive tillers per plant and Balakrishna *et al.* (2015b) for test weight.

Thus the trait plant height showed positive direct effect coupled with significant positive correlation coefficients with grain yield per plant. These results also indicate that there is considerable amount of contribution through the indirect effects via kernel breadth, productive tillers per plant, test weight, grains per panicle, days to maturity and days to 50% flowering towards the positive correlation. In such situations, these indirect casual factors are to be considered along with plant height during selection for improvement of grain yield per plant.

4.3.5 Panicle length (cm)

Panicle length expressed significant positive association (0.4826**) and negative direct effect (-0.0190) on grain yield per plant. Similar results were earlier reported by Eradasappa *et al.* (2007), Rani and Reddy (2010) and Sudharani *et al.* (2013).

It also exhibited the positive casual factors via kernel breadth (0.1896), productive tillers per plant (0.1800), grains per panicle (0.1243), test weight (0.1072), days to 50% flowering (0.0184), plant height (0.0173) and days to maturity (0.0148). Similar indirect effects were indicated by Sateeshkumar and Saravanan (2012) for grains per panicle; Aditya and Bhartiya (2013) for days to maturity and kernel breadth; Balakrishna *et al.* (2015b) for days to 50% flowering, productive tillers per plant and test weight and Tejaswini (2016) for plant height.

Thus the trait showed negative direct effect coupled with highly significant positive association on grain yield per plant. For improvement of grain yield per plant, this type of correlation does not explain the true relationship and direct selection through this trait will not be rewarding. In such situations the casual factors showing positive indirect effect on grain yield per plant viz., kernel breadth, productive tillers per plant, grains per panicle, test weight, days to 50% flowering, plant height days to maturity are responsible for positive correlation. Therefore these traits are to be considered simultaneously during selection process for improvement of the dependent variable.

4.3.6 Grains per panicle

This character recorded significant positive association (0.5644**) and positive direct effect (0.2727) on grain yield per plant. Similar results for both association and direct effect were recorded by Janardhanam *et al.* (2001), Nagajyothi (2001), Kumar and Bapu (2005) and Panwar (2006).

It also possessed positive indirect effect via productive tillers per plant (0.1357), kernel breadth (0.1334), test weight (0.0878), days to maturity (0.0424), days to 50% flowering (0.0319), plant height (0.0056) and L/B ratio (0.0035). Similar findings were earlier reported by Kumari *et al.* (2011) for days to 50% flowering and test weight; Aditya and Bhartiya (2013) for days to maturity, productive tillers per plant, plant height and kernel breadth and Ashok (2015) for L/B ratio.

Thus this trait showed positive direct effect coupled with highly significant positive association on grain yield per plant. This indicates that direct effect of grains per panicle accounted for the major portion in the total correlation between them, hence, direct selection through grains per panicle will be effective.

4.3.7 Test weight (g)

It showed positive and highly significant association (0.5233**) and positive direct effect (0.2001) on grain yield per plant. These findings were in agreement with the results of Kumar and Bapu (2005) and Gangasetty *et al.* (2013).

It also possessed positive causal factors through kernel breadth (0.1478), productive tillers per plant (0.1397), grains per panicle (0.1197), days to maturity (0.0231), days to 50% flowering (0.0141) and plant height (0.0113). Similar indirect effects were indicated by Panwar (2006) and Rani and Reddy (2010) for plant height and grains per panicle; Kumari *et al.* (2011) and Premkumar *et al.* (2015) for days to 50% flowering, productive tillers per plant and kernel breadth and Aditya and Bhartiya (2013) for days to maturity.

This trait showed positive direct effect coupled with highly significant positive association on grain yield per plant. This indicates direct effect of test weight on grain yield per plant accounted for major portion in the total correlation between them, therefore direct selection through test weight will be effective.

4.3.8 Kernel length (mm)

Kernel length exhibited significant positive correlation (0.1481*) and negative direct effect (-0.5919) on grain yield per plant. Similar result for direct effect was recorded by Kumari *et al.* (2011), Aditya and Bhartiya (2013) and Tejaswini (2016).

This trait also recorded positive indirect effects via kernel breadth (0.4775), L/B ratio (0.1134), grains per panicle (0.0645), days to maturity (0.0357), days to 50% flowering (0.0215), plant height (0.0166) and test weight (0.0220). Similar indirect effects were indicated by Sateeshkumar and Saravanan (2012) for days to 50% flowering and plant height; Aditya and Bhartiya (2013) for days to maturity and L/B ratio; Kumari *et al.* (2011) for grains per panicle; Parvathi *et al.* (2011) and Allam *et al.* (2015) for test weight and Tejaswini (2016) for kernel breadth.

Thus this trait had negative direct effect coupled with significant positive correlation. Here the contribution of high positive indirect effects nullified the negative direct effect. In such situations, the above mentioned high positive casual factors viz., kernel breadth, L/B ratio, grains per panicle, days to maturity, days to 50% flowering, plant height and test weight are to be considered during selection process for improvement of grain yield per plant.

4.3.9 Kernel breadth (mm)

Kernel breadth showed significant positive correlation (0.3025**) and positive direct effect (1.0616) on grain yield per plant. Similar result for direct effect was earlier reported by Kumari *et al.* (2011), Aditya and Bhartiya (2013) and Tejaswini (2016).

It also possessed positive indirect effects through productive tillers per plant (0.0429), grains per panicle (0.0343), test weight (0.0279), plant height (0.0180), days to maturity (0.0074) and days to 50% flowering (0.0027). Similar effects of indirect casual factors were indicated by Aditya and Bhartiya (2013) for grains per panicle; Venkanna *et al.* (2014) for productive tillers per plant and Tejaswini (2016) for test weight, plant height, days to maturity and days to 50% flowering.

As kernel breadth recorded high positive direct effect coupled with significant positive association on grain yield per plant and accounted for the major portion in the total correlation between them, direct selection through kernel breadth will be effective for improvement of grain yield per plant.

4.3.10 L/B ratio

This trait exhibited significant negative association (-0.2167*) and positive direct effect (0.7713) on grain yield per plant. Similar result for direct effect was recorded by Pal *et al.* (2011), Nagaraju *et al.* (2013), Aditya and Bhartiya (2013) and Tejaswini (2016).

This trait also had positive indirect effects via days to maturity (0.0149), days to 50% flowering (0.0105), panicle length (0.0025) and grains per panicle (0.0012). Similar indirect effects were indicated by Aditya and Bhartiya (2013) and Allam *et al.* (2015) for days to maturity; Premkumar *et al.* (2015) for days to 50% flowering; Venkanna *et al.* (2014) and Tejaswini (2016) for panicle length and Ashok (2015) for grains per panicle.

Thus the trait, L/B ratio recorded positive direct effect and significant negative association with grain yield per plant. Since, the direct effect is positive and the correlation coefficient is significantly negative, the indirect casual factors which are having positive effects viz., days to maturity, days to 50% flowering, panicle length and grains per panicle are to be considered simultaneously along with L/B ratio during selection for improvement of dependent variable.

In plant breeding it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of the possible independent variables which were not included in the study on the dependent variable. In the present study, the residual effect is 0.6406 indicating that the characters included in present investigation had contributed around 36 percent of variability pertaining to the dependent variable *i.e.*, yield.

In the present investigation, path analysis revealed that kernel breadth, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant height showed true relationship with grain yield per plant by establishing significant positive association and positive direct effect.

4.4 GENETIC DIVERGENCE

Conservation of germplasm resources is basic to crop improvement programmes. However, to understand the usable variability, grouping or classification of genetic stocks based on suitable scale is quite imperative. Similarly, choice of genetically divergent parents for hybridization under transgressive breeding programme is also

dependent upon categorization of breeding materials on the basis of appropriate criteria. Systematic classification rests exclusively upon easily distinguishable qualitative attributes. This represents phylogenetic hierarchy or descriptive account of individuals or group of individuals. But it does not consider quantitative traits showing continuous variation which constitutes the backbone of plant breeding practices.

On the other hand, quantitative classification offers a quantified degree of divergence among genotypes or populations. This serves as a sound basis of grouping any two or more genotypes based on minimum divergence or resemblance between them. The models of multivariate analysis (*i.e.*, simultaneous statistical treatment of a set of correlated metric traits in a group of populations) which satisfy this proposition are more than one; for instance Duncon's multiple range test, metroglyph and index score method, D^2 -statistic, Principal component analysis, factor analysis. However, out of all these, D^2 -statistic and Principal component analysis are now most frequently used for classificatory purposes. While the former gives a quantitative measurement of divergence among genotypes, the latter serves the same purpose in terms of spatial distance. Besides, both venture to define the relative contribution of different characters to differentiation among genotypes. This narrows down the problem of identifying the characters responsible for the discrimination between the populations.

The data collected on 11 grain yield and yield contributing characters from 40 genotypes of rice were subjected to genetic divergence analysis employing Mahalanobis' D^2 statistic (whose group constellations are confirmed by PCA) and hierarchial cluster analysis using Ward's method. The magnitude of values suggested that there is considerable variability in the genotypes studied, which led to genetic diversity.

4.4.1 Mahalanobis' D^2 analysis

4.4.1.1 Test with Wilk's criterion ' Λ '

Univariate analysis of variance revealed the significant difference for all the eleven characters under study in the 40 rice genotypes. This significance of difference among 40 genotypes for all characters justify further calculation of D^2 values. However pooled differences are determined by Wilk's criterion. Wilk's statistic ' Λ ' which follows v-statistic representing χ^2 -distribution at 429 df was calculated and found to be highly significant with a magnitude of 1395.57. Therefore, pooled differences (aggregate of all traits) among the 40 genotypes were significant justifying the need to calculate D^2 values.

4.4.1.2 Mahalanobis' D^2 values

To estimate the D^2 values, correlated means of characters were transformed into uncorrelated variables using Pivotal Condensation Method. It measures the degree of diversification and determines the relative contribution of each component character to total divergence. The D^2 values between any two genotypes was obtained as the sum of squares of the differences of their corresponding uncorrelated values. Thus D^2 values were obtained for all the possible 780 pairs of genotypes.

The percent contribution of all the 11 characters in the 40 genotypes towards genetic divergence is presented in Table 4.6. Among the characters studied test weight (33.97%) showed maximum contribution followed by panicle length (18.08%), kernel length (14.74%), kernel breadth (10.51%), L/B ratio (8.21%), plant height (6.03%), grains per panicle (3.21%), days to 50% flowering (2.44%), grain yield per plant (1.41%), productive tillers per plant (1.15%) and days to maturity (0.26%).

4.4.1.3 Grouping of genotypes into various clusters

The 40 genotypes were grouped into seven clusters using the Tocher's method (Table 4.7), with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values.

The distribution of 40 genotypes into seven clusters was at random with maximum number of genotypes in cluster III (13 genotypes). Cluster II is having 12 genotypes followed by cluster I with nine genotypes and cluster IV with three genotypes. Clusters V, VI and VII were solitary clusters, hence no intra-cluster distances (D^2 values). The formation of distinct solitary cluster may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes must be responsible for this genetic diversity (Arunachalam and Ram, 1967).

4.4.1.4 Average intra and inter-cluster D^2 value

The average intra and inter-cluster D^2 values were estimated as per the procedure given by Singh and Chaudhary (1977) and are presented in the Table 4.8. The nearest and farthest cluster for each of the seven clusters are indicated in Table 4.9 and Fig 4.2 and Fig 4.3.

Inter-cluster divergence expresses the diversification among clusters (group of genotypes resembling each other, hence with low intra-cluster divergence). Intra-cluster D^2 values ranged from 0.00 (cluster V, VI and VII) to 34.99 (cluster IV). The intra-cluster distance indicated the diversity among the genotypes grouped in that clusters. Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured.

General notion exists that the larger is the divergence between the parental genotypes, the higher will be the heterosis in crosses (Falconer, 1964). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced. In the present study, inter-cluster distances were worked out considering 11 characters and these distances ranged from 16.01 (between cluster II and V) to 173.85 (between cluster IV and VII).

Cluster I consists of 9 genotypes. It was nearest to cluster III (22.09) followed by cluster II (24.06) and was farthest from cluster VII (116.15) followed by cluster VI (63.95).

Cluster II is with 12 genotypes and its nearest cluster is cluster V (16.01) followed by cluster III (20.29) while the farthest is cluster IV (65.40) followed by cluster VII (53.11).

Cluster III with 13 genotypes was the largest of all clusters. It was nearest to cluster II (20.09) followed by cluster I (22.29) and it was farthest from cluster VII (80.31) followed by cluster IV (61.52).

Cluster IV consisted three genotypes. It was nearest to the cluster I (35.97) followed by cluster III (61.52) and it was farthest from cluster VII (173.85) followed by cluster VI (97.62).

Cluster V was monogenotypic (MTU 2071-13-1-1). It was nearest to the cluster II (16.01) followed by cluster VI (21.21) and was farthest from cluster IV (76.15) followed by cluster I (39.81).

Cluster VI was again monogenotypic (NLR 3385). It was closest to the cluster VII (20.45) followed by cluster V (21.21) and was farthest from cluster IV (97.62) followed by cluster I (63.95).

Cluster VII was also monogenotypic (BPT 2658) as that of clusters V and VII. It was closest to the cluster VI (20.45) followed by cluster V (35.37) and was farthest from cluster IV (173.85) followed by cluster I (116.15).

The maximum inter-cluster distance was between cluster IV and VII (173.85), followed by cluster I and VII (116.15), cluster IV and VI (97.62), cluster III and VII (80.31), cluster IV and V (76.15) and cluster II and Cluster IV (65.40). This suggested that there is wide genetic diversity between these clusters. The genotypes BPT 5204 and BPT 2658 belonging to same geographical area *i.e.*, Guntur district were grouped in two different clusters *i.e.*, cluster I and VII respectively, which are second farthest pair of clusters (116.15). Similarly NLR 3390 and NLR 3385 which are from Nellore were also grouped in two different clusters, IV and VI respectively. And these are third farthest pair of clusters (97.62). This indicate that geographical divergence and genetic diversity are not correlated. These results are in accordance with those of Shanmugasundaram *et al.* (2000), Vanaja and Bapu (2006) and Sandhyakishore *et al.* (2007).

4.4.1.5 Cluster mean values

Cluster means indicate average performance of all genotypes present in a particular cluster. The cluster mean values for 11 characters are presented in Table 4.10. Days to 50% flowering had a range of 104.33 days for cluster V to 114.33 days for cluster VI, days to maturity had a range of 143 days for cluster V to 150.33 days for cluster VI, productive tillers per plant had a range of 5.78 for cluster IV to 10.67 for cluster V, plant height had a range of 105.33 cm for cluster V to 130.67 cm for cluster VI, panicle length had a range of 18.33 cm for cluster IV to 29.67 cm for cluster VII, grains per panicle had ranged from 128.67 for cluster IV to 226 for cluster VII, test weight had range of 15.16g for cluster IV to 29.32 g for cluster VII, kernel length had range of 5.46 mm for clusters I, II and V to 6.23 mm for cluster VI, kernel breadth had range of 1.95 mm for cluster I and III to 2.34 mm for cluster V, L/B ratio had range of 2.41 mm for cluster V to 2.97 mm for cluster III and grain yield per plant 12.96 g for cluster IV to 24.93 g for cluster VII. The above results indicated a wide range of mean values between the clusters.

For a successful breeding programme selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence in rice was

already indicated by Shanmugasundaram *et al.* (2000), Shanthi and Singh (2001), Mishra *et al.* (2003), Das *et al.* (2004), Awasthi *et al.* (2005), Devi *et al.* (2006), Sarawgi and Bisne (2007), Ramya and Senthilkumar (2008), Sabesan *et al.* (2009), Padmaja *et al.* (2010), Chaturvedi *et al.* (2011), Kulsum *et al.* (2011), Chanmundeswari *et al.* (2012), Karuppaiyan *et al.* (2013), Haque *et al.* (2015), and Krishnaveni *et al.* (2015).

4.4.1.6 Principal component analysis

Principal component analysis or Canonical (vector) analysis is a sort of multivariate analysis where canonical vectors and roots representing different axis of differentiation and the amount of variation accounted for by each of such axis, respectively, are derived (Rao, 1952). It is called principal component analysis as it reflects the importance of the largest contributor to the total variation at each axis of differentiation. It measures divergence between varieties in terms of spatial distance rather than quantifying it as D^2 does. Thus, it confirms the group constellations obtained by D^2 analysis as varietal distribution in two-way pictorial graph fixing the relative position of each genotype.

In principal component analysis on correlation matrix, the standardization of columns (here characters) created 11 new variables for 40 genotypes without changing their relative positions. These 11 new variables are the principal components (PC_1 , PC_2 PC_{11}). Each principal component is a linear combination of the 11 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal component. Like regression coefficients, loadings sign (+ / -) are indicative of the direction of contribution. But unlike regression, only the relative contributions are important, so all signs can be changed without affecting the analysis (Jackson, 1991).

The loadings for first principal component were chosen so as to make its variance as large as possible. Loadings of second principal component were chosen such that the variance of PC_2 is as large as possible, subject to the constraint that PC_1 and PC_2 are uncorrelated. The process was continued to create 11 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984).

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating several significant principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are discussed here under.

Principal components (Eigen value greater than one), Eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table 4.11.

In the present study, the first four principal components with eigen values more than one contributed 78.913 per cent towards the total variability. The principal component with eigen values less than one were considered as non- significant. It was therefore inferred that the essential features of data set had been represented in the first four principal components.

The first principal component (PC_1) contributed maximum towards variability (39.895%). The characters viz., grain yield per plant (0.447), grains per panicle (0.366), panicle length (0.362), test weight (0.351), productive tillers per plant (0.341), plant height (0.312), days to maturity (0.308), days to 50% flowering (0.276), L/B ratio (0.126), kernel breadth (0.097) and kernel length (0.052) which were positively loaded.

The second principal component (PC_2) contributed 18.746 per cent of total variance and it reflected significant positive loading of the characters viz., L/B ratio (0.571), days to 50% flowering (0.111), productive tillers per plant (0.076), test weight (0.048), days to maturity (0.031), panicle length (0.017), grain yield per plant (0.005) and kernel breadth (-0.571), kernel length (-0.517), plant height (-0.242) and grains per panicle (-0.014) were negatively loaded.

The third principal component (PC_3) was characterized by 13.810 per cent contribution towards the total variability. The characters viz., Days to maturity (0.519), days to 50% flowering (0.512), kernel length (0.317), L/B ratio (0.179), plant height (0.031), grains per panicle (0.005) were positively loaded. While, Productive tillers per plant (-0.397), panicle length (-0.272), test weight (-0.311), kernel breadth (-0.081) and seed yield per plant (-0.001) were negatively loaded.

The fourth principal component (PC₄) contributed 6.462 per cent towards the total variability and it reflected significant positive loading of the characters viz., Grains per panicle (0.624), kernel breadth (0.277), productive tillers per plant (0.075), test weight (0.074), days to 50% flowering (0.069) and days to maturity (0.064). While, Plant height (-0.656), panicle length (-0.248), L/B ratio (-0.091), kernel length (-0.088) and grain yield per plant (-0.078) were negatively loaded.

The PCA scores for 40 rice genotypes in the first four principal components were computed. Principal component I, II, III and IV were considered as four axis and squared distance of each genotype from these four axis were calculated and presented in Table 4.12.

The analysis thus identified the maximum contributing variables *i.e.*, L/B ratio, days to maturity, days to 50% flowering, seed yield per plant, grains per panicle, panicle length, test weight, productive tillers per plant and plant. It is important to study the variance as the relative contribution than the signs (indicative of direction) in principal component analysis.

Results of cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in describing clusters in the two dimensional and three dimensional scattered diagrams. The genotypes falling in same cluster were present closer to each other in scattered diagram. The genotypes falling in same cluster were present closer to each other in scattered diagram.

Two dimensional and three dimensional scatter diagrams were shown in Fig 4.4 and 4.5 respective, which are obtained using the first two PCA scores *i.e.*, PCA I and PCA II. The genotypes numbered 22, 5 and 25 *i.e.*, NLR 3390, MTU 2195-105-1-5 and MTU 2195-201-1-3 which are scattered away from other genotypes formed a separate cluster *i.e* cluster IV. Similarly genotypes numbered 12 (NLR 3385) and 17 (BPT 2658) were also scattered and formed two separate monogenotypic clusters (Table 4.7). While the genotypes which are closer to each are grouped in a single cluster.

But in choosing genotypes for hybridization programme we have to consider the inter-cluster distances. It is evident from the Table 4.12 that the maximum inter cluster distance was recorded between cluster IV and cluster VII (173.85). This indicate that the genotypes existing cluster IV and cluster VII are much divergent as per the Tocher's method of D² analysis and may be suitable for hybridization, subjected to have good *per*

se performance for the desirable characters. Similar studies of divergence using D^2 analysis (Tocher's method) which are confirmed by PCA were earlier done by Padmaja *et al.* (2010), Chaturvedi *et al.* (2011), Kulsum *et al.* (2011), Chamundeswari *et al.* (2012), Chakravorthy and Gosh (2012), Hasan *et al.* (2012), Singh *et al.* (2012), Tushara *et al.* (2013), Role *et al.* (2014), Haque *et al.* (2015) and Ravikumar *et al.* (2015).

4.4.2 Hierarchical cluster analysis

The cluster analysis using Euclidean² distances provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to characters considered together. The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and to confirm the results of principal component analysis.

4.4.2.1 Grouping of genotypes into various clusters

Fourty genotypes were grouped into seven clusters using the Ward's minimum variance procedure (Anderberg, 1993) and the distributions of the genotypes into different clusters are presented in figure 4.6.

The 40 genotypes were grouped into seven clusters. The distribution of genotypes into seven clusters is presented in Table 4.13. Among all the clusters, cluster V was the largest containing twelve genotypes followed by cluster I containing ten genotypes, cluster III with seven genotypes, cluster II with six genotypes cluster IV and VII each containing two genotypes and cluster VI is monogenotypic having only one genotype. The mutual relationship between clusters is represented diagrammatically (Fig.4.7) by taking average intra and inter-cluster Euclidean² distances.

4.4.2.2 Average intra and inter-cluster Euclidean² distance values

The average intra and inter-cluster Euclidean² distance were estimated based on Ward's minimum variance and are presented in the Table 4.14.

By Ward's method, the 40 genotypes were grouped into seven clusters. Of the seven clusters formed, cluster VI doesn't have intra-cluster Euclidean² distance because it is a monogenotypic cluster, cluster VII has minimum intra-cluster Euclidean² distance value of 9.88 followed by cluster V (22.36), cluster II (33.51), cluster I (38.56), cluster III (46.56) and cluster IV (61.36). The inter-cluster Euclidean² distances varied from 56.34 (between cluster I and cluster II) to 463.06 (between clusters IV and VII). All the inter-cluster Euclidean² values were lying between these values.

Cluster I comprised of 10 genotypes. It was nearest to cluster II (56.34) followed by cluster III (75.42) and farthest from cluster VII (203.84) followed by cluster VI (140.07).

Cluster II comprised of 6 genotypes. It was nearest to cluster I (56.34) followed by cluster III (66.33) and farthest from cluster VII (250.99) followed by cluster VI (249.56).

Cluster III consisted of seven genotypes. It was closest to cluster V (63.82) followed by cluster II (66.33) and farthest from cluster VI (225.99) followed by cluster IV (181.66).

Cluster IV was consisted of two genotypes. It was nearest to cluster II (111.94) followed by cluster I (127.42) and farthest from cluster VII (463.06) followed by cluster VI (295.51).

Cluster V was comprised of 12 genotypes (the largest one). It was closest to cluster III (63.82) followed by cluster I (69.94) and farthest from cluster IV (255.08) followed by cluster VI (150.43).

Cluster VI was monogenotypic having only one genotype. It was nearest to cluster I (140.07) followed by cluster V (150.43) and farthest from cluster IV (295.51) followed by cluster II (249.56).

Cluster VII was consisted two genotypes. It was nearest to cluster V (89.09) followed by cluster III (167.67) and farthest from cluster IV (463.06) followed by cluster II (250.99).

Of the seven clusters formed, maximum intra-cluster distance (Euclidean² distance) was recorded by cluster IV (61.36) followed by cluster III (46.56) and cluster I (38.56) and maximum inter-cluster distance was observed between cluster IV and cluster VII (463.06) followed by cluster IV and VI (295.51) and cluster IV and cluster V (255.08). This suggested that there was wide genetic diversity between these clusters. Genotypes belonging to different districts in India were distributed in different clusters. The genotypes NLR 3385 and NLR 3390 belonging to same geographical area *i.e* Nellore district were grouped in two different clusters, which are second farthest pair of clusters (IV and VI). This indicated that geographical diversity and genetic diversity are not related. Similar conclusion was drawn by Shanmugasundaram *et al.* (2000), Vanaja and Bapu (2006) and Sandhyakishore *et al.* (2007).

4.4.2.3 Cluster mean values

Cluster means were computed for the 11 characters studied by Ward's minimum variance method are presented in Table 4.15.

Cluster I registered high mean value for productive tillers per plant (10.40), low mean value for L/B ratio (2.64) and second high mean value for grain yield per plant (21.30) among all the clusters.

Cluster II recorded low mean value for kernel length (5.44 mm) and second highest mean values for productive tillers per plant (10.33), panicle length (26.22 cm), grains per panicle (220.33) and test weight (21.39 g) and second lowest mean values for days to maturity (144.28) and plant height (105.61 cm).

Cluster III recorded highest L/B ratio (3.05) and lowest kernel breadth (1.84 mm) and second lowest mean value for panicle length (21.86 cm).

Cluster IV recorded high mean value for Days to 50% flowering (113.17), days to maturity (150.17), plant height (127.67 cm), panicle length (27.50 cm), grains per panicle (225.33), test weight (26.64 g) and grain yield per plant (24.87 g).

Cluster V registered second highest mean value for L/B ratio (2.87) and second lowest mean values for Days to maturity (110.50), grains per panicle (164.92), kernel length (5.58 mm), kernel breadth (1.95 mm) and grain yield per plant (14.16 g).

Cluster VI recorded second high mean value for kernel length (6.99 mm) and kernel breadth (2.55 mm), second highest mean values for Days to 50% flowering (112.00), days to maturity (148.33), plant height (123.67 cm) and second lowest mean values for productive tillers per plant (6.33) and test weight (16.07 g).

Cluster VII recorded low mean values for Days to 50% flowering (105.33), days to maturity (141.50), productive tillers per plant (5.50), plant height (101.67 cm), panicle length (16.33 cm), grains per panicle (91.50), test weight (14.70 g), L/B ratio (2.64) and grain yield per plant (10.77 g).

Thus, cluster IV showed high mean values for most of the yield contributing traits like Days to 50% flowering, days to maturity, plant height, panicle length, grains per panicle, test weight and grain yield per plant. So the genotypes from this cluster can be used for rice yield improvement programme.

4.4.3 Comparison of clusters obtained by Tocher's method and Ward's method

Mahalanobis's D^2 Statistic (Tocher's method) and Jackson's PCA are tools for analyzing multivariate data. PCA confirms the group constellations obtained by D^2 analysis. It determines the effective number of axis of differentiation primary and secondary or so based on number of canonical vectors. The advantage of PCA over D^2 analysis is that it reduces the dimensionality of the data set by creating significant principal components which contributed towards maximum variability of the genotypes. The largest element (absolute value) in each vector constitutes the greatest contributor for divergence. In PCA, standardization of data made attributes to contribute equally towards the divergence studies irrespective of the units taken.

The principal component analysis sorted only significant principal components out of the total 11 attributes. The contribution of the main characters for variance was easily identified by the characters loaded on the PC_1 with high loading values. While, Ward's method of grouping of genotypes was done using the Euclidean² values.

Both D^2 analysis and Ward's method grouped the 40 rice genotypes into seven clusters each, the clusters are different in different methods with respect to total number as well as genotypes included in each cluster. In D^2 analysis, cluster III is the largest with 13 genotypes followed by cluster II with 12 genotypes, cluster I with nine genotypes, cluster IV with 3 genotypes and cluster V, VI and VII were monogenotypic clusters having only one genotype. In Ward's method cluster V was the largest containing 12 genotypes followed by cluster I containing 10 genotypes, cluster III with 7 genotypes, cluster II with 6 genotypes and cluster IV & VII containing two genotypes each.

The pattern of distribution of genotypes into different clusters was at random. Further, the two clustering methods grouped differently and clustering pattern for genotypes is also not same for. There was only one solitary cluster in Ward's minimum variance method *i.e.*, cluster VI, where as in D^2 analysis there were three solitary clusters *viz.*, cluster V, cluster VI and cluster VII. This indicate that genetic diversity was the outcome of several factors along with geographic diversity and the selection for hybridization should be more based on genetic diversity.

Two important points are to be considered while selecting genotypes for hybridization programmes: (i) Choice of the particular cluster from which genotypes are

to be used as parents and (ii) selection of particular genotype from selected cluster. The clusters selected should be separated by largest statistical distance *i.e.*, maximum divergence. Genotypes from these divergent clusters should be selected based on their *per se* performance for different yield contributing characters. However the selected genotype should be tested for their combining ability using other biometrical techniques like Line $\times$ Tester or Diallel analysis.

Based on results of Mahalanobis D^2 analysis the genotypes grouped in cluster IV (NLR 3390, MTU 2195-201-1-3 and MTU 2195-105-1-5) are having maximum genetic distance with the genotypes placed in the cluster VII (BPT 2658) (Table 4.8). This indicates that crosses between the genotypes present in these two clusters are expected to be much heterotic. But as a rule along with genetic distance, *per se* yield and yield contributing characters should be taken into consideration. The genotypes MTU 2195-105-1-5 and MTU 2195-105-1-5 are poor yielders hence cannot be included in the crossing programme to obtain superior hybrids. Therefore cross between NLR 3390 and BPT 2658 may only produce superior hybrids or transgressive segregants depending on the gene action.

Similarly the clusters obtained using Ward's method indicate that the genotypes grouped in cluster IV (NLR 3385 and BPT 2658) are much divergent from the genotypes present in cluster VII (MTU 2195-201-1-3 and MTU 2195-105-1-5) (Table 4.14). But both the genotypes in cluster VII are having very less *per se* performance with regard to yield. However the genotype NLR 3385 which is placed in cluster IV of Ward's method was placed in cluster VI of D^2 analysis (Table 4.7) which is having an inter cluster distance of 97.62 with cluster IV of D^2 analysis where NLR 3390 is placed hence it can be concluded that F_1 s obtained by crossing BPT 2658 with NLR 3390 and/ or NLR 3385 are having a good chance of producing heterotic hybrid varieties in presence of dominance and may result in good transgressive segregants if additive component of gene action is predominant. So, these genotypes should be tested for their gene action and combining ability using suitable mating design before using them in hybridization programme.

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif* 2015 at Agricultural College Farm, Bapatla, Guntur, Andhra Pradesh with 40 genotypes of rice (*Oryza sativa* L.) with the prime objective of grouping the genotypes into distinct classes based on their genetic diversity.

Other parameters like mean, genetic variability, heritability, genetic advance as per cent of mean, character association and the magnitude of direct and indirect effects of yield component traits on rice grain yield were also studied for 11 characters viz., Days to 50% flowering, days to maturity, productive tillers per plant, plant height (cm), panicle length (cm), grains per panicle, test weight (g), kernel length (mm), kernel breadth (mm), L/B ratio and grain yield per plant (g).

The analysis of variance indicated significant differences among 40 genotypes for all the characters studied. High PCV and moderate GCV were recorded for Productive tillers per plant, grains per panicle and grain yield per plant, moderate PCV with GCV were recorded for panicle length and test weight, moderate PCV coupled with low GCV was recorded only for kernel breadth. While low PCV coupled with low GCV were recorded for days to 50% flowering, days to maturity, plant height, kernel length and L/B ratio. These results indicate that there is considerable amount of variability for majority of the characters studied.

The estimates of heritability and genetic advance as per cent of mean were high for panicle length, grains per panicle, test weight and grain yield per plant indicating the predominance of additive gene action and hence direct selection is useful with respect to these traits.

The traits, Productive tillers per plant, grains per panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50% flowering and kernel length were found to possess significant positive association with grain yield per plant. Further, path analysis revealed that kernel breadth, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant height showed true relationship with grain yield per plant by establishing significant positive association and positive direct effect.

Considering the nature and magnitude of character associations and their direct and indirect effects, it can be inferred that productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering, kernel breadth and plant height could serve as important traits in any selection programme for selecting high yielding genotypes in rice.

The results of multivariate analysis revealed considerable genetic divergence among the 40 genotypes studied. In principal component analysis, four principal components all together explained 78.913% of the total variability. All the 11 characters were significant and positively loaded in PC₁, maximum divergence was contributed by grain yield per plant followed by grains per panicle, panicle length, test weight and productive tillers per plant.

Both D² analysis (whose group constellations are confirmed by PCA) and Ward's method grouped the 40 rice genotypes into seven clusters. However the clusters are different in different methods with respect to total number of genotypes and the actual genotypes included in each cluster. In D² analysis, cluster III is the largest with 13 genotypes followed by cluster II with 12 genotypes, cluster I with nine genotypes, cluster IV with 3 genotypes and cluster V, VI and VII were monogenotypic clusters having only one genotype. In Ward's method cluster V was the largest containing 12 genotypes followed by cluster I containing 10 genotypes, cluster III with 7 genotypes, cluster II with 6 genotypes and cluster IV & VII containing two genotypes each.

The pattern of distribution of genotypes into different clusters was at random. Further, the two clustering methods grouped differently and clustering pattern for genotypes is also not same. There was only one solitary cluster in Ward's minimum variance method *i.e.*, cluster VI, whereas in D² analysis there were three solitary clusters *viz.*, cluster V, cluster VI and cluster VII. This indicates that genetic diversity was the outcome of several factors along with geographic diversity and the selection for hybridization should be more based on genetic diversity.

According to the Mahalanobis D² analysis the genotypes grouped in cluster IV (NLR 3390, MTU 2195-201-1-3 and MTU 2195-105-1-5) are having maximum genetic distance with the genotypes placed in the cluster VII (BPT 2658). This indicates that crosses between the genotypes present in these two clusters are expected to be much heterotic. But the genotypes MTU 2195-105-1-5 and MTU 2195-105-1-5 are poor

yielders hence cannot be included in the crossing programme to obtain superior hybrids. Therefore cross between NLR 3390 and BPT 2658 may only produce superior hybrids or transgressive segregants depending on the gene action.

Similarly the clusters obtained using Ward's method indicate that the genotypes grouped in cluster IV (NLR 3385 and BPT 2658) are much divergent from the genotypes present in cluster VII (MTU 2195-201-1-3 and MTU 2195-105-1-5). But both the genotypes in cluster VII are having very less *per se* performance with regard to yield. However the genotype NLR 3385 which is placed in cluster IV of Ward's method was placed in cluster VI of D² analysis which is having an inter cluster distance of 97.62 with cluster IV of D² analysis where NLR 3390 is placed hence it can be concluded that F₁s obtained by crossing BPT 2658 with NLR 3390 and/ or NLR 3385 are having a good chance of producing heterotic hybrid varieties in presence of dominance and may result in good transgressive segregants if additive component of gene action is predominant. So, these genotypes should be tested for their gene action and combining ability using suitable mating design before using them in hybridization programme.

Table 2.3. Review of literature on association of component characters with grain yield per plant in rice (*Oryza sativa* L.)

S. No.	Character	Direction	Significance	P/G	Reference
1.	Days to 50% flowering	Positive	S	P, G P, G -- P, G P, G --	Panwar (2006) Swain and Reddy (2006) Neelima <i>et al.</i> (2007) Sharma and Sharma (2007) Chandra <i>et al.</i> (2009) Tushara <i>et al.</i> (2013)
		Positive	NS	P, G P, G P, G P	Rangare <i>et al.</i> (2012) Nagaraju <i>et al.</i> (2013) Ashok (2015) Tejaswini (2016)
		Negative	S	P, G -- P, G P, G	Eradasappa <i>et al.</i> (2007) Dey <i>et al.</i> (2010) Gangashetty <i>et al.</i> (2013) Bornare <i>et al.</i> (2014)
		Negative	NS	P, G P, G G P, G P, G --	Borbora <i>et al.</i> (2005) Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Panwar and Ali (2007) Seyoum <i>et al.</i> (2012) Gopikannan and Ganesh (2013)
2.	Days to maturity	Positive	S	P, G P, G	Bornare <i>et al.</i> (2014) Rashid <i>et al.</i> (2014)
		Positive	NS	P, G P	Ashok (2015) Tejaswini (2016)
3.	Productive tillers per plant	Positive	S	P, G P P P, G p G P, G P, G P, G P, G -- P P, G P, G	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Chaudhary and Motiramani (2003) Shashidhar <i>et al.</i> (2005) Manna <i>et al.</i> (2006) Panwar (2006) Swain and Reddy (2006) Eradasappa <i>et al.</i> (2007) Panwar and Ali (2007) Sharma and Sharma (2007) Chandra <i>et al.</i> (2009) Rani and Reddy (2010) Kumar <i>et al.</i> (2013) Bornare <i>et al.</i> (2014)

Table 2.3 (cont.)

S. No.	Character	Direction	Significance	P/G	Reference
		Positive	S	G P, G P, G	Neha <i>et al.</i> (2014) Rashid <i>et al.</i> (2014) Ashok (2015)
		Positive	NS	-- G	Neelima <i>et al.</i> (2007) Rani and Reddy (2010)
		Negative	NS	P P G	Bhavana (2003) Borbora <i>et al.</i> (2005) Binse <i>et al.</i> (2006)
4.	Plant height (cm)	Positive	S	P, G P, G P, G P, G -- P P, G P, G P, G P, G	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Shashidhar <i>et al.</i> (2005) Eradasappa <i>et al.</i> (2007) Neelima <i>et al.</i> (2007) Rani and Reddy (2010) Sheet <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Idris and Mohamed (2013)
		Positive	NS	P, G G P, G P, G G P, G P, G P	Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Swain and Reddy (2006) Sharma and Sharma (2007) Rani and Reddy (2010) Rangare <i>et al.</i> (2012) Ashok (2015) Tejaswini (2016)
		Negative	S	P, G P, G P, G P, G	Borbora <i>et al.</i> (2005) Panwar and Ali (2007) Gangashetty <i>et al.</i> (2013) Rashid <i>et al.</i> (2014)
		Negative	NS	P, G -- P, G P, G P, G P, G P, G P, G P, G	Chaudhary and Motiramani (2003) Krishnaveni and Sobharani (2006) Manna <i>et al.</i> (2006) Panwar (2006) Chandra <i>et al.</i> (2009) Dey <i>et al.</i> (2010) Akhtar <i>et al.</i> (2011) Iaxuman <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012)

Table 2.3 (cont.)

S. No.	Character	Direction	Significance	P/G	Reference
5.	Panicle length (cm)	Positive	S	P, G P, G P P, G -- P P P, G -- P, G P, G P, G P, G P P, G P, G P, G P	Hasib (2005) Kumar and Bapu (2005) Sharma and Sharma (2007) Eradasappa <i>et al.</i> (2007) Chandra <i>et al.</i> (2009) Parmhansh <i>et al.</i> (2010) Rani and Reddy (2010) Laxuman <i>et al.</i> (2011) Ghosh and Sharma (2012) Rangare <i>et al.</i> (2012) Sheet <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Ashim and Gosh (2013) Gangashetty <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Sudharani <i>et al.</i> (2013) Bornare <i>et al.</i> (2014) Tejaswini (2016)
		Positive	NS	P, G P, G P, G P, G -- P, G -- -- G P, G P, G	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Bhavana (2003) Borbora <i>et al.</i> (2005) Krishnaveni and Sobharani (2006) Panwar (2006) Neelima <i>et al.</i> (2007) Gulzar and Parry (2010) Rani and Reddy (2010) Seyoum <i>et al.</i> (2012) Ashok (2015)
		Negative	S	P, G	Rashid <i>et al.</i> (2014)
6.	Grains per panicle	Positive	S	P, G P P, G P, G -- P, G --	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Borbora <i>et al.</i> (2005) Kumar and Bapu (2005) Krishnaveni and Sobharani (2006) Panwar (2006) Neelima <i>et al.</i> (2007)

Table 2.3 (cont.)

S. No.	Character	Direction	Significance	P/G	Reference
		Positive	S	P, G P P, G	Panwar and Ali (2007) Sharma and Sharma (2007) Ashok (2015)
		Positive	NS	P, G -- P, G P -- P, G	Eradasappa <i>et al.</i> (2007) Chandra <i>et al.</i> (2009) Gulzar and Parry (2010) Parmhansh <i>et al.</i> (2010) Rani and Reddy (2010) Rashid <i>et al.</i> (2014)
		Negative	NS	P, G	Manna <i>et al.</i> (2006)
7.	Test weight (g)	Positive	S	G P, G P, G -- -- G -- P G P, G P, G P, G -- P, G P, G P, G P, G	Nagajyothi (2001) Bhavana (2003) Kumar and Bapu (2005) Krishnaveni and Sobharani (2006) Neelima <i>et al.</i> (2007) Sharma and Sharma (2007) Chandra <i>et al.</i> (2009) Parmhansh <i>et al.</i> (2010) Rani and Reddy (2010) Seyoum <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Gopikannan and Ganesh (2013) Sudharani <i>et al.</i> (2013) Rashid <i>et al.</i> (2014) Bornare <i>et al.</i> (2014) Ashok (2015)
		Positive	NS	P, G P, G P, G P, G -- P P, G	Chaudhary and Motiramani (2003) Borbora <i>et al.</i> (2005) Eradasappa <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Gulzar and Parry (2010) Rani and Reddy (2010) Ngaraju <i>et al.</i> (2013)
		Negative	S	G	Swain and Reddy (2006)

Table 2.3 (cont.)

S. No.	Character	Direction	Significance	P/G	Reference
		Negative	NS	P, G P, G P, G P, G P	Hasib (2005) Panwar and Ali (2007) Babu <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Tejaswini (2016)
8.	Kernel length (mm)	Positive	S	P, G P, G	Satheeshkumar and Saravanan (2012) Premkumar <i>et al.</i> (2015)
		Positive	NS	P, G	Allam <i>et al.</i> (2015)
		Negative	NS	P	Tejaswini (2016)
9.	Kernel breadth (mm)	Positive	S	P, G P, G	Satheeshkumar and Saravanan (2012) Premkumar <i>et al.</i> (2015)
		Positive	NS	P, G	Allam <i>et al.</i> (2015)
		Negative	NS	P	Tejaswini (2016)
10.	L/B ratio	Positive	S	P	Parmhansh <i>et al.</i> (2010)
		Positive	NS	P, G P, G	Parvathi <i>et al.</i> (2011) Ashok (2015)
		Negative	S	G	Krishnaveni and Sobharani (2006)
		Negative	NS	P, G P	Garg <i>et al.</i> (2010) Tejaswini (2016)

S: Significant

NS: Non-significant

P: Phenotypic correlation

G: Genotypic correlation

Table 2.4. Review of literature on association of yield components among themselves in rice (*Oryza sativa* L.)

S.No.	Character	Direction	Significance	P/G	Reference
I.Association of Days to 50% flowering with					
1.	Days to maturity	Positive	S	P P P,G P P P,G P,G P,G P	Panwar (2006) Akinwale <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Aditya and Bhartiya (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Ashok (2015) Tejaswini (2016)
		Positive	NS	G P,G G	Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	NS	P	Idris and Mohammad (2013)
2.	Productive tillers per plant	Positive	S	P P,G P,G	Panwar (2006) Sateeshkumar and Saravanan (2012) Ashok (2015)
3.	Plant height (cm)	Positive	S	P,G P,G P,G P P,G P P,G P,G P	Panwar (2006) Sateeshkumar and Saravanan (2012) Babu <i>et al.</i> (2012) Aditya and Bhartiya (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Ashok (2015) Tejaswini (2016)
		Positive	NS	P P,G P,G	Idris and Mohammad (2013) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013)
		Negative	S	P	Akinwale <i>et al.</i> (2011)
		Negative	NS	P,G P,G P	Hasan <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Bekele <i>et al.</i> (2013)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
4.	Panicle length (cm)	Positive	S	P P,G P,G P P,G	Akinwale <i>et al.</i> (2011) Babu <i>et al.</i> (2012) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Khare <i>et al.</i> (2014)
		Positive	NS	P,G P P,G P,G P P,G	Hasan <i>et al.</i> (2012) Idris and Mohammad (2013) Nagaraju <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Patel <i>et al.</i> (2014)
		Negative	S	P,G	Sravan <i>et al.</i> (2012)
		Negative	NS	P,G P,G P	Panwar (2006) Ashok (2015) Tejaswini (2016)
5.	Grains per panicle	Positive	S	P,G P	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)
		Negative	NS	P,G	Panwar (2006)
6.	Test weight (g)	Positive	S	P,G P P,G P	Panwar (2006) Sharma and Sharma (2007) Patel <i>et al.</i> (2014) Tejaswini (2016)
		Positive	NS	P,G P,G P P,G P P P,G P,G	Borbora <i>et al.</i> (2005) Panwar and Ali (2007) Akinwale <i>et al.</i> (2011) Dwivedi <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Idris and Mohammad (2013) Khare <i>et al.</i> (2014) Ashok (2015)
		Negative	S	G	Swain and Reddy (2006)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Negative	NS	P,G G P,G -- P,G P,G	Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Eradasappa <i>et al.</i> (2007) Chandra <i>et al.</i> (2009) Garg <i>et al.</i> (2010) Nagaraju <i>et al.</i> (2013)
7.	Kernel length (mm)	Positive	S	-- P	Krishna <i>et al.</i> (2008) Tejaswini (2016)
		Positive	NS	P	Aditya and Bhartiya (2013)
		Negative	NS	P,G P, G P	Sateeshkumar and Saravanan (2012) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014)
8.	Kernel breadth (mm)	Positive	S	P,G p	Sateeshkumar and Saravanan (2012) Ogunbayo <i>et al.</i> (2014)
		Positive	NS	P P	Aditya and Bhartiya (2013) Tejaswini (2016)
		Negative	S	P,G	Lakshmi <i>et al.</i> (2014)
		Negative	NS	P,G P,G	Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
9.	L/B ratio	Positive	S	P P,G	Aditya and Bhartiya (2013) Ashok (2015)
		Positive	NS	P P,G P,G	Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
		Negative	S	P	Arulmozi and Muttuswamy (2013)
		Negative	NS	P,G P,G P	Sateeshkumar and Saravanan (2012) Nagaraju <i>et al.</i> (2013) Tejaswini (2016)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
II. Association of Days to maturity with					
1.	Productive tillers per plant	Positive	S	P,G P,G	Panwar (2006) Ashok (2015)
2.	Plant height (cm)	Positive	S	P,G P,G P P,G P,G P,G P	Panwar (2006) Abarshahr <i>et al.</i> (2011) Aditya and Bhartiya (2013) Lakshmi <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Ashok (2015) Tejaswini (2016)
		Positive	NS	P,G	Sanghera <i>et al.</i> (2013)
		Negative	NS	P P,G P,G P P	Idris and Mohammad (2013) Nagaraju <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
3.	Panicle length (cm)	Positive	S	P P P,G P,G P,G P,G	Akinwale <i>et al.</i> (2011) Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Lakshmi <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014)
		Positive	NS	P,G P,G P	Nagaraju <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Tejaswini (2016)
		Negative	NS	P,G P,G P P	Panwar (2006) Abarshahr <i>et al.</i> (2011) Idris and Mohammad (2013) Allam <i>et al.</i> (2015)
4.	Grains per panicle	Negative	NS	P,G	Panwar (2006)
5.	Test weight (g)	Positive	S	P,G P,G P	Panwar (2006) Patel <i>et al.</i> (2014) Tejaswini (2016)
		Positive	NS	P P P,G P,G	Akinwale <i>et al.</i> (2011) Aditya and Bhartiya (2013) Khare <i>et al.</i> (2014) Lakshmi <i>et al.</i> (2014)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Negative	S	P p	Bekele <i>et al.</i> (2013) Idris and Mohammad (2013)
		Negative	NS	P,G P,G P P P	Abarshahr <i>et al.</i> (2011) Nagaraju <i>et al.</i> (2013) Khare <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
6.	Kernel length (mm)	Positive	S	P	Tejaswini (2016)
		Positive	NS	P p P,G P,G p	Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
		Negative	S	P, G	Sanghera <i>et al.</i> (2013)
		Negative	NS	P	Ogunbayo <i>et al.</i> (2014)
7.	Kernel breadth (mm)	Positive	NS	P,G P P	Lakshmi <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014) Tejaswini (2016)
		Negative	S	P P,G	Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013)
		Negative	NS	P p	Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)
8.	L/B ratio	Positive	S	P	Allam <i>et al.</i> (2015)
		Positive	NS	P p P,G P,G P,G	Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Patel <i>et al.</i> (2014)
		Negative	NS	P	Tejaswini (2016)
III. Association of productive tillers per plant with					
1.	Plant height (cm)	Negative	NS	P,G	Sateeshkumar and Saravanan (2012)
2.	Panicle length (cm)	Positive	S	P,G P,G P	Janardhanam <i>et al.</i> (2001) Eradasappa <i>et al.</i> (2007) Rani and Reddy (2010)
		Positive	NS	P,G --	Panwar and Ali (2007) Chandra <i>et al.</i> (2009)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Positive	NS	P G P,G	Garg <i>et al.</i> (2010) Rani and Reddy (2010) Sateeshkumar and Saravanan (2012)
		Negative	S	P	Manna <i>et al.</i> (2006)
		Negative	NS	P,G G P,G -- P,G	Borbora <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Panwar (2006) Neelima <i>et al.</i> (2007) Sharma and Sharma (2007)
3.	Grains per panicle	Positive	S	P,G P,G P,G	Janardhanam <i>et al.</i> (2001) Panwar (2006) Eradasappa <i>et al.</i> (2007)
		Positive	NS	P,G -- P	Borbora <i>et al.</i> (2005) Neelima <i>et al.</i> (2007) Garg <i>et al.</i> (2010)
		Negative	NS	G P,G P,G -- P,G G P,G P	Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Sharma and Sharma (2007) Chandra <i>et al.</i> (2009) Rani and Reddy (2010) Garg <i>et al.</i> (2010) Sateeshkumar and Saravanan (2012) Idris and Mohammad (2013)
4.	Test weight (g)	Positive	S	P G P,G P,G	Rani and Reddy (2010) Hasan <i>et al.</i> (2012) Sravan <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2014)
		Positive	NS	P,G -- P,G P,G P,G P,G	Panwar (2006) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Ashok (2015)
		Negative	S	P P,G P,G P,G	Chaudhary and Motiramani (2003) Borbora <i>et al.</i> (2005) Swain and Reddy (2006) Eradasappa <i>et al.</i> (2007)
		Negative	NS	G P,G	Binse <i>et al.</i> (2006) Bhattacharyya <i>et al.</i> (2007)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Negative	NS	P,G -- P,G P,G	Sharma and Sharma (2007) Chandra <i>et al.</i> (2009) Sanghera <i>et al.</i> (2013) Khare <i>et al.</i> (2014)
5.	Kernel length (mm)	Positive	S	P,G	Ashok (2015)
		Negative	S	P,G	Sateeshkumar and Saravanan (2012)
6.	Kernel breadth (mm)	Negative	NS	P,G	Sateeshkumar and Saravanan (2012)
7.	L/B ratio	Negative	NS	P,G	Sateeshkumar and Saravanan (2012)
IV. Association of Plant height with					
1.	Panicle length (cm)	Positive	S	P,G P P,G -- P,G P P,G P,G P,G P P,G P P	Janardhanam <i>et al.</i> (2001) Chaudhary and Motiramani (2003) Kumar and Bapu (2005) Chandra <i>et al.</i> (2009) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Babu <i>et al.</i> (2012) Datt <i>et al.</i> (2012) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Minnie <i>et al.</i> (2013) Allam <i>et al.</i> (2015) Tejaswini (2016)
		Positive	NS	P,G G P,G P,G -- P,G P,G P,G G P,G	Borbora <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Panwar (2006) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Sharma and Sharma (2007) Eradasappa <i>et al.</i> (2007) Rani and Reddy (2010) Abarshahr <i>et al.</i> (2011)
		Negative	NS	--	Krishnaveni and Sobharani (2006)
2.	Grains per panicle	Positive	S	P,G	Sateeshkumar and Saravanan (2012)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
3.	Test weight (g)	Positive	S	P P,G	Aditya and Bhartiya (2013) Ashok (2015)
		Negative	NS	P,G	Panwar (2006)
		Positive	S	G -- P,G P P,G	Binse <i>et al.</i> (2006) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Rani and Reddy (2010) Minnie <i>et al.</i> (2013)
		Positive	NS	P,G P,G P,G -- G P P P	Borbora <i>et al.</i> (2005) Eradasappa <i>et al.</i> (2007) Sharma and Sharma (2007) Chandra <i>et al.</i> (2009) Rani and Reddy (2010) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015) Tejaswini (2016)
		Negative	S	--	Krishnaveni and Sobharani (2006)
		Negative	NS	P,G P,G P,G P,G P P,G P	Chaudhary and Motiramani (2003) Kumar and Bapu (2005) Panwar (2006) Swain and Reddy (2006) Garg <i>et al.</i> (2010) Abarshahr <i>et al.</i> (2011) Ogunbayo <i>et al.</i> (2014)
4.	Kernel length (mm)	Positive	S	P,G P	Patel <i>et al.</i> (2014) Tejaswini (2016)
		Positive	NS	P	Aditya and Bhartiya (2013)
		Negative	S	P,G P	Sateeshkumar and Saravanan (2012) Ogunbayo <i>et al.</i> (2014)
		Negative	NS	P P,G P	Bekele <i>et al.</i> (2013) Sanghera <i>et al.</i> (2013) Allam <i>et al.</i> (2015)
5.	Kernel breadth (mm)	Positive	S	P P,G P	Bekele <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Ogunbayo <i>et al.</i> (2014)
		Positive	NS	P,G P,G P	Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Tejaswini (2016)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Negative	NS	P,G p p	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)
6.	L/B ratio	Positive	S	P,G P,G	Sateeshkumar and Saravanan (2012) Patel <i>et al.</i> (2014)
		Positive	NS	P P,G P,G P P	Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Tejaswini (2016)
		Negative	S	P	Bekele <i>et al.</i> (2013)
		Negative	NS	G	Arulmozi and Muttuswamy (2013)
		V. Association of Panicle length with			
1.	Grains per panicle	Positive	S	P,G p	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)
2.	Test weight (g)	Positive	S	P,G P,G P P P,G P,G	Borbora <i>et al.</i> (2005) Hasib (2005) Sharma and Sharma (2007) Rani and Reddy (2010) Babu <i>et al.</i> (2012) Minnie <i>et al.</i> (2013)
		Positive	NS	G P,G -- G -- P	Binse <i>et al.</i> (2006) Panwar and Ali (2007) Chandra <i>et al.</i> (2009) Rani and Reddy (2010) Gulzar and Parry (2010) Parmhansh <i>et al.</i> (2010)
		Negative	S	P,G P	Abarshahr <i>et al.</i> (2011) Tejaswini (2016)
		Negative	NS	P,G P,G --	Kumar and Bapu (2005) Panwar (2006) Neelima <i>et al.</i> (2007)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Negative	NS	P,G P	Garg <i>et al.</i> (2010) Aditya and Bhartiya (2013)
3.	Kernel length (mm)	Positive	S	P,G P,G	Patel <i>et al.</i> (2014) Lakshmi <i>et al.</i> (2014)
		Positive	NS	P,G p,G p p	Sateeshkumar and Saravanan (2012) Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Tejaswini (2016)
		Negative	NS	P	Aditya and Bhartiya (2013)
4.	Kernel breadth (mm)	Positive	S	--	Krishna <i>et al.</i> (2008)
		Positive	NS	P,G P P,G	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Lakshmi <i>et al.</i> (2014)
		Negative	S	P P	Ogunbayo <i>et al.</i> (2014) Tejaswini (2016)
		Negative	NS	P,G P,G	Sanghera <i>et al.</i> (2013) Patel <i>et al.</i> (2014)
5.	L/B ratio	Positive	NS	P,G G p,G p,G p	Sateeshkumar and Saravanan (2012) Arulmozi and Muttuswamy (2013) Sanghera <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Tejaswini (2016)
		Negative	NS	P G	Aditya and Bhartiya (2013) Nagaraju <i>et al.</i> (2013)
VI. Association of grains per panicle with					
1.	Test weight (g)	Positive	S	P P,G	Chaudhary and Motiramani (2003) Panwar <i>et al.</i> (2006)
		Positive	NS	G -- P	Binse <i>et al.</i> (2006) Gulzar and Parry (2010) Aditya and Bhartiya (2013)
		Negative	S	P,G P P,G P,G	Borbora <i>et al.</i> (2005) Sharma and Sharma (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Negative	NS	P	Parmhansh <i>et al.</i> (2010)
2.	Kernel length (mm)	Negative	NS	P,G P	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)
3.	Kernel breadth (mm)	Positive	S	P	Aditya and Bhartiya (2013)
		Negative	S	P,G	Sateeshkumar and Saravanan (2012)
4.	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
		Negative	NS	P,G	Sateeshkumar and Saravanan (2012)
VII. Association of Test weight with					
1.	Kernel length (mm)	Positive	S	P P P,G P P P,G P	Chaudhary and Motiramani (2003) Bhattacharya <i>et al.</i> (2007) Sarkar <i>et al.</i> (2007) Aditya and Bhartiya (2013) Bekele <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Tejaswini (2016)
		Positive	NS	P,G P P,G	Sanghera <i>et al.</i> (2013) Ogunbayo <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
		Negative	S	--	Krishnaveni and Sobharani (2006)
2.	Kernel breadth (mm)	Positive	S	P P,G P P,G P,G P	Bhattacharya <i>et al.</i> (2007) Sarkar <i>et al.</i> (2007) Bekele <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Tejaswini (2016)
		Positive	NS	P P,G	Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013)
		Negative	S	P	Ogunbayo <i>et al.</i> (2014)
		Negative	NS	P,G	Allam <i>et al.</i> (2015)
3.	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
		Negative	S	P	Tejaswini (2016)
VIII. Association of Kernel length with					
1.	Kernel breadth (mm)	Positive	S	P P,G	Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013)

Table 2.4 (cont.)

S.No.	Character	Direction	Significance	P/G	Reference
		Positive	NS	G P,G	Ashishbinodh <i>et al.</i> (2007) Sateeshkumar and Saravanan (2012)
		Negative	S	-- P,G P G P P,G	Krishnaveni and Sobharani (2006) Sarkar <i>et al.</i> (2007) Shivani <i>et al.</i> (2007) Ashifshikari <i>et al.</i> (2008) Ogunbayo <i>et al.</i> (2014) Ashok (2015)
		Negative	NS	P	Tejaswini (2016)
2.	L/B ratio	Positive	S	P,G P P,G P,G P,G P,G P	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Sanghera <i>et al.</i> (2013) Lakshmi <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Tejaswini (2016)
IX. Association of Kernel breadth with					
1.	L/B ratio	Positive	S	P	Aditya and Bhartiya (2013)
		Positive	NS	P,G	Sanghera <i>et al.</i> (2013)
		Negative	S	P,G P,G P,G P	Lakshmi <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015) Tejaswini (2016)
		Negative	NS	P,G	Sateeshkumar and Saravanan (2012)

S : Significant

NS: Non-significant

P: Phenotypic

G: Genotypic

Table 2.2. Review of literature on heritability and genetic advance as per cent of mean of yield and yield components in rice (*Oryza sativa* L.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
1.	Days to 50% flowering	High	High	Baradwaj <i>et al.</i> (2007) Sharma and Sharma (2007) Vijayalakshmi <i>et al.</i> (2008) Lal and Chauhan (2011) Prasad <i>et al.</i> (2011) Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011) Neha <i>et al.</i> (2014) Balakrishna <i>et al.</i> (2015a)
		High	Moderate	Patil <i>et al.</i> (2003) Chand <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Vaithiyalingan and Nadarajan (2006) Singh <i>et al.</i> (2007) Padmaja <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Kuchanur <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Gangashetty <i>et al.</i> (2013) Paikhomba <i>et al.</i> (2014)
		High	Low	Sreeparvathy <i>et al.</i> (2010) Osman <i>et al.</i> (2012)
2.	Days to maturity	High	High	Kumar and Ramesh (2008) Neha <i>et al.</i> (2014)
		High	Moderate	Tejaswini (2016)
		High	Low	Madhavalatha and Suneetha (2005) Karim <i>et al.</i> (2007) Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011) Osman <i>et al.</i> (2012)

Table 2.2 (cont.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
3.	Productive tillers per plant	High	High	Zada (2002) Chaudhary and Motiramani (2003) Patil <i>et al.</i> (2003) Chaudhary <i>et al.</i> (2004) Mall <i>et al.</i> (2005) Singh <i>et al.</i> (2005) Singh and Singh (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Vaithiyalingan and Nadarajan (2006) Sharma and Sharma (2007) Singh <i>et al.</i> (2007) Nayudu <i>et al.</i> (2007) Padmaja <i>et al.</i> (2008) Vijayalakshmi <i>et al.</i> (2008) Anbanandan <i>et al.</i> (2009) Chandra <i>et al.</i> (2009) Parvathi (2010) Saidaiah <i>et al.</i> (2010) Sreeparvathy <i>et al.</i> (2010) Lal and Chauhan (2011) Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011) Gangashetty <i>et al.</i> (2013) Sharma and Koutu (2013) Dhurai <i>et al.</i> (2014)
		Moderate	Moderate	Manna <i>et al.</i> (2006) Baradwaj <i>et al.</i> (2007) Garg <i>et al.</i> (2010)
		High	Low	Prasad <i>et al.</i> (2011)
		Moderate	High	Mishra and Pravin (2004) Krishna <i>et al.</i> (2008)
		Low	Low	Prasad <i>et al.</i> (2009) Paikhomba <i>et al.</i> (2014)
4.	Plant height (cm)	High	High	Nagajyothi (2001) Chaudhary and Motiramani (2003)

Table 2.2 (cont.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
				Elayaraja <i>et al.</i> (2005) Mall <i>et al.</i> (2005) Singh and Singh (2005) Singh <i>et al.</i> (2006) Baradwaj <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Sharma and Sharma (2007) Karad and Pol (2008) Kumar and Ramesh (2008) Padmaja <i>et al.</i> (2008) Vijayalakshmi <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Anjaneyulu <i>et al.</i> (2010) Saidaiah <i>et al.</i> (2010) Lal and Chauhan (2011) Parvathi <i>et al.</i> (2011) Prasad <i>et al.</i> (2011) Bhadru <i>et al.</i> (2012) Sateeshkumar and Saravanan (2012) Bekele <i>et al.</i> (2013) Gangashetty <i>et al.</i> (2013) Karupaiyan <i>et al.</i> (2013) Bornare <i>et al.</i> (2014) Dhurai <i>et al.</i> (2014) Neha <i>et al.</i> (2014)
		High	Moderate	Chand <i>et al.</i> (2005) Vaithiyalingan and Nadarajan (2006) Singh <i>et al.</i> (2007) Paikhomba <i>et al.</i> (2014) Tejaswini (2016)
		High	Low	Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011)
		Moderate	Low	Kuchanur <i>et al.</i> (2009)
		Low	High	Mishra and Pravin (2004) Krishna <i>et al.</i> (2008)

Table 2.2 (cont.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
		Low	Low	Manna <i>et al.</i> (2006)
5.	Panicle length (cm)	High	High	Chaudhrary and Motiramani (2003) Chaudhary <i>et al.</i> (2004) Naik (2004) Elayaraja <i>et al.</i> (2005) Vaithiyalingan and Nadarajan (2006) Baradwaj <i>et al.</i> (2007) Nayudu <i>et al.</i> (2007) Sharma and Sharma (2007) Vijayalakshmi <i>et al.</i> (2008) Sateeshkumar and Saravanan (2012) Gangashetty <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014)
		High	Moderate	Singh and Singh (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Karthikeyan <i>et al.</i> (2007)
		High	Low	Singh <i>et al.</i> (2007) Prasad <i>et al.</i> (2009)
		Low	High	Mishra and Pravin (2004)
		Low	Moderate	Manna <i>et al.</i> (2006)
		Moderate	Low	Bhavana (2003) Paikhomba <i>et al.</i> (2014)
		Moderate	High	Patil <i>et al.</i> (2003)
		Moderate	Moderate	Parvathi <i>et al.</i> (2011)
		Low	Low	Krishna <i>et al.</i> (2008) Chandra <i>et al.</i> (2009)
		High	High	Hossain and Hossain (2001) Chaudhrary and Motiramani (2003) Patil <i>et al.</i> (2003) Chaudhary <i>et al.</i> (2004) Singh and Singh (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006)
6.	Grains per panicle	High	High	Hossain and Hossain (2001) Chaudhrary and Motiramani (2003) Patil <i>et al.</i> (2003) Chaudhary <i>et al.</i> (2004) Singh and Singh (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006)

Table 2.2 (cont.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
				Panwar (2006) Vaithiyalingan and Nadarajan (2006) Karim <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Sharma and Sharma (2007) Kuchanur <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Sharma and Koutu (2013) Dhurai <i>et al.</i> (2014)
		Moderate	High	Baradwaj <i>et al.</i> (2007)
7.	Test weight (g)	High	High	Sarawgi <i>et al.</i> (2000) Shanthi and Singh (2001) Zada (2002) Chaudhray and Motiramani (2003) Patil <i>et al.</i> (2003) Elayaraja <i>et al.</i> (2005) Hasib (2005) Singh and Singh (2005) Binse <i>et al.</i> (2006) Vaithiyalingan and Nadarajan (2006) Baradwaj <i>et al.</i> (2007) Karim <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Sharma and Sharma (2007) Karad and Pol (2008) Vijayalakshmi <i>et al.</i> (2008) Anbanandan <i>et al.</i> (2009) Chandra <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Lal and Chauhan (2011) Prasad <i>et al.</i> (2011) Bhadru <i>et al.</i> (2012) Sateeshkumar and Saravanan (2012)

Table 2.2 (cont.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
				Gangashetty <i>et al.</i> (2013) Bornare <i>et al.</i> (2014) Tejaswini (2016)
		High	Low	Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011)
		High	Moderate	Satish (2000) Elayaraja <i>et al.</i> (2005)
		Low	High	Krishna <i>et al.</i> (2008) Paikhomba <i>et al.</i> (2014)
		Moderate	Low	Singh and Singh (2005)
		Moderate	Moderate	Kuchanur <i>et al.</i> (2009)
8.	Kernel length (mm)	High	Low	Krishnaveni and Niveditha (2014)
		High	Moderate	Tejaswini (2016)
		Moderate	Moderate	Venkanna <i>et al.</i> (2014)
9.	Kernel breadth (mm)	High	Moderate	Krishnaveni and Niveditha (2014) Tejaswini (2016)
		Moderate	Moderate	Venkanna <i>et al.</i> (2014)
10.	L/B ratio	High	High	Sarawgi <i>et al.</i> (2000) Zada (2002) Chaudhary <i>et al.</i> (2004) Madhavalatha and Suneetha (2005) Devi <i>et al.</i> (2006) Vanaja and Babu (2006) Baradwaj <i>et al.</i> (2007) Manonmani <i>et al.</i> (2010) Rajeswari <i>et al.</i> (2010) Sateeshumar and Saravanan (2012) Gangashetty <i>et al.</i> (2013) Karuppaiyan <i>et al.</i> (2013) Kumar <i>et al.</i> (2013) Tejaswini (2016)
		High	Moderate	Krishnaveni and Niveditha (2014)
		High	Low	Lal and Chauhan (2011) Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011)

Table 2.2 (cont.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
11.	Grain yield per plant (g)	High	High	Chaudhary <i>et al.</i> (2004) Elayaraja <i>et al.</i> (2005) Madhavalatha and Suneetha (2005) Sankar <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Panwar (2006) Karthikeyan <i>et al.</i> (2007) Nayudu <i>et al.</i> (2007) Sharma and Sharma (2007) Kumar and Ramesh (2008) Padmaja <i>et al.</i> (2008) Anbanandan <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Anjaneyulu <i>et al.</i> (2010) Garg <i>et al.</i> (2010) Sreeparvathy <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Singh <i>et al.</i> (2011) Bhadru <i>et al.</i> (2012) Sateeshkumar and Saravanan (2012) Gangashetty <i>et al.</i> (2013) Sharma and Koutu (2013) Neha <i>et al.</i> (2014) Paikhomba <i>et al.</i> (2014) Tejaswini (2016)
		High	Low	Saidaiah <i>et al.</i> (2010) Prasad <i>et al.</i> (2011)
		Moderate	High	Singh <i>et al.</i> (2007) Chandra <i>et al.</i> (2009)
		Low	High	Krishna <i>et al.</i> (2008)

Table 2.5. Review of literature on direct effects of component characters on grain yield per plant in rice (*Oryza sativa* L.)

S. No.	Character	P/G	Positive direct effect	P/G	Negative direct effect
1.	Days to 50 % flowering	P P P P P,G G G P,G G G P	Panwar (2006) Jaiswal <i>et al.</i> (2007) Pal <i>et al.</i> (2011) Basavaraja <i>et al.</i> (2012) Rangare <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Seesang <i>et al.</i> (2013) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015) Tejaswini (2016)	G P G P,G P P,G P,G P P,G P	Borbora <i>et al.</i> (2005) Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Swain and Reddy (2006) Eradasappa <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Abarshahr <i>et al.</i> (2011) Babu <i>et al.</i> (2012) Sateeshkumar and Saravanan (2012) Bekele <i>et al.</i> (2013)
2.	Day to maturity	P P,G	Aditya and Bhartiya (2013) Kundu and Kundagrami (2015)	P P,G P,G G P	Panwar (2006) Abarshahr <i>et al.</i> (2011) Krishna <i>et al.</i> (2011) Kundu and Kundagrami (2015) Tejaswini (2016)
3.	Productive tillers per plant	P,G G P,G P P,G P P P P G P,G P,G G G	Nagajyothi (2001) Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Panwar (2006) Swain and Reddy (2006) Eradasappa <i>et al.</i> (2007) Jaiswal <i>et al.</i> (2007) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Sateeshkumar and Saravanan (2012) Kumar <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)	P,G G P,G	Janardhanam <i>et al.</i> (2001) Rani and Reddy (2010) Sudharani <i>et al.</i> (2013)
4.	Plant height (cm)	P,G P P P,G	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Kumar and Bapu (2005) Shashidhar <i>et al.</i> (2005)	G P G P,G P	Nagajyothi (2001) Panwar (2006) Manna <i>et al.</i> (2006) Abarshahr <i>et al.</i> (2011) Babu <i>et al.</i> (2012)

Table 2.5 (cont.)

S. No.	Character	P/G	Positive direct effect	P/G	Negative direct effect
		G P P,G P P P G P,G P P P,G P G P	Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Swain and Reddy (2006) Bhattacharyya <i>et al.</i> (2007) Jaiswal <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Seyoum <i>et al.</i> (2012) Rangare <i>et al.</i> (2012) Basavaraja <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Sudharani <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Premkumar <i>et al.</i> (2015) Tejaswini (2016)	P,G G	Sateeshkumar and Saravanan (2012) Balakrishna <i>et al.</i> (2015b)
5.	Panicle length (cm)	P,G G P G P P P P P G P P P,G G G G P	Nagajyothi (2001) Borbora <i>et al.</i> (2005) Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Panwar (2006) Jaiswal <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Babu <i>et al.</i> (2012) Basavaraja <i>et al.</i> (2012) Rangare <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015) Tejaswini (2016)	P,G G G P P G G P,G G G P,G	Janardhanam <i>et al.</i> (2001) Borbora <i>et al.</i> (2005) Manna <i>et al.</i> (2006) Bhattacharyya <i>et al.</i> (2007) Eradasappa <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Sateeshkumar and Saravanan (2012) Gopikannan and Ganesh (2013) Seesang <i>et al.</i> (2013) Sudharani <i>et al.</i> (2013)
6.	Grains per panicle	P,G P,G G P P P P P P	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Borbora <i>et al.</i> (2005) Kumar and Bapu (2005) Panwar (2006) Swain and Reddy (2006) Jaiswal <i>et al.</i> (2007) Bhattacharyya <i>et al.</i> (2007)	G P,G G G	Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Swain and Reddy (2006) Rani and Reddy (2010)

Table 2.5 (cont.)

S. No.	Character	P/G	Positive direct effect	P/G	Negative direct effect
		G P P,G	Rani and Reddy (2010) Garg <i>et al.</i> (2010) Sateeshkumar and Saravanan (2012)		
7.	Test weight (g)	P,G P G P P P P G P P G P,G P,G P,G G	Nagajyothi (2001) Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Panwar (2006) Swain and Reddy (2006) Bhattacharyya <i>et al.</i> (2007) Eradasappa <i>et al.</i> (2007) Rani and Reddy (2010) Garg <i>et al.</i> (2010) Pal <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Rangare <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Kumar <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b)	G G G P,G G P	Swain and Reddy (2006) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Sudharani <i>et al.</i> (2013) Premkumar <i>et al.</i> (2015) Tejaswini (2016)
8.	Kernel length (mm)	P,G P,G	Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012)	P,G P P G P	Krishna <i>et al.</i> (2011) kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015) Tejaswini (2016)
9.	Kernel breadth (mm)	P P G P	Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015) Tejaswini (2016)	P,G P,G P,G	Krishna <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012)
10.	L/B ratio	P P,G P P,G P P,G P	Pal <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Madhusoodanan <i>et al.</i> (2013) Nagaraju <i>et al.</i> (2013) Kumar <i>et al.</i> (2013) Tejaswini (2016)	P,G G	Garg <i>et al.</i> (2010) Premkumar <i>et al.</i> (2015)

P: Phenotypic level

G: Genotypic level

Table 2.6. Review of literature on indirect effects of component characters on grain yield per plant in rice (*Oryza sativa* L.).

S.No.	Character	Positive indirect effect	Negative indirect effect
I. Days to 50% flowering on grain yield per plant through			
1.	Days to maturity	Panwar (2006) Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Tejawini (2016)	Hasan <i>et al.</i> (2012) Bhabendra <i>et al.</i> (2013)
2.	Productive tillers per plant	Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Panwar (2006) Jaiswal <i>et al.</i> (2007) kumari <i>et al.</i> (2011) Hasan <i>et al.</i> (2012)	Binse <i>et al.</i> (2006) Jaiswal <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)
3.	Plant height(cm)	Kumar and Bapu (2005) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Borbora <i>et al.</i> (2005) Panwar (2006) Sateeshkumar and Saravanan (2012) Hasan <i>et al.</i> (2012)
4.	Panicle length (cm)	Binse <i>et al.</i> (2006) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Hasan <i>et al.</i> (2012) Aditya and Bhartiya (2013)	Borbora <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Panwar (2006) Kumari <i>et al.</i> (2011) Garg <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015) Tejawini (2016)
5.	Grains per panicle	Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Panwar and Ali (2007) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)	Borbora <i>et al.</i> (2005) Panwar (2006) Jaiswal <i>et al.</i> (2007) Kumari <i>et al.</i> (2011)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
6.	Test weight (g)	Binse <i>et al.</i> (2006) Panwar (2006) Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Tejawini (2016)	Borbora <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Jaiswal <i>et al.</i> (2007) Hasan <i>et al.</i> (2012) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)
7.	Kernel length (mm)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014)
8.	Kernel breadth (mm)	Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Tejawini (2016)	Krishna <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015)
9.	L/B ratio	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014)	Premkumar <i>et al.</i> (2015) Tejawini (2016)
II. Days to maturity on grain yield per plant through			
1.	Days to 50% flowering	Hasan <i>et al.</i> (2012) Bhabendra <i>et al.</i> (2013) Allam <i>et al.</i> (2015)	Panwar (2006) Abarshahr <i>et al.</i> (2011) Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Tejawini (2016)
2.	Productive tillers per plant	Krishna <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Aditya and Bhartiya (2013)	Panwar (2006) Bhabendra <i>et al.</i> (2013) Allam <i>et al.</i> (2015)
3.	Plant height (cm)	Hasan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)	Panwar (2006) Abarshahr <i>et al.</i> (2011) Krishna <i>et al.</i> (2011) Kundu and Kundagrami (2015) Tejawini (2016)
4.	Panicle length (cm)	Panwar (2006) Hasan <i>et al.</i> (2012) Aditya and Bhartiya (2013) Tejawini (2016)	Krishna <i>et al.</i> (2011) Kundu and Kundagrami (2015)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
5.	Grains per panicle	Panwar (2006) Aditya and Bhartiya (2013)	Kundu and Kundagrami (2015)
6.	Test weight (g)	Hasan <i>et al.</i> (2012)	Panwar (2006) Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Kundu and Kundagrami (2015) Tejawini (2016)
7.	Kernel length (mm)	Krishna <i>et al.</i> (2011)	Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015) Tejawini (2016)
8.	Kernel breadth (mm)	Allam <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Tejawini (2016)
9.	L/B ratio	Aditya and Bhartiya (2013) Tejawini (2016)	Allam <i>et al.</i> (2015)
III. Productive tillers per plant on grain yield per plant through			
1.	Days to 50% flowering	Binse <i>et al.</i> (2006) Panwar (2006) Panwar and Ali (2007) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013)	Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)
2.	Days to maturity	Panwar (2006) Krishna <i>et al.</i> (2011) Allam <i>et al.</i> (2015)	Aditya and Bhartiya (2013)
3.	Plant height (cm)	Shashidhar <i>et al.</i> (2005) Panwar (2006) Neelima <i>et al.</i> (2007) Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Sudharani <i>et al.</i> (2013) Allam <i>et al.</i> (2015) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)	Binse <i>et al.</i> (2006) Panwar and Ali (2007) Kumari <i>et al.</i> (2011)
4.	Panicle length (cm)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)	Panwar (2006) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Allam <i>et al.</i> (2015)
5.	Grains per panicle	Shashidhar <i>et al.</i> (2005) Binse <i>et al.</i> (2006)	Panwar (2006) Jaiswal <i>et al.</i> (2007)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
			Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012)
6.	Test weight (g)	Panwar (2006) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b)	Binse <i>et al.</i> (2006) Jaiswal <i>et al.</i> (2007) Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Allam <i>et al.</i> (2015)
7.	Kernel length (mm)	Krishna <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Premkumar <i>et al.</i> (2015)	Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
8.	Kernel breadth (mm)	Allam <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015)
9.	L/B ratio	Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015)	Sateeshkumar and Saravanan (2012) Allam <i>et al.</i> (2015)
IV. Plant height on grain yield per plant through			
1.	Days to 50% flowering	Panwar and Ali (2007) Sudhrani <i>et al.</i> (2013) Premkumar <i>et al.</i> (2015)	Kumar and Bapu (2005) Panwar (2006) Yadav <i>et al.</i> (2010) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Balakrishna <i>et al.</i> (2015b) Tejawini (2016)
2.	Days to maturity	Aditya and Bhartiya (2013)	Panwar (2006) Krishna <i>et al.</i> (2011) Allam <i>et al.</i> (2015) Tejawini (2016)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
3.	Productive tillers per plant	Shashidhar <i>et al.</i> (2005) Panwar (2006) Jaiswal <i>et al.</i> (2007) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Parvathi <i>et al.</i> (2011) Premkumar <i>et al.</i> (2015)	Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b)
4.	Grains per panicle	Shashidhar <i>et al.</i> (2005) Panwar (2006) Jaiswal <i>et al.</i> (2007) Neelima <i>et al.</i> (2007) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)	Kumar and Bapu (2005) Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011)
5.	Panicle length (cm)	Jaiswal <i>et al.</i> (2007) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Premkumar <i>et al.</i> (2015) Balakrishna <i>et al.</i> (2015b)	Panwar (2006) Sudharani <i>et al.</i> (2013) Tejawini (2016)
6.	Test weight (g)	Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Kumari <i>et al.</i> (2011) Balakrishna <i>et al.</i> (2015b)	Kumar and Bapu (2005) Panwar (2006) Jaiswal <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Yadav <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Tejawini (2016)
7.	Kernel length (mm)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Venkanna <i>et al.</i> (2014)	Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015) Tejawini (2016)
8.	Kernel breadth (mm)	Sateeshkumar and Saravanan (2012)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
			Parvathi <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015) Tejawini (2016)
9.	L/B ratio	Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015)	Sateeshkumar and Saravanan (2012) Tejawini (2016)
V. Panicle length per plant on grain yield per plant through			
1.	Days to 50% flowering	Jaiswal <i>et al.</i> (2007) Hasan <i>et al.</i> (2012) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b)	Kumar and Bapu (2005) Panwar. (2006) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Premkumar <i>et al.</i> (2015) Tejawini (2016)
2.	Days to maturity	Hasan <i>et al.</i> (2012) Aditya and Bhartiya (2013)	Panwar (2006) Krishna <i>et al.</i> (2011) Allam <i>et al.</i> (2015) Tejawini (2016)
3.	Productive tillers per plant	Jaiswal <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Premkumar <i>et al.</i> (2015)	Panwar (2006) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Rani and Reddy (2010) Kumari <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Allam <i>et al.</i> (2015)
4.	Plant height(cm)	Kumar and Bapu (2005) Panwar (2006) Neelima <i>et al.</i> (2007) Garg <i>et al.</i> (2010) Rani and Reddy (2010) Sudharani <i>et al.</i> (2013) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Panwar and Ali (2007) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Balakrishna <i>et al.</i> (2015b)
5.	Grains per panicle	Kumar and Bapu (2005) Panwar (2006) Jaiswal <i>et al.</i> (2007) Neelima <i>et al.</i> (2007)	Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
		Rani and Reddy (2010) Sateeshkumar and Saravanan (2012)	
6.	Test weight (g)	Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sudharani <i>et al.</i> (2013) Allam <i>et al.</i> (2015) Balakrishna <i>et al.</i> (2015b)	Kumar and Bapu (2005) Panwar (2006) Neelima <i>et al.</i> (2007) Panwar and Ali (2007) Garg <i>et al.</i> (2010) Hasan <i>et al.</i> (2012) Tejawini (2016)
7.	Kernel length (mm)	Krishna <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Tejawini (2016)	Kumari <i>et al.</i> (2011) Premkumar <i>et al.</i> (2015)
8.	Kernel breadth (mm)	Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)	Parvathi <i>et al.</i> (2011) Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Tejawini (2016)
9.	L/B ratio	Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)
VI. Grains per panicle on grain yield per plant through			
1.	Days to 50% flowering	Binse <i>et al.</i> (2006) Panwar (2006) Kumari <i>et al.</i> (2011)	Panwar and Ali (2007) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)
2.	Days to maturity	Panwar (2006) Aditya and Bhartiya (2013)	
3.	Productive tillers per plant	Neelima <i>et al.</i> (2007) Aditya and Bhartiya (2013)	Panwar (2006) Jaiswal <i>et al.</i> (2007) Panwar and Ali (2007) Kumari <i>et al.</i> (2011)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
			Sateeshkumar and Saravanan (2012)
4.	Plant height(cm)	Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Neelima <i>et al.</i> (2007) Aditya and Bhartiya (2013)	Borbora <i>et al.</i> (2005) Panwar (2006) Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012)
5.	Panicle length (cm)	Binse <i>et al.</i> (2006) Neelima <i>et al.</i> (2007) Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)	Panwar (2006)
6.	Test weight (g)	Kumar and Bapu (2005) Binse <i>et al.</i> (2006) Panwar (2006) Neelima <i>et al.</i> (2007) Kumari <i>et al.</i> (2011)	Borbora <i>et al.</i> (2005) Panwar and Ali (2007) Jaiswal <i>et al.</i> (2007) Aditya and Bhartiya (2013)
7.	Kernel length (mm)	Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)	
8.	Kernel breadth (mm)	Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013)	Sateeshkumar and Saravanan (2012)
9.	L/B ratio		Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)
VII. Test wait on grain yield per plant through			
1.	Days to 50% flowering	Binse <i>et al.</i> (2006) Panwar (2006) Kumari <i>et al.</i> (2011) Premkumar <i>et al.</i> (2015)	Hasan <i>et al.</i> (2012) Sudharani <i>et al.</i> (2013) Balakrishna <i>et al.</i> (2015b) Tejawini (2016)
2.	Days to maturity	Panwar (2006) Aditya and Bhartiya (2013)	Krishna <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Allam <i>et al.</i> (2015) Tejawini (2016)
3.	Productive tillers per plant	Panwar (2006) Neelima <i>et al.</i> (2007) Garg <i>et al.</i> (2010)	Binse <i>et al.</i> (2006) Rani and Reddy (2010) Sudharani <i>et al.</i> (2013)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
		Kumari <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Premkumar <i>et al.</i> (2015)	Allam <i>et al.</i> (2015) Balakrishna <i>et al.</i> (2015b)
4.	Plant height(cm)	Binse <i>et al.</i> (2006) Panwar (2006) Neelima <i>et al.</i> (2007) Rani and Reddy (2010) Sudhrani <i>et al.</i> (2013) Hasan <i>et al.</i> (2012) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)	Garg <i>et al.</i> (2010) Kumari <i>et al.</i> (2011) Balakrishna <i>et al.</i> (2015b) Tejawini (2016)
5.	Panicle length (cm)	Binse <i>et al.</i> (2006) Kumari <i>et al.</i> (2011) Hasan <i>et al.</i> (2012) Sudahrani <i>et al.</i> (2013) Allam <i>et al.</i> (2015) Balakrishna <i>et al.</i> (2015b) Tejawini (2016)	Panwar (2006) Rani and Reddy (2010) Garg <i>et al.</i> (2010) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)
6.	Grains per panicle	Panwar (2006) Rani and Reddy (2010) Aditya and Bhartiya (2013)	Binse <i>et al.</i> (2006) Garg <i>et al.</i> (2010) kumari <i>et al.</i> (2011)
7.	Kernel length (mm)	Kumari <i>et al.</i> (2011) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015) Tejawini (2016)
8.	Kernel breadth (mm)	Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Tejawini (2016)
9.	L/B ratio	Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
VIII. Kernel length on grain yield per plant through			
1.	Days to 50% flowering	Parvathi <i>et al.</i> (2011) Krishna <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012)	Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015) Tejawini (2016)
2.	Days to maturity	Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Tejawini (2016)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
3.	Productive tillers per plant	Krishna <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)
4.	Plant height(cm)	Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Allam <i>et al.</i> (2015) Tejawini (2016)
5.	Panicle length (cm)	Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)	Parvathi <i>et al.</i> (2011) Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Tejawini (2016)
6.	Grains per panicle	Kumari <i>et al.</i> (2011)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013)
7.	Test weight (g)	Parvathi <i>et al.</i> (2011) Allam <i>et al.</i> (2015)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015) Tejawini (2016)
8.	Kernel breadth (mm)	Parvathi <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Tejawini (2016)	Krishna <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)
9.	L/B ratio	Aditya and Bhartiya (2013)	Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015) Tejawini (2016)
IX. Kernel breadth on grain yield per plant through			
1.	Days to 50% flowering	Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013)	Parvathi <i>et al.</i> (2011) Krishna <i>et al.</i> (2011)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
		Venkanna <i>et al.</i> (2014) Tejawini (2016)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)
2.	Days to maturity	Krishna <i>et al.</i> (2011) Aditya and Bhartiya (2013) Tejawini (2016)	Allam <i>et al.</i> (2015)
3.	Productive tillers per plant	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Venkanna <i>et al.</i> (2014)	Parvathi <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Premkumar <i>et al.</i> (2015)
4.	Plant height(cm)	Krishna <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014) Tejawini (2016)	Kumari <i>et al.</i> (2011) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)
5.	Panicle length (cm)	Krishna <i>et al.</i> (2011) Kumari <i>et al.</i> (2011) Sateeskumar and Saravanan (2012) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)	Parvathi <i>et al.</i> (2011) Venkanna <i>et al.</i> (2014) Tejawini (2016)
6.	Grains per panicle	Aditya and Bhartiya (2013)	Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012)
7.	Test weight (g)	Kumari <i>et al.</i> (2011) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Krishna <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014)
8.	Kernel length (mm)	Krishna <i>et al.</i> (2011) Parvathi <i>et al.</i> (2011) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015)	Kumari <i>et al.</i> (2011) Sateeshkumar and Saravanan (2012) Tejawini (2016)
9.	L/B ratio	Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014)	Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015) Tejawini (2016)

Table 2.6 (cont.)

S.No.	Character	Positive indirect effect	Negative indirect effect
X. L/B ratio on grain yield per plant through			
1.	Days to 50% flowering	Premkumar <i>et al.</i> (2015)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Tejawini (2016)
2.	Days to maturity	Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)	Allam <i>et al.</i> (2015) Tejawini (2016)
3.	Productive tillers per plant	Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015)
4.	Plant height(cm)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Allam <i>et al.</i> (2015) Premkumar <i>et al.</i> (2015) Tejawini (2016)	Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015)
5.	Panicle length (cm)	Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015) Tejawini (2016)	Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)
6.	Grains per panicle	Ashok (2015)	Aditya and Bhartiya (2013)
7.	Test weight (g)	Allam <i>et al.</i> (2015) Tejawini (2016)	Sateeshkumar and Saravanan (2012) Aditya and Bhartiya (2013) Venkanna <i>et al.</i> (2014) Premkumar <i>et al.</i> (2015)
8.	Kernel length (mm)	Premkumar <i>et al.</i> (2015) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015)	Aditya and Bhartiya (2013) Sateeshkumar and Saravanan (2012) Tejawini (2016)
9.	Kernel breadth (mm)	Sateeshkumar and Saravanan (2012) Venkanna <i>et al.</i> (2014) Allam <i>et al.</i> (2015)	Aditya and Bhartiya (2013) Premkumar <i>et al.</i> (2015)

Chapter II

REVIEW OF LITERATURE

The review of work done on Rice (*Oryza sativa* L.) relevant to the present investigation is furnished under the following headings.

2.1 Genetic variability

2.2 Heritability and genetic advance as per cent of mean

2.3 Character association

2.4 Path co-efficient analysis

2.5 Genetic divergence

2.1 GENETIC VARIABILITY

An insight into the magnitude of variability present in a crop species is of utmost importance as it provides the basis for effective selection. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait.

The literature on genetic variability studies on rice is reviewed and presented in Table 2.1.

2.2 HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN (GAM)

Heritability measures the relative amount of the heritable portion of variability. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. Basic information on heritability is a pre-requisite for planning any breeding programme.

Genetic advance helps to measure the amount of progress that could be expected with selection for a particular character. Estimates of heritability along with estimates of genetic advance are more useful in choice of selection method rather than heritability or genetic advance alone (Johnson *et al.*, 1955).

The available literature on heritability and genetic advance as per cent of mean in rice was reviewed and presented in Table 2.2.

2.3 CHARACTER ASSOCIATION

Plant yield is a complex and is a polygenically inherited trait. Therefore direct selection for yield is not much effective. But, it could be improved by selecting various component characters which are correlated to yield and are simple in inheritance with less environmental influence. Hence, correlation studies paved a path in order to find out the association between highly heritable independent character and most economic but dependent character like yield which would help the breeder in obtaining improved yields.

The available literature on the association of component characters with grain yield per plant and the associations among the yield component characters are presented in Tables 2.3 and 2.4, respectively.

2.4 PATH CO-EFFICIENT ANALYSIS

The estimation of path coefficients gives an exact picture of relative importance of the direct and indirect contribution of the component characters to yield. Path analysis proposed by Dewey and Lu (1959) facilitates the partitioning of the correlation coefficients into direct and indirect effects of various characters on grain yield. Thus path analysis would give a better insight into the cause and effect relationship between the pairs of characters.

The literature on direct and indirect effects of yield components on grain yield are reviewed and presented in Tables 2.5 and 2.6, respectively.

2.5 STUDIES ON GENETIC DIVERGENCE

The assessment of genetic diversity using quantitative traits has got prime importance in many contexts particularly in differentiating well defined population. The germplasm in a self-pollinated crop can be considered as a heterogeneous set of groups since each group being homozygous within it. Selecting parents for hybridization programme in these crops is difficult because, the success depends upon the segregates of hybrid derivatives between the parents, particularly when the aim is to improve the quantitative characters like yield.

To identify the parents that nick better, several methods of divergence analysis based on quantitative characters have been proposed to suit various objectives. Among them, Mahalanobis's generalized distance occupies a unique place and is an efficient method to measure the extent of diversity among genotypes, which quantify the differences among several quantitative traits.

2.5.1 Mahalanobis D^2 analysis

Divergence analysis is performed to identify the diverse genotypes for hybridization purpose. Clustering by D^2 analysis is useful in this matter. The genotypes grouped together are less divergent than the ones, which fall into different clusters. Clusters separated by largest statistical distance (D^2) show maximum divergence (Singh and Chaudhary, 1977).

For the first time, Nair and Mukherjee (1960) used D^2 statistic as a measure of genetic divergence in the classification of natural and plantation Teak. The basic importance of genetic diversity in breeding for high yield has long been recognised and is evident from the results supported by several workers.

Shanmugasundaram *et al.* (2000) studied the genetic diversity using Mahalanobis D^2 statistic of 38 cultivars which were grouped into 4 clusters, revealed sufficient amount of variability among the cultivars. Cluster I had 25 varieties of local origin and other clusters had genotypes obtained through recombination. The clustering pattern did not follow the geographical origin, but followed the breeding method and selection for different objectives. The most divergent clusters were I and III. Two genotypes from cluster I, one from Cluster III and one from IV were the potential parents for further breeding programmes. The major contributors to the total divergence were plant height, panicle length, grain yield and tiller number.

Shanthi and Singh (2001) studied the genetic divergence by using Mahalanobis's D^2 statistic and Tocher's method and grouped them into four clusters. The first cluster had nine genotypes, the second had six while the third and fourth had one genotype. The recommended genotypes for inclusion in a hybridization programme were genotypes from clusters II and III which had greater cluster distance and the genotypes were expected to produce good segregants.

Mishra *et al.* (2003) evaluated the nature and magnitude of genetic diversity in 16 rice cultivars and their 72 F₁ hybrids. Based on the relative magnitude of multivariate D² values, the genotypes were grouped into 12 clusters. Cluster XII had highest number of genotypes. The highest genetic distance was observed between clusters III and VIII and lowest between cluster VII and VIII. It was found that there was no close correspondence between geographical distribution and genetic divergence.

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

Awasthi *et al.* (2005) studied the genetic divergence of 21 Indian aromatic rice genotypes and grouped them into 6 clusters for different characters. The intra-cluster distance ranged from 0.00 for clusters IV, V and VI to 40.21 for cluster III. The inter-cluster distance was observed to be highest between clusters II and III, indicating that the genotypes of these 2 clusters were genetically more diverse. The highest per cent contribution towards total genetic divergence was shown by the number of grains per panicle, grain yield per plant, days to 50 % flowering, leaf length and leaf width.

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

Devi *et al.* (2006) evaluated genetic diversity in 54 rice cultivars for yield and yield components and the genotypes were grouped into 9 clusters. High mean values for plant height (140.33cm), flag leaf length (48.11cm) and flag leaf width (2.10cm) were recorded in cluster VI. Major contribution towards genetic divergence (40.16%) was recorded by plant height followed by flag leaf width (20.12%) and yield per plant (15.79%).

Mundhe *et al.* (2006) studied genetic diversity in 39 rice genotypes and grouped them into 7 clusters and observed that intra-cluster distance was maximum in cluster III followed by cluster II and cluster I and inter-cluster distance was maximum between cluster V and VII followed by cluster III and V, and cluster II and V.

Vanaja and Bapu (2006) estimated the genetic diversity in 56 rice genotypes and grouped them into 9 clusters and they observed that there was no association between the geographical distribution and genetic diversity. Maximum intra-cluster distance was observed in cluster I which could be made use of in the yield improvement through recombination breeding. Maximum inter-cluster distance was noticed between the clusters II and IV, followed by that between the clusters II and IV, which could be made use of in heterosis and recombination breeding.

Sarawgi and Bisne (2007) studied genetic divergence in 81 scented rice genotypes based on D^2 statistics and the genotypes were grouped into 9 clusters. The genotypes from cluster II had desired mean for characters like hulling %, milling % and head rice recovery and panicle length. While cluster VII had high value for kernel length and L/B ratio and cluster V had low value for days to 50% flowering but highest value for grain yield in Kg per hectare.

Sandhyakishore *et al.* (2007) studied genetic divergence for different yield attributing traits in 70 rice genotypes and grouped them into 9 clusters. They found that geographical diversity and genetic diversity were not related which was indicated by the mode of distribution of genotypes from different eco-regions into various clusters at random.

Kumar (2008) estimated genetic divergence by using Mahalanobis D^2 statistic in 30 genetically diverse genotypes of rice and grouped them into 8 clusters. They observed that the inter-cluster distance was highest between cluster V and VI which indicated 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 Senthilkumar (2008) assessed the genetic diversity in 50 rice genotypes and grouped them into 11 clusters with cluster I as the largest with consisting of 35 genotypes. The recorded inter cluster distance between clusters IV and VIII was maximum. The highest per cent contribution towards genetic divergence was given by number of grains per panicle, number of productive tillers per plant and grain yield per plant.

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 monogenotypic clusters. The maximum inter cluster distance was recorded between clusters II and III. Cluster XII recorded highest mean value for grain yield per plant and lowest mean value for days to first flower. Maximum total divergence was contributed by number of grains per panicle (42.71%) followed by days to first flower (25.62%).

Rouf *et al.* (2009) used D^2 statistic to measure the genetic divergence in 75 genotypes and grouped them into 11 clusters. Greater genetic separation was shown by Clusters VI, IX and X among themselves, though Cluster II and I had more strength which would help in achieving high genetic gain.

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

Chaturvedi *et al.* (2011) studied the nature and magnitude of genetic divergence in 35 rice genotypes by using Mahalanobis D^2 statistic and grouped them into 8 clusters. Maximum contributors towards divergence were panicle weight followed by effective tillers per plant and yield per plant. To achieve greater variability in the segregating generations, the genotypes of cluster VII could be utilized as diverse parents in hybridization programme with the genotypes of clusters II and VIII.

Sharma *et al.* (2011) assessed the genetic divergence by using D^2 statistic in 63 rice genotypes and grouped them into 8 clusters of which cluster VII was the largest having 16 genotypes. 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, based on mean performance, genetic distances and clustering pattern.

Chamundeswari *et al.* (2012) evaluated sixty four rice germplasm lines to study the degree and magnitude of genetic diversity by using Mahalanobis D^2 technique and grouped them into 8 clusters of which cluster I was the largest with 23 genotypes followed by cluster V with 11 genotypes and clusters II and VIII with 8 genotypes each. The traits which gave maximum contribution towards genetic divergence were 50% flowering followed by iron content, grain yield per plant, gel consistency and test weight.

Chakravorty and Ghosh (2012) studied 51 land races of rice and grouped them into 11 clusters. The grouping showed 6 multigenotypic, 3 digenotypic, and two monogenotypic clusters. The maximum intra cluster D^2 value was shown by the cluster X followed by cluster IX, III and I, while the intra cluster distance was maximum between genotypes present in cluster IX. Maximum contribution towards genetic divergence came from the characters, culm length and grain length. Cluster VII recorded highest mean value for plant height, ligule length, culm length, culm diameter, culm number, panicle length and maturity. Hybridization among these genotypes from the cluster I, III and IX which had maximum inter cluster distances and desirable values for flag leaf angle, grain breadth, grain weight, kernel weight, no of primary branches for panicle, likely to produce heterotic combinations and wide variability in segregating generations.

Karupaiyan *et al.* (2013) studied 27 genotypes were grouped into 4 clusters. Yield ha^{-1} (20.80%) contributed maximum towards divergence followed by plant height (16.81%), grain breadth (16.52%) and grain length (15.10%).

Kar *et al.* (2013) studied 65 indigenous aromatic rice genotypes and the genotypes were grouped into thirteen clusters. Based on clustering pattern, the maximum genetic distance among genotypes existed between cluster IV, V and XI. The clusters, V and X, were ascertained outstanding on the basis of higher cluster means for most of the component characters.

Tushara *et al.* (2013) studied genetic divergence of 19 medium duration genotypes of rice for 20 characters and grouped them into five clusters. Protein percentage (43.27) showed maximum contribution towards genetic divergence followed by alkali digestion value (27.49), amylose content (9.94), grain length (5.26), grain width (5.26), water uptake (2.92), kernel breadth (1.17), test weight (1.17), days to 50% flowering (1.17), filled grains per panicle (0.58), kernel length after cooking (0.58),

panicle length (0.58) and tillers per plant (0.58). The maximum inter cluster D^2 values was observed between clusters II and III, followed by clusters II and V and clusters I and II.

Krishnaveni *et al.* (2015) studied genetic divergence of 70 rice genotypes and genotypes were grouped into five clusters. Maximum genetic divergence was contributed by 50% flowering (34.29%) followed by test weight (24.43%) and grain yield per plant (15.82%).

2.5.2 Principal component analysis and cluster analysis

Principal component analysis was carried out to perform the inter dependent traits into a set of independent traits as well as to reduce the dimensionality of the data structure (Banfield, 1978). It is defined as a method of data reduction to clarify the relationship between two or more characters into limited number of uncorrelated new variables. The reduction is achieved by linear transformation of the original characters into a new set of correlated variables known as principal components (PC_s).

Kulsum *et al.* (2011) studied the genetic divergence of thirty six restorer lines through Mohalanobis's D^2 and principal component analysis for nine characters and grouped the restorers into five different clusters. Cluster III comprised of maximum number of genotypes (eleven) followed by cluster I and IV. The inter-cluster distance was maximum between clusters II and IV (14.064) indicating wide genetic diversity between these two clusters. Among the characters, number of tillers/hill, panicle length, number of filled spikelets/ panicle, spikelet fertility % and yield/plant contributed most for divergence in the studied genotypes.

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

Maji and shaibu (2012) studied 123 rice germplasm lines from India and Africa. Cluster analysis using Ward's method classified the 123 populations into six clusters, large number of genotypes was placed in cluster 5 followed by cluster 1, cluster 4,

cluster 3, cluster 2 and cluster 6. The maximum inter-cluster distance was observed between clusters II and III and it indicating the possibility of high heterosis if individuals from these clusters are cross-bred. Principal component analysis resulted in the first two components with Eigen value greater than 1 accounting for 78% of the total variation.

Hasan *et al.* (2012) determined the genetic divergence of 40 parental lines comprising of 30 restorers and 10 maintainer lines through Mohalanobis's D^2 and principal component analysis for eleven characters. Genotypes were grouped into five different clusters. Cluster V had maximum number of genotypes followed by cluster I and II. The inter-cluster distance was maximum between clusters I and V (13.495) indicating wide genetic diversity between these two clusters. The minimum inter-cluster distance was observed between cluster II and cluster III (3.034) indicating that the genotypes of these clusters were genetically close. The intra cluster distance in the entire five clusters was more or less low which indicated that the genotypes within the same cluster were closely related.

Ashfaq *et al.* (2012) studied 40 rice genotypes through principal component analysis among the various morphological traits. The results found that the highest variability was observed in plant height followed by tillers per plant, panicle length and flag leaf area. The combined variation among these traits was 67.7%. The seed length and seed width showed maximum variation (88%) with respect to other seed traits.

Role *et al.* (2014) studied 307 traditional rice varieties newly conserved at the PhilRice genebank were characterized to assess their phenotypic diversity using 57 morphological traits. Cluster analysis separated the different varieties into various groups. Principal component analysis (PCA) showed that seven independent principal components accounted for 74.95% of the total variation. Each principal component showed morphological characters, such as culm number, panicle number and caryopsis ratio that were among the phenotypic traits contributing positive projections in three principal components that explained 48% of variation.

Haque *et al.* (2015) studied diversity among sixty rice genotypes and contribution of thirteen traits towards diversity were analyzed using cluster analysis based on Mahalanobis's D^2 statistics and principal component analysis and classified them into 7 clusters. The highest intra- cluster distance (21.95) was observed in cluster II whereas that was lowest (7.62) for cluster VI. Maximum inter-cluster distance was

observed between cluster III & VII (46.75) followed by cluster II & VII (42.91), cluster V & VII (38.48) and cluster III & VI (30.87). Inter-cluster distance was higher than the intra-cluster distance suggesting wider diversity among the genotypes. First three principal components explained about 81% of the total variation.

Ravikumar *et al.* (2015) used cluster analysis and principal component analysis in 34 released and pre-released rice genotypes and cluster analysis grouped all these varieties into five clusters by PCA and six clusters in Tochers' method. The genotypes from cluster III and cluster I having high genetic divergence coupled with high mean performance may be selected for yield and its components viz., test weight (51%) followed by mother panicle length (22%) and tiller panicle length (7%) indicating the significance of these traits in selection procedures for increasing yield.

**Table 2.1. Review of literature on genetic variability of yield and yield components in rice
[*Oryza sativa* L.]**

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
1.	Days to 50% flowering	High	High	Sharma and Sharma (2007) Seyoum <i>et al.</i> (2012) Niteshkumar <i>et al.</i> (2015)
		Moderate	Moderate	Jaiswal <i>et al.</i> (2007) Vijayalakshmi <i>et al.</i> (2008) Lal and Chauhan (2011) Bekele <i>et al.</i> (2013)
		Low	Low	Bhavana (2003) Patil <i>et al.</i> (2003) Naik (2004) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Vaithiyalingan and Nadarajan (2006) Singh <i>et al.</i> (2007) Kole <i>et al.</i> (2008) Krishna <i>et al.</i> (2008) Padmaja <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Kuchanur <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Parvathi (2010) Sreeparvathy <i>et al.</i> (2010) Prasad <i>et al.</i> (2011) Ghosh and Sharma (2012) Sravan <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Idris and Mohamed (2013) Paikhomba <i>et al.</i> (2014) Neha <i>et al.</i> (2014) Balakrisna <i>et al.</i> (2015a) Tejaswini (2016)
2.	Days to maturity	High	High	Prasad <i>et al.</i> (2011) Neha <i>et al.</i> (2014)
		Low	Low	Chaudhary and Motiramani (2003)

Table 2.1 (cont.)

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
				Naik (2004) Souroush <i>et al.</i> (2004) Tejaswini (2016)
3.	Productive tillers per plant	High	High	Souroush <i>et al.</i> (2004) Vaithiyalingan and Nadarajan (2006) Karim <i>et al.</i> (2007) Nayudu <i>et al.</i> (2007) Panwar and Ali (2007) Sarkar <i>et al.</i> (2007) Singh <i>et al.</i> (2007) Kole <i>et al.</i> (2008) Kumar and Ramesh (2008) Padmaja <i>et al.</i> (2008) Roy <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Babu <i>et al.</i> (2011) Lal and Chauhan (2011) Prasad <i>et al.</i> (2011) Selvaraj <i>et al.</i> (2011) Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Bornare <i>et al.</i> (2014)
		Moderate	High	Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Singh <i>et al.</i> (2006) Vijayalakshmi <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Balakrisna <i>et al.</i> (2015a)
		Low	Moderate	Karthikeyan <i>et al.</i> (2007) Kuchanur <i>et al.</i> (2009)
4.	Plant height (cm)	High	High	Karad and Pol (2008) Padmaja <i>et al.</i> (2008) Lal and Chauhan (2011) Selvaraj <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Bornare <i>et al.</i> (2014)

Table 2.1 (cont.)

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
				Neha <i>et al.</i> (2014) Tejaswini (2016)
		Moderate	High	Kumar and Ramesh (2008) Balakrisna <i>et al.</i> (2015a)
		Moderate	Moderate	Nagajyothi (2001) Patil <i>et al.</i> (2003) Mishra and Pravin (2004) Naik (2004) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Jaiswal <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Sharma and Sharma (2007) Krishna <i>et al.</i> (2008) Vijayalakshmi <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Parvathi <i>et al.</i> (2011) Prasad <i>et al.</i> (2011) Ghosh and Sharma (2012) Sateeshkumar and Saravanan (2012) Sravan <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Idris and Mohamed (2013) Sharma and Koutu (2013) Krishnaveni and Niveditha (2014)
		Low	Low	Ogunbayo <i>et al.</i> (2014)
5.	Panicle length (cm)	High	High	Chaudhary <i>et al.</i> (2004) Nayudu <i>et al.</i> (2007)
		Moderate	Moderate	Naik (2004) Hasib (2005) Devi <i>et al.</i> (2006) Sharma and Sharma (2007) Vijayalakshmi <i>et al.</i> (2008) Saidaiah <i>et al.</i> (2010) Prasad <i>et al.</i> (2011) Gangashetty <i>et al.</i> (2013)

Table 2.1 (cont.)

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
				Idris and Mohamed (2013)
		Low	Low	Tejaswini (2016)
		Low	Moderate	Chaudhrary and Motiramani (2003) Patil <i>et al.</i> (2003) Vaithiyalingan and Nadarajan (2006) Chandra <i>et al.</i> (2009) Parvathi <i>et al.</i> (2011) Ghosh and Sharma (2012)
		Low	Low	Bhavana (2003) Singh <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Manna <i>et al.</i> (2006) Karthikeyan <i>et al.</i> (2007) Singh <i>et al.</i> (2007) Kole <i>et al.</i> (2008) Krishna <i>et al.</i> (2008) Padmaja <i>et al.</i> (2008) Prasad <i>et al.</i> (2009) Laxuman <i>et al.</i> (2011) Sravan <i>et al.</i> (2012) Paikhomba <i>et al.</i> (2014) Balakrisna <i>et al.</i> (2015a)
6.	Grains per panicle	High	High	Hossain and Hossain (2001) Nagajyothi (2001) Chaudhrary and Motiramani (2003) Patil <i>et al.</i> (2003) Chaudhary <i>et al.</i> (2004) Mishra and Pravin (2004) Naik (2004) Borkakati <i>et al.</i> (2005) Hasib (2005) Devi <i>et al.</i> (2006) Kumar <i>et al.</i> (2006) Karim <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Panwar and Ali (2007) Krishna <i>et al.</i> (2008) Padmaja <i>et al.</i> (2008) Chandra <i>et al.</i> (2009)

Table 2.1 (cont.)

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
				Prasad <i>et al.</i> (2009) Parvathi <i>et al.</i> (2011) Seyoum <i>et al.</i> (2012) Gangashetty <i>et al.</i> (2013) Dhurai <i>et al.</i> (2014)
		High	Moderate	Borkakati <i>et al.</i> (2005) Panwar (2006)
		Moderate	High	Kuchanur <i>et al.</i> (2009) Laxuman <i>et al.</i> (2011)
		Low	Low	Bhavana (2003)
7.	Test weight (g)	High	High	Nagajyothi (2001) Bhavana (2003) Chaudhray and Motiramani (2003) Patil <i>et al.</i> (2003) Mishra and Pravin (2004) Hasib (2005) Binse <i>et al.</i> (2006) Gangashetty <i>et al.</i> (2013) Tejaswini (2016)
		Moderate	Moderate	Satish (2000) Naik (2004) Kumar and Bapu (2005) Vaithiyalingan and Nadarajan (2006) Sarkar <i>et al.</i> (2007) Singh <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Sharma and Sharma (2007) Krishna <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Sharma and Koutu (2013)
		Low	Moderate	Vijayalakshmi <i>et al.</i> (2008) Kuchanur <i>et al.</i> (2009)
		Low	Low	Satish (2000) Paikhomba <i>et al.</i> (2014)
8.	Kernel length(mm)	Low	Low	Krishnaveni and Niveditha (2014) Venkanna <i>et al.</i> (2014) Tejaswini (2016)
9.	Kernel breadth (mm)	Moderate	Low	Tejaswini (2016)

Table 2.1 (cont.)

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
		Low	Low	Krishnaveni and Niveditha (2014) Venkanna <i>et al.</i> (2014)
10.	L/B ratio	High	High	Chaudhary <i>et al.</i> (2004) Saxena <i>et al.</i> (2005) Lal and Chauhan (2011)
		Moderate	Moderate	Sarkar <i>et al.</i> (2007) Rajeswari <i>et al.</i> (2010) Sateeshkumar and Saravanan (2012) Bekele <i>et al.</i> (2013) Shejul <i>et al.</i> (2013) Tejaswini (2016)
		Low	Low	Krishnaveni and Sobharani (2006) Krishnaveni and Niveditha (2014)
11.	Grain yield per plant (g)	High	High	Hossain and Hossain (2001) Chaudhary and Motiramani (2003) Patil <i>et al.</i> (2003) Chaudhary <i>et al.</i> (2004) Mishra and Pravin (2004) Borkakati <i>et al.</i> (2005) Saxena <i>et al.</i> (2005) Singh <i>et al.</i> (2005) Binse <i>et al.</i> (2006) Devi <i>et al.</i> (2006) Kumar <i>et al.</i> (2006) Jaiswal <i>et al.</i> (2007) Karim <i>et al.</i> (2007) Karthikeyan <i>et al.</i> (2007) Nayudu <i>et al.</i> (2007) Panwar and Ali (2007) Sarkar <i>et al.</i> (2007) Sharma and Sharma (2007) Krishna <i>et al.</i> (2008) Padmaja <i>et al.</i> (2008) Roy <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Prasad <i>et al.</i> (2009) Sreeparvathy <i>et al.</i> (2010)

Table 2.1 (cont.)

S.No.	Character	Coefficient of variation		Reference
		GCV	PCV	
				Lal and Chauhan (2011) Parvathi <i>et al.</i> (2011) Prasad <i>et al.</i> (2011) Selvaraj <i>et al.</i> (2011) Singh <i>et al.</i> (2011) Verma <i>et al.</i> (2011) Bhadru <i>et al.</i> (2012) Idris <i>et al.</i> (2012) Seyoum <i>et al.</i> (2012) Bekele <i>et al.</i> (2013) Gangashetty <i>et al.</i> (2013) Idris and Mohamed (2013) Bornare <i>et al.</i> (2014) Dhurai <i>et al.</i> (2014) Tejaswini (2016)
		Moderate	Moderate	Satish (2000) Bhavana (2003) Kumar <i>et al.</i> (2006) Kole <i>et al.</i> (2008) Chandra <i>et al.</i> (2009) Saidaiah <i>et al.</i> (2010) Paikhomba <i>et al.</i> (2014)
		Moderate	High	Nagajyothi (2001) Borkakati <i>et al.</i> (2005) Manna <i>et al.</i> (2006) Panwar (2006) Kumar and Ramesh (2008) Laxuman <i>et al.</i> (2011)

PCV: Phenotypic coefficient of variation

GCV: Genotypic coefficient of variation