ABSTRACT

Name of the Author	**:**	**HARIKRISHNAN.P.J**
Title of the Thesis	**:**	**SCREENING OF ELITE PARENTAL LINES FOR PROVEN *Rf* GENES AND IDENTIFICATION OF HETEROTIC HYBRIDS IN RICE**
Degree to which it is submitted	**:**	**Master of Science in Agriculture**
Faculty	**:**	**Agriculture**
Major field of study	**:**	**GENETICS AND PLANT BREEDING**
Major Advisor	**:**	**Dr. P.V. SATYANARAYANA**
University	**:**	**Acharya N.G. Ranga Agricultural University**
Year of Submission	**:**	**2013**

In the present investigation, elite restorer lines were screened for the presence of proven *Rf* genes and the identified restorers were evaluated for their *per se* performance in different hybrid combinations and promising hybrids were identified.

During *kharif*, 2012, fifty-five restorers and 2 CMS lines (WA type) developed at Maruteru were evaluated for variability, genetic parameters and genetic divergence for nine yield and yield component traits at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, West Godavari district, Andhra Pradesh. DNA was isolated from the leaf tissues collected from parental lines at tillering stage and screened for the presence of proven *Rf* genes using published SSR markers and molecular cluster analysis was performed. The 55 restorers were then crossed with two CMS lines in a line x tester design and the hybrids obtained were evaluated during *rabi,* 2012-13.

The analysis of variance of parental lines revealed significant differences among the genotypes for all the nine characters studied. Genetic variability studies revealed high variability for the character, no. of filled grains panicle^{-1}. High heritability coupled with high genetic advance was observed in case of ear bearing tillers plant^{-1}, number of filled grains panicle^{-1}, test weight and grain yield plant^{-1} suggesting the role of additive gene action in the inheritance of these traits.

The estimation of genetic divergence employing both Mahalanobis D^2 statistic and molecular cluster analysis revealed the existence of considerable genetic diversity among the parental lines studied.

High genetic variability was observed in the hybrids for number of filled grains per panicle, spikelet fertility and grain yield per plant. High heritability coupled with high genetic advance was observed in case of ear bearing tillers per plant, number of filled grains panicle^{-1}, spikelet fertility, test weight and grain yield plant^{-1} suggesting the

role of additive gene action in the inheritance of these traits and directional selection could be profitably applied on these traits.

The analysis of variance for combining ability showed significance of crosses for all the characters under study. The variance due to lines was significant for all the characters studied whereas testers showed significance for all the characters except plant height, number of grains per panicle and spikelet fertility. All the traits showed significance for line × tester interaction. The SCA variances were higher than GCA variances for all the characters indicating the predominance of non-additive gene action.

Among lines, TCNP 23 and RP 13 and APMS 6A in testers were identified as good general combiners for grain yield plant^{-1}, based on *gca* effects.

Based on overall performance, the hybrids TC 11 (APMS 6A × RP 13), TC 7 (APMS 6A × RP 5), TC 1(APMS 6A × RP 2), TC 34 (APMS 10A × TCNP 23), TC 20 (APMS 10A × RP 18) and TC 69 (APMS 6A × TCNP 29) were identified as promising heterotic hybrids for grain yield per plant over higher yielding check, MTU 1121.

These hybrids may be further evaluated for grain quality traits and also for their stability by testing over more number of environments in different seasons before being commercially exploited.

Twenty three restorers were identified as best ones based on spikelet fertility of the hybrids. Four and five primers were found to distinguish the restorer checks (Swarna and BPT 5204) and CMS lines for *Rf3* and *Rf4* genes respectively. Leaving a few exceptions, all the identified restorers showed similar banding pattern with the restorer checks indicating the presence of *Rf3* and *Rf4* genes in those restorers.

The identified test crosses with good restoration ability may be evaluated in F_2 generation for further confirmation of the presence of *Rf* genes.

DECLARATION

I**, Mr. HARIKRISHNAN P.J** hereby declare that the thesis entitled "**SCREENING OF ELITE PARENTAL LINES FOR PROVEN *Rf* GENES AND IDENTIFICATION OF HETEROTIC HYBRIDS IN RICE"** submitted to the **Acharya N.G. Ranga Agricultural University** for the degree of **Master of Science** in the major field of **Genetics and Plant Breeding** 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: **(HARIKRISHNAN. P.J)**

Date: **I.D. No. BAM-11-17**

CERTIFICATE

This is to certify that thesis entitled **"SCREENING OF ELITE PARENTAL LINES FOR PROVEN *Rf* GENES AND IDENTIFICATION OF HETEROTIC HYBRIDS IN RICE** " submitted in partial fulfilment of the requirements for the degree of **'Master of Science in Agriculture'** of the Acharya N. G. Ranga Agricultural University, Hyderabad is a record of the bonafide original research work carried out by **Mr. HARIKRISHNAN. P. J** 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.

(P. V. SATYANARAYANA)
Chairman of the Advisory Committee

Thesis approved by the student's advisory committee

Chairman : **Dr. P. V. SATYANARAYANA** _____
Principal Scientist (PB)
APRRI & RARS, Maruteru

Member : **Dr. LAL AHAMED M.** _____
Assistant Professor
Department of Genetics & Plant Breeding,
Agricultural College, Bapatla

Member : **Dr. B. N. V. S. R. RAVI KUMAR** _____
Scientist (PB)
APRRI & RARS, Maruteru

Member : **Dr.V. SRINIVASA RAO** _____
Associate Professor & Head
Department of Statistics & Mathematics
Agricultural College, Bapatla

Date of final viva-voce:

CERTIFICATE

Mr. HARIKRISHNAN. P.J has satisfactorily prosecuted the course of research and that the thesis entitled **"SCREENING OF ELITE PARENTAL LINES FOR PROVEN *Rf* GENES AND IDENTIFICATION OF HETEROTIC HYBRIDS IN RICE "** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him for a degree of any university.

Date:

(P.V. SATYANARAYANA)

Chairperson
Principal Scientist
APRRI & RARS, Maruteru

LIST OF TABLES

4.10	Estimates of genetic components of variance and proportional contribution of lines, testers and line x tester interaction to total variance for different characters in rice (*Oryza sativa* L.).	
4.11	General combining ability effects of parental lines for yield and yield component characters in rice (*Oryza sativa* L.) during *rabi*, 2012-13.	
4.12	Specific combining ability effects of hybrids for yield and yield component characters during *rabi*, 2012-13.	
4.13	Standard heterosis of hybrids for yield and yield component characters during *rabi*, 2012-13.	
4.14	Superior hybrids identified character wise based on *per se* performance, *sca* effects and standard heterosis	
4.15	Molecular clustering pattern among the 57 parental lines, 2 maintainers and 2 checks in rice (*Oryza sativa* L.).	
4.16	List of primers polymorphic for *Rf3* and *Rf4* genes.	
4.17	Best restorers and spikelet fertility of corresponding hybrids.	

LIST OF PLATES

LIST OF FIGURES

LIST OF CONTENTS

LIST OF APPENDICES

LIST OF SYMBOLS AND ABBREVIATIONS

A.M	:	Before noon
ANOVA	:	Analysis of variance
APRRI	:	Andhra Pradesh Rice Research Institute
^{0}C	:	Degree centigrade
CD	:	Critical difference
cm	:	Centimeter
CMS	:	Cytoplasmic male sterility
CV	:	Coefficient of variation
df	:	Degrees of freedom
et al.	:	and coworkers
F_1	:	First filial generation of a cross
Fig	:	Figure
g	:	Grams
GAM	:	Genetic advance as per cent of mean
GCV	:	Genotypic coefficient of variation
gca	:	General combining ability
ha	:	Hectare
h^2 (bs)	:	Heritability in broad sense
II	:	Indica/Indica
kg	:	Kilogram
kg ha $^{-1}$	:	Kilogram per hectare
L x T	:	Line x Tester
MSS	:	Mean sum of squares
mha	:	Million hectare
min	:	Minutes

mm	:	Milli meter
ml	:	Milli litre
mt	:	Million tonnes
No.of	:	Number of
PCV	:	Phenotypic coefficient of variation
Per se	:	As such with mean
RARS	:	Regional Agricultural Research Station
RBD	:	Randomized block design
sca	:	Specific combining ability
SEm	:	Standard error of mean
t/ha	:	Tonnes per hectare
%	:	per cent
viz.,	:	Namely
WA	:	Wild abortive
$\overline{X}$	:	Grand mean
/	:	Per

ACKNOWLEDGEMENTS

In everyone's life, the day arises when one has to shape ones feelings in words. Though only my name appears on the cover of this thesis, a great many people have contributed to its production. I owe my gratitude to all those people who have made this thesis possible and because of whom my post graduate experience has been one that I will cherish forever.

I feel a great pleasure in expressing my whole hearted sense of gratitude to ***Dr. P. V. Satyanarayana****, Chairman of Advisory Committee, Principal Scientist, Plant Breeding, APRRI and RARS Maruteru for his scholastic guidance, unceasing interest, valuable knowledge, technical advice, patient audience, scientific view, amiable dealing, providing each and every facility, warm affection and mental support, without whom it would have been impossible to complete the research project. I could not have imagined having a better advisor and mentor for my research work.*

My deepest admiration and heartfelt thanks to ***Dr. Lal Ahamed. M****, Member of Advisory Committee, Assistant Professor, Department of Genetics and Plant Breeding, Agricultural College, Bapatla for his sustained interest, caring nature, immense help, constant inspiration and fruitful advice and co-operation throughout my P.G programme.*

I express my profound sense of reverence to ***Dr. B. N. S.V. R. Ravi Kumar****, Member of Advisory Committee, Scientist, Plant Breeding, APRRI and RARS, Maruteru for his constant guidance, support, motivation , good counsel and untiring help during the course of my research work. His guidance has served me well and I owe him my heartfelt appreciation.*

Iam also grateful to ***Dr. V. Srinivasa Rao****, Member of Advisory Committee, Associate Professor, Department of Statistics and Mathematics, Agricultural College, Bapatla for his guidance and support during the course of this work.*

Iam very much grateful to ***Dr. J. S. V. SambaMurthy,*** *Professor and Head, Department of Genetics and Plant Breeding for his fruitful counsel, guidance, motivation and support during the course of my P.G programme.*

Iam very much indebted to my Professors, ***Dr. P.V Rama Kumar*** *and* ***Dr. V. Satyanarayana Rao*** *and Assistant Professor,* ***Dr. D. Ratna Babu****, Department of Genetics and Plant breeding, Agricultural College, Bapatla for their cooperation and help during the P.G. Programme.*

I take this opportunity to express my sincere gratitude to ***Dr. Bharatha Lakshmi****, Associate Director of Research, APPRI and RARS, Maruteru for giving me permission to work in the Molecular Biology lab of the esteemed institute.*

Its my privilege to extend heartfelt thanks to all the scientists at APRRI and RARS Maruteru, ***Dr. Y. Suryanarayana (P.S Rice) , Dr. N. Chamundeshwari, Smt. M.Girija Rani,***

Dr. P. V Ramana Rao and Dr.Vishnuvardhan *and all other staff working there, for their constant help and needy inspiration in carrying out the entire research work smoothly.*

It is my pleasure to acknowledge all the SRFs and Technical Assistants at APRRI and RARS Maruteru, specially ***Prasad, Karteek, Ramakrishna, Neeraja, Kumari, Manasa, Kondayya, Ganga, Venkat and Shiva*** *for their enormous support and providing a good atmosphere in the lab. I will always be grateful to them for patiently clearing my doubts and helping me to develop a scientific approach and attitude.*

A truly outstanding quality of 'Hybrid Rice' division of APRRI, Maruteru is its dedicated and experienced field staff; without them I would have been lost. Iam very much grateful to ***Sarojini, Satyaveni, Suryakantham, Varalaxmi, Thayaru*** *and all the remaining labourers for their crucial assistance during my research work.*

Most importantly, none of this would have been possible without the unflagging love, support and patience of my family. I would like to express my heart-felt gratitude to my parents, ***Sri. Premachandra kumar*** *and* ***Smt. Jayakumary*** *and my beloved sister* ***Krishnapriya*** *who have been a constant source of love, concern, support and strength all these years. Iam very much indebted to them, specially my mom for believing in me and the decisions I made and for bearing my long absence from home during my studies.*

Many seniors, friends and juniors aided me a lot during this tenure. Their support and care helped me overcome setbacks and stay focused on my work. I use this opportunity to thank my seniors, ***Balu, Padmavathi, Jhansi, Udayabhanu, Basavaraj and Venketesh*** *., classmates,* ***Dhanu, Nishit, Anu, Anitha, Rajitha, Bhargavi and Sreelekshmi*** *., juniors,* ***Patil, Vinay, Raj, Lohith, Ravi and Muthu*** *and special friend* ***Prakasham*** *for everything they have done for me. I greatly value their friendship and I deeply appreciate their belief in me.*

I humbly thank the authorities of Acharya N.G. Ranga Agricultural University, Government of Andhra Pradesh for availing me the opportunity to do my PG in this prestigious institution.

Last but not the least, I thank ***Almighty*** *for blessing, protecting and guiding me throughout this period.*

For any errors or inadequacies that may remain in this work, of course, the responsibility is entirely my own.

Date: *(HARIKRISHNAN.P.J)*

Place: Bapatla

Chapter - I

INTRODUCTION

Rice *(Oryza sativa L.)* is the primary source of food for more than half of the world's population. Globally, it is cultivated in an area of about 154 million hectares with an annual production of 600 million tonnes. China (202.67 mt) ranked first in production of rice followed by India (155.70 mt), Indonesia (65.74 mt), Bangladesh (50.63 mt) and Vietnam (42.33 mt), in 2011.

Rice is the most important cereal food crop of our country, and occupies about 24 per cent of gross cropped area of the country. In India it is cultivated in an area of 44.10 mha with a production of 95.32 mt in 2010. West Bengal (18.73 mt) ranked first in production of rice followed by Uttar Pradesh (14.02 mt), Andhra Pradesh (12.90 mt), Punjab (10.54 mt) and Tamil Nadu (8.20 mt), in 2011-12.

Production of rice in India has increased during last 60 years by about 3.5 times from 25.03 million tonnes during the first five year plan period to 85.73 million tonnes (milled rice) during the tenth five year plan period. The average productivity of rice in India, at present, is 2.2 tonnes/ ha, which is far below the global average of 2.7 tonnes/ ha. At the current rate of population growth of 1.58% in India, the requirement of rice by 2025 is estimated to be around 140.7 million tonnes (http://worldfood.apionet.or.jp). To make India self sufficient in rice, it is needed to improve the productivity to a greater extent (Hossain, 1996; Mishra, 2002). The task is quite challenging and the options available are very limited.

Exploitation of hybrid vigour is one of the readily available alternatives to boost up the rice yield potential. In India research on hybrid rice was initiated way back in late 70s and early 80s owing to success of this technology in China (Ilyas Ahamed, 2006). India is the second country which has commercially exploited heterosis in rice with the release of hybrid varieties having an yield advantage of 1-1.5 t/ha over the existing high yielding varieties. The hybrid rice research initiated in India has resulted in the development and release of 53 rice hybrids so far including 21 hybrids from private research organizations. Presently hybrid rice covers an area of 2 million hectares in our country. Keeping in view the advantage of this technology a major project on hybrid rice was initiated under National Agricultural Technology Project in 1989.

In the initial years, the entire research program was highly dependent on the parental lines imported from other countries, basically from Phillipines. The three line breeding approach involving a A line-cytoplasmic male sterile (CMS) line, B line-maintainer line and R line - fertility restorer line for the development of rice hybrids, first standardized in China, has led to significant yield improvement by 20-30% over the high yielding pureline varieties.

The commercial use of cytoplasmic genic male sterility is possible only when effective restorers are identified. The identification of restorers for different cytoplasmic male sterile sources will increase cytoplasmic diversification and will help in the development of hybrids with greater adaptability and reduced vulnerability to different pests and diseases, which otherwise may arise due to genetic uniformity resulting from large scale cultivation of hybrids based on only a few CMS lines. Strong restoring ability in hybrids also results in realizing high yield by virtue of higher spikelet fertility in the hybrids.

The process of screening for the trait of fertility restoration is laborious and time consuming as it involves test crossing with a set of CMS lines and evaluation of F1 for pollen and spikelet fertility. The use of molecular markers linked to fertility restoring *Rf* genes can enhance the selection efficiency, save time and avoid the complications associated with phenotype-based screening. The fertility restorer genes *Rf-3* and *Rf-4* for WA-type CMS have been mapped on chromosome 1 and 10, respectively (Yao *et al*., 1997).

DNA based markers are increasingly being recognized as useful tools for various applications in plant breeding; since they are not influenced by the environment (Lee, 1995). DNA markers detect genetic variation among genotypes and are useful as landmarks to tag functional genes. RAPD are dominant markers, while RFLP and AFLP are difficult to perform. Therefore, Simple Sequence Repeat (SSR) markers are a better choice as they are abundant, easy to detect and codominant.

SSRs are tandem repeats of di, tri or a higher number of nucleotide sequence motifs flanked by unique sequences in the DNA of plants. SSRs are abundantly distributed throughout the nuclear genome of all plant species, which make them useful for both genetic mapping and for characterization of cultivars or populations. They generally display higher levels of polymorphism (Beckmann and Soller, 1990 and Senor *et al*., 1998) and are amenable to automated genotyping strategies. They can be

amplified by PCR and efficiently detect DNA polymorphism (Pejic *et al*., 1998). SSR marker technology has been developed and used for genome mapping and DNA fingerprinting in different plant species including rice (Wu and Tanksley, 1993).

The present study was undertaken with an aim to screen the elite parental lines developed at APRRI and RARS, Maruteru for proven *Rf* genes and for the identification of heterotic hybrids with the following objectives.

1) To study the presence of major fertility restoration genes in elite parental lines.
2) To validate the identified restorers for their *per se* performance in different hybrid combinations.
3) To identify promising heterotic hybrids

Chapter - II

REVIEW OF LITERATURE

The present investigation in rice was undertaken to study the extent of variability, heritability and genetic advance, to estimate the combining ability effects, to determine the genetic divergence among parental lines, to estimate the heterosis of hybrids and to screen the parental lines for proven *Rf* genes. The literature available on the main objectives of the present study has been comprehensively reviewed under the following headings.

2.1 Variability

2.2 Heritability and genetic advance

2.3 Genetic divergence

2.4 Combining ability

2.5 Heterosis

2.6 Screening for *Rf* genes

2.1 VARIABILITY

Improvement in any crop species depends upon the amount of variation present in a given population. The variability expressed by a genotype can be partitioned into genotypic and phenotypic components. The genotypic component being the heritable part of the total variability, its magnitude for yield and its component characters influences the selection strategies to be adopted by the breeders.

The character wise chronological report of review of literature on phenotypic coefficient of variability and genotypic coefficient of variability is presented in the table 2.1.

2.2 HERITABILITY AND GENETIC ADVANCE

Heritability (h^2) measures the relative amount of the heritable portion of variability, while the genetic advance (GA) helps to measure the amount of progress that could be expected with selection in a character.

The review of literature on heritability and genetic advance is presented character wise in the table 2.2

Table 2.1. Review of literature on phenotypic coefficient of variance and genotypic coefficient of variance in rice (*Oryza sativa* L.)

S.No.	Character	Variability	Reference
1.	Days to 50% flowering	High PCV, GCV	Sharma and Sharma (2007) Seyoum *et al*. (2012)
		Moderate PCV, GCV	Jaiswal *et al.* (2007) Vijayalakshmi *et al* .(2008) Mohan Lal and Chauhan (2011)
		Low PCV, GCV	Sobita Devi *et al.* (2006) Rita Binse *et al.* (2006) Vaithiyalingan and Nadarajan (2006) Mamta Singh *et al.* (2007) Krishna *et al.* (2008) Kole *et al.* (2008) Padmaja *et al.* (2008) Prasad *et al.* (2009) Satish Chandra *et al.* (2009) Kuchanur *et al.* (2009) Rita Bisne *et al.* (2009) Siva Parvathy *et al*. (2011) Shiva Prasad *et al*. (2011)
2.	Plant height (cm)	High PCV, GCV	Karad and Pol (2008) Padmaja *et al.* (2008) Mohan Lal and Chauhan (2011) Selvaraj *et al.* (2011) Bhadru *et al.* (2012) Seyoum *et al*. (2012)
		Moderate to High PCV, GCV	Kumar and Ramesh (2008)
		Moderate GCV, PCV	Sobita Devi *et al.* (2006) Rita Binse *et al.* (2006) Karthikeyan *et al.* (2007) Sharma and Sharma (2007) Jaiswal *et al* .(2007) Krishna *et al.* (2008) Vijayalakshmi *et al.* (2008) Satish Chandra *et al.* (2009) Prasad *et al.* (2009) Rita Binse *et al.* (2009) Saidaiah *et al*. (2010b)
		Low PCV, GCV	Monalisa Manna *et al. (*2006) Vaithiyalingan and Nadarajan (2006) Mamta Singh *et al.* (2007) Kole *et al.* (2008) Kuchanur *et al.* (2009)

Table 2.1 (Contd…)

3.	No: of ear bearing tillers per plant	High PCV, GCV	Sarkar *et al.* (2005) Vaithiyalingan and Nadarajan (2006) Mamta Singh *et al.* (2007) Nayudu *et al.* (2007) Kole *et al.* (2008) Padmaja *et al.* (2008) Roy *et al.* (2008) Prasad *et al.* (2009) Mohan Lal and Chauhan (2011) Selvaraj *et al.* (2011) Singh *et al.* (2011) Shiva Prasad *et al*. (2011) Seyoum *et al*. (2012)
		High PCV, Moderate GCV	Sobita Devi *et al.* (2006) Rita Binse *et al.* (2006) Singh *et al.* (2006) Vijayalakshmi *et al.* (2008) Satish Chandra *et al.* (2009) Saidaiah *et al.(*2010b)
		Moderate PCV, GCV	Singh *et al*. (2005) Monalisa Manna *et al*. (2006) Karthikeyan *et al.* (2007) Krishna *et al*. (2008) Rita Binse *et al.* (2009) Saidaiah *et al.* (2010b) Siva Parvathi *et al.* (2011) Shiva Prasad *et al*. (2011)
		Moderate PCV, Low GCV	Karthikeyan *et al.* (2007) Kuchanur *et al*. (2009)
4.	Days to maturity	High PCV, GCV	Shiva Prasad *et al*. (2011)
		Low GCV, PCV	Karim *et al.* (2007) Kumar and Ramesh (2008)
5.	Panicle length	High PCV, GCV	Nayudu *et al.* (2007)
		Moderate PCV, GCV	Hasib (2005) Sobita Devi *et al.* (2006) Sharma and Sharma (2007) Vijayalakshmi *et al.* (2008) Saidaiah *et al*. (2010b) Shiva Prasad *et al*. (2011)
		Moderate PCV low GCV	Vaithiyalingan and Nadarajan (2006) Satish Chandra *et al.*(2009) Siva Parvathi *et al.* (2011)
		Low PCV, GCV	Singh *et al.* (2005) Monalisa Manna *et al.* (2006) Rita Binse *et al.* (2006) Mamta Singh *et al.* (2007) Karthikeyan *et al.* (2007) Krishna *et al.* (2008) Kole *et al.* (2008)

Table 2.1 (Contd…)

			Padmaja *et al.* (2008) Prasad *et al.* (2009) Rita Binse *et al.* (2009)
6.	Number of filled grains per panicle	High PCV, GCV	Borkakati *et al*. (2005) Hasib (2005) Sobita Devi *et al.*(2006) Karim *et al.* (2007) Karthikeyan *et al.* (2007) Kumar *et al.* (2007) Krishna *et al.* (2008) Padmaja *et al.* (2008) Prasad *et al.* (2009) Rita Binse *et al.* (2009) Satish Chandra *et al.* (2009) Saidaiah *et al.* (2010b) Siva Parvathi *et al.* (2011) Seyoum *et al*. (2012)
		High PCV, Moderate GCV	Kuchanur *et al.* (2009)
		Moderate to high PCV, GCV	Panwar (2005)
		Moderate PCV, GCV	Singh *et al.* (2005) Monalisa Manna *et al.* (2006)
		Low PCV, GCV	Bhavana (2003)
7.	Spikelet fertility	Low PCV, GCV	Kole *et al.* (2008) Saidaiah *et al.* (2010b) Sravan *et al.*(2012)
8.	Test Weight	High GCV, PCV	Hasib (2005) Rita Binse *et al.*(2006) Karim *et al.* (2007) Nayudu *et al.* (2007) Karad and Pol (2008) Satish Chandra *et al.* (2009) Rita Binse *et al.* (2009) Bhadru *et al.* (2012)
		Moderate PCV, GCV	Vaithiyalingan and Nadarajan (2006) Mamta Singh *et al*. (2007) Sarkar *et al*. (2007) Sharma and Sharma (2007) Karthikeyan *et al. (*2007) Krishna *et al*. (2008) Satish Chandra *et al*. (2009) Saidaiah *et al.* (2010b) Mohan Lal and Chauhan (2011) Shiva Prasad *et al*. (2011)
		Moderate PCV Low GCV	Vijayalakshmi *et al.* (2008) Kuchanur *et al.* (2009)

Table 2.1 (Contd…)

		Low GCV, PCV	Kole *et al.* (2008)
9	Grain yield/plant	High PCV, GCV	Sarkar *et al.* (2005) Saxena *et al.* (2005) Rita Binse *et al.* (2006) Singh *et al.* (2006) Sobita Devi *et al.* (2006) Jaiswal *et al* .(2007) Karim *et al.* (2007) Karthikeyan *et al.* (2007) Kumar *et al.* (2007) Mamta Singh *et al.* (2007) Nayudu *et al.* (2007) Sharma and Sharma (2007) Roy *et al.* (2008) Padmaja *et al.* (2008) Krishna *et al.* (2008) Prasad *et al.* (2009) Sreeparvathy *et al.* (2010) Selvaraj *et al.* (2011) Singh *et al.* (2011) Idris *et al.* (2012) Bhadru *et al.* (2012) Seyoum *et al.* (2012)
		High PCV Moderate GCV	Monalisa Manna *et al.* (2006)
		Moderate to High GCV, PCV	Borkakati *et al.* (2005) Kumar and Ramesh (2008) Panwar (2005)
		Moderate GCV, PCV	Kumar *et al.* (2007) Kole *et al.* (2008) Satish Chandra *et al.* (2009)

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

S.No.	Character	Heritability	Genetic advance as % of mean	Reference
1.	Days to 50% flowering	High	High	Sharma and Sharma (2007) Bharadwaj *et al.* (2007) Vijayalakshmi *et al.* (2008) Mohan Lal and Chauhan (2011) Shiva Prasad *et al*. (2011) Singh *et al.* (2011)
		High to Moderate	High to Moderate	Seyoum *et al*. (2012)
		High	Moderate	Uttam Chand and Vijay Kumar (2005) Rita Binse *et al.* (2006) Sobita Devi *et al.* (2006) Vaithiyalingan and Nadarajan (2006) Mamta Singh *et al.* (2007) Padmaja *et al.* (2008) Rita Binse *et al.* (2009) Satish Chandra *et al.* (2009) Prasad *et al.* (2009) Kuchanur *et al.* (2009) Saidaiah *et al*. (2010b) Siva Parvathi *et al.* (2011)
		High	Low	Sreeparvathy *et al*. (2010) Osman *et al.* (2012)
2.	Plant height	High	High	Elayaraja *et al.* (2005) Singh *et al* .(2005) Rita Binse *et al*. (2006) Singh *et al*. (2006) Sobita Devi *et al*. (2006) Bharadwaj *et al.* (2007) Karthikeyan *et al.* (2007) Sharma and Sharma (2007) Karad and Pol (2008) Kumar and Ramesh (2008) Padmaja *et al.* (2008) Vijayalakshmi *et al.* (2008) Prasad *et al.* (2009) Satish Chandra *et al.*(2009) Saidaiah *et al*. (2010b) Shiva Prasad *et al*. (2011) Siva Parvathi *et al.* (2011) Bhadru *et al.* (2012)
		High to Moderate	High to Moderate	Seyoum *et al*. (2012)
		High	Moderate	Uttam Chand and Vijay Kumar

Table 2.2 (Contd…)

				(2005) Vaithiyalingan and Nadarajan (2006) Mamta Singh *et al.* (2007)
		High	Low	Singh *et al.* (2011)
		Moderate	High	Mohan Lal and Chauhan (2011)
		Moderate	Low	Kuchanur *et al.* (2009)
		Low	High	Krishna *et al.* (2008)
		Low	Low	Monalisa Manna *et al.* (2006)
3.	Ear bearing tillers per plant	High	High	Singh and Singh (2005) Singh *et al.* (2005) Rita Binse *et al.* (2006) Sobita Devi *et al.* (2006) Vaithiyalingan and Nadarajan (2006) Sharma and Sharma (2007) Nayudu *et al.* (2007) Padmaja *et al.* (2008) Vijayalakshmi *et al.*(2008) Anbanandan *et al.*(2009) Satish Chandra *et al.*(2009) Saidaiah *et al*.(2010b) Sreeparvathy *et al.* (2010) Mohan Lal and Chauhan (2011) Singh *et al.* (2011) Siva Parvathi *et al.* (2011)
		High	High to Moderate	Elayaraja *et al*. (2005) Kole *et al.* (2008)
		High to Moderate	High to Moderate	Seyoum *et al*. (2012)
		High	Low	Shiva Prasad *et al*. (2011)
		Moderate	High	Mamta Singh *et al*. (2007) Prasad *et al.* (2009)
		Moderate	Moderate	Monalisa Manna *et al.* (2006) Bharadwaj *et al.* (2007)
		Low	High	Krishna *et al.* (2008)
		Low	Low	Karthikeyan *et al.* (2007) Kuchanur *et al* .(2009)
4.	Days to maturity	High	High	Kumar and Ramesh (2008)
		High	Low	Madhavilatha *et al*. (2005) Karim *et al.* (2007) Singh *et al.* (2011) Osman *et al.* (2012)

Table 2.2 (Contd…)

5.	Panicle length	High	High	Elayaraja *et al.* (2005) Vaithiyalingan and Nadarajan (2006) Bharadwaj *et al.* (2007) Nayudu *et al.* (2007) Sharma and Sharma (2007) Vijayalakshmi *et al.* (2008) Mohan Lal and Chauhan (2011)
		High	Moderate	Singh *et al.* (2005) Rita Binse *et al.* (2006) Sobita Devi *et al.* (2006) Karthikeyan *et al.* (2007) Padmaja *et al.* (2008) Rita Binse *et al.* (2009) Saidaiah *et al*. (2010b)
		High	Low	Mamta Singh *et al.* (2007) Prasad *et al.* (2009) Shiva Prasad *et al*. (2011)
		Moderate	High	Patil *et al.* (2003)
		Moderate	Low	Bhavana (2003)
		Low	High	Mishra and Pravin (2004)
		Low	Moderate	Monalisa Manna *et al.* (2006)
		Low	Low	Krishna *et al*. (2008) Satish Chandra *et al*. (2009)
6.	Number of filled grains per panicle	High	High	Panwar (2005) Singh *et al.* (2005) Rita Binse *et al.* (2006) Sobita Devi *et al.* (2006) Vaithiyalingan and Nadarajan (2006) Karim *et al.* (2007) Karthikeyan *et al.* (2007) Sharma and Sharma (2007) Prasad *et al.* (2009) Kuchanur *et al.* (2009) Saidaiah *et al*. (2010b) Siva Parvathi *et al.* (2011)
		High	High to Moderate	Hossain and Hossain (2001)
		High	Moderate	Monalisa Manna *et al*. (2006)
		High to Moderate	High to Moderate	Seyoum *et al*. (2012)
		High	Low	Bhavana (2003)
		Moderate	High	Bharadwaj *et al.* (2007)
		Low	High	Krishna *et al*. (2008)
7.	Spikelet fertility	High	Moderate	Sravan *et al.*(2012)
		High	Low	Kole *et al.*(2008) Saidaiah *et al.*(2010b)

Table 2.2 (Contd…)

8.	Test weight	High	High	Elayaraja *et al.* (2005) Hasib (2005) Singh and Singh (2005) Rita Binse *et al.* (2006) Vaithiyalingan and Nadarajan (2006) Bharadwaj *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) Satish Chandra *et al*. (2009) Saidaiah *et al*. (2010) Mohan Lal and Chauhan (2011) Shiva Prasad *et al*. (2011) Bhadru *et al.* (2012)
		High	High to Moderate	Hossain and Hossain (2001)
		High to moderate	High to Moderate	Seyoum *et al*. (2012)
		High	Low	Singh *et al.* (2011)
		Moderate	Moderate	Kuchanur *et al.* (2009)
		Moderate	Low	Singh *et al.* (2005)
		Low	High	Krishna *et al.* (2008)
9.	Grain yield per plant	High	High	Madhavilatha *et al*. (2005) Sarkar *et al.* (2005) Singh *et al*. (2005) Panwar (2005) Kumar *et al*. (2006) Monalisa Manna *et al.* (2006) Sobita Devi *et al.* (2006) Rita Binse *et al.* (2006) Nayudu *et al.* (2007) Sharma and Sharma (2007) Karthikeyan *et al.* (2007) Kumar and Ramesh (2008) Padmaja *et al.* (2008) Anbanandan *et al.*(2009) Prasad *et al.*(2009) Rita Binse *et al.* (2009) Sreeparvathy *et al*. (2010) Uma Devi *et al*. (2010) Siva Parvathi *et al.* (2011) Singh *et al.* (2011) Bhadru *et al.* (2012)
		High	High to Moderate	Elayaraja *et al.* (2005) Kole *et al.* (2008)
		High	Moderate	Mohan Lal and Chauhan (2011)

Table 2.2 (Contd…)

		High	Low	Saidaiah *et al*. (2010b) Shiva Prasad *et al*. (2011)
		Moderate	High	Mamta Singh *et al.* (2007) Satish Chandra *et al.* (2009)
		Low to Moderate	Low to Moderate	Bharadwaj *et al.* (2007)
		Low	High	Krishna *et al.* (2008)

2.3 GENETIC DIVERGENCE

The selection of parental lines plays a vital role in developing ideal combinations. The performance and heterosis of hybrids are associated with genetic divergence between their parental lines. Therefore, it is essential to study the relationship and genetic diversity among parental lines in hybrid rice. Plant breeders often select parental lines in combinations with morphological trait and pedigree information. However, this breeding method is less effective and accurate due to environmental effect. Hence, molecular markers have been widely used to study the genetic diversity of breeding materials as they are less influenced by temporal, spatial and environmental conditions.

Duan *et al.*(2002) studied the genetic variation among thirty-five restorer lines of hybrid rice (*Oryza sativa* L.) utilizing twenty-five SSR primer pairs, dispersed on 12 chromosomes in rice. The primers detected 65 alleles among 35 restorer lines of hybrid rice with an average of 2.6 alleles per primer. The result from cluster analysis showed that hybrid rice restorer lines had abundant resource in China, but the genetic diversity was small and this seriously limited the utilization of heterosis for yield improvement.

Wang *et al.* (2006) studied the genetic diversity of 41 parental lines which popularized `commercial hybrid rice production in China using cluster analysis of morphological traits and simple sequence repeat (SSR) markers. Forty-one entries were assigned into two clusters (i.e., early or medium-maturing cluster., medium or late maturing cluster) and further assigned into six sub-clusters based on morphological trait cluster analysis. The SSR cluster analysis classified 41 entries into two groups (i.e., maintainer line group and restorer line group) and seven sub-groups. The maintainer line group consisted of all 19 maintainer lines and two thermosensitive genic male sterile lines while the restorer line group was composed of all 20 restorer lines.

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.* (2011) used a set of morphological traits and SSR markers to determine the genetic relationship among 12 elite thermosensitive genic male sterile (TGMS) lines. Analysis with 30 SSR markers (20 EST-SSRs and 10 genomic SSRs) revealed 27 markers as polymorphic, amplifying a total of 83 alleles. Each SSR marker amplified 2–6 alleles with an average of 2.76 alleles per marker and a PIC value varying from 0.54 to 0.96. Cluster analysis based on SSR and morphological data clearly differentiated the lines according to their source of origin.

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 (thirteen) 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.

Genetic distance analysis of twelve commercial hybrid rice parental lines was carried out by Rajendran *et al.* (2012) using simple sequence repeats (SSR) markers. Out of hundred SSR markers screened, sixty two were found to be polymorphic. A total of 203 alleles were recorded as 0 to 1 data set (presence-1 and absence-0) with an average of 3.2 alleles per loci. NTSYS cluster analysis of genotypic data set distinguished maintainer and restorer groups into two different clusters with the mean genetic distance value of about 22%.

Baluch-Zehi *et al.*(2013) investigated the genetic distance among the parental lines of hybrid rice based on cluster analysis of morphological traits. Sixteen hybrid rice parental lines including 6 restorer lines and 5 CMS lines with their maintainers were grouped into 4 clusters based on cluster analysis.

2.4 COMBINING ABILITY

The ability of a parent to transmit desirable performance to its hybrid progeny is called combining ability. Combining ability helps in the identification of parents with good general and specific combining ability and also to determine the gene action. The concept of combining ability as a measure of gene action was proposed by Sprague and Tatum (1942). They defined general combining ability as an average performance of a strain in a series of hybrid combinations, whereas specific combining ability is the deviation of actual performance of a cross from its expected performance based on the general combining ability of the parents involved. They further reported that general combining ability was primarily due to additive gene effect, while specific combining ability was due to non-additive gene effect.

The review of literature on gene action governing the inheritance of different traits in rice is summarized and presented in Table 2.3.

2.5 HETEROSIS

Shull (1914) coined the term heterosis and it is the phenomenon in which the F_1 of two genetically dissimilar parents show increased or decreased vigour for various characters over the mid parent (relative or mid parent heterosis) or over the better parent (heterobeltiosis) or over the superior check (standard heterosis). Heterotic performance can be used as the measure of nicking ability of any inbred line when crossed with a common tester. The manifestation of heterosis and its utilization as a means of maximizing the yield of agricultural crops has been one of the most important techniques in plant breeding.

Mather and Jinks (1971) proposed the term standard heterosis to denote the expression of hybrid vigour over the best commercial variety. Virmani *et al.* (1981) suggested that there should be at least 20-30% yield advantage for the hybrid varieties over the standard commercial varieties, to offset the cost of hybrid seed production

The literature pertaining to standard heterosis over the superior check in rice is summarized in Table 2.4.

Table 2.3. Review of literature on gene action for yield and yield component characters in rice (*Oryza sativa* L.)

Days to 50 % flowering		
Gene action		
Additive	**Non additive**	**Additive and non-additive**
Rosamma and Vijayakumar (2005)	Panwar (2005)	Manuel and Palanisamy (1989)
Anand Kumar *et al.*(2006)	Jayasudhan and Deepak Sharma (2009)	Ganesan *et al*. (1997)
Gnanasekaran *et al.* (2006)	Kumar Babu *et al.* (2010a)	Gupta *et al*. (1999)
Dalvi and Patel (2009)	Nadali Bagheri and Babaeian (2010)	Honarnejad (1999)
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Sanghera and Hussain (2013)	

Plant Height		
Additive	**Non additive**	**Additive and non-additive**
Anand Kumar *et al.* (2006)	Panwar (2005)	Manuel and Palanisamy (1989)
Gnanasekaran *et al.* (2006)	Singh *et al.* (2005)	Li *et al*. (1998)
Nadali Bagheri and Babaeian (2010)	Dalvi and Patel (2009)	Honarnejad (1999)
	Jayasudhan and Deepak Sharma (2009)	Singh (2002)
	Kumar Babu *et al.* (2010a)	
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Sanghera and Hussain (2013)	

Table 2.3 (cont.)

Number of ear bearing tillers plant $^{-1}$		
Additive	**Non additive**	**Additive and non-additive**
Rosamma and Vijayakumar (2005)	Panwar (2005)	Ganesan *et al*. (1997)
Gnanasekaran *et al.* (2006)	Singh *et al.* (2005)	Li *et al*. (1998)
Dalvi and Patel (2009)	Anand Kumar *et al.* (2006)	Meenakshi and Amirthadevarathinam (1999)
	Jayasudhan and Deepak Sharma (2009)	Sharma *et al.* (2001)
	Kumar Babu *et al.* (2010a)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Sanghera and Hussain (2013)	

Days to Maturity		
Gene action		
Additive	**Non additive**	**Additive and non-additive**
Anand Kumar *et al.*(2006)	Jayasudhan and Deepak Sharma (2009)	Ganesan *et al*. (1997)
Gnanasekaran *et al.* (2006)	Kumar Babu *et al.* (2010a)	Gupta *et al*. (1999)
Dalvi and Patel (2009)	Nadali Bagheri and Babaeian (2010)	Honarnejad (1999)
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Sanghera and Hussain (2013)	

Table 2.3 (cont.)

Panicle length		
Additive	**Non additive**	**Additive and non-additive**
Kalita and Upadhaya (2000)	Panwar (2005)	Manuel and Palanisamy (1989)
	Gnanasekaran *et al.*(2006)	Ganesan *et al*. (1997)
	Dalvi and Patel (2009)	Li *et al*. (1998)
	Jayasudhan and Deepak Sharma (2009)	Honarnejad (1999)
	Kumar Babu *et al*. (2010a)	Sharma *et al*. (2001)
	Saidaiah *et al.* (2010a)	Singh (2002)
	Saidaiah *et al.* (2011)	Anand Kumar *et al.* (2006)
	Sanghera and Hussain (2013)	

Number of filled grains panicle^{-1}		
Additive	**Non additive**	**Additive and non-additive**
Ganesan and Rangaswamy (1998)	Panwar (2005)	Anand Kumar *et al.* (2006)
Rosamma and Vijayakumar (2005)	Gnanasekaran *et al.* (2006)	
	Dalvi and Patel (2009)	
	Kumar Babu *et al.* (2010a)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Sanghera and Hussain (2013)	

Table 2.3 (Contd..)

Spikelet fertility		
Additive	**Non additive**	**Additive and non-additive**
Ganesan and Rangaswamy (1998)	Panwar (2005)	Anand Kumar *et al.* (2006)
Kumar Babu *et al.* (2010a)	Gnanasekaran *et al.* (2006)	
	Dalvi and Patel (2009)	
	Jayasudhan and Deepak Sharma (2009)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Sanghera and Hussain (2013)	

Test weight		
Additive	**Non additive**	**Additive and non-additive**
Rosamma and Vijayakumar (2005)	Panwar (2005)	Manuel and Palanisamy (1989)
Gnanasekaran *et al.* (2006)	Anand Kumar *et al.* (2006)	Ganesan *et al*. (1997)
Gnanamalar and Vivekanandan (2013)	Kumar Babu *et al.* (2010a)	Dwivedi *et al*. (1999)
		Honarnejad (1999)
		Patil *et al.*(2003)

Table 2.3 (Contd..)

Grain yield plant^{-1}		
Additive	**Non additive**	**Additive and non-additive**
	Panwar (2005)	Ganesan *et al*. (1997)
	Rosamma and Vijayakumar (2005)	Sharma *et al.* (2001)
	Singh *et al.* (2005)	
	Anand Kumar *et al.* (2006)	
	Gnanasekaran *et al.* (2006)	
	Dalvi and Patel (2009)	
	Jayasudhan and Deepak Sharma (2009)	
	Kumar Babu *et al.* (2010a)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al.* (2010a)	
	Saidaiah *et al.* (2011)	
	Gnanamalar and Vivekanandan (2013)	
	Sanghera and Hussain (2013)	

Table 2.4.Range of standard heterosis reported for grain yield and yield components in rice (*Oryza sativa* L.)

Character	Range	Reference
Days to 50% flowering	-8.43 to 7.28	Aananthi and Jebaraj (2006)
	-20.19 to -0.39	Pandya and Tripathi (2006)
	-21.00 to 14.00	Singh *et al.* (2006)
	-16.3 to -3.3	Chaudhry *et al.*(2007)
	-2 to 2.67	Eradasappa *et al.* (2007)
	-8.2 to 13.6	Rosamma and Vijayakumar (2007)
	-11.90 to -8.93	Chandirakala *et al.* (2010)
	-21.89 to 14.35	Gouri Shankar *et al.* (2010)
	0 to 20.33	Kumar Babu *et al.* (2010b)
	-16.57 to 12.65	Tiwari *et al.* (2011)
	-25.35 to 28.13	Sen and Singh (2011)
	-7.944 to 14.953	Kumar *et al.*(2012)
Plant height	-21.66 to -4.47	Aananthi and Jebaraj (2006)
	-35.40 to -15.08	Pandya and Tripathi (2006)
	-25.00 to 21.00	Singh *et al.* (2006)
	-5.40 to 69.04	Chaudhry *et al.* (2007)
	-11.20 to 34.40	Rosamma and Vijayakumar (2007)
	-16.32 to -12.60	Chandirakala *et al.* (2010)
	-24.83 to 2.06	Gouri Shankar *et al.* (2010)
	-7.06 to 2.84	Kumar Babu e*t al.* (2010b)
	-8.3 to 79.8	Rahimi *et al.* (2010)
	-16.40 to 0.18	Tiwari *et al.* (2011)
	-7.87 to 23.22	Sen and Singh (2011)
	-22.915 to 35.698	Kumar *et al.* (2012)
Number of ear bearing tillers plant $^{-1}$	-62.11 to 14.60	Aananthi and Jebaraj (2006)
	0.51 to 48.84	Pandya and Tripathi (2006)
	-45.00 to 105.00	Singh *et al.* (2006)
	34.54 to 38.55	Eradasappa *et al.* (2007)
	-18.1 to 131.9	Rosamma and Vijayakumar (2007)

Table 2.4 (Contd..)

	23.55 to 33.22	Chandirakala *et al.* (2010)
	-25.37 to 34.23	Gouri Shankar *et al.* (2010)
	-28.33 to 92.22	Kumar Babu e*t al.* (2010b)
	-38.7 to 13.6	Rahimi *et al.* (2010)
	-8.33 to 75.00	Tiwari *et al* .(2011)
	2.554 to 66.67	Sen and Singh (2011)
	3.922 to 138.552	Kumar *et al.* (2012)
Days to maturity	-24.4 to 7.9	Rahimi *et al.* (2010)
	-19.84 to 21.43	Sen and Singh (2011)
Panicle length	-18.19 to 22.42	Aananthi and Jebaraj (2006)
	0.97 to 34.31	Pandya and Tripathi (2006)
	-24.00 to 19.00	Singh *et al.* (2006)
	38.92 to 40.37	Eradasappa *et al.* (2007)
	-31.98 to 70.67	Singh *et al.* (2007)
	16.94 to 30.09	Chandirakala *et al.* (2010)
	-30.60 to -0.50	Gouri Shankar *et al.* (2010)
	-4.04 to 21.62	Kumar Babu e*t al.* (2010b)
	-18.9 to 6.9	Rahimi *et al.* (2010)
	-40.63 to 23.20	Tiwari *et al.* (2011)
	-26.19 to 9.52	Sen and Singh (2011)
	-6.757 to 14.189	Kumar *et al.* (2012)
Number of filled grains panicle^{-1}	-34.35 to 17.74	Aananthi and Jebaraj (2006)
	4.13 to 14.38	Pandya and Tripathi (2006)
	-91.00 to 63.00	Singh *et al.* (2006)
	-28.85 to 11.86	Singh *et al.* (2007)
	42.3` to 45.11	Eradasappa *et al.* (2007)
	36.40 to 76.96	Chandirakala *et al.* (2010)
	-43.69 to 19.04	Gouri Shankar *et al.* (2010)
	-93.53 to 26.64	Kumar Babu e*t al.* (2010b)
	-15.4 to 10.80	Rahimi *et al.* (2010)
	-33.58 to 12.08	Tiwari *et al.* (2011)

Table 2.4 (Contd..)

	-17.43 to 56.88	Sen and Singh (2011)
	-51.503 to 236.229	Kumar *et al.* (2012)
Spikelet fertility	-18.70 to -2.44	Aananthi and Jebaraj (2006)
	-38.42 to -13.38	Pandya and Tripathi (2006)
	-88.00 to 69.00	Singh *et al.* (2006)
	28.81 to 34.34	Chandirakala *et al.* (2010)
	-11.27 to 8.06	Gouri Shankar *et al.* (2010)
	-95.87 to 7.02	Kumar Babu e*t al.* (2010b)
	-0.81 to 16.31	Tiwari *et al.* (2011)
Test weight	-38.95 to -11.42	Aananthi and Jebaraj (2006)
	0.00 to 26.00	Pandya and Tripathi (2006)
	-23.00 to 30.53	Singh *et al.* (2006)
	-28.3 to -0.70	Rosamma and Vijayakumar (2007)
	-28.62 to 42.48	Singh *et al.* (2007)
	37.12 to 49.50	Chandirakala *et al.* (2010)
	-12.15 to 9.43	Gouri Shankar *et al.* (2010)
	-26.67 to 8.33	Kumar Babu e*t al.* (2010b)
	-4.6 to 18.1	Rahimi *et al.*(2010)
	-43.47 to 41.25	Tiwari *et al.*(2011)
	-24.71 to 41.57	Sen and Singh (2011)
	-14.921 to 29.319	Kumar *et al.* (2012)
Grain yield plant^{-1}	65.3 to 211.00	Chaudhry *et al.* (2007)
	51.57 to 57.94	Eradasappa *et al.* (2007)
	-38.30 to 70.60	Rosamma and Vijayakumar (2007)
	-60.35 to 22.64	Singh *et al.* (2007)
	24.05 to 28.97	Chandirakala *et al.* (2010)
	-29.19 to 20.14	Gouri Shankar *et al.* (2010)
	-85.78 to 69.43	Kumar Babu e*t al.* (2010b)
	-47.3 to 20.9	Rahimi *et al.* (2010)
	-28.57 to 71.56	Tiwari *et al.* (2011)
	-21.66 to 40.87	Sen and Singh (2011)
	-12.698 to 309.524	Kumar *et al.* (2012)

2.6 SCREENING FOR *Rf* GENES

Komori *et al.* (2004) carried out map based cloning of a fertility restorer gene ,*Rf1* in rice (*Oryza sativa* L.).Genomic fragments carrying *Rf* were identified by conducting chromosome walking and a series of complementation tests. Isolation and analysis of cDNA clones corresponding to the clones demonstrated that Rf-1 encodes a mitochondrially targeted protein containing 16 repeats of the 35-aa pentatricopeptide repeat (PPR) motif.

Fujii and Toriyama (2005) carried out molecular mapping of the fertility restorer gene for *ms-CW*-type cytoplasmic male sterility of rice. The 1:1 segregation of fertile and sterile plants in a BC_1F_1 population from a cross between W1-R and a maintainer line demonstrated that fertility restoration is controlled by a single gene which functions gametophytically and designated the fertility restorer gene as *Rfcw* and localized *Rfcw* to chromosome 4 with a genetic distance of 0.6 cM from the nearest SSR marker.

Li *et al.* (2005) studied the distribution of fertility restorer genes for Wild - Abortive and Honglian CMS lines of rice in the AA genome species of genus *Oryza.* by investigating the fertility of microspores identified by I2–KI staining and by following the seed-setting rate of spikelets. Fertility analysis showed that 21 out of 35 HL-type F_1 s and 13 out of 31 WA-type F_1 s were fertile and reported that the frequency of Rf gene in wild rice was 60% for HL-CMS and 41.9% for WA-CMS, respectively. The fertility restorer accessions, especially those with complete restoring ability, aggregated mainly in two species of *O. rufipogon* and *O.nivara*.

Ahmadikhah *et al.* (2007) studied the inheritance of the fertility restoration and carried genotyping of rice lines at the restoring fertility (*Rf*) loci using molecular markers and crossed 38 lines with a sterile tester (*rfrf*) line and identified fertile F_1 hybrids which were then self-pollinated to obtain F_2 seeds. Pollen fertility test was performed to identify sterile and fertile individuals in F_2 and reported that lines IR 28, Amol 1 and Amol 2 carry *Rf4* gene linked with SSR marker RM 171 on the long arm of chromosome 10., lines IR 36 and IR 60966 carry *Rf3* gene linked with SSR marker RM1 on the short arm of chromosome 1., line IR 62030 carries *Rf5* gene on the short arm of chromosome 10, and line IR 24 carries *Rf4* gene on the long arm of chromosome 10 and an unknown *Rf* gene, respectively.

Huang *et al*. (2007) carried out genetic analysis and mapping of genes involved inthe fertility restoration of Pingxiang Dominant Genic Male Sterile Rice and found that E823, an indica inbred rice variety, restored the fertility of PDGMSR and the genetic pattern was found to be consistent with a dominant epistatic model, therefore, the dominant epistatic fertility restorer gene was designated as *Rfe*. The fertility restoring gene *Rfe* was mapped to one side of the microsatellite markers RM311 and RM3152 on rice chromosome 10 with genetic distances of 7.9 cM and 3.6 cM, respectively.

Bazrkar *et al*. (2008) carried out tagging of restorer genes for wild abortive (WA) CMS source by studying the F_2 population of a cross between IR58025A and IR42686R. Four *Rf* genes were tagged to simple sequence repeats (SSR) markers on chromosomes 1, 7, 10, 12 by recessive class analysis and found a new *Rf* locus designated as *Rf7* on chromosome 12 linked to RM7003 at a genetic distance of 13.3 cM .

Alavi *et al*. (2009) mapped the fertility restorer gene Rf_3 using SSR and CAPS markers in rice line IR 36 in a F_2 population developed from the cross Neda-A×IR36 and reported that three SSR markers, RM1, RM3233 and RM3878 and one CAPS marker, RG140/EcoRI on the short arm of chromosome 1 were linked to *Rf3* and that the *Rf3* gene is flanked by two SSR markers RM1 and RM3873 at distances of 5.6 and 14 cM, respectively.

Sheeba *et al.* (2009) carried out validation of molecular markers linked to fertility restorer gene(s) for WA-CMS lines of rice. Nine SSR and three CAPS markers reported to be linked to *Rf* genes along with two previously unreported SSR markers were analyzed in the mapping populations. The marker RM6100 amplified the *Rf-4* linked allele in a majority of the restorers with a selection accuracy of 94.87%.

Hossain *et al.* (2010) studied the genetics of fertility restoration of 'WA'-based cytoplasmic male sterility system in rice using indica and japonica derivative restorers. Study using three indica/japonica restorers (P1277-100, P1266-89, and P1266-8) and three 'WA'-type cytoplasmic male sterile lines (Pusa 3A, Pusa 5A, and Pusa 6A) revealed that two or three major genes govern the fertility restoration with epistatic interactions that differed from cross to cross.

Nematzadeh and Kiani (2010) studied the crosses between Iranian CMS line Neda-A and three lines DN-33-18 ,DN-33-18 and DN-32-6 and found that only the

cross of Neda-A/DN-33-18 had more than 80% pollen and grain fertility in F_1 generation. Molecular tagging of fertility restorer genes with SSR markers showed that four markers RM258, RM171, RM591 and RM3148 produced polymorphic bands between two parents. Linkage analysis on F_2 recessive class showed that RM258 and RM171 (on chromosome 10) were flanked to restorer gene *Rf4* at distances of 3.1 and 6.3 cm, respectively. They also reported a new SSR marker RM3148 linked with *Rf* locus at a genetic distance of 19.7 cm.

Toriyama *et al.* (2010) carried out molecular comparison of fertility restorer genes Rf_1, *Rf*2 and *Rf* 17 for cytoplasmic male sterility in rice. They achieved positional cloning of the fertility restorer genes *RF1* for BT-CMS originated from Chinsurah Boro II, *RF2* for LD-CMS originated from Lead Rice and *Rf17* for CW-CMs from Chinese wild rice.

Tan *et al*. (2011) studied the relationship between cytoplasmic male sterility and fertility restoration-related genes in *Oryza* species through genetic and molecular analysis. They studied 41 accessions from 7 *Oryza* species with AA genome for analyzing the evolutionary relationships between the CMS factors and *Rf* candidates on chromosome 10 using RFLP and SSR markers. The phylogenetic tree of CMS-associated mitochondrial genes showed that these 41 *Oryza* accessions fell into 3 distinct groups.

Balaji Suresh *et al.* (2012) carried out fine mapping of *Rf3* and *Rf4* fertility restorer loci of WA-CMS of rice *(Oryza sativa* L.) and did validation of the developed marker system for identification of restorer lines.

Gholizadeh *et al*. (2012) crossed 5 cytoplasmic male sterile lines with 10 pure lines as testers and evaluated the fertility in F_1 population and reported the parental line IR-9 to be an effective restorer. Molecular analysis using the SSR marker RM1 confirmed the presence of *Rf3* gene in IR-9 conferring the fertility restoration in F_1 hybrids.

Hu *et al.* (2012) studied the molecular mechanism of fertility restoration by *Rf5* gene in Hong-Lian Cytoplasmic Male-Sterile lines in rice and found that GRP162 (a Gly-rich protein encoding 162 amino acids) physically interact with RF5 (a pentatricopeptide repeat protein), to form a restoration of fertility complex (RFC) that is 400 to 500 kD in size and can cleave CMS-associated transcripts in vitro.

Shah *et al.* (2012) studied the genetic diversity among 22 rice genotypes representative of restorer, maintainer and male sterile lines using SSR markers. Among 30 SSR markers used, 25 SSR loci generated polymorphic patterns and a total of 231 alleles were amplified. The number of alleles per locus ranged from 5 to 17 with a mean of 9.4 alleles per locus. The PIC values for 25 SSR markers varied from 0.74 (RM195, RM10318, and RM258) to 0.92 (RM302).

Tan *et al*. (2012) carried out molecular characterization of latent fertility restorer loci for Honglian cytoplasmic male sterility in *Oryza* species. They analyzed the restoring ability and the diversity of molecular markers cosegregated with *Rf5* (Milyang23) and *Rf6(t)* (9311) for HL-CMS. Molecular and genetic analyses revealed that eight accessions, including one cultivar and seven wild rice, showed polymerase chain reaction (PCR) patterns different from *Rf5* and *Rf6(t)*, and each of them harboured a pair of *Rf* genes unallelic to *Rf5* and *Rf6(t)* for HL-CMS.

Wang *et al*. (2012) employed the rice variety Wanlun 422 with wide compatibility, WA-type restorer lines Shuhui 527, Miyang 46, and Miyang 42 as the parent materials, and selected the *Japonica* rice restorer line for Yinshui type cytoplasmic male sterility (YS-CMS) from the hybrid combinations F_2 and F_4 using molecular marker-assisted selection combined with conventional breeding method.

Chapter - III

MATERIAL AND METHODS

In the present investigation, elite parental lines were screened for the presence of proven *Rf* genes using SSR markers and crossing programme of CMS lines and restorer lines was undertaken during *kharif,* 2012 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, West Godavari district of Andhra Pradesh State located at 81.44^0 E longitude, 26.38^0 N latitude, in Godavari Zone of Andhra Pradesh. During *rabi,* 2012-13 evaluation of hybrids was carried out at the same location.

3.1 MATERIAL

Experimental material of the present investigation which was carried out in *kharif*, 2012 comprised two cytoplasmic male sterile (CMS) lines (WA type) and fifty-five elite restorers developed at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru. The experimental material used in the crossing is presented in table 3.1.

3.2 METHODS

3.2.1 Screening of Parental Lines for Proven *Rf* genes using SSR Markers

The parental lines comprising 55 restorer lines and 2 CMS lines were screened for the presence of proven *Rf* genes using published SSR markers.

3.2.1.1 DNA extraction and quantification

DNA was extracted from the leaf tissue of all the parental lines using the modified Cetyl Tri Methyl Ammonium Bromide (CTAB) method of Dellaporta *et al.* (1983) described as under:

Reagents

- CTAB Extraction Buffer. Composition and concentrations of CTAB extraction buffer is presented in table 3.2.

Table 3.1. Experimental material used in the crossing programme during *kharif*, 2012

Parent	Designation	Source	Origin
CMS lines	APMS 6A	WA	Maruteru
	APMS 10A	WA	Maruteru
R lines	**Culture**	**Parentage**	**Origin**
RP2	II 218-5-1	MTU 1061/MTU 1071	Maruteru
RP3	MTU II-156-13-1-2	MTU 1071/BPT 5204	Maruteru
RP4	II 110-9-1-1-1-1	[(BPT 5204/IET 9762)/Swarna] /MTU 2716	Maruteru
RP5	II 110-11-1-1-1-6	[(BPT 5204/IET 9762)/Swarna] /MTU 2716	Maruteru
RP12	MTU 1851-6-1-1-1	MTU 1576-4-3-1/JGL 1798	Maruteru
RP13	II 178-28-1-1-1	BPT 5204/DP-13	Maruteru
RP14	MTU II 193-22-1-3	BPT 5204/MTU 1071	Maruteru
RP15	PS 219	Selection from MTU 1064	Maruteru
RP17	II 290-2-1-1	MTU 1071/BPT 5204	Maruteru
RP18	II 193-1-1-1	BPT 5204/MTU 1071	Maruteru
RP19	II 193-41-1-12-1	BPT 5204 / MTU 1071	Maruteru
RP20	II 282-7-1	MTU 2077/IRBBN 39	Maruteru
RP22	II 283-7-1-1	MTU 1071/PAUPR 106	Maruteru
TCNP7	MTU 1770-24-3-1-1	(Eramallelu / RNR19994)/ BPT 5204	Maruteru
TCNP13	II 137-32-1	MTU 7029/BPT 5204	Maruteru
TCNP22	_	Selection from MTU 1071	Maruteru
TCNP23	II 110-11-1-1-1-15	[(BPT 5204/IET 9762)/Swarna)] /MTU 2716	Maruteru
TCNP38	II 318-1-2-1	BPT 5204/IR 64	Maruteru
TCNP50	II 225-16-1	MTU 1071/MTU 1003	Maruteru

Table 3.1 (Contd..)

Parent	Designation	Source	Origin
TCNP53	II 139-1-1-1-1-1	BPT 5204//II 110-79-1-1-2	Maruteru
TCNP56	II 139-1-1-1-1-1	BPT 5204//II110-79-1-1-2	Maruteru
TCNP60	MTU II 110-47-2-1-1-1	BPT 5204/II-104-3	Maruteru
TCNP61	II 110-9-1-1-1-1	[(BPT 5204/IET 9762)/Swarna] /MTU 2716	Maruteru
TCNP62	MTU II 156-13-1-2	MTU 1071/BPT 5204	Maruteru
TCNP73	II 178-28-1-1-1	BPT 5204/DP-13	Maruteru
TCNP83	II 192-38-1-1	(BPT 5204/BM71)/BPT 5204	Maruteru
TCNP85	II 193-3-2	BPT 5204/MTU 1071	Maruteru
TCNP87	II 193-20-1-1	BPT 5204/MTU 1071	Maruteru
TCNP89	II 193-22-1-1-1	BPT 5204/MTU 1071	Maruteru
TCNP92	II 197-7-12-1	(BPT 5204/MTU 1061)/ BPT 5204	Maruteru
TCNP93	II 197-38-1-1	(BPT5204/MTU1061)/BPT5204	Maruteru
TCNP94	II 236-12-1-1	MTU 27116/MTU 1071	Maruteru
TCNP97	II 240-8-1	MTU 1071/PLA 1100	Maruteru
RP1	MTU 1071	–	Maruteru
RP6	II 187-6-1-1	MTU-II129-9-1/NSN-26	Maruteru
RP7	II 190-1-1-1-1-1	(BPT 1235/JGL 384)/MTU 1010	Maruteru
RP9	II 225-19-1	MTU 1071/MTU 1003	Maruteru
RP11	II 124-41-1-1	JGL 1798/MTU1001	Maruteru
RP16	II150-16-1-1	BPT 5204/DP7	Maruteru
RP21	II 255-1-1-1	MTU 1071/DP4	Maruteru

Table 3.1 (Contd..)

Parent	Designation	Source	Origin
TCNP1	MTU 1632-10-1-1	(BPT 1235/ Veluthacheera)/ BPT 5204	Maruteru
TCNP14	II 138-82-1	(JGL 1798/MTU 1001)/ MTU 3626	Maruteru
TCNP21	AESg-133PS 198-3-1	BPT 5204/MTU II104-3	Maruteru
TCNP26	II 133-11-1-1	BPT 5204/IET8585	Maruteru
TCNP29	II 308-1-1-2-2	MTU 7029/ DP11	Maruteru
TCNP51	II 218-5-1	MTU 1061/MTU 1071	Maruteru
TCNP54	II 315-2-1-1	MTU 1071/MTU 3626/BPT 5204	Maruteru
TCNP57	MTU 1064	_	Maruteru
TCNP58	II 236-12-1-1	MTU 2716/MTU 1071	Maruteru
TCNP75	II 187-6-1-1	II 124-9-1/NSM-26	Maruteru
TCNP76	II 187-6-1-1	II 124-9-1/NSM-26	Maruteru
TCNP82	II 192-4-2-1-1	(BPT 5204/BM 71)/BPT 5204	Maruteru
TCNP90	II 193-41-1-1-2	BPT 5204/MTU 1071	Maruteru
TCNP96	II 237-40-2	(JGL 1798/BM 71)/MTU 1010	Maruteru
TCNP100	II 256-4-1	BPT 5204/PR 108	Maruteru

Table 3.2. Composition and concentrations of CTAB extraction buffer

S. No	Components	Stock concentration	Working concentration	Volume required for 500ml
1	Tris HCl	1M	200mM	100ml
2	EDTA	0.5M	20mM	20ml
3	NACl	5M	1.4mM	140ml
4	CTAB	2%	2g	10g
5	PVP	2%	2g	10g

- RNase 10mg/ml
- Absolute ethanol

Methodology followed

- Healthy leaf samples were collected at tillering stage in a sterile plastic bag or cover, which was labelled, sealed and placed in a freezer.
- The leaf was cut into 0.5cm long pieces.
- 400 micro litres of DNA extraction buffer was added using micropipette and the tissue was ground until the buffer turned dark green.
- The dark green colour solution obtained was transferred in to a fresh, labelled micro centrifuge tube.
- To this tube 200 micro litres of Tris saturated phenol and 200 micro litres of chloroform was added & centrifuged at 10,000 rpm for 10 min in a cooling centrifuge.
- The supernatant thus obtained was transferred in to another labelled tube using a micropipette.
- To the aqueous supernatant, 10 micro litres of RNase was added and incubated at 37^{o}C for about 30-45 min.
- After incubation, 400 micro litres of chloroform was added, mixed gently and centrifuged at 10,000 rpm for 10 min.
- The top aqueous phase i.e, supernatant was transferred to another labelled tube.
- To this solution, equal volume of chilled isopropanal was added, mixed well and centrifuged at 10,000 rpm for 10 min.

- After centrifugation the supernatant was discarded and to the DNA pellet settled down at the bottom of the tube, 200 micro litres of 70% ethanol was added and centrifuged at 10,000 rpm for 10min.
- The supernatant was discarded and the tubes containing DNA pellet were air dried for about 1-2 hrs till the ethanol got evaporated completely.
- After the pellet got completely dried with no smell of alcohol, it was suspended in 100-200 micro liters of Tris EDTA buffer and stored at -20^{o}C.
- The DNA thus obtained was subjected to quantification.

3.2.1.2 Estimation of Quality and Quantity of DNA

DNA quantification was done by spectrophotometric technique using Thermo scientific Nano drop 8000 (spectrophotometer). The measurement of absorbance was done at 260 nm. DNA has maximum absorbance at 260nm, one optical density (OD) corresponded approximately to 50µl/ml of double stranded DNA, 40 µg/ml of single stranded DNA/RNA and 20 µg/ml of oligonucleotide.

An aliquot of 10µl of the DNA was diluted in TE buffer in a ratio of 1:1000 in a microcuvette, mixed well and absorbance was determined at 260nm against TE buffer blank. The DNA concentration was calculated using the following formula:

Amount of DNA (µg/ml) = Dilution factor × standard (50µl/ml) × OD at 260nm

The ratio of OD 260 to OD 280 provided information on the purity of the DNA

1) If the ratio is 1.8 to 2.0 the sample of DNA is relatively pure
2) If the ratio is < 1.8 the sample of the DNA is either contaminated with phenol or protein

3.2.1.3 Polymerase Chain Reaction

The *in vitro* amplification of DNA by repeated cycles of strand separation and polymerization, by DNA polymerase activity is called polymerase chain reaction (PCR). This technique was developed by Kary.B.Mullis at Cites Corporation, California in 1985 and he was awarded with the noble prize in chemistry in 1993. PCR is now considered as a basic tool for molecular biology. The polymerase chain reaction technique is used for generating large quantities of a specified DNA segment of interest. The PCR components are presented in table 3.3.

Table 3.3. Components of Polymerase Chain Reaction

PCR Components	1X
PCR Buffer	1 micro litre
dNTPS	1 micro litre
Forward primer (5pM)	1 micro litre
Reverse primer(5pM)	1 micro litre
Template	3 micro litre
Taq polymerase	1 micro litre
Water	2 micro litre
Total	10 micro litres

3.2.1.3.1 PCR with Microsatellite Markers

SSR markers are very powerful tools in Marker Assisted Selection (MAS) due to their hyper polymorphism, abundance in the genome, co-dominant inheritance, simplicity of assay, most important being already mapped both physically and genetically in the rice genome. Amplification of single SSR involves two different primers- F (Forward) and R (Reverse) primers. SSR primers are usually in the size range of 18 to 25 bases. *Taq* DNA polymerase is the most vital ingredient of a PCR reaction. *Taq* DNA polymerase is a special category of DNA polymerase, which is obtained from a thermophilic bacterium, *Thermus aquaticus* and is highly thermo stable. The steps involved in PCR were given below:

- Master Mix consisting of PCR buffer, dNTPs, Forward primer, Reverse primer, Milli Q water, *Taq* DNA polymerase was prepared.
- Inorder to avoid minor pippeting errors, a little extra quantity of master mix was prepared to ensure that adequate quantity was available for the samples. Empirically, for every 10 reactions, one extra reaction was taken.
- The tube containing master mix was spun for about 10 to 15 seconds and kept in ice until added to PCR tubes.
- Master mix was added equally to all the wells in the PCR plate, given a spin and kept inside the thermocycler (Applied Biosystem's Veriti PCR machine).

The actual technique of PCR involves repeated cycles for amplification of target DNA.

Each cycle has 3 stages.

1. Denaturation
2. Annealing
3. Extension

On raising the temperature to 94^{o}C for about 0.5 min, the DNA gets denatured and the two strands are separated. When the temperature of mixture is slowly cooled to about 58^{o}C for 0.5 min the primers base pair with the complementary regions flanking the target DNA segments. The initiation of DNA synthesis occurs at 3-hydroxyl end of each primer by the enzyme *Taq* DNA polymerase. The primers are extended by joining the bases complementary to DNA strands. However the temperature has to be kept optimal as required by the enzyme *Taq* DNA polymerase, the optimum temperature is around 72^{o} C for 1 min. It is estimated that the end of 35 cycles of PCR, about a million fold target DNA is synthesized. The thermo profile for PCR is given in table 3.4

Table 3.4. The thermo profile for Polymerase Chain Reaction (PCR)

Activity	Temperature (^{0}C)	Duration (min)	Number of cycles
Initial Denaturation	94	5.0	1
Denaturation	94	0.5	35
Annealing	58	0.5	35
Extension	72	1.0	35
Final Extension	72	7.0	1

After completion of 35 cycles PCR plate was taken out and stored at 4^{o}C.

3.2.1.4 Agarose Gel Electrophoresis

The migration of charged particles under the influence of direct electric field is known as electrophoresis. The electrophoresis technique was first developed in 1930s by A. Tiselius of Sweden. Many important biological molecules such as amino acids, peptides, proteins, nucleic acids and nucleotides possess ionizable groups. When they are subjected to electric field the charged molecules migrate towards either cathode or anode under the influence of electric field. Agarose gel electrophoresis is useful in identification and separation of DNA molecules.

3.2.1.4.1 Gel Preparation

- Prepared 1X TAE buffer by diluting 50X TAE buffer.
- Agarose gel was prepared by adding 15g agarose to 500ml of 1X TAE buffer (3%) and boiled till agarose dissolves completely and a clear solution is formed.
- The electrophoresis apparatus and the combs were washed with distilled water and the combs were placed approximately 2cm away from the cathode.
- When the temperature of molten Agarose was around 50^{o}C, ethidium bromide was added at a concentration of 15µl/500ml mixed and poured into the central part of the tank without any air bubbles.
- The gel casting set was kept undisturbed till the Agarose solidified.
- Upon solidification, 1X TAE buffer was poured in to the gel tank till the level reached 0.6-0.8 cms above the gel surface.
- The combs were lifted gently ensuring that the wells remained intact.

3.2.1.4.2 Loading DNA

PCR plate was taken out from the refrigerator and tracking dye, bromophenol blue (0.25% bromophenol blue and 40% sucrose mixed in water) was added and given one spin for uniform mixing of bromophenol blue. The samples were then loaded carefully into the wells.

3.2.1.4.3 Electrophoresis

- After loading all DNA samples in to the wells electrophoresis unit was made air tight with a lid and power supply was switched on.
- DNA molecules with in an Agarose gel matrix are subjected to steady electric field; it will migrate through the gel towards the positive electrode, anode since DNA has a strong negative charge at neutral pH. The pores in the gel separate the linear fragments of DNA according to their size.
- The gel was run at 80 to120V till the dye front reached 3/4 th of the gel.

3.2.1.4.4 Gel Documentation

The resolved PCR bands were documented using Syngene gel doc system.

3.2.1.5 Screening with Microsatellites

The 55 restorer lines and 2 CMS lines were screened for the presence of *Rf3* and *Rf4* genes located on chromosomes 1 and 10, respectively using a set of microsatellites or SSR markers (simple sequence repeats).The list of microsatellite markers studied and the primers used are given in tables 3.5 and 3.6, respectively. The scoring of the population was done based on the presence or absence of the band. Cluster analysis and dendrogram construction was done by UPGMA (Unweighted Pair Group Method with Arithmetic Averages) clustering algorithm using NTSYSpc version 2.0 (Rohlf, 1994).

3.2.2 Field Evaluation of Parents and Hybridization

A total of 110 crosses were obtained involving the two CMS lines and fifty-five restorers in a line × tester fashion during *kharif,* 2012. The crosses made are given in table 3.7. Three staggered sowings of the parents (females and males) were undertaken at an interval of ten days to ensure synchronous flowering to produce adequate crossed seed. Twenty three days old seedlings were transplanted at a spacing of 20×15cm in RBD with 2 replications. The plot size was 1.60 m^2 with 4 rows per plot. The crop was raised using the recommended practices and necessary plant protection measures were adopted. The parental lines were also evaluated for different characters.

3.2.2.1 Clipping

Healthy male sterile plants of the female lines with just emerged panicles were uprooted and potted in the evening hours of the day into plastic buckets filled with mud and were transferred to the net house. Productive tillers with healthy panicles were selected and the leaf sheaths were removed carefully. Further, florets that had completed anthesis (at the top) and young florets at the bottom of the panicle were removed. Florets due to flower on the next day alone were used for crossing. Top 1/3rd of each floret was clipped with scissors and the clipped florets were covered with butter paper bags and labelled properly. The clipping process was carried out during evening hours.

3.2.2.2 Pollination

Next day morning, panicles ready for anthesis were selected from healthy male parents and were brought to the crossing chamber in which temperature, relative humidity and light conducive for anthesis were maintained. When the male parent was ready for dehiscence the female parent was brought inside the crossing chamber.

Table 3.5.The list of microsatellite markers studied in rice (*Oryza sativa* L.)

Marker	Chromosome number	QTL linked	Citation
RM 1, RM 315, RM 443, RM 576, RM1201, RM 3148, RM 3233, RM3520, RM 3627, RM 3740, RM 3873, RM 5359, RM 8146, RM 10287, RM 10305, RM 10318, DRCG Rf3-1, DRCG Rf3-2, DRCG Rf3-3, DRCG Rf3-4, DRCG Rf3-5, DRCG Rf3-6, DRCG Rf3-7, DRCG Rf3-8, DRCG Rf3-9, DRCG Rf3-10, DRCG Rf3-11, DRCG Rf3-12, DRCG Rf3-13, DRCG Rf3-14, DRCG Rf3-15, DRCG Rf3-16, DRCG Rf3-17, DRCG Rf3-18, DRCG Rf3-19, DRCG Rf3-20, DRCG Rf3-21, DRCG Rf3-22, DRCG Rf3-23, DRRM Rf3-5, DRRM Rf3-6, DRRM Rf3-10, DRRM Rf3-15, DRRM Rf3-24, DRRM Rf3-27	1	*Rf3*	Ahmadikhah *et al.* (2007), Tada. (2007), Bazrkar *et al.* (2008), Alavi *et al*. (2009), Nematzadeh and Kiani (2010), Shah *et al*.(2012), Balaji Suresh *et al.* (2012)
RM 171, RM 216, RM 228, RM 244, RM 258, RM 294, RM 311, RM 591, RM 1108, RM 3123,RM 5373, RM 6100, RM 6344, RM 6737, DRCG Rf4-1, DRCG Rf4-2, DRCG Rf4-3, DRCG Rf4-4, DRCG Rf4-5, DRCG Rf4-6, DRCG Rf4-7, DRCG Rf4-8, DRCG Rf4-9, DRCG Rf4-10, DRCG Rf4-11, DRCG Rf4-12, DRCG Rf4-13 DRCG Rf4-14, DRCG Rf4-15, DRCG Rf4-16, DRCG Rf4-17, DRCG Rf4-18, DRCG Rf4-19, DRCG Rf4-20, DRCG Rf4-21, DRRM Rf4-10, DRRM Rf4-20, DRRM Rf4-72, DRRM Rf4-74	10	*Rf4*	Mishra *et al.* (2001), Ahmadikhah *et al*.(2007), Bazrkar *et al.*(2008), Sheeba *et al.*(2009), Shah *et al*.(2012), Balaji Suresh *et al.* (2012)

Table 3.6. Primers used in screening for *Rf* genes in rice (*Oryza sativa* L.)

S.No.	Primer	Chromosome number	Forward Sequence	Reverse Sequence
1	RM 1	1	GCGAAAACACAATGCAAAAA	GCGTTGGTTGGACCTGAC
2	RM 315	1	GAGGTACTTCCTCCGTTTCAC	AGTCAGCTCACTGTGCAGTG
3	RM 443	1	GGGAGTTAGGGTTTTGGAGC	TCCAGTTTCACACTGCTTCG
4	RM 576	1	GGACGGCGAGTTCATAAATAG	CTTGATGGGATAAAAGCATCAG
5	RM 1201	1	TTACCGCGCCACATATACAC	CGTACGAGCCCTAGTTACCG
6	RM 3148	1	GACTATTGCTCGAACACTTTG	TTGTCTGCTTTGGTATTTGC
7	RM 3233	1	GAAATTCGAAATGGAGGGAGAGC	GGTGAGTAAACAGTGGTGGTGAGC
8	RM 3530	1	GTAGATCCGGTCAGCTCCTC	CAAGGAGATTCCCTTCCATG
9	RM 3627	1	GGCTACTCGAGCAAGCTCTG	ACCTACCCGTCATCCCTCTC
10	RM 3740	1	ATCCCAACTCTAAGCCACCC	CTACCCGTCACCAACTCACC
11	RM 3873	1	GCTATAGACGCCTCCTCCTTATCC	AAAGCTAGCTAGGACCGACATGC
12	RM 5359	1	CGTGATCTCGTGCATCCC	CCCTCAGGAGCTTCATGAAC
13	RM 8146	1	GACTCCTCCAAGTGCAACG	GTAGCTTCCCCACAATGTCA
14	RM 10287	1	GTATTCCTTGCTGCTGCTGATGG	GACTGGAGATGTGATCGGAAACC
15	RM 10305	1	CAGGAACCAACCTTCTTCTTGACC	GTCAGACTCCGATCTGGGATGG
16	RM 10318	1	TGTCTCACACATTGCACACTTACC	GGCCTAACCCAACACATGTCC
17	DRCG Rf3-1	1	AAGCGTGACATCCCTAATCG	GTCGTGGCCATCTGATCTCT
18	DRCG Rf3-2	1	CTTCCCCTTCCACTTGTCTG	GTGCGGCTGACCTTGATG
19	DRCG Rf3-3	1	CTTCGCTTCCTCCCCATCT	TGGAGCGAGGTAAGGTTCAC
20	DRCG Rf3-4	1	TCTTTTATGCTTGGTTCTGTTTTT	AACTGAACAAGATGGTCCCTGT
21	DRCG Rf3-5	1	TTTCTGTGGGCAGTTAGCAA	GGCTTTGCTGGTCCAGTTAC
22	DRCG Rf3-6	1	TCCCCGAATTGTTCTAGC	AGCGCCACAAGATTTTCGAT
23	DRCG Rf3-7	1	CTGTTAAGTGTGCAGTGTCCTG	CGCTTTAGCACGGTCAAGTT
24	DRCG Rf3-8	1	TGCCACTCCTGGAAAAGGTA	TGGAGGGAACTTCATCATTTG
25	DRCG Rf3-9	1	TGGGCAGTTATTTTGTATGTGC	TGGTATTCTCAATCATCCAGAGTT
26	DRCG Rf3-10	1	TCTGTGCATTGCCTGAACAT	TCGTATGGAACGATGTGATGA

Table 3.6 (Contd..)

27	DRCG Rf3-11	1	AATGCTGTGCTTCTGGCTTT	GCTTCCGTCAGGTCATGTCT
28	DRCG Rf3-12	1	TGTTAAGCAATGTCGGTGGA	AAAGACAAGGCAAGCTTTGAA
29	DRCG Rf3-13	1	CTCCACGTCGATGGACAC	CTCTCCTCTCGCGGTTGTAT
30	DRCG Rf3-14	1	AAAGGCAGGACAACTTGTGG	TCCACACACATACAAACTTCCA
31	DRCG Rf3-15	1	CTGCACTGATGGGTGAATTG	ATGTCTTCGGAATGCTCGAT
32	DRCG Rf3-16	1	GAACACCGTGACATGGAACA	GTGCTCTGGTCCTCGGATT
33	DRCG Rf3-17	1	AGTAGGCGGCGAGGATCT	CCATGGAATCGCCTCCTC
34	DRCG Rf3-18	1	ATGGAACAGCCGTTCAAAAA	GATTTGAAGGCCTTGCTGAC
35	DRCG Rf3-19	1	CTGACAGCCTCCCATCTCTC	TGGATGTCGAATTCACAGGA
36	DRCG Rf3-20	1	AGCAATCTTGCCAATGAAGC	ATGGGCCTTTCCTCTCACTT
37	DRCG Rf3-21	1	TGAGTGCGTCTTCAATCCTG	GCATACCATTTCTTGCCTCCT
38	DRCG Rf3-22	1	GATGGTTTGGTGGTTCATGG	AGGTCGGAGTTGGAGTAGCA
39	DRCG Rf3-23	1	TTTGGGCAGTATTGCAGATG	TGATGTCACGTTGAGGCATT
40	DRRM Rf3- 5	1	GATGGCACAGCTTCAGAACA	CTAATTCTGGGCGAGCAAAG
41	DRRM Rf3- 6	1	AAAGGCAGGACAACTTGTGG	TCCACACACATACAAACTTCCA
42	DRRM Rf3- 10	1	TCACCTCTTCCTGCTTCGAC	CTCCACCAGTGCAGGTTTTT
43	DRRM Rf3-15	1	TACGCGTGGTAGTCCAGTCA	CGTGCCGCTATCCTCGAC
44	DRRM Rf3- 24	1	ATTCGAAATGGAGGGAGAGC	CGGTTTTTCACTGGTTGCTT
45	DRRM Rf3-27	1	GTCCCCGTTCTTTCTCACTG	CTCGTGATCAACCGACAA
46	RM 171	10	AACGCGAGGACACGTACTTAC	ACGAGATACGTACGCCTTTG
47	RM 216	10	GCATGGCCGATGGTAAAG	TGTATAAAACCACACGGCCA
48	RM 228	10	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC
49	RM 244	10	CCGACTGTTCGTCCTTATCA	CTGCTCTCGGGTGAACGT
50	RM 258	10	TGCTGTATGTAGCTCGCACC	TGGCCTTTAAAGCTGTCGC
51	RM 294	10	TTGGCCTAGTGCCTCCAATC	GAGGGTACAACTTAGGACGCA
52	RM 311	10	TGGTAGTATAGGTACTAAACAT	TCCTATACACATACAAACATAC
53	RM 591	10	CGGTTAATGTCATCTGATTGG	TTCGAGATCCAAGACTGACC
54	RM 1108	10	GCTCGCGAATCAATCCAC	CTGGATCCTGGACAGACGAG
55	RM 3123	10	ATTTCCCACACATCTCGCTG	GTGTCGCCGGTCAAGAAC

Table 3.6 (Contd..)

56	RM 5373	10	GGAGATGCTATAGCAGCAGTG	ATTGCTCCTTACCACCTTGC
57	RM 6100	10	TCCTCTACCAGTACCGCACC	GCTGGATCACAGATCATTGC
58	RM 6344	10	ACACGCCATGGATGATGAC	TGGCATCATCACTTCCTCAC
59	RM 6737	10	CATTGGGGGTGGATAAAGAG	TATCCTCTACTCCCTCGGCC
60	DRCG Rf4-1	10	TCACGAATTCGATTAGGTTGTC	CAACGTCCATCCTGTTTTGA
61	DRCG Rf4-2	10	CGACTCCTTCCGTATTTCCA	TTCTTAATGACATTGCCCAAG
62	DRCG Rf4-3	10	CATTCTCATCGGTTCCTGCT	AAGGGCTCCTTTGGTAGCAT
63	DRCG Rf4-4	10	TATGACCAAGAGGGGCCTAA	TTCTTTTGCAGCAGCAGTTC
64	DRCG Rf4-5	10	GGAGATGGAGAGCAGTGGTG	GGCATCAAAGGCAGAACATAA
65	DRCG Rf4-6	10	TTGACGAGATTCCATGGTCA	GATGGACGGTCCTGATTGAT
66	DRCG Rf4-7	10	GAGTTAGGGTTTGGGCTGCT	ATCTCTTGCGCAGTTGTGTG
67	DRCG Rf4-8	10	TTGCAACGCAAGGGTAATTT	TCACTGCGCATCTTTTTGAG
68	DRCG Rf4-9	10	AGTGGTGTCATGCCTGATTG	TTCCAACTGAGACCATGCTG
69	DRCG Rf4-10	10	GGTGTGAAGCCCGATATCAT	TCCCTCCTCTAATCGGACTG
70	DRCG Rf4-11	10	TTTCCGTCCAAGAGATAGCC	AGATGGCAGGGATGGTGTAG
71	DRCG Rf4-12	10	GGTGGGAGAGAAGGGACATT	TTGAGAAGAATGGTGCAGGA
72	DRCG Rf4-13	10	CATAGTGCTCCGCAGAATGA	GCATCGTCTACACTGCCTGA
73	DRCG Rf4-14	10	GCAATGCTTGTATTCAGCAAA	TCCAGCTGTAAATCCGTCAA
74	DRCG Rf4-15	10	TAATCCTTCATGGGCTTTGC	CACAATGTTGGATCTAATGTCAAA
75	DRCG Rf4-16	10	GCAACATTTAAGCACCACATT	GGGCCATTTTCAGTCCATTT
76	DRCG Rf4-17	10	GGACTGAAAATGGCCCATAG	AATGCCGTAGGTGCACAAGT
77	DRCG Rf4-18	10	CCTCGATCTACGGCTTGAAC	TCCATGCATCTTCCGTTCTT
78	DRCG Rf4-19	10	CTCAAAAAGATGCGCAGTGA	AACTAACGCGTCTTCCATCC
79	DRCG Rf4-20	10	TTCTGGCATGGTCTCAGTTG	CAAAGCTGCAAAATGCTTCA
80	DRCG Rf4-21	10	AGCATCCACTGCTTCCTTGT	CTTCCCAACCAATCACAACC
81	DRRM Rf4- 10	10	GCCGGTAAATGGATGAGTTC	AATTAAGCAACACGGGATGG
82	DRRM Rf4- 20	10	GAAGAGGTGGAGGCCATGT	CGACGAAGGCAGATAAGTCG
83	DRRM Rf4-72	10	AGCCGGGAGTAGGAAGAAAG	ATTGGATGGGGCTAATGACA
84	DRRM Rf4-74	10	CCCTCCGTCCAAAGCTTATT	CGTGACAATGTTTGACTGTCC

Table 3.6 (Contd..)

Table 3.7. The crosses made in rice (*Oryza sativa* L.) during *kharif*, 2012

S.No.	Designation	Cross combination	S.No.	Designation	Cross combination
1	TC1	APMS 6A × RP2	56	TC56	APMS10A × TCNP87
2	TC2	APMS10A × RP2	57	TC57	APMS 6A × TCNP89
3	TC3	APMS 6A × RP3	58	TC58	APMS10A × TCNP89
4	TC4	APMS10A × RP3	59	TC59	APMS 6A × TCNP92
5	TC5	APMS 6A × RP4	60	TC60	APMS10A × TCNP92
6	TC6	APMS10A × RP4	61	TC61	APMS 6A × TCNP93
7	TC7	APMS 6A × RP5	62	TC62	APMS10A × TCNP93
8	TC8	APMS10A × RP5	63	TC63	APMS 6A × TCNP94
9	TC9	APMS 6A × RP12	64	TC64	APMS10A × TCNP94
10	TC10	APMS10A × RP12	65	TC65	APMS 6A × TCNP97
11	TC11	APMS 6A × RP13	66	TC66	APMS10A × TCNP97
12	TC12	APMS10A × RP13	67	TC67	APMS 6A × RP1
13	TC13	APMS 6A × RP14	68	TC68	APMS10A × RP1
14	TC14	APMS10A × RP14	69	TC69	APMS 6A × RP6
15	TC15	APMS 6A × RP15	70	TC70	APMS10A × RP6
16	TC16	APMS10A × RP15	71	TC71	APMS 6A × RP7
17	TC17	APMS 6A × RP17	72	TC72	APMS10A × RP7
18	TC18	APMS10A × RP17	73	TC73	APMS 6A × RP9
19	TC19	APMS 6A × RP18	74	TC74	APMS10A × RP9
20	TC20	APMS10A × RP18	75	TC75	APMS 6A × RP11
21	TC21	APMS 6A × RP19	76	TC76	APMS10A × RP11
22	TC22	APMS10A × RP19	77	TC77	APMS 6A × RP16
23	TC23	APMS 6A × RP20	78	TC78	APMS10A × RP16
24	TC24	APMS10A × RP20	79	TC79	APMS 6A × RP21
25	TC25	APMS 6A × RP22	80	TC80	APMS10A × RP21
26	TC26	APMS10A × RP22	81	TC81	APMS 6A × TCNP1
27	TC27	APMS 6A × TCNP7	82	TC82	APMS10A × TCNP1
28	TC28	APMS10A × TCNP7	83	TC83	APMS 6A × TCNP14
29	TC29	APMS 6A × TCNP13	84	TC84	APMS10A × TCNP14
30	TC30	APMS10A × TCNP13	85	TC85	APMS 6A × TCNP21
31	TC31	APMS 6A × TCNP22	86	TC86	APMS10A × TCNP21
32	TC32	APMS10A × TCNP22	87	TC87	APMS 6A × TCNP26
33	TC33	APMS 6A × TCNP23	88	TC88	APMS10A × TCNP26
34	TC34	APMS10A × TCNP23	89	TC89	APMS 6A × TCNP29
35	TC35	APMS 6A × TCNP38	90	TC90	APMS10A × TCNP29
36	TC36	APMS10A × TCNP38	91	TC91	APMS 6A × TCNP51
37	TC37	APMS 6A × TCNP50	92	TC92	APMS10A × TCNP51
38	TC38	APMS10A × TCNP50	93	TC93	APMS 6A × TCNP54
39	TC39	APMS 6A × TCNP53	94	TC94	APMS10A × TCNP54
40	TC40	APMS10A × TCNP53	95	TC95	APMS 6A × TCNP57
41	TC41	APMS 6A × TCNP56	96	TC96	APMS10A × TCNP57
42	TC42	APMS10A × TCNP56	97	TC97	APMS 6A × TCNP58
43	TC43	APMS 6A × TCNP60	98	TC98	APMS10A × TCNP58
44	TC44	APMS10A × TCNP60	99	TC99	APMS 6A × TCNP75
45	TC45	APMS 6A × TCNP61	100	TC100	APMS10A × TCNP75
46	TC46	APMS10A × TCNP61	101	TC101	APMS 6A × TCNP76
47	TC47	APMS 6A × TCNP62	102	TC102	APMS10A × TCNP76
48	TC48	APMS10A × TCNP62	103	TC103	APMS 6A × TCNP82
49	TC49	APMS 6A × TCNP73	104	TC104	APMS10A × TCNP82
50	TC50	APMS10A × TCNP73	105	TC105	APMS 6A × TCNP90
51	TC51	APMS 6A × TCNP83	106	TC106	APMS10A × TCNP90
52	TC52	APMS10A × TCNP83	107	TC107	APMS 6A × TCNP96
53	TC53	APMS 6A × TCNP85	108	TC108	APMS10A × TCNP96
54	TC54	APMS10A × TCNP85	109	TC109	APMS 6A × TCNP100
55	TC55	APMS 6A × TCNP87	110	TC110	APMS10A × TCNP100

Butter paper bags covering clipped panicles of the female parents were removed. Further, the panicles were gently shaken so that the sterile extruded anthers fell off. Panicles of male parents were then gently shaken over the female parents (CMS lines) until adequate pollen was deposited on the stigmas of the clipped spikelets.

The pollinated spikelets were then covered with fresh butter paper bags, duly labelled and fixed against the support of bamboo stakes. The process of pollination was continued upto 11.00 AM. Crossed seeds were collected after four weeks from the plants maintained in the pots. The seeds were then sun dried, dehusked, counted and stored in small envelops.

3.2.3 Field Evaluation of Hybrids

Crossed seeds of hybrids and their parents were treated with carbendazim solution (0.1%) and germinated in petridishes. Satisfactory germination was observed on the 4^{th} and 5^{th} day of soaking. The seedlings were transferred to small raised beds covered with a layer of sand and sufficient care was taken to avoid water logging and complete drying up of the nursery beds.

Top dressing was given with urea and need based plant protection measures were undertaken for raising healthy seedlings. Four weeks aged seedlings were subsequently utilized for transplanting in the main field.

3.2.4 Experimental Design for Variability, Heritability, Genetic Advance and Heterosis

The 110 hybrids obtained from crossing programme were evaluated with 2 B lines, 55 R lines and four checks during *rabi,* 2012-13 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru in a randomized block design (RBD) with two replications. A spacing of 20 × 15 cm was adopted. The plot size was 1.60 m^2 with 4 rows per plot.

Fertilizers were applied at the rate of 180 kg nitrogen, 90 kg phosphorus and 90 kg K_2O $hectare^{-1}$. The package of practices recommended to the location adopted for raising a good crop.

3.2.4.1 Recording of observations

Plants were selected randomly from each replication and observations were recorded on ten randomly selected plants for plant height (cm), number of tillers plant^{-1}, panicle length (cm), number of filled grains panicle^{-1}, spikelet fertility (%) and grain yield plant^{-1} (g). The characters, days to 50 % flowering, days to maturity and test weight (g) were recorded on plot basis. In case of CMS lines (cytoplasmic male sterile lines) the observations were recorded on their respective maintainer (B) lines.

The details of the observations recorded and methods followed are presented here under character wise.

3.3 YIELD AND YIELD COMPONENTS

3.3.1 Days to 50% Flowering

The total number of days taken for 50 per cent flowering from the date of sowing was recorded.

3.3.2 Plant Height (cm)

It was measured at maturity from bottom of the plant to the tip of the panicle and expressed in cm.

3.3.3 Number of Ear Bearing Tillers Plant^{-1}

Total number of panicle bearing tillers were counted in each of the 10 randomly selected plants at maturity.

3.3.4 Days to Maturity

The total number of days taken for maturity from the date of sowing was recorded

3.3.5 Panicle Length (cm)

The length from base of the panicle to the tip was measured in cm.

3.3.6 Number of Filled Grains Panicle^{-1}

The number of filled grains per panicle were counted and recorded.

3.3.7 Spikelet Fertility (%)

Spikelet fertility per cent was calculated as the ratio of fertile grains per panicle to the total number of grains in a panicle and was expressed as percentage.

3.3.8 Test Weight (g)

Thousand well filled grains were counted at random and the weight was recorded in grams.

3.3.9 Grain Yield Plant^{-1} (g)

The matured panicles were harvested, threshed, cleaned and seed dried to 12% moisture level. The grain yield per plant was recorded in grams.

3.4 STATISTICAL ANALYSIS

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

3.4.1 Analysis of Variance

The analysis of variance for each character was found as per the standard statistical procedure given by Panse and Sukhatme (1978).

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

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

μ = general mean

b_i = True effect of i^{th} block

t_j = True effect of j^{th} genotype

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

Analysis of variance was carried out for each character as indicated below.

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

Where,

r = Number of replications

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^2_e = Environmental variance

σ^2_r = Variance due to replications

σ^2_g = Variance due to genotypes

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

3.4.2 Estimation of Genetic Parameters

3.4.2.1 Phenotypic and genotypic variance

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

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

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

3.4.2.2 Coefficient of Variation

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

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

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

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

Low = Less than 10%

Moderate = 10-20%

High = More than 20%

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

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

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

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

Low = 0 - 30 %

Moderate = 31- 60 %

High = 61 % and above

3.4.2.4 Genetic advance as per cent of mean (GAM)

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

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

Where,

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

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

σ_p = Phenotypic standard deviation.

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

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

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

3.4.3 Genetic Divergence Using Mahalanobi's Generalized Distance (D^2)

Genetic diversity among the parental lines during *kharif*, 2012 was estimated using D^2 statistics given by Mahalanobis (1936).

3.4.3.1 Test of significance

Variances were calculated for all the nine characters studied and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1978). After testing the difference between genotypes for each of the character, a simultaneous test of significance for differences in the mean values for a number of correlated variables with regard to pooled effect of 9 characters was carried out using 'V' statistic, which in turn utilizes Wilk's Criterion. The sum of squares and sum of products of error and error + variety variance – covariance matrix were used for this purpose. The estimation of 'V' (Wilk's criterion) was done by using the following relationship.

'V' = W/S

Where, 'V' = Wilk's criterion

W = Determinant of error matrix and

S = Determinant of error + variety matrix

The significance of 'V' was tested by V (stat):

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

Where,

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

p = number of characters (or) variable observations

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

n = degrees of freedom for error + genotypes at base of

natural log = 2.7183

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

3.4.3.2 Transformation of correlated variables

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

3.4.3.3 Computation of D2 values

The D^2 value between i^{th} and j^{th} genotypes for 'p' character was calculated as:

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

Where,

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

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

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

3.4.3.4. Grouping of genotypes into various clusters

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

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

inclusion in that cluster. Similarly, a second cluster was formed. The process was continued till all the genotypes were included in one or the other clusters.

3.4.3.5 Intra and inter cluster distance

Average intra cluster distance

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

Average inter cluster distance

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

$$\text{Average inter cluster distance} = \frac{D^2}{n1 \times n2}$$

n1 and n2 are number of genotypes of two clusters

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

3.4.3.6 Cluster Diagram

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

The D^2 analysis was performed using WINDOWSTAT computer programme.

3.4.4 Combining Ability Analysis

Estimates of combining ability variances and effects were obtained using line x tester method suggested by Kempthorne (1957) and detailed by Singh and Chaudhary (1985). The mathematical model is given below.

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

Y_{ijk} = Any measurable character of the cross i x j in the k^{th} replication

μ = Population mean effect

g_i = General combining ability effect of line or female parent

g_j = General combining ability effect of tester or male parent

s_{ij} = Specific combining ability effect of i x j^{th} cross

r_k = Effect due to k^{th} replication

e_{ijk} = Environmental effect on ijk^{th} individual

Table 3.8. Analysis of Variance (ANOVA) for Combining Ability

Source	d.f	Mean sum of squares	F test
Replications	r-1	M_r	M_r / M_e
Genotypes	(g-1)	M_g	M_g / M_e
Parents	(p-1)	M_p	M_p / M_e
Parents *Vs* crosses	1	M_{pc}	M_{pc} / M_e
Crosses	(c-1)	M_c	M_c / M_e
Lines	(l-1)	M_l	M_l / M_{lt}
Testers	(t-1)	M_t	M_t / M_{lt}
Lines x testers	(l-1) (t-1)	M_{lt}	M_{lt} / M_e
Error	(r-1) (g-1)	M_e	

Where,

r = Number of replication

g = Number of genotypes

p = Number of parents

c = Number of crosses

l = Number of females

t = Number of males

M_r = Replication mean sum of squares

M_g = Genotype mean sum of squares

M_p = Parent mean sum of squares

M_c = Cross mean sum of squares

M_{pc} = Mean squares due to parents and crosses

M_l = Mean sum of squares due to lines

M_t = Mean sum of squares due to testers

M_{lt} = Mean sum of squares due to lines x testers

M_e = Mean sum of squares due to error

df = Degrees of freedom

The significant differences between the variances of genotypes, replications, parents, crosses, lines, testers, parents *vs.* crosses, lines x testers was tested by applying the F test of Fisher and Yates (1963).

The *gca* and *sca* effects were estimated as follows:

$$g_i = \frac{x_{i..}}{tr} - \frac{x..}{ltr}$$

Where

x_i = total of ith lines over all testers and replications

x = Mean of lines, testers and replications

i = number of lines

t = number of testers

r = number of replications

While, the *gca* effects of lines were estimated as follows

$$g_j = \frac{x_j}{lr} - \frac{x..}{ltr}$$

Where, x_j .= total of jth line over testers and replications

$$s_{ij} = \frac{x_{ij..}}{r} - \frac{x_i..}{tr} - \frac{x_{j.}}{lr} + \frac{x..}{ltr}$$

Where, x_{ij} = total of ijth combination over replications

The standard errors (SE) pertaining to *gca* effects of lines and testers and *sca* effects of combinations were calculated as shown below:

SE (g_i) (gca for female) = $\sqrt{\frac{M_e}{r\,x\,t}}$

SE $\left(g_j\right)$ (gca for males) = $\sqrt{\frac{M_e}{(r\,x\,l)}}$

SE $\left(s_{ij}\right)$ (sca effects) = $\sqrt{\frac{M_e}{r}}$

SE $\left(g_i - g_j\right)$ female = $\sqrt{\frac{2M_e}{r\,x\,t}}$

SE $\left(g_i - g_j\right)$ male = $\sqrt{\frac{2M_e}{r\,x\,l}}$

SE $\left(S_{ij} - S_{kl}\right)$ = $\sqrt{\frac{2M_e}{r}}$

The covariance of half sibs (H.S) and full sibs (F.S.) was used to obtain the estimates of general and specific combing ability and their variances.

Cov H.S. (female) = $\frac{M_l - M_{lt}}{r\,x\,t}$

Cov H.S. (male) = $\frac{M_t - M_{lt}}{r\,x\,l}$

Cov H.S. (average) = $\frac{1}{r(2lt - l - t)}\left[\frac{(l-1)(M_l)+(t-1)(M_t)}{1+(t-2)} - M_{lt}\right]$

Covariance of (F.S.) =

$$\frac{(M_l - M_e)+(M_t - M_e)+(M_{lt} - M_e)}{3r} + \frac{6r\,Cov\,HS - r(1+t)Cov.(H.S)}{3r}$$

The *gca* and *sca* variances were obtained as follows:

$\sigma^2\,gca$ = Cov. H.S. (average)

$\sigma^2\,sca = \frac{M_{lt} - M_e}{r}$

gca to *sca* ratio was calculated to know the type of gene action involved *i.e.*, additive or non-additive. The *gca* and *sca* effects were tested against zero for significance by calculating t-value, by using the following formulae

$$t - cal = \frac{|g_i - 0|}{SE(g_i)}; \; t - cal. = \frac{|g_j - 0|}{SE(g_j)}; \; t - cal. = \frac{|s_{ij} - 0|}{SE(s_{ij})};$$

t-calculated value is compared with t-table value at error degrees of freedom.

The Line × Tester analysis was performed using WINDOWSTAT computer programme.

3.4.5 Estimation of Standard Heterosis

Standard heterosis was expressed as per cent increase or decrease observed in F_1 over standard check as per the following formula given by Liang *et al.* (1971).

$$\text{Standard heterosis (\%)} = \frac{\overline{F_1} - \text{Mean of superior check}}{\text{Mean of superior check}} \times 100$$

Chapter - IV

RESULTS AND DISCUSSION

The present investigation was carried out to study the presence of major fertility restorer genes in elite restorer lines developed and validate the identified restorers for their *per se* performance in different hybrid combinations and identify promising heterotic hybrids in rice. The results obtained are presented below under the following headings

4.1 Evaluation of parental lines

4.2 Evaluation of hybrids

4.3 Identification of *Rf* genes in the restorers

4.1 EVALUATION OF PARENTAL LINES

The evaluation of 57 parental lines (2 CMS lines and 55 restorers) for yield and yield component traits was carried out at Maruteru during *kharif,* 2012.

4.1.1 Analysis of Variance

The analysis of variance (ANOVA) of 57 parental lines (2 CMS lines and 55 restorer lines) for yield and yield component traits were presented in the table 4.1. The results revealed existence of significant differences among the parental lines for all the characters under study.

4.1.2 Mean Performance

The mean performance of parental lines evaluated during *kharif,* 2012 for nine characters were presented in table 4.2.

4.1.2.1 Days to 50% flowering

Days to 50% flowering ranged from 81.00 (TCNP 73) to 114.50 (RP 13) days with an overall mean of 105.14.

Table 4.1. Analysis of variance for yield and yield contributing characters in parental lines of rice (*Oryza sativa* L.) during *kharif*, 2012

Source of variations	df	Days to 50 % flowering	Plant height	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight	Grain yield plant^{-1}
Mean Sum of Squares										
Replications	1	2.84	23.09	1.90	2.25	5.09	163.67	3.54	1.55	3.01
Treatments	56	82.83**	308.69**	2.75**	82.57**	3.70**	8805.38**	147.93**	11.21**	8.65**
Error	56	0.79	7.29	0.60	1.12	1.46	399.05	11.57	1.50	2.07

** Significant at 1 % level

4.1.2.2 Plant height

Plant height varied from 84.00 (APMS 10A) to 149.05 cm (TCNP 38) with a general mean of 126.73 cm. The CMS lines recorded the lowest plant height values with APMS 10A (84 cm) being the shortest followed by APMS 6A (91 cm).

4.1.2.3 Number of ear bearing tillers plant^{-1}

Number of ear bearing tillers plant^{-1} ranged from 5.00 (RP 15) to 10.70 tillers plant^{-1} (RP 1) with a general mean of 8.02.

4.1.2.4 Days to maturity

Days to maturity varied from 111.00 (TCNP 73) to 144.50 (RP 13) days and recorded an overall mean of 135.09 days.

4.1.2.5 Panicle length

An average panicle length of 23.82cm was recorded ranging from 20.22 (TCNP 97) to 26.40 cm (TCNP 21).

4.1.2.6 Number of filled grains panicle^{-1}

The general mean of filled grains panicle^{-1} was 204.75 with a range of 112.06 (TCNP 62) to 400.89 (TCNP 85) grains panicle^{-1}.

4.1.2.7 Spikelet fertility

The general mean for spikelet fertility was 83.09 per cent with a range of 47.03 (TCNP 62) to 93.09 (RP 20) per cent.

4.1.2.8 Test weight

The parental lines recorded test weight ranging from 13.30 (TCNP 92) to 22.94g (TCNP 94) with an average weight of 18.48 g.

4.1.2.9 Grain yield plant^{-1}

The range of grain yield plant $^{-1}$ among parental lines was from 9.36 (TCNP 92) to 18.47 g (TCNP 38) with a general mean of 13.90 g.

4.1.3 Variability and Genetic Parameters

Improvement in any crop species depends upon the amount of variability present in a given population as greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are useful in determining the genetic variability in a population.

The estimate of heritability act as predictive instrument in expressing the reliability of phenotypic value and indicates the relative degree of transmissibility of character from parents to offsprings. Therefore, high heritability helps in effective selection for a particular character. Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). High heritability values indicate that the character is less influenced by the environment and such characters could be improved upon by selection.

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance would give a more reliable index of selection value (Johnson *et al*. 1955). The estimates of variances, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean for 9 characters in parental lines were furnished in table 4.3. The results were presented here character wise.

4.1.3.1 Days to 50% flowering

The parental lines exhibited low phenotypic and genotypic coefficient of variation (6.15 and 6.09), indicating low amount of variability among the genotypes studied for the concerned trait. Similar results were reported by Krishna *et al*. (2008), Prasad *et al*. (2009), Rita Binse *et al.* (2009), Satish Chandra *et al*. (2009), Kuchanur *et al*. (2009), Saidaiah *et al.* (2010b), Siva Parvathi *et al.* (2011) and Shiva Prasad *et al*. (2011).

High heritability (98.11) coupled with moderate genetic advance as per cent of mean (12.43) was observed for this trait in the parental lines. This indicated the presence of both additive and non-additive gene action. These results were in conformity with the findings of Prasad *et al.* (2009), Kuchanur *et al.* (2009), Saidaiah *et al*. (2010b) and Siva Parvathi *et al.* (2011).

Table 4.3. Estimation of genetic variability and genetic parameters in parental lines for yield and yield contributing characters in rice (*Oryza sativa* L.) during *kharif, 2*012.

Character	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability(h^2_{bs}) (%)	Genetic advance (%) (at 5%)	GAM (at 5%)
Days to 50 % flowering	41.81	41.02	6.15	6.09	98.11	13.07	12.43
Plant height	157.99	150.70	9.92	9.69	95.38	24.70	19.49
No. of ear bearing tillers plant^{-1}	1.67	1.07	16.11	12.92	64.31	1.71	21.34
Days to maturity	41.85	40.73	4.79	4.72	97.32	12.97	9.60
Panicle length	2.58	1.12	6.74	4.44	43.48	1.44	6.04
No. of filled grains panicle^{-1}	4602.21	4203.16	33.13	31.66	91.33	127.63	62.33
Spikelet fertility	79.75	68.18	10.75	9.94	85.49	15.73	18.93
Test weight	6.36	4.85	13.64	11.92	76.36	3.97	21.46
Grain yield plant^{-1}	5.36	3.29	16.66	13.05	61.38	2.93	21.06

4.1.3.2 Plant height

The estimates of PCV and GCV for plant height were low (9.92 and 9.69) indicating less variability for the trait among the lines studied. Similar results were reported by Mamta Singh *et al.* (2007), Kole *et al.* (2008) and Kuchanur *et al.*(2009).

High heritability (95.38) coupled with moderate genetic advance as per cent of mean (19.49) was noticed in the parental lines indicating the role of both additive and non additive gene action in the inheritance of this trait. This was in agreement with the results of Uttam Chand and Vijay Kumar (2005), Vaithiyalingan and Nadarajan (2006) and Mamta Singh *et al.* (2007).

4.1.3.3 Number of ear bearing tillers per plant

Moderate estimates of PCV (16.11) and GCV (12.92) were observed for this trait in the parental lines indicating the existence of moderate level of variability for this trait. Similar findings were reported by Saidaiah *et al.* (2010b), Siva Parvathi *et al.* (2011) and Shiva Prasad *et al*. (2011)

High heritability (64.31) and high genetic advance as per cent of mean (21.34) were recorded for this trait indicating the operation of additive gene action in the expression of this trait. This was in conformity with the findings of Saidaiah *et al.* (2010b), Sreeparvathy *et al.* (2010), Mohan Lal and Chauhan (2011) and Siva Parvathi *et al.* (2011).

4.1.3.4 Days to maturity

Low PCV and GCV were observed in the parental lines (4.79 and 4.72) for days to maturity indicating presence of narrow variability among the genotypes for this trait. These results were in conformity with the findings of Karim *et al*. (2007) and Kumar and Ramesh (2008).

High heritability (97.32) coupled with low genetic advance (9.60) was observed in the parental lines indicating the involvement of non-additive gene action in the expression of this trait. Similar observations were reported by Karim *et al.* (2007), Singh *et al.* (2011) and Osman *et al.* (2012).

4.1.3.4 Panicle length

Both PCV and GCV estimates were low (6.74, 4.44) in parental lines indicating low variability for this trait. These results were in conformity with Monalisa Manna *et al*. (2006), Rita Binse *et al*. (2006), Mamta Singh *et al*. (2007), Karthikeyan *et al.* (2007), Krishna *et al*. (2008), Prasad *et al.* (2009) and Rita Binse *et al.* (2009).

Moderate heritability (43.48) coupled with low genetic advance as per cent of mean (6.04) was observed indicating the importance of non-additive gene action. This was in agreement with the results of Bhavana (2003).

4.1.3.5 Number of filled grains per panicle

High estimates of PCV (33.13) and GCV (31.66) values were recorded for this trait in the parental lines indicating high genetic variability and less environmental influence for this trait. The results were in agreement with those of Saidaiah *et al*. (2010b), Siva Parvathi *et al.*(2011) and Seyoum *et al.*(2012).

High heritability (91.33) and high genetic advance as per cent of mean (62.33) were recorded for this trait revealing the presence of additive gene action in the expression of this trait. Thus, the trait can be easily improved through simple selection procedure. Similar findings were reported by Karthikeyan *et al.* (2007), Sharma and Sharma (2007), Prasad *et al*. (2009), Kuchanur *et al*. (2009) Saidaiah *et al.* (2010b) and Siva Parvathi *et al.* (2011).

4.1.3.6 Spikelet fertility

Moderate PCV (10.75) and low GCV (9.94) values were recorded in the parental lines for this trait.

The parental lines recorded high heritability (85.49) and moderate GAM (18.93) value for spikelet fertility, indicating the role of both additive and non-additive gene action in the expression of this trait. This was in agreement with the observations of Sravan *et al*. (2012).

4.1.3.7 Test weight

Moderate estimates of PCV (13.64) and GCV (11.92) were recorded for this trait in the parental lines. Similar findings were reported by Saidaiah *et al.* (2010b), Mohan Lal and Chauhan (2011) and Shiva Prasad *et al.* (2011).

High heritability (76.36) coupled with high genetic advance as per cent of mean (21.46) was observed in the parents indicating the operation of additive gene action. These results were in consonance with the findings of Saidaiah *et al*. (2010b), Mohan Lal and Chauhan (2011), Shiva Prasad *et al*. (2011) and Bhadru *et al.* (2012).

4.1.3.8 Grain yield per plant

Estimates of PCV and GCV were moderate (16.66 and 13.05) for grain yield in the parental lines which was in agreement with the observations of Kumar *et al.* (2006), Kole *et al.* (2008) and Satish Chandra *et al.* (2009).

High heritability (61.38) coupled with high genetic advance as per cent of mean (21.06) was observed for grain yield in the parental lines indicating the presence of additive gene action in the expression of this trait. Hence grain yield can be easily improved through simple selection procedures in the present breeding material. These results were in consonance with the findings of Kumar *et al*. (2006), Monalisa Manna *et al*. (2006), Sobita Devi *et al*. (2006), Rita Binse *et al*. (2006), Sharma and Sharma (2007), Karthikeyan *et al.* (2007), Prasad *et al*. (2009), Umadevi *et al.* (2010) and Siva Parvathi *et al.* (2011), Singh *et al*. (2011) and Bhadru *et al.* (2012).

In the present investigation the magnitude of difference between PCV and GCV was relatively low for all the traits which indicated the least influence of environment on the expression of these traits.

In case of parental lines, high estimates of PCV and GCV were observed for the character, number of filled grains per panicle. The traits viz., number of ear bearing tillers per plant, test weight and grain yield exhibited moderate PCV and GCV values while spikelet fertility showed moderate PCV and low GCV. Low estimates of PCV and GCV were observed in case of days to 50% flowering, plant height, days to maturity and panicle length.

High heritability coupled with high genetic advance was observed in case of ear bearing tillers per plant, number of filled grains panicle^{-1}, test weight and grain yield plant^{-1} suggesting the role of additive gene action in the inheritance of these traits and directional selection could be profitably applied on these traits. High heritability and moderate genetic advance were observed in case of days to 50% flowering, plant height and spikelet fertility which when accompanied by low to moderate PCV and GCV indicated the presence of both additive and non-additive gene action. The traits, days to maturity and panicle length, exhibited high and moderate heritability, respectively. This along with low estimates of GAM, PCV and GCV indicated the preponderance of non-additive gene action.

4.1.4 Genetic Divergence

The quantitative assessment of genetic divergence among the parental lines was done using cluster analysis by adopting Mahalanobis D^2 statistic for yield and its contributing characters using WINDOWSTAT computer programme. The results obtained from the study were presented below

4.1.4.1 Mahalanobis's D^2 analysis

The fifty seven parental lines under study were grouped into eight clusters using D^2 statistic such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters was presented in Table 4.4. Out of eight clusters, cluster II was the largest comprising of twenty eight genotypes followed by cluster I and cluster VII with seven genotypes each, cluster IV with six genotypes, cluster V with four genotypes and cluster III and VI with only one genotype each. Both the CMS lines (APMS 6B and APMS 10B) along with one restorer line (TCNP 97) were found within a single cluster indicating their relatedness. The dendrogram was given in Figure 4.1.

4.1.4.1.1 Average intra and inter cluster distances

The average intra and inter cluster D^2 values were presented in Table 4.5. Intra cluster D^2 values ranged from 0.00 (cluster III and cluster VI) to 99.88 (cluster VII). Maximum intra cluster distance was observed in cluster VI (99.88), followed by cluster I (88.30), cluster VIII (77.17), cluster V (74.79), cluster IV (63.45) and

Table 4.4. Clustering pattern (D^2 analysis) among 57 parental lines in rice (*Oryza sativa* L.).

Cluster no.	No: of genotypes	Name of the genotypes
Cluster I	7	RP 2, RP 5, RP 3, RP 6, TCNP 60,RP 18,TCNP 61
Cluster II	28	RP 4, TCNP 53, RP 20, RP 9, TCNP 7, TCNP 58, TCNP 82, RP 19, TCNP 100, TCNP 90, RP 7, TCNP 92, TCNP 26, RP 13, TCNP 96, RP 1, TCNP 54, RP 17, TCNP 56, TCNP 87, TCNP 93, TCNP 89, RP 22, TCNP 22, RP 14, RP 11, RP 16, RP 15
Cluster III	1	TCNP 62
Cluster IV	6	TCNP 13, TCNP 14, TCNP 21, TCNP 57, RP 12, TCNP 1
Cluster V	4	TCNP 38, TCNP 29, TCNP 83, TCNP 85
Cluster VI	1	TCNP 73
Cluster VII	7	TCNP 50, TCNP 51, TCNP 75, TCNP 76, TCNP 23, TCNP 94, RP 21
Cluster VIII	3	TCNP 97, APMS 6A, APMS 10A

Figure 4.1. Dendrogarm for parental lines in rice (*Oryza sativa*.L)

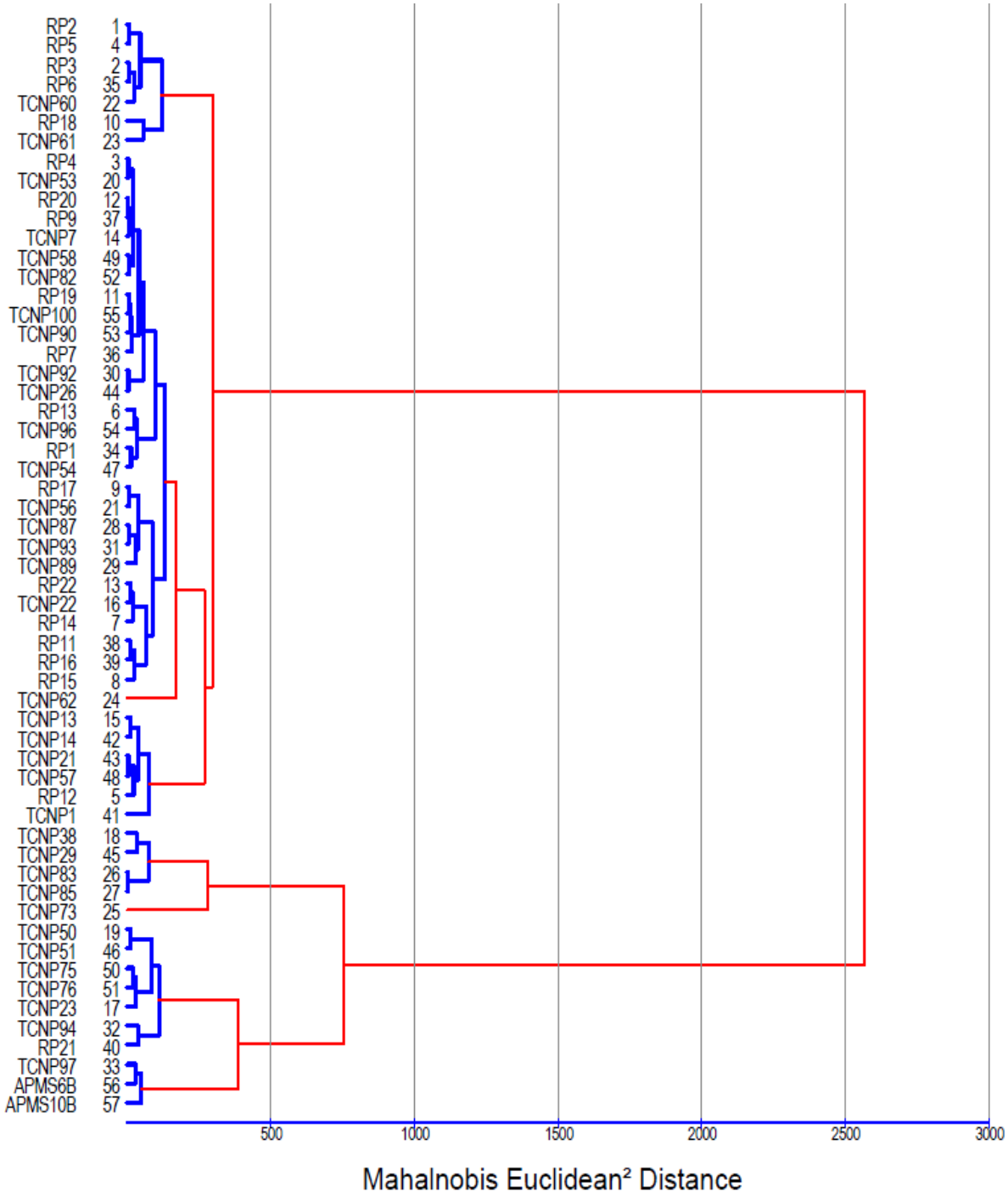
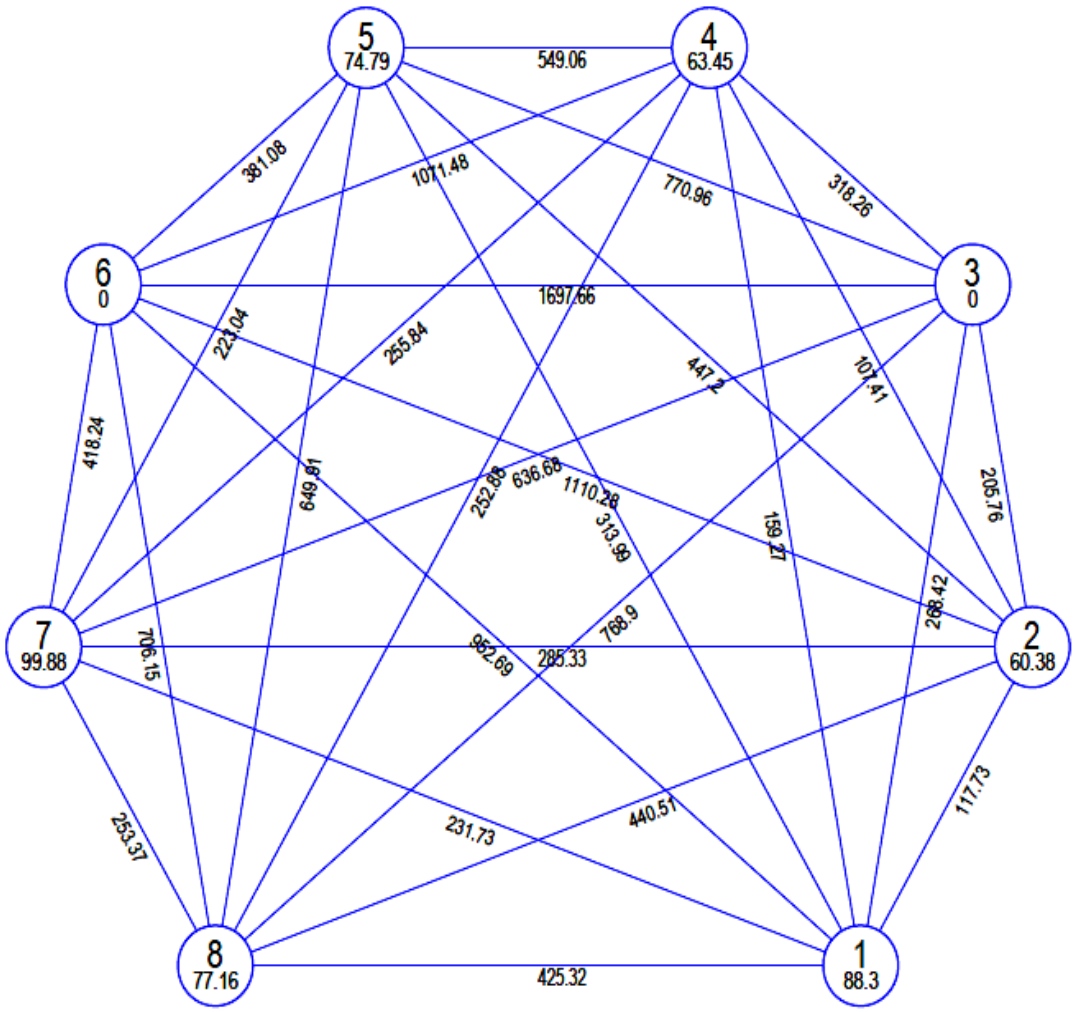


Table 4.5. Intra (diagonal) and Inter cluster average of D2 values of 57 parental lines in rice (*Oryza sativa* L.)

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**
Cluster I	**88.30**	117.73	268.42	159.27	313.99	952.69	231.73	425.32
Cluster II		**60.38**	205.76	107.41	447.20	1110.28	285.33	440.51
Cluster III			**0.00**	318.26	770.96	1697.66	636.68	768.90
Cluster IV				**63.45**	549.06	1071.48	255.84	252.88
Cluster V					**74.79**	381.08	223.04	649.91
Cluster VI						**0.00**	418.24	706.15
Cluster VII							**99.88**	253.37
Cluster VIII								**77.17**

Figure 4.2. D^2 Cluster Diagram of parental lines in rice (*Oryza sativa* L.).



cluster II (60.38) indicating that considerable genetic divergence existed among the genotypes within the same cluster. This could be made use of for yield improvement through recombination breeding.

From the inter cluster D^2 values of eight clusters, it can be seen that the highest divergence occurred between cluster III and cluster VI (1697.66) followed by cluster II and cluster VI (1110.28) and cluster IV and cluster VI (1071.48), suggesting that the crosses involving lines from these clusters would manifest greater heterosis and give wider and desirable recombinations which can be successfully exploited for yield improvement.

The lowest divergence was noticed between cluster II and cluster IV (107.41) followed by cluster I and cluster II (117.73) and cluster I and cluster IV (159.27).The cluster diagram was depicted in the Figure 4.2.

4.2 EVALUATION OF HYBRIDS

The evaluation of 110 hybrids obtained from the crossing programme was carried out along with their parental lines and 4 checks during *rabi*, 2012-13. Since data for certain characters cannot be obtained for A lines, the data recorded on corresponding B lines were given here under for the purpose of statistical analysis.

4.2.1 Analysis of Variance

The analysis of variance (ANOVA) of 110 hybrids and 4 checks for yield and yield component traits were presented in the table 4.6. The results revealed existence of significant differences among the hybrids for all the characters under study.

4.2.2 Mean Performance

Based on single plant yield, the variety MTU 1121 having the highest yield (20.92g) was selected as the standard check for comparing the mean performance of the hybrids for different characters. The mean performance of hybrids during *rabi*, 2012-13 were presented in table 4.7.

4.2.2.1 Days to 50% flowering

For the crosses, days to 50% flowering ranged from 84.50 (TC 92) to 109.50 (TC 18) days with an overall mean value of 96.27 days. The hybrid TC 92 (84.50) registered the lowest number of days for 50% flowering followed by TC 71(85.00), TC 80 (85.00) and TC 91 (86.50).

4.2.2.2 Plant height

Plant height varied from 93.10 (TC 79) to 139.20 (TC 17) with a general mean of 113.39 cm. The hybrid TC 79 (93.10 cm) recorded the lowest value followed by TC 41 (95.10) and TC 35 (96.00).

4.2.2.3 Number of ear bearing tillers plant^{-1}

The trait, number of ear bearing tillers plant^{-1} ranged from 5.01 (TC 102) to 9.10 (TC 63) tillers plant^{-1} with a general mean of 6.45 tillers plant^{-1}.The highest number of ear bearing tillers per plant was recorded by the hybrid TC 63 (9.10) followed by TC 80 (9.05) and TC 20 (8.90). None of the hybrids tested recorded significantly greater number of ear bearing tillers plant^{-1} than the standard check, MTU 1121 (8.30).

4.2.2.4 Days to maturity

For the hybrids, days to maturity varied from 114.50 (TC 71) to 139.50 (TC 18) days, recording an overall mean of 126.24 days. The hybrid TC 71 (114.5) recorded the lowest number of days to maturity followed by TC 80 (115.5).

4.2.2.5 Panicle length

A mean panicle length of 25.91cm was recorded ranging from 22.21(TC 66) to 28.71 cm (TC 16). The highest value for panicle length was recorded by the hybrid TC 16 (28.71) followed by TC 68 (28.54) and TC 18 (28.22).Seventeen hybrids were found to have significantly greater panicle length than the standard check MTU 1121 (25.06 cm).

4.2.2.6 Number of filled grains per panicle

The general mean of filled grains panicle^{-1} was 172.10 with a range of 9.46 (TC 94) to 321.43 (TC 63) grains panicle^{-1}.The hybrid TC 63 (321.43) recorded the highest number of filled grains panicle^{-1}. A total of five hybrids (TC 63, TC 100, TC 45,

TC 34 and TC 22) were found to have significantly higher number of filled grains panicle^{-1} compared to the standard check MTU 1121 (232.71).

4.2.2.7 Spikelet fertility

The general mean for spikelet fertility was 67.37 per cent with a range of 4.88 (TC 93) to 91.49 per cent (TC 106). Among the hybrids, TC 106 (91.49%) recorded the highest value for spikelet fertility followed by TC 34 (90.71%) and TC 91 (90.66%). None of the hybrids tested were found superior to the standard check, MTU 1121 (93.34%).

4.2.2.8 Test weight

The hybrids exhibited test weight ranging from 13.05 (TC 31) to 26.35g (TC 57) with an average weight of 19.55 g. The hybrid TC 57 (26.35g) recorded the highest test weight followed by TC 94 (25.45) and TC 96 (25.15).

4.2.2.9 Grain yield per plant

In case of hybrids, the range of variation for grain yield plant $^{-1}$ was from 0.90 (TC 93) to 27.50 g (TC 11) with a general mean of 15.28 g. The highest single plant yield was recorded for the hybrid TC 11 (27.50 g) followed by TC 7 (27.03 g). A total of six hybrids recorded significantly higher single plant yield than the standard check, MTU 1121 (20.92g).

4.2.3 Variability and Genetic Parameters

The estimates of variances, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean for 9 characters in hybrids were furnished in the table 4.8. The results are presented here character wise.

4.2.3.1 Days to 50% flowering

The hybrids exhibited low phenotypic (5.52) and genotypic coefficient of variation (5.33), indicating low amount of variability among the genotypes for days to 50% flowering. Similar results were reported by Krishna *et al*. (2008), Prasad *et al*. (2009), Rita Binse *et al.* (2009), Satish Chandra *et al*. (2009),

Table 4.8. Estimation of genetic variability and genetic parameters in hybrids for yield and yield contributing characters in rice (*Oryza sativa* L.) during *rabi, 2*012-13

Character	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability(h^2_{bs}) (%)	Genetic advance (%) (at 5%)	GAM (at 5%)
Days to 50 % flowering	28.29	26.42	5.52	5.33	93.37	10.23	10.62
Plant height	107.19	101.35	9.10	8.85	94.55	20.17	17.73
No. of ear bearing tillers plant^{-1}	0.97	0.66	15.25	12.63	68.61	1.39	21.55
Days to maturity	24.54	22.26	3.92	3.74	90.72	9.26	7.33
Panicle length	2.26	1.14	5.78	4.11	50.49	1.56	6.02
No. of filled grains panicle^{-1}	4209.54	3965.80	38.08	36.96	94.21	125.92	73.91
Spikelet fertility	393.46	386.06	29.77	29.49	98.12	40.09	60.17
Test weight	6.21	5.97	12.75	12.49	96.06	4.93	25.22
Grain yield plant^{-1}	41.81	38.87	42.69	41.16	92.95	12.38	81.75

Kuchanur *et al*. (2009), Saidaiah *et al.* (2010b), Siva Parvathi *et al.* (2011) and Shiva Prasad *et al*. (2011).

High heritability (93.37) coupled with moderate genetic advance as per cent of mean (10.62) was observed for this trait in hybrids. This indicated the presence of both additive and non-additive gene action. These results were in conformity with the findings of Prasad *et al.* (2009), Kuchanur *et al.* (2009), Saidaiah *et al*. (2010b) and Siva Parvathi *et al.* (2011).

4.2.3.2 Plant height

The estimates of PCV and GCV for plant height were low (9.10 and 8.85) for the hybrids indicating less amount of variability. Similar results were reported by Mamta Singh *et al.* (2007), Kole *et al.* (2008) and Kuchanur *et al.* (2009).

High heritability (94.55) and moderate GAM (17.73) values were exhibited by the hybrids, which when coupled with low PCV and GCV indicated the role of both additive and non-additive gene action in the inheritance of this trait. Similar results were reported by Uttam Chand and Vijay Kumar (2005), Vaithiyalingan and Nadarajan (2006) and Mamta Singh *et al.* (2007).

4.2.3.3 Number of ear bearing tillers plant^{-1}

The hybrids exhibited moderate PCV (15.25) and GCV (12.63) values for this trait indicating the existence of moderate level of variability for this trait. Similar findings were reported by Saidaiah *et al.* (2010b), Siva Parvathi *et al.* (2011) and Shiva Prasad *et al*. (2011)

High heritability (68.61) and high genetic advance as per cent of mean (21.55) were recorded for this trait, indicating the operation of additive gene action in expression of this trait. This was in conformity with the findings of Saidaiah *et al*. (2010b), Sreeparvathy *et al.* (2010), Mohan Lal and Chauhan (2011) and Siva Parvathi *et al.* (2011)

4.2.3.4 Days to maturity

Low PCV and GCV were observed in the hybrids (3.92 and 3.74) for days to maturity indicating low amount of variability in the genotypes for this trait. These

results were in conformity with the findings of Karim *et al.*(2007) and Kumar and Ramesh (2008).

High heritability (90.72) coupled with low genetic advance (7.33) was observed in the hybrids indicating the involvement of non-additive gene action in the expression of this trait. Similar observations were reported by Karim *et al.* (2007), Singh *et al.* (2011) and Osman *et al.* (2012).

4.2.3.5 Panicle length

Both PCV and GCV estimates were low in the hybrids (5.78, 4.11) for panicle length indicating low variability for this trait. The results were in conformity with Monalisa Manna *et al*. (2006), Rita Binse *et al*. (2006), Mamta Singh *et al*. (2007), Karthikeyan *et al.* (2007), Krishna *et al*. (2008), Prasad *et al.* (2009) and Rita Binse *et al.*(2009).

Moderate heritability (50.49) coupled with low genetic advance as per cent of mean (6.02) was observed in the hybrids indicating the importance of non-additive gene action in the inheritance of this trait. This was in agreement with the results of Bhavana (2003).

4.2.3.6 Number of filled grains per panicle

High estimates of PCV and GCV values were recorded for this trait in the hybrids (38.08 and 36.96) indicating presence of high genetic variability for this trait. The results were in agreement with those of Saidaiah *et al*.(2010b), Siva Parvathi *et al.*(2011) and Seyoum *et al.*(2012).

High heritability (94.21) and high genetic advance as per cent of mean (73.91) were recorded for this trait by the hybrids revealing the presence of additive gene action in the expression of this trait. Hence simple selection can be practiced for the further improvement of this trait. Similar findings were reported by Karthikeyan *et al.* (2007), Sharma and Sharma (2007), Prasad *et al.* (2009), Kuchanur *et al*. (2009), Saidaiah *et al.* (2010b) and Siva Parvathi *et al.* (2011).

4.2.3.7 Spikelet fertility

The hybrids exhibited high PCV (29.77) and GCV (29.49) values for spikelet fertility, indicating high genetic variability.

The hybrids recorded high values for heritability (98.12) and GAM (60.17).The result indicated the presence of additive gene action which can be exploited through simple selection procedures.

4.2.3.8 Test weight

Moderate estimates of PCV and GCV were recorded in the hybrids (12.75 and 12.49). Similar findings were reported by Saidaiah *et al.* (2010b), Mohan Lal and Chauhan (2011) and Shiva Prasad *et al*. (2011).

High heritability coupled with high genetic advance as per cent of mean was observed in hybrids (96.06 and 25.22) indicating the operation of additive gene action. These results were in consonance with the findings of Saidaiah *et al*. (2010b), Mohan Lal and Chauhan (2011), Shiva Prasad *et al*. (2011) and Bhadru *et al.* (2012).

4.2.3.9 Grain yield per plant

The hybrids exhibited high PCV (42.69) and GCV (41.16) for grain yield per plant which was in accordance with the results of Selvaraj *et al*. (2011), Singh *et al.* (2011), Idris *et al.* (2012), Bhadru *et al.* (2012) and Seyoum *et al*. (2012).

High heritability (92.95) coupled with high genetic advance as per cent of mean (81.75) was observed for grain yield per plant, indicating the presence of additive gene action in the expression of this trait. Hence grain yield can be easily improved through simple selection in the present breeding material. These results were in consonance with the findings of Kumar *et al*. (2006), Monalisa Manna *et al.* (2006), Sobita Devi *et al*. (2006), Rita Binse *et al*. (2006), Sharma and Sharma (2007), Karthikeyan *et al.* (2007), Prasad *et al*. (2009), Umadevi *et al.* (2010) and Siva Parvathi *et al.* (2011), Singh *et al*.(2011) and Bhadru *et al.*(2012).

In the present investigation the magnitude of difference between PCV and GCV was relatively low for all the traits which indicated the least influence of environment on the expression these traits. In case of hybrids, high estimates of PCV and GCV were observed for the characters number of filled grains per panicle, spikelet fertility and grain yield. The traits *viz.,* ear bearing tillers per plant and test weight exhibited moderate PCV and GCV values while days to 50% flowering, days to maturity, plant height and panicle length exhibited low values.

High heritability coupled with high genetic advance was observed in case of ear bearing tillers per plant, number of filled grains panicle^{-1}, spikelet fertility, test weight and grain yield plant^{-1} suggesting the role of additive gene action in the inheritance of these traits and directional selection could be profitably applied on these traits in a genetically diverse material. High heritability and moderate genetic advance were observed in case of days to 50% flowering and plant height which when accompanied by moderate to low PCV and GCV indicated the presence of both additive and non-additive gene action. Such traits can be improved by the simultaneous exploitation of both additive and non-additive components by adopting breeding procedures like biparental mating, diallel selective mating system or cyclic hybridization. The traits days to maturity and panicle length exhibited high and moderate heritability respectively. This along with low estimates of GAM, PCV and GCV indicated the preponderance of non-additive gene action which may be exploited through heterosis breeding.

4.2.4 Combining Ability Analysis

Analysis of variance for combining ability was carried out and the mean sums of squares obtained were presented in table 4.9. The crosses were observed to be highly significant for all the traits studied. The mean sum of squares for crosses was further partitioned into lines, testers and line × tester components. The variance due to lines was significant for all the characters studied whereas testers showed significance for all the characters except plant height, number of grains per panicle and spikelet fertility. All the traits were observed significant for line × tester interaction.

The estimates of GCA and SCA variances and percentage contribution of lines, testers and line × tester interaction towards total variance were presented in table 4.10. General combining ability was generally associated with additive gene action, while specific combining ability was due to non-additive gene action i.e., dominance and epistasis. Non-additive gene action of a trait is an indicator for the selection of a hybrid combination.

In the present investigation SCA variances were higher than GCA variances for all the characters indicating the predominance of non-additive gene action for all the characters studied.

Table 4.9. Analysis of variance of combining ability for different characters in rice (*Oryza sativa* L.) during *rabi,* 2012-13

Source of variation	df	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
Replication	1	2.62	14.66	0.66	2.40	2.56	526.51	9.33	0.42	6.39
Crosses	109	54.71**	208.54**	1.63**	46.80**	3.40**	8175.35**	779.50**	12.18**	80.68**
Lines Effect	54	96.37**	366.74**	2.00*	81.09**	4.97**	12708.51**	1366.49**	14.46*	146.85**
Testers Effect	1	59.07*	4.92	9.79**	60.11*	8.16*	7636.74	523.51	129.67**	86.16*
Line × Tester	54	12.97**	54.13**	1.11**	12.27**	1.73*	3652.17**	197.26**	7.73**	14.40**
Error	109	1.88	5.84	0.30	2.28	1.12	243.75	7.40	0.24	2.95
Total	219	28.18	106.77	0.97	24.44	2.26	4192.73	391.70	6.19	41.65

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

Table 4.10. Estimates of genetic components of variance and proportional contribution of lines, testers and line x tester interaction to total variance for different characters in rice (*Oryza sativa* L.)

	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
σ^2 *gca*	1.14	2.31	0.08	1.02	0.08	114.39	13.12	1.13	1.79
σ^2 *sca*	5.74	24.04	0.41	5.25	0.19	1701.40	94.09	3.71	5.85
σ^2*gca* / σ^2 *sca*	0.20	0.10	0.21	0.20	0.44	0.067	0.14	0.30	0.31
Contribution %									
Line (%)	87.26	87.12	60.90	85.83	72.50	77.01	86.85	58.81	90.18
Tester (%)	0.99	0.02	5.51	1.18	2.20	0.86	0.62	9.77	0.98
Line × Tester	11.75	12.86	33.59	12.99	25.30	22.13	12.54	31.43	8.84

General combining ability effects of parents and specific combining ability effects of crosses were estimated and presented in tables 4.11 and 4.12. The results were discussed character wise here under

4.2.4.1 Days to 50% flowering

The general combining ability effects for days to 50% flowering ranged from -10.85 (TCNP 51) to 11.15 (RP 17) in lines and the testers APMS 6A and APMS 10A registered the values -0.52 and 0.52, respectively. Significant negative *gca* effects for days to 50% flowering was recorded in twenty four lines with TCNP 51 (-10.85) registering the lowest value followed by RP 7 (-10.35), RP 12 (-8.35) and RP 19 (-8.35). Among the testers, APMS 6A (-0.52) recorded significant negative value for this trait. This suggested that they were good general combiners with favourable genes for earliness and can be used in future breeding programmes for improving this trait.

The proportional contribution to total genetic variance due to lines was high (87.26 %) followed by line × tester (11.75 %) and testers (0.99 %). The estimated component of variance due to *sca* (5.74) was higher than *gca* (1.14) for days to 50% flowering indicating the preponderance of non-additive gene action. Similar results were earlier reported by Panwar (2005), Jayasudhan and Deepak Sharma (2009), Kumar Babu e*t al.* (2010a), Nadali Bagheri and Babaeian (2010), Saidaiah *et al.* (2010a) and Saidaiah *et al.* (2011).

Specific combining ability effects for days to 50% flowering varied from -4.98 (TC 43) to 4.98 (TC 44). Significant negative *sca* effects desirable for this trait were recorded by twelve cross combinations. The hybrid TC 43 (-4.98) recorded the most desirable value for *sca* effect followed by TC 80 (-4.52), TC 28 (-4.02), TC 70 (-4.02), TC 12 (-3.52), TC 21(-3.48) and TC 99 (-3.48).

Based on *per se* performance and *sca* effects, the crosses *viz.*, TC 92- APMS 10A × TCNP 51 (Low x High), TC 71- APMS 6A × RP 7 (High x High), TC 80- APMS 10A × RP 21 (Low x High), TC 9- APMS 6A × RP 12 (High x High) and TC 70- APMS 10A × RP 6 (Low x High) were identified as superior cross combinations. The crosses between low × high and high x low resulted in superior cross combinations due to complementary gene action which had arisen out of both additive and non-additive gene actions while the cross combinations involving

high × high general combiners revealed additive and additive × additive genetic components of variance where the characters could be easily improved through simple selection procedures in recombination breeding.

4.2.4.2 Plant height

Estimates of *gca* effects for plant height ranged from -18.26 (RP 21) to 22.74 (RP 15) among lines and testers recorded the values 0.15 (APMS 6A) and -0.15 (APMS 10A). The *gca* effects were significant in the desired direction for twenty lines with the line RP 21 (-18.26) registering the best value followed by TCNP 14 (-16.36) and TCNP 56 (-15.81). None of the testers registered significantly negative *gca* effect for this trait.

The proportional contribution to total genetic variance due to lines was high (87.12 %) followed by line × tester (12.86 %) and testers (0.02 %). The variance due to specific combining ability (24.04) was higher than the general combining ability (2.31) for this trait indicating the influence of non-additive gene action (Table 4.12). Similar results were given by Panwar (2005), Singh *et al.* (2005), Dalvi and Patel (2009), Jayasudhan and Deepak Sharma (2009), Kumar Babu *et al.* (2010a), Saidaiah *et al.* (2010a) and Saidaiah *et al.* (2011).

The estimates of *sca* effects for plant height varied from -11.80 (TC 19) to 11.80 (TC 20) among crosses and significant negative *sca* effects were recorded by fourteen hybrids. The top eight crosses showing significant and desirable *sca* effects were TC 19 (-11.80), TC 35 (-10.45), TC 73 (-6.80), TC 65 (-6.05), TC 85 (-6.05), TC 4 (-6.00), TC 46 (-5.75) and TC 102 (-5.75).

Based on *per se* performance and desirable *sca* effects, the crosses *viz.*, TC 79- APMS 6A × RP 21 (Low x High), TC 41- APMS 6A × TCNP 56 (Low x High) and TC 35- APMS 6A × TCNP 38 (Low x High), TC 93- APMS 6A × TCNP 54 (Low x High) and TC 37- APMS 6A × TCNP 50 (Low x High) were identified as superior cross combinations for plant height. The cross between low × high resulted in superior cross combination due to complementary gene action which had arisen out of both additive and non-additive gene action.

4.2.4.3 Number of ear bearing tillers plant^{-1}

The *gca* effects for ear bearing tillers plant^{-1} exhibited a range of -1.14 (TCNP 51) to 2.01 (RP 21) among lines. The testers APMS 6A and APMS 10A recorded the values 0.21 and -0.21 respectively. The line RP 21 (2.01) recorded the highest positive value for *gca* effect followed by the lines RP 2 (1.54), RP 13 (1.54) and RP 18 (1.24). This suggested that they were good general combiners with favourable genes for ear bearing tillers and can be used in future breeding programmes for improving this trait. Among the testers, APMS 6A (0.21) recorded significant positive *gca* effect.

The proportional contribution to total genetic variance due to lines was high (60.90 %) followed by line × tester (33.59 %) and testers (5.51 %). The variance due to specific combining ability (0.41) was higher than the general combining ability (0.08) and the ratio of *gca* variance to *sca* variance was low (0.21) indicating the importance of non-additive gene action and this component can be better exploited through heterosis breeding. These are in agreement with the reports of Panwar (2005), Singh *et al.* (2005), Anand Kumar *et al.* (2006), Jayasudhan and Deepak Sharma (2009), Kumar Babu *et al.* (2010a), Nadali Bagheri and Babaeian (2010), Saidaiah *et al.* (2010a) and Saidaiah *et al.* (2011).

The *sca* effects for ear bearing tillers plant^{-1} ranged from -1.64 (TC 64) to 1.64 (TC 63). Significant positive *sca* effects were exhibited by six hybrids *viz.*, TC 63 (1.64), TC 106 (1.46), TC 20 (1.42), TC 72 (0.96), TC 29(0.91) and TC 80(0.80).

Based on *per se* performance and *sca* effects, the crosses TC 63- APMS 6A × TCNP 94 (High x High), TC 80- APMS 10A × RP 21 (Low x High), TC 20- APMS 10A × RP 18 (Low x High), TC 11- APMS 6A × RP 13 (High x High) and TC 1- APMS 6A × RP2 (High x High) and were identified to be superior for this trait.

The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance which are fixable and this character could be easily improved through simple selection procedures in recombination breeding such as pedigree method. The crosses between low × high general combiners resulted in superior cross combinations due to complementary gene action.

4.2.4.4 Days to maturity

The *gca* effects for days to maturity ranged from -10.82 (RP 7) to 11.18 (RP 17) among lines and from -0.52 (APMS 6A) to 0.52 (APMS 10A) among testers. Twenty five lines recorded significantly negative and desirable *gca* effects. Among the lines RP 7 (-10.82) registered the best value followed by TCNP 51 (-8.82) and TCNP 90 (-7.82). Among the testers, APMS 6A (-0.52) recorded desirable *gca* effect. Thus these parental lines can be used for developing early maturing varieties in rice.

The proportional contribution to total genetic variance due to lines was high (85.83 %) followed by line × tester (12.99 %) and testers (1.18 %). The component of variance due to *sca* (5.25) was higher than the *gca* variance (1.02). The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.20) revealing the role of non-additive gene action. Similar findings were reported by Jayasudhan and Deepak Sharma (2009) and Nadali Bagheri and Babaeian (2010).

The sca effects for crosses varied from -4.98 (TC 43) to 4.98 (TC 44). A total of ten hybrids were found to possess significantly negative *sca* effects with TC 43 (-4.98) being the most desirable followed by TC 80 (-4.52), TC 28 (-4.02), TC 70 (-4.02), TC 12 (-3.52), TC 99 (-3.48), TC 94 (-3.02) and TC 21 (-2.98).

Based on the *per se* performance and *sca* effects, the crosses, TC 71- APMS 6A × RP 7 (High x High), TC 80- APMS 10A × RP 21 (Low x High), TC 70- APMS 10A × RP 6 (Low x High), TC 92- APMS 10A × TCNP 51 (Low x High) and TC 9- APMS 6A × RP 12 (High x High) were found to be superior for earliness in maturity. The superior cross combinations obtained from low x high general combiners may be due to complementary gene action arising from both additive and non-additive gene action. The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance which are fixable and this character could be easily improved through simple selection procedures in recombination breeding such as pedigree method.

4.2.4.5 Panicle length

Estimates of *gca* effects for panicle length, varied from -2.85 (TCNP 97) to 2.41(RP 15) among the lines and from -0.19 (APMS 6A) to 0.19 (APMS 10A) among the testers (Table 4.13). Significant positive *gca* effects were recorded by eight lines of which RP 15 (2.41), TCNP 96 (1.96), TCNP 75 (1.77) and RP 4 (1.55) registered highly significant values. None of the testers exhibited significant positive *gca* effect.

The proportional contribution to total genetic variance due to lines was high (72.50%) followed by line × tester (25.30%) and testers (2.20%). For this trait the estimated component of variance due to *sca* (0.19) was higher than *gca* (0.08) variance. It indicates the predominance of non-additive gene action which can be better exploited through heterosis breeding. This is in accordance with the earlier reports of Panwar (2005), Gnanasekaran *et al.*(2006), Dalvi and Patel (2009), Jayasudhan and Deepak Sharma (2009), Kumar Babu e*t al.* (2010a), Saidaiah *et al.* (2010a) and Saidaiah e*t al.* (2011).

The *sca* effects for crosses varied from -1.43 (TC 30) to 1.43 (TC 29). Among the 110 hybrids evaluated, none of them registered significant positive *sca* effects.

Based on *per se* performance and *sca* effects, the crosses TC 16- APMS 10A × RP15 (Low x High), TC 68- APMS 10A × RP1 (Low x High), TC 18 - APMS 10A × RP 17 (Low x High), TC 107 - APMS 6A × TCNP 96 (Low x High) and TC 5- APMS 6A × RP 4 (Low x High) were identified as superior ones for the trait concerned. Parental lines with low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene action.

4.2.4.6 Number of filled grains per panicle

Estimates of *gca* effects for number of filled grains panicle^{-1} ranged from -160.34 (TCNP 54) to 107.53 (TCNP 61) among the lines and from -5.89 (APMS 10A) to 5.89 (APMS 6A) among the testers. The estimates of *gca* effects were positive and significant for twenty- three lines of which TCNP 61 (107.53) exhibited the highest value followed by TCNP 75 (100.02) and RP 19 (75.80). Among the testers, APMS 6A (5.89) recorded highly significant and positive *gca* effect. These were identified as good general combiners for improving this trait.

The proportional contribution to total genetic variance due to lines was high (77.01 %) followed by line × tester (22.13%) and testers (0.86 %). Component of variance due to *sca* (1701.40) was higher than *gca* (114.39) for number of filled grains panicle^{-1}, indicating the prevalence of non-additive gene action which can be better exploited through heterosis breeding. Similar results were observed by Panwar (2005), Gnanasekaran *et al.*(2006), Dalvi and Patel (2009), Kumar Babu e*t al.* (2010a), Nadali Bagheri and Babaeian (2010), Saidaiah *et al.* (2010a) and Saidaiah e*t al.* (2011).

Among the crosses, *sca* effects for number of filled grains panicle^{-1} ranged from -70.60 (TC 64) to 70.60 (TC 63). Significant positive *sca* effects were exhibited by twenty-five hybrids. The top eight promising crosses for this trait were TC 63 (70.60), TC 43 (61.96), TC 86 (60.30), TC 27 (57.99), TC 100 (52.10), TC 34 (51.57), TC 22 (47.90) and TC 105 (47.08).

Based on *per se* performance and *sca* effects, the crosses TC 63- APMS 6A × TCNP 94 (High x High), TC 100- APMS 10A × TCNP 75 (Low x High), TC 45 - APMS 6A × TCNP 61 (High x High), TC 34 - APMS 10A × TCNP 23 (Low x High) TC 22- APMS 10A × RP 19 (Low x High) were identified as superior ones for the trait concerned. The superior cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance which could be easily improved through simple selection procedures in recombination breeding. Parental lines with low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene action.

4.2.4.7 Spikelet fertility

The estimates of *gca* effects for spikelet fertility varied from -61.57 (TCNP 54) to 23.79 (TCNP 23) among lines while in testers, range was from -1.54 (APMS 10A) to 1.54 (APMS 10A). A total of twenty- nine lines showed significant and positive *gca* effects. The line TCNP 23 (23.79) recorded the highest value followed by TCNP 50 (22.83) and TCNP 90 (19.49). Among the testers, APMS 6A (1.54) recorded significant positive *gca* effect. Thus these were identified as potent parental lines for the development of hybrids having higher spikelet fertility.

The proportional contribution to total genetic variance due to lines was high (86.85 %) followed by line × tester (12.54 %) and testers (0.62 %). In the present investigation, spikelet fertility seems to be mostly under the control of non- additive gene action as the *sca* variance (94.09) was higher than *gca* variance (13.12). The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.14) revealing the preponderance of non-additive gene action in the inheritance of this trait. The present findings are in accordance with the results of Dalvi and Patel (2009), Jayasudhan and Deepak Sharma (2009), Nadali Bagheri and Babaeian (2010) and Saidaiah e*t al.* (2011).

The estimates of *sca* effects varied from -23.53 (TC 101) to 23.53(TC 102). Nineteen hybrids recorded significant positive *sca* effects. Top performing crosses identified among them were TC 102 (23.53) followed by TC 86 (19.62), TC 1(14.63), TC 43 (12.81), TC 84 (11.75), TC 91(11.12), TC 57(11.00), TC 41(10.84), TC 61 (10.46) and TC 36 (10.05).

From the above crosses TC 106- APMS 10A × TCNP 90 (Low x High), TC 34- APMS 10A × TCNP 23 (Low x High), TC 91- APMS 6A × TCNP 51 (High x High), TC 38- APMS 10A × TCNP 50 (Low x High) and TC 39- APMS 6A × TCNP 53 (High x High) were identified as best specific combiners as per their *per se* performance and *sca* effects. The cross combinations involving high × high general combiner revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding and the crosses with low × high combiners resulted in superior combinations which may be due to complementary gene action.

4.2.4.8 Test weight

Among the lines, *gca* effects for test weight ranged from -3.88 (TCNP 22) to 3.59 (TCNP 54 and TCNP 57). The testers registered the values -0.77 (APMS 6A) to 0.77 (APMS 10A) respectively. A total of twenty one lines registered significant positive gca effects of which the highest value recorded was 3.59 (TCNP 54 and TCNP 57) followed by 3.37 (TCNP 75) and 3.09 (TCNP 89). APMS 10A (0.77) registered significant and positive value among the testers. These may serve as useful source for improvement of this trait in hybridization programmes.

The proportional contribution to total genetic variance due to lines was high (58.81 %) followed by line × tester (31.43 %) and testers (9.77 %). The variance due to *gca* (1.13) was lesser than the *sca* (3.71) for test weight indicating the contribution of non-additive gene action in the inheritance of this trait. Results supporting the present investigation were put forth by Panwar (2005), Anand Kumar *et al.* (2006) and Kumar Babu *et al.* (2010a).

The sca effects for test weight, exhibited a range from -4.47 (TC 58) to 4.47 (TC 57) among crosses . Thirty-five hybrids showed significant positive *sca* effects of which TC 57 (4.47) registered the highest value followed by TC 69 (3.07), TC 28 (2.96), TC 17 (2.84), TC 9 (2.12) and TC 35 (2.07).

The crosses viz., TC 57- APMS 6A × TCNP 89 (Low x High), TC 94- APMS 10A × TCNP 54 (High x High), TC 96- APMS 10A × TCNP 57 (High x High), TC 28- APMS 10A × TCNP 7 (High x High) and TC 100- APMS 10A × TCNP 75 (High x High) were identified as superior cross combinations for the concerned trait. The cross combination involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding. The superior cross combinations obtained from low x high general combiners may be due to complementary gene action arising from both additive and non-additive gene action.

4.2.4.9 Grain yield per plant

The range of *gca* effects for grain yield was from -13.65 (TCNP 54) to 10.00 (TCNP 23) among lines and from -0.63 (APMS 10A) to 0.63(APMS 6A) among testers. A total of twenty - four lines registered significant positive gca effects of which TCNP 23 (10.00) possessed the highest value followed by RP 13 (9.83) and TCNP 50(9.60). Among testers APMS 6A (0.63) recorded the significant positive value. These parents may be utilized in future breeding programmes for improving grain yield.

The proportional contribution to total genetic variance due to lines was high (90.18%) followed by line × tester (8.84%) and testers (0.98 %). The estimated component of variance due to *sca* (5.85) was higher than the *gca* (1.79) for grain yield. The ratio of *gca* variance to *sca* variance was low (0.31) indicating the presence of non-additive gene action which can be better exploited through heterosis breeding. Comparable results were earlier reported by Panwar (2005), Rosamma and Vijayakumar (2005), Singh *et al.* (2005), Anand Kumar *et al.* (2006), Gnanasekaran *et al.* (2006), Dalvi and Patel (2009), Jayasudhan and Deepak Sharma (2009), Kumar Babu *et al.* (2010a), Nadali Bagheri and Babaeian (2010), Saidaiah *et al.* (2010a) and Saidaiah *et al.* (2011).

The *sca* effects for grain yield varied from -5.18 (TC 2) to 5.18(TC 1). Among the 110 hybrids evaluated, fourteen hybrids recorded significant positive *sca* effects for grain yield. The highest value was registered by TC 1 (5.18) followed by TC 86 (4.08), TC 91 (3.92), TC 102 (3.89), TC 72(3.68), TC 81(3.01), TC 20(3.00), TC 77(2.87), TC 4(2.63), TC 76(23.20), TC 104(2.52), TC 89(2.50), TC 36(2.39) and TC 7(2.39).

The crosses TC 11- APMS 6A × RP 13 (High x High), TC 7- APMS 6A× RP 5 (High x High), TC 1- APMS 6A × RP 2 (High x High), TC 34- APMS 10A × TCNP 23 (Low x High), TC 38- APMS 10A × TCNP 50 (Low x High), TC 39- APMS 6A × TCNP 53 (High x High), TC 20- APMS 10A × RP 18 (Low x High), and TC 69- APMS 6A × RP 6 (High x High) were identified as good specific cross combinations based on *per se* performance and favourable positive *sca* effects. The superior cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance which could be easily improved through simple selection procedures in recombination breeding. The crosses with low × high combiners resulted in superior combinations which may be due to complementary gene action arising from both additive and non-additive gene action.

The ratio between *gca* and *sca* variance was low for all the characters studied, indicating the predominance of non-additive gene action in the expression of these traits. These traits may be exploited by biparental mating or diallel selective mating or heterosis breeding.

The proportional contribution of lines towards the total genetic variance was high for all the characters studied followed by the contribution of line × tester and tester components respectively.

Based on *gca* effects, the lines TCNP 51 and RP 7 were identified as good general combiners for days to 50% flowering and days to maturity. RP 21 and TCNP 14 were identified as good general combiners for plant height while RP 15 and TCNP 96 were chosen for panicle length. TCNP 61 and TCNP 75 showed good general combining ability for number of filled gains per panicle while the lines TCNP 23 and TCNP 50 registered the best values for spikelet fertility. The lines TCNP 54 and TCNP 57 were identified as good general combiners for test weight, while TCNP 23 and RP 13 were chosen for grain yield plant^{-1}.Among the testers, APMS 6A registered good general combining ability for no: of ear bearing tillers per plant, spikelet fertility, grain yield plant^{-1} while APMS 10A showed good results for days to 50% flowering, days to maturity and test weight.

The cross combinations involving high × high general combiners producing crosses with significant *sca* effect revealed the role of additive and additive × additive genetic component of variance which could be easily improved through simple selection procedures. The crosses between high × low or low × high

combiners resulted in superior cross combinations due to complementary gene action which has arisen out of both additive and non-additive gene action. These crosses may likely throw superior trangressive segregants. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system.

Similar findings were reported by Dalvi and Patel (2009), Jayasudhan and Deepak Sharma (2009), Kumar Babu e*t al.* (2010a), Nadali Bagheri and Babaeian (2010) and Saidaiah *et al.* (2010a).

4.2.5 Standard Heterosis

Heterosis refers to the increase (or) decrease in F_1 value over the mean parental value. From the view point of plant breeding, increased yield of F_1 over the better (or) best commercial variety is more relevant (Virmani *et al.*, 1981). A higher yield over high yielding check varieties and wider adaptability has been instrumental in rapid spread of hybrid rice in India.

Commercial exploitation of heterosis in rice is profitable and it is important that the crosses are compared with released superior varieties and hybrids rather than merely comparing with their mid / better parents. So in the present study, the performance of experimental crosses were compared with that of the most popular varieties (MTU 1075, MTU 1121 and MTU 1081) and hybrid (Arize 6444 Gold) in order to estimate the magnitude of standard heterosis. So that the crosses with high heterotic potential could be exploited for further evaluation and commercial cultivation.

The estimates of standard heterosis over high yielding check MTU 1121 were presented in table 4.13.

4.2.5.1 Days to 50% flowering

Standard heterosis for days to 50% flowering ranged from -7.14 (TC 92) to 20.33 (TC 18). Out of 110 hybrids evaluated, a total of nine hybrids recorded significant negative heterosis over the standard check, MTU 1121. The highest significant negative heterosis was recorded in the hybrid TC 92 (-7.14) followed by TC 71 (-6.59) and TC 80 (-6.59).

Negative standard heterosis for this trait was also reported by Pandya and Tripathi (2006), Rosamma and Vijayakumar (2007) and Chandirakala *et al.* (2010).

4.2.5.2 Plant height

Estimates of standard heterosis for plant height ranged from -10.48 (TC 79) to 33.85 (TC 17). Significant negative standard heterosis over the check MTU 1121 was registered by nine hybrids .The highest significant negative heterosis was recorded in the hybrid TC 79 (-10.48) followed by the hybrids TC 41 (-8.56) and TC 35 (-7.69).

For the trait plant height, similar results were reported by Chaudhary *et al.* (2007), Rosamma and Vijayakumar (2007), Chandirakala *et al.* (2010), Gouri Shankar *et al.* (2010), Kumar Babu *et al.* (2010b) and Tiwari *et al.* (2011).

4.2.5.3 Number of ear bearing tillers per plant

The standard heterosis for number of ear bearing tillers plant^{-1} ranged from -39.64 (TC 102) to 9.64 (TC 63). None of the hybrids recorded significant positive heterosis over the superior check, MTU 1121.

Singh *et al.* (2006), Rosamma and Vijayakumar (2007), Gouri Sankar *et al.* (2010), Kumar Babu *et al.* (2010b) and Tiwari *et al.* (2011) also reported similar results.

4.2.5.4 Days to maturity

The standard heterosis estimated over the superior check for days to maturity ranged from -5.37 (TC 71) to 15.29 (TC 18). A total of seven hybrids were found to have highly significant negative heterosis over the standard check, MTU 1121.The highest significant negative heterosis was recorded in the hybrid, TC 71(-5.37) followed by TC 80 (- 4.55) and TC 70 (- 3.72).

Negative standard heterosis for this trait was also reported by Rahimi *et al.* (2010) and Sen and Singh (2011).

4.2.5.5 Panicle length

The panicle length of hybrids showed standard heterosis over superior check ranging from -11.37 (TC 66) to 14.57 (TC 16). A total of fourteen hybrids were found to possess significant positive heterosis over the standard check, MTU 1121. The highest positive standard heterosis was recorded in the hybrid TC 16 (14.57) followed by TC 68 (13.89) and TC 18 (12.61).

Earlier workers Pandya and Tripathi (2006) and Chandirakala *et al.* (2010) reported positive standard heterosis for panicle length.

4.2.5.6 Number of filled grains per panicle

Among the hybrids, standard heterosis for number of filled grains panicle^{-1} ranged from -95.94 (TC 94) to 38.12 (TC 63). Out of the 110 hybrids evaluated, five hybrids viz. TC 63 (38.12), TC 100 (36.04), TC 45 (31.50), TC 34 (24.85) and TC 22 (23.83) registered highly significant positive heterosis over the standard check, MTU 1121.

Positive standard heterosis for number of filled grains was also reported by Singh *et al.* (2006), Singh *et al.* (2007), Gouri Shankar *et al.* (2010), Kumar Babu *et al.* (2010b) and Tiwari *et al.* (2011).

4.2.5.7 Spikelet fertility

Range of standard heterosis for spikelet fertility was from -94.77 (TC 93) to -1.97 (TC 106). None of the hybrids evaluated registered significant positive standard heterosis for spikelet fertility over the standard check, MTU 1121.

Positive standard heterosis for spikelet fertility was reported by Singh *et al.* (2006), Gouri Shankar *et al.* (2010), Kumar Babu *et al.* (2010b) and Tiwari *et al.* (2011).

4.2.5.8 Test weight

The range of standard heterosis for test weight was from -31.68 (TC 31) to 37.96 (TC 57). Forty four hybrids were observed to have significant positive standard heterosis for test weight over the superior check, MTU 1121. The highest positive standard heterosis was recorded in the hybrid TC 57 (37.96) followed by TC 94 (33.25) and TC 96 (31.68).

Similar results were reported by Singh *et al.* (2006), Singh *et al.* (2007), Gouri Shankar *et al.* (2010), Kumar Babu *et al.* (2010b) and Tiwari *et al.* (2011).

4.2.5.9 Grain yield per plant

Among the 110 crosses evaluated against standard check, MTU 1121, the hybrid TC 93 (-95.70) recorded lowest standard heterosis and TC 11 (31.48) recorded highest

standard heterosis. Ten hybrids recorded significant positive standard heterosis over the superior check. The hybrid TC 11 exhibited the highest heterosis of 31.48% followed by TC 7 (29.21), TC 1 (25.15), TC 34 (23.60), TC 38 (20.49), TC 33 (16.90), TC 37 (16.18), TC 39 (15.95), TC 20 (15.71) and TC 69 (15.71).

Positive standard heterosis for grain yield per plant was also reported by Singh *et al.*(2006), Rosamma and Vijayakumar (2007), Singh *et al.* (2007), Gouri Shankar *et al.* (2010), Kumar Babu *et al.* (2010b) and Tiwari *et al.*(2011).

Superior hybrids identified character wise based on *per se* performance, *sca* effects and standard heterosis were given in table 4.14.

Promising hybrids based on *per se* performance, *sca* effect and standard heterosis

Based on *per se* performance, favourable *sca* effects and heterosis for yield the crosses TC 11, TC 7, TC 1, TC 34, TC 20 and TC 69 which recorded high *per se* performance (27.50, 27.03, 26.18, 25.85, 24.20 and 24.20 g), favourable positive *sca* effects (1.90, 2.39, 5.18, 1.33, 3.00 and 1.02 respectively) and significant standard heterosis (31.48%, 29.21%, 25.15 %, 23.60%, 15.71 % and 15.71 %) over the best check MTU 1121 for grain yield plant^{-1} were identified as promising heterotic hybrids. Besides the grain yield, these crosses also showed good *per se* performance, favourable *sca* effects and positive standard heterosis for other important yield contributing characters like number of ear bearing tillers plant^{-1}, panicle length, number of filled grains panicle^{-1} and test weight.

4.3 IDENTIFICATION OF *Rf* GENES IN THE RESTORERS

A total of eighty four primers specific to *Rf3* and *Rf4* gene linked markers, were used for screening 57 parental lines, 2 maintainers and 2 checks, of which thirty three primers were found to be polymorphic. Scoring was done based on the presence (1) or absence (0) of bands. The polymorphic primers amplified a set of 66 alleles.

4.3.1 Molecular Cluster Analysis

Molecular cluster analysis was carried out employing UPGMA (Unweighted Pair Group Method with Arithmetic Averages) clustering algorithm using NTSYSpc version 2.0 (Rohlf, 1994), which grouped the 57 parental lines, 2 maintainers and 2

checks (Swarna and BPT 5204) into 2 major clusters, I and II. The details of the genotypes in each cluster are given in Table 4.15. The two CMS lines (APMS 6A and APMS 10A) and their maintainers were grouped under cluster I along with the restorer line TCNP 76. Remaining all other restorers and the 2 checks under study were grouped into major cluster II.

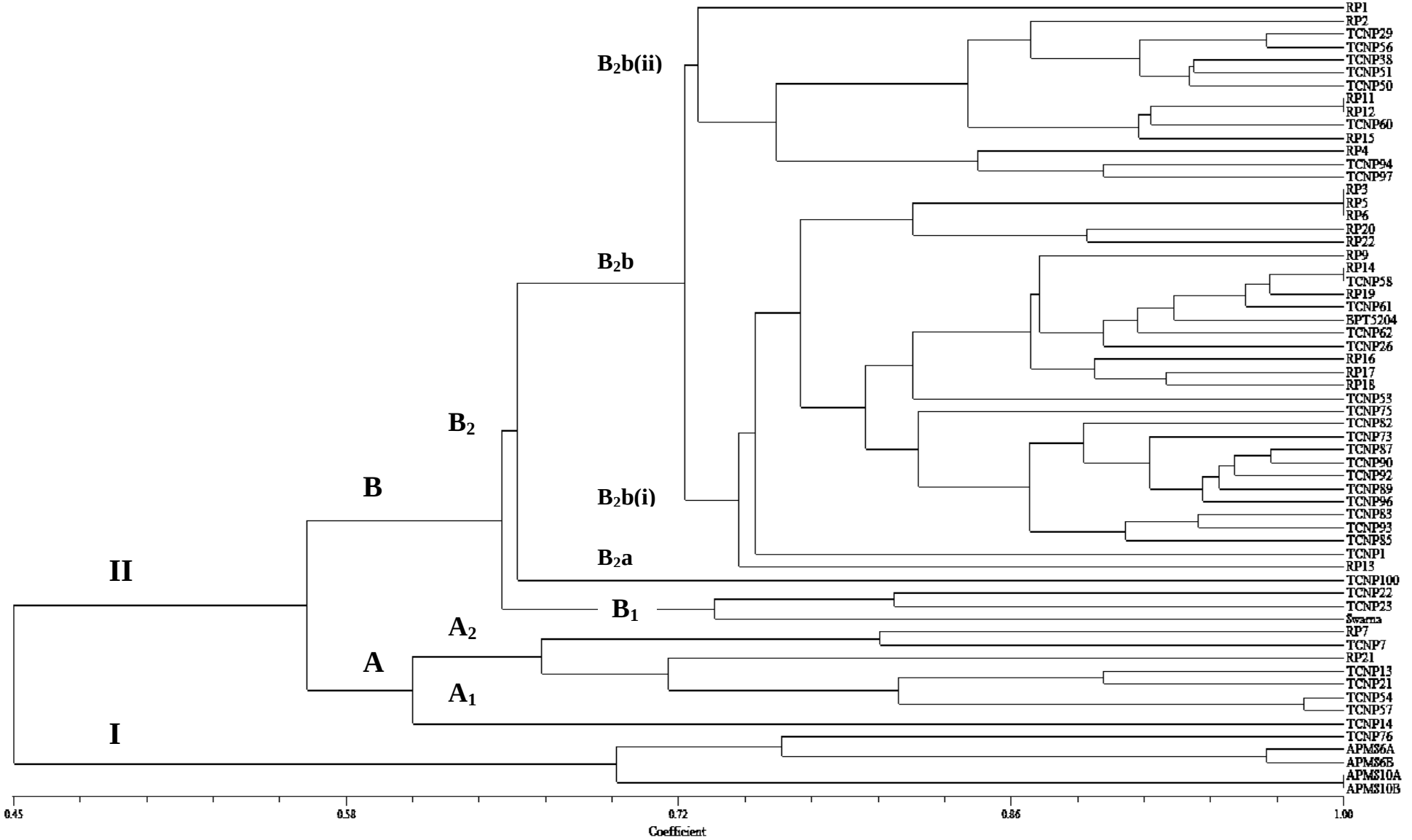
The major cluster II was subdivided into two clusters, cluster A with eight genotypes and cluster B with forty eight genotypes. The cluster A was again subdivided into clusters A_1 and A_2 having one and seven genotypes, respectively. The cluster B got subdivided into clusters B_1 and B_2 comprising of three and forty five genotypes, respectively. The check varieties, Swarna and BPT 5204 fell into these two clusters, respectively. The cluster B_2 was again subdivided into cluster B_2a containing a single restorer line (TCNP 100) and cluster B_2b having 44 genotypes. The cluster B_2b got again separated into clusters $B_2b(i)$ and $B_2b(ii)$ containing thirty and fourteen genotypes, respectively. The dendrogram of the parental lines is given in figure 4.3.

The coefficient of similarities among genotypes ranged from 0.45 to 1.00 with an average similarity index of 0.72. The results indicated presence of high genetic diversity among the parental lines used in the crossing programme.

Table 4.15. Molecular clustering pattern among the 57 parental lines, 2 maintainers and 2 checks in rice (*Oryza sativa* L.)

S. No.	Cluster	Number of genotypes	Genotypes
1	**I**	5	APMS 6A, APMS 10A, APM6B, APMS 10A,TCNP 76
2	**II**	56	Remaining 56 genotypes (54 restorers + 2 checks)
3	**A**	8	
4	A_1	1	TCNP 14
5	A_2	7	RP 7,TCNP 7,RP 21,TCNP 13,TCNP 21,TCNP 54,TCNP 57
6	**B**	48	
7	B_1	3	Swarna, TCNP 22,TCNP 23
8	B_2	45	TCNP 100, RP 13, TCNP 1,TCNP 85, TCNP 93,TCNP 83, TCNP 96, TCNP 89,TCNP 92,TCNP 90, TCNP 87, TCNP 73, TCNP 82, TCNP 75, TCNP 53, RP 18, RP 17, RP 16, TCNP 26, TCNP 62, BPT 5204, TCNP 61, RP 19, TCNP 58, RP 14, RP 9, RP 22, RP 20, RP 6, RP 5, RP 3, TCNP 97,TCNP 94, RP 4, RP 15, TCNP 60, RP 12, RP 11, TCNP 50,TCNP 51,TCNP 38,TCNP 56,TCNP 29, RP 2, RP 1
9	B_2a	1	TCNP 100
10	B_2b	44	RP 13, TCNP 1, TCNP 85, TCNP 93, TCNP 83, TCNP 96, TCNP 89, TCNP 92, TCNP 90,TCNP 87, TCNP 73, TCNP 82, TCNP 75, TCNP 53, RP 18, RP 17, RP 16, TCNP 26, TCNP 62, BPT5204, TCNP 61, RP 19, TCNP 58, RP 14, RP 9, RP 22, RP 20, RP 6, RP 5, RP 3,TCNP 97, TCNP 94, RP 4, RP 15, TCNP 60, RP 12, RP 11, TCNP 50, TCNP 51, TCNP 38, TCNP 56, TCNP 29, RP 2, RP 1
11	$B_2b(i)$	30	RP 13, TCNP 1, TCNP 85, TCNP 93, TCNP 83, TCNP 96, TCNP 89, TCNP 92, TCNP 90, TCNP 87, TCNP 73, TCNP 82, TCNP 75, TCNP 53, RP 18, RP 17, RP 16, TCNP 26, TCNP 62, BPT5204, TCNP 61, RP 19, TCNP 58, RP 14, RP 9, RP 22, RP 20, RP 6, RP 5, RP 3
12	$B_2b(ii)$	14	TCNP 97, TCNP 94, RP 4, RP 15, TCNP 60, RP 12, RP 11, TCNP 50, TCNP 51, TCNP 38, TCNP 56, TCNP 29, RP 2, RP 1

Figure 4.3 Molecular cluster analysis dendrogram of the parental lines in rice (*Oryza sativa* L.)



4.3.2 Screening for *Rf* Genes

In the present investigation, a total of 55 elite restorer lines were studied and out of which 23 were identified as best restorers based on spikelet fertility of the hybrids. The list of best restorers identified and spikelet fertility of the corresponding hybrids is presented in table 4.17.

The 55 restorers, two CMS lines and their maintainers were screened for the presence of *Rf3* and *Rf4* genes using a set of forty five and thirty nine SSRs, respectively. Among these, seventeen primers were found polymorphic for *Rf3* gene while sixteen showed polymorphism for *Rf4* gene. The list of primers polymorphic for *Rf3* and *Rf4* genes is given in table 4.16.

Table 4.16. List of primers polymorphic for *Rf3* and *Rf4* genes

Gene	Polymorphic primers	Number of polymorphic primers
Rf3	RM 315, RM 443, RM 576, RM 1201, RM 3148, RM 3530, RM 3627, RM 3740, RM 3873, RM 5359, RM 10287, RM 10305, RM 10318, DRRM Rf3-5, DRRM Rf3-6, DRRM Rf3-10, DRRM Rf3-24	17
Rf4	RM 171, RM 216, RM 228, RM 244, RM 258, RM 294, RM 311, RM 591, RM 1108, RM 3123, RM 6100, RM 6344, DRCG Rf4-8, DRCG Rf4-14, DRRM Rf4-10, DRRM Rf4-20	16

Two proven restorers, Swarna and BPT 5204 were taken as checks for further confirming the *Rf* genes in the restorers under study. The polymorphism generated between both the restorer checks and CMS lines along with field spikelet fertility of hybrids obtained in the test crosses was taken as criteria for identifying presence or absence of *Rf* genes present in the restorers under study.

Four primers (RM 576, RM 10287, RM 10305 and DRRM Rf3-5) were found to distinguish the restorer checks and CMS lines for *Rf3* gene while five primers

Table 4.17. Best restorers and spikelet fertility of corresponding hybrids

S. No.	Restorer lines	Cross Combinations	Spikelet fertility (%)	Grain yield plant $^{-1}$ (g)
1	RP4	APMS 6A × RP 4	82.10	21.15
		APMS 10A × RP 4	76.48	18.23
2	RP5	APMS 6A × RP 5	81.10	27.03
		APMS 10A × RP 5	77.22	21.00
3	RP6	APMS 6A × RP 6	82.40	24.20
		APMS 10A × RP 6	80.58	20.90
4	RP11	APMS 6A × RP 11	81.25	19.25
		APMS 10A × RP 11	83.28	23.20
5	RP13	APMS 6A × RP 13	82.45	27.50
		APMS 10A × RP 13	80.95	22.45
6	RP18	APMS 6A × RP 18	78.62	19.45
		APMS 10A × RP 18	80.55	24.20
7	RP19	APMS 6A × RP 19	83.16	19.70
		APMS 10A × RP 19	81.13	19.15
8	RP21	APMS 6A × RP 21	78.21	16.60
		APMS 10A × RP 21	80.03	18.20
9	TCNP 13	APMS 6A × TCNP 13	75.39	18.40
		APMS 10A × TCNP 13	80.85	19.30
10	TCNP 23	APMS 6A × TCNP 23	90.14	24.45
		APMS 10A × TCNP 23	90.71	25.85
11	TCNP 50	APMS 6A × TCNP 50	88.68	24.30
		APMS 10A × TCNP 50	90.25	25.20
12	TCNP 53	APMS 6A × TCNP 53	89.78	24.25
		APMS 10A × TCNP 53	78.20	19.40
13	TCNP 61	APMS 6A × TCNP 61	85.90	20.35
		APMS 10A × TCNP 61	80.03	20.50
14	TCNP 75	APMS 6A × TCNP 75	82.42	22.75
		APMS 10A × TCNP 75	82.29	20.90
15	TCNP 90	APMS 6A × TCNP 90	80.75	18.15
		APMS 10A × TCNP 90	91.49	18.00
16	TCNP 94	APMS 6A × TCNP 94	85.85	23.10
		APMS 10A × TCNP 94	80.95	19.40
17	TCNP 97	APMS 6A × TCNP 97	80.15	19.00
		APMS 10A × TCNP 97	82.07	17.80
18	TCNP 100	APMS 6A × TCNP 100	82.65	20.30
		APMS 10A × TCNP 100	81.28	19.35
19	RP2	APMS 6A × RP 2	88.14	26.18
20	RP7	APMS 10A × RP 7	83.22	21.20
21	RP16	APMS 6A × RP 16	81.48	21.40
22	TCNP 51	APMS 6A × TCNP 51	90.66	23.20
23	TCNP 89	APMS 6A × TCNP 89	81.20	19.20

(RM 294, RM 311, RM 1108, RM 6100 and DRCG Rf4-14) specific to *Rf4* gene distinguished the checks and CMS lines. All the identified restorers showed similar banding pattern with the restorer checks except RP13 for DRRM Rf3-5, TCNP 100 for RM 311 and RP 7, RP 21 and TCNP 13 for primers DRCG Rf4-14 and RM 6100. For DRRM Rf3-5 and RM 10287, all the identified restorers showed similar banding pattern with the checks. Molecular profile of 55 restorers, two checks and two CMS lines along with their maintainers using primers RM 10287, DRRM Rf3-5 and RM 6100 are presented in plates 1, 2 and 3 respectively.

Since Swarna and BPT 5204 showed polymorphism for both *Rf3* and *Rf4* specific primers, it can be inferred that both *Rf3* and *Rf4* genes may be present in the restorer checks. All the identified restorers which are co segregating with the restorer checks may also have *Rf3* and *Rf4* genes. In the identified restorers having different segregating pattern, some other *Rf* gene may be present. Similar findings were reported by Balaji Suresh *et al.* (2012).

For further confirmation of the presence or absence of *Rf* genes, F_2 population has to be screened for the presence of *Rf* genes and field restoration has to be studied.

Table 4.14. Superior hybrids identified character wise based on *per se* performance *sca* effects and standard heterosis

Character	Hybrids	*Per se* performance	sca effects	Standard heterosis
Days to 50% flowering	TC 92	84.50	-1.52	-7.14**
	TC 71	85.00	-0.48	-6.59**
	TC 80	85.00	-4.52**	-6.59**
	TC 9	87.00	-0.48	-4.40**
	TC 70	87.00	-4.02**	-4.40**
Plant height	TC 79	93.10	-2.55	-10.48**
	TC 41	95.10	-3.00	-8.56**
	TC 35	96.00	-10.45**	-7.69**
	TC 93	96.50	-2.25	-7.21**
	TC 37	97.10	-2.05	-6.63**
No. of ear bearing tillers plant^{-1}	TC 63	9.10	1.64**	9.64
	TC 80	9.05	0.80*	9.04
	TC 20	8.90	1.42**	7.23
	TC 11	8.82	0.62	6.20
	TC 1	8.75	0.54	5.36
Days to maturity	TC 71	114.50	-0.48	-5.37**
	TC 80	115.50	-4.52**	-4.55**
	TC 70	116.50	-4.02**	-3.72**
	TC 92	116.50	-1.52	-3.72**
	TC 9	117.00	-1.23	-3.31**
Panicle length	TC 16	28.71	0.14	14.57**
	TC 68	28.54	1.03	13.89**
	TC 18	28.22	0.68	12.61**
	TC 107	28.21	0.48	12.57**
	TC 5	28.13	0.8	12.25**
No. of filled grains per panicle	TC 63	321.43	70.60**	38.12**
	TC 100	316.59	52.10**	36.04**
	TC 45	306.02	22.24*	31.50**
	TC 34	290.54	51.57**	24.85**
	TC 22	288.18	47.90**	23.83**
Spikelet fertility	TC 106	91.49	6.92**	-1.97
	TC 34	90.71	1.83	-2.81
	TC 91	90.66	11.12**	-2.87
	TC 38	90.25	2.33	-3.31
	TC 39	89.78	4.25*	-3.81
Test weight	TC 57	26.35	4.47**	37.96**
	TC 94	25.45	1.53**	33.25**
	TC 96	25.15	1.23**	31.68**
	TC 28	24.75	2.96**	29.58**
	TC 100	24.55	0.86*	28.53**
Grain yield plant^{-1}	TC 11	27.50	1.9	31.48**
	TC 7	27.03	2.39*	29.21**
	TC 1	26.18	5.18**	25.15**
	TC 34	25.85	1.33	23.60**
	TC 38	25.20	1.08	20.49*
	TC 39	24.25	1.80	15.95*
	TC 20	24.20	3.00	15.71*
	TC 69	24.20	1.02	15.71*

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

Table 4.6. Analysis of variance for yield and yield contributing characters of hybrids and checks in rice (*Oryza sativa* L.) during *rabi* 2012-13

Source of variations	df	Days to 50 % flowering	Plant height	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight	Grain yield plant^{-1}
		Mean Sum of Squares								
Replications	1	3.44	13.46	0.47	3.20	2.78	518.68	7.08	0.67	5.36
Genotypes	113	55.10**	210.67**	1.67**	47.46**	3.52**	8131.23**	783.28**	12.00**	78.91**
Error	113	1.87	5.70	0.32	2.26	1.16	236.87	7.24	0.24	2.91

** Significant at 1% level

Table 4.11.General combining ability effects of parental lines for yield and yield component characters in rice (*Oryza sativa* L.) during *rabi,* 2012-13

Parents	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
Lines - Restorer lines									
RP 2	-3.85 **	-1.41	1.54 **	-3.82**	-0.32	37.42**	5.33**	1.57**	5.23**
RP 3	-1.85 **	13.69**	-0.46	-1.82**	1.13	6.52	-1.67	1.79**	0.15
RP 4	-0.85	13.94**	0.19	-0.82	1.55**	44.04**	12.66**	-0.13	4.54**
RP 5	-2.85 **	4.14 **	0.51	-2.82**	0.93	29.18**	12.53**	2.84**	8.87**
RP 12	-8.35 **	-0.31	-0.18	-7.57**	0.09	-55.42**	-18.74**	1.49**	-6.62**
RP 13	-0.35	12.24 **	1.54 **	1.18	0.54	52.22**	15.07**	-2.23**	9.83**
RP 14	-0.85	11.94 **	-0.04	0.18	-1.04	4.78	6.07**	-0.66*	0.74
RP 15	5.65 **	22.74 **	-0.43	5.68**	2.41**	-8.41	0.02	-1.16**	1.83*
RP 17	11.15 **	19.94 **	0.18	11.18**	1.38*	39.37**	2.73	-1.53**	3.73**
RP 18	-2.35 **	-1.01	1.24 **	-2.32**	0.15	50.51**	12.95**	0.44	6.68**
RP 19	1.65 **	5.19 **	-0.12	1.68*	0.83	75.80**	15.51**	-0.83**	4.28**
RP 20	-1.85 **	3.89 **	-0.42	-2.07**	1.17*	-16.43*	0.62	0.79**	0.77
RP 22	-1.35 *	8.14 **	-0.21	-1.32*	0.72	16.26*	1.60	0.54	-1.82*
TCNP 7	0.15	-6.63 **	-0.10	0.18	-1.08	-18.59*	7.82**	1.47**	-0.30
TCNP 13	-2.85 **	-14.46 **	1.02 **	-2.82**	-1.61**	-43.85**	11.49**	-1.41**	3.70**
TCNP 22	-0.85	-4.29 **	0.25	-0.82	-0.55	-17.72*	-10.51**	-3.88**	-0.68
TCNP 23	-2.85 **	0.19	0.44	-1.82**	0.43	74.50**	23.79**	-0.66*	10.00**
TCNP 38	-2.10 **	-7.46 **	0.86 **	-0.82	-2.35**	-13.39	0.97	-2.31**	-1.28
TCNP 50	-3.35 **	-14.76 **	0.25	-1.82**	0.04	56.58**	22.83**	-0.73**	9.60**
TCNP 53	7.65 **	1.19	-0.39	7.18**	-1.91**	16.09*	17.36**	-1.88**	6.68**
TCNP 56	-0.35	-15.81 **	0.78 **	-1.82**	-2.21**	-79.22**	8.08**	2.99**	-1.95*
TCNP 60	3.65 **	12.44 **	0.69 *	1.18	0.57	-16.71*	-8.27**	1.49**	-0.59

Table 4.11 (Contd..)

Parents	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TCNP 61	6.15 **	1.34	-0.55 *	3.68**	0.44	107.53**	16.33**	-2.96**	5.28**
TCNP 62	8.15 **	2.69 *	0.09	5.68**	0.10	-39.51**	-17.25**	-0.66*	-5.30**
TCNP 73	7.65 **	5.14 **	0.12	5.18**	-0.30	1.04	3.17*	-1.61**	-1.65*
TCNP 83	-1.85 **	-0.81	-0.10	-3.82**	-1.29*	-119.39**	-38.38**	2.99**	-10.50**
TCNP 85	-1.85 **	3.59 **	0.67 *	-3.82**	-0.10	-101.69**	-36.06**	1.84**	-12.45**
TCNP 87	7.65 **	6.29 **	0.05	5.68**	0.26	-3.21	-3.42*	-0.71*	-4.10**
TCNP 89	4.65 **	11.44 **	0.45	2.68**	-1.00	-15.08	2.02	3.09**	1.55
TCNP 92	8.15 **	4.29 **	-0.21	6.93**	1.08	44.60**	2.37	-2.36**	-3.02**
TCNP 93	7.65 **	-2.21	-0.27	7.18**	-0.46	-15.89*	-15.75**	-1.61**	-4.50**
TCNP 94	-0.85	-8.61 **	0.80 **	-1.32*	-0.12	74.58**	16.77**	0.89**	6.10**
TCNP 97	9.15 **	-5.16 **	-0.33	8.68**	-2.85**	12.31	14.48**	-1.61**	3.25**
RP 1	2.65 **	-0.36	-0.14	2.18**	1.35*	34.13**	4.09**	-2.36**	-3.08**
RP 6	-5.85 **	-1.21	-0.25	-6.32**	0.19	41.46**	14.86**	-0.71*	7.40**
RP 7	-10.35 **	-3.76 **	0.01	-10.82**	-1.24*	25.55**	10.44**	-0.06	3.00**
RP 9	1.15	3.19 *	0.54 *	0.68	-0.58	-3.58	4.12**	2.19**	-1.06
RP 11	-2.85 **	4.29 **	-1.10 **	-3.32**	0.93	54.08**	15.63**	-0.66*	6.08**
RP 16	-1.85 **	11.04 **	-0.69 *	-1.82**	-0.01	-21.57**	9.06**	0.94**	2.75**
RP 21	-7.35 **	-18.26 **	2.01 **	-6.82**	-1.28*	-7.38	12.48**	0.79**	2.25**
TCNP 1	2.40 **	-14.01 **	0.41	3.68**	-0.50	-0.10	1.34	-1.83**	-2.61**
TCNP 14	3.15 **	-16.36 **	-0.32	5.18**	0.76	-111.45**	-43.04**	0.04	-13.60**
TCNP 21	-0.85	-7.06 **	-0.90 **	1.18	0.94	-60.69**	-28.25**	0.94**	-10.30**
TCNP 26	-0.35	4.79 **	-0.48	1.68*	0.04	42.29**	5.17**	-2.38**	0.88
TCNP 29	0.15	11.59 **	-1.09 **	2.18**	0.26	-11.23	-0.62	0.07	-3.57**
TCNP 51	-10.85 **	-12.06 **	-1.14 **	-8.82**	-1.29*	-13.04	11.36**	1.64**	3.50**
TCNP 54	-5.35 **	-15.16 **	-0.84	-3.32**	1.18*	-160.34**	-61.57**	3.59**	-13.65**
TCNP 57	-2.35 **	-14.01 **	-0.59 *	-1.82**	0.12	-122.04**	-47.32**	3.59**	-12.05**
TCNP 58	2.15 **	-4.41 **	-0.55 *	2.68**	-0.09	-4.15	-7.82**	-2.11**	-4.62**

Table 4.11 (Contd..)

Parents	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TCNP 75	1.65 **	9.04 **	-0.81 **	2.18**	1.77**	100.02**	15.72**	3.37**	6.68**
TCNP 76	0.15	-2.16	-1.02 **	0.68	0.68	-60.85**	-19.33**	2.19**	-7.58**
TCNP 82	-1.85 **	-4.86 **	-0.52	-1.32*	-0.76	16.41*	-1.44	-1.61**	-4.04**
TCNP 90	-8.35 **	-7.11 **	0.26	-7.82**	-0.53	39.00**	19.49**	-2.81**	2.93**
TCNP 96	-0.35	-0.76	0.39	0.18	1.96**	-25.24**	-12.14**	0.09	-2.13*
TCNP 100	-2.35 **	-4.01 **	-1.06 **	-2.82**	-0.43	69.87**	15.33**	-0.26	4.68**
Testers-CMS lines									
APMS6A	-0.52 **	0.15	0.21 **	-0.52**	-0.19	5.89**	1.54**	-0.77**	0.63**
APMS10A	0.52 **	-0.15	-0.21 **	0.52**	0.19	-5.89**	-1.54**	0.77**	-0.63**
CD 95% GCA(Line)	1.21	2.44	0.54	1.32	1.15	15.65	2.99	0.54	1.63
CD 95% GCA(Tester)	0.23	0.46	0.10	0.25	0.22	2.98	0.57	0.10	0.31
Heritability (Narrow Sense) %	29.20	18.90	26.25	28.24	17.43	16.01	24.98	39.46	35.67
Genetic Advance 5 %	1.82	2.25	0.47	1.70	0.37	15.38	5.90	2.05	2.46

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

Table 4.12. Specific combining ability effects of hybrids for yield and yield component characters during *rabi,* 2012-13

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 1	0.02	-2.50	0.54	0.02	-0.02	41.91**	14.63**	0.04	5.18**
TC 2	-0.02	2.50	-0.54	-0.02	0.02	-41.91**	-14.63**	-0.04	-5.18**
TC 3	0.02	6.00**	0.14	0.02	0.13	-1.13	1.22	-1.33**	-2.63*
TC 4	-0.02	-6.00**	-0.14	-0.02	-0.13	1.13	-1.22	1.33**	2.63*
TC 5	0.02	0.45	0.09	0.02	0.80	26.11*	1.27	-1.26**	0.83
TC 6	-0.02	-0.45	-0.09	-0.02	-0.80	-26.11*	-1.27	1.26**	-0.83
TC 7	-0.98	3.05	0.28	-0.98	0.56	7.16	0.40	-0.78*	2.39*
TC 8	0.98	-3.05	-0.28	0.98	-0.56	-7.16	-0.40	0.78*	-2.39*
TC 9	-0.48	3.80*	-0.32	-1.23	0.54	45.59**	4.58*	2.12**	-0.25
TC 10	0.48	-3.80*	0.32	1.23	-0.54	-45.59**	-4.58*	-2.12**	0.25
TC 11	3.52**	-0.65	0.62	3.52**	0.46	3.68	-0.79	0.79*	1.90
TC 12	-3.52**	0.65	-0.62	-3.52**	-0.46	-3.68	0.79	-0.79*	-1.90
TC 13	-0.98	2.45	0.04	-0.48	0.18	31.06**	0.26	0.72	0.94
TC 14	0.98	-2.45	-0.04	0.48	-0.18	-31.06**	-0.26	-0.72	-0.94
TC 15	0.02	1.75	-0.27	0.02	-0.14	-26.54*	-4.11	-1.68**	-0.90
TC 16	-0.02	-1.75	0.27	-0.02	0.14	26.54*	4.11	1.68**	0.90
TC 17	-1.48	5.35**	-0.26	-1.48	-0.68	-21.56	0.01	2.84**	-0.20
TC 18	1.48	-5.35**	0.26	1.48	0.68	21.56	-0.01	-2.84**	0.20
TC 19	1.02	-11.80**	-1.42**	1.02	-0.72	-45.27**	-2.51	0.82*	-3.00*
TC 20	-1.02	11.80**	1.42**	-1.02	0.72	45.27**	2.51	-0.82*	3.00*
TC 21	-3.48**	-1.10	0.34	-2.98**	-0.37	-47.90**	-0.53	0.09	-0.35
TC 22	3.48**	1.10	-0.34	2.98**	0.37	47.90**	0.53	-0.09	0.35
TC 23	1.02	1.50	0.24	0.77	0.25	21.89	-0.22	0.87*	0.59
TC 24	-1.02	-1.50	-0.24	-0.77	-0.25	-21.89	0.22	-0.87*	-0.59
TC 25	1.52	0.35	0.44	1.52	0.69	-14.13	2.12	0.32	-0.80
TC 26	-1.52	-0.35	-0.44	-1.52	-0.69	14.13	-2.12	-0.32	0.80

Table 4.12 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 27	4.02**	2.25	0.34	4.02**	-0.10	57.99**	2.47	-2.96**	-0.08
TC 28	-4.02**	-2.25	-0.34	-4.02**	0.10	-57.99**	-2.47	2.96**	0.08
TC 29	1.02	-0.05	0.91*	1.02	1.43	0.10	-4.27*	0.57	-1.08
TC 30	-1.02	0.05	-0.91*	-1.02	-1.43	-0.10	4.27*	-0.57	1.08
TC 31	-0.98	-2.42	-0.26	-0.98	1.04	-0.71	-10.03**	-1.86**	-0.46
TC 32	0.98	2.42	0.26	0.98	-1.04	0.71	10.03**	1.86**	0.46
TC 33	-0.98	3.10	0.45	-0.98	0.22	-51.57**	-1.83	-0.18	-1.33
TC 34	0.98	-3.10	-0.45	0.98	-0.22	51.57**	1.83	0.18	1.33
TC 35	0.27	-10.45**	0.60	0.02	0.54	-21.43	-10.05**	2.07**	-2.39*
TC 36	-0.27	10.45**	-0.60	-0.02	-0.54	21.43	10.05**	-2.07**	2.39*
TC 37	-0.98	-2.05	0.39	-0.98	-0.17	-20.33	-2.33	-0.81*	-1.08
TC 38	0.98	2.05	-0.39	0.98	0.17	20.33	2.33	0.81*	1.08
TC 39	0.02	0.50	-0.36	0.02	-0.48	10.04	4.25*	-0.96*	1.80
TC 40	-0.02	-0.50	0.36	-0.02	0.48	-10.04	-4.25*	0.96*	-1.80
TC 41	-1.98*	-3.00	-0.14	-0.98	-1.18	-10.21	10.84**	1.97**	0.37
TC 42	1.98*	3.00	0.14	0.98	1.18	10.21	-10.84**	-1.97**	-0.37
TC 43	-4.98**	-0.15	-0.72	-4.98**	1.05	61.96**	12.81**	-1.43**	1.33
TC 44	4.98**	0.15	0.72	4.98**	-1.05	-61.96**	-12.81**	1.43**	-1.33
TC 45	-1.48	5.75**	0.14	-1.48	0.44	22.24*	1.39	0.72	-0.70
TC 46	1.48	-5.75**	-0.14	1.48	-0.44	-22.24*	-1.39	-0.72	0.70
TC 47	-0.48	3.60*	0.59	-0.48	-0.75	-5.14	0.67	-0.88*	-0.18
TC 48	0.48	-3.60*	-0.59	0.48	0.75	5.14	-0.67	0.88*	0.18
TC 49	0.02	0.15	0.62	0.02	-0.27	-12.69	1.22	-0.93*	1.07
TC 50	-0.02	-0.15	-0.62	-0.02	0.27	12.69	-1.22	0.93*	-1.07
TC 51	1.02	1.30	-0.30	1.02	-0.34	-8.16	0.58	0.97*	-1.48
TC 52	-1.02	-1.30	0.30	-1.02	0.34	8.16	-0.58	-0.97*	1.48
TC 53	-0.98	-0.90	-0.10	-0.98	-1.28	-10.16	2.68	-0.18	-1.13
TC 54	0.98	0.90	0.10	0.98	1.28	10.16	-2.68	0.18	1.13
TC 55	-0.48	1.60	-0.51	-0.48	0.16	32.17**	6.60**	-0.88*	1.52
TC 56	0.48	-1.60	0.51	0.48	-0.16	-32.17**	-6.60**	0.88*	-1.52

Table 4.12 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No: of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 57	1.52	4.45*	0.39	1.52	-0.95	6.39	11.00**	4.47**	1.87
TC 58	-1.52	-4.45*	-0.39	-1.52	0.95	-6.39	-11.00**	-4.47**	-1.87
TC 59	1.02	-2.50	-0.06	0.27	-0.15	-27.63*	-0.12	-0.78*	0.75
TC 60	-1.02	2.50	0.06	-0.27	0.15	27.63*	0.12	0.78*	-0.75
TC 61	-0.48	0.60	-0.11	-0.48	-0.48	35.30**	10.46**	0.07	-0.88
TC 62	0.48	-0.60	0.11	0.48	0.48	-35.30**	-10.46**	-0.07	0.88
TC 63	-1.98*	-2.80	1.64**	-1.98*	0.93	70.60**	0.91	-0.13	1.22
TC 64	1.98*	2.80	-1.64**	1.98*	-0.93	-70.60**	-0.91	0.13	-1.22
TC 65	0.02	-6.05**	-0.41	0.02	1.10	-0.92	-2.51	0.97*	-0.03
TC 66	-0.02	6.05**	0.41	-0.02	-1.10	0.92	2.51	-0.97*	0.03
TC 67	-1.48	0.05	-0.01	-1.48	-1.03	-10.39	0.55	0.42	0.71
TC 68	1.48	-0.05	0.01	1.48	1.03	10.39	-0.55	-0.42	-0.71
TC 69	4.02**	-3.30	-0.12	4.02**	-0.02	7.68	-0.63	3.07**	1.02
TC 70	-4.02**	3.30	0.12	-4.02**	0.02	-7.68	0.63	-3.07**	-1.02
TC 71	-0.48	-2.15	-0.96*	-0.48	-0.69	-13.50	-7.68**	-0.58	-3.68**
TC 72	0.48	2.15	0.96*	0.48	0.69	13.50	7.68**	0.58	3.68**
TC 73	-1.98*	-6.80**	0.10	-1.98*	-1.40	-32.30**	0.15	0.07	0.38
TC 74	1.98	6.80**	-0.10	1.98*	1.40	32.30**	-0.15	-0.07	-0.38
TC 75	1.02	1.20	-0.02	1.02	0.25	-8.74	-2.56	0.12	-2.60*
TC 76	-1.02	-1.20	0.02	-1.02	-0.25	8.74	2.56	-0.12	2.60*
TC 77	2.02*	3.45*	0.19	1.52	-0.19	4.40	4.24*	-1.58**	2.87*
TC 78	-2.02*	-3.45*	-0.19	-1.52	0.19	-4.40	-4.24*	1.58**	-2.87*
TC 79	4.52**	-2.55	-0.80*	4.52**	-0.27	-22.07	-2.46	1.47**	-1.43
TC 80	-4.52**	2.55	0.80*	-4.52**	0.27	22.07	2.46	-1.47**	1.43
TC 81	0.77	2.00	0.64	0.02	0.12	32.54**	2.95	-1.31**	3.01*
TC 82	-0.77	-2.00	-0.64	-0.02	-0.12	-32.54**	-2.95	1.31**	-3.01*
TC 83	-0.48	-0.25	0.45	-0.48	0.10	-38.31**	-11.75**	-0.98*	-1.18
TC 84	0.48	0.25	-0.45	0.48	-0.10	38.31**	11.75**	0.98*	1.18
TC 85	-0.48	-6.05**	-0.32	-0.48	-0.75	-60.30**	-19.62**	1.72**	-4.08**
TC 86	0.48	6.05**	0.32	0.48	0.75	60.30**	19.62**	-1.72**	4.08**

Table 4.12 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 87	0.02	3.40	-0.10	0.02	0.13	-35.64**	-3.57	0.54	1.25
TC 88	-0.02	-3.40	0.10	-0.02	-0.13	35.64**	3.57	-0.54	-1.25
TC 89	-1.48	0.10	-0.23	-1.48	0.12	25.08*	9.82**	-0.66	2.50*
TC 90	1.48	-0.10	0.23	1.48	-0.12	-25.08*	-9.82**	0.66	-2.50*
TC 91	1.52	0.15	-0.11	1.52	0.17	34.22**	11.12**	-0.18	3.92**
TC 92	-1.52	-0.15	0.11	-1.52	-0.17	-34.22**	-11.12**	0.18	-3.92**
TC 93	3.02**	-2.25	0.09	3.02**	-0.73	-5.32	-1.72	-1.53**	-1.23
TC 94	-3.02**	2.25	-0.09	-3.02**	0.73	5.32	1.72	1.53**	1.23
TC 95	-1.48	-0.30	0.04	-1.48	-0.25	-11.80	-3.85	-1.23**	0.57
TC 96	1.48	0.30	-0.04	1.48	0.25	11.80	3.85	1.23**	-0.57
TC 97	0.02	1.70	-0.26	0.02	-0.53	2.26	5.05*	0.07	1.90
TC 98	-0.02	-1.70	0.26	-0.02	0.53	-2.26	-5.05*	-0.07	-1.90
TC 99	-3.48**	1.35	-0.13	-3.48**	-0.04	-52.10**	-1.47	-0.86*	0.30
TC 100	3.48**	-1.35	0.13	3.48**	0.04	52.10**	1.47	0.86*	-0.30
TC 101	1.02	5.75**	0.21	1.02	1.19	-30.98**	-23.53**	-2.03**	-3.89**
TC 102	-1.02	-5.75**	-0.21	-1.02	-1.19	30.98**	23.53**	2.03**	3.89**
TC 103	0.02	-2.95	-0.06	0.02	-0.21	20.78	6.52**	-0.13	-2.52*
TC 104	-0.02	2.95	0.06	-0.02	0.21	-20.78	-6.52**	0.13	2.52*
TC 105	1.52	-1.40	-1.46**	1.52	1.13	47.08**	-6.92	0.07	-0.55
TC 106	-1.52	1.40	1.46**	-1.52	-1.13	-47.08**	6.92**	-0.07	0.55
TC 107	-0.48	5.15**	-0.53	-0.48	0.48	-0.53	-4.89*	1.27**	-0.01
TC 108	0.48	-5.15**	0.53	0.48	-0.48	0.53	4.89*	-1.27**	0.01
TC 109	-0.48	2.10	-0.16	0.52	-0.03	-0.73	-0.86	-1.08**	-0.15
TC 110	0.48	-2.10	0.16	-0.52	0.03	0.73	0.86	1.08**	0.15
CD 95% SCA	1.71	3.45	0.76	1.87	1.63	22.13	4.22	0.77	2.31

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

Table 4.2. Mean performance of parental lines for yield contributing traits in rice (*Oryza sativa* L.) during *kharif*, 2012

	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No: of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
B lines									
APMS 6B	99.00	91.00	8.60	129.00	22.35	187.13	85.80	16.95	16.95
APMS 10B	105.00	84.00	9.00	135.00	23.55	137.09	83.93	16.83	15.90
R lines									
RP 2	106.00	129.60	8.70	136.00	24.05	238.47	88.77	20.50	16.97
RP 3	106.50	132.00	9.70	136.00	23.82	288.36	82.81	22.53	12.51
RP 4	107.00	134.50	9.30	137.00	24.75	195.23	89.98	15.18	15.25
RP 5	105.50	123.00	9.10	135.50	24.56	210.85	82.85	22.84	15.65
RP 12	105.00	123.10	8.15	135.00	23.43	158.12	91.29	17.36	12.77
RP 13	114.50	129.70	7.10	144.50	23.79	250.13	89.19	19.91	15.16
RP 14	108.50	125.90	7.70	138.50	25.04	240.60	76.19	16.55	11.81
RP 15	107.00	138.00	5.00	137.00	24.75	178.31	89.47	19.11	13.67
RP 17	107.00	127.60	8.30	137.00	24.62	112.91	66.53	21.74	16.30
RP 18	110.50	123.20	7.00	141.00	22.00	378.55	81.11	16.58	15.44
RP 19	108.50	131.40	8.55	138.00	22.10	175.87	90.57	16.51	15.95
RP 20	108.00	131.00	7.00	138.00	24.70	205.16	93.09	18.13	12.28
RP 22	105.50	134.20	6.70	135.50	26.15	246.32	87.90	18.43	13.24
TCNP 7	109.50	126.00	7.00	139.00	24.45	201.14	89.40	18.20	12.65
TCNP 13	110.00	110.50	8.00	140.00	25.48	259.44	91.71	20.56	16.21
TCNP 22	108.50	126.40	6.90	138.50	25.30	239.27	88.79	16.14	14.09
TCNP 23	97.00	130.15	8.55	127.00	26.05	192.19	84.32	16.43	14.91
TCNP 38	95.50	149.05	9.50	125.50	24.55	337.06	88.46	18.56	18.47
TCNP 50	93.50	123.80	8.00	123.50	24.00	240.61	87.82	21.08	14.79
TCNP 53	108.00	129.90	10.00	138.00	24.65	208.64	90.96	17.30	15.66

Table 4.2 (Contd..)

	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No: of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TCNP 56	108.00	125.05	8.30	138.00	23.94	141.08	75.39	20.89	12.11
TCNP 60	105.00	138.90	7.40	135.00	26.11	238.22	79.13	21.33	9.96
TCNP 61	105.50	120.00	8.20	135.50	22.95	212.15	62.07	17.76	15.32
TCNP 62	112.50	130.20	8.00	142.50	22.35	112.06	47.03	15.42	11.47
TCNP 73	81.00	133.05	9.30	111.00	25.35	258.39	89.97	17.76	13.97
TCNP 83	91.50	144.60	7.50	121.50	22.35	398.83	86.24	17.38	10.28
TCNP 85	92.50	144.50	8.00	122.50	25.00	400.89	86.65	19.36	11.61
TCNP 87	109.50	121.80	7.00	139.50	22.05	122.55	66.49	15.70	11.38
TCNP 89	107.50	137.30	8.10	137.50	24.05	138.53	70.00	15.97	14.49
TCNP 92	110.50	126.10	9.00	140.50	22.90	156.07	86.28	13.30	9.36
TCNP 93	108.50	121.50	8.10	138.50	22.30	153.07	74.93	14.91	11.03
TCNP 94	104.50	106.10	6.70	134.50	23.20	217.98	89.45	22.94	17.19
TCNP 97	99.50	106.50	8.00	130.00	20.22	160.64	82.03	20.10	15.43
RP 1	111.50	126.50	10.70	141.50	24.25	203.84	74.39	15.98	14.09
RP 6	107.00	129.20	8.00	137.00	23.59	267.80	78.16	22.79	14.64
RP 7	108.00	141.50	7.90	138.00	22.16	131.46	90.69	18.42	15.34
RP 9	106.50	130.40	8.00	136.50	24.08	198.62	89.47	17.28	12.09
RP 11	104.50	137.90	7.50	134.00	24.25	167.41	73.70	19.20	15.53
RP 16	105.00	134.90	6.00	135.00	20.59	147.67	76.65	20.36	15.83
RP 21	98.50	118.70	6.10	128.50	24.25	279.66	90.93	21.65	17.53
TCNP 1	114.00	102.00	6.30	144.00	23.20	155.72	86.82	15.14	12.14
TCNP 14	108.50	115.10	6.80	138.50	25.36	195.62	92.17	20.94	14.12
TCNP 21	108.50	113.00	9.00	138.00	26.40	149.82	84.75	19.26	13.06
TCNP 26	111.00	125.10	8.20	141.00	22.70	134.47	87.23	15.04	12.05
TCNP 29	96.50	146.90	6.30	127.00	26.00	250.83	83.49	17.86	11.64
TCNP 51	92.50	121.50	8.40	122.00	24.15	150.99	78.53	21.46	14.74
TCNP 54	111.50	126.60	10.50	141.50	23.35	220.21	87.71	17.46	11.18
TCNP 57	107.50	111.60	7.70	137.50	24.68	119.08	78.77	20.40	13.66

Table 4.2 (Contd..)

	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No: of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TCNP 58	108.50	130.75	8.20	138.50	21.95	183.57	84.16	17.08	11.78
TCNP 75	99.50	130.00	8.20	129.00	23.45	185.17	76.80	20.59	15.11
TCNP 76	97.50	139.10	6.40	127.50	23.10	222.66	86.53	22.12	11.67
TCNP 82	108.50	129.60	9.20	138.00	22.55	220.98	81.12	17.13	11.83
TCNP 90	106.50	130.50	7.50	136.50	23.50	132.85	84.09	17.41	14.91
TCNP 96	110.50	138.80	10.40	140.50	24.70	204.96	91.15	18.22	14.37
TCNP 100	109.50	134.10	8.60	139.00	22.43	155.61	82.00	17.35	14.97
Grand mean	105.14	126.73	8.02	135.09	23.82	204.75	83.09	18.48	13.90
S.E.m	0.63	1.91	0.55	0.75	0.85	14.13	2.41	0.87	1.02
C.D.(5%)	1.78	5.41	1.55	2.12	2.42	40.01	6.81	2.46	2.88
CV(%)	0.84	2.13	9.63	0.78	5.07	9.76	4.09	6.63	10.35

Table 4.7. Mean performance of crosses and checks for yield and yield contributing traits in rice (*Oryza sativa* L.) during *rabi*, 2012-13

Crosses	Parentage	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TC 1	APMS 6A × RP 2	92.00	110.00	8.75	122.00	25.43	255.59	88.14	20.40	26.18
TC 2	APMS 10A × RP 2	93.00	114.70	7.24	123.00	25.86	159.98	55.78	21.85	14.57
TC 3	APMS 6A × RP 3	94.00	133.60	6.34	124.00	27.03	181.65	67.72	19.25	13.30
TC 4	APMS 10A × RP 3	95.00	121.30	5.64	125.00	27.16	172.12	62.20	23.45	17.30
TC 5	APMS 6A × RP 4	95.00	128.30	6.94	125.00	28.13	246.41	82.10	17.40	21.15
TC 6	APMS 10A × RP 4	96.00	127.10	6.34	126.00	26.91	182.40	76.48	21.45	18.23
TC 7	APMS 6A × RP 5	92.00	121.10	7.45	122.00	27.26	212.60	81.10	20.85	27.03
TC 8	APMS 10A × RP 5	95.00	114.70	6.46	125.00	26.53	186.50	77.22	23.95	21.00
TC 9	APMS 6A × RP 12	87.00	117.40	6.16	117.00	26.40	166.42	54.01	22.40	8.90
TC 10	APMS 10A × RP 12	89.00	109.50	6.37	120.50	25.71	63.46	41.77	19.70	8.15
TC 11	APMS 6A × RP 13	99.00	125.50	8.82	130.50	26.78	232.15	82.45	17.35	27.50
TC 12	APMS 10A × RP 13	93.00	126.50	7.16	124.50	26.24	213.01	80.95	17.30	22.45
TC 13	APMS 6A × RP 14	94.00	128.30	6.66	125.50	24.92	212.10	74.51	18.85	17.45
TC 14	APMS 10A × RP 14	97.00	123.10	6.16	127.50	24.94	138.20	70.89	18.95	14.33
TC 15	APMS 6A × RP 15	101.50	138.40	5.97	131.50	28.05	141.30	64.09	15.95	16.70
TC 16	APMS 10A × RP 15	102.50	134.60	6.07	132.50	28.71	182.60	69.22	20.85	17.25
TC 17	APMS 6A × RP 17	105.50	139.20	6.58	135.50	26.47	194.07	70.92	20.10	19.30
TC 18	APMS 10A × RP 17	109.50	128.20	6.68	139.50	28.22	225.40	67.80	15.95	18.45
TC 19	APMS 6A × RP 18	94.50	101.10	6.48	124.50	25.21	181.50	78.62	20.05	19.45
TC 20	APMS 10A × RP 18	93.50	124.40	8.90	123.50	27.03	260.26	80.55	19.95	24.20
TC 21	APMS 6A × RP 19	94.00	118.00	6.87	124.50	26.23	204.15	83.16	18.05	19.70
TC 22	APMS 10A × RP 19	102.00	119.90	5.77	131.50	27.36	288.18	81.13	19.40	19.15
TC 23	APMS 6A × RP 20	95.00	119.30	6.48	124.50	27.20	181.72	68.58	20.45	17.13
TC 24	APMS 10A × RP 20	94.00	116.00	5.58	124.00	27.08	126.16	65.92	20.25	14.70
TC 25	APMS 6A × RP 22	96.00	122.40	6.89	126.00	27.18	178.38	71.91	19.65	13.15
TC 26	APMS 10A × RP 22	94.00	121.40	5.59	124.00	26.19	194.87	64.57	20.55	13.50
TC 27	APMS 6A × TCNP 7	100.00	109.53	6.90	130.00	24.60	215.65	78.47	17.30	15.40
TC 28	APMS 10A × TCNP 7	93.00	104.73	5.79	123.00	25.18	87.90	70.45	24.75	14.30

Table 4.7 (Contd..)

Crosses	Parentage	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TC 29	APMS 6A × TCNP 13	94.00	99.40	8.59	124.00	25.59	132.51	75.39	17.95	18.40
TC 30	APMS 10A × TCNP 13	93.00	99.20	6.34	123.00	23.12	120.52	80.85	18.35	19.30
TC 31	APMS 6A × TCNP 22	94.00	107.20	6.65	124.00	26.26	157.82	47.63	13.05	14.63
TC 32	APMS 10A × TCNP 22	97.00	111.75	6.75	127.00	24.57	147.47	64.62	18.30	14.30
TC 33	APMS 6A × TCNP 23	92.00	117.20	7.54	123.00	26.42	199.18	90.14	17.95	24.45
TC 34	APMS 10A × TCNP 23	95.00	110.70	6.23	126.00	26.37	290.54	90.71	19.85	25.85
TC 35	APMS 6A × TCNP 38	94.00	96.00	8.13	125.00	23.96	141.44	59.09	18.55	12.10
TC 36	APMS 10A × TCNP 38	94.50	116.60	6.50	126.00	23.27	172.52	76.11	15.95	15.63
TC 37	APMS 6A × TCNP 50	91.50	97.10	7.30	123.00	25.64	212.50	88.68	17.25	24.30
TC 38	APMS 10A × TCNP 50	94.50	100.90	6.11	126.00	26.37	241.38	90.25	20.40	25.20
TC 39	APMS 6A × TCNP 53	103.50	115.60	5.91	133.00	23.38	202.39	89.78	15.95	24.25
TC 40	APMS 10A × TCNP 53	104.50	114.30	6.21	134.00	24.73	170.53	78.20	19.40	19.40
TC 41	APMS 6A × TCNP 56	93.50	95.10	7.30	123.00	22.38	86.82	87.09	23.75	14.20
TC 42	APMS 10A × TCNP 56	98.50	100.80	7.15	126.00	25.13	95.47	62.34	21.35	12.20
TC 43	APMS 6A × TCNP 60	94.50	126.20	6.63	122.00	27.40	221.50	72.71	18.85	16.52
TC 44	APMS 10A × TCNP 60	105.50	126.20	7.64	133.00	25.68	85.80	44.02	23.25	12.60
TC 45	APMS 6A × TCNP 61	100.50	121.00	6.24	128.00	26.65	306.02	85.90	16.55	20.35
TC 46	APMS 10A × TCNP 61	104.50	109.20	5.55	132.00	26.16	249.76	80.03	16.65	20.50
TC 47	APMS 6A × TCNP 62	103.50	120.20	7.35	131.00	25.13	131.61	51.60	17.25	10.30
TC 48	APMS 10A × TCNP 62	105.50	112.70	5.73	133.00	27.01	130.10	47.17	20.55	9.40
TC 49	APMS 6A × TCNP 73	103.50	119.20	7.40	131.00	25.21	164.60	72.56	16.25	15.20
TC 50	APMS 10A × TCNP 73	104.50	118.60	5.74	132.00	26.13	178.20	67.04	19.65	11.80
TC 51	APMS 6A × TCNP 83	95.00	114.40	6.25	123.00	24.15	48.70	30.37	22.75	3.80
TC 52	APMS 10A × TCNP 83	94.00	111.50	6.44	122.00	25.21	53.24	26.12	22.35	5.50
TC 53	APMS 6A × TCNP 85	93.00	116.60	7.23	121.00	24.40	64.40	34.80	20.45	2.20
TC 54	APMS 10A × TCNP 85	96.00	118.10	7.01	124.00	27.34	72.94	26.35	22.35	3.20
TC 55	APMS 6A × TCNP 87	103.00	121.80	6.20	131.00	26.20	205.22	71.36	17.20	13.20
TC 56	APMS 10A × TCNP 87	105.00	118.30	6.80	133.00	26.26	129.09	55.07	20.50	8.90
TC 57	APMS 6A × TCNP 89	102.00	129.80	7.50	130.00	23.83	167.56	81.20	26.35	19.20
TC 58	APMS 10A × TCNP 89	100.00	120.60	6.29	128.00	26.11	143.00	56.11	18.95	14.20

Table 4.7 (Contd..)

Crosses	Parentage	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TC 59	APMS 6A × TCNP 92	105.00	115.70	6.39	133.00	26.70	193.23	70.43	15.65	13.50
TC 60	APMS 10A × TCNP 92	104.00	120.40	6.08	133.50	27.39	236.70	67.58	18.75	10.75
TC 61	APMS 6A × TCNP 93	103.00	112.30	6.28	132.50	24.84	195.66	62.88	17.25	10.39
TC 62	APMS 10A × TCNP 93	105.00	110.80	6.08	134.50	26.18	113.28	38.89	18.65	10.90
TC 63	APMS 6A × TCNP 94	93.00	102.50	9.10	122.50	26.59	321.43	85.85	19.55	23.10
TC 64	APMS 10A × TCNP 94	98.00	107.80	5.40	127.50	25.11	168.45	80.95	21.35	19.40
TC 65	APMS 6A × TCNP 97	105.00	102.70	5.91	134.50	24.03	187.64	80.15	18.15	19.00
TC 66	APMS 10A × TCNP 97	106.00	114.50	6.32	135.50	22.21	177.70	82.07	17.75	17.80
TC 67	APMS 6A × RP 1	97.00	113.60	6.51	126.50	26.09	200.00	72.81	16.85	13.40
TC 68	APMS 10A × RP 1	101.00	113.20	6.10	130.50	28.54	209.00	68.63	17.55	10.74
TC 69	APMS 6A × RP 6	94.00	109.40	6.30	123.50	25.94	225.40	82.40	21.15	24.20
TC 70	APMS 10A × RP 6	87.00	115.70	6.11	116.50	26.37	198.25	80.58	16.55	20.90
TC 71	APMS 6A × RP 7	85.00	108.00	5.71	114.50	23.84	188.30	70.93	18.15	15.10
TC 72	APMS 10A × RP 7	87.00	112.00	7.20	116.50	25.61	203.52	83.22	20.85	21.20
TC 73	APMS 6A × RP 9	95.00	110.30	7.30	124.50	23.80	140.38	72.45	21.05	15.10
TC 74	APMS 10A × RP 9	100.00	123.60	6.68	129.50	26.98	193.20	69.06	22.45	13.08
TC 75	APMS 6A × RP 11	94.00	119.40	5.54	123.50	26.96	221.60	81.25	18.25	19.25
TC 76	APMS 10A × RP 11	93.00	116.70	5.16	122.50	26.84	227.29	83.28	19.55	23.20
TC 77	APMS 6A × RP 16	96.00	128.40	6.16	125.50	25.57	159.09	81.48	18.15	21.40
TC 78	APMS 10A × RP 16	93.00	121.20	5.36	123.50	26.34	138.50	69.92	22.85	14.40
TC 79	APMS 6A × RP 21	93.00	93.10	7.88	123.50	24.22	146.80	78.21	21.05	16.60
TC 80	APMS 10A × RP 21	85.00	97.90	9.05	115.50	25.15	179.17	80.03	19.65	18.20
TC 81	APMS 6A × TCNP 1	99.00	101.90	7.71	129.50	25.40	208.70	72.47	15.65	16.18
TC 82	APMS 10A × TCNP 1	98.50	97.60	6.01	130.50	25.54	131.84	63.48	19.80	8.90
TC 83	APMS 6A × TCNP 14	98.50	97.30	6.79	130.50	26.63	26.50	13.38	17.85	1.00
TC 84	APMS 10A × TCNP 14	100.50	97.50	5.47	132.50	26.82	91.33	33.79	21.35	2.10
TC 85	APMS 6A × TCNP 21	94.50	100.80	5.43	126.50	25.97	55.26	20.30	21.45	1.40
TC 86	APMS 10A × TCNP 21	96.50	112.60	5.66	128.50	27.85	164.09	56.46	19.55	8.30
TC 87	APMS 6A × TCNP 26	95.50	122.10	6.08	127.50	25.95	182.90	69.78	16.95	17.90
TC 88	APMS 10A × TCNP 26	96.50	115.00	5.87	128.50	26.07	242.40	73.83	17.40	14.15

Table 4.7 (Contd..)

Crosses	Parentage	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TC 89	APMS 6A × TCNP 29	94.50	125.60	5.34	126.50	26.16	190.10	77.39	18.20	14.70
TC 90	APMS 10A × TCNP 29	98.50	125.10	5.38	130.50	26.30	128.17	54.65	21.05	8.45
TC 91	APMS 6A × TCNP 51	86.50	102.00	5.40	118.50	24.65	197.43	90.66	20.25	23.20
TC 92	APMS 10A × TCNP 51	84.50	101.40	5.21	116.50	24.70	117.21	65.32	22.15	14.10
TC 93	APMS 6A × TCNP 54	93.50	96.50	5.91	125.50	26.22	10.60	4.88	20.85	0.90
TC 94	APMS 10A × TCNP 54	88.50	100.70	5.31	120.50	28.07	9.46	5.24	25.45	2.10
TC 95	APMS 6A × TCNP 57	92.00	99.60	6.11	122.50	25.65	42.42	17.01	21.15	4.30
TC 96	APMS 10A × TCNP 57	96.00	99.90	5.61	126.50	26.53	54.24	21.62	25.15	1.90
TC 97	APMS 6A × TCNP 58	98.00	111.20	5.86	128.50	25.15	174.37	65.41	16.75	13.05
TC 98	APMS 10A × TCNP 58	99.00	107.50	5.95	129.50	26.60	158.06	52.21	18.15	8.00
TC 99	APMS 6A × TCNP 75	94.00	124.30	5.72	124.50	27.51	224.18	82.42	21.30	22.75
TC 100	APMS 10A × TCNP 75	102.00	121.30	5.55	132.50	27.97	316.59	82.29	24.55	20.90
TC 101	APMS 6A × TCNP 76	97.00	117.50	5.85	127.50	27.65	84.42	25.33	18.95	4.30
TC 102	APMS 10A × TCNP 76	96.00	105.70	5.01	126.50	25.65	134.60	69.29	24.55	10.83
TC 103	APMS 6A × TCNP 82	94.00	106.10	6.08	124.50	24.81	213.45	73.26	17.05	9.21
TC 104	APMS 10A × TCNP 82	95.00	111.70	5.77	125.50	25.61	160.10	57.13	18.85	13.00
TC 105	APMS 6A × TCNP 90	89.00	105.40	5.46	119.50	26.38	262.33	80.75	16.05	18.15
TC 106	APMS 10A × TCNP 90	87.00	107.90	7.95	117.50	24.50	156.40	91.49	17.45	18.00
TC 107	APMS 6A × TCNP 96	95.00	118.30	6.51	125.50	28.21	150.48	51.14	20.15	13.64
TC 108	APMS 10A × TCNP 96	97.00	107.70	7.16	127.50	27.64	139.76	57.84	19.15	12.40
TC 109	APMS 6A × TCNP 100	93.00	112.00	5.43	123.50	25.32	245.40	82.65	17.45	20.30
TC 110	APMS 10A × TCNP 100	95.00	107.50	5.34	123.50	25.76	235.07	81.28	21.15	19.35
Checks										
MTU 1075		102.00	104.80	5.18	132.00	22.80	226.29	85.52	18.15	19.20
MTU 1081		88.00	95.00	6.10	118.00	24.68	254.91	82.05	17.95	18.10
MTU 1121		91.00	104.00	8.30	121.00	25.06	232.71	93.34	19.10	20.92
ARIZE 6444 GOLD		95.00	108.70	5.90	125.00	24.67	164.40	89.57	22.65	17.35
Grand mean		96.27	113.39	6.45	126.24	25.91	172.09	67.37	19.55	15.28
C.D.(5%)		2.71	4.73	1.12	2.98	2.13	30.49	5.33	0.98	3.38
CV(%)		1.42	2.11	8.77	1.19	4.15	8.94	3.99	2.52	11.16

Table 4.13. Standard heterosis of hybrids for yield and yield component characters during *rabi,* 2012-13

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 1	1.10	5.77*	5.36	0.83	1.48	9.83	-5.57	6.81*	25.15**
TC 2	2.20	10.29**	-12.77	1.65	3.19	-31.25**	-40.23**	14.40**	-30.34**
TC 3	3.30*	28.46**	-23.61**	2.48*	7.86	-21.94**	-27.44**	0.79	-36.41**
TC 4	4.4 **	16.63**	-31.99**	3.31**	8.38	-26.04**	-33.36**	22.77**	-17.28*
TC 5	4.4 **	23.37**	-16.39*	3.31**	12.25**	5.89	-12.04**	-8.90**	1.12
TC 6	5.49 **	22.21**	-23.55**	4.13**	7.38	-21.62**	-18.06**	12.30**	-12.84
TC 7	1.10	16.44**	-10.24	0.83	8.78	-8.64	-13.11**	9.16**	29.21**
TC 8	4.40**	10.29**	-22.17**	3.31**	5.87	-19.86**	-17.27**	25.39**	0.41
TC 9	-4.40**	12.88**	-25.78**	-3.31**	5.35	-28.49**	-42.13**	17.28**	-57.45**
TC 10	-2.20	5.29*	-23.25**	-0.41	2.59	-72.73**	-55.25**	3.14	-61.06**
TC 11	8.79**	20.67**	6.20	7.85**	6.86	-0.24	-11.66**	-9.16**	31.48**
TC 12	2.20	21.63**	-13.73	2.89**	4.71	-8.47	-13.27**	-9.42**	7.34
TC 13	3.30*	23.37**	-19.76**	3.72**	-0.56	-8.86	-20.17**	-1.31	-16.57*
TC 14	6.59**	18.37**	-25.78**	5.37**	-0.48	-40.61**	-24.04**	-0.79	-31.51**
TC 15	11.54**	33.08**	-28.13**	8.68**	11.93*	-39.28**	-31.34**	-16.49**	-20.15*
TC 16	12.64**	29.42**	-26.81**	9.50**	14.57**	-21.53**	-25.83**	9.16**	-17.52*
TC 17	15.93**	33.85**	-20.72**	11.98**	5.63	-16.60*	-24.02**	5.24	-7.72
TC 18	20.33**	23.27**	-19.46**	15.29**	12.61**	-3.14	-27.35**	-16.49**	-11.79
TC 19	3.85**	-2.79	-21.93**	2.89**	0.60	-22.01**	-15.77**	4.97	-7.00
TC 20	2.75*	19.62**	7.23	2.07	7.86	11.84	-13.70**	4.45	15.71*
TC 21	3.30*	13.46**	-17.17**	2.89**	4.67	-12.27	-10.90**	-5.50	-5.81
TC 22	12.09**	15.29**	-30.42**	8.68**	9.18	23.83**	-13.08**	1.57	-8.44

Table 4.13 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 23	4.40**	14.71**	-21.99**	2.89**	8.54	-21.91**	-26.53**	7.07*	-18.12*
TC 24	3.30*	11.54**	-32.77*	2.48*	8.06	-45.79**	-29.37**	6.02*	-29.72**
TC 25	5.49**	17.69**	-16.93*	4.13**	8.46	-23.34**	-22.96**	2.88	-37.13**
TC 26	3.30*	16.73**	-32.71**	2.48*	4.51	-16.26*	-30.82**	7.59**	-35.45**
TC 27	9.89**	5.31*	-16.93*	7.44**	-1.84	-7.33	-15.93**	-9.42**	-26.37**
TC 28	2.20	0.70	-30.18**	1.65	0.48	-62.23**	-24.52**	29.58**	-31.63**
TC 29	3.30*	-4.42	3.49	2.48*	2.11	-43.06**	-19.23**	-6.02*	-12.02
TC 30	2.20	-4.62	-23.55**	1.65	-7.74	-48.21**	-13.38**	-3.93	-7.72
TC 31	3.30*	3.08	-19.88**	2.48*	4.79	-32.18**	-48.96**	-31.68**	-30.07**
TC 32	6.59**	7.45**	-18.67**	4.96**	-1.96	-36.63**	-30.77**	-4.19	-31.63**
TC 33	1.10	12.69**	-9.10	1.65	5.43	-14.41*	-3.43	-6.02*	16.90*
TC 34	4.40**	6.44**	-25.00**	4.13**	5.23	24.85**	-2.81	3.93	23.60**
TC 35	3.30*	-7.69**	-2.11	3.31**	-4.39	-39.22**	-36.69**	-2.88	-42.15**
TC 36	3.85**	12.12**	-21.69**	4.13**	-7.14	-25.87**	-18.46**	-16.49**	-25.29**
TC 37	0.55	-6.63**	-12.05	1.65	2.31	-8.68	-4.99	-9.69**	16.18*
TC 38	3.85**	-2.98	-26.45**	4.13**	5.23	3.73	-3.31	6.81*	20.49*
TC 39	13.74**	11.15**	-28.80**	9.92**	-6.70	-13.03	-3.81	-16.49**	15.95*
TC 40	14.84**	9.90**	-25.18**	10.74**	-1.32	-26.72**	-16.22**	1.57	-7.24
TC 41	2.75*	-8.56**	-12.05	1.65	-10.69*	-62.69**	-6.69*	24.35**	-32.11**
TC 42	8.24**	-3.08	-13.80*	4.13**	0.28	-58.98**	-33.21**	11.78**	-41.67**
TC 43	3.85**	21.35**	-20.12**	0.83	9.34*	-4.82	-22.09**	-1.31	-21.04**
TC 44	15.93**	21.35**	-7.95	9.92**	2.47	-63.13**	-52.84**	21.73**	-39.76**
TC 45	10.44**	16.35**	-24.76**	5.79**	6.34	31.50**	-7.97*	-13.35**	-2.70
TC 46	14.84**	5.00*	-33.13**	9.09**	4.39	7.33	-14.26**	-12.83**	-1.98

Table 4.13 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 47	13.74**	15.58**	-11.51	8.26**	0.28	-43.45**	-44.72**	-9.69**	-50.75**
TC 48	15.93**	8.37**	-30.90**	9.92**	7.78	-44.09**	-49.46**	7.59**	-55.06**
TC 49	13.74**	14.62**	-10.84	8.26**	0.60	-29.27**	-22.25**	-14.92**	-27.32**
TC 50	14.84**	14.04**	-30.84**	9.09**	4.27	-23.42**	-28.18**	2.88	-43.58**
TC 51	4.40**	10.00**	-24.64**	1.65	-3.63	-79.07**	-67.46**	19.11**	-81.83**
TC 52	3.30*	7.21**	-22.41**	0.83	0.60	-77.12**	-72.01**	17.02**	-73.70**
TC 53	2.20	12.12**	-12.89	0.00	-2.63	-72.33**	-62.72**	7.07*	-89.48**
TC 54	5.49**	13.56**	-15.54*	2.48*	9.10	-68.66**	-71.77**	17.02**	-84.70**
TC 55	13.19**	17.12**	-25.30**	8.26**	4.55	-11.81	-23.54**	-9.95**	-36.89**
TC 56	15.38**	13.75**	-18.07**	9.92**	4.79	-44.53**	-40.99**	7.33*	-57.45**
TC 57	12.09**	24.81**	-9.58	7.44**	-4.91	-27.99**	-13.00**	37.96**	-8.20
TC 58	9.89**	15.96**	-24.16**	5.79**	4.19	-38.55**	-39.89**	-0.79	-32.11**
TC 59	15.38**	11.25**	-23.07**	9.92**	6.54	-16.97*	-24.55**	-18.06**	-35.45**
TC 60	14.29**	15.77**	-26.69**	10.33**	9.30*	1.71	-27.59**	-1.83	-48.63**
TC 61	13.19**	7.98**	-24.28**	9.50**	-0.88	-15.92*	-32.62**	-9.69**	-50.35**
TC 62	15.38**	6.54**	-26.81**	11.16**	4.47	-51.32**	-58.34**	-2.36	-47.88**
TC 63	2.20	-1.44	9.64	1.24	6.11	38.12**	-8.02*	2.36	10.45
TC 64	7.69**	3.65	-35.00**	5.37**	0.20	-27.61**	-13.27**	11.78**	-7.24
TC 65	15.38**	-1.25	-28.73**	11.16**	-4.11	-19.37**	-14.13**	-4.97	-9.16
TC 66	16.48**	10.10**	-23.86**	11.98**	-11.37*	-23.64**	-12.06**	-7.07*	-14.89
TC 67	6.59**	9.23**	-21.57**	4.55**	4.11	-14.06*	-21.99**	-11.78**	-35.93**
TC 68	10.99**	8.85**	-26.51**	7.85**	13.89**	-10.19	-26.47**	-8.12**	-48.67**
TC 69	3.30*	5.19*	-24.16**	2.07	3.51	-3.14	-11.72**	10.73**	15.71*
TC 70	-4.40**	11.25**	-26.39**	-3.72**	5.23	-14.81*	-13.67**	-13.35**	-0.07

Table 4.13 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1} (g)
TC 71	-6.59**	3.85	-31.20**	-5.37**	-4.87	-19.08**	-24.00**	-4.97	-27.80**
TC 72	-4.40**	7.69**	-13.19*	-3.72**	2.19	-12.54	-10.84**	9.16**	1.36
TC 73	4.40**	6.06*	-12.05	2.89**	-5.03	-39.68**	-22.37**	10.21**	-27.80**
TC 74	9.89**	18.85**	-19.58**	7.02**	7.66	-16.98*	-26.01**	17.54**	-37.46**
TC 75	3.30*	14.81**	-33.31**	2.07	7.58	-4.78	-12.95**	-4.45	-7.96
TC 76	2.20	12.21**	-37.83**	1.24	7.10	-2.33	-10.77**	2.36	10.93
TC 77	5.49**	23.46**	-25.78**	3.72**	2.04	-31.64**	-12.70**	-4.97	2.32
TC 78	2.20	16.54**	-35.36**	2.07	5.11	-40.48**	-25.09**	19.63**	-31.15**
TC 79	2.20	-10.48**	-5.12	2.07	-3.35	-36.92**	-16.21**	10.21**	-20.63*
TC 80	-6.59**	-5.87*	9.04	-4.55**	0.36	-23.01**	-14.26**	2.88	-12.98
TC 81	8.79**	-2.02	-7.11	7.02**	1.36	-10.32	-22.35**	-18.06**	-22.64**
TC 82	8.24**	-6.15*	-27.59**	7.85**	1.92	-43.35**	-31.99**	3.66	-57.45**
TC 83	8.24**	-6.44**	-18.19**	7.85**	6.26	-88.61**	-85.66**	-6.54*	-95.22**
TC 84	10.44**	-6.25**	-34.10**	9.50**	7.02	-60.75**	-63.79**	11.78**	-89.96**
TC 85	3.85**	-3.08	-34.52**	4.55**	3.63	-76.25**	-78.25**	12.30**	-93.31**
TC 86	6.04**	8.27**	-31.81**	6.20**	11.13*	-29.49**	-39.50**	2.36	-60.32**
TC 87	4.95**	17.40**	-26.75**	5.37**	3.55	-21.40**	-25.24**	-11.26**	-14.42
TC 88	6.04**	10.58**	-29.34**	6.20**	4.03	4.16	-20.90**	-8.90**	-32.35**
TC 89	3.85**	20.77**	-35.66**	4.55**	4.39	-18.31**	-17.09**	-4.71	-29.72**
TC 90	8.24**	20.29**	-35.24**	7.85**	4.95	-44.93**	-41.45**	10.21**	-59.60**
TC 91	-4.95**	-1.92	-34.88**	-2.07	-1.64	-15.16*	-2.87	6.02*	10.93
TC 92	-7.14**	-2.50	-37.23**	-3.72**	-1.44	-49.63**	-30.01**	15.97**	-32.58**
TC 93	2.75*	-7.21**	-28.73**	3.72**	4.63	-95.44**	-94.77**	9.16**	-95.70**
TC 94	-2.75*	-3.17	-36.02**	-0.41	12.01*	-95.94**	-94.39**	33.25**	-89.96**

Table 4.13 (Contd..)

Hybrids	Days to 50% flowering	Plant Height (cm)	Ear bearing tillers/ plant	Days to maturity	Panicle length (cm)	No. of filled grains per panicle	Spikelet fertility (%)	Test weight (g)	Grain yield plant $^{-1}$ (g)
TC 95	1.10	-4.23	-26.45**	1.24	2.35	-81.77**	-81.78**	10.73**	-79.44**
TC 96	5.49**	-3.94	-32.41**	4.55**	5.87	-76.69**	-76.83**	31.68**	-90.92**
TC 97	7.69**	6.92**	-29.46**	6.20**	0.36	-25.07**	-29.92**	-12.30**	-37.60**
TC 98	8.79**	3.37	-28.37**	7.02**	6.15	-32.08**	-44.06**	-4.97	-61.75**
TC 99	3.30*	19.52**	-31.08**	2.89**	9.78*	-3.67	-11.69**	11.52**	8.77
TC 100	12.09**	16.63**	-33.07**	9.50**	11.61*	36.04**	-11.84**	28.53**	-0.07
TC 101	6.59**	12.98**	-29.52**	5.37**	10.34*	-63.72**	-72.87**	-0.79	-79.44**
TC 102	5.49**	1.63	-39.64**	4.55**	2.35	-42.16**	-25.76**	28.53**	-48.24**
TC 103	3.30*	2.02	-26.81**	2.89**	-1.00	-8.28	-21.51**	-10.73**	-55.99**
TC 104	4.40**	7.40**	-30.42**	3.72**	2.19	-31.20**	-38.79**	-1.31	-37.84**
TC 105	-2.20	1.35	-34.22**	-1.24	5.27	12.73	-13.48**	-15.97**	-13.22
TC 106	-4.40**	3.75	-4.22	-2.89**	-2.23	-32.79**	-1.97	-8.64**	-13.94
TC 107	4.40**	13.75**	-21.51**	3.72**	12.57**	-35.33**	-45.21**	5.50	-34.81**
TC 108	6.59**	3.56	-13.80*	5.37**	10.30*	-39.94**	-38.03**	0.26	-40.71**
TC 109	2.20	7.69**	-34.52**	2.07	1.04	5.45	-11.45**	-8.64**	-2.94
TC 110	4.40**	3.37	-35.66**	2.07	2.79	1.02	-12.92**	10.73**	-7.48
SED	1.22	2.46	0.54	1.33	1.16	15.79	3.01	0.55	1.65
CD 95%	2.41	4.87	1.07	2.64	2.30	31.30	5.97	1.09	3.26
CD 99%	3.19	6.45	1.42	3.49	3.04	41.40	7.90	1.44	4.32

*Significant at 5% level, ** Significant at 1% level

Chapter - V

SUMMARY AND CONCLUSIONS

The study was undertaken with an objective to identify major fertility restorer genes in elite restorer lines developed at APRRI and RARS, Maruteru, to validate the identified restorers for their *per se* performance in different hybrid combinations and to identify promising heterotic hybrids.

In the present investigation, fifty five elite restorer lines and two CMS lines (WA type) developed at Maruteru were evaluated for variability, genetic parameters and genetic divergence for yield and yield component traits in *kharif*, 2012 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, West Godavari district, Andhra Pradesh. DNA was isolated from the leaf tissues collected from parental lines at tillering stage and screened for the presence of proven *Rf* genes using identified SSR markers. Molecular cluster analysis was also performed based on marker data. The 55 restorer lines were then crossed with 2 CMS lines in a line x tester fashion and the hybrids obtained were evaluated in *rabi*, 2012-13.

The analysis of variance of parental lines revealed significant differences among the genotypes for all the nine characters studied. The genetic variability studies indicated high variability for the character, no. of filled grains panicle^{-1}. High heritability coupled with high genetic advance was observed in case of ear bearing tillers plant^{-1}, number of filled grains panicle^{-1}, test weight and grain yield plant^{-1} suggesting the role of additive gene action in the inheritance of these traits and directional selection could be profitably applied for their improvement.

The estimation of genetic divergence employing both Mahalanobis D^2 statistic and molecular cluster analysis revealed the existence of considerable genetic diversity among the parental lines studied.

During *rabi*, 2012-13, the 110 hybrids were evaluated for variability, genetic parameters, combining ability and heterosis and promising heterotic hybrids were identified.

The hybrids exhibited high genetic variability for number of filled grains panicle^{-1}, spikelet fertility and grain yield plant^{-1}. High heritability coupled with high

genetic advance was observed in case of ear bearing tillers per plant, number of filled grains panicle^{-1}, spikelet fertility, test weight and grain yield plant^{-1} suggesting the role of additive gene action in the inheritance of these traits.

The analysis of variance for combining ability showed high significance of crosses for all the traits studied. The variance due to lines was significant for all the characters studied whereas testers showed significance for all the characters except plant height, number of grains per panicle and spikelet fertility. All the traits were observed significant for line × tester interaction. The SCA variances were higher than GCA variances for all the characters indicating the predominance of non-additive gene action.

The lines, TCNP 23 and RP 13 were identified as good general combiners for grain yield plant^{-1} while APMS 6A registered good general combining ability for no. of ear bearing tillers plant^{-1}, spikelet fertility and grain yield plant^{-1} among testers.

Based on *per se* performance and *sca* effects the hybrids, TC 11, TC 7 and TC1 were identified as superior ones for grain yield plant^{-1}. Ten hybrids *viz.*, TC 11, TC 7, TC 1, TC 34, TC 38, TC 33, TC 37, TC 39, TC 20, and TC 69 were observed to possess significant positive standard heterosis for grain yield plant^{-1} over the superior check, MTU1121.

Based on overall performance for yield, the crosses, TC 11, TC 7, TC 1, TC 34, TC 20 and TC 69, were identified as promising heterotic hybrids for grain yield plant^{-1}.

Twenty three restorers were identified as best ones based on spikelet fertility of the hybrids. Four primers (RM 576, RM 10287, RM 10305 and DRRM Rf3-5) were found to distinguish the restorer checks (Swarna and BPT 5204) and CMS lines for *Rf3* gene while five primers (RM 294, RM 311, RM 1108, RM 6100 and DRCG Rf4-14) specific to *Rf4* gene distinguished the checks and CMS lines. All the identified restorers showed similar banding pattern with the restorer checks with few exceptions.

Since Swarna and BPT 5204 showed polymorphism for both *Rf3* and *Rf4* specific primers, it can be inferred that both *Rf3* and *Rf4* genes may be present in the restorer checks. All the identified restorers which are co segregating with the restorer checks may also have *Rf3* and *Rf4* genes and in the identified restorers having different segregating pattern, some other *Rf* genes may be present.

Future line of work

- The promising heterotic hybrids identified in the present study *viz.*, TC 11, TC 7, TC 1, TC 34, TC 20 and TC 69 may be evaluated for quality traits and also grown over more number of environments in different seasons for further confirmation before being commercially exploited.

- The identified test crosses with good restoration ability can be evaluated in F_2 generation for further confirmation of the presence or absence of *Rf* genes.

LITERATURE CITED

Aananthi, N and Jebaraj, S. 2006. Heterosis in two line rice hybrids. *Indian Journal of Agricultural Research*. 40(3): 178 - 183.

Ahmadikhah, A., Karlov, G.I., Nematzadeh, G and Bezdi, K.G. 2007. Inheritance of the fertility restoration and genotyping of rice lines at the restoring fertility (*Rf*) loci using molecular markers. *International Journal of Plant Production* . 1: 13-21.

Alavi, M., Ahmadikhah, A., Kamkar, B and Kalateh, M. 2009. Mapping *Rf3* locus in rice by SSR and CAPS markers. *International Journal of Genetics and Molecular Biology*. 1(7).121-126.

Allard, R.W. 1960. *Principles of Plant Breeding*. John Wiley and Sons Inc., New York. 485.

Anand Kumar., Singh, N.K and Sharma, V.K. 2006. Combining ability analysis for identifying elite parents for heterotic rice hybrids. *Oryza*. 43(2): 82-86.

Anbanandan, V., Saravanan, K and Sabesan, T. 2009. Variability, heritability and genetic advance in rice (*Oryza sativa* L.). *International Journal of Plant Sciences*. 4(1): 61- 63.

Ashvani Panwar Dhaka, R.P.S and Vinod Kumar. 2007. Genetic variability and heritability studies in rice. *Advances in Plant Sciences*. 20(1): 47-49.

Balaji Suresh, P., Srikanth, B., Kishore, V.H., Rao, I.S., Vemireddy, L.R., Dharika, N., Sundaram, R.M., Ramesha, M.S., Rao, K.R.S.S., Viraktamath, B.C and Neeraja, C.N. 2012. Fine mapping of *Rf3* and *Rf4* fertility restorer loci of WA-CMS of rice (*Oryza sativa* L.) and validation of the developed marker system for identification of restorer lines. *Euphytica*. 187(3): 421-435.

Baluch-Zehi, A., Kiani, Gh and Bagheri, N. 2013. Investigation of genetic distance among parental lines of hybrid rice based on cluster analysis of morphological traits. *Journal of Crop Production and Processing*. 3(7): 73-83.

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.

Bazrkar, L., Ali, A.J., Babaeian, N.A., Ebadi, A.A., Allahgholipour, M., Kazemitabar, K and Nematzadeh, G. 2008. Tagging of four fertility restorer loci for wild abortive cytoplasmic male sterility system in rice (*Oryza sativa* L.) using microsatellite markers. *Euphytica*. 164: 669-677.

Beckmann, J.S and Soller, M. 1990. Towards a unified approach to genetic mapping of eukaryotes based on sequence tagged micro satellite sites. *Biotechnology*. 8: 930-932.

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.). *Journal of Breeding and Genetics.* 44(1): 129-137.

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.

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.

Burton, G.W and Devane, E.W. 1953. Estimating heritability in tall fescue (*Festuca arundiraceae*) from replicated clonal material. *Agronomy Journal*. 45: 478-481.

Chandirakala, R., Kandasamy, G and Thiyagarajan, K. 2010. Heterotic expression of two line hybrids in rice. *Oryza*. 47(3): 248-251.

Chaudhry, A., Sharma, P., Singh, H., Pradhan, S.K and Pandey, M.P. 2007. Study on heterosis for yield and physiological characters in rice hybrids. *Oryza*. 44(1): 7-13.

Dalvi, V.V and Patel, D.V. 2009. Combining ability analysis for yield in hybrid rice. *Oryza*. 46(2): 97-102.

Dellaporta, S.L., Wood, J and Hicks, J.B. 1983. A plant DNA minipreparation: version 2. *Plant Molecular Biology Reporter*. 1: 19-22.

Duan, S.H., Mao, J.N and Zhu, Y.G. 2002. Genetic variation of main restorer lines of hybrid rice in China was revealed by microsatellite microsatellite markers. *Journal of Genetics and Genomics.* 29(3): 250-254.

Dwivedi, D.K., Pandey, M.P., Pandey, S.K and Rongbai, L.I. 1999. Combining ability over environments in rice involving indica and tropical japonica lines. *Oryza*. 36(2): 101-107.

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., Ganapathy, K.N., Satish, R.G., Shanthala, J and Nadarajan, N. 2007. Heterosis studies for yield and yield components using CMS lines in rice (*Oryza sativa* L.). *Crop Research.* 34(1, 2 & 3): 152-155.

Fisher, R.A and Yates, F. 1963. *Statistical Tables for Biological, Agricultural and Medical Research.* Oliver and Boyd, London. 46-63.

Fujii, S and Toriyama, K. 2005. Molecular mapping of the fertility restorer gene for *ms-CW*-type cytoplasmic male sterility of rice. *Theoretical and Applied Genetics.* 111(4): 696-701.

Ganesan, K.N and Rangaswamy, M. 1998. Combining ability studies in rice hybrids involving wild abortive (WA) and *Oryza perennis* sources of CMS lines. *Oryza.* 35(2): 113-116.

Ganesan, K., Subramanian, M., Manuel, W.W and Sundaram, T. 1997. Genetic studies in F_2 and F_3 generations of rice. *Madras Agricultural Journal*. 84(6): 319-323.

Gholizadeh, A., Nematzadeh, G., Bagheri, N., Ebrahimi, A and Oladi, M. 2012. Molecular and cytological evaluation of male sterile and restorer lines in hybrids rice. *International Research Journal of Applied and Basic Sciences.* 3(1): 183-189.

Gnanamalar, R.P and Vivekanandan, P. 2013. Combining ability analysis of grain quality traits in rice (*Oryza sativa* L.). *Asian Journal of Plant Science and Research.* 3(2): 145-149.

Gnanasekaran, M., Vivekanandan, P and Muthuramu, S. 2006. Combining ability and heterosis for yield and grain quality in two line rice (*Oryza sativa* L.) hybrids. *Indian Journal of Genetics and Plant Breeding.* 66(1): 6-9.

Gouri Shankar, V., Ansari, N.A., Ilyas Ahamed, M and Venkata Ramana Rao, P. 2010. Heterosis studies using thermo-sensitive genetic male sterile lines in rice. *Oryza.* 47(2): 100-105.

Gupta, A., Sharma, R.K., Mani, V.P and Chauhan, V.S. 1999. Variability and association analysis for grain yield and its components in hill rices. *Journal of Hill Research.* 12(2): 99-101.

Hasan, M.J., Kulsum, U., Rahman, M. M. H., Chowdhury, M.M.H and Chowdhury, A.Z.M.K.A. 2012. Genetic diversity analysis of parental lines for hybrid development in rice (*Oryza sativa* L.). *Bangladesh Journal of Agricultural Research.* 37(4): 617-624.

Hasib, K.M. 2005. Genetic variability, interrelations and path analysis for panicle characters in scented rice. *Crop Research* . 30(1): 37-39.

Honarnejad, R. 1999. Combining ability of characteristics and gene effects in segregating populations (F_2) of rice (*Oryza sativa* L.). *Agricultural Sciences and Technology*. 13(1): 53-65.

Hossain, B.R and Hossain, M.F. 2001. Genetic variability in yield components of rice (*Oryza sativa)*. *Environment and Ecology*. 19(1): 186-189.

Hossain, M. 1996. *Economic prosperity in Asia: Implications for Rice Research*. In: Khush, G.S. (ed) *Rice genetics III*. IRRI, Manila, Philippines. 3-16.

Hossain, M.S., Singh, A.K and Zaman, F. 2010. Genetics of fertility restoration of 'WA'-based cytoplasmic male sterility system in rice (*Oryza sativa* L.) using indica/japonica derivative restorers. *Science Asia.* 36:94-99.

Huang, J., Hu, J., Xu, X., Li, S., Yi, P., Yang, D., Ren, F., Liu, X and Zhu, Y. 2007. Fine mapping of the nuclear fertility restorer gene for HL cytoplasmic male sterility in rice. *Botanical Bulletin of Academia Sinica.* 44: 285-289.

Hu, J., Wang, K., Huang, W., Liu, G., Gao, Y., Wang, J., Huang, Q., Ji, Y., Qin, X., Wan, L., Zhu, R., Li, S., Yang, D and Zhu, Y. 2012. The rice pentatricopeptide repeat protein RF5 restores fertility in hong-lian cytoplasmic male sterile lines via a complex with the glycine-rich protein GRP162. *Plant Cell*. Advance Online Publication.

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.

Ilyas Ahamed, M., Mangal Sain, M and Ramesha, M.S. 2006. *Winter School on New Frontiers in 'Hybrid Rice Technology.'* Directorate of Rice Research, Rajendranagar, Andhra Pradesh.

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.

Jayasudhan, S and Deepak Sharma. 2009. Combining ability and gene action analysis for yield and its components in rice (*Oryza sativa* L.). *Journal of Research, ANGRAU*. 2(2): 105-110

Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.

Kalita, U.C and Upadhaya, L.P. 2000. Line × tester analysis of combining ability in rice under irrigated low land condition. *Oryza*. 37(1): 15-19.

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.

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.

Karthikeyan, 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.

Kempthorne, O. 1957. *An Introduction to Genetic Statistics*. John Wiley and Sons Inc., New York. pp: 458-471.

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 Agricultutal Research and Extension*. 11: 60-64.

Komori, T., Ohta, S., Murai, N., Takakura, Y., Kuraya, Y., Suzuki, S., Hiei, Y., Imaseki, H and Nitta, N. 2004. Map-based cloning of a fertility restorer gene, *Rf-1*, in rice (*Oryza sativa* L.). *The Plant Journal*. 37: 315–325.

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.

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 Babu, G., Satyanarayana, P.V., Panduranga Rao, C and Srinivasa Rao, V. 2010a. Combining ability for yield, components and quality traits in hybrid rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*. 57(2): 143-147.

Kumar Babu, G., Satyanarayana, P.V., Panduranga Rao, C and Srinivasa Rao, V. 2010b. Heterosis for yield, components and quality traits in rice (*Oryza sativa* L.). *The Andhra Agricultural Journal*. 57(3): 226-229.

Kumar, A., Singh, S and Singh, S.P. 2012. Heterosis for yield and yield components in Basmati rice. *Asian Journal of Agricultural Research*. 6(1):21-29.

Kumar, S., Gautam, A.S and Chandel, S. 2007. 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, P and Ramesh, B. 2008. Genetic variability and character associations in rice. *Progressive Agriculture*. 8(2): 260-262.

Lee, M. 1995. DNA markers in plant breeding programmes. *Advances in Agronomy*. 55: 265-234.

Liang, G.H., Reddy, C.R and Dayton, A.D. 1971. Heterosis, inbreeding depression and heritability estimates in a systematic series of grain sorghum genotypes. *Crop Science*. 12: 409-411.

Li, S., Yang, G., Li, S., Li, Y., Chen, Z and Zhu, Y. 2005. Distribution of fertility-restorer genes for Wild-abortive and Honglian CMS lines of rice in the AA genome species of genus *Oryza*. *Annals of Botany*. 96: 461-466.

Li, X.F., He, K.M., Lin, H., Zhu, X.Y., Liang, N., Wu, D.H., Zen, H., Li, X.F., He, K.M., Lin, H., Zhu, X.Y., Liang, N., Wu, D.H and Zhen, H. 1998. Combining ability analysis for main traits in the rice cultivars with blast resistance and/or good quality. *Chinese Journal of Rice Science*. 12(1): 55-58.

Lush, J.L. 1940. Intra-sire correlation on regression of off-spring on dams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Production*. 33: 292-301.

Madhavilatha, L., Sekhar, M.R., Suneetha, Y and Srinivas, T. 2005. Genetic variability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). *Research on Crops*. 6(3): 527-534.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proceedings of the National Institute of Sciences of India*. 2: 49-55.

Manuel, W and Palanisamy, S. 1989. Heterosis and correlation in rice. *Oryza*. 26: 238-242.

Mamta Singh., Kumar, K and Singh, R.P. 2007. Study of coefficient of variation, heritability and genetic advance in hybrid rice. *Oryza.* 44(1): 160-162.

Mather, K and Jinks, J.L. 1971. *Introduction to Biometrical Genetics*. Chapman and Hall Limited, London pp: 249-252.

Meenakshi, T and Amirthadevarathinam, A. 1999. Combining ability for yield and physiological characters in semi dry rice. *Oryza.* 36(2): 111-113.

Mishra, G.P., Singh, R.K., Mohapatra, T., Singh, A.K., Prabhu, K.V and Zaman, F.U. 2001. Molecular mapping of a fertility restorer gene in basmati rice using microsatellite markers. *Indian Journal of Genetics*. 61(4): 348-349.

Mishra, M. 2002. Rice in India. *Agrolook*, 3:10-15.

Mohan Lal 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.

Monalisa Manna, M.D., Ali, N and Samal, B.G. 2006. Variability, correlation and path coefficient analysis in some important traits of low land rice. *Crop Research.* 31(1):153-156.

Nadali Bagheri and Babaeian, N. J. 2010. Heterosis and combining ability for yield and related yield traits in hybrid rice. *Interational Journal of Biology*. 2(2): 222-231.

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.

Nematzadeh, G.A and Kiani, G. 2010. Genetic analysis of fertility restoration genes for WA type cytoplasmic male sterility in Iranian restorer rice line DN-33-18. *African Journal of Biotechnology*. 9(38). 6273-6277.

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., Subba Rao, 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.

Pandya, R and Tripathi, R.S. 2006. Heterosis breeding in hybrid rice. *Oryza.* 43(2): 87-93.

Panse, V.G and Sukhatme, P.V. 1978. *Statistical Methods for Agricultural Workers.* ICAR, New Delhi. 103-108.

Panwar, L.L. 2005. Genetic variability, heritability and genetic advance for panicle characters in transplanted rice. *Research on Crops.* 6(3): 505-508.

Patil, D.V., Thiyagarajan, K and Kable, P. 2003. Combining ability of parents for yield and yield contributing traits in two line hybrid rice (*Oryza sativa* L.). *Crop Research.* 25(3): 520-524.

Patil, P.V., Sarawgi, A.K and Shrivastava, M.N. 2003. Genetic analysis of yield and quality traits in tradional aromatic accessions of rice. *Journal of Maharastra Agricultural Universities.* 28(3): 255-258.

Pejic, I., Ajmone-marsan, P., Morgante, M., Kozumplick, V., Castiglioni, P.L., Taramino, G and Motto, M . 1998. Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs and AFLPs. *Theoretical and Applied Genetics*. 97: 1248-1255.

Prasad, R., Prasad, L.C and Agarwal, R.K. 2009. Genetic diversity in Indian germplasm of aromatic rice. *Oryza.* 46(3): 197-201.

Rahimi, M., Rabiei, B., Samizadeh, H and Ghasemi, A.K. 2010. Combining ability and heterosis in rice (*Oryza sativa* L.) cultivars. *Journal of Agricultural Science and Technology*. 12: 223-231.

Rajendran, N., Mukherjee, L., Reddy, K.K and Shashidhar, H.E. 2012. DNA fingerprinting and estimation of genetic diversity among hybrid rice parental lines (*Oryza sativa* L.) using simple sequence repeats (SSR) markers. *Journal of Plant Breeding and Crop Science*. 4(11): 169-174.

Rita Binse., Motiramani, N.K and Sarawgi. 2006. Association analysis and variability analysis in rice. *Mysore Journal of Agricultural Sciences.* 40(3):375-380.

Rita Binse., Sarawgi, A.K and Verulkar, S.B. 2009. Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh Journal of Agricultural. Research.* (2): 175-179.

Rohlf, H.J. 1994. NTSYS-pc: Numerical taxonomy and multivariate analysis system, version 2.0. Exeter Software, Setauket, Newyork.

Rosamma, C.A and Vijayakumar, N.K. 2005. Variation in quantitative characters and heterosis in F_1 rice (*Oryza sativa* L.) hybrids as affected by male sterile cytoplasm. *Indian Journal of Genetics and Plant Breeding.* 67(1): 23-27.

Roy, S., Edpuganti, N., Senapati, B.K and Sarkar, G. 2008. Polygenic variation and character association in M_4 progenies of rice (*Oryza sativa* L.). *Indian Agriculturist*. 52(3/4): 159-167.

Saidaiah, P., Ramesha, M.S and Sudheer Kumar, S. 2010a. Line x tester analysis in rice (*Oryza sativa* L.). *Madras Agricultural Journal.* 97(4-6): 110-113.

Saidaiah, P., Ramesha, M.S., Sudheer Kumar, S and Suresh, J. 2011. Combining ability analysis for yield and yield component traits in rice (*Oryza sativa* L.). *Journal of Research ANGRAU.* 39(1 & 2): 28-33.

Saidaiah, P., Sudheer Kumar, S and Ramesha, M.S. 2010b. Variability for yield and yield component attributes in rice. *Crop Research.* 39(1, 2, & 3): 91-93.

Sanghera, G.S and Hussain,W. 2013.Gene action and combining ability studies using CMS system for development of hybrid rice under temperate conditions. *American Journal of Agricultural Science and Technology*.1: 27-44.

Sarkar, K.K., Bhutia, K.S., Senapati, B.K and Roy, S.K. 2005. Genetic variability and character association of quality traits in rice (*Oryza sativa* L.). *Oryza.* 44(1): 64-67.

Satish Chandra, B., Dayakar Reddy, T and Sudheer Kumar, S. 2009. Variability parameters for yield, its components and quality traits in rice (*Oryza sativa* L.). *Crop Research.* 38: 144-146.

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 Interacademicia*. 9(4): 487-489.

Selvaraj, C.I., Thiyagarajan, K.P.N., 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.

Sen, C and Singh, R.P. 2011. Study on heterosis in Boro × High yielding rice hybrids. *International Journal of Plant Breeding and Genetics.* 5(2): 141-149.

Senor, M.L., Murthy, J.P., Goodman, M.M and Stuber, C.W. 1998. Utility of SSRs for determining genetic similarities and relationships in maize using an agarose gel system. *Crop Science.* 38: 1088-1098.

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.

Shah, G., Sasidharan, N., Chakraborty, S., Trivedi, R., Ravikiran, R and Davla, D. 2012.

Genetic diversity and molecular analysis for fertility restorer genes in rice (*Oryza sativa* L.) for wild abortive (*WA*) cytoplasm using microsatellite markers. *Journal of Agricultural Technology*. 8(1): 261-271.

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., Pandey, M.P., Dwivedi, D.K and Shukla, S.K. 2001. Combining ability, heterosis and inbreeding depression among elite bacterial blight resistance lines in rice (*Oryza sativa* L.). *'Diamond Jubilee Symposium on Hundred years of Post Mendelian Genetics and Plant Breeding – Restrospect and Prospects'* held on November 6-9, 2001, New Delhi: 127.

Sheeba, N.K., Viraktamath, B.C., Sivaramakrishnan,S., Gangashetti, M.G., Khera, P and Sundaram, R.M. 2009. Validation of molecular markers linked to fertility restorer gene(s) for WA-CMS lines of rice. *Euphytica*. 167: 217-227.

Shiva Prasad, G., Sujatha, M., Chaitanya, U and Subba Rao, L.V. 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.

Shull, G.H. 1914. Duplicate genes for capsule form in Bursa bursa – pastoris Zectscher, *Induki Abstramm Verebungsi*. 12: 97- 149

Singh, J., Dey, K., Sanjeev Singh 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, N.K., Singh, S., Singh, A.K., Sharma, C.L., Singh, P.K and Singh, O.N. 2007. Study of heterosis in rice (*Oryza sativa* L.) using line × tester mating system. *Oryza*. 44(3): 260-263.

Singh, R.K and Chaudhary, B.D. 1985. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. 205-214.

Singh, R. K and Omkar Singh. 2005. Genetic variation for yield and quality characters in mutants of aromatic rice. *Annals of Agricultural Research*. 26(3): 406-410.

Singh, R.V., Maurya, D.M., Dwivedi, J.L and Verma, O.P. 2005. Combining ability studies on yield and its components using CMS lines in rice (*Oryza sativa* L.). *Oryza*. 42 (4): 306-309.

Singh, R.V., Verma, O.P., Dwivedi, J.L and Singh, R.K. 2006. Heterosis studies in rice hybrids using CMS systems. *Oryza*. 43(2): 154-156.

Singh, S.K. 2002. Combining ability studies for yield and it's components in rice. *Madras Agricultural Journal*. 89(1-3): 157-161.

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.

Singh, V.K., Upadhyay, P., Sinha, P., Mall, A.K., Jaiswal, S.K., Singh, A., Ellur, R.K., Biradar, S., Sundaram, R.M., Singh, S., Ahmed, I., Mishra, B., Singh, A.K and Kole, C. 2011. Determination of genetic relationships among elite thermosensitive genic male sterile lines (TGMS) of rice (*Oryza sativa* L.) employing morphological and simple sequence repeat (SSR) markers. *Journal of Genetics*. 90(1): 11-19.

Singh, S.P., Singhara, G.S., Parray, G.A and Bhat, G.N. 2006. Genetic variability and character association in rice (*Oryza sativa* L.). *Agricultural Science Digest*. 26(3): 212-214.

Siva Parvathi, P., Satyanarayana Rao, V., Lal Ahamed, M and Anil Kumar, P. 2011. Variability, heritability and genetic advance for yield and grain quality charactes in rice. *The Andhra Agricultural Journal*. 58(1): 116-118.

Sobita Devi, L., Raina, F.A., Manish, K., Pandey and Kole, C.R. 2006. Genetic parameters of variation for yield and its components in rice (*Oryza sativa* L.). *Crop Research*. 32(1): 69-71.

Sprague, G.F and Tatum, L.A. 1942. General vs. specific combining ability in single crosses of corn. *Journal of American Society of Agronomy*. 34: 923- 932.

Sravan, T., Rangare, N.R., Suresh, B.G and Ramesh kumar, S. 2012. Genetic Variability and Character Association in Rainfed Upland Rice (*Oryza sativa* .L). *Journal of Rice Research*. 5(1): 24-28.

Sreeparvathy, P.V., Vashi, R.D and Kodappully, V.C. 2010. Genetic variability, heritability and genetic advance in rice, *Oryza sativa*. *Journal of Ecobiology*. 26(3/4): 205-210.

Subramanian, P.S and Menon, P.M. 1973. Genotypic and phenotypic variability in rice. *Madras Agricultural Journal*. 60: 1093-1096.

Tada, Y. 2007. Effects of *Rf1, Rf3* and *Rf6(t)* genes on fertility restoration in rice (*Oryza sativa* L.) with WA and BT-type cytoplasmic male sterility. *Breeding Science*. 57: 223-229.

Tan, Y.P., Xie, H.W., Li, N.W., Li, S.Q and Zhu, Y.G. 2012. Molecular characterization of latent fertility restoration loci for Honglian cytoplasmic male sterility in *Oryza* species. *Molecular Breeding*. 30(4): 1699-1706.

Tan, Y.P., Li, S.Q., Xie, H.W., Duan, S.H., Wang, T and Zhu, Y.G. 2011. Genetical and molecular analysis reveals a cooperating relationship between cytoplasmic male sterility and fertility restoration related genes in *Oryza* species. *Theoretical and Applied Genetics*. 122: 9–19.

Tiwari, D.K., Pandey, P., Giri, S.P and Dwivedi, J.L. 2011. Heterosis studies for yield and its components in rice hybrids using CMS system. *Asian Journal of Plant Sciences*. 10(1): 29-42.

Toriyama, K., Fujii, S., Itabashi, E and Kazama, T. 2010. Molecular comparison of fertility restorer genes *Rf1*, *Rf2* and *Rf17* for cytoplasmic male sterility in rice. Proceedings of the International Rice Research Conference, 8-12 November 2010, Hanoi, Vietnam.36-42.

Umadevi, M., Veerabadhiran, P., Manonmani, S and Shanmugasundaram, P. 2010. Physico-chemical and cooking characteristics of rice genotypes. *Electronic Journal of Plant Breeding*. 1(2): 114-123.

Uttam Chand Katoch, P.C and Vijay Kumar. 2005. Variability studies in some macro mutations induced by EMS and Gamma rays in Basmathi rice T - 23. *Annals of Biology*. 21(2):137-141.

Vaithiyalingan, M and Nadarajan, N. 2006. Genetic variability and genetic advance in F_2 population of inter sub- specific crosses of rice. *Crop Research.* 31(3): 476-477.

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: 212-214.

Virmani, S.S., Chaudhary, R.C and Khush, G.S. 1981. Current outlook on hybrid rice. *Oryza.* 18: 67-84.

Wang, S.J., Lu, Z.M and Wan, J.M. 2006. Genetic diversity among parents of hybrid rice based on cluster analysis of morphological traits and simple sequence repeat markers. *Rice Science*. 13(3): 155-160.

Wang, X., Tan, X., Shao, G., Ma, H., Chen, Y., Zhang, C and Shang, W. 2012. Marker-Assisted Selection of Japonica restorers used for Yinshui CMS system. *Rice Genomics and Genetics*.4:19-24.

Wu, K.S and Tanksley, S.D. 1993. Abundance, polymorphism and genetic mapping of microsatellites in rice. *Molecular General Genetics.* 241: 225-235.

Yao, F.Y., Xu, C.G., Yu, S.B., Li, J.X., Gao, Y.J., Li, X.H and Zhang, Q.1997. Mapping and genetic analysis of two fertility restorer loci in the wild abortive cytoplasmic male sterility system of rice (*Oryza sativa* L.). *Euphytica* . 98:183.

***Original not seen**

Note: The literature is cited following the guidelines given by Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad – 500 030

Appendix-1: Mean performance of parental lines for yield contributing traits in rice (*Oryza sativa* L.) during *rabi* 2012-13

	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
B lines									
APMS 6B	98.50	89.60	8.25	127.00	21.82	181.83	84.90	16.80	16.25
APMS10B	104.50	82.00	8.45	133.00	22.96	131.00	82.93	16.70	15.30
Mean	101.50	85.80	8.35	130.00	22.39	156.42	83.91	16.75	15.78
R lines									
RP2	102.00	111.30	6.15	132.00	26.75	229.56	90.58	20.95	18.25
RP3	102.50	118.00	4.77	132.50	26.86	277.59	84.50	22.98	13.45
RP4	103.00	108.10	5.62	133.00	24.87	187.94	91.82	15.63	16.40
RP5	101.50	117.10	5.30	131.50	24.47	202.98	84.54	23.29	16.83
RP12	101.00	120.30	6.47	131.00	23.43	152.21	93.15	17.81	13.74
RP13	110.50	119.30	5.51	140.50	26.56	240.78	91.01	20.36	16.30
RP14	104.50	113.00	5.24	134.50	25.53	231.61	77.75	17.00	12.70
RP15	103.00	120.40	4.71	133.00	26.76	171.65	91.30	19.56	14.70
RP17	103.00	114.50	6.04	133.00	23.62	110.52	68.38	22.19	16.45
RP18	106.50	113.00	5.14	136.50	26.88	370.53	83.36	17.03	16.60
RP19	104.50	95.70	4.92	134.50	22.10	172.14	93.08	16.96	17.15
RP20	103.00	108.50	5.94	133.00	25.54	200.82	95.68	18.58	13.20
RP22	100.50	117.70	5.83	130.50	26.16	236.60	90.33	18.88	14.24
TCNP7	104.50	99.20	4.02	134.50	27.00	193.20	91.88	18.65	13.60
TCNP13	105.00	99.80	7.65	135.00	26.38	249.20	94.26	21.01	17.43
TCNP22	103.50	108.60	4.02	133.50	25.30	229.82	91.25	16.59	15.15
TCNP23	92.00	114.70	4.59	122.00	25.34	184.60	86.66	16.88	16.39
TCNP38	90.50	127.60	7.25	120.50	27.37	323.75	90.92	19.01	20.30
TCNP50	88.50	98.70	5.14	118.50	24.09	228.50	90.07	21.53	16.25
TCNP53	103.00	113.90	6.48	133.00	23.47	198.13	93.29	17.75	17.20
TCNP56	103.00	107.60	6.62	133.00	23.05	133.98	77.32	21.34	13.30

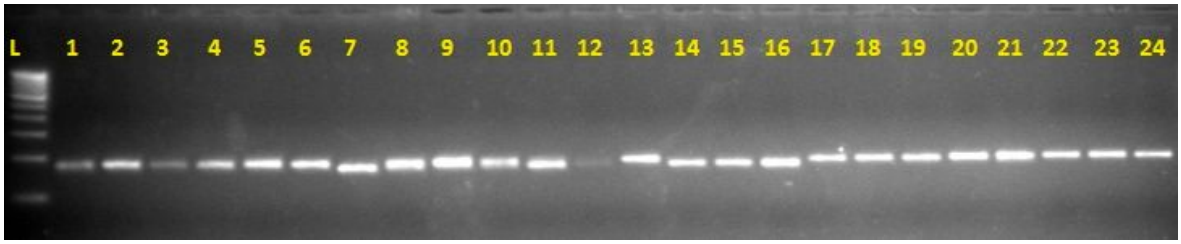
(Contd..)

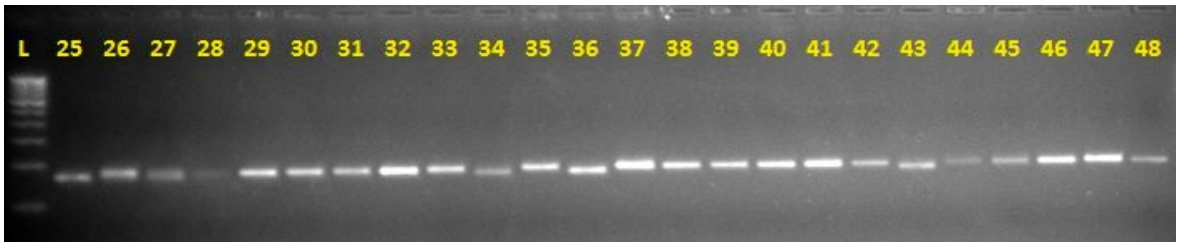
	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No. of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TCNP60	100.00	133.00	4.43	130.00	27.31	226.23	81.16	21.78	10.95
TCNP61	100.50	90.62	4.64	130.50	25.95	201.47	63.66	18.21	16.84
TCNP62	107.50	115.90	7.25	137.50	26.05	106.42	48.24	15.87	12.60
TCNP73	76.00	111.70	8.09	106.00	26.59	245.39	92.27	18.21	15.35
TCNP83	86.50	120.10	6.09	116.50	24.24	378.75	88.45	17.83	11.30
TCNP85	87.50	125.70	6.15	117.50	26.07	391.59	88.88	19.81	12.35
TCNP87	104.50	99.00	4.98	134.50	21.74	128.16	76.55	16.15	11.20
TCNP89	102.50	109.20	5.67	132.50	23.61	131.56	71.80	16.42	16.10
TCNP92	105.50	99.60	6.47	135.50	21.93	146.86	88.50	13.75	10.40
TCNP93	103.50	89.60	4.41	133.50	22.49	144.48	77.09	15.36	12.25
TCNP94	99.50	91.20	4.52	129.50	23.20	205.74	92.03	23.39	19.10
TCNP97	94.50	91.60	5.46	124.50	25.22	151.62	84.40	20.55	17.14
RP1	106.50	103.30	5.78	136.50	24.38	192.40	76.53	16.43	15.65
RP6	102.00	103.90	3.85	132.00	24.39	252.77	80.41	23.24	16.27
RP7	103.00	98.40	4.71	133.00	25.55	124.08	93.30	18.87	17.05
RP9	101.50	109.50	5.78	131.50	21.48	187.47	92.05	17.73	13.00
RP11	98.50	116.60	6.15	128.50	25.83	158.01	75.82	19.65	16.70
RP16	99.00	117.90	5.41	129.00	24.44	139.38	78.85	20.81	17.03
RP21	92.50	96.40	8.93	122.50	24.76	271.43	93.55	22.10	19.05
TCNP1	108.00	93.20	4.86	138.00	25.78	150.37	88.86	15.59	13.20
TCNP14	102.50	94.70	4.46	132.50	24.91	188.89	94.34	21.39	15.35
TCNP21	102.50	105.90	5.02	132.50	25.24	144.23	86.48	19.71	14.20
TCNP26	105.00	97.80	4.81	135.00	26.00	129.45	89.01	15.49	13.10
TCNP29	92.50	134.30	4.24	122.50	27.40	241.46	85.19	18.31	12.65
TCNP51	88.50	93.70	5.13	118.50	24.58	145.35	80.13	21.91	16.03
TCNP54	107.50	96.60	4.75	137.50	24.85	211.99	89.50	16.91	12.15
TCNP57	103.50	97.50	4.86	133.50	24.54	114.64	80.38	19.85	14.85
TCNP58	104.50	101.40	5.02	134.50	21.90	176.71	85.88	16.53	12.45
TCNP75	95.50	114.70	4.13	125.50	26.57	178.25	78.37	20.04	16.25

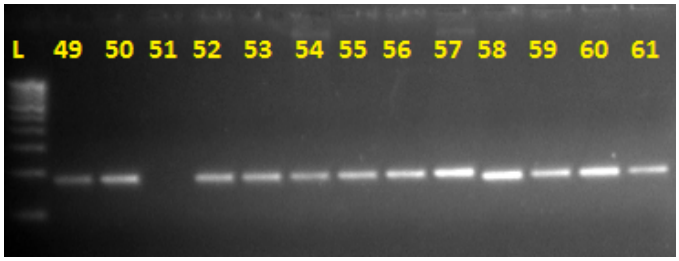
(Contd..)

	Days to 50 % flowering	Plant height (cm)	No. of ear bearing tillers plant^{-1}	Days to maturity	Panicle length (cm)	No: of filled grains panicle^{-1}	Spikelet fertility	Test weight (g)	Grain yield plant^{-1} (g)
TCNP76	93.50	109.30	5.40	123.50	22.29	214.34	88.30	21.57	12.40
TCNP82	104.50	117.50	6.37	134.50	24.46	212.72	82.78	16.58	13.26
TCNP90	102.50	102.10	5.51	132.50	25.09	127.89	85.80	16.86	16.04
TCNP96	106.50	101.50	5.51	136.50	23.13	197.31	93.01	17.67	15.45
TCNP100	105.50	112.75	6.43	135.50	22.43	149.80	83.67	16.80	16.10
Mean	100.53	108.06	5.50	130.53	24.84	198.06	85.21	18.82	14.97
Grand mean	100.56	107.28	5.60	130.50	24.75	196.60	85.16	18.75	15.00
S.E.m	0.61	1.81	0.36	0.64	0.93	11.50	2.49	0.45	1.07
C.D.(5%)	1.73	5.13	1.03	1.82	2.63	33.58	7.05	1.28	3.03
CV(%)	0.86	2.39	9.19	0.70	5.31	8.27	4.13	3.4	10.09

Plate 3. Molecular profile of 55 restorers, two checks and two CMS lines along with their maintainers using RM 6100



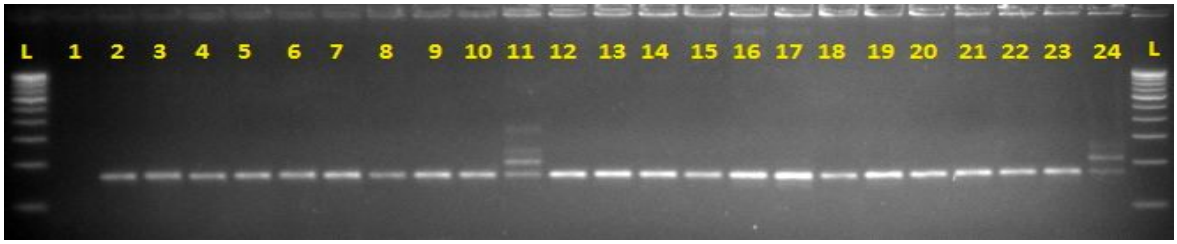


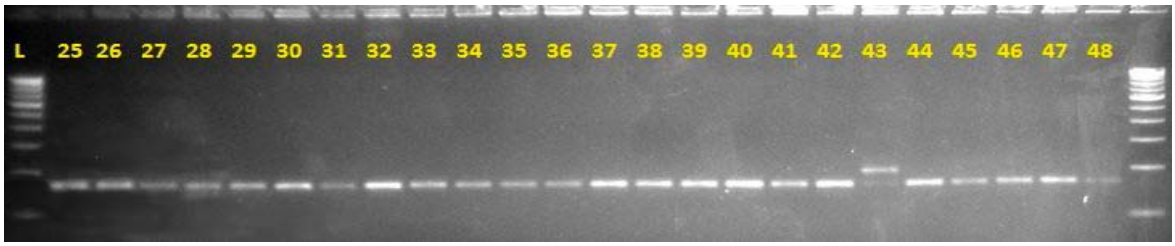


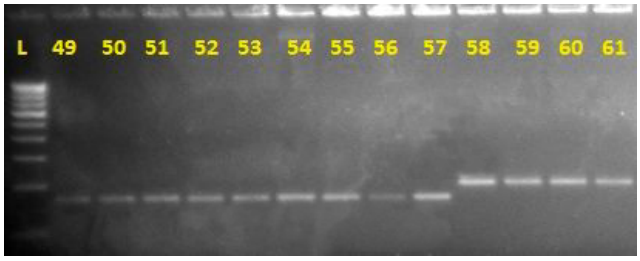
INDEX

L	100 bp ladder	**16**	TCNP 14	**32**	TCNP 51	**48**	TCNP 89
1	RP 1	**17**	RP 11	**33**	TCNP 53	**49**	TCNP 90
2	RP 2	**18**	RP 12	**34**	TCNP 54	**50**	TCNP 92
3	RP 3	**19**	RP 13	**35**	TCNP 56	**51**	TCNP 93
4	RP 4	**20**	RP 14	**36**	TCNP 57	**52**	TCNP 94
5	RP 5	**21**	RP 15	**37**	TCNP 58	**53**	TCNP 96
6	RP 6	**22**	RP 16	**38**	TCNP 60	**54**	TCNP 97
7	RP 7	**23**	RP 17	**39**	TCNP 61	**55**	TCNP 100
8	RP 9	**24**	RP 18	**40**	TCNP 62	**56**	SWARNA
9	RP 19	**25**	TCNP 21	**41**	TCNP 73	**57**	BPT 5204
10	RP 20	**26**	TCNP 22	**42**	TCNP 75	**58**	APMS 6A
11	RP 21	**27**	TCNP 23	**43**	TCNP 76	**59**	APMS 6B
12	RP 22	**28**	TCNP 26	**44**	TCNP 82	**60**	APMS 10A
13	TCNP 1	**29**	TCNP 29	**45**	TCNP 83	**61**	APMS 10B
14	TCNP 7	**30**	TCNP 38	**46**	TCNP 85		
15	TCNP 13	**31**	TCNP 50	**47**	TCNP 87		

Plate 2. Molecular profile of 55 restorers, two checks and two CMS lines along with their maintainers using RM 10287



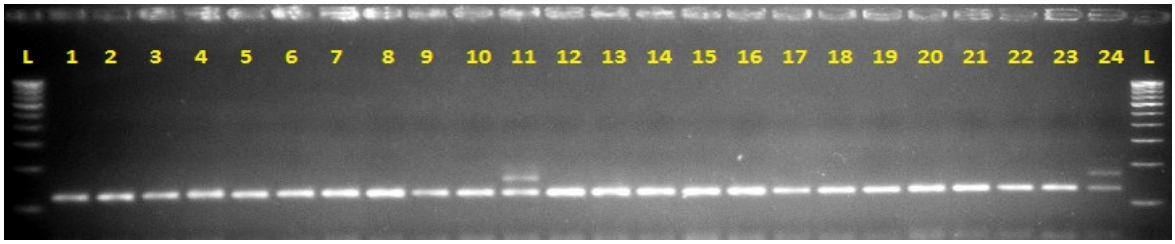


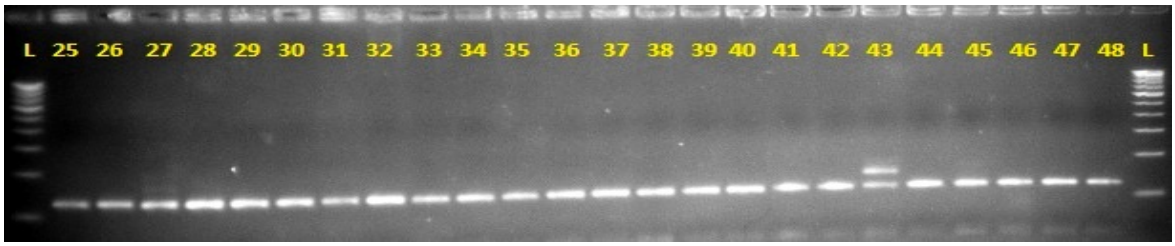


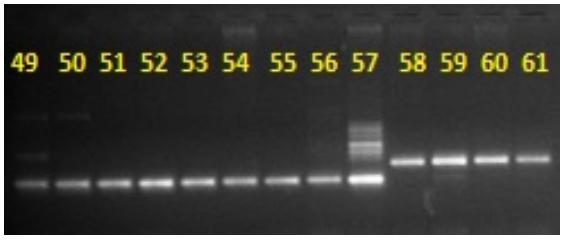
INDEX

L	100 bp ladder	**16**	RP 18	**32**	TCNP 51	**48**	TCNP 89
1	RP 1	**17**	RP 19	**33**	TCNP 53	**49**	TCNP 90
2	RP 2	**18**	RP 20	**34**	TCNP 54	**50**	TCNP 92
3	RP 3	**19**	RP 21	**35**	TCNP 56	**51**	TCNP 93
4	RP 4	**20**	RP 22	**36**	TCNP 57	**52**	TCNP 94
5	RP 5	**21**	TCNP 1	**37**	TCNP 58	**53**	TCNP 96
6	RP 6	**22**	TCNP 7	**38**	TCNP 60	**54**	TCNP 97
7	RP 7	**23**	TCNP 13	**39**	TCNP 61	**55**	TCNP 100
8	RP 9	**24**	TCNP 14	**40**	TCNP 62	**56**	SWARNA
9	RP 11	**25**	TCNP 21	**41**	TCNP 73	**57**	BPT 5204
10	RP 12	**26**	TCNP 22	**42**	TCNP 75	**58**	APMS 6A
11	RP 13	**27**	TCNP 23	**43**	TCNP 76	**59**	APMS 6B
12	RP 14	**28**	TCNP 26	**44**	TCNP 82	**60**	APMS 10A
13	RP 15	**29**	TCNP 29	**45**	TCNP 83	**61**	APMS 10B
14	RP 16	**30**	TCNP 38	**46**	TCNP 85		
15	RP 17	**31**	TCNP 50	**47**	TCNP 87		

Plate 1. Molecular profile of 55 restorers, two checks and two CMS lines along with their maintainers using DRRM Rf 3-5







INDEX

L	100 bp ladder	**16**	RP 18	**32**	TCNP 51	**48**	TCNP 89
1	RP 1	**17**	RP 19	**33**	TCNP 53	**49**	TCNP 90
2	RP 2	**18**	RP 20	**34**	TCNP 54	**50**	TCNP 92
3	RP 3	**19**	RP 21	**35**	TCNP 56	**51**	TCNP 93
4	RP 4	**20**	RP 22	**36**	TCNP 57	**52**	TCNP 94
5	RP 5	**21**	TCNP 1	**37**	TCNP 58	**53**	TCNP 96
6	RP 6	**22**	TCNP 7	**38**	TCNP 60	**54**	TCNP 97
7	RP 7	**23**	TCNP 13	**39**	TCNP 61	**55**	TCNP 100
8	RP 9	**24**	TCNP 14	**40**	TCNP 62	**56**	SWARNA
9	RP 11	**25**	TCNP 21	**41**	TCNP 73	**57**	BPT 5204
10	RP 12	**26**	TCNP 22	**42**	TCNP 75	**58**	APMS 6A
11	RP 13	**27**	TCNP 23	**43**	TCNP 76	**59**	APMS 6B
12	RP 14	**28**	TCNP 26	**44**	TCNP 82	**60**	APMS 10A
13	RP 15	**29**	TCNP 29	**45**	TCNP 83	**61**	APMS 10B
14	RP 16	**30**	TCNP 38	**46**	TCNP 85		
15	RP 17	**31**	TCNP 50	**47**	TCNP 87		