GENETIC CHARACTERIZATION AND MOLECULAR STUDIES FOR BRAN OIL USING SSR MARKERS IN RICE (*Oryza sativa* L.).

BY

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THESIS SUBMITTED TO THE PROFESSOR JAYA SHANKAR TELANGANA STATE AGRICULTURAL UNIVERSITY PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF

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2015

CERTIFICATE

Mr. **M. RAJENDAR REDDY** has satisfactorily prosecuted the course of research and that the thesis entitled **"Genetic characterization and molecular studies for bran oil using SSR markers in rice (*Oryza sativa* L.)"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him for a degree of any university.

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Chairperson

DECLARATION

I, **Mr. RAJENDAR REDDY** hereby declare that the thesis entitled **"GENETIC CHARACTERIZATION AND MOLECULAR STUDIES FOR BRAN OIL USING SSR MARKERS IN RICE (*Oryza sativa* L.)"** submitted to the **Professor Jaya Shankar Telangana State Agricultural University** (Formerly part of Acharya N.G. Ranga Agricultural University) for the degree of **Doctor of philosophy in Agriculture** is the result of original research work done by me. I also declare that any material contained in the thesis has not been published earlier in any manner.

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Date :

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LIST OF CONTENTS

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

CERTIFICATE

This is to certify that the thesis entitled " **GENETIC CHARACTERIZATION AND MOLECULAR STUDIES FOR BRAN OIL USING SSR MARKERS IN RICE (*Oryza sativa* L.)"** submitted in partial fulfilment of the requirements for the degree of "**Doctor of philosophy in Agriculture"** of the **Professor Jaya Shankar Telangana State Agricultural University** (Formerly part of Acharya N.G. Ranga Agricultural University) is a record of the bonafide original research work carried out by Mr. M.Rajendar reddy 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 has been duly acknowledged by the author of thesis.

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Date of Final Viva-Voce: 23-02-2015

LIST OF TABLES

Sl.No	Particulars	Page No.
2.1	Review of literature on gene action for yield, yield component characters in rice (*Oryza sativa* L.)	
2.1.1	Review of literature on gene action for days to 50 % flowering	
2.1.2	Review of literature on gene action for plant height (cm)	
2.1.3	Review of literature on gene action for number of productive tillers per plant	
2.1.4	Review of literature on gene action for panicle length (cm)	
2.1.5	Review of literature on gene action for number of filled grains per panicle	
2.1.6	Review of literature on gene action for 1000-grain weight (g)	
2.1.7	Review of literature on gene action for grain yield per plant (g)	
2.3.1	Association of yield component characters with grain yield per plant in rice	
2.3.2	Association of days to 50 % flowering with	
2.3.3	Association of plant height (cm)	
2.3.4	Association of panicle length (cm)	
2.3.5	Association of number of productive tillers per plant	
2.3.6	Association of 1000-grain weight (g)	
2.3.7	Association of grain yield per plant (g)	
2.3.8	Association of kernel length (mm) with	
2.3.9	Association of L/B ratio with	

2.4.1	Direct effects of different characters on grain yield per plant (g)	
2.4.2	Indirect effects of days to 50% flowering on grain yield per plant through	
2.4.3	Indirect effects of plant height on grain yield per plant through	
2.4.4	Indirect effects of panicle length on grain yield per plant through	
2.4.5	Indirect effects of number of productive tillers per plant on grain yield per plant through	
2.4.6	Indirect effects of number of filled grains per panicle on grain yield per plant through	
2.4.7	Indirect effects of 1000-grain weight on grain yield per plant through	
2.4.8	Indirect effects of kernel length on grain yield per plant through	
2.4.9	Indirect effects of L/B ratio on grain yield per plant through	
2.6.1	Review on QTL Mapping for protein content.	
3.1	Some of the promising genotypes with medium to high bran oil content	
3.2	Details of the eleven genotypes used in the study	
3.3	Details of SSR markers used and their chromosomal locations	
3.4	Master mix used for 35 reactions in PCR	
3.5	PCR Profile used for DNA amplification	
4.1.	Analysis of variance (Mean squares)for yield and its components, Quality traits and bran oil content in three different locations	
4.1.2	The cross combinations used in the present study and their codings	
4.2.1-4.2.6	Mean performance of yield and its components, quality traits and bran oil content in three different locations and over locations	

4.3.1	Analysis of variance of combining ability for different characters in rice at Jagtial location	
4.3.2	Analysis of variance of combining ability for different characters in rice at Warangal location	
4.3.3	Analysis of variance of combining ability for different characters in rice at Hyderabad location	
4.3.4	Analysis of variance of combining ability for different characters in rice in pooled analysis	
4.3.5	Estimates of gca effects for yield, its components and quality traits in rice (O.*sativa)* in 3 locations.	
4.3.6	Estimates of gca effects for yield, its components and quality traits in pooled analysis	
4.3.7	Promising general combiners for yield , its components and quality traits	
4.3.8	Estimates sca effects for yield, its components and quality traits and bran oil content in rice at 3 locations	
4.3.9	Estimates sca effects for yield, its components and quality traits and bran oil content in rice in pooled analysis	
4.3.10	Type of gene action for different characters based on GCA/ SCA variance ratio	
4.3.11	Promising specific combiners for Yield and other traits	
4.3.12	Promising specific combiners for bran oil content, yield attributes and quality traits	
4.4.1	Standard heterosis for bran oil content, yield and quality traits in rice (*Oryza sativa* L.) at different locations and in pooled analysis	
4.4.2	Most promising cross combinations for yield and quality characters based on *sca* effects, *per se* performance and heterosis	
4.4.3	Most promising cross combinations for bran oil content based on *per se* performance correlating with optimum grain yield	
4.5.1	Analysis of variance for yield and yield components and bran oil content for stability in rice	

4.5.2	Analysis of variance for kernel characters and bran oil content for stability in rice	
4.5.3	Environment indices for bran oil, yield and quality components for three locations	
4.5.4	Mean performance and stability parameters for bran oil, yield and its components.	
4.5.5	Classification of cross combinations for different based on stability parameters	
4.6	Simple correlation coefficients for yield and its components, quality traits, bran oil for three different locations and pooled analysis	
4.7	Direct and Indirect effects for yield components, Kernel characters and bran oil on grain yield for three different locations and pooled analysis	
4.8.1	Variance of parents, F1 and F2 generation for bran oil in Keshari and Swarna cross combination	
4.8.2	PCV, GCV, Heritability and GA for bran oil content in F2 generation	
4.9.1	Parental polymorphism survey between Keshari and Swarna	
4.9.2	Single Marker Analysis for bran oil with RM1 and RM5140 Markers	

LIST OF PLATES

Sl. No.	Title	Page No.
1	Segregation pattern of RM-1 marker in F_2 population of Keshari × Swarna	

LIST OF ILLUSTRATIONS

Sl. No.	Title	Page No.
1	Standard heterosis exhibited by promising cross combinations for days to 50% flowering	
2	Standard heterosis exhibited by promising cross combinations for panicle length	
3	Standard heterosis exhibited by promising cross combinations for 1000-grain weight	
4	Comparison of parents, F_1s and heterosis for number of grains per panicle	
5	Comparison of parents, F_1s and heterosis for grain yield per plant	
6	Mean performance, *sca effect* and standard heterosis in promising cross combinations for grain yield per plant	
7	Most promising cross combinations for bran oil content based on *per se* performance correlating with optimum grain yield per plant.	

LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
AFLP	:	Amplified Fragment Length Polymorphism
bp	:	Base pairs
CV	:	Coefficient of variation
CTAB	:	Cetyl-trimethyl-ammonium bromide
DAS	:	Days after sowing
ddw	:	Double distil water
df	:	Degrees of freedom
DH	:	Double hapliod
DNA	:	Deoxyribonucleic acid
dNTP	:	Deoxynucleotide triphosphate
DRR	:	Directorate of Rice Research
EDTA	:	Ethyl diamino tetra acetic acid
EMS	:	Ethylmethane sulphonate
et.al	:	And co-authors.
F_1	:	First ffilialgeneration.
F_2	:	Second ffilialgeneration.
g	:	Gram
GA	:	Genetic advance
gca	:	General combining ability
GCV	:	Genotypic coefficient of variaion
ha	:	Hectare
HCl	:	Hydro chloric acid
hr	:	Hour
i.e.,	:	Which is to say in other words
Ij	:	environment index
M	:	Molar
MAS	:	Marker assisted selection
mg	:	Milli gram
m ha	:	Million hectares.
min	:	Minute

ml	:	Micro litre
mM	:	Milli molar
Nacl	:	Sodium chloride
ng	:	Nanogram
nm	:	Nanometer
^{o} C	:	Degree centigrade
^{0}F	:	Degree Foreignheat
PCR	:	Polymerase chain reaction
PCV	:	Phenotypic coefficient of variaion
PVP	:	Polyvinyl pyrollidone
QTL	:	Quantitative Trait Loci
RAPD	:	Random Amplified Polymorphic DNA
RFLP	:	Restriction Fragment Length Polymorphism
RIL	:	Recombinant inbred line
rpm	:	revolutions per minute
sca	:	Specific combining ability
S.E	:	Standard error
S.Em	:	Standard error of means
SSR	:	Simple sequence repeats
Taq	:	Thermostable DNA polymerase
TAE	:	Tris Actate EDTA buffer
TBE	:	Tris Borate EDTA buffer
UV	:	Ultra violet
v/v	:	Volume/ volume
viz.,	:	namely
w/v	:	weight/volume
µL	:	Micro litre
µM	:	Micro molar

ABSTRACT

Name of the Author	**:**	**M.RAJENDAR REDDY**
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The present investigation in rice was undertaken to estimate GCA, SCA effects (L × T mating), heterosis and to study stability of hybrids for bran oil, yield, yield components and quality traits across locations of Telangana state, to study the association and direct and indirect effects between yield and bran oil and to map the gene(s) for bran oil.

Six lines with medium to high bran oil content (Keshari, Ishwarya, Mandhya Vijaya, PR116, Kandhagiri and Phalguna) and five popular high yielding varieties (NDR359, IR64, Swarna, RPBio226 and MTU1010) with low bran oil were crossed in a line × tester design during *kharif*, 2012 at DRR Farm, Directorate of Rice Research, Hyderabad, Telangana state. During *rabi,* 2012-13 the 30 cross combinations along with their parents were evaluated at three different locations *viz.,* Jagitial, Warangal, and Hyderabad for bran oil content, yield, yield components and quality characters.

The analysis of variance of 41 genotypes (Six lines, five testers and 30 cross combinations) revealed significant differences among the lines, testers and hybrids evaluated at different locations for all the characters under study.

The combining ability analysis of variance, in pooled analysis, showed significant differences due to locations, parents, hybrids and various interactions indicating the existence of sufficient variation in the material under study. The g*ca* and *sca* variances indicated that non additive gene action was predominant in the expression of bran oil content, yield, yield component traits and quality characters except for plant height and gel consistency where additive gene action was predominant.

In pooled analysis, none of the lines and testers were found to exhibit significant *gca* effects for all the characters studied. Keshari and MTU1010 among lines and IR64 and Swarna among testers were good general combiners for bran oil

content whereas lines Mandhya Vijaya and Phalguna and testers NDR359 and MTU1010 were found to be promising general combiners for grain yield per plant and other traits.

Based on significant *sca* effects, in pooled analysis, for bran oil content eight crosses recorded significant positive *sca* effects. On the whole, six cross combinations *viz.,* Mandhya Vijaya × NDR359, Keshari × MTU1010, Phalguna × NDR359, Mandhya Vijaya × Swarna, Kandhagiri × RP Bio226 and Phalguna × Swarna have been identified as promising based on *per se* performance, *sca* effects and heterosis for yield and its attributes in pooled analysis. Besides yield these cross combinations also possessed desirable quality characters like milling per cent, head rice recovery per cent, kernel length, kernel breadth, L/B ratio, gel consistency and amylose content. But in case of bran oil content, none of the cross combination showed significant heterosis in desirable direction though Keshari × IR64, Kandhagiri × RPBIO226, Keshari × NDR359, Phalguna × MTU1010 and Kandhagiri × MTU1010 had high bran oil content among all cross combinations with optimum yield.

Genotype × environment interaction studies with 30 hybrids at different locations for bran oil content, yield and yield attributing traits by Eberhart and Russell revealed four hybrids *viz.,* Mandhya Vijaya × NDR359, Phalguna × NDR359, PR116 × NDR359 and Phalguna × MTU1010 were identified as stable hybrids for grain yield per plant while in case of bran oil content the hybrid, Kandhagiri × Swarna was considered as stable cross combination.

The character association studies revealed that the attributes *viz.* kernel breadth, panicle length, 1000-grain weight, number of grains per panicle, days to 50 % flowering, plant height and kernel length were showed a significant positive association along with direct effect on grain yield per plant suggesting selection of these traits will be useful for the improvement of grain yield.

Based on the present study, it can be emphasized that Mandhya Vijaya × NDR359 and Phalguna × NDR359 are stable with the desirable *sca* effects, heterosis and *per se* performance for grain yield and other important attributes. Keshari × IR64 and Kandhagiri × RPBio226 had high bran oil content among all cross combinations with optimum yield. These hybrids may be further tested over locations, seasons and years and recommended for commercial release.

During *Kharif, 2013*, F_2 generation of Keshari × Swarna was grown at DRR Farm, Directorate of Rice Research, Hyderabad, for the estimation of genetic parameters. The estimated value of PCV is higher than GCV, it means that the apparent variation is not only due to genotypes but also due to the influence of environment and selection for this trait sometimes may be misleading. Medium heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the presence of additive gene action. Hence this trait can be improved through simple selection procedures.

Till now there are no reports about the markers related to bran oil. Attempt has been made with 30 SSR markers representing 12 chromosomes of rice in cross Keshari × Swarna to find out the bran oil related markers and concluded that RM5140 marker – can be used as bran oil related marker in future studies as it showed the highest F value (Probability less than 0.005).

Chapter I

INTRODUCTION

Rice (*Oryza sativa*L.) is one of the predominant food crops of the world. Worldwide, rice is grown in an area of 163 million hectares with a production of 730 million tonnes and with an average productivity of 4.48 tonnes per hectare (FAO, 2013), out of which 90 per cent of world's rice is produced and consumed in Asia. While, China produces 206 million tonnes from an area of 30.05 million hectare with the productivity of 6.7 tonnes per hectare (FAO, 2013). It is a grain of life for more than 70 per cent of the Asian population and it has great importance in Indian culture.

Rice is produced in very large quantities in nine countries of South-east Asia. Considerable amounts are also produced in the USA, Europe and Latin America. China is the largest rice producing country followed by India. India is the world's second largest producer 104.32 million tonnes of rice on an area of 43.97 million hectares and with the productivity of 2.37 tonnes per hectare. In Andhra Pradesh it is grown in an area of 41.31 lakh hectares with production of 130.8 lakh tonnes and productivity of 3.17 tonnes per hectare (Directorate of Economics and Statistics, 2012).

Rice bran is a byproduct of rice processing industry and upon extraction yields rice bran oil. The oil content of rice bran varies in each variety and depends to an even greater extent on the processes and conditions obtained during rice milling. Rice bran, as such, has 15 to 25% of oil associated with it. The total world production of about 4000 million tons of paddy may yield about 6-7 million tons of edible grade oil. Modern techniques of recovery would yield oil and other by-products of better quality than the old technologies, still being used in India, China and other Asian countries.

Under-nourishment is the problem that all the developing countries face to-day. Studies carried out by the United Nations have indicated that diets of the people in these countries are deficient in calories. Similar is the case with India, where the prices of oils and fats are always on the ascent. The reasons for this are-(i) increasing population and (ii) rise in standard of living of bulk of the lower echelons of the population. These factors have increased and continue to increase the demand for oils and fats both for edible and non-edible purposes. But the increase in the production of

oil seed crop is not in keeping with the increasing demand. India, an exporter of oil twenty years ago, is forced to-day to import oil for domestic consumption. This is true for both edible and essential oils.

Rice bran oil (also known as rice bran extract) is the oil extracted from the germ and inner husk of rice. It is notable for its high smoke point of 213 °C (415 °F) and its mild flavor, making it suitable for high-temperature cooking methods such as stir frying and deep frying. It belongs to vitamin E family – a natural antioxidant, which prevents cardio vascular diseases.A rich source of gamma – oryzanol (anti-oxidant) used to treat nerve imbalance and disorders of menopause. It has no cholesterol and no trans-fatty acids and rich in oleic and linoleic fatty acids.It is popular as a cooking oil in several Asian countries, including Japan and China.

A wide range of vegetable oils are available in the market. However, some vegetable oils are not up to standards to meet consumer satisfaction in terms of their physicochemical properties and stability.Blending of vegetable oils is gaining popularity due to its advantages like improved thermal stability, oxidative stability and nutritional benefits. Blending of oil with rice bran oil has been found to improve the stability of the blend during frying and storage. In addition, rice bran oil is less expensive non-conventional oil and blending it with other expensive conventional vegetable oils will produce lower cost rice bran oil blends

Rice bran oil has a composition similar to that of peanut oil, with 38% monounsaturated, 37% polyunsaturated, and 25% saturated. Rice bran oil and its active constituents improve blood cholesterol by reducing total plasma cholesterol and triglyceride concentration and increasing the proportion of HDL cholesterol. The antioxidant stability in rice bran oil remains almost constant even when heated at frying temperatures. The oxidative stability of rice bran oil was equivalent to or better than soybean, corn, canola, cottonseed, and safflower oil in a model system that simulated deep frying condition. Other potential properties of rice bran oil include modulation of pituitary secretion, inhibition of gastric acid secretion, antioxidant action and inhibition of platelet aggregation.

The plant breeders should focus their attention towards the improvement of rice bran oil content, grain quality and high yield potential. Yield is a complex character determined by a large number of component characters which are considered important

in plant breeding. There were no systematic studies on rice bran oil content in improved high yielding varieties in India.

Keeping in view, the situation presented in the foregoing paragraphs, an attempt has been made in the present investigation to identify the promising rice crosses having high bran oil content coupled with optimum yield with the specific objectives being:

Objectives:

1. To study the general combining ability ***(gca)*** and specific combining ability ***(sea)*** effects for bran oil, grain yield and its components through Line x Tester design.
2. To estimate the heterosis for quality, yield and its component traits.
3. To study the interrelationship between bran oil and yield through direct and indirect effect.
4. To analyze G x E interaction and stability of hybrids for bran oil content and grain yield.
5. To study genetics related to bran oil content.
6. Mapping of the gene(s) for Bran oil using SSR markers.

Chapter II

REVIEW OF LITERATURE

The present investigation in rice was undertaken to estimate GCA, SCA effects (L × T mating), heterosis and to study stability of hybrids for bran oil, yield, yield components and quality traits across locations, to study the association and direct and indirect effects between yield and bran oil and to map the gene(s) for bran oil. The literature available on the main objectives of the present study has been comprehensively reviewed under the following headings.

2.1 Combining Ability Analysis

Combining ability studies are useful in classifying parental lines in terms of their hybrid performance. In self pollinated crops, these studies are useful in assessing the nicking ability of parents and thus aid in selecting parents which when crossed would give rise to more desirable segregants, as the choice of the parents is the first important step in any plant breeding programme aimed at improving yield or other attributes.

Combining ability is the ability of an inbred line to transmit desirable performance to its hybrid progenies. Sprague and Tatum (1942) defined general combining ability (*gca*) as the average performance of a line in hybrid combinations. The term specific combining ability (*sca*) was applied to designate the crosses in which certain combinations do relatively better or worse than would be expected on the basis of average performance of line involved. The estimation of *gca* and *sca* gives an idea of performance of parents. In cross combinations *gca* is associated with additive effect of genes and *sca* is attributed primarily to deviation from the additive scheme caused by dominance and epistasis.

The results of earlier work on combining ability studies in rice revealed that most of yield components and quality characters were under the influence of all three types of gene action *viz.*, additive, non-additive and both additive and non-additive gene actions. A brief review of studies on combining ability for oil, yield and quality characters was presented below.

The studies in general revealed significant *gca* and *sca* variances indicating the importance of both additive and non additive gene effects. A perusal of the literature on *gca* effects of the parents with regard to hybrid performance revealed that superior crosses with high *sca* effects for grain yield plant^{-1} were obtained from both the parents having high *gca* effects [Ganesan *et al.* (1997), Meenakshi and Devarathinam (1999) and Kalitha and Upadhaya (2000)], one parent with high *gca* and other with low *gca* effect [Annandurai and Nadarajan (2001), Anand Kumar *et al.* (2006) and Pradhan and Singh (2008)] and both low combiner parents (Swamy *et al.,* 2003), as a result of Additive x Additive, Additive x dominance and over dominance or epistatic gene interactions, respectively.

2.1.1 Combining ability for oil

Sabaghnia, N *et al*. (2010) carried out studies on combining ability in Rapeseed for 36 F_1 combinations and reported the importance of non-additive gene action for oil content.

Ghaffari, M *et al*. (2011) conducted experiment in Sunflower to study combining ability of 24 F_1 combinations and reported the importance of additive gene action for oil content.

Amir Jose Klein Werle *et al*. (2013) studied combining ability in maize and reported both additive and non-additive effects were involved in the genetic control of the oil content and crude protein. The estimates of the components showed predominance of non-additive genetic effects in the oil content.

Mahesh, N *et al*. (2013) evaluated 88 single cross hybrids of Maize through Line x Tester analysis for starch, protein and oil content. He noticed YP-15 as a good general combiner for grain yield and starch content. While inbred lines YP-25 and YP - 16 were good general combiners for protein and oil content respectively. The hybrids such as ARBMH-09-28 and ARBMH-09-42 for oil content were performed better with high significant SCA effects.

Sunita, J *et al*. (2013) did experiment to study combining ability in Safflower through Diallel analysis for yield and oil content. The germplasm lines GMU 7359 and GMU 5394 were good general combiners for characters *viz.*, seed yield, total capitula per plant, 100 seed weight, biological yield, harvest index and oil content. For SCA effects the

best crosses identified in pooled analysis were GMU 5815 x GMU 217and GMU 5815 x GMU 217for seed yield. Whereas, GMU 5267 x GMU 5815, GMU 3714 x GMU 7359 and GMU 5394 x GMU 217 exhibited maximum SCA effect for oil content.

Binod Kumar *et al*. (2014) carried out combining ability analysis in Indian mustard through Line x Tester analysis for yield and oil quality traits. Among the lines and testers, RH-30, RAURD 214, EC 401574 and Rajendra Sufalam be proved to good general combiners by exhibiting desirable negative and highly significant gca effect for days to 50% flowering and days to maturity and positive and highly significant for number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, siliqua length, siliqua density, 1000 seed weight, biological yield per plant, stearic acid, oleic acid, oil content and seed yield per plant indicating the presence of additive gene action or additive x additive interaction effects.

Table 2.1. Review of literature on gene action for yield, yield component characters in rice (*Oryza sativa* L.)

Table 2.1.1. Review of literature on gene action for days to 50% flowering

Gene action		
Additive	**Non additive**	**Additive and non additive**
Sharma and Koranne (1995)	Manuel and Rangaswamy (1995)	
Sreedhar and Kulkarni (1995)	Ramalingam *et al*. (1997)	
Ganesan and Rangaswamy (1998)	Singh and Maurya (1997)	
Patil *et al* .(2003a)	Yadav *et al.* (1999)	
Rosamma and Vijayakumar (2005)	Babu *et al*. (2000)	
Anand Kumar *et al*.(2006)	Satyanarayana *et al.* (2000)	
Gnanasekaran *et al.* (2006)	Banumathy *et al.* (2003)	
Dalvi and Patel (2009)	Bhave *et al.* (2003)	
	Swamy *et al.* (2003)	
	Panwar (2005)	
	Jayasudhan and Deepak Sharma (2009)	
	Kumar Babu e*t al.* (2010a)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al*. (2010a)	
	Saidaiah e*t al*. (2011)	

Table 2.1.2. Review of literature on gene action for plant height (cm)

Additive	Non additive	Additive and non additive
Manuel and Rangaswamy (1995)	Sreedhar and Kulkarni (1995)	
Sharma and Koranne (1995)	Yadav *et al.* (1999)	
Ramalingam *et al*. (1997)	Kalita and Upadhaya (2000)	
Ganesan and Rangaswamy (1998)	Satyanarayana *et al.* (2000)	
Shanthakumar *et al.* (1998)	Bhave *et al.* (2003)	
Anand Kumar *et al.* (2006)	Swamy *et al.* (2003)	
Gnanasekaran *et al.* (2006)	Panwar (2005)	
Nadali Bagheri and Babaeian (2010)	Singh *et al.* (2005)	
	Dalvi and Patel (2009)	
	Jayasudhan and Deepak Sharma (2009)	
	Kumar Babu e*t al.* (2010a)	
	Saidaiah *et al.* (2010a)	
	Saidaiah e*t al.* (2011)	

Table 2.1.3. Review of literature on gene action for number of productive tillers plant $^{-1}$

Additive	Non additive	Additive and non additive
Rosamma and Vijayakumar (2005)	Sharma and Koranne (1995)	
Gnanasekaran *et al.* (2006)	Sreedhar and Kulkarni (1995)	
Dalvi and Patel (2009)	Ramalingam *et al.* (1997)	
	Ganesan and Rangaswamy (1998)	
	Yadav *et al.* (1999)	
	Babu *et al.* (2000)	
	Kalita and Upadhaya (2000)	
	Satyanarayana *et al.* (2000)	
	Banumathy *et al.* (2003)	
	Bhave *et al.* (2003)	
	Patil *et al.*(2003a)	
	Swamy *et al.* (2003)	
	Panwar (2005)	
	Singh *et al.* (2005)	
	Anand Kumar *et al.*(2006)	
	Jayasudhan and Deepak Sharma (2009)	
	Kumar Babu e*t al.* (2010a)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al.* (2010a)	
	Saidaiah e*t al.* (2011)	

Table 2.1.4. Review of literature on gene action for panicle length (cm)

Additive	Non additive	Additive and non additive
Kalita and Upadhaya (2000)	Sreedhar and Kulkarni (1995)	Anand Kumar *et al.* (2006)
	Ramalingam *et al*. (1997)	
	Singh and Maurya (1997)	
	Ganesan and Rangaswamy (1998)	
	Yadav *et al.* (1999)	
	Babu *et al.* (2000)	
	Satyanarayana *et al.* (2000)	
	Bhave *et al.* (2003)	
	Banumathy *et al.* (2003)	
	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)	
	Saidaiah e*t al.* (2011)	

Table 2.1.5. Review of literature on gene action for number of filled grains panicle^{-1}

Additive	Non additive	Additive and non additive
Ganesan and Rangaswamy (1998)	Ramalingam *et al.* (1997)	Anand Kumar *et al.* (2006)
Rosamma and Vijayakumar (2005)	Yadav *et al*. (1999)	
	Babu *et al.* (2000)	
	Banumathy *et al*. (2003)	
	Patil *et al.*(2003a)	
	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)	
	Saidaiah e*t al.* (2011)	

Table 2.1.6. Review of literature on gene action for 1000-grain weight (g)

Additive	Non additive	Additive and non additive
Ganesan and Rangaswamy (1998)	Sharma and Koranne (1995)	Patil *et al.* (2003a)
Rosamma and Vijayakumar (2005)	Ramalingam *et al*. (1997)	
Gnanasekaran *et al.* (2006)	Babu *et al.* (2000)	
	Kalita and Upadhaya (2000)	
	Satyanarayana *et al.* (2000)	
	Banumathy *et al.* (2003)	
	Bhave *et al.* (2003)	
	Swamy *et al.* (2003)	
	Panwar (2005)	
	Anand Kumar *et al.* (2006)	
	Kumar Babu e*t al.* (2010a)	

Table 2.1.7. Review of literature on gene action for grain yield per plant (g)

Additive	Non additive	Additive and non additive
	Sharma and Koranne (1995)	
	Ramalingam *et al.* (1997)	
	Singh and Maurya (1997)	
	Ganesan and Rangaswamy (1998)	
	Yadav *et al.* (1999)	
	Babu *et al.* (2000)	
	Satyanarayana (2000)	
	Banumathy *et al.* (2003)	
	Bhave *et al.* (2003)	
	Patil *et al.*(2003a)	
	Swamy *et al.* (2003)	
	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 e*t al.* (2010a)	
	Nadali Bagheri and Babaeian (2010)	
	Saidaiah *et al.* (2010a)	
	Saidaiah e*t al.* (2011)	

2.1.2 Quality characters

Dhaliwal and Sharma (1990) carried out studies on combining ability and reported the importance of non-additive gene action for grain characters like grain length and breadth.

Verma *et al.* (1994) reported the presence of non-allelic interactions for grain length, breadth and L/B ratio which is of additive x dominance in combination with dominance x dominance type. They also reported predominance of dominance components for these characters.

Vivekanandan and Girdhan (1995) while studying combing ability for grain quality characters reported higher *gca* variances than *sca* variances for kernel length, kernel breadth, kernel L/B ratio, kernel length after cooking, kernel breadth after cooking, linear elongation ratio, breadth wise expansion ratio and elongation index suggesting the prevalence of additive gene action in the expression of these traits.

In a study of grain characters Paramasivan *et al.* (1996) opinionated that *gca* effects were significant for IR50 and White ponni. Parents TKM 6 and ADT 37 were best for improving cooking quality. ADT 39 proved to be a good donor for improving hulling and milling percentage. Predominance of additive gene action was indicated by high *gca* values recorded.

Sharma and Mani (1997) observed predominance of non-additive gene effect for alkali spreading value, water uptake and amylose content. However, both additive and non-additive gene effects were equally important for kernel elongation and volume expansion ratio.

Sharma and Mani (1998) estimated gene action and combining ability for physical grain quality characters in a set of diallel crosses involving nine genotypes. Non-additive gene action appeared to be predominant for kernel length, L/B ratio, milling and head rice recovery, while both additive and non-additive gene action were equally important for kernel breadth. Predominance of non-additive genetic variance supports the idea for the exploitation of hybrid vigour in improving physical quality traits.

Munhot *et al.* (2000) carried out combining ability analysis in rice through Line x Tester analysis for yield, yield attributes and quality traits. The predominance of dominance gene action was observed for milling percentage, head rice recovery, kernel breadth, elongation ratio and alkali value. The predominance of additive gene action

was recorded for expression of kernel length, L/B ratio, and kernel elongation. In addition to grain yield plant^{-1}, crosses also had significant and positive *sca* effect for different traits like hulling percentage, kernel length, L/B ratio, kernel elongation ratio, head rice recovery, milling percentage, kernel breadth, and alkali spreading value.

Bisne and Motiramani (2005) indicated that non additive gene effect was predominant for characters like length and breadth of paddy kernels. Further, Ganasekaran *et al.* (2006) revealed that the line GD 98014 had significant and desirable *gca* effects for kernel elongation after cooking and amylose content. Among the testers, IR 72 had good *gca* effects for kernel L/B ratio, followed by CB 97033 which has shown high *gca* effects for six traits. Among the 32 crosses generated, the hybrid GD 98049/IR 72 recorded high mean values for all the traits except for kernel elongation at cooking and amylose content.

Venkatesan *et al.* (2007) studied ten physical characters in rice through Line x Tester analysis involving eight lines and four testers. The mean squares of variance for Line x Tester interaction were significant for all the characters except for grain length and grain breadth. The combining ability analysis revealed non-additive gene action governing the characters *viz.*, days to first flower, plant height, panicles per plant, grain yield per plant and grain L/B ratio. Predominance of *gca* variance was recorded for days to first flower, plant height, grains per panicles and grain yield per plant.

Sharma *et al.* (2007) reported variety Basanthabahar exhibited high *gca* for grain length, L/B ratio and water uptake, while Malbhog-I exhibited high *gca* for alkali digestion value. Crosses identified best for other important traits were Haripua x Nilaji for L/B ratio and Aijuri x Hasakumra for alkali digestion value, all these crosses had high *sca* effects.

Pradhan and Singh (2008) studied 30 hybrids generated from crossing three lines with ten testers. The *gca* and *sca* effects were significant for all the characters, indicating the importance of both additive and non additive genetic components. But it was found that there was predominance of non-additive genetic components for expression of different traits. Among the parental lines, RP 3392-75-11-1 and RP 3644-41-9-5-5 were best general combiners for grain yield along with other traits. The most specific combiners for grain yield and other traits were Pusa3A x RP3392-75-11-1, IR 68281A x BTCE 10-98, IR 58025A X HKR 97-401, Pusa x RP3644-36-15-8-4 and IR68281A x RP3644-41-9-5-6.

Dalvi and Patel (2009) studied sixty hybrids along with parents for 13 yield attributing characters. Among the male parental lines BR-827-35-3-1, RTN-3, IR-46 appeared as the best general combiner for grain yield and most of the component characters. The female line IR-58025A was found to be good general combiner for all the traits except for plant height and L/B ratio of grain.

Shivani *et al*. (2009) stated that, eighteen *indica/indica* hybrids developed by crossing three lines with six testers were screened for various grain quality traits to assess the combining ability of the parents. For head rice recovery, the crosses involving IR 58025A with MTU 9992 and KMR-3, IR 62829A with MTU 9992 and IR 68886A with IR 40750R and IR 21567 showed significant positive specific combining ability (*sca*) effects. For kernel length, IR 58025A and IR 688886A among lines and MTU 9992 and IR 21567 among testers showed positive significant general combining ability *(gca)* effects. The magnitude of s^2 *gca*/s^2*sca* revealed the predominance of non-additive genetic variance for most of the quality characters.

Tyagi *et al*. (2010) based on the general combining ability estimates for 11 grain quality characters in a set of crosses involving nine parents of indica rice observed that none of parental line was found excellent for all the 11 qualitative characters. Among the nine lines, three lines *viz.,* Pusa-1121 (L7), Pusa-1463 (L9) and Pusa-1176 (L6) showed good general combining ability effects for maximum quality characters. Among all the crosses, P-1463 x P-44 showed high specific combining ability effects as well as high heterosis. P-1173 x Heibao, Shah-Pasand x P-44 and Bas-370 x Heibao were good specific combiners for different characters.

Kumar Babu *et al.* (2010) studied 96 hybrids generated from crossing four CMS lines and twenty four testers along with parents to estimate combining ability for quality characters. Predominance of non-additive gene action was observed for grain length and L/B ratio. The line IR58025A and tester MTUII 161-28- 1-1 were found to be good general combiners for grain quality characters. Crosses PMS10A X MTU II 161-28-1-1 and PMS10A X MTU II 193-23-1 were identified as most promising crosses for yield based on *sca* effects, *per se* performance and with more than 55 per cent standard heterosis.

Gonya Nayak (2011) evaluated sixteen crosses developed from four aromatic lines and four normal testers for various grain quality traits to assess the combining ability of the parents and to identify best combinations. The predominance of non-

additive genetic variance was noticed for most of the quality characters *viz.*, milling and head rice recovery, kernel length after cooking, kernel breadth after cooking, kernel elongation ratio and aroma. Kernel length, kernel breadth and L/B ratio were under the influence of additive gene action. Parents Yamini, Pusa-1121 and MTU-1010 appeared to have contributed maximum favourable genes for physical and cooking quality traits. Cross RNR-2354 x MTU-1081 was found to be good specific combiner for head rice recovery, kernel length, kernel breadth and L/B ratio. Cross RNR-2354 x BM-71 was found to be good specific combiner for kernel length after cooking, kernel elongation ratio and aroma. Pusa-1121 x BM-71 was found to be good specific combiner for kernel length and L/B ratio.

Combining ability studies by Roy and Senapathi (2012) revealed predominance of non-additive gene action for kernel elongation ratio; additive gene action for kernel length, kernel breadth, L/B ratio and both additive and non-additive gene action for cooked kernel length. Among the lines IET 5656 was found to be best general combiner for grain yield as well as its components and quality characters. In testers Kalounnunia was best general combiner for grain yield, where as for quality characters Dudheswar was best general combiner. The three crosses IET 5656 x Kalounnunia, IR 50 x Basmati 385 and IR 62 x Samba Mashuri were superior over their superior grain quality parents.

2.2 Heterosis

Heterosis is the phenomenon in which the F_1 of two genetically dissimilar parents show increased vigour or size for various characters over the mid parent value (relative or mid parent heterosis) or over the better parent (heterobeltiosis) or over the standard check (standard heterosis).

The term heterosis was coined by Shull (1908) and is used to refer to the phenomenon in which the F_1 obtained by crossing two genetically dissimilar individuals showed an increase or decrease in vigour over mid-parent value.

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.

In rice, heterosis was first reported by Jones (1926) who observed that some F_1 hybrids had more culms and higher yield than their parents. Since then several rice

researchers also confirmed its occurrence for yield and yield contributing characters (Virmani, 1994). However, most of these reports were on relative heterosis and heterobeltiosis and are not on standard heterosis. It was only after the successful development and cultivation of F_1 rice hybrids in China since 1976, the standard heterosis useful in commercial agriculture is being considered. Pertinent literature available on heterosis in rice and oil seeds has been reviewed and summarized in below

2.2.1 Heterosis for oil content

Habibullah Habi *et al*. (2006) studied sunflower hybrids for high heterosis and reported that highest positive heterosis and heterobeltiosis for oil content was observed in crosses ORI-6 x RL-27 and ORI-47 x RL-69 with a value of 26 and 17.1 percent resperctively.

Huang Zesu *et al.* (2010) estimated heterosis for oil content in rapeseed and observed both positive and negative heterosis in crosses ranging from -4.5% to 9.6% with a mean of 8%.

Abou-Delif, M.H *et al.* (2012) studied heterosis in 15 maize hybrids and reported that positive standard heterosis for oil content only in 7 hybrids *viz.*, K5 x L162B (11.29%), K5 x Rg59 (10.69%), K11 x K62 (10.69%), K7 x K11 (10.67%), K11xRg59 (10.65%), K5 x K11 (10.55%) and K5 x K7 (10.21%) which was in a rang 10.21-11.29 percent.

Boraiah *et al.* (2012) conducted experiments in groundnut to study the superiority of hybrids and reported that negative heterosis was observed over mid parent, better parent and standard check for oil content.

2.2.2 Heterosis for yield, its components and quality characters in rice

Krishna Veni *et al*. (2005) reported that standard heterosis for the kernel length ranged from -14.75 to 1.54 and In case of breadth minimum -8.5 to maximum13.9 percent. For Length/Breadth ratio standard heterosis ranged from -24.67 to 8.66 percent. For kernel length after cooking standard heterosis ranged from -13.16 to 3.16 percent. For kernel elongation standard heterosis from -10.99 to 8.39 percent was documented. Significant positive standard heterosis was observed for alkali spread value.

Singh (2005) reported significant positive standard heterosis for the quality characters like head rice recovery ranged from-4.92 to 39.41 percent, kernel length range from -9.03 to 12.63 percent, Length/Breadth ratio ranged from -20.55 to 8.02

percent, kernel elongation ratio ranged from 6.47 to16.47 percent and alkali spread value range was 15.6 to 123.4 percent.

Singh and Lal (2005) studied 14 hybrids and reported significant positive standard heterosis in 13 hybrids for head rice recovery ranging from 7.81 to 33.66 percent, as well as negative standard heterosis for head rice recovery recorded in only one hybrid while, significant positive standard heterosis for volume expansion ratio ranged from 11.42 to 60.00 percent and significant negative standard heterosis for water uptake ranged from -35.17 to -11.45 percent and for alkali spread value all the 14 hybrids recorded negative standard heterosis ranging from -35.71 to -15.71 percent.

Biju *et al.* (2006) reported that the magnitude of standard heterosis and *per se* performance of thirty four hybrids developed by International Rice Research Institute was studied for yield and yield contributing characters. The hybrid IR 80784 H recorded maximum significant positive standard heterosis (46.61%) for grain yield. The hybrids manifested significant positive standard heterosis for spikelet fertility grain yield and significant negative heterosis for plant height and days to 50% flowering. This study suggests that the high yielding hybrids IR 80784 H, IR 79172 H and IR 80634 H can be exploited for increasing yield in southern regions of India.

Verma *et al*. (2006) evaluated forty-five rice hybrids generated from crossing three lines with 15 testers during *kharif* 2002 and 2003 in Uttar Pradesh, India, to determine the nature and magnitude of heterosis over better parent (BP) and standard variety (SV) *i.e.* Sarjoo-52 for yield and yield traits. The manifestation of heterosis for yield per plant was obtained over BP from 54.90 to 82.58% and over SV from 68.66 to 40.34%. Moreover, the hybrids, in general showed superiority over BP and SV for grain yield per plant and also exhibited significant heterosis for panicle bearing tillers per plant, panicle length, number of spikelets per panicle, number of filled grains per panicle, biological yield per plant and harvest index.

Eradasappa *et al*. (2007) crossed three lines and 11 testers in a line x tester fashion to work out heterosis over standard parent for nine yield and yield components in rice. Three F_1s *viz.,* IR 68886A x ADT 36, IR 68886A x ADT 45 and IR 68886A x ASD 16 exhibited significant negative standard heterosis for earliness. Two crosses, namely, PMS 10A x ADT 41 and IR 68886A x ADT 43 recorded significant standard heterosis for dwarfness. For productive tillers per plant 21 crosses, for panicle length 32

crosses, all 33 crosses for filled grains per panicle and grain yield per plant showed significant standard heterosis.

Munisonnappa and Vidyachandra (2007) studied heterosis for 5 quantitative traits in 7 newly developed rice hybrids (APRH-2, DRRH-1, PA 6201, Sahyadri, PHB-71, KMRH-4 and KRH-2) and 2 control cultivars (Jaya and IR 30864) grown in 6 environments (created through different dates of sowing with 15-days interval from 10th July to 23rd September) during *kharif* 2000, in Mandya, Karnataka, India. All hybrids showed significant positive heterosis for all the traits in at least one environment over the control cultivars. APRH-2 showed significant positive heterosis in a maximum number of environments, followed by KMRH-4, DRRH-1, KRH-2, PA 6201, Sahyadri and PHB-7. DRRH-1 proved to be superior to the other hybrids as it recorded significant positive heterosis for grain yield in most of the environments, followed by Sahyadri and KRH-2.

Kumar *et al*. (2008) studied F_1 heterosis over better parent, standard variety (Narendra Usar 2) and standard hybrid (NUSD 3) in 40 crosses of rice for yield and five other yield attributing traits under saline-alkali soil. Highly significant positive heterosis for grain yield plant^{-1} was expressed over better parent, standard variety and standard hybrid in nine crosses, IR 58025 A x IR 72048-B-R-2-2-2-1-B, IR58025 A x NDR9830119, NMS 4A x NDRK 5094, NMS 4A x CSR(S) 14-1-4-0, IR 58025 A x Narendra Usar 3, IR 58025 A x IR 71829-3R-73-1-2-B, IR 58025 A x 21-2-5-B-1-1, IR 58025 A x NDRK 5086 and NMS x IR 64.

Mahalingam and Nadarajan (2010) reported that four aromatic varieties *viz*., ADT 41, Pusa Basmati 1, Basmati 370 and Taroari Basmati and the three TGMS lines (TS29, TS 6, and GD 98013) were crossed to generate 12 F_1 hybrids with normal fertility. Observations were recorded for quality characters. Overall two hybrids TS29 x ADT 41 and TS 29 x Pusa Basmati 1 were found to be superior and could be utilized commercially for exploitation of heterosis.

Vaithiyalingan and Nadarajan (2010) studied forty two inter and intra sub-specific hybrids utilising seven wide compatible varieties (WCVs) including two *indicas* (Dular and ASD 16) and five tropical *japonicas* (WCR 6, IR 65600-32-4-6-1, IR 65601-120-3-5, IR 66158-38-3-2-1 and IR 67323-46-2-1) for nine biometrical characters including grain yield. The combinations with significant standard heterosis over local variety MDU 5 for grain yield along with important yield components

recommended for heterosis breeding were Dular x IET 16114 (*indica/japonica*); IR 65601-120-3-5 x ADT 43, IR 67323-46-2-1 x ADT 43 (tropical *japonica/indica*) and IR 66158-38-3-2-1 x Odaebayeo (tropical *japonica/japonica*).

Chandirakala *et al.* (2010) studied that the heterosis in 88 crosses using four Thermo-sensitive Genetic Male Sterile (TGMS) lines and 22 non-TGMS testers. The magnitude of standard heterosis with check (CORH 2 and ADTRH 1) were estimated. The top yielding hybrids *viz.*, GD 98049 x IR 63875-196-2-2-1-3, GD 98014 x TKM11, GD 98049 x TKM 11, GD 99017 x TKM 12 exhibited significant standard heterosis over CORH 2 and ADTRH 1.

Kumar Babu *et al.* (2010) studied 96 hybrids derived from crossing 4 CMS lines with 24 testers and evaluated for the extent of heterosis over mid parent, better parent and standard check. The hybrid IR58025A X MTUII 161-28-1-1 recorded maximum standard heterosis for kernel length. The hybrid IR58025A X MTUITJ 201-12-1 recorded maximum standard heterosis for kernel breadth. The hybrid IR58025A X MTUII 226-18-1-1-2 recorded maximum standard heterosis for the L/B ratio.

Rahimil *et al.* (2010) assessed the standard heterosis based on check variety Dorfak which showed that there was significant heterosis for all the traits studied in the 15 hybrids. For grain yield, the Dorfak×Domsefid cross had the highest heterosis. For grain yield, only the Dorfak×Domsefid hybrid showed significant positive heterosis. The observed heterosis ranged from -47.33 to 20.95 percent for the Binam×Dorfak and Dorfak×Domsefid hybrids, respectively. It seems that the Dorfak×Domsefid cross is the best promising combination for developing high yielding hybrid rice varieties.

Muthuramu *et al.* (2010) carried out diallel analysis in three different environments namely, managed stress, rainfed and dry conditions to study the combining ability and heterosis for 13 yield and drought tolerant traits The hybrids *viz.*, NPT 107 / MDU 5 for rainfed and dry condition and NPT 107 / Nootripathu for managed stress condition were observed to have parallelism between desirable mean, sca effects and standard heterosis for most of the drought tolerant traits besides grain yield and hence these hybrids were recommended for commercial exploitation of heterosis. Under rainfed condition, the hybrid NPT 107 / MDU 5 performed well by possessing favourable mean, sca effects and standard heterosis for nine traits including single plant yield. The same hybrid showed parallelism between high mean, sca effects and standard heterosis for eight traits under dry conditions. It is concluded that, the

above said hybrids are highly suitable for commercial exploitation of heterosis under drought situations

Satheeshkumar *et al*. (2011) evaluated 7 lines and 4 testers to estimate the heterosis (heterobeltiosis and standard heterosis) for 7 traits. Heterosis to the extent of 64.65 and 74.69 percentage over better parent and standard parent respectively, was recorded for grain yield per plant, 2 hybrids *viz.*, CRAC 2221-67 x JAYA and IR 6331-1-B-3R-B-24-3 x JAYA were identified as promising for grain yield per plant and other desirable traits, no. of grains per panicle and L/B ratio.

2.3 Character Association

Study of character association helps the breeder in fixing a selection criteria for grain yield in parental lines, such that selections will be effective in isolating the plants with desired combination of characters.

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

2.3.1 Correlation between yield and oil

Kumar and Kumar (2000) concluded that Maize grain yield and oil content were contrasting selection criteria. Selection based on greater plant height, ear weight, number of kernel rows per ear and number of kernels per ear was desirable for grain yield. However, for improved oil content, late maturing and dwarf plant types with lower number of kernel rows and kernels per ear in addition to lower 100 grain weight were desirable. Hence a balanced selection of high yielding hybrids with moderate oil content need to be emphasized while breeding for both grain yield and oil content.

According to Venu Gopal (2000), there was negative and non significant correlation between grain yield and oil content of maize kernels.

Ravindra Babu (2002) reported in his studies on maize that oil and protein contents had significant positive correlation with each other and negative correlation with yield.

Satyanarayana *et al.* (2003) recorded that the grain yield had significant and positive correlation with all the traits studied except oil and protein content. Oil content was positively correlated with protein content and vice versa. Thus

selection for grain yield in addition to oil and protein content should involve high yielding lines with average oil and protein content.

Mijice *et al.* (2009) assessed the interrelationships between oil yield and its components on 14 sunflower hybrids developed within a breeding program of the Agricultural Institute Osijek, Croatia. Field trials were set up according to completely randomized block design (CRBD) on three locations during two growing seasons (2002 and 2003) for analysis of plant height, 1000 grain weight, test weight, grain yield, oil content and oil yield. Highly significant positive correlation was observed between grain yield and oil yield, but the association between grain yield and oil content was negative and low. A positive correlation coefficient was estimated between 1000 grain weight and grain yield, and a negative one between 1000 grain weight and oil content. Grain yield and oil content expressed the strongest direct effect on oil yield.

Ahmad Reza Golparvar (2011) reported in his studies on safflower showed positive and significant relation of 1000-seed weight, seed number plant-^{1}, seed yield plant-^{1} and seed oil per cent with oil yield.

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

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

Character	**Nature of association**	**Reference**
Days to 50 per cent flowering	Positive significant	Sarkar *et al.* (2006) Krishna *et al*. (2008) Abdul Fiyaz *et al*. (2011)
	Negative significant	Eradasappa *et al.* (2007) Pankaj Garge *et al*. (2010) Ravindra Babu *et al*. (2012) Yadhav *et al*. (2012)
Plant height (cm)	Positive significant	Eradasappa *et al.* (2007) Krishna *et al.* (2008) Sebesan *et al*. (2009) Abdul Fiyaz *et al*. (2011)
Panicle length and no. of productive tillers per plant	Positive significant	Satish Chandra *et al*. (2009) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012) Ravindra Babu *et al*. (2012)

Character	Nature of association	Reference
Number of filled grains per panicle	Positive significant	Satish Chandra *et al.* (2009) Pankaj Garg *et al*. (2010) Padmaja *et al.* (2011) Zulqarnain *et al.* (2012)
1000-grain weight (g)	Positive significant	Satish Chandra *et al.* (2009) Yadav *et al*. (2010) Basavaraja *et al*. (2011) Yadav *et al*. (2012) Zulqarnain *et al*. (2012)
Kernel length (cm)	Positive significant	Mareker and Siddiqui (1996)
	Negative significant	Krishna *et al.* (2008)
L/B ratio	Positive significant	Marekar and Siddiqui (1996) Tara Satyavathi *et al.* (2010) Pankaj Garg *et al*. (2010)

2.3.2. Association of days to 50 per cent flowering with

Character	Nature of association	Reference
Plant height (cm)	Positive significant	Sakthivel (2001) Madhavi Latha (2002) Ravindra Babu *et al* (2012)
	Negative significant	Nayak *et al*. (2004) Satish Chandra *et al.* (2009)
Panicle length (cm)	Positive significant	Madhavi Latha (2002) Satish Chandra *et al.* (2009) Ravindra Babu *et al.* (2012)
	Negative significant	Nandan *et al*. (2010)
No. of productive tillers per plant	Positive significant	Sakthivel (2001)
	Negatively significant	Ravindrababu *et al*. (2012)
Number of filled grains per panicle	Positive significant.	Nayak *et al.* (2001) Madhavi Latha (2002) Mulugeta seyoum *et al.* (2012)
1000-grain weight (g)	Positive significant	Yadav *et al*.(2011)

Character	Nature of association	Reference
	Negative significant	Nayak *et al.* (2001) Sakthivel (2002) Bhadru *et al* (2012)
Kernel length (mm)	Negative significant	Nayak *et al.* (2001) Krishna *et al.* (2008) Yadav *et al.(*2012)
Kernel breadth (mm)	Negative non-significant	Nandan *et al.*(2010)
L/B ratio	Positive significant	Madhavi Latha (2002)
	Negative significant	Yadav *et al.*(2012)

2.3.3. Association of plant height (cm) with

Character	Nature of association	Reference
No. of productive tillers per plant	Positive significant	Janardhanam *et al.* (2001) Kavitha and Sree Rama Reddy (2001) Surender Raju (2002) Satish Chandra *et al.* (2009)
	Negative significant	Nayak *et al.* (2001) Nayak (2008) Bhadru *et al*. (2012)
Panicle length (cm)	Positive significant	Sabesan *et al*. (2009) Satish Chandra *et al.* (2009) Yadav *et al*. (2010) Rajamadhan *et.al*. (2011) Bhadru *et al*. (2012)
	Negative significant	Ananda kumar (1992)
Number of grains per panicle	Positive significant	Nayak *et al.* (2001) Madhavi Latha (2002) Satish Chandra *et al.* (2009)
	Negative significant	Debchoudhury and Das (1998) Surender Raju (2002)
1000-grain weight (g)	Positive significant	Suman (2003) Yogameenakshi *et al.* (2004) Krishna *et al*. (2008)

Kernel length (mm)	Negative significant	Nayak *et al.* (2001)
Kernel breadth (mm)	Positively significant	Krishna *et al*. (2008) Sebesan *et al*. (2009)
L/B ratio	Positive non-significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddy (2001)
	Negative non-significant	Nayak *et al.* (2001) Tara Satyavathi *et al*. (2001) Nandan *et al.* (2010)

2.3.4. Association of panicle length (cm) with

Character	Nature of association	Reference
No. of productive tillers per plant	Positive significant	Bala (2001)
	Negative and significant	Ravindra Babu *et al* (2012)
Number of grains per panicle	Positive significant	Satish Chandra *et al.* (2009) Abdus salman khan *et al*. (2009) Padmaja *et al*. (2011)
Kernel length (mm)	Positive significant	Reddy *et al*. (1997b) Ramesh Babu (1999) Krishna *et al*. (2008)
L/B ratio	Negative significant	Nayak *et al*. (2001)
1000-grain weight (g)	Positive significant	Yogameenakshi *et al.* (2004) Krishna *et al.* (2008) Ravindra Babu *et al*. (2012)
	Negative significant	Sukanya Subramanian and Rathinam (1984)

2.3.5. Association of number of productive tillers per plant with

Character	Nature of association	Reference
Panicle length (cm)	Positive significant	Janardhanam *et al.* (2001) Sakthivel (2001) Padmaja *et al.*(2011)
	Negative significant	Chaubey and Richharia (1993) Tara Satyavathi *et al.* (2001) Suman (2003)

Plant height (cm)	Positive significant	Meenakshi and Devarathinam (1999) Janardhanam *et al.* (2001) Sakthivel (2001)
No. of filled grains per panicle	Negative significant	Chaubey and Richharia (1993)
Kernel length (mm)	Positive significant	Hussain *et al.* (1989) Chauhan *et al.* (1994)
	Negative significant	Ramesh Babu (1999)
L/B ratio	Positive non-significant	Kavitha and Sree Rama Reddy (2001) Nayak *et al.* (2001)
	Negative significant	Tara Satyavathi *et al.* (2001)
	Negative non-significant	Ramesh Babu (1999)
1000-grain weight (g)	Positive and significant	Suryanarayana (2000) Sakthivel (2001)
	Negative significant	Nayak *et al.* (2001) Padmaja *et al.*(2011)

2.3.6. Association of number of grains per panicle with

Character	**Nature of association**	**Reference**
1000- grain weight (g)	Negative significant	Nayak *et al.* (2001) Yadav *et al.*(2010) Bhadru *et al.* (2012)
Kernel length (mm)	Negative significant	Ramesh Babu (1999) Krishna *et al.*(2008) Nayak *et al.* (2001)
L/B ratio	Negative significant	Kavitha and Sree Rama Reddy (2001)

2.3.7. Association of 1000 grain weight (g) with

Character	**Nature of association**	**Reference**
Kernel length and kernel breadth	Positive and significant	Krishna *et al.* (2008)

2.3.8. Association of kernel length (mm) with

Character	Nature of association	Reference
Kernel breadth	Positive significant	Krishna *et al.*(2008)
L/B ratio	Positive significant	Madhavi Latha (2002) Nayak *et al.* (2003) Krishna *et al.* (2008)
1000-grain weight (g)	Positive significant	Nayak *et al.* (2001) Madhavi Latha (2002)

2.3.9. Association of L/B ratio with

Character	Nature of association	Reference
1000-grain weight	Positive significant	Nayak *et al.* (2001) Tara Satyavathi *et al.* (2001)
	Negative significant	Sarwar *et al.* (1999)

2.4 Path Coefficient Analysis

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

Mohan Y *et al.* (2002) performed the path analysis for oil and grain yields of 169 high oil maize genotypes reported that the ear length exhibited the maximum positive direct effect on oil content followed by days to 50% tasselling and ear girth. The traits which had negative direct effects on oil content exhibited strong positive indirect effects via ear length, days to 50% tasselling and ear girth. The results emphasize the need for selection based on plant type with higher ear length, days to 50% tasselling and ear girth values for improvement of oil content.

Siddiquey, M. N. H *et al*. (2006) carried path coefficient analysis also revealed that pods per plant, 100-pod weight and oil content gave the highest direct positive effects on nut yield per plant and contributed the highest variation in yield of groundnut. The other direct positive effects were days to maturity, plant height and protein content in seeds. Therefore, selection based on number of mature pods per plant, 100-pod weight and oil content in seeds may be appropriate in yield improvement of groundnut.

Hladni N *et al* (2010) in sunflower reported that weight of 1,000 seeds had a highly significant direct negative effect on seed oil content and a highly significant direct positive effect on seed yield. The total number of seeds per head has demonstrated a highly significant direct positive effect on seed yield and oil content. The total number of seeds per head was the most important trait that determined seed yield and oil content. The obtained results can be used in sunflower breeding programs aimed at the development of sunflower hybrids that combine high genetic potentials for seed yield and seed oil content.

Dutta (2013) in sunflower reported that the estimates of direct and indirect effects of different traits revealed that the seed yied had the highest positive direct effect on oil percent.

The findings of earlier workers on the relative contribution of different characters are furnished here under in a tabular form:

2.4.1. Direct effects of different characters on grain yield per plant (g)

Character	**Positive direct effect on grain yield**	**Negative direct effect on grain yield**
Days to 50 per cent flowering	Satish Chandra *et al*. (2009) Basavaraja *et al*. (2011) Padmaja *et al.* (2011) Mulugeta *et al.* (2012)	Yadav *et al*.(2010) Pankaj Garg *et al*. (2010) Rajamadhan *et al.* (2011) Pandey *et al*. (2012) Ravindra Babu *et al.* (2012)

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Plant height (cm)	Nandeshware *et al*. (2010) Basavaraja *et al*. (2011) Yadav *et al*. (2011) Mulugeta suyoum *et al*. (2012) Pandey *et al*. (2012) Ravindra Babu *et al.* (2012)	Tara Satyavathi *et al.* (2001) Suman (2003) Karad and Pol (2008) Satish Chandra *et al.* (2009) Akhtar *et al.* (2011)
Number of productive tillers per plant	Satish Chandra *et al*. (2009) Basavaraja *et al*. (2011) Padmaja *et al.* (2011) Ravindra Babu *et al.* (2012) Pandey *et al.* (2012) Bhadru *et al*. (2012)	Valarmathi and Leenakumari (1998) Kavitha and Sree Rama Reddy (2001) Mulugeta seyoum *et al*. (2012)
Panicle length (cm)	Basavaraja *et al*. (2011) Mulugeta seyoum *et al.* (2012) Ravindra Babu *et al*. (2012)	Kole and Hasib (2008) Krishna *et al*.(2008) Satish Chandra *et al.* (2009) Pankaj *et al*. (2010)
No. of filled Grains per panicle	Satish Chandra *et al*. (2009) Nandan and Sweta Singh (2010) Mulugeta seyoum *et al*. (2012) Badhru *et al*. (2012) Yadhav *et al*. (2012)	Gupta *et al*. (1998) Akhtar *et al.(*2011) Rajamadhan *et al*. (2011) Ravindra Babu *et al.* (2012)
1000-grain weight (g)	Satish Chandra *et al*. (2009) Akhtar *et al. (*2011) Padmaja *et al*. (2011) Bhadru *et al*. (2012) Yadav *et al*. (2012)	Karad and Pol (2008) Pankaj Garg *et al*. (2010) Basavaraja *et al*. (2011) Mulugeta seyoum *et al*. (2012) Ravindra Babu *et al*. (2012)

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Kernel length (mm)	Nayak *et al.* (2001) Rajamadhan *et al.* (2011)	Vivekanandan and Giridharan (1998) Madhavi Latha (2002)
Kernel breadth (mm)	Krishna *et al.* (2008) Yadav *et al.* (2012)	
L/B ratio	Krishna *et al.* (2008) Sabesan *et al.*(2009) Nandeshwar *et al.* (2010)	Pankaj Garg *et al.* (2010)

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

Character	Positive indirect effect	Negative indirect effect
Plant height (cm)	Basavaraja *et al*. (2011) Padmaja *et al.* (2011) Rajamadhan *et al*. (2011) Yadav *et al*. (2012) Bhadru *et al.* (2012)	Kole and Hasib (2008) Satish Chandra *et al*. (2009) Ravindra Babu *et al*. (2012)
Number of productive tillers per plant	Rajamadhan *et al*. (2011) Ravindra Babu *et al*. (2012) Bhadru *et al*. (2012)	Kavitha and Sree Rama Reddy (2001) Basavaraja *et al*. (2011) Padmaja *et al*. (2011) Yadav *et al.* (2012)
Panicle length (cm)	Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012)	Kole and Hasib (2008) Satish Chandra *et al.* (2009) Ravindra Babu *et al*. (2012)
Number of filled grains per panicle	Madhavi Latha (2002) Bhadru *et al*. (2012) Yadav *et al*. (2012)	Satish Chandra *et al.* (2009) Padmaja *et al.* (2011) Rajamadhan *et al*. (2011) Ravindra Babu *et al*. (2012)
1000-grain weight (g)	Madhavi Latha (2002) Basavaraja *et al*. (2011) Yadav *et al*. (2012)	Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Ravindra Babu *et al*. (2012)
Kernel length (mm)	Yadav *et al.* (2012)	Rajamadhan *et al*. (2011) Bhadru *et al*. (2012)
Kernel breadth (mm)	Yadav *et al*. (2012)	
L/B ratio	Madhavi Latha (2002)	Nayak *et al.* (2001) Yadav *et.al*. (2012)

2.4.3. Indirect effects of plant height on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Yadav *et al.* (2010) Rajamadhan *et al*. (2011) Ravindra Babu *et al*. (2012)	Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Bhadru *et al*. (2012) Yadav *et al*. (2012)

Number of productive tillers per plant	Yadav *et al*. (2010) Basavaraja *et al*. (2011) Pandey *et al*. (2012) Bhadru *et al*. (2012)	Nayak *et al.* (2001) Padmaja *et al.* (2011) Ravindra Babu *et al*. (2012) Yadav *et al.* (2012)
Panicle length (cm)	Yadav *et al*. (2010) Basavaraja *et al.* (2011) Rajamadhan *et al*. (2011) Ravindra Babu *et al*. (2012) Pandey *et al*. (2012)	Kole and Hasib (2008) Padmaja *et al*. (2011) Bhadru *et al*. (2012)
Number of filled grains per panicle	Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Ravindra Babu *et al*. (2012) Yadav *et al.* (2012)	Suryanarayana (2000) Bhadru *et al.* (2012)
1000-grain weight (g)	Kole and Hasib (2008) Satish Chandra *et al.* (2009) Rajamadhan *et al*. (2011) Bhadru *et al.* (2012)	Padmaja *et al*. (2011) Ravindra Babu *et al*. (2012) Pandey *et al*. (2012)
Kernel length (mm)	Madhavi Latha (2002) Yadav *et al.* (2012)	Ganesan *et al.* (1997) Reddy *et al.* (1997b) Rajamadhan *et al.* (2011)
Kernel breadth (mm)	Yadav *et al*.(2012)	
L/B ratio	Ramesh Babu (1999) Nagajyothi (2001)	Madhavi Latha (2002) Yadav *et al.* (2012)

2.4.4. Indirect effects of panicle length on grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 per cent flowering	Satish Chandra *et al.* (2009) Rajamadhan *et al*. (2011) Ravindra Babu *et al*.(2012) Bhadru *et al*. (2012)	Debchoudhury and Das (1998) Padmaja *et al*. (2011)

Character	Positive indirect effect	Negative indirect effect
Plant height (cm)	Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Bhadru *et al.* (2012) Ravindra Babu *et al*. (2012)	Janardhanam *et al.* (2001) Yadav *et al.* (2010)
Number of productive tillers per plant	Basavaraja *et al*. (2011) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Bhadru *et al.* (2012) Ravindra Babu *et al*. (2012)
Number of grains per panicle	Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Mulugeta seyoum *et al*. (2012) Bhadru *et al.* (2012)	Amirthadevarathinam (1990) Satish Chandra *et al.* (2009)
1000-grain weight	Kole and Hasib (2008) Basavaraja *et al*. (2011) Padmaja *et al*. (2011) Ravindra Babu *et al*. (2012)	Satish Chandra *et al.* (2009) Pandey *et al*. (2012) Bhadru *et al*. (2012)

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

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Madhavi Latha (2002) Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Yadav *et al*. (2010) Basavaraja *et al*. (2011) Ravindra Babu *et al*. (2012)
Plant height (cm)	Yadav *et al*. (2010) Basavaraja *et al.* (2011) Rajamadhan *et al*. (2011)	Reddy *et al.* (1997b) Satish Chandra *et al.* (2009) Ravindra Babu *et al*. (2012)
Panicle length (cm)	Madhavi Latha (2002) Basavaraja *et al*. (2011) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Nayak *et al.* (2001) Yadav *et al*. (2010) Satish Chandra *et al.* (2009) Ravindra Babu *et al*. (2012)

Character	Positive indirect effect	Negative indirect effect
Number of filled grains per panicle	Tara Satyavathi *et al.* (2001) Satish Chandra *et al.* (2009) Rajamadhan *et a.l* (2011) Mulugeta seyoum *et al.* (2012)	Nayak *et al.* (2001) Madhavi Latha (2002) Ravindra Babu *et al.* (2012)
Kernel length (mm)	Ramesh Babu (1999)	Madhavi Latha (2002) Rajamadhan *et al*. (2011)
L/B ratio	Nayak *et al.* (2001) Madhavi Latha (2002)	Ramesh Babu (1999)
1000-grain weight (g)	Reddy *et al.* (1997b) Nagajyothi (2001) Tara Satyavathi *et al.* (2001)	Satish Chandra *et al.* (2009) Yadav *et al.* (2010) Padmaja *et al*. (2011) Ravindra Babu *et al*. (2012)

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

Character	Positive indirect effect	Negative indirect effect
Days to50 per cent flowering	Kole and Hasib (2008) Satish Chandra *et al*. (2009) Padmaja *et al*. (2011)	Nayak *et al*. (2001) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012)
Plant height (cm)	Akhtar *et al.* (2011) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012)	Kole and Hasib (2008) Satish Chandra *et al.* (2009)
Number of productive tillers per plant	Akhtar *et al.* (2011) Rajamadhan *et al* (2011) Bhadru *et al*. (2012)	Nayak *et al.* (2001) Madhavi Latha (2002) Satish Chandra *et al.* (2009) Padmaja *et al*. (2011)
Panicle length (cm)	Reddy *et al.* (1997b) Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Kole and Hasib (2008) Bhadru *et al.* (2012)

Character	Positive indirect effect	Negative indirect effect
1000-grain weight (g)	Satish Chandra *et al*. (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012)	Tara Satyavathi *et al.* (2001) Kole and Hasib (2008)
Kernel length (mm)	Ganesan *et al*. (1997) Madhavi Latha (2002)	Reddy *et al.* (1997b) Nayak *et al.* (2001) Rajamadhan *et al*. (2011)
L/B ratio	Tara Satyavathi *et al.* (2001) Madhavi Latha (2002)	

2.4.7. Indirect effects of 1000-grain weight on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Kole and Hasib (2008) Satish Chandra *et al.* (2009) Yadav *et al*. (2012)	Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012) Ravindra Babu *et al*. (2012)
Plant height (cm)	Kole and Hasib 2008) Rajamadhan *et al*. (2011) Ravindra Babu *et al.* (2012)	Satish Chandra *et al.* (2009) Yadav *et al*.(2010) Padmaja *et al*. (2011) Bhadru *et al*. (2012)
Number of productive tillers per plant	Nagajyothi (2001) Bhadru *et al*. (2012)	Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Ravindra Babu *et al*. (2012)
Panicle length (cm)	Nayak *et al.* (2001) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Satish Chandra *et al.* (2009) Yadav *et al.* (2010) Ravindra Babu *et al*. (2012) Bhadru *et al*. (2012)
Number of filled grain per panicle	Madhavi Latha (2002) Satish Chandra *et al.* (2009) Padmaja *et al*. (2011) Yadav *et al*. (2012)	Kole and Hasib (2008) Rajamadhan *et al*. (2011)

Kernel length (mm)	Reddy *et al.* (1997b) Rajamadhan *et al*. (2011)	Madhavi Latha (2002) Yadav *et al*. (2012)
L/B ratio	Nagajyothi (2001) Yadav *et al*. (2012)	Madhavi Latha (2002)

2.4.8. Indirect effects of kernel length on grain yield per plant through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 per cent flowering	Krishna *et al*. (2008) Rajamadhan *et al*. (2011) Yadav *et al*. (2012)	
Plant height (cm)	Ganesan *et al.* (1997)	Krishna *et al*. (2008) Rajamadhan *et al.* (2011) Nandadeshwar *et al*. (2010)
Productive tiller per plant	Madhavi Latha (2002) Yadav *et al*. (2012)	Krishna *et al.* (2008) Rajamadhan *et al*. (2011)
Panicle length (cm)	Reddy *et al.* (1997) Nayak *et al.* (2001)	Krishna *et al*. (2008) Rajamadhan *et al*. (2011)
Number of filled grains per panicle	Krishna *et al*. (2008) Rajamadhan *et al*. (2011) Yadav *et al.* (2012)	Madhavi Latha (2002) Nandeshwar *et al.* (2010)
Kernel breadth (mm)	Nandeshwar *et al*. (2010) Yadav *et al*. (2012)	Krishna *et al*. (2008)
L/B ratio	Nandeshwar *et al.* (2010) Yadav *et al*. (2012)	Ramesh Babu (1999) Krishna *et al*. (2008)
1000-grain weight (g)	Madhavi Latha (2002) Nandeshwar *et al*. (2010)	Krishna *et al.* (2008) Rajamadhan *et al*. (2011) Yadav *et al.* (2012)

2.4.9. Indirect effects of L/B ratio on grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 per cent flowering	Madhavi Latha (2002) Yadav *et al.* (2012)	Krishna *et al*. (2008)

Plant height (cm)	Nagajyothi (2001) Krishna *et al*. (2008)	Nandeshwar *et al*. (2010) Yadav *et al*. (2012)
Number of productive tillers per plant	Madhavi Latha (2002) Yadav *et al*. (2012)	Nayak *et al.* (2001) Krishna *et al*. (2008)
Panicle length (cm)	Nayak *et al.* (2001) Krishna *et al.* (2008)	Madhavi Latha (2002) Nandeshwar *et al*. (2010)
Number of filled grain per panicle	Madhavi Latha (2002)	Krishna *et al*. (2008) Nandeshwar *et al*. (2010) Yadav *et al*. (2012)
1000-grain weight (g)	Nayak *et al.* (2001) Nandeshwar *et al.* (2010)	Madhavi Latha (2002) Yadav *et al*. (2012)
Kernel length (mm)	Nayak *et al.* (2001) Krishna *et al*. (2008)	Nandeshwar *et al*. (2010) Yadav *et al.* (2012)
Kernel breadth (mm)	Nandeshwar *et al.* (2010)	Krishna *et al*. (2008) Yadav *et al*. (2012)

2.5 Stability Analysis

2.5.1 Genotype x environment interaction and stability analysis.

A stable variety is one which has high mean, unit regression coefficient and minimum deviation from regression line. A breeder would usually desire to develop a variety that exhibits high yield performance across many locations and seasons. The genetic effects are not independent of the non-genetic environmental effects. This interplay of genetic and non genetic effects is the G x E interaction (Eberhart and Russell, 1966).

Halaswamy *et al*. (2000) conducted stability analysis for l6 genotypes in 4 locations in India They observed genetic differences in all the 4 locations for all the traits except stem diameter, number of filled seeds and oil yield per plant. G X E interactions were found to be significant for all the five characters considered for stability analysis. Significant environmental (linear) effect was observed for all the six traits. The variance due to genotype x environment (linear) was non-significant for head diameter. The effect due to pooled deviation (non-linear) was found to be significant for all the traits. Among the 16 genotypes studied, nine showed stability for seed yield of which two hybrids (234 A x 851 B) x RHA 274 and MSFH-17 had average stability (bi=l). The TWC hybrids (851 A x 300 B) x RHA 274 and (234 A x 851 B) x 60-1 were found to be stable for majority of the characteristics.

Lavanya *et al.* (2005) studied thirty rice hybrids and their parents for their stability in two seasons with different nitrogen levels. The study indicated that a substantial portion of the G x E interaction was due to the linear component for tiller number, plant height, panicle length, spikelet fertility percentage, test weight and harvest index. Several high yielding hybrids and parents were identified for favourable and poor environments. The study revealed that stable hybrids were developed from stable parents but stable parents may not necessarily generate a stable hybrid.

Shanmuganathan and Ibrahim (2005) evaluated eleven rice hybrids in six different environments for their stability. Significant mean sum of square due to genotypes, environments and G x E interaction was observed. Both linear and non-linear components of G x E interaction were important for the expression of most of the traits; however, linear component was larger in magnitude than the non-linear component. The hybrid CORH 2 was found stable for most of the characters.

Ali *et al*. (2006) evaluated 16 genotypes of rice in nine locations of Punjab and

revealed that the combined analysis of variance showed highly significant differences among varieties, environment and variety x environment interaction. Highly significant difference in genotypes may be due to the differences in their genetic makeup and diverse nature of origin. Highly significant differences in locations indicated an existence of variation in the prevailing environments.

Deshpande and Dalvi (2006) evaluated the performance of 12 rice hybrids in respect of grain yield and other characters under five environments in Maharastra and revealed that stability in the yield of the hybrid appeared to differ in respect of level of stability in the component traits. It was found that stability in grain yield was due to stability in yield components only and plasticity in others. The yield behaviour in almost all the genotypes except KRH 2 and DRRH 1 was highly predictable. The hybrid KRH 2 was found to be stable for yield as it has average yield performance, regression coefficient is near to unity and minimum deviation from regression.

Pande *et al*. (2006) studied the stability of twelve high yielding varieties of rice for boro season of eastern India. Assessment of varieties based on individual parameters of adaptability (X, bi, S^2di) for grain yield revealed that all the 12 genotypes tested showed significant response to different environments by their significant values of regression coefficient from unity. Ten genotypes exhibited stable performance for grain yield.

Arumugam *et al.* (2007) evaluated twelve rice genotypes for the stability of grain yield and its component characters in six environments. The genotypes were found to interact significantly with the environments for days to 50 % flowering, plant height, number of productive tillers, panicle length, spikelet fertility, 1000 - grain weight, grain density, harvest index and grain yield per plot.

Dushyanthakumar and Shadadshari (2007) evaluated 15 rice mutants of PUB local for the stability of yield and yield components across three environments in Karnataka. Significant pooled deviations observed for all the traits, suggested that there is a considerable genotypic differences. Significant linear sensitivity with insignificant non linear sensitivity suggested that the performance of genotypes could be predicted with great precision across the environments.

Bhakta and Das (2008) evaluated twenty six rice genotypes over eight environments for the assessment of yield and yield stability. Pooled analysis of variance for grain yield over environments showed highly significant differences among genotypes, environments and genotype - environment (G x E) interaction indicating

diverse and variable nature of cropping environments. The difference in performance of genotypes in different environments indicated the presence of significant genotype - environment (G x E) interaction for the expression of the character.

Forty eight hybrid combinations were studied along with their 14 parents and two standard checks for their stability performance at three locations in Andhra Pradesh for eight quantitative characters. The G x E interaction was significant for days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle and grain yield per plant. Linear component was also significant for the above mentioned characters, while non-linear component was found significant for all the traits studied (Gouri Shanker *et al.*, 2008).

Panwar *et al*. (2008) studied genotype x environment interaction for grain yield, its components and grain quality traits in 10 parents and their 45 F1s of scented rice under four environments. Significant genotype x environment interactions were observed for all the eleven characters having homogenous error variance in environments. Among the linear and non - linear components of G x E interaction, linear component was predominant for most of the characters, suggesting variation in the performance of different genotypes grown over environments could be predicted. Mean squares due to environment (linear) was also found significant for all the characters, indicating differences between environments and their influence on genotypes for expression of these characters.

Ramya and Senthilkumar (2008) evaluated twenty three rice genotypes in three different environments created by staggering the date of sowing during the year 2006 for their stability. G x E interaction was significant for six characters viz., days to 50 percent flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle and grain yield per plant. The genotype, MDU 3 was the most stable and consistent one for most of the traits studied in the entire environment.

Saidaiah (2008) studied 115 hybrids and reported that CRMS 32 A x 517, APMS 6A x 118, PUSA x IR 55, PUSA x 124 and APMS 6A x GQ 120 are stable with the desirable sca effects, heterosis and per se performance for grain yield and important attributes.

Das *et al.* (2009) conducted yield trials on 12 late duration (145-165 days) rice genotypes and revealed that four of the seven genotypes realize above average yield and showed adaptability to all environments, whereas, OR 1901-14-32 and Jagabandhu showed specific adaptaion to poor environments. The G x E interaction was significant

for grain yield indicating differential response of genotypes to changes in environments and some genotypes showed stable performance over the range of environments, while many showed unstable performance due to high G x E interaction.

Krishnappa *et al.* (2009) conducted an experiment to evaluate 40 rice genotypes in six environments. Pooled analysis of variance indicated the presence of genetic variability. Linear and non-linear components also revealed that yield and its contributing characters were subjected to environmental changes. The genotypes viz., Andrewsal, IET-5784, IET-7191, IET-13870, IET-14211, IMRYT/91/1708, IET-30864, IVT/91(SHW) 10607 and IVT (SHW) 93 /10608 were stable for high mean yield with non-significant bi and S2di values.

Bhadru (2010) studied stability of hundred rice hybrids and reported that IR-79156A x R-52 and IR-79156A x IR-13419 possessed stability for wider environments and DRR-14A x R-47, IR-79156A x R-49 and IR-80555A x IR-66 exhibited stability for favourable environments with the desirable sca effects, heterosis and per se performance for grain yield and quality and other important attributes.

Das *et al.* (2010) conducted multilocation yield trials of 11 mid-early rice genotypes at Bhubaneswar, Chiplima, Jeypore and Ranital over 3 years 2003-05, during kharif season. Anova of yield data of the 12 environments revealed significant G x E interaction and indicated differential performance of genotypes over environments. Further partitioning of E+G x E effects revealed that E (linear) component was highly significant. G x E (linear) component was significant and pooled deviation was highly significant, indicating that some genotypes showed linear effects over environments, while others showed significant deviation from linear relationship.

Dushyantha kumar *et al.* (2010) studied G x E interaction and stability for grain yield and some associated traits during the year 2002-06 in 8 halugidda local rice mutants in the hill zone of Karnataka. Significant G X E interaction was observed for all the traits studied. The pooled deviation was significant for the majority of the traits including grain yield and considerable genotypic difference was observed. Both linear and non-linear components of G x E interaction were significant.

Saidaiah *et al.* (2010c) tested one hundred and fifteen hybrids, their parents and four checks for their stability at three locations. The study indicated that a substantial portion of G × E interaction was due to linear component for days to fifty per cent flowering, productive tillers plant-1, panicle weight, filled grains panicle-1, grain yield plant-1 and productivity day-1. Several high yielding hybrids and parents

were identified for general (CRMS 32 A × 517 and APMS 6A × 118), favourable (PUSA 5A × 1096, IR 58025A × KMR-3 and CRMS 32 A × GQ-120) and poor (CRMS 32A × GQ-70) environment.

Ahmad Ramezanil *et al.* (2011) studied the stability of yield and some phenological parameters with 13 genotypes of rice under various environment conditions. Combined variance analysis of data showed that the genotype and environment at differences were significant relative to days to 50%flowering, plant height and grain yield which indicated a wide range of variability among the genotypes performance. Based on the stability in yield and qualitative parameter genotype 4 is superior to other genotypes so that it can be recommended for commercial cultivation in the Isfahan zone of Iran.

Biswas *et al*. (2011) evaluated 28 rice genotypes for their stability in respect of grain yield and growth duration during boro season of 2007-08 over five locations. The G x E interactions were highly significant for growth duration and grain yield, which indicated significant differences among the regression coefficients and that might be extended for stability analysis. The linear components of G x E interactions were insignificant but non-linear component (pooled deviation) were significant for both the traits. Considering both growth duration and grain yield based on stability parameters, the genotypes Ropa and Sera were identified as most stable and could be recommended for release as varieties.

Balalic *et al*. (2011) studied stability of twenty Sunflower hybrids grown in 13 locations According to non-parametric stability parameters Si(1) and Si(2), hybrids Baća and Vranac were most stable in all locations. Baća also had high oil yield in 2008 and 2009. In 2010 twonew hybrids (NS-H-6612, NS-H-2069) were high yielding and stable for oil yield. Hybrid NS-H-111 was also stable in all locations in 2009 and 2010 and its oil yield was above average.

Maji *et al.* (2011) multi-locational rice trials were conducted in 6 locations across Nigeria. G x E analysis of transformed data showed that there was no significant differences in grain yield among varieties and locations. There was however a high interaction of G x E and location x year. Joint regression analysis which gives a measure of stability showed that WAB 96-1-1, IDSA86, M2 and IR47701-6-3-1 were the most stable varieties across the locations.

Sreedhar *et al.* (2011) studied 82 genotypes including 60 hybrids, 17 parents and 5 checks for the eight characters. The pooled analysis of variance revealed that G x E interactions were significant for five characters viz., panicle weight, no. of productive tillers per plant, no. of. filled grains per panicle and 1000 seed weight and single plant yield implying differential response of genotypes under three locations for these characters. Among the 60 hybrids, superior performing stable hybrids APMS 6 A x IR-24R, APMS 6 AxBR-827-35-R, IR-80555AxIR-54742R, IR-80559AxIR-54742R, IR-80559AxKMR-3R and IR-80151AxIR-54742R are across the three different environmental conditions.

Lal and Singh (2012) studied G x E interaction for grain yield and its components characters in 15 genotypes of rice under 6 environments during kharif 2005-06. Pooled analysis also indicated highly significant differences among the genotypes and environments for all the characters under study. Based on stability parameters, genotypes like Pusa Basumati-1, PR-114 and Sahib-140 were found promising with stable performance for plant height, effective tillers per plant and grain yield per plant.

Subudhi *et al.* (2012) evaluated 20 popular rice varieties of eastern India were evaluated to study the G x E interaction and stability nature of different yield traits. In pooled analysis the G x E interaction was highly significant and both linear and nonlinear compounds are equally important in determining the stability of different characters. For grain yield, Gouri, IR-8, Jaya and IR-36 are stable varieties and can perform better in all types of environment.

2.6 Genetic Parameters in F_2 Generation for Oil Content

Noubissie *et al.* (2012) estimated heritability and genetic advance in ground nut for oil and protein content and revealed that moderate heritability coupled with low genetic advance for oil content while high heritability and low genetic advance for protein content.

Ashutosh Kumar Shukla and Prashant Kumar Rai (2014) evaluated thirty groundnut genotypes for yield and quality traits and revealed that the PCV was higher than GCV for all the characters studied indicating the role of environmental variance in the total variance. The magnitude of PCV and GCV was moderate to high for primary branches/plant at 40 DAS, pod yield, kernel yield, oil yield and oleic acid. Heritability in broad sense was higher in most of the characters like oil yield, oleic acid, kernel

yield, plant height, pod yield (q/ha), hundred kernel weight, sound mature kernel %, oil content, days to maturity, field emergence, plant height at 60 DAS, kernel uniformity, pod yield/plant, shelling %, primary branches/plant 40 DAS, primary branches/plant 60 DAS and days to 50 % flowering. High heritability coupled with high genetic advance was observed for oil yield.

Liala Fayyaz *et al.* (2014) conducted genetic variability studies in F2 population of brassica and reported that high heritability was coupled with high genetic advance for oil content.

2.7 Molecular Markers and Mapping

One of the most exciting developments in rice biotechnology is the advent of molecular markers. With the development of molecular markers techniques and especially PCR-based markers, tremendous progress has been made in rice breeding and genetics. Recent advances in rice genomics have now made it possible to identify and map a number of genes through linkage to existing DNA markers. A series of molecular markers, e.g. random fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP) and microsatellites, have become available. These markers offer new opportunities for various studies in genetic and breeding research, particularly in the construction of saturated molecular maps, gene tagging, QTL mapping, marker-assisted breeding, gene pyramiding, physical mapping of genome, map-based gene cloning, alien introgression and DNA finger-printing of pathogen populations (Tanskley *et al.*, 1983, Paterson *et al.*, 1996).

Markers can also be used for dissecting polygenic traits into their Mendelian components or Quantitative Trait Loci (QTL) and this increasing understanding of the inheritance and gene action for such traits allows the use of markers -selection procedures (Anderson *et al.*, 1993).

One of the most widely used applications of the molecular technique is the identification of markers linked to traits of interest without the necessity for mapping the entire genome. With finding linked markers to the loci controlling the desirable traits, using molecular breeding methods, it is possible to select the plants with desirable traits and with few or no unwanted traits. Once the linked markers to genes or quantitative trait loci (QTLs) of interest are identified, prior to field evaluation of a large number of plants and at the early stages of growth, breeders may use specific DNA

marker alleles as a diagnostic tool to identify plants carrying the genes or QTLs (Collard *et al.*, 2005). Tightly linked DNA markers to the important genes may be used as molecular tools for marker-assisted selection (MAS) in plant breeding, which helps in more efficient, reliable and commercial phenotype selection compared to the classical plant breeding methods (Collard *et al.*, 2005).

Among the available molecular markers, microsatellites or simple sequence repeats (SSRs) are ideal genetic markers, which are tandem repeats of one to six nucleotide long DNA motifs, have gained considerable importance in plant genetics and breeding owing to many desirable genetic attributes including hypervariability, multiallelic nature, codominant inheritance, reproducibility of microsatellites is such that they can be used efficiently by different research laboratories to produce consistent data (Saghai Maroof *et al.*, 1994), relative abundance, extensive genome coverage including organellar genomes, chromosome specific location and amenability to automation and high throughput genotyping. High degree of allelic variation revealed by microsatellite markers results from variation in number of repeat-motifs at a locus caused by replication slippage and/or unequal crossing-over during meiosis.

Locus-specific microsatellite based markers have been reported from many plant species such as rice (*Oryza Sativa L.*) (Wu and Tanksley, 1993). Barley (*Hordeum vulgare L.*) (Saghai Maroof *et al.*, 1994) and lettuce (*Lactuca sativa L.*) (Van de Wiel *et al.*, 1999).

2.7.1 Construction of Linkage Map

A linkage map may be thought of as a ‘road map’ of the chromosomes derived from two different parents (Paterson, 1996). Linkage maps indicate the position and relative genetic distances between markers along chromosomes, which is analogous to signs or landmarks along a highway. The most important use for linkage maps is to identify chromosomal locations containing genes and QTLs associated with traits of interest; such maps may then be referred to as ‘QTL’ (or ‘genetic’) maps. ‘QTL mapping’ is based on the principle that genes and markers segregate via chromosome recombination (called crossing-over) during meiosis (i.e. sexual reproduction), thus allowing their analysis in the progeny (Paterson, 1996).

Genes or markers that are close together or tightly-linked will be transmitted together from parent to progeny more frequently than genes or markers that are located further apart. In a segregating population, there is a mixture of parental and recombinant genotypes. The frequency of recombinant genotypes can be used to calculate

recombination fractions, which may be used to infer the genetic distance between markers. By analyzing the segregation of markers, the relative order and distances between markers can be determined the lower the frequency of recombination between two markers, the closer they are situated on a chromosome (conversely, the higher the frequency of recombination between two markers, the further away they are situated on a chromosome). Markers that have a recombination frequency of 50 per cent are described as ‘unlinked’ and assumed to be located far apart on the same chromosome or on different chromosomes.

Liu *et al*. (2009) reported 14 QTLs for crude fat content in brown rice distributing on chromosomes 1, 3, and 5-9. One of which is a major QTL, qCFC5, locating on chromosome 5.

Ying *et al*. (2012) identified QTLs for fatty acid composition, and 29 associated QTLs were identified throughout the rice genome except chromosomes 9 and 10.

Chapter III

MATERIAL AND METHODS

EXPERIMENT-I

The present investigation on "Genetic Characterization and molecular studies for Bran oil using SSR markers in Rice (*Oryza sativa* L.)" was taken up at Directorate of Rice Research, Rajendranagar, Hyderabad.

3.1 Description of the experimental material

3.1.1 Screening of germplasm lines

Fifty lines were screened during *rabi*, 2011-12, at DRR, Hyderabad and selected 6 lines with medium to high bran oil content while five popular varieties with high yield were used as testers. For the estimation of bran oil content, after harvest, samples were sent to National Institute of Nutrition (NIN), Hyderabad.

3.1.2 Generation of the experimental material

The eleven selected genotypes chosen as parents were raised in the pots at DRR, Hyderabad, during *kharif* 2012. Crossing was carried out by Line × Tester Model (Kempthorne, 1957). Clipping method of emasculation followed by pollination was carried out among the plants (Plate1). Details of selected genotypes are presented in the Table 3.1.

3.3 Field Evaluation of Hybrids and Parents

Field Evaluation of all the parents and 30 F_1s was carried out at three locations *viz.*, at Directorate of Rice Research, Hyderabad, Regional Agricultural Research Station, Warangal (Central Telangana agro-climatic zone), Regional Agricultural Research Station, Jagtial (Northern Telangana agro-climatic zone) representing different agroclimatic zones of Telangana during *Rabi* season 2013. F_1 seeds and parents were sown in the raised nursery bed, the seedlings were transplanted on 26 DAS in the main field and each entry was planted in two rows each having ten plants with a spacing of 20 cm between rows and 10 cm between plants. The experiment was laid out in completely randomized block design with

three replications. The crop was grown under irrigated conditions, with recommended package of practices of Acharya N.G. Ranga Agricultural University.

Quality analysis of promising hybrids was carried out at rice quality lab, Directorate of Rice Research, Hyderabad.

3.4 Recording of Observations

Plants were selected randomly from each replication and observations were recorded on five randomly selected plants for days to 50 % flowering, plant height, number of tillers per plant, panicle length, number of grains per panicle, 1000- grain weight and grain yield per plant. Quality characters *viz.*, milling per cent, head rice recovery, kernel length, kernel breadth, L/B ratio, grain type, grain chalkiness, water uptake, volume expansion ratio, gel consistency, alkali spreading value, amylose content and bran oil content were recorded for hybrids at three locations. The details of the observations recorded and methods followed are presented here under character wise.

3.4.1. Yield Contributing Characters

3.4.1.1. Days to 50% Flowering: The number of days from sowing to the emergence of 50 per cent of the panicles in each experimental plot.

3.4.1.2. Plant height (cm): Plant height was measured in centimeters from ground level to the tip of the mother panicle of each plant at the time of harvest.

3.4.1.3. Number of productive tillers per plant: Number of ear bearing tillers per plant was counted at the time of harvest.

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

3.4.1.5. Number of filled grains per panicle: The number of well filled grains was counted in mother panicle of each entry expressed as filled grains per panicle.

3.4.1.6. 1000-grain weight (g): One thousand filled grains were counted at random from bulk seed of each plant and weighed after thorough drying at 12 per cent moisture content and the weight was recorded in grams.

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

3.4.2. Quality Characters

3.4.2.1. Milling per cent: The hulled rice was transferred to rice miller Model (6704) and milling was carried out. The milled rice obtained was weighed in grams and the milling per cent was calculated by using the formula.

$$\text{Milling per cent} = \frac{\text{Total weight of milled rice (g)}}{\text{Total weight of rough rice (g)}} \times 100$$

3.4.2.2. Head rice recovery per cent: The milled rice obtained from the rice miller was separated into broken and non brokens in a sizing device (Model 6701). The weight of non-brokens was recorded in grams and head rice recovery percentage was calculated by using the formula.

$$\text{Head rice recovery per cent} = \frac{\text{Total weight of head rice (g)}}{\text{Total weight of rough rice (g)}} \times 100$$

3.4.2.3. Kernel Length (mm): Ten polished kernels were randomly selected and length of the kernel was recorded in mm using dial micrometer.

3.4.2.4. Kernel Breadth (mm): Breadth of the kernel was recorded on the same polished kernels used for length in mm using Dial micrometer.

3.4.2.5. Kernel L/B Ratio: The L/B ratio was calculated using the following formula of Murthy and Govindaswamy (1967).

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

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

Grain type	Length (mm)	Shape	L/B ratio
Extra long	More than 7.5	Slender	More than 3.0
Long	6.61-7.5	Medium	2.1-3.0
Medium	5.51-6.60	Bold	1.1-2.0
Short	Less than 5.5	Round	Less than 1.1

Classification of grain length and shape as per DUS characters published by Directorate of rice research, Hyderabad, 2006.

Class	Length(mm)	L/ B ratio
Long slender	>6.00	>3.0
Long bold	>6.0	<3.0
Short slender	<6.0	>3.0
Short bold	<6.0	<3.0
Medium slender	5.5 – 6.0	2.5- 3.0

3.4.2.6 Water uptake

Two grams of the milled rice was soaked for thirty minutes in a test tube by putting 10 ml of water. Then it was boiled for 45 minutes at 77^{o}C- 80^{o}C in a constant temperature water bath. Two test tubes were kept with 10 ml of water as a control along with the samples in the water bath. Immediately the tubes were placed in a beaker containing cold water for cooling. The supernatant water in the test tube was poured into graduated cylinder after cooling and the water level was noted (DRR, 2006).

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

3.4.2.7. Gel consistency (mm)

Gel consistency was analyzed based on the method described by Cagampang *et al.* (1973). One hundred milligrams of the rice flour of each sample was weighed accurately, in duplicate, into long narrow pyrex tubes and kept at

room temperature for 24 hours, to obtain moisture equilibrium, the sample as wetted with wet 0.2 ml of 95 per cent ethanol containing 0.025 per cent thymol blue. The tubes were shaken to suspend the starch and 2 ml of 0.2 N KOH was added immediately. The tubes were placed on a vortex mixer for vigorous shaking and then put in a boiling water bath for 5 minutes of refluxing. Later the tubes were taken out and cooled at room temperature for 15 minutes and then cooled in an ice water bath (5-7^{0}C) for 20 minutes.

After drying the surface moisture, tubes were placed horizontally over a graph paper graduated in mm without any disturbance. The length of the blue coloured gel was measured from inside bottom of the test tube to the gel front after 30 minutes. This value is given in mm.

Based on the length of the gel, rice samples can be categorized as follows.

1. Very flaky rice with hard gel consistency (length of gel <40 mm)
2. Flaky rice with medium gel consistency (length of gel 40-60 mm)
3. Soft rice with soft gel consistency (length of gel >60 mm)

3.4.2.8. Alkali spreading value (Gelatinization Temperature score)

The method of Little *et al*. (1958) was used. Six whole milled grains without cracks were taken from each replication and spaced evenly in small petri dishes containing 10 ml of 1.7 per cent Potassium hydroxide (KOH). The dishes were kept at 30^{o}C for 23 hours undisturbed and replicated twice.

The spreading and clearing of kernels noted in seven point scale was recorded as detailed hereunder (Jennings *et al*., 1979).

Scoring with seven point scale was recorded as detailed here under (Jennings *et al.*, 1979)

S.No.	Spreading	Score	Clearing
1	Kernel not effected	1	Kernel chalky
2	Kernel swollen	2	Kernel chalky, collar powdery
3	Kernel swollen, collar incomplete and narrow	3	Kernel chalky, collar cloudy
4	Kernel swollen, collar complete and wide	4	Centre cottony, collar cloudy
5	Kernel split or segmented,	5	Centre cottony, collar cloudy

	collar complete and wide		
6	Kernel dispersed, merging with collar	6	Centre cloudy, collar cleared
7	All kernels dispersed and inter mingled	7	Centre and collar cleared

The above scoring was adopted for all the grains selected and expressed as the average Gelatinization Temperature (GT) score. A rating of 1 to 2 was classified as high gelatinization temperature (> 74^0C), 3 high to intermediate, 4 to 5 intermediate (70 to 74^0C) and 6 to 7 low gelatinization temperature (< 55^0C – 69^0C).

3.4.2.9. Amylose content

Amylose, a linear fraction of starch has a major influence on cooking and eating quality characteristics of rice. It also plays an important role in determining the texture of cooked rice. Simplified procedure of Juliano (1971) was used for the estimation of amylose content.

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

Amylose content was determined by reference to a standard curve and expressed on dry weight basis. For preparing the standard curve, 40 mg of potato amylose (sigma) was taken and wet with 1 ml ethyl alcohol and 9 ml 1 N NaOH, heated for 10 minute in beakers containing water on an electric heater. Then the content was cooled and volume was made up to 100 ml with several distilled water washings. From this solution 1, 2, 3, 4 and 5 ml portion were placed with a pipette in 100 ml volumetric flask and then these are acidified with 1 N acetic acid (0.2,

0.4, 0.6, 0.8 and 1.0 ml of acetic acid to 1, 2, 3, 4 and 5 ml amylose solutions respectively) and then 2 ml of iodine solution was added. After 20 minutes, absorbance values at 620 nm were recorded on spectrophotometer and were plotted against the concentrations of anhydrous amylose (mg) to determine the conversion factor. The dilution factor of 20 for the sample was included in the conversion factor.

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

3.4.2.10 Bran oil content (%)

For the estimation of bran oil content, after harvest the samples were sent to National Institute of Nutrition (NIN), Hyderabad. The procedure which is followed at NIN is described hereunder.

Rice powder of 0.5g was taken into a 50ml centrifuge tube and 5ml of 6N HCL was added, subjected to vortex, kept in water bath for 1hr incubation at 80^0C. Then 10ml of 2:1 ratio of chloroform: methanol mixture was added, subjected to vertex and kept for incubation in cold room (4^0C) for overnight. Chloroform layer was transferred into another 50ml tube which was kept in cold room. Again 10ml of chloroform: methanol was added to the sample tube, contents were mixed for 3 minutes on a vertex and kept for incubation in cold room (4^0C) for 4 hours. Again chloroform layer was collected into the second tube, 2ml of Milli Q water was added, contents were mixed by vortex for 1 minute, and centrifuged at 1500rpm for 10 minutes. After centrifugation, water layer was discarded, chloroform layer was taken in a glass beaker of known weight (W1) and it was kept in oven maintained at 60^0C for overnight to evaporate chloroform. After incubation, weight (W2) of the beaker was noted. Simultaneously, Moisture percentage was also estimated and values were substituted into the following equation (Bligh *et al*.1959).

Calculation

$$\text{Total oil content (fat \%)} = \frac{W2-W1}{\text{Weight of sample}} \times 100 \times \frac{\text{Total solids (g \%)}}{100}$$

Total solids = 100- moisture percent

3.4.2.11. Chalkiness

Materials:

1.Light Box 2.Florescence Light

Procedure:

1.Select whole grains from a sample and place approximately ten grains of whole grain on Light Box .

2.Visually identify grains with chalk content and classify according to the given procedure

Scoring	**Kernal area (Extent)**
A - Absent	None
VOC- Very occassionally present	Small (less than 10%) kernel
OC- occassionally present	Medium (11% to 20%)
P- Present	Long (More than 20%)

3.5 Statistical Analysis

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

1. Analysis of variance
2. Combining ability analysis
3. Estimation of standard heterosis.
4. Estimation of simple correlation coefficients.
5. Direct and indirect effects of characters using Path coefficient analysis.
6. Stability Analysis.
7. Estimation of genetic parameters in F_2 generation

3.5.1 Analysis of Variance

The analysis of variance for each character was carried out 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 (1967).

3.5.2 Combining Ability Analysis

3.5.2.1. Line × Tester analysis

The data recorded on the material generated as per Line × Tester model of Kempthorne (1957) was subjected to analysis of variance as per Line × Tester model given by Singh and Chaudhary (1985).

ANOVA for Lines × Testers

Sources of Variation	Degrees of freedom (df)	Mean sum of squares (MSS)
Replications	r-1	
Genotypes	g-1	
Parents	p-1	
Crosses	c-1	
Parents vs. crosses	1	
Females	f-1	Mm
Males	m-1	Mf
Females × males	(f-1) (m-1)	M(f × m)
Error	(r-1) (g-1)	Me

where,

R = number of replication

G = number of genotypes

P = number of parents

C = number of crosses

F = number of lines

M = number of testers

Mf = mean sum of squares due to lines

Mm = mean sum of squares due to testers

M (f × m) = mean sum of squares due to lines and testers

Me = mean sum of squares due to error

Df = degrees of freedom

The significant differences among the genotypes and replications were verified by applying 'F' test (Fisher and Yates, 1967).

3.5.3.2. Combining ability analysis

The variations among the hybrids was further partitioned into genetic components attributed to general combining ability (*gca*) and specific combining ability (*sca*) as per the method suggested by Kempthorne (1957).

The analysis was based on the following mathematical model.

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

where,

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

μ : Population mean

g_i : *gca* effect of i^{th} parent

g_j : *gca* effect of j^{th} parent

S_{ij} : *sca* effect of $(i \times j)^{th}$ cross

r_k : Effect due to k^{th} replication

e_{ijk} : Random error effect associated with $(ijk)^{th}$ observation in k^{th} replication

ANOVA for combining ability

Sources of variation	Degrees of freedom (df)	Mean sum of squares (MSS)	Expected MSS
Replication	(r-1)	-	-
Hybrids	(lt-1)	-	-
Lines (Females)	(l-1)	M_1	$\sigma^2e + r$ [Cov(FS) - 2Cov(HS) + rt [Cov(HS)]
Testers (Males)	(t-1)	M_2	$\sigma^2e + r$ [Cov(FS) - 2Cov(HS) + rl [Cov(HS)]
Line × Tester	(l-1) (t-1)	M_3	$\sigma^2e + r$ [Cov(FS) - 2Cov(HS)]
Error	(r-1) (lt-1)	M_4	σ^2e

where,

r : Number of replications

l : Number of female parents

t : Number of male parents

$\sigma^2 e$: Random error

Cov(FS) : Covariance of full sibs

Cov(HS) : Covariance of half sibs

M_1 : Mean sum of squares due to females (lines)

M_2 : Mean sum of squares due to males (testers)

M_3 : Mean sum of squares due to females × males

M_4 : Mean sum of squares due to error

i. Estimation of combining ability effects

The following effects were calculated from two way table of lines verses testers in which each figure was a total of the two replications.

$$\mu = \frac{X\ldots}{ltr}$$

$$\hat{g}_i = \frac{Xi..}{tr} - \frac{X}{ltr}\frac{..}{}$$

$$\hat{g}_j = \frac{X.j.}{lr} - \frac{X\ldots}{ltr}$$

$$\hat{S}_{ij} = \frac{Xij.}{r} - \frac{Xi..}{tr} - \frac{X.j.}{Lr} - \frac{X\ldots}{ltr}$$

where,

X. . . = Total of all hybrids

X_i. . = Total of i^{th} line over all testers and replications

$X_{.j}$. = Total of j^{th} tester over all lines and replications

X_{ij}. = Total of ij^{th} cross over all the replications

ii. Standard errors of the effects

The standard errors of the estimates were compared as the square roots of their variances as shown below.

i. S.E. (*gca* for line) = $(M4/rt)^{1/2}$

ii. S.E. (*gca* for testers) = $(M4/rt)^{1/2}$

iii. S.E. (*sca* effect) $= (M4/r)^{1/2}$

where,

M_4 : MSS due to error
r : Number of replications
l : Number of femalparents
t : Number of male parents

Tests of significance for *gca* and *sca* effects

The *gca* and *sca* effects were tested for significance by calculating‘t’ value by using the following formula.

$$t\ cal = \frac{gi - O}{SE\ (gi)}$$

$$t\ cal = \frac{gi - O}{SE\ (gj)}$$

$$t\ cal = \frac{Sij - O}{SE\ (Sij)}$$

The values are compared with‘t’ table value at error degrees of freedom.

iii. Estimates of genetic components of variation

The GCA and SCA variance were expressed in terms of co variances of full sibs (FS) and half-sibs (HS) as indicated below.

$$Cov\ (HS) = GCA\ variance = \frac{M1 + M2 - 2M3}{r\ (1+ t)}$$

$$Cov\ (HS)\ lines = \frac{M1 - M3}{rt}$$

$$Cov\ (HS)\ testers = \frac{M2 - M3}{rl}$$

$$\sigma^2_{SCA} = Cov\ (FS) - 2\ Cov\ (HS) = \frac{M3 - M4}{R} - = \sigma^2_{lt}$$

where,

σ^2_{GCA} : General combining ability variance

σ^2_{SCA} : Specific combining ability variance

3.5.3. 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).

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

3.5.5. Estimation of Simple correlation coefficients

Simple correlation coefficients (r) for bran oil content, grain yield, its components and physical quality characters were calculated involving both hybrids and varieties by using the method given by Johnson *et al*. (1955):

Simple correlation coefficients were estimated location wise and also based on pooled data including both hybrids and varieties.

$$r_g(xy) = \frac{Cov(xy)}{\sqrt{\text{var}(x).\text{var}(y)}}$$

$$Cov(xy) = \frac{1}{n}\left[xy - \frac{(xy)}{n} \right]$$

$$Var(x) = \frac{1}{n}\left[x^2 - \frac{(x^2)}{n} \right]$$

where,

r(xy)	=	correlation between x and y
Cov(xy)	=	covariance for characters x and y
Var(x)	=	variance for x
Var(y)	=	variance for y
r	=	correlation coefficient
xy	=	two independent variables

3.4.6. Path coefficient analysis

The direct and indirect effects at genotypic level were estimated by taking seed yield as dependent variable for yield characters, using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959). The following equations

were formed and solved simultaneously for estimating the various direct and indirect effects. Direct and indirect effects were estimated based on pooled data of three locations and also location wise including both hybrids and varieties.

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

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

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

Where,

1, 2 . . . . . n	=	Independent variable
y	=	Dependent variable (yield per plant)
$r_{1y}, r_{2y} \ldots\ldots\ldots r_{ny}$	=	Coefficient of correlation between causal factors '1' to 'n' on dependent character 1
$p_{1y}, P_{2y} \ldots\ldots P_{ny}$	=	Direct effect of characters 1 to n on character Y

The above equations can be written in matrix form as:

$$A = C \times B$$

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ \vdots \\ r_{ny} \end{pmatrix} = \begin{pmatrix} 1 & r_{12} & r_{13} & \ldots\ldots r_{1n} \\ r_{21} & 1 & r_{23} & \ldots\ldots r_{2n} \\ & \vdots & \vdots & \vdots \\ & \vdots & \vdots & \vdots \\ r_{n1} & r_{n2} & r_{n3} & \ldots\ldots 1 \end{pmatrix} \begin{pmatrix} p_{1y} \\ p_{2y} \\ \vdots \\ \vdots \\ p_{ny} \end{pmatrix}$$

Then

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

$$\begin{pmatrix} c_{11} & c_{12} & c_{13} & \ldots\ldots c_{1n} \\ c_{21} & c_{22} & c_{23} & \ldots\ldots c_{2n} \\ \vdots & \vdots & \vdots & \\ \vdots & \vdots & \vdots & \\ c_{n1} & c_{n2} & c_{n3} & \ldots\ldots c_{nn} \end{pmatrix}$$

Direct effects were as follows:

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

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

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

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

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

Where, p_{ny} = Direct effect of x_n on Y

r_{ny} = Correlation coefficient of x_n on y.

3.5.7. Stability Analysis

Analysis of variance of genotype means was computed for each agronomic variable in each location. The data were pooled over environments as the coefficient of variation values in each environment were generally low, though the Bartlett's Chi-square values showed significance in case of certain characters (Gomez and Gomez, 1984.)

3.5.7.1. Eberhart and Russell's (1966) model

Stability parameters were computed as given by Eberhart and Russell (1966). The model is

$$Y_{ij} = \mu + \beta_i I_j + S_{ij}$$

i varies from 1 to 30 genotypes

j varies from 1 to 3 environments

Where,

Y_{ij} = Mean of i^{th} genotype in j^{th} environment

μ = Mean of all genotypes over all environments

β_i = Regression coefficient of i[th] genotype on the environmental index which measures the response of this genotype to varying environments.

I_j = The environmental index which is defined as the deviation of the mean of all the genotypes at a given location from the overall mean.

S_{ij} = The deviation from regression of the i[th] genotype at j[th] environment.

3.4.7.1.1. Analysis of variance for stability

The analysis of variance as proposed by Eberhart and Russell (1966) is given in Table

Analysis of variance as proposed by Eberhart and Russell (1966)

Source	Degrees of freedom	Sum of squares	Mean squares
Total	(ge-1)	$\sum_i \sum_j Y_{ij}^2 - C.F$	
Genotypes	(g-1)	$1/e \sum_i Y_{i.}^2 - C.F$	MS_1
Environment+ (Genotype x Environment)	g(e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_{i.}^2 / e$	
Environment (Linear)	1	$1/g \left(\sum_j Y._j I_j \right)^2 \Big/ \sum_j I_j^2$	
Genotype x Environment (Linear)	(g-1)	$\sum_j \left((\sum_j Y_{ij} I_j)^2 \Big/ \sum_j I_j^2 \right)$ - Environment (linear) ss	MS_2
Pooled deviations	g(e-2)	$\sum_i \sum_j S_{ij}^2$	MS_3
Deviation due to genotype 1	(e-2)	$\left[\sum_j Y_{ij}^2 - (Y_{i.})^2 / e \right] - \left(\sum_j Y_{ij}^2 I_j \right)^2 / \sum_j I_j^2 = \sum_j S_{ij}^2$	
Pooled error	e(r-1)(g-1)		

g = Genotype e = Environment r = Replication

3.5.7.1.2. Estimation of stability parameters

The regression coefficient (b) and the deviation from the line of regression (S^2d) were estimated as follows:

a) Regression coefficient:

$$b = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

Where,

$\sum_j Y_{ij} I_j$ = The sum of products of environmental index (I_j) with corresponding mean of that genotype at each environment (Y_{ij})

$\sum_j I_j^2$ = The sum of squares of the environmental index (I_j)

b) Mean square deviations (S^2d) from linear regression:

$$S^2 d = \frac{\sum_j S_{ij}^2}{(e-2)} - \frac{S_e^2}{r}$$

Where,

$$\sum_j S_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g} \right] - \frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2}$$

Where,

$\sum_j S_{ij}^2$ = Variance due to deviation from regression for a genotype

$\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g}$ = Variance due to dependent variable

$\sum_j (Y_{ij} I_j)^2 / \sum_j I_j^2$ = Variance due to regression

S_e^2 = The estimate of pooled error

e = Number of environments

g = Number of genotypes

r = Number of replications

The various computational steps involved in the estimation are as follows:

3.5.7.1.3 Computation of environmental index (I_j)

$$I_j = \frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge}$$

with $\sum_j I_j = 0$

3.5.7.1.4 Computation of regression coefficient (b) for each genotype

$$b = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

a) For each value of regression coefficient, $\sum_j I_j^2$ is common.

b) $\sum_j Y_{ij} I_j$ for each genotype is the sum of products of environmental index (I_j) with the corresponding mean $(\overline{X})$ of that genotype in each environment.

These values may be obtained in the following manner

$$\left[\overline{X}\right]\left[I_j\right] = \left[\sum_j Y_{ij} I_j\right] = \left[S\right]$$

Where,

$\left[\overline{X}\right]$ = Matrix of means

$\left[I_j\right]$ = Vector for environmental index and

$\left[S\right]$ = Vector for sum of products, i.e., $\sum_j Y_{ij} I_j$

3.5.7.1.5 Computation of S^2d

In a regression analysis, it is possible to partition the variance of the dependent variable (Y) into two parts, the one which explains the linearity between dependent and independent variables (variance due to regression) and the other which explains the variance due to deviations from linearity.

$\sigma_Y^2 = \sigma^2$ regression + σ^2 deviation from the regression

The variance of mean over different locations with regard to individual genotype may be obtained in the following way.

$$\sigma_{g_i}^2 = \sum_j Y_{ij}^2 - (Y_{i.}^2 / g)$$

The variance due to deviations from regression $\left(\sum_j S_{ij}^2\right)$ for a genotype being

$$\sum_j S_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g}\right] - \frac{\left(\sum_j Y_{ij} I_j\right)^2}{\sum_j I_j^2}$$

Where,

$\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g}$ = Variance due to dependent variable and

$(\sum_j Y_{ij} I_j)^2 / \sum_j I_j^2$ = The variance due to regression

because $$\frac{\left(\sum_j Y_{ij} I_j\right)^2}{\sum_j I_j^2} = \frac{\left(\sum_j Y_{ij} I_j\right)\left(\sum_j Y_{ij} I_j\right)}{\sum_j I_j^2}$$

$$= b\sum_j Y_{ij} I_j$$

From $\sum_j S_{ij}^2$ Values, the stability parameters S^2d for each variety is computed as follows:

$$S^2 d = \left[\sum_j S_{ij}^2 /(e-2)\right] - \left(S_e^2 / r\right)$$

$$\text{Mean square deviation} = \frac{\text{Deviation from regression}}{\text{Degrees of freedom for environment}} = \frac{\text{Pooled error}}{\text{Number of replications}}$$

The variance due to genotypes, environments and the pooled error were the same as those calculated in the pooled analysis of data, except that the total sum of squares was mainly partitioned into 3 main components namely (1) sum of squares due to genotypes (2) sum of squares due to environments + (genotype x environment) and (3) pooled error. Again sum of squares due to genotype x environment was further partitioned into 2 parts namely (a) sum of squares due to genotype x environment (linear) which is in fact sum of squares due to regression and (b) sum of squares due to deviations from linearity of response (i.e., sum of squares due to deviation).

Sum of squares due to environment + Genotype x environment

$$= \sum_i \sum_j Y_{ij}^2 - \left(\sum_j Y_{i.}^2 / e\right)$$

Sum of squares due to environment (linear)

$$= \frac{1}{g}\left(\sum_j Y_{.j} I_j\right)^2 / \left(\sum_j I_j^2\right)$$

Sum of squares due to genotype x environment (linear)

$$= \sum_j \left[\left(\sum_j Y_{ij} I_j \right)^2 / \left(\sum_j I_j^2 \right) \right]$$ - SS environment (linear)

Where,

$$\left(\sum_j Y_{ij} I_j \right)^2 / \left(\sum_j I_j^2 \right) = b \sum_j Y_{ij} I_j$$ for each genotype

3.5.7.1.6 Tests of significance

The following tests of significance were carried out :

1. To test the significance of the differences among genotype means namely, $H_o = \mu_1 = \mu_2 = \mu_3 = ...\mu_{10}$

the 'F' test used was,

$$F = \frac{\text{Mean square due to genotypes}}{\text{Mean square due to pooled deviation}} = \frac{MS_1}{MS_3}$$

2. To test that the genotypes did not differ due to regression on environmental index, i.e., $H_0 = b_1 = b_2 = ...b_{10}$,

the 'F' test used was

$$F = \frac{\text{Mean square due to genotype x environment (linear)}}{\text{Mean square due to pooled deviation}} \quad \frac{MS_2}{MS_3}$$

3. Individual deviation from linear regression was tested as follows:

$$F = \left[\left(\sum_j S_{ij}^2 \right) / (e-2) \right] /$$ pooled error mean sum of squares

t value at (g-2) d.f at P=0.05 and 0.01 levels.

4. The hypothesis that any regression coefficient does not differ from unity or from zero was tested by the appropriate't' test, i.e,

$$t = \frac{|1-b|}{SE(b)} \qquad SE(b) = \sqrt{\left[\sum_j S_{ij}^2 / (e-2) \right] / \sum_j I_j^2}$$

t-value at (g-2) d.f at p = 0.05 and 0.01 levels

3.5.8 Estimation of Genetic Parameters in F_2 Generation for Bran Oil Content

3.5.8.1 Genotypic and phenotypic coefficients of variation: The genotypic and phenotypic coefficients of variation in F_2 were calculated according to the formula given by Emphig *et al.* (1970).

$$GCV = \frac{(Vg)^{1/2}}{\bar{X}} \times 100$$

Where, $$Vg = VF_2 - V\left(\frac{(P_1) + V(P_2) + V(F_1)}{3}\right)$$

Where, $$VF_2 = \frac{\sum X^2 - \frac{(\sum X)^2}{N}}{N-1}$$

Variance was estimated based on single plant observations

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{(Vp)^{1/2}}{\bar{X}} \times 100$$

Where, Vp = Phenotypic variance of F_2

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

< 10%	:	Low
10-20%	:	Moderate
> 20%	:	High

3.4.8.2 Heritability and genetic advance

Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense for all characters in F_2 was computed as per formula given by Allard (1960).

$$h^2(b) = \frac{VF_2 - \left(\frac{V P_1 + V P_2 + V F_1}{3} \right)}{V F_2}$$

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

VF_2 = variance among F_2 plants

VP_1, VP_2, VF_1 = variance among female, male and F_1 plants, Respectively

as suggested by Johnson *et al.* (1955) heritability estimates were categorized as

Low : 0-30%

Medium : 30-60%

High : above 60%

Genetic advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1953).

$$GA = K.\, h^2(b).\, \sigma p$$

Where,

GA = Expected genetic advance

K = Selection differential, the value of which is 1.76 at 10 per cent selection intensity

σp = Phenotypic standard deviation of F_2

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

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

$$\text{Genetic advance as per cent of mean} = \frac{GA}{\overline{X}} \times 100$$

Where, $\overline{X}$ = mean of F_2 population

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%

EXPERIMENT-II: Mapping of the Gene(S) for Bran Oil Using Rice SSR Markers

3.6 Plant material used:

The present investigation was carried out with the cross between Keshari × Swarna. Swarna a popular variety but low in bran oil content and Keshari is released variety with high bran oil content. F_2 mapping population derived from the above two varieties comprising 132 individuals was used for the mapping purpose.

3.6.1 Mapping of Gene(s) for bran oil content:

For the parental polymorphism survey, parents were tested with 30 SSR markers representing 12 chromosomes of rice.

3.6.2 DNA extraction from leaf samples:

3.6.2.1. Materials and equipments required:

1. Spot test plate (30 well) – available from Thomas Scientific, USA. This is required only for mini-preps (small scale preparations). The spot test plate should be autoclaved or alcohol sterilized before use.
2. Alcohol sterilized glass rods
3. Micropipettes (1 ml, 20 and 200 µl range)
4. 1.5 ml micro-centrifuge tubes (autoclaved and dried)
5. 1 ml and 200 µl tips (autoclaved and dried)

6. Pestle and mortar (required for maxi-preps)
7. Micro-centrifuge
8. Fume hood

3.6.2.2. Preparation of stock solutions

a) 1 M Tris HCl (pH 8.0): Tris base of about 30.28 g was dissolved in 200 ml distilled water. Then the pH was adjusted to 8.0 with 10.5 ml of concentrated HCl and the solution was cooled to room temperature. After cooling, the final volume was made to 250 ml with distilled water and the solution was sterilized by autoclaving at 121^0 C temperature, 15 Psi pressure for 20 minutes. Then it was stored in transparent reagent bottle.

b) 0.5 M EDTA (pH 8.0): 46.53 g of Disodium Ethylene Diamine Tetra Acetate (EDTA) was added in 200 ml of distilled water. The pH is adjusted to 8.0 by adding 4 g of NaOH pellets and stirred vigorously on a magnetic stirrer. The total volume was adjusted to 250 ml with distilled water and sterilized by autoclaving, and it was stored in transparent reagent bottle.

c) 5 M NaCl: 73.05 g of NaCl was dissolved in 200 ml of distilled water and final volume was made to 250 ml with distilled water. Then it was sterilized by autoclaving and stored at room temperature in transparent reagent bottle.

3.6.2.3 Procedure:

Total genomic DNA was isolated from the parental lines and F_2 plants using the method of Zheng e*t al.* (1991) with modifications as given below:

1) Healthy leaf pieces (2-3 cm) from the youngest leaves of a 20-25 day old rice seedlings were taken. These were cut into 3-4 small pieces and taken into the well of a spot test plate (M/s Thomas Scientific, USA). 400 ml of extraction buffer (50 mM Tris HCL, pH 8.0, 25 mM EDTA, 300 mM NaCl and 1 % SLS) was added to the well. The leaf tissues were macerated using an alcohol sterilized blunt ended glass rod for about 15-20 seconds till it was completely homogenized. Another 400 µl of extraction buffer was added to the well containing the leaf sample.

2) Using a micropipette of 1 ml capacity (the tip was cut at the bottom using a sterile scissor), the entire content from the well was transferred to a 1.5 ml capacity

micro centrifuge tube. About 400-500 µl Phenol (pH 8.0): Chloroform: Isoamyl alcohol (25:24:1) was then added to the micro centrifuge tube. The contents were mixed well by inversion for about 10 minutes and centrifuged at 12000 rpm for about 10 minutes at room temperature.

3) After the centrifugation, the supernatant was aliquoted from the micro-centrifuge tube without disturbing the intermediate layer into a fresh 1.5 ml micro-centrifuge tube. If the supernatant was not clear, the Phenol: Chloroform: Isoamyl alcohol purification step was repeated once again.

To the clear supernatant, 5-10 µl of RNAase (10 mg per ml) was added and incubated for 45-60 minutes at room temperature (~ 37 ^{o}C). After completion of the incubation period, about 500 µl of Chloroform: Isoamyl alcohol (24:1) was added to the micro-centrifuge tube and mixed well by inversion for 10 minutes. The content was centrifuged at 12000 rpm for 10 minutes and the supernatant was collected into another fresh 1.5 ml micro-centrifuge tube without disturbing the intermediate layer.

5) To the clear supernatant equal volume (~500-600 ml) of chilled isopropanol was added. The contents were mixed gently and centrifuged at 12000 rpm for 10 minutes at room temperature.

6) The supernatant was drained gently without disturbing the DNA pellet. About 150-200 µl of 70 % ethanol was added to the pellet at the bottom of the micro-centrifuge tube. It was ensured that the pellet was completely immersed in 70 % alcohol. Then the content was centrifuged at 5000 rpm for 5 minutes at room temperature. After centrifugation, the supernatant was drained and 70 % alcohol wash was repeated once again. Finally, after centrifugation and draining out the supernatant, the pellet was left overnight air drying at room temperature. After complete drying of the pellet, depending upon the size of the pellet, about 50-100 µl of sterile distilled water was added for dissolving the pellet.

7) About 3 µl of the DNA sample was taken and loaded in 0.8 % ethidium bromide stained agarose-TBE (concentration of TBE) gel, electrophoresed for about an hour and the bands of genomic DNA were visualized and documented in a UV gel documentation system (M/s Alpha Innotech Corporation, USA).

3.6.3 Quantification of DNA isolated:

The purity and concentration of the isolated genomic DNA samples were estimated by UV- absorption spectrophotometer (Beckman DU 650 model) as per the procedure described in Sambrook *et al*. (2001). The ratio of absorbance at 260 nm and 280 nm was used as an indicator of DNA purity. A ratio between 1.4 and 1.9 was considered as relatively pure DNA samples as it did not show any effect on PCR reaction.

The genomic DNA concentration was measured by using the formula:

Genomic DNA concentration in µg µl^{-1} = OD 260 x 50 µg µl $^{-1}$ × dilution factor

Agarose gel electrophoresis (0.8%) was carried out for confirming the quality and quantity of the isolated DNA using a known concentration of λ DNA. Based on the number of DNA samples to be electrophoresed, appropriate amount of Agarose gel was weighed and dissolved in required quantity of 0.5 X TBE buffer to make a final concentration of 0.8%. The agarose was melted in a micro oven. The appropriate gel tray was fixed into the gel cast and the combs were placed on the gel tray. To the melted Agarose, Ethidium Bromide (to a final concentration of 0.5 µg ml^{-1}) was added, mixed well by swirling and poured into the gel with prefixed combs, carefully avoiding air bubbles. The gel was allowed to solidify at room temperature for one hour. Then the solidified gel was transferred to Hoefer Super Submarine electrophoresis unit (Pharmacia Biotech) containing 0.5 X TBE buffer. The DNA samples were mixed with 1/3rd volume of gel loading-cum-tracking dye (0.25% Sucrose: 0.25% Bromo phenol blue) and loaded on the gel. The electrophoresis was carried out at 100 volts/cm at room temperature for about one hour. After the gel run, the gel was visualized in a UV light transmitted gel documentation system. After checking the concentration of the DNA based on the band intensity, the DNA samples were diluted to 20 ng µl^{-1} for further polymerase chain reaction (PCR) analysis.

3.6.4 Rice microsatellite markers used for analysis

In the present study, 30 rice SSR markers were used. Chromosome number of the respective marker is given in Table 3.3. The SSR markers, which showed clear polymorphism between the parental lines, were used for mapping analysis of the F_2 progeny.

3.6.4.1. Polymerase Chain Reaction (PCR)

The genomic DNA of parental lines and the mapping population were subjected to PCR amplification as per the procedure described by Chen *et al.* (1997). PCR was carried out using a programmable thermocycler (Corbett Research, Australia). The PCR protocol used is given in the Table 3.4.

PCR plates were taken and 3 µl of template DNA was pipetted into each of the PCR tubes after proper labelling and kept the PCR plate at 4^0 C. Then the master mixwas prepared by taking 0.5 µl of each primer (both forward and reverse primers), 0.5 µl of 2.5 mM deoxy ribonucleotides (dNTPs), 1 µl of Genei 10 X assay buffer (10 mM Tris-Cl (pH 8.3, 50 mM KCl, 1.5 mM $MgCl_2$, 0.01 % gelatin) and 0.2 µl of 3 $U\mu l^{-1}$ Taq DNA polymerase (Bangalore Genei Private Limited, Bangalore). Usually there will be minor errors while pipetting. Hence to avoid these errors, master mix was prepared a little bit extra, to ensure that the adequate quantity is available for all the samples. Empirically, for every 10 reactions, one reaction is taken extra.

Then the master mix was centrifuged for short duration of about 10 sec for thorough mixing of the components. Then 7 µl of master mix was added to each of PCR tube having 3 µl of template DNA to make the final reaction volume to 10 µl. Then PCR plate was covered and kept in a thermal cycler for the reaction to take place, which was set to the thermal profile as described in Table 3.5.

Materials used:

1. Thermal Cycler (PCR machine)
2. PCR tubes/PCR plates (sterile)
3. 1.5 ml micro centrifuge tubes (sterile)
4. 0.5 ml micro centrifuge tubes (sterile)
5. Micropipettes and micropipette tips (sterile)
6. Gel electrophoresis unit
7. Gel documentation system (or UV-transilluminator)

Table 3.4 Master Mix used for 35 reactions in PCR

Component	Stock conc.	Final conc.	Quantity required for one reaction (µl)	Quantity required for 35 reactions (µl)
Sterile water	----	----	2.5	87.5
PCR buffer	10 X	1 X	1.0	35.0
DNTPs	2.5 mM	125 µM	0.5	17.5
Primer F	5 µM	0.5 µM	1.0	35.0
Primer R	5 µM	0.5 µM	1.0	35.0
***Taq* DNA polymerase**	0.5 U μl^{-1}	0.05 U/µl	1.0	35.0
Total			7.0	245.0

Table 3.5 PCR profile used for DNA amplification

Activity	Temperature (^{0}C)	Duration (min)	Cycles(No.)
Initial Denaturation	94	5.0	1
Denaturation	94	0.5	35
Annealing	55	0.5	
Extension	72	1.0	
Final extension	72	7.0	1
Storage	4	∞	

3.6.5. Agarose Gel Electrophoresis for resolution of SSR markers

The SSR-PCR products were resolved in a 3% Agarose gel prepared in 0.5 X TBE buffer stained with Ethidium Bromide.

Materials used:

1. Gel casting unit
2. Gel trays
3. Power supply unit
4. Microwave oven
5. Reagent bottle
6. Electronic balance
7. Gel documentation system including UV trans-illuminator

Chemicals used:

1. Agarose.
2. 10 X TBE buffer, 1000 ml: Add 108 g of Tris (0.9 M) base in 500 ml double distilled water, then add 55 g of Boric acid, mix well by stirring and add 40 ml of 0.5 M EDTA and make up the volume to 1000 ml using double distilled water. Filter sterilize the solution using 0.45 µm filter. Store at room temperature.
3. Ethidium Bromide: 10 mg ml^{-1} solution (prepared in sterile ddW) was prepared by dissolving 1 g of Ethidium Bromide in 100ml of distilled water.
4. Bromophenol blue dye (0.0025% bromophenol blue in 40% sucrose). This dye is to be used in the ratio of 1:6 (dye: DNA solution).

Procedure:

1. 12.0 g of agarose was weighed and put into two 500 ml conical flask each having 6.0 g of agarose.
2. 300 ml of 0.5X TBE added in both flasks and boiled gently in a microwave oven.
3. Mixed vigorously several times during heating in the microwave oven. After proper melting, when the solution is crystal clear with no floating particulate matter taken out and allowed it to cool down.

4. When the boiled agarose has cooled down substantially (when the heat is bearable, ~ 45^0C), 5.0 µl of ethidium bromide was added to the solution and mixed gently.
5. Melted agarose poured in the casting unit and left to solidify (20-30 min).
6. The gel tank was filled with 0.5 X TBE buffer till the buffer reaches 0.5 cm above the gel surface.
7. The DNA mixed with bromophenol dye is filled into the wells and electrodes were connected to power supply unit.
8. Then the gel was allowed to run for about 2 to 3 hours and after that it was documented using gel documentation system.

3.6.6 Mapping population analysis:

The markers which were found to be polymorphic in the parental polymorphic studies were used for analysis of all the 132 individuals. Each gel was scored for maternal, paternal and heterozygous banding pattern and scored accordingly.

3.6.7. Statistical analysis

3.6.7.1 Scoring of gels:

Gels were analyzed for status of the genotype by a microsatellite marker. The maternal band was designated as 'A', paternal band 'B' and heterozygous band 'H'.

3.6.8. Mapping of the chromosomal regions associated with bran oil content in the rice:

The total genomic DNA was isolated from the leaf samples of the parents and F_2 mapping population by using the same procedure as described earlier in 3.5.2. The quality and quantity of the isolated genomic DNA was checked using the procedure depicted in 3.5.3. Further, the genomic DNA of both the parents and F_2 population was subjected to PCR amplification as per the procedure given in 3.5.4.1. In addition of reported, a total of 30 SSR primers were employed for

studying the parental polymorphism. The SSR- PCR products were subjected to Agarose Gel Elctrophoresis as per the procedure presented in 3.5.5. Gels were analyzed for the status of the genotype by a SSR marker. The maternal band was designated as 'A', parental band 'B' and heterozygous band 'H'.

3.6.9. Single marker analysis

Single marker analysis can be conducted using a variety of statistical analysis, including t-tests, ANOVA, regression, maximum likelihood estimation and log likelihood ratios. The fact that molecular marker genotypes can be classified into groups means that marker genotypes can be used as classifying variables for a t-test or ANOVA, or as variables for regression analysis. The null hypothesis tested is that genotypic classes do not differ in phenotype for a given molecular marker. Single marker analysis calculates whether phenotype values differ among genotypes for a given molecular marker.

$$Y = \mu + f(\text{marker}) + \text{error}$$

where,

Y is equal to the trait value
μ is equal to the population mean
f (marker) is a function of the molecular marker

Analysis of R^2 value was calculated by STATISTICA 4.5 software

Table 3.2. Details of the eleven genotypes used as parents in the study

S.No	Genotypes	Parentage	Released in the year
	Lines		
1	Keshari	Kumar x Jagannath,	1985
2	Ishwarya	Jyothi x BR-51-46-1	1993
3	Mandhya Vijaya	Sona x Mahsuri	1986
4	PR116	IR 5657-33-2-1/IR 2061-465-1-5-5	1985
5	Kandhagiri	Parijat x IR-13429-94-3-2-2	1994
6	Phalguna	IR-8 x Siam-29	1978
	Testers		
1	NDR359	BG-90-2-4 x 08677	1994
2	IR64	IR 5657-33-2-1/IR 2061-465-1-5-5	1985
3	Swarna	Vasisatha /Mahsuri	1979
4	RPBIO226	BPT 5204*4/SS1113,	2007
5	MTU1010	Krishnaveni /IR 64	2000

Table 3.3 Details of SSR markers used and their chromosomal locations

S.No	Markers	Chromosome number
1	RM1	1
2	RM283	1
3	RM5	1
4	RM154	2
5	RM6307	2
6	RM3763	2
7	RM15337	3
8	RM15580	3
9	RM16343	3
10	RM16757	3
11	RM18888	5
12	RM18857	5
13	RM5140	5
14	RM20096	6
15	RM20672	6
16	RM11	7
17	RM455	7
18	RM118	7
19	RM125	7
20	RM477	8
21	RM22622	8
22	RM22524	8
23	RM6543	9
24	RM160	9
25	RM271	10
26	RM484	10
27	RM144	11
28	RM552	11
29	RM19	12
30	RM277	12

Chapter IV

RESULTS AND DISCUSSION

The results obtained from the statistical analysis of the data from 6 lines, 5 testers and 30cross combinations of rice at three locations for bran oil content, yield, its components and quality characters are presented here under.

4.1 Analysis of Variance

The analysis of variance (ANOVA) of 41 genotypes (6 lines, 5 testers and 30 cross combinations) for bran oil content, yield, yield components and quality traits at 3 locations *viz*., Jagitial , Warangal and Hyderabad are presented in table 4.1. The results revealed the existence of significant differences among the genotypes studied for all the characters at different locations.In the present study the cross combinations were given with codes and discussed as per the table 4.1.2.

4.2 Mean Performance

Results on mean performance of parents and F_1 cross combinations for seventeen characters at different locations are presented character wise in tables 4.2.1 to 4.2.6.

4.2.1 Days to 50% Flowering

At Jagitial location, days to 50% flowering ranged from 82.00to 128.33 days with an overall mean value of 112.01days (Table 4.2.1). Among the lines, this trait ranged from 82.00 (L5) to 123.00 days (L2) and in testers it ranged from 101.33 (T5) to 122.33 (T3) days. This trait had mean values ranging from 89.67 (L1T2) and 128.33 (L2T3) in case of cross combinations.

Days to 50% flowering at Warangal location, exhibited variation from 81.00 to 123.33 days with a mean of 107.48days. The lines flowered between 81.00 (L1) to 120.00 (L2) days, whereas the testers flowered between 99.00 (T2 and T5) to 117.67 days (T3). Among the cross combinations this trait ranged from 83.00 (L1T2) to 123.33 (L1T3) days.

At Hyderabad location, this trait varied from 70.00 to 116.33 days with a mean of 96.96 days. The lines exhibited a range of 76.00 (L1) to113.00 days (L2) and the testers showed a range of 91.33(T2) to 111.33 days (T3). For cross combinations, it ranged from 70.00 (L1T2) to 116.33 days (L1T3).

4.2.2 Plant height (cm)

Plant height at Jagitial location, varied from 75.27 to 115.60 cm with a general mean 92.07cm. Among the lines, it ranged from 78.63 (L5) to 109.16 cm (L2) and in testers it varied from 86.33 (T5) to 110.33 cm (T1). The cross combinations exhibited a range from 75.27(L3T2) to 115.60 cm (L4T1).

At Warangal location, this character ranged from 80.03 to 138.83cm with a general mean of 112.24cm. The lines exhibited a range from 80.03 (L4) to 114.46 cm (L2) and for testers it ranged from 88.83(T2) to 119.53 cm (T1). In cross combinationsthis character ranged from 90.77 (L5T3) to 138.83 cm (L6T1).

Mean plant height at Hyderabad location, revealed a range from 86.30 to 142.67 cm with an average of 112.40cm. The range of this trait among the lines was from 86.30 (L5) to 119.63 cm (L2) and in testers, the range was from 89.2(T2) to 129.93 cm (T1). Among the cross combinations the plant height ranged from 101.10 (L3T2) to 142.67 cm (L2T1).

4.2.3 Number of productive tillers per plant

At Jagitial location, the genotypes manifested a mean number of productive tillers per plantof 9.51 with a range of 5.67 to 12.00 tillers per plant. The lines ranged from 8.33 (L1 and L2) to 10.33 (L4) tillers plant^{-1}, whereas the testers varied from 7.67 (T2) to 11.00 (T4 and T5) tiller number. Among the cross combinations, it ranged between 5.67 (L2T4) to 12.00 (L6T5) tillers plant^{-1}.

Number of productive tillers per plan at Warangal location, showed a variation from 8.33 to 14.33 with a mean of 11.10 tillers plant^{-1}. Estimates of tiller number in lines ranged from 10.00 (L3) to 12.00 (L6) and among testers it varied from 9.00 (T3) to 13.33 (T5). The cross combinations possessed tiller number from 8.33 (L2T1) to 14.33 (L1T5).

The genotypes at Hyderabad location, exhibited tillers range from 7.33 to 14.00 with a mean of 10.76 tillers plant^{-1}. Among lines, it varied from 9.33 (L1 and L3) to 12.67 (L4) tillers plant^{-1} whereas in testers, its range was from 8.67(T3) to 12.00 (T5). Tiller number in cross combinations varied from 7.33 (L2T1) to 14.00 (L3T2 and L3T5).

4.2.4 Panicle Length (cm)

Panicle length at Jagitial location, varied from 14.33 to 27.43 cm with a general mean of 22.66 cm. Among the lines it varied from 20.69 (L5) to 23.10 cm (L6) and among testers, it ranged from 16.93 (T4) to 25.53 cm (T1). The cross combinations exhibited a variation from 14.33 (L5T4) to 27.43 cm (L2T1). The cross combination L2T1 (27.43) registered highest panicle length followed by L1T1 (26.80) and L5T5 (26.53).

At Warangal location, it ranged from 17.80 to 28.53 cm with a general mean of 23.88cm. The lines exhibited a variation from 22.43 (L5) to 24.27 (L6) cm and for testers, it ranged from 18.60 (T4) to 27.13 cm (T1). In hybrids, it ranged from 17.80(L5T4) to 28.53 cm (L1T1).

The variation for panicle length at Hyderabad location, ranged from 15.27 to 24.47 cm with an average of 19.28 cm. It varied from 18.20 (L5) to 22.13 cm (L6) in lines while in testers, it ranged from 18.17 cm (T3) to 24.47 cm (T1). The hybrids possessed a range from 15.27 (L2T4 and L5T5) to 24.10 cm (L6T1).

4.2.5 Number of grains per panicle

The general mean of number of grains per panicle at Jagitial location was 139.72 with a range of 90.67 to 221.67 grains panicle^{-1}. The range of number of grains varied from 102.33 (L5) to 123.33 (L3) among the lines and from 105.67 (T2) to 134.67 (T4) among the testers. In hybrids number of grains ranged from 90.67 (L5T3) to 221.67 (L3T3). The hybrid L3T3 (221.67) registered highest number of grains followed by L6T4 (186.33) and L4T1 (186.00).

At Warangal location, the variation for number of grains panicle^{-1} ranged from 102.33to 211.00 with an overall mean of 147.63 grains panicle^{-1}. The lines exhibited a range of 110.00 (L5) to 143.67(L3) whereas the testers ranged between 122.33 (T2) to 151.33 (T5) grains panicle^{-1}. Among the hybrids, it varied from 102.33 (L4T3) to

211.00 (L3T3) filled grains panicle^{-1}. Highest number of grains were recorded in L3T3 (211.00) hybrid followed by L6T4 (191.00) and L6T1 (185.00).

Number of grains panicle^{-1} at Hyderabad location, exhibited variation from 71.00 to 205.33 with a mean of 123.33 grains panicle^{-1}. The lines varied between 99.00 (L1) to 138.33 (L3) grains panicle^{-1} while in testers, it ranged from 125.00 (T2) to 148.00 (T3). For this trait the hybrids showed a range of 71.00 (L5T1) to 205.33 (L4T1).Highest number of grains (205.33) was noted in L3T3 hybrid followed by L2T1(181.00) and L3T3(152.67).

4.2.61000 grain weight (g)

The genotypes at Jagitial location, exhibited a 1000-grain weight range from 14.10 to 31.43 g with an average weight of 20.98 g. The lines ranged from 16.74 (L1) to 25.48 g (L2) and the testers ranged from 16.01 (T3) to 25.93 g (T1). The hybrid L2T4 recorded the least test weight of 14.10 g and L2T1 showed a highest test weight of 31.43g.

1000-grain weight at Warangal location, displayed a variation from 15.57 to 30.43g with an overall mean of 21.40 g. Among the lines, it ranged from 17.47 (L3) to 24.23 g (L6), whereas the testers varied from 16.30 (T4) to 28.43 g (T1). The hybrids exhibited test weight range from 15.57 (L6T4) to 30.43 g (L6T1).

Among the genotypes at Hyderabad, the mean test weight ranged from 14.50 to 31.67g with a general mean of 20.53 g. The test weight among the lines varied from 15.30 (L1) to 21.50 g (L6) and among the testers it varied from 15.80(T4) to 22.47 g (T1). Hybrids showed test weight range from 14.50 (L5T2) to 31.67 g (L2T1).

4.2.7 Grain yield per plant (g)

The range of variation for grain yield plant $^{-1}$ at Jagitial location was from 13.43 to 36.13 g with a general mean of 24.22 g. The estimates of grain yield in lines ranged from 16.92 (L5) to 28.87 g (L4) whereas in testers, it varied from 15.63 (T2) to 29.47 g (T1). Among hybrids, it ranged from 13.43 (L1T3) to 36.13 g (L1T5).Out of 30 hybrids evaluated, the best among them were L1T5 (36.13), L3T1 (34.10) and L3T1(34.10).

The grain yield among the genotypes at Warangal location, ranged between 14.37and 36.33 g with a general mean of 26.53 g. The lines exhibited a range from 20.90 (L1) to 29.53 g (L6) and among the testers it recorded from 19.37 (T2) to 30.07g

(T1). In hybrids it varied from 14.37 (L1T3) to 36.33 g (L6T1). The hybrid L6T1 (36.33) recorded higher grain yield followed by L3T1 (35.77) and L4T1 (34.00).

At Hyderabad location, grain yield plant^{-1} varied from 11.10to 32.57 g with an average of 21.85g. In lines it ranged from 14.90 (L1) to 30.43 g (L6) while in testers, the range was from 15.10 (T3) to 32.13 g (T1). The hybrid L3T4 recorded the minimum grain yield of 11.10g and L1T5 hybrid exhibited maximum yield of 32.57 g. High yielding hybrids were L1T5 (32.57), L3T1 (32.53) and L5T5(30.53).

4.2.8 Mean Performance of Quality Characters

Quality in rice is quite complex in nature and it is determined by indices of milling, cooking, eating and nutritional quality characteristics. Market value is determined largely by grain size, shape, appearance and color, while percentage of milling and head rice recovery are the principal indices from trader's point of view. Physico-chemical properties of starch, like water uptake, gel consistency and amylose content constitute the cooking and eating qualities.

4.2.8.1 Kernel length (mm)

At Jagitial location, kernel length ranged from 4.15to 6.99 mm with an overall mean value of 5.90 mm. Among the lines, this trait ranged from 4.90 (L1) to 6.62 mm (L6) and in testers it ranged from 4.67 (T3) to 6.93 (T1) mm.Among the hybrids the kernel length ranged from 4.15 (L1T3) to 6.99 mm (L4T1).

Kernel length at Warangal location, showed a variation from 4.49 to 7.05 mm with a mean of 5.84 mm. Estimates of kernel length in lines ranged from 4.91 (L5) to 6.52 mm (L6) and among testers it varied from 4.72 (T3) to 7.01 mm (T1). The hybrids possessed kernel length from 4.49 (L4T3) to 7.05 mm (L4T1).

The genotypes at Hyderabad location, exhibited kernel length range from 4.33 to 7.02 with a mean of 5.88 mm. Among lines, it varied from 4.83 (L1) to 6.70 (L4) mm whereas in testers, its range was from 4.82 (T3) to 6.83mm (T1). Kernel length in hybrids varied from 4.33 (L1T3) to 7.02 (L4T1).

4.2.8.2 Kernel breadth (mm)

Kernel breadth at Jagitial location, varied from 1.65 to 2.72 mm with a general mean of 2.02 mm. Among the lines it varied from 1.84 (L1) to 2.20 mm (L6) and among testers, it ranged from 1.68 (T3) to 2.31 mm (T1). The hybrids exhibited a

variation from 1.65 (L2T3) to 2.72 mm (L6T1). The hybrid L2T3 (1.65) registered lowest kernel breadth followed by L3T3 (1.69) and L2T4 (1.75) desired direction.

At Warangal location, it ranged from 1.75 to 2.70 mm with a general mean of 2.08mm. The lines exhibited a variation from 1.81 (L1) to 2.15 mm (L6) and for testers, it ranged from 1.75 (T3) to 2.25 mm (T1). In hybrids, it ranged from 1.77 (L3T3) to 2.70 mm (L6T1).

The variation for kernel breadth at Hyderabad location, ranged from 1.73 to 2.72 mm with an average of 2.06 mm. It varied from 1.83 (L2) to 2.29 mm (L6) in lines while in testers, it ranged from 1.78 mm (T3) to 2.27 mm (T1). The hybrids possessed a range from 1.73 (L3T3) to 2.72 mm (L6T1).

4.2.8.3 L/B Ratio

At Jagitial location, the general mean for L /B ratio was 2.93 with a range of 2.31 to 3.66. The mean ranged from 2.53 (L5) to 3.14 (L4) in lines and from 2.78 (T3) to 3.04 (T2)among the testers. In hybrids this trait range varied from 2.31 (L1T3) to 3.66 (L2T2). The highest L/ B ratio was noted in L2T2 (3.66) hybrid followed by L3T2 (3.66) and L5T4 (3.50).

A range of 2.02 to 3.43 was observed for this trait at Warangal location, with a mean of 2.82. The mean of lines varied from 2.48 (L5) to 3.03 (L6), while in testers, its range was from 2.70 (T3) to 3.16 (T1). The hybrids exhibited a range of 2.02 (L4T3) to 3.43 (L3T3).

At Hyderabad location, the genotypes manifested a mean L / B ratio of 2.87 with a range of 2.26 to 3.66. In lines it was observed to range from 2.52 (L1) to 3.07 (L4) and among testers, it varied from 2.71(T3) to 3.03 (T2). The hybrids exhibited L /B ratio variation from 2.26 (L4T3) to 3.66 (L3T3).

4.2.4 Bran oil content (%)

The genotypes at Jagitial location, exhibited a bran oil content range from 9.67 to 17.80 % with an average bran oil content of 12.58%. The lines ranged from 12.31 (L2) to 17.30 (L1) % and the testers ranged from 10.25 (T2) to 11.26 (T5). The hybrid L3T2 recorded the least bran oil of 9.67 % and L1T3 showed a highest bran oil of 17.80 %. Only one hybrid (L1T3) was found superior to best check Keshari (17.30 %).

Bran oil content at Warangal location, displayed a variation from 9.65 to 17.40 with an overall mean of 12.20 %. Among the lines, it ranged from 11.53 (L2) to 17.25 % (L1), whereas the testers varied from 9.97 (T2) to 11.11% (T3). The hybrids exhibited bran oil range from 9.65 (L6T1) to 17.40 % (L1T3).

Among the genotypes at Hyderabad, the mean bran oil content ranged from 9.99 to 17.00 with a general mean of 12.87 %. The bran oil content among the lines varied from 11.72 (L2) to 16.85 % (L1) and among the testers it varied from 9.99 (T2) to 11.30 % (T3). Hybrids showed bran oil range from 10.20 (L4T1) to 17.00 % (L1T2).

4.2.8.5 Milling per cent

The genotypes at Jagitial location, exhibited a milling per cent range from 62.30 to 76.30 per cent with an average milling of 70.85 per cent. The lines ranged from 67.90 (L2) to 72.20 (L5) per cent and the testers ranged from 66.52 (T2) to 71.32 (T3) per cent. The hybrid L2T1 recorded the least milling per cent of 62.30 and L1T5 showed a highest milling per cent of 76.30 per cent.

Milling per cent at Warangal location, displayed a variation from 65.20 to 74.90 per cent with an overall mean of 71.48 per cent. Among the lines, it ranged from 69.20 (L4) to 73.20 (L3) per cent whereas the testers varied from 65.20 (T2) to 72.20 per cent (T3). The hybrids exhibited milling per cent range from 65.70 (L2T3) to 74.90 (L3T4 and L5T1) per cent.

Among the genotypes at Hyderabad, the mean milling per cent ranged from 64.20 to 73.40per cent with a general mean of 69.50 per cent. The milling per cent among the lines varied from 67.60 (L2) to 72.30 (L4) and among the testers it varied from 68.20 (T5) to 71.40 (T4) per cent. Hybrids showed milling per cent range from 64.20 (L5T2) to 73.40 (L4T1) per cent.

4.2.8.6 Head rice recovery (%)

At Jagitial location, the general mean for head rice recovery per cent was 57.52 per cent with a range of 48.20to 65.27 per cent. The mean ranged from 48.20 (L2) to 63.73 per cent (L4) in lines and from 48.66 (T2) to 61.50 (T4) per cent among the testers. In hybrids head rice recovery range varied from 51.20 (L2T1) to 65.27 (L4T3) per cent.

A range of 54.47 to 65.30 per cent was observed for this trait at Warangal location, with a mean of 60.16 per cent. The mean of lines varied from 54.67 (L2) to 59.50 (L1 and L3) per cent, while in testers, its range was from 54.47 (T2) to 63.97 (T5) per cent. The hybrids exhibited a range of 56.30 (L1T2) to 65.30 (L3T4) per cent.

At Hyderabad location, the genotypes manifested a mean head rice recovery of 59.12 per cent with a range of 64.20 to 73.40 per cent. In lines it was observed to range from 67.60(L2) to 72.30 (L4) per cent and among testers, it varied from 68.20 (T5) to 71.40 (T4) per cent. The hybrids exhibited head rice recovery variation from 64.20 (L5T2) to 73.40 (L4T1) per cent.

4.2.8.7 Alkali spreading value

Alkali spreading value at Jagitial location, varied from 3.11 to 6.68 with a general mean of 4.88. Among the lines it varied from 3.78 (L2 and L5) to 6.67 (L6) and among testers, it ranged from 3.78 (T1) to 5.83 (T4). The hybrids exhibited a variation from 3.11 (L5T4) to 6.68 (L6T4).

At Warangal location, it ranged from 3.27 to 6.81 with a general mean of 4.93. The lines exhibited a variation from 3.53 (L5) to 6.37 (L6) and for testers, it ranged from 3.95 (T1) to 5.66 (T4). In hybrids, it ranged from 3.27 (L5T1) to 6.81 (L6T4).

The variation for alkali spreading value at Hyderabad location, ranged from 3.42 to 6.58 with an average of 4.99. It varied from 3.42 (L5) to 6.58 (L6) in lines while in testers, it ranged from 4.08 (T5) to 6.06 (T4). The hybrids possessed a range from 3.46 (L5T4) to 6.42 (L6T4).

4.2.8.8 Water uptake (ml)

The general mean of water uptake at Jagitial location was 258.90 with a range of 193.33 to 340.00 ml. The range of water uptake varied from 245.00 (L4) to 340.00 ml (L2) among the lines and from 193.33 (T1) to 280.00 (T2) ml among the testers. In hybrids water uptake ranged from 210.00 (L3T2) to 320.00 ml(L2T2).The hybrid L2T2(320.00) registered highest water uptake followed by L5T4 (318.33) and L2T4(310.00).

At Warangal location, the variation for water uptake ranged from 190.00 to 363.33 with an overall mean of 270.65 ml. The lines exhibited a range of 235.00 (L4) to

316.67 (L5) whereas the testers ranged between 190.00 (T3) to 263.33 (T2) ml. Among the hybrids, it varied from 208.33 (L3T2) to 363.33 (L2T4) ml.

Water uptake at Hyderabad location, exhibited variation from 183.33 to 390.00 with a mean of 276.10. The lines varied between 235.00 (L1) to 365.0 ml (L5) while in testers, it ranged from 183.33 (T1) to 306.67 (T2) ml. The hybrids showed a range of 208.33 (L3T4) to 390.00 (L5T4) ml. Highest water uptake (390.00) was noted in L5T4 hybrid followed by L2T1 (356.67) and L2T3 (350.00).

4.2.8.9 Gel consistency (mm)

At Jagitial location, gel consistency ranged from 52.67 to 83.33 mm with an overall mean value of 68.50 mm. Among the lines, this trait ranged from 52.67 (L2) to 73.33 mm (L5) and in testers it ranged from 62.00 (T4) to 79.33 (T1) mm. Among the hybrids the gel consistency ranged from 56.00 (L2T1) to 83.33 mm (L6T5).

Gel consistency at Warangal location, showed a variation from 54.00 to 79.00 mm with a mean of 66.64 mm. Estimates of gel consistency in lines ranged from 54.00 (L2) to 71.67 mm (L4) and among testers it varied from 64.33 (T4) to 75.00 mm (T1). The hybrids possessed gel consistency from 55.67(L6T4) to 79.00 mm (L2T1).

The genotypes at Hyderabad location, exhibited gel consistency range from 54.00 to 77.33 with a mean of 67.18 mm. Among lines, it varied from 57.00 (L4) to 73.33 (L5) mm whereas in testers, its range was from 60.00 (T3) to 77.33 mm (T5). Gel consistency in hybrids varied from 54.00 (L4T3) to 77.00 (L2T5).

4.2.8.10 Amylose content (%)

Amylose content at Jagitial location, varied from 18.10 to 27.27% with a general mean of 22.34%. Among the lines it varied from 20.47 (L5) to 25.97 % (L2) and among testers, it ranged from 20.40 (T1) to 24.13 % (T2). The hybrids exhibited a variation from 18.10 (L1T2) to 27.27 % (L2T2).

At Warangal location, it ranged from 17.67 to 26.33 % with a general mean of 23.38 %. The lines exhibited a variation from 19.47(L4) to 26.33 %(L2) and for testers, it ranged from 19.73 (T1) to 25.00 (T2). In hybrids, it ranged from 17.67 (L1T5) to 26.17 % (L2T2).

The variation for amylose content at Hyderabad location, ranged from 18.97to 26.57 with an average of 22.33%. It varied from 21.77 (L5) to 24.63 (L6) % in lines while in testers, it ranged from20.83 (T3 and T4) to 23.23% (T5). The hybrids possessed a range from 18.97 (L3T1) to 26.57(L2T1).

4.2.8.11 Grain type

Based on kernel length and L/B ratio grains are classified long slender, long bold, short slender, short bold and medium slender as per DDR procedure. Among all these grains types long slender and medium slender grains are preferred by consumers.

Among lines, L5 had long slender grains in all locations and over locations while in L6 long slender grains observed at Jagitial and Warangal locations. In testers, T1 and T2 possessed long slender grains whereas T5 had medium slender grains at all locations and over locations.

Among 30 cross combinations, four crosses *viz.*, L2T2, L3T3, L4T5 and L5T2 recorded long slender grains and two crosses (L3T2 and L3T5) had medium slender grains in all locations and over locations.

4.2.8.12 Grain chalkiness

In lines L6 had no chalky grains at all locations as well as in pooled while in L4 and L6 grain chalkiness was absent at Warangal and Hyderabad and in pooled analysis respectively. Among testers, absence of grain chalkiness was observed in T5 at all locations and in pooled.

Grain chalkiness was absent in cross combinations L1T4, L3T5, L5T5 and L6T1 which is desirable in consumer point of view and also for fetching higher price for produce.

4.3 Combining Ability Analysis

Analysis of variance for combing ability was carried at different locations and presented in tables 4.3.1 to 4.3.3. The mean sum of squares of crosses was partitioned into lines, testers and line × tester effects.

Mean squares due to genotypes were highly significant for all the seventeen characters at all locations. Further, partitioning of the genotypes into parents and crosses

and comparison of parents *Vs* crosses showed significant differences among themselves for all the seventeen characters indicating that the crosses performed well compared to parents except for productive tillers per plant, alkali spreading value at Jagitial location, for productive tillers per plant, L/B ratio, alkali spreading value at Warangal, for L/B ratio, bran oil, milling recovery, head rice recovery and amylose content at Hyderabad location in case of parents vs crosses interaction. The differences among lines and testers were also significant. Line × tester mean sum of squares were found to be highly significant for yield, yield attributing traits and bran oil content studied at different locations.

4.3.1 Line × Tester Pooled Analysis for Combining Ability

The pooled analysis of variance for combining ability over three locations recorded significant differences for all the characters studied (Table 4.3.4). The differences among the parents, parents *Vs* crosses (except panicle length and L/B ratio) and crosses were observed to be significant for all the characters studied. Partitioning of crosses into lines, testers and line × tester revealed that the variance due to lines were significant for plant height, bran oil, head rice recovery and water uptake, whereas for testers 17 characters studied nine were found to be significant. The interaction due to lines x testers were significant for all the traits studied.

Interaction effect of parents *Vs* crosses× locations, crosses × locations were significant for all the characters, except for kernel length, alkali spreading value and amylose content in parents *Vs* crosses× locations interaction. Further, lines × locations interaction showed significant differences for days to 50% flowering, L/B ratio and head rice recovery. While, testers × locations were significant for grain yield per plant, L/B ratio, bran oil, milling recovery, head rice recovery and water uptake. Interaction effects of line ×tester × location were significant for all the characters studied.

4.3.2 Combining Ability Variances and Gene Action

The estimates of GCA and SCA variances in pooled analysis were presented in table 4.3.10. General combining ability is generally associated with additive gene action while specific combining ability is due to non-additive gene action. In the present investigation SCA variances were higher than GCA variances in pooled analysis for all the characters except plant height and gel consistency indicating the predominance of non-additive gene action for these characters.

4.3.3 Combining Ability Effects

General combining ability effects of parents at different locations and over locations (pooled) were estimated and presented in tables 4.3.5 and 4.3.6 whereas, specific combining ability effects of cross combinations were given in tables 4.3.8 and 4.3.9. The results are discussed character wise here under.

4.3.3.1 Days to 50% Flowering

***gca* effects**

At Jagitial, general combining ability effects for days to 50% flowering ranged from -7.44 (L5) to 4.02 (L3 and L4) in lines and from -6.39 (T2) to 8.44 (T3) in testers. Further, significant *gca* effects in desired direction was recorded for this trait in L1 (-3.64) and L5 (-7.44) lines and in testers *viz.*, T2 (-6.39), T5 (-3.11) and T1 (-2.83).

At Warangal location, the *gca* effects for this trait ranged from -5.01 (L1) to 5.92 (L6) in lines and from -6.26 (T2) to 9.86 (T3) in testers. Further, the lines L1 (-5.01), L5 (-3.88) and L2 (-1.61) and testers T2 (-6.26), T5 (-4.53) and T1 (-1.87) recorded significant *gca* effects in desired direction for this trait.

General combining ability effects for days to 50% flowering at Hyderabad location, varied from -3.04 (L1) to 3.89 (L4) in lines and from -7.36 (T2) to 8.70 (T3) in testers. Significant and negative *gca* effects desirable for the trait were noticed in L1 (-3.04), L5 (-2.84) and L2 (-1.64) lines and T2 (-7.36), T5 (-3.13) and T1 (-0.52) testers.

The estimated component of variance due to *sca* (68.32) was higher than *gca* (13.55) for days to 50% flowering in pooled analysis 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 e*t al.* (2011).

From the pooled analysis, among six lines involved three lines L5 (-4.72), L1 (-3.90) and L2 (-0.57) and three testers *viz.*, T2 (-6.67), T5 (-3.59) and T1 (-1.74) showed significant negative *gca* effects suggesting that they were good general combiners with favorable genes for earliness. The lines L1 and L5 and testers *viz.*, T1, T2 and T5 exhibited significant *gca* effects at different locations and as well as in pooled analysis.

***sca* effects**

Specific combining ability effects for days to 50% flowering at Jagitial location, varied from -13.74 (L1T2) to 11.70 (L4T1). Significant negative *sca* effects desirable for the trait were recorded by 14 cross combinations. The cross L1T2 (-13.74) recorded highest *sca* effect followed by L5T5 (-9.55) and L2T4 (-7.22).

At Warangal location, *sca* effects for this trait ranged from -13.87 (L1T2) to 11.40 (L1T4) and eleven cross combinations exhibited significant negative *sca* effects. The cross combinations L1T2 (-13.87) registered highest *sca* effect followed by L5T5 (-11.40) and L2T4 (-10.33).

Estimates of *sca* effects at Hyderabad location, ranged from -15.84 (L1T2) to 14.43 (L1T3). Fourteen crosses exhibited significant negative *sca* effects and the best among them were L1T2 (-15.84) followed by L5T5 (-11.26) and L2T4 (-10.57).

From the pooled analysis, out of thirty crosses fifteen cross combinations showed significant *sca* effects in desirable direction. The superior cross combinations identified among them were L1T2 (-14.49), L5T5 (-10.74), L2T4 (-9.39) and L1T1 (-7.53). Based on *per se* performance and negative *sca* effects L1T2 (high × high), L5T5 (high × high), L1T1 (high × high), L2T2 (high × high) and L5T1 (high × high) cross combinations were superior for days to 50% flowering. The cross combinations involving high × high general combiner revealed additive and additive × additive genetic component of variance where the characters can be easily improved through simple selection procedures in recombination breeding.

4.3.3.2 Plant height (cm)

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -4.42 (L5) to 6.80 (L6) among lines and from -5.36 (T4) to 12.76 (T1) among testers. The *gca* effects were significantly negative for L5 (-4.42) and L1 (-3.41) in lines while in testers, T4 (-5.36), T2 (-3.63) and T3 (-3.28) recorded significant negative *gca* effects for this trait.

Among the lines at Warangal location, *gca* effects ranged from -11.48 (L5) to 8.41(L3) and from -5.71 (T2) to 7.18 (T1) among testers. The estimates of *gca* effects

were significant and negative for L5 (-11.48) and L1 (-9.49) in lines and among testers T2 (-5.71), T4 (-1.76) and T3 (-1.50).

Range of *gca* effects at Hyderabad location, for plant height was from -6.69 (L5) to 5.81 (L2) among lines and from -8.35 (T2) to 10.41(T1) among testers. Lines L5 (-6.69), L4 (-5.22) and L1 (-2.21) recorded significant negative *gca* effects whereas in testers, T2 (-8.35) and T3 (-1.92) exhibited significant negative *gca* effects.

The variance due to specific combining ability (20.32) was lesser than the general combining ability (26.51) for this trait in pooled analysis indicating the influence of additive gene action. Conformity results were given by Ganasekaran *et al.* (2006) and Nadali Bagheri and Babaeian (2010).

In pooled analysis three lines L5 (-7.53), L1 (-5.04) and L4 (-1.28) recorded significant negative *gca* effect, while in testers T2 (-5.90), T4 (-2.44) and T3 (-2.23) registered significant *gca* effects in desired direction. These were found to be good combiners for producing dwarf plant types. The lines L1 and L5 and in testers *viz.*, T2 and T3 recorded significant negative *gca* effects at all locations as well as in pooled analysis.

***sca* effects**

At Jagitial location, estimates of *sca* effects for plant height varied from -14.30 (L5T1) to 16.86 (L5T2). Among cross combinations significant negative *sca* effects were recorded by 9 cross combinations. Top three crosses among them were L5T1 (-14.30), L3T2 (-12.71) and L4T3 (-11.15).

Range of *sca* effects at Warangal location was from -17.98 (L1T1) to 12.93 (L1T3).Thirteen cross combinations possessed significant negative *sca* effects at this location. The best among them were L1T1 (-17.98) followed by L5T3 (-13.55) and L6T5 (-9.87).

Among the cross combinations tested at Hyderabad location, *sca* effects ranged from-18.86 (L4T1) to 11.56 (L4T2). Thirteen cross combinations recorded significant negative *sca* effects. Highest *sca* effects were recorded by L4T1 (-18.86), L3T2 (-11.87) and L6T4 (-9.09).

In pooled analysis, fourteen cross combinations had recorded significant *sca* effects in desired direction. Some of the top specific combiners were L3T2 (-9.45), L6T4 (-7.30), L2T5 (-7.03), L4T3 (-5.74) and L4T1 (-4.67). The hybrids L2T5, L3T2, L4T3 and L6T4 exhibited significant negative *sca* effect at all locations and also in pooled analysis. Based on *per se* performance and negative *sca* effects cross combinations, L1T2 (High × high) and L5T3 (High × high) were identified as best specific cross combination for plant height. The cross combination involving high × high general combiner revealed additive and additive × additive genetic component of variance where the characters can be easily improved through simple selection procedures in recombination breeding

4.3.3.3 Panicle Length (cm)

***gca* effects**

Estimates of *gca* effects at Jagitial location, varied from -1.73 (L5) to 1.24 (L2) among the lines and from -1.83 (T4) to 2.69 (T1) among the testers. Highly significant positive *gca* effects were recorded by line L2 (1.24) and in testers, T1 (2.69) and T5 (1.29).

Among the lines at Warangal location, *gca* effects exhibited a range from -1.01 (L5) to 0.79 (L6) and among testers it varied from -1.58 (T2) to 2.23 (T1). The estimates of *gca* effects were positive and significant for lines L6 (0.79) and L2 (0.68) while, in testers T1 (2.23) and T5 (1.38).

At Hyderabad location, lines showed *gca* effects from -1.18 (L3) to 1.81 (L6) whereas testers ranged from -1.44 (T4) to 2.13 (T1). Significant positive *gca* effects were recorded by line L6 (1.81) whereas, in testers T1 (2.13) and T5 (0.82).

For this trait the estimated component of variance due to *sca* (2.42) was higher than *gca* (1.28) variance in pooled analysis. It indicates the predominance of non-additive gene action. This is in accordance with the earlier reports of Panwar (2005), Ganasekaran *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).

Among lines, L6 (0.81), L2 (0.62) and L1 (0.42) and among testers T1 (2.35) and T5 (1.16) revealed positive *gca* effects over pooled environments, implying that

they are good general combiners. For the character panicle length, T1 and T5 registered significant positive *gca* effects at all locations and also in pooled analysis.

***sca* effects**

For panicle length at Jagitial location exhibited *sca* effects for crosses from -5.10 (L5T4) to 4.92 (L5T2) and among hybrids evaluated four crosses registered significant positive *sca* effects. Some of the top specific crosses identified among them were L5T2 (4.92), L4T4 (3.18) and L5T1 (2.29).

At Warangal location, *sca* effects varied from -3.83 (L5T4) to 2.94 (L2T4) and significant positive *sca* effects were recorded by six cross combinations. The crosses L2T4 (2.94) recorded the highest *sca* effect followed by L5T2 (2.62) and L3T5 (2.06).

At Hyderabad location, crosses showed *sca* effects from -3.52 (L5T5) to 3.19 (L5T2). Out of 30 cross combinations tested only eight crosses recorded significant positive *sca* effects. The highest *sca* effect was recorded by cross L5T2 (3.19) followed by L4T5 (2.53) and L4T4 (2.47).

Seven cross combinations showed significant *sca* effects in positive direction and top four crosses among them were L5T2 (3.58), L4T4 (2.50), L5T1 (1.55) and L1T1 (1.48). Among the hybrids, 2crosses L4T4 and L5T2recorded significant positive *sca* effects at all locations as well as in pooled analysis. When compared over their *per se* performance and *sca* effects the crosses L6T1 (High × High), L1T1 (High × High), L5T1 (Low × High), L3T5 (Low × high) and L5T2 (Low × Low) found superior for this trait. 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 while 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 and the cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.4 Number of productive tillers per plant

***gca* effects**

Among the lines at Jagitial location, *gca* effects exhibited a range from -1.28 (L2) to 1.66 (L6) and in testers it recorded a range from -1.27 (T4) to 0.90 (T2). Line

L6 (1.66) showed significant positive *gca* effect and among testers, T2 (0.90) and T5 (0.62) recorded significant positive *gca* effects.

At Warangal location, *gca* effects for number of productive tillers per plant ranged from -1.16 (L4) to 1.11 (L6) in lines and from -1.21 (T1) to 1.07 (T5) among the testers. Further, significant and positive *gca* effects for this trait were noticed in L6 (1.11) in Lines and T5 (1.07) and T4 (0.40) in testers.

At Hyderabad location, *gca* effects for number of productive tillers varied from -0.80 (L2) to 1.00 (L6) in lines and from -0.49 (T4) to 1.01 (T5) in testers. Significant and positive *gca* effects were recorded in L6 (1.00), L3 (0.53) and L1 (0.40) among lines and T5 (1.01) and T2 (0.34) in testers.

The ratio of *gca* variance to *sca* variance was low (0.26) in pooled analysis 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 e*t al.* (2010a), Nadali Bagheri and Babaeian (2010), Saidaiah *et al.* (2010a) and Saidaiah e*t al.* (2011).

From the pooled analysis the lines L6 (1.26), L3 (0.26) and L1 (0.23) and two testers *viz*., T5 (0.90) and T2 (0.47) registered positive *gca* effects implying their good general combining ability. The line L6 and tester T5 recorded significant positive *gca* effect at all locations and also in pooled analysis. These parents may be involved in crossing programmes for improving this trait.

***sca* effects**

The *sca* effects at Jagitial location, ranged from -2.08 (L4T5) to 1.44 (L2T5). Further, significant positive *sca* effects displayed by six cross combinations. Top three specific combiners were L2T5 (1.44), L6T4 (1.40) and L3T2 (1.10).

At Warangal location, *sca* effects for tillers varied from -2.06 (L4T5) to 2.30 (L5T3) and only six cross combinations *viz.*,L5T3, L1T5, L4T1, L3T5, L6T1 and L4T4 exhibited significant positive *sca* effects. Among them L5T3 (2.30) followed by L1T5 (1.86) and L4T1 (1.54) were found superior.

Lowest and highest *sca* effects recorded at Hyderabad location, were -3.54 (L4T5) and 3.56 (L4T1). Among the crosses, eight hybrids recorded significant positive *sca* effects. The top performing ones were L4T1 (3.56), L2T4 (3.02) and L4T3 (2.56).

Among 30 cross combinations evaluated, 11 crosses showed significant positive *sca* effects over locations and top five specific cross combinations among them were L4T1 (1.95), L3T2 (1.28), L5T1 (1.15), L1T5 (1.10) and L4T3 (0.97) and none of the crosses revealed significant positive *sca* effects at all locations as well as in pooled analysis. However based on *per se* performance and *sca* effects the cross combinations L1T5 (high × high), L3T2 (high × high) and L3T5 (high × high) were detected as promising specific cross combination. The cross combination 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.

4.3.3.5 Number of grains per panicle

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -18.39 (L5) to 9.08 (L3) among the lines and from -13.51 (T2) to 26.38 (T1) among the testers. The estimates of *gca* effects were positive and significant for lines L3 (9.08), L4 (7.94) and L6 (1.88), and in testers, T1 (26.38) and T3 (7.77).

At Warangal location, *gca* effects for number of grains varied from -15.52 (L4) to 10.01 (L6) in lines and from -10.06 (T5) to 14.83 (T1) among testers. Further, significant and positive *gca* effects desirable for the trait were noticed in lines L6 (10.01), L3 (8.88), L1 and L2 (2.34) lines and the testers *viz.*, T1 (14.83) and T3 (6.44).

A range of -25.61 (L5) to 18.66 (L4) was observed for lines at Hyderabad location whereas, testers recorded a range from -15.79 (T4) to 18.04 (T1). The line L4 (18.66), L2 (13.32) and L6 (7.86) and the testers T1 (18.04), T5 (1.88) and T3 (1.60) exhibited significant positive *gca* effect.

Component of variance due to *sca* (208.86) was higher than *gca* (65.14) for number of grains panicle^{-1} in pooled analysis, indicating the prevalence of non-additive gene action. Similar results were observed by Panwar (2005), Ganasekaran *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).

From pooled analysis, L6 (6.58), L3 (5.96), L2 (4.60) and L4 (3.69) lines and two testers *viz.*,T1 (19.75) and T3 (5.27) registered significant positive *gca* effects indicating the good combining ability for grains panicle^{-1}.The line L6 and T1 and T3testers were identified as good general combiners at different locations as well as in pooled analysis. They may be utilized in future breeding programmers for improving the number of grains panicle^{-1}.

***sca* effects**

Among the crosses at Jagitial location, *sca* effects for number of grains per panicle ranged from -52.02 (L3T4) to 57.36 (L3T3) and significant positive *sca* effects were exhibited by fourteen hybrids. The top three promising crosses were L3T3 (57.37), L6T4 (50.17) and L4T2 (23.11).

Estimates of *sca* effects at Warangal location, ranged from -43.43 (L3T4) to 43.95 (L3T3). Among crosses, 12 crosses revealed significant positive *sca* effects for this trait. Top three superior crosses were L3T3 (43.95), L6T4 (34.10) and L5T4 (25.83).

Specific combining ability effects for grains panicle^{-1} at Hyderabad location ranged from -42.44 (L5T1) to 47.62 (L4T1). Significant positive *sca* effects were observed in sixteen hybrids. Highest performance was recorded by crosses L4T1 (47.62) followed by L5T2 (46.66) and L3T3 (30.13).

In pooled analysis, out of 30 crosses evaluated, 11 crosses showed significant *sca* effect in positive direction and some of the superior crosses among them were L3T3 (43.82), L6T4 (28.73), L4T1 (24.72) and L5T2 (17.39). The hybrids L1T2, L2T5, L3T3, L3T5 and L4T1displayed significant positive *sca* effect at all locations and also in pooled analysis. The superior cross combinations identified based on their *per se* performance and *sca* effects were L3T3 (High × High), L4T1 (High × High), L6T4 (High × Low), L2T5 (High × low), L3T5 (High × low) and L1T2 (Low × low). 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. The

crosses involving high × low *gca* effects resulted in superior combinations which may be due to complementary gene action and the crosses between two low combiners producing crosses with significant *sca* effect indicating the presence of non-additive inter allelic interaction. The cross between two low combiners revealed the presence of non-additive inter allelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.6 1000-grain weight (g)

***gca* effects**

Among the lines at Jagitial location, *gca* effects ranged from -0.74 (L5) to 0.72 (L6) and among testers, *gca* effects varied from –4.00 (T4) to 5.02 (T1). The line L6 (0.72) and testers *viz.*, T1 (5.02) and T5 (2.00) recorded significant positive *gca* effects.

Estimates of *gca* effects at Warangal location, varied from -1.40 (L3) to 0.85 (L4) among lines and from -3.33 (T4) to 4.71 (T1) in testers. The lines L4 (0.85) and L2 (0.78) and the testers T1 (4.71) and T5 (2.30) recorded significant positive *gca* effect.

For 1000-grain weight, *gca* effects at Hyderabad location, exhibited a range from -0.64 (L5) to 0.68 (L1) among lines whereas in testers, range was from -4.38 (T4) to 5.81 (T1). The line L1 (0.68) showed significant positive *gca* effects. Among testers T1 (5.81) and T5 (2.02) recorded significant *gca* effects in desired direction.

In pooled analysis the variance due to *gca* (5.81) was lesser than the *sca* (8.21) 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 Banumathy *et al.* (2003), Bhave *et al.* (2003), Swamy *et al.* (2003), Panwar (2005), Anand Kumar *et al.* (2006) and Kumar Babu e*t al*. (2010a).

For 1000-grain weight in pooled analysis, two lines L1 (0.49) and L2 (0.40) and two testers *viz.*, T1 (5.18) and T5 (2.11) were identified as potential general combiners based on their *gca* effects. The testers T1 and T5 were good general combiners at different locations and over locations. These may serve as useful source for improvement of this trait in hybridization programmes.

***sca* effects**

1000-grain weight *sca* effects at Jagitial location, exhibited a range from -5.40 (L5T2) to 5.03 (L2T1) among crosses. Ten cross combinations showed significant positive *sca* effects at this location. Top three specific crosses among them were L2T1 (5.02), L3T2 (4.34) and L1T4 (4.21).

At Warangal location *sca* effects ranged from -5.14 (L1T1) to 4.76 (L1T4) and nine crosses recorded significant positive *sca* effects. The top three crosses were L1T4 (4.76) followed by L3T2 (4.10) and L6T1 (3.99).

Estimates of *sca* effects at Hyderabad location, varied from -6.12 (L1T1) to 5.39 (L1T4) and nine crosses exhibited significant positive *sca* effects. Top three specific crosses were L1T4 (5.39), L2T1 (4.51) and L3T3 (2.97).

From pooled analysis 11 cross combinations showed significant *sca* effects in positive direction and the top five specific cross combinations identified among them were L1T4 (4.79), L2T1 (4.17), L6T1 (3.28), L3T2 (2.85) and L2T3 (2.40). Four hybrids *viz.*, L1T4, L2T1, L5T1 and L6T1 recorded significant positive *sca* effect at all locations and also in pooled analysis. The best specific cross combinations identified based on positive *sca* effect and *per se* performance were L2T1 (High × High), L6T1 (Low × High), L5T1 (Low × High), L1T2 (High × low), L1T4 (high × low), L4T5 (low × high), L5T5 (low × high), L1T5 (high × high) and L3T2 (low × low). 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. The crosses involving low × high *gca* effects resulted in superior combinations which may be due to complementary gene action and the crosses between two low combiners producing crosses with significant *sca* effect indicating the presence of non-additive interallelic interaction. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.7 Grain yield per plant (g)

***gca* effects**

Range of *gca* effects at Jagitial location, for grain yield was from -5.21(L2) to 2.45 (L6) among lines and from -5.97 (T4) to 4.72 (T1) among testers. Out of six lines,

L6 (2.45), L3 (2.17) and L4 (1.77) lines recorded significant positive *gca* effect whereas in testers T1 (4.72), T2 (1.83) and T5 (1.60).

General combining ability effects at Warangal location, varied from -2.71 (L4) to 2.55 (L3) in lines and in testers it ranged from -4.51 (T3) to 6.42 (T1). The lines L3 (2.55), L6 (1.97) and L2 (1.33) and in testersT1 (6.42) possessed significant positive *gca* effects.

At Hyderabad location, *gca* effects ranged from -3.67 (L2) to 2.09 (L5) among lines. Similarly, in testers it ranged from -4.22 (T2) to 3.70 (T1). Highly significant *gca* effects were recorded by L5 (2.09), L6 (1.31) and L4 (1.28) lines, and in testers, T1 (3.70) and T5 (3.42).

The estimated component of variance due to *sca* (11.87) was higher than the *gca* (2.87) for grain yield in pooled analysis. The ratio of *gca* variance to *sca* variance was low (0.24) indicating the presence of non-additive gene action. Comparable results were earlier reported by Panwar (2005), Rosamma and Vijayakumar (2005), Singh *et al.*(2005), Anand Kumar *et al.*(2006), Ganasekaran *et al.*(2006), Dalvi and Patel (2009), 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).

In pooled analysis, L6 (1.91) and L3 (1.48) lines and T1 (4.95) and T5 (1.60) testers showed significant positive *gca* effects and were considered to be good general combiners for grain yield plant^{-1}. The parent, L6 in lines and T1in testers recorded significant positive *gca* effects at different locations and also in pooled analysis.

sca effects

Range of *sca* effects at Jagitial location for grain yield was from -8.34 (L1T3) to 10.57 (L1T5). Among 30 hybrids evaluated, eight hybrids recorded significant positive *sca* effects for grain yield. The top three crosses were L1T5 (10.57) followed by L3T3 (9.21) and L4T2 (4.49).

At Warangal location, *sca* effects of grain yield varied from –7.35 (L1T3) to 5.90 (L2T3) and significant *sca* effects were noted by 10 hybrids. Top three specific crosses among them were L2T3 (5.90) followed by L1T5 (4.29) and L3T5 (3.46).

Among the cross combinations at Hyderabad location, *sca* effects ranged from -8.28 (L3T4) to 8.24 (L1T5) and ten crosses exhibited significant positive *sca* effects. Highest *sca* effect recorded by L1T5 (8.24) followed by L3T1 (7.48) and L2T3 (7.04).

In pooled analysis, ten crosses showed significant *sca* effects in positive direction out of 30 crosses evaluated. The crossesL1T5, L3T3 and L5T4recorded significant positive *sca* effect at all the locations and over all locations. The top five specific crosses among them were L1T5 (7.70), L3T3 (6.00), L2T3 (3.39), L3T1 (3.16) and L5T4 (3.10). The cross combinations L3T1 (High × High), L6T1 (High × High), L1T5 (Low× High), L3T2 (high × low), L6T3 (high × low), L1T4 (low × low), L2T2 (low × low), L2T3 (low × low), L4T4 (low × low) and L5T4 (low × low) were identified as good specific cross combinations based on positive *sca* effects and *per se* performance. 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 with low × high or high × low combiners resulted in superior combinations which may be due to complementary gene action. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.8 Kernel length (mm)

***gca* effects**

At Jagitial, general combining ability effects for kernel length ranged from -0.47 (L1) to 0.50 (L6) in lines and from -0.69 (T3) to 0.49 (T1) in testers (Table). Further, significant *gca* effects in desired direction was recorded for this trait in L6 (0.50) and L4 (0.14) lines and in testers *viz.*, T1 (0.49), T2 (0.25) and T5 (0.21).

At Warangal location, the *gca* effects for this trait ranged from -0.16 (L1) to 0.55 (L6) in lines and from -0.61 (T3) to 0.52 (T1) in testers. Further, the line L6 (0.55) and testers T1 (0.52), T2 (0.24) and T5 (0.21) recorded significant *gca* effects in desired direction for this trait.

General combining ability effects for kernel length at Hyderabad location, varied from –0.33(L5) to 0.40 (L6) in lines and from -0.77 (T3) to 0.43 (T1) in testers.

Significant and positive *gca* effects desirable for the trait were noticed in L6 (0.40) and L4 (0.23) lines and T1 (0.43), T2 (0.40) and T5 (0.20) testers.

The estimated component of variance due to *sca* (0.31) was higher than *gca*(0.10) for kernel length in pooled analysis indicating the preponderance of non-additive gene action. Similar results were earlier reported by Bisne and Motiramani (2005) and Shivani *et al.* (2009).

From the pooled analysis, among six lines involved two lines L6 (0.48) and L4 (0.11) and three testers *viz.*, T1 (0.48), T2 (0.29) and T5 (0.21) showed significant positive *gca* effects suggesting that they were good general combiners with favorable genes for kernel length. The line L6 and testers *viz.*, T1, T2 and T5exhibited significant *gca* effects at different locations and as well as in pooled analysis.

***sca* effects**

Specific combining ability effects for kernel length at Jagitial location, varied from -1.41 (L5T1) to 0.92 (L3T3). Significant positive *sca* effects desirable for the trait were recorded by11 cross combinations. The cross L3T3 (0.92) recorded highest *sca* effect followed by L2T2 (0.66) and L1T5 (0.64).

At Warangal location, *sca* effects for this trait ranged from -1.23 (L5T1) to 0.88 (L3T3) and nine crosses exhibited significant positive *sca* effects. The cross L3T3 (0.88) registered highest *sca* effect followed by L4T1 (0.66) and L4T5 (0.64).

Estimates of *sca* effects at Hyderabad location, ranged from -1.62 (L5T1) to 1.09 (L3T3). Thirteencrosses exhibited significant positive *sca* effects and the best among them were L3T3 (1.09) followed by L2T2 (0.57) and L5T2 (0.52).

From the pooled analysis, out of thirty crosses, eleven cross combinations showed significant *sca* effects in desirable direction. The superior crosses identified among them were L3T3 (0.97), L2T2 (0.58), L5T2 (0.56), L4T1 (0.49), and L5T4 (0.48). The crosses *viz*., L2T1, L2T2, L3T1, L3T3, L4T1, L5T2, L5T3 and L5T4 showed significant positive *sca* effects at all locations and also in pooled analysis.

Based on *per se* performance and positive *sca* effects the crosses *viz*., L4T1 (High × High), L2T1 (Low × High) and L2T2 (Low × High), L1T1 (low × high), L1T5 (low × high), L3T1 (low × high), L3T3 (low × low), L4T5 (high × high), L5T2 (low ×

high) and L5T4 (low × low) were identified as superior for kernel length. The crosses between low × high resulted in superior cross combinations due to complementary gene action which had resulted out of both additive and non-additive gene action while 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. The cross between two low combiners revealed the presence of non-additive inter allelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents.

4.3.3.9 Kernel breadth (mm)

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -0.12 (L5) to 0.15 (L6) among lines and from -0.17 (T3) to 0.38 (T1) among testers. The *gca* effects were significantly negative for L5 (-0.12) and L2 (-0.11) in lines while in testers, T3 (-0.17), T4 (-0.16) and T2 (-0.08) recorded significant negative *gca* effects for this traits.

Among the lines at Warangal location, *gca* effects ranged from -0.16 (L5) to 0.15 (L6) and from -0.17 (T3) to 0.31 (T1) among testers. The estimates of *gca* effects were significant and negative for L5 (-0.16) and L2 (-0.05) in lines and among testers T3 (-0.17), T4 (-0.09) and T2 (-0.04).

Range of *gca* effects at Hyderabad location, for kernel length was from -0.13 (L5) to 0.15 (L6) among lines and from -0.15 (T4) to 0.37(T1) among testers. Lines L5 (-0.13), L3 (-0.05) and L1 (-0.04) recorded significant negative *gca* effects whereas in testers, T4 (-0.15), T3 (-0.13) and T2 (-0.12) exhibited significant negative *gca* effects.

The variance due to specific combining ability (0.026) was higher than the general combining ability (0.023) for this trait in pooled analysis indicating the influence of non-additive gene action. Conformity results were given by Bisne and Motiramani (2005) and Shivani *et al.* (2009).

In pooled analysis three lines L5 (-0.14), L2 (-0.05) and L3 (-0.03) recorded significant negative *gca* effect, while in testers T3 (-0.16), T4 (-0.13) and T2 (-0.08) registered significant *gca* effects in desired direction. These were found to be good

combiners for kernel breadth. The line L5 and in testers *viz.,* T3 and T4 recorded significant negative *gca* effects at all locations as well as in pooled analysis.

***sca* effects**

At Jagitial location, estimates of *sca* effects for kernel breadth varied from -0.44 (L5T1) to 0.36 (L5T3) among crosses and significant negative *sca* effects were recorded by7 hybrids. Top three crosses among them were L5T1 (-0.44), L6T3 (-0.24) and L4T2 (-0.15).

Range of *sca* effects at Warangal location was from -0.43 (L5T1) to 0.28 (L5T3). Nine crosses possessed significant negative *sca* effects at this location. The best among them were L5T1 (-0.43) followed by L6T3 (-0.21) and L4T2 (-0.18).

Among the crosses tested at Hyderabad location, *sca* effects ranged from-0.51 (L5T1) to 0.28 (L5T3). Eight cross combinations recorded significant negative *sca* effects. Highest *sca* effects were recorded by L5T1 (-0.51), L6T3 (-0.25) and L3T3 (-0.17).

In pooled analysis, eight cross combinations had recorded significant *sca* effects in desired direction. Some of the top specific combiners were L5T1 (-0.46), L6T3 (-0.24), L1T2 (-0.16), L3T3 (-0.16) and L4T4 (-0.11). The hybridsL3T3, L4T2, L4T4, L5T1 and L6T3exhibited significant negative *sca* effect at all locations and also in pooled analysis. Based on *per se* performance and *sca* effects L3T3 (High × High), L1T3 (low × high), L4T2 (low × high), L4T4 (low × high), L5T1 (high × low) and L6T3 low × high) were identified as best specific cross combination. The cross combination 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. The crosses between low × high or high × low resulted in superior cross combinations due to complementary gene action which had arised out of both additive and non-additive gene action.

4.3.3.10 L/B ratio

***gca* effects**

Among the lines at Jagitial location, *gca* effects exhibited a range from -0.26 (L1) to 0.13 (L2) and in testers it recorded a range from -0.27 (T1) to 0.24 (T2). Lines

L2 (0.13) and L5 (0.11) showed significant positive *gca* effect and among testers, T2 (0.24) and T4 (0.10) recorded significant positive *gca* effects.

At Warangal location, *gca* effects for L/B ratio ranged from -0.10 (L4) to 0.14 (L5) in lines and from -0.14 (T1) to 0.17 (T2) among the testers. Further, significant and positive *gca* effects for this trait were noticed in L5 (0.14) line and T2 (0.17) and T5 (0.08) in testers.

At Hyderabad location, *gca* effects for L/B ratio varied from -0.08 (L1) to 0.11 (L3) in lines and from -0.28 (T1) to 0.36 (T2) in testers. Significant and positive *gca* effects were recorded in L3 (0.11) line and T2 (0.36) and T4 (0.07) in testers.

The ratio of *gca* variance to *sca* variance was low (0.12) in pooled analysis 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 Bisne and Motiramani (2005), Shivani *et al.* (2009) and Kumar Babu *et al.* (2010)

From the pooled analysis the line L5 (0.09) and two testers *viz*., T2 (0.26) and T5 (0.05) registered positive *gca* effects implying their good general combining ability. The tester T2 recorded significant positive *gca* effect at all locations and also in pooled analysis. This parent may be involved in crossing programmes for improving this trait.

***sca* effects**

The *sca* effects at Jagitial location, ranged from -0.39 (L4T3) to 0.75 (L3T3). Further, significant positive *sca* effects displayed by eight crosses. Top three specific combiners were L3T3 (0.75), L6T3 (0.45) and L5T4 (0.35).

At Warangal location, *sca* effects for L/B ratio varied from -0.30 (L5T3) to 0.71 (L3T3) and only six crosses exhibited significant positive *sca* effects. Among them L3T3 (0.71) followed by L4T5 (0.37) and L6T3 (0.36) were found superior.

Range of *sca* effects at Hyderabad location was from -0.46 (L3T2) to 0.86 (L3T3). Among the crosses, eight hybrids recorded significant positive *sca* effects. The top performing ones were L3T3 (0.86), L6T3 (0.31) and L1T2 (0.30).

Among 30 cross combinations evaluated, nine crosses showed significant positive *sca* effects and top three specific cross combinations among them were

L3T3 (0.78), L6T3 (0.38), L2T2 (0.33), L5T4 (0.29) and L4T5 (0.26) and the crosses L2T2, L3T3, L5T4 and L6T3 revealed significant positive *sca* effects at all locations as well as in pooled analysis. However based on *per se* performance and *sca* effects the crosses L3T3 (Low × Low), L2T2 (Low × High), L4T4 (low × low), L4T5 (low × high), L5T4 (high × low), L6T3 (low × low) and L5T2 (High × High) were detected as promising specific cross combinations. The cross combinations involving high × high general combiner 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. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents. Low × high or high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.3.11Bran oil content (%)

***gca* effects**

At Jagitial location, estimates of *gca* effects varied from -1.62 (L4) to 2.30 (L1) among lines while in testers, range was from -0.86 (T1) to 0.83 (T4). Only two lines L1 (2.30) andL5 (1.20) showed significant positive *gca* effect and in testers T4 (0.83) and T3 (0.55).

Range of *gca* effects at Warangal location was from -1.73 (L2) to 2.11 (L1) in lines and from -1.22 (T1) to 1.25 (T3) in testers. Significant positive *gca* effects exhibited by L1 (2.11) and L5 (1.45) lines and in testers T3 (1.25) and T2 (1.02).

At Hyderabad location, estimates of *gca* effects varied from -1.35 (L4) to 1.36 (L1) in lines while in testers, range was from -1.18 (T5) to 2.07 (T2). Only two lines L1 (1.36) and L5 (0.99) and one tester T2 (2.07) showed significant positive *gca* effect.

In the present investigation, bran oil content seems to be mostly under the control of non -additive gene action in pooled analysis as the *gca* variance (0.86) was lower than *sca* variance (0.93).The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.92) revealing the preponderance of non- additive gene action in the inheritance of this trait.

The present findings are in accordance with the results of Sabaghnia N *et al*. (2010) and Amir Jose Klein Werle *et al*. (2013).

In pooled analysis, the estimates of *gca* effects revealed that L1 (1.92) and L5 (1.22) among lines and T2 (1.07) and T3 (0.55) among testers were good general combiners. Among the lines L1 and L5 were identified with significant positive *gca* effects at all locations as well as in pooled analysis. These lines can be utilized in basic breeding programmes for improvement of this trait.

***sca* effects**

At Jagitial location, estimates of *sca* effects varied from -3.91 (L1T5) to 2.51 (L1T3). Six hybrids recorded significant positive *sca* effects. Top performing crosses identified among them were L1T3 (2.51) followed by L3T4 (2.08) and L2T5 (1.53).

Range of *sca* effects at Warangal location, for bran oil was from -2.13 (L1T5) to 2.74 (L6T2). Six crosses possessed significant *sca* effects at this location. The superior crosses identified among them were L6T2 (2.74), L1T3 (1.94) and L5T5 (1.17).

For bran oil at Hyderabad location, *sca* effects ranged from -1.94 (L1T5) to 3.01 (L6T5). Among crosses, six crosses displayed significant positive *sca* effects. The top three crosses were L6T5 (3.01) followed by L4T3 (1.96) and L2T1 (1.69).

In pooled analysis, eight crosses recorded significant positive *sca* effects. The top performing three specific crosses among them were L1T3 (1.89), L6T5 (1.43), L3T4 (1.39), L6T2 (1.33) and L2T1 (0.92). Among the cross, L1T3exhibited significant positive *sca* effects at all locations and also in pooled analysis. From the above crosses, none of the cross was identified as best specific combiners as per their *per se* performance and *sca* effects.

4.3.3.12 Milling %

***gca* effects**

Among the lines at Jagitial location, *gca* effects ranged from -4.11 (L2) to 1.66 (L1) and among testers, *gca* effects varied from –1.61 (T1) to 1.52 (T4). The lines L1 (1.66), L5 (0.72), L6 (0.65) and L3 (0.63) and testers *viz.*, T4 (1.52) and T5 (0.78) recorded significant positive *gca* effects.

Estimates of *gca* effects at Warangal location, varied from -0.73 (L4) to 0.86 (L5) among lines and from -1.70 (T2) to 1.88 (T1) in testers. The lines L5 (0.86) and L6 (0.57) recorded significant positive *gca* effect and in testers T1 (1.88), T5 (0.73) and T4 (0.59).

gca effects at Hyderabad location, exhibited a range from -2.79 (L2) to 1.95 (L4) among lines whereas in testers, range was from -0.73 (T5) to 0.91 (T1). The lines L4 (1.95) and L3 (1.67) showed significant positive *gca* effects. Among testers T1 (0.91) and T3 (0.37) recorded significant *gca* effects in desired direction.

In pooled analysis the variance due to *gca* (0.18) was lesser than the *sca* (1.77) for milling recovery indicating the contribution of non-additive gene action in the inheritance of this trait. Results supporting the present investigation were put forth by Sharma and Mani (1998), Munhot *et al.* (2000) and Gonya Nayak (2011).

For milling percent in pooled analysis, four lines L3 (0.85), L4 (0.56), L1 (0.51) and L6 (0.43) and three testers *viz.*, T4 (0.59), T1 (0.39) and T5 (0.26) were identified as potential general combiners based on their *gca* effects. None of the lines and testers were good general combiners at different locations and over locations.

***sca* effects**

Milling percent *sca* effects at Jagitial location, exhibited a range from -3.77 (L2T3) to 5.34 (L2T2) among crosses. Nine hybrids showed significant positive *sca* effects at this location. Top three specific crosses among them were L2T2 (5.34), L6T1 (4.12) and L4T3 (3.43).

At Warangal location *sca* effects ranged from -4.07 (L2T3) to 4.22 (L2T2) and 10 crosses recorded significant positive *sca* effects. The top three crosses were L2T2 (4.22) followed by L5T3 (3.68) and L3T4 (2.30).

Estimates of *sca* effects at Hyderabad location, varied from -4.64 (L3T1) to 2.41 (L5T1) and ten crosses exhibited significant positive *sca* effects. Top three specific crosses were L5T1 (2.41), L6T1 (2.32) and L1T5 (2.27).

From pooled analysis 13 crosses showed significant *sca* effects in positive direction and the top three specific cross combinations identified among them were L2T2(3.89), L6T1(2.34), L1T5(2.10), L5T2 (1.87) and L4T4 (1.68). Two hybrids *viz.*,

L1T5 and L2T2 recorded significant positive *sca* effect at all locations and also in pooled analysis. The best specific cross combinations identified based on positive *sca* effect and *per se* performance were L6T1 (high × high), L1T5 (high × high), L4T4 (high × high), L1T1 (high × high), L3T5 (high × high), L2T4 (low × high), L3T2 (high × low), L3T4 (high × low), L4T3 (high × low), L5T1 (low × high), L5T5 (low × high), (L2T2 low × low) and (L5T3 low × low). 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. The cross between two low combiners revealed the presence of non-additive inter allelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents. Low × high or high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.3.13 Head rice recovery (%)

***gca* effects**

Estimates of *gca* effects at Jagitial location, varied from -5.05 (L2) to 2.02 (L1) among the lines and from -2.67 (T2) to 2.09 (T5) among the testers. Highly significant positive *gca* effects were recorded by lines L1 (2.02), L3 (1.66), L6 (0.97) and L4 (0.83) and in testers, T5 (2.09), T3 (1.67) and T4 (0.89).

Among the lines at Warangal location, *gca* effects exhibited a range from -1.41 (L2) to 0.82 (L3) and among testers it varied from -1.94 (T2 and T3) to 1.94 (T1). The estimates of *gca* effects were positive and significant for lines L3 (0.82) and L6 (0.52) while, in testers T1 (1.94), T4 (1.11) and T5 (0.84).

At Hyderabad location, lines showed *gca* effects from -2.82 (L2) to 2.61 (L4) whereas testers ranged from -1.19 (T4) to 1.37 (T1). Significant positive *gca* effects were recorded by lines L4 (2.61) and L3 (2.18) whereas, in testers T1 (1.37) and T3 (0.67).

For this trait the estimated component of variance due to *sca* (2.58) was higher than *gca* (0.25) variance in pooled analysis. It indicates the predominance of non-additive gene action. This is in accordance with the earlier reports of Sharma and Mani (1998), Munhot *et al.* (2000) and Gonya Nayak (2011).

Among lines, L4 (1.41), L3 (0.86) and L1 (0.76) and among testers T5 (0.73) T1 (0.44) and T4 (0.27) revealed positive *gca* effects, implying that they are good general combiners. For the character head rice recovery, line L3 registered significant positive *gca* effects at all locations and also in pooled analysis.

***sca* effects**

For head rice recovery at Jagitial location *sca* effects in crosses varied from -5.14 (L6T5) to 6.17 (L6T1) and among hybrids evaluated eight hybrids registered significant positive *sca* effects. Some of the top specific crosses identified among them were L6T1 (6.17), L5T5 (4.03) and L4T3 (3.79).

At Warangal location, *sca* effects varied from -5.13 (L3T1) to 2.87 (L2T2) and significant positive *sca* effects were recorded by 11 crosses. The crosses L2T2 (2.87) recorded the highest *sca* effect followed by L3T4 (2.79) and L4T4 (2.55).

At Hyderabad location, crosses showed *sca* effects from -4.55 (L3T1) to 3.63 (L5T1). Out of 30 hybrids tested 12 hybrids recorded significant positive *sca* effects. The highest *sca* effect was recorded by cross L5T1 (3.63) followed by L6T1 (3.37) and L4T4 (2.44).

Eleven cross combinations showed significant *sca* effects in positive direction and top 5 crosses among them were L6T1 (3.87), L2T2 (2.39), L4T4 (1.90), L3T2 (1.83) and L1T5 (1.77). Among the hybrids, L2T2 and L6T1 recorded significant positive *sca* effects at all locations as well as in pooled analysis. When compared over their *per se* performance and *sca* effects the crosses L6T1 (low × high) was found superior for this trait. The cross combinations involving 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.

4.3.3.14 Alkali spreading value

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -0.51 (L5) to 0.55 (L6) among the lines and from -0.76 (T1) to 0.46 (T2 and T3) among the testers. The estimates of *gca* effects were positive and significant for lines L6 (0.55) and L3 (0.52), and in testers, T2 and T3 (0.46).

At Warangal location, *gca* effects for alkali spreading value varied from -0.60 (L5) to 0.57 (L3) in lines and from -0.71 (T1) to 0.56 (T2) among testers. Further, significant and positive *gca* effects desirable for the trait were noticed in L3 (0.57), L6 (0.56) and L4 (0.13) among the lines and T2 (0.56), T3 (0.26) and T5 (0.13) among testers.

A range of -0.53 (L5) to 0.67 (L6) was observed for lines at Hyderabad location whereas, testers recorded a range from -0.61(T1) to 0.48 (T3). The lines L6 (0.67), L3 (0.53) and L4 (0.17) exhibited significant positive *gca* effect, whereas in testers T3 (0.48) and T2 (0.46).

Component of variance due to *sca* (0.45) was higher than *gca* (0.16) for alkali spreading value in pooled analysis, indicating the prevalence of non-additive gene action. Similar results were observed by Sharma and Mani (1998) and Munhot *et al.* (2000).

From pooled analysis, L6 (0.59), L3 (0.54) and L4 (0.14) lines and two testers *viz.*, T2 (0.50) and T3 (0.40) registered significant positive *gca* effects indicating the good combining ability for alkali spreading value. The lines L3, L6 and T2 and T3testers were identified as good general combiners at different locations as well as in pooled analysis. They may be utilized in future breeding programmers for improving this trait.

***sca* effects**

Among the crosses at Jagitial location, *sca* effects for alkali spreading value ranged from -1.02 (L5T4) to 1.49 (L6T4) and significant positive *sca* effects were exhibited by 12 hybrids. The top three promising crosses were L6T4 (1.49), L1T1 (0.72) and L2T1 (0.67).

Estimates of *sca* effects at Warangal location, ranged from -0.91 (L6T1) to 1.53 (L6T4) among crosses and 10 crosses revealed significant positive *sca* effects for this trait. Top three superior crosses were L6T4 (1.53), L1T1 (0.93) and L4T3 (0.65).

Specific combining ability effects for alkali spreading value at Hyderabad location ranged from -0.87 (L2T4) to 0.92 (L6T4). Significant positive *sca* effects were observed in 12 hybrids. Highest performance was recorded by cross L6T4 (0.92) followed by L1T1 (0.88) and L2T1 (0.75).

In pooled analysis, out of 30 crosses evaluated, 13 crosses showed significant *sca* effect in positive direction and some of the superior crosses among them were L6T4 (1.32), L1T1(0.85), L2T1 (0.82), L5T2 (0.48) and L2T2 (0.440). The hybrids L1T1, L1T3, L2T1, L4T5, L5T2 and L6T4 displayed significant positive *sca* effect at all locations and also in pooled analysis. The superior cross combinations identified based on their *per se* performance and *sca* effects were L6T2 (high × high), L4T5 (high × high). L4T4 (high × low), L3T5 (high × low), L6T4 (high × low), L1T3 (low × high), L2T2 (low × high), L5T2 (low × high), L5T3 (low × high), L1T1 (low × low), L2T1 (low × low) and L5T5 (low × low). 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. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents. Low × high or high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.3.15 Water uptake

***gca* effects**

Among the lines at Jagitial location, *gca* effects ranged from -16.61 (L3) to 39.72 (L2) and among testers, *gca* effects varied from –17.78 (T3) to 18.33 (T2). The lines L2 (39.72) and L5 (11.39) and testers *viz.*, T2 (18.33) and T4 (7.50) recorded significant positive *gca* effects.

Estimates of *gca* effects at Warangal location, varied from -21.89 (L3) to 37.11 (L2) among lines and from -24.50 (T1) to 25.78 (T4) in testers. The lines L2 (37.11) and L5 (2.78) recorded significant positive *gca* effect and in testers T4 (25.78), T2 (12.44) and T5 (5.50).

gca effects at Hyderabad location, exhibited a range from -40.33 (L3) to 21.00 (L2) among lines whereas in testers, range was from -25.78 (T5) to 20.33 (T1). The lines L2 (21.00), L5 (12.67), L6 (4.33) and L1 (3.00) showed significant positive *gca* effects. Among testers T1 (20.33) and T3 (8.11) recorded significant *gca* effects in desired direction.

In pooled analysis the variance due to *gca* (75.32) was lesser than the *sca* (406.15) for water uptake indicating the contribution of non-additive gene action in the

inheritance of this trait. Results supporting the present investigation were put forth by Sharma and Mani (1998).

For water uptake in pooled analysis, two lines L2 (32.61) and L5 (8.94) and two testers *viz.,* T4 (10.65) and T2 (9.82) were identified as potential general combiners based on their *gca* effects. The lines L2 and L5 were good general combiners at different locations and over locations. These may serve as useful source for improvement of this trait in hybridization programmes.

***sca* effects**

Water uptake *sca* effects at Jagitial location, exhibited a range from -52.00 (L3T2) to 39.17 (L5T4). Among crosses 11 hybrids showed significant positive *sca* effects at this location. Top three specific crosses among them were L5T4 (39.17), L3T5 (33.83) and L3T1 (26.88).

At Warangal location *sca* effects ranged from -59.78 (L3T2) to 56.22 (L4T2) and twelve crosses recorded significant positive *sca* effects. The top three crosses were L4T2 (56.22) followed by L1T5 (45.16) and L3T3 (36.89).

Estimates of *sca* effects at Hyderabad location, varied from -58.22 (L2T5) to 100.67 (L5T4) and 13 crosses exhibited significant positive *sca* effects. Top three specific crosses were L5T4 (100.67), L2T3 (42.89) and L6T2 (39.00).

From pooled analysis twelve crosses showed significant *sca* effects in positive direction and the top five specific cross combinations identified among them were L5T4 (49.57), L4T2 (31.52), L3T1 (30.35), L1T5 (27.82) and L2T1 (23.13). Hybrids *viz.,* L1T5, L2T1, L3T1, L4T2 and L5T4 recorded significant positive *sca* effect at all locations and also in pooled analysis. The best specific cross combinations identified based on positive *sca* effect and *per se* performance were L5T4 (high × high), L2T4 (high × high), L2T2 (high × high), L5T2 (high × high), L2T1 (high × low), L2T3 (high × low), L4T2 (low × high), L6T2 (low × high), L1T5 (low × low), L3T1 (low × low), L3T5 (low × low) and L6T5 (low × low). 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. The crosses involving high x low or low × high *gca* effects resulted in superior

combinations which may be due to complementary gene action. The cross between two low combiners revealed the presence of non-additive interallelic interaction.

4.3.3.16 Gel consistency

***gca* effects**

Range of *gca* effects at Jagitial location, for gel consistency was from -2.94 (L2) to 2.52 (L6) among lines and from -2.40 (T4) to 3.60 (T5) among testers. Out of six lines, L6 (2.52), L1 (1.39) and L5 (0.86) lines recorded significant positive *gca* effect whereas in testers T5 (3.60).

General combining ability effects at Warangal location, varied from -4.36 (L6) to 3.58 (L4) in lines and in testers it ranged from -1.53 (T3) to 1.74 (T1). The lines L4 (3.58), L1 (1.58) and L5 (1.04) and in testers T1 (1.74) possessed significant positive *gca* effects.

At Hyderabad location, *gca* effects ranged from -5.54 (L4) to 1.86 (L6) among lines. Similarly, in testers it ranged from -1.88 (T3) to 1.57 (T2). Highly significant *gca* effects were recorded by L6 (1.86), L2 (1.39), L1 (1.19) and L5 (1.12) lines and in testers, T2 (1.57) and T5 (1.46).

The estimated component of variance due to *sca* (0.10) was lesser than the *gca* (0.58) for gel consistency in pooled analysis. The ratio of *gca* variance to *sca* variance was high (5.80) indicating the presence of additive gene action.

In pooled analysis, L1 (1.39) and L5 (1.01) lines and T5 (1.60) and T1 (0.90) testers showed significant positive *gca* effects and were considered to be good general combiners for gel consistency. The parents, L1 and L5 recorded significant positive *gca* effects at different locations and also in pooled analysis.

***sca* effects**

Range of *sca* effects at Jagitial location for gel consistency was from -12.52 (L6T2) to 9.53 (L6T1). Among 30 hybrids evaluated, fourteen hybrids recorded significant positive *sca* effects for gel consistency. The top three crosses were L6T1 (9.53) followed byL6T5 (8.20) and L3T4 (7.93).

At Warangal location, *sca* effects of gel consistency varied from –11.68 (L2T2) to 9.32 (L2T1) and significant *sca* effects were noted by 12 hybrids. Top three specific crosses among them were L2T1 (9.32) followed by L3T2 (7.86) and L6T5 (7.52).

Among the hybrids at Hyderabad location, *sca* effects ranged from -8.78 (L2T4) to 7.54 (L5T3) and twelve crosses exhibited significant positive *sca* effects. Highest *sca* effect recorded by L5T3 (7.54) followed by L2T5 (7.28) and L6T1 (7.26).

In pooled analysis, ten hybrids showed significant *sca* effects in positive direction out of 30 crosses evaluated. The crossesL4T2 and L4T4recorded significant positive *sca* effect at all the locations and over all locations. The top 5 specific crosses among them were L4T4 (4.73), L6T5 (4.73), L4T2 (4.54), L2T5 (3.64) and L6T1 (3.44). The cross L6T5 (low × high) was identified as good specific cross combination based on positive *sca* effects and *per se* performance. The cross involving low x high *gca* effects resulted in superior combinations which may be due to complementary gene action

4.3.3.16 Amylose content

***gca* effects**

At Jagitial location, estimates of *gca* effects varied from -1.34 (L6) to 1.69 (L2) among lines while in testers, range was from -0.96 (T5) to 0.55 (T1). Three lines L6 (-1.34), L3 (-1.32) and L1 (-0.76) showed significant negative *gca* effect and in testers *viz.*, T5 (-0.96).

Range of *gca* effects at Warangal location was from -1.44 (L1) to 1.16 (L5) in lines and from -0.96 (T5) to 0.93 (T3) in testers. Significant negative *gca* effects exhibited by L1 (-1.44) and L6 (-0.66) lines and in testers T5 (-0.96) and T1 (-0.47).

At Hyderabad location, estimates of *gca* effects varied from -1.68 (L6) to 1.70 (L2) in lines while in testers, range was from -0.80 (T5) to 0.36 (T4).Three lines L6 (-1.68), L3 (-1.11) and L1 (-0.35) showed significant negative *gca* effect and in testers, T5 (-0.80).

In the present investigation, amylose content seems to be mostly under the control of non-additive gene action since in pooled analysis the *gca* variance (0.10) was less than *sca* variance (3.47).The present findings are in accordance with the results of Sharma and Mani (1998).

In pooled analysis, the estimates of *gca* effects revealed that L6 (-1.22), L1 (-0.85) and L3 (-0.75) among lines and T5 (-0.91) among testers were good general

combiners. Among the lines L1 and L6and in testers T5 were identified with significant negative *gca* effects at all locations as well as in pooled analysis. These lines can be utilized in basic breeding programmes for improvement of this trait.

***sca* effects**

At Jagitial location, estimates of *sca* effects varied from -4.38 (L2T4) to 3.59 (L2T2). Thirteen hybrids recorded significant negative *sca* effects. Top performing crosses identified among them were L2T4 (-4.38) followed by L5T4 (-3.60) and L1T2 (-3.12).

Range of *sca* effects at Warangal location, for amylose content was from -3.39 (L2T4) to 2.96 (L2T2). 12 crosses possessed significant *sca* effects at this location. The superior crosses identified among them were L2T4 (-3.40), L6T3 (-3.20) and L1T5 (-2.16).

For amylose content at Hyderabad location, *sca* effects ranged from -2.53 (L5T4) to 3.74 (L3T5). Among crosses, ten hybrids displayed significant negative *sca* effects. The top three crosses were L5T4 (-2.53) followed by L2T3 (-2.41) and L5T5 (-2.34).

In pooled analysis, twelve crosses recorded significant negative *sca* effects. The top performing three specific crosses among them were L2T4 (-3.07), L5T4 (-2.38) and L2T3 (-1.92). Among the crosses, L1T2, L2T3, L2T4, L3T1, L3T2, L4T3, L5T4 and L6T2exhibited significant negative *sca* effects at all locations and also in pooled analysis. From the above crosses LIT5 (high × high), L6T2 (high × low), L1T2 (high × low), L3T1 (high × low), L3T2 (high × low), L4T5 (low × high), L5T4 (low × high), L2T3 (low × low), L2T4 (low × low), L4T1 (low × low), L4T3 (low × low) and L5T4 (low × low) 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. The crosses involving high × low or low high effects resulted in superior combinations which may be due to complementary gene action. The cross between two low combiners revealed the presence of non-additive inter allelic interaction.

A perusal of *gca* effects from pooled analysis revealed that none of the parent recorded significant *gca* effects for all the characters studied. Among lines, L3

(MandhyaVijaya) and L6 (Phalguna) lines recorded significant positive *gca* effects for grain yield plant^{-1}. In addition to this, L6 had significant positive *gca* effect for productive tillers per plant, panicle length, number of grains per panicle, kernel length, milling per cent, alkali spreading value and it showed significant negative effect for amylose content. L3line exhibited significant positive *gca* effect for number of grains per panicle, milling recovery and head rice recovery while negative effects for kernel breadth and amylose content. In case of bran oil content, L1 (Keshari) and L5 (Kandagiri) lines exhibited significant positive gca effects.

Among testers T1(NDR359) and T5 (MTU1010) recorded significant positive *gca* effects for most of the characters *viz*., grain yield per plant, panicle length, 1000-grain weight, kernel length, milling percent, head rice recovery, water uptake while negative significant *gca* effects was recorded for days to 50 % flowering. In addition to these characters, T1 tester exhibited desirable significant positive *gca* effect for number of grains per panicle and the tester T5 possessed significant positive *gca* effect for L/B ratio whereas negative effects for amylose content. However, among testers, T2 (IR64) and T3 (Swarna) showed significant positive *gca* effects in desired direction for bran oil content.

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 transgressive segregants. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system. The crosses between two low combiners producing crosses with significant *sca* effect revealed the role of non-additive interallelic interaction. This may be due to high nicking ability/genetic diversity of parents involved. This component may be exploited through heterosis breeding. Similar findings were observed by Shivani *et al.* (2009).

4.4 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).

Commercial exploitation of heterosis in rice is profitable and it is important that the crosses are compared with released varieties rather than merely comparing with their mid / better parents. So in the present study the performance of the experimental crosses were compared with that of the most popular varieties 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 MTU1010 for yield and quality characters but over Keshari for bran oil content at different locations and in pooled analysis are presented in table 4.4.1. Based on overall performance (*per se* performance, positive *sca* effect and standard heterosis) the best heterotic cross combinations identified for yield, its components and quality characters were presented in table 4.4 .2 and were discussed character-wise hereunder.

4.4.1 Days to 50% Flowering

Standard heterosis for days to 50% flowering at Jagitial location ranged from -11.51 (L1T2) to 26.64 (L2T3). Three cross combinations recorded significant negative heterosis at this location. The range of standard heterosis at Warangal location was from -16.16 (L1T2) to 24.58 (L1T3) and three cross combinations exhibited significant negative standard heterosis over standard check.

At Hyderabad location, standard heterosis for this trait varied from -23.64 (L1T2) to 26.91 (L1T3) and six cross combinations exhibited significant negative standard heterosis.

From the pooled analysis, standard heterosis range for days to 50% flowering was from -16.89 (L1T2) to 25.91 (L1T3) and four hybrids recorded significant standard heterosis over standard check in desired direction. Two cross combinations exhibited significant negative standard heterosis at all locations and also in pooled analysis. Based on overall performance (*per se, sca* effect and standard heterosis) the top specific combiners identified for this trait were L1T2 (-16.89), L5T5 (-10.73), L1T1 (-4.68)and L2T2 (-1.94).

For this trait both positive and negative standard heterosis was observed by Singh *et al.* (2006), Gouri Shankar *et al.* (2010) and Tiwari *et al.* (2011).

4.4.2 Plant Height

Estimates of standard heterosis for plant height at Jagitial location was from -12.82 (L3T2) to 33.90 (L4T1). Significant negative heterosis was recorded by 7 cross

combinations. At Warangal location, estimates of standard heterosis varied from -16.16 (L5T3) to 24.58 (L1T3) among cross combinations. Further, significant negative heterosis was recorded by three cross combinations.

Standard heterosis for plant height at Hyderabad location, ranged from -3.96 (L3T2) to 35.83 (L2T1) and three cross combinations exhibited significant negative heterosis.

In pooled analysis, plant height range was from -2.97 (L1T2) to 34.36 (L2T1) and only one cross combination (L1T2) exhibited significant negative standard heterosis. None of the cross combinations recorded significant negative standard heterosis at different locations as well as pooled analysis. Highest significant negative heterosis was recorded by L1T2 (-2.97) and superiority of this cross combination confirmed by *per se* performance and high *sca* effects.

For the trait plant height, both positive and negative heterosis over standard check were recorded by Chaudhary *et al.* (2007), Rosamma and Vijayakumar (2007), Chandirakala *et al.* (2010), Gouri Shankar *et al.* (2010), Kumar Babu *etal*. (2010) and Tiwari *et al.* (2011).

4.4.3 Panicle length

At Jagitial location, panicle length showed standard heterosis over standard check from -40.69 (L5T4) to 13.52 (L2T1). Out of 30 cross combinations only five cross combinations possessed significant positive standard heterosis. Estimates of standard heterosis at Warangal location varied from -29.08 (L5T4) to 13.68 (L1T1). Four cross combinations recorded significant positive heterosis over standard check MTU1010.

Panicle length at Hyderabad location, exhibited standard heterosis ranging from -21.44 (L2T4 and L5T5) to 24.01 (L6T1) and among 30 cross combinations, five cross combinations revealed significant positive standard heterosis over check MTU1010.

In pooled analysis, a range from -28.09 (L5T4) to 14.99 (L6T1) was recorded for panicle length and six cross combinations exhibited significant positive standard heterosis over standard check MTU 1010. Out of 30 cross combinations evaluated only two cross combinations (L1T1 and L6T1) were found to have highly significant positive heterosis over standard check MTU 1010 at all locations and over locations. The

potential specific cross combinations identified as per *per se* performance and *sca* effects were L6T1 (14.99), L1T1 (14.65), L5T1 (7.89) and L3T5 (5.14). Earlier workers Seetaramaiah *et al.* (1999), Pandya and Tripathi (2006) and Chandirakala *et al.* (2010) reported positive standard heterosis for panicle length.

4.4.4 Number of productive tillers per plant

Among the cross combinations at Jagitial location standard heterosis ranged from -48.48 (L2T4) to 9.09 (L6T5) whereas at Warangal location, it varied from -37.50 (L2T1) to 7.50 (L1T5) and none of the cross combinations showed significant positive standard heterosis in both the locations.

The range of standard heterosis at Hyderabad location was from -38.89 (L2T1) to 16.67 (L3T2 and L3T5) and four cross combinations recorded significant positive heterosis over superior check MTU1010.

A range of -37.61 (L2T1) to 8.26 (L6T5) was observed for number of productive tillers per plant in pooled analysis. Two cross combinations *viz.*, L6T5 and L1T5 recorded significant positive standard heterosis over standard check. This trait directly contributes towards grain yield. None of the cross combinations possessed significant positive standard heterosis at all locations and also in pooled analysis. The best heterotic cross combination identified based on *per se* performance and *sca* effects was L1T5 (5.50).

Singh *et al.* (2006), Rosamma and Vijayakumar (2007), GouriSankar *et al.* (2010), Kumar Babu *et al.* (2010) and Tiwari *et al.* (2011) reported both positive and negative heterosis in their studies.

4.4.5 Number of grains per panicle

Among the cross combinations at Jagitial location, standard heterosis ranged from -26.09 (L5T3) to 80.71 (L3T3) and twenty three cross combinations recorded significant positive standard heterosis. At Warangal location, standard heterosis varied from -32.38 (L4T3) to 39.43 (L3T3). Among cross combinations, twelve cross combinations showed significant positive standard heterosis at this location.

Standard heterosis for grains per panicle at Hyderabad location ranged from -47.92 (L5T1) to 50.61 (L4T1) and four cross combinations exhibited significant positive standard heterosis.

A range of standard heterosis from -32.82 (L3T4) to 42.65 (L3T3) was observed in pooled analysis. Eleven cross combinations *viz.,* L1T1, L2T1, L2T3, L2T5, L3T1, L3T3, L3T5, L4T1, L6T1, L6T3 and L6T4 showed significant standard heterosis for number of grains per panicle over standard check. Three cross combinations *viz.*, L2T1, L3T3 and L4T1 exhibited significant positive standard heterosis at all locations as well as in pooled analysis. Based on overall performance the best specific cross combinations were L3T3 (42.65), L4T1(37.61), L6T4 (19.98), L1T1 (19.42), L2T5 (10.56) and L3T5 (9.75).Standard heterosis of both positive and negative was observed by Singh *et al*. (2006), Gouri Shankar *et al*. (2010), Kumar Babu e*t al.* (2010) and Tiwari *et al.* (2011).

4.4.6 1000-grain weight

At Jagitial location, the cross combination L2T4 (-35.42) recorded lowest test weight and L2T1 (43.97) recorded highest 1000-grain weight. Eight cross combinations exhibited significant positive standard heterosis. The range of standard heterosis at Warangal location, varied from – 32.71 (L6T4) to 31.56 (L6T1). Six cross combinations recorded significant positive standard heterosis over standard check.

1000-grain weight at Hyderabad location, exhibited a range from -27.98 (L5T2) to 57.28 (L2T1). Eleven cross combinations revealed significant positive standard heterosis over standard check.

In pooled analysis this trait recorded a range from -30.62 (L5T2) to 43.22 (L2T1). Nine cross combinations showed significantly greater standard heterosis over standard check MTU 1010. The cross combinations L1T5, L2T1, L4T1, L4T5, L5T1 and L6T1 displayed significant positive standard heterosis for 1000-grain weight at all locations and also in pooled analysis. The best performing cross combinations identified based on *per se* performance, heterosis and *sca* effects were L2T1 (43.22), L6T1 (38.66), L5T1 (27.65), L1T5 (18.43), L4T5 (12.95) and L5T5 (12.80).

Annadurai and Nadarajan (2001), Singh *et al.* (2006), Gouri Shankar *et al.* (2010), Kumar Babu e*t al*. (2010) and Tiwari *et al.* (2011) reported both positive and negative standard heterosis for this trait.

4.4.7 Grain yield per plant

Range of standard heterosis at Jagitial location for grain yield was from -33.28 (L1T3) to 79.47 (L1T5) and seventeen cross combinations recorded significant positive standard heterosis over check.

Among the 30 cross combinations evaluated against standard check, L1T3 (-43.36) recorded lowest standard heterosis and L6T1 (43.23) recorded highest standard heterosis at Warangal location. Significant positive standard heterosis was exhibited by twelve cross combinations *viz.,* L1T1, L1T5, L2T1, L2T3, L3T1, L3T2, L3T5, L4T1, L5T1, L6T1, L6T4 and L6T5.

Standard heterosis at Hyderabad location was ranged from -50.88 (L3T4) to 44.10 (L1T5) and eight cross combinations *viz.*, L1T5, L3T1, L3T3, L4T1, L4T4, L4T5, L5T5 and L6T1recorded significant positive standard heterosis over standard check.

Standard heterosis for grain yield ranged from -39.45 (L1T3) to 50.37 (L3T1) in pooled analysis and sixteen cross combinations *viz.,* L1T1, L1T5, L2T1, L3T1,L3T2, L3T3, L3T5, L4T1, L4T5, L5T1, L5T4, L5T5, L6T1, L6T3, L6T4 and L6T5 registered significant positive standard heterosis. The cross combination L3T1 exhibited the highest heterosis (50.37%) followed by L1T5 (45.37%), L6T1 (44.54%), L4T1 (35.49%) and L3T3 (29.86%).

The present investigation recorded a high order of standard heterosis for grain yield. Four cross combinations L1T5, L3T1, L4T1 and L6T1 registered significant positive standard heterosis over standard check at all locations and also in pooled analysis. Based on *per se* performance positive *sca* effects and heterosis superior combinations identified were L3T1 (50.37), L1T5 (45.37), L6T1 (44.54), L3T3 (29.86), L6T3 (11.26) and L5T4 (9.10).

Negative to positive heterosis over standard check reported by Singh *et al.* (2006), Rosamma and Vijayakumar (2007), Gouri Shankar *et al.* (2010), Kumar Babu e*t al.* (2010) and Tiwari *et al.* (2011).

The cross combinations L1T5 and L6T5 in pooled analysis showed significant positive standard heterosis for number of productive tillers per plant and 1000-grain

weight. This indicates that yield attributes helped the cross combinations to get high heterosis for grain yield per plant.

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

Based on *per se* performance, significant *sca* effects and heterosis for yield in pooled analysis the crossesL3T1, L1T5, L6T1, L3T3, L6T3 and L5T4 recorded high *per se* performance (34.13, 33.00, 32.81, 29.48, 25.26, 24.77 g), significant *sca* effects (3.16, 7.70, 1.41, 6.00, 1.34, 3.09 respectively) and standard heterosis (50.37%, 45.37%, 44.54%, 29.86% , 11.26%, 9.10%) over the standard check MTU 1010 for grain yield per plant.

4.4.8 Kernel length

At Jagitial location, kernel length showed standard heterosis over standard check from -29.00 (L1T3) to 19.54 (L4T1). Out of 30 cross combinations fourteen cross combinations possessed significant positive standard heterosis. Estimates of standard heterosis at Warangal location varied from -23.04 (L4T3) to 20.93 (L4T1). Twelve cross combinations recorded significant positive heterosis over standard check.

Kernel length at Hyderabad location, exhibited standard heterosis ranging from -26.73 (L1T3) to 18.84 (L4T1) and among cross combinations, fourteen cross combinations revealed significant positive standard heterosis over check MTU 1010.

In pooled analysis, a range from -22.34 (L1T3) to 19.77 (L4T1) was recorded for kernel length and fourteen cross combinations exhibited significant positive standard heterosis over standard check MTU 1010. Out of 30 cross combinations evaluated nine cross combinations *viz.*, L1T1, L2T1, L2T2, L3T1, L4T1, L4T5, L5T2, L6T1, L6T2, L6T4 and L6T5 were found to have highly significant positive heterosis over standard check MTU 1010 at all locations and over locations. The top 3 potential specific cross combinations identified as per *per se* performance and *sca* effects wereL4T1 (19.77), L2T1 (15.75) and L2T2 (15.12). Earlier workers Krishna Veni *et al. (*2005) and Singh (2005) reported both positive and negative standard heterosis for kernel length.

4.4.9 Kernel breadth

Estimates of standard heterosis for kernel breadth at Jagitial location was from -15.67 (L2T3) to 39.01 (L6T1). Significant negative heterosis was recorded by six cross combinations. At Warangal location, estimates of standard heterosis varied from -10.15

(L3T3) to 37.06 (L6T1) among cross combinations. Six cross combinations recorded significant negative heterosis.

Standard heterosis for kernel breadth at Hyderabad location, ranged from -12.48 (L3T3) to 37.77 (L6T1) and seven cross combinations exhibited significant negative heterosis.

In pooled analysis, kernel breadth range was from -12.03 (L3T3) to 37.94 (L6T1) and six cross combinations (L1T3, L2T3, L3T3, L5T1, L5T4, L6T3) exhibited significant negative standard heterosis. Highest significant negative heterosis was recorded by L3T3(-12.03), L5T1 (-6.78), L6T3 (-6.66) and L1T3 (-6.55) and superiority of these hybrids confirmed by *per se* performance and high *sca* effects.

For the trait kernel breadth, both positive and negative heterosis over standard check were recorded by Krishna Veni *et al. (*2005).

4.4.10 L/B ratio

Among the cross combinations at Jagitial location, standard heterosis effects ranged from -22.60 (L1T3) to 22.82 (L2T2) and five cross combinations recorded significant positive standard heterosis. At Warangal location, standard heterosis varied from -31.95 (L4T3) to 15.86 (L3T3). Among the cross combinations, only three cross combinations showed significant positive standard heterosis at this location.

Standard heterosis for L/B ratio at Hyderabad location ranged from -24.53 (L4T3) to 22.41 (L3T3) and five cross combinations exhibited significant positive standard heterosis.

A range of standard heterosis from -25.37 (L4T3) to 20.34 (L3T3) was observed in pooled analysis. Six cross combinations *viz.*, L2T2, L3T3, L4T5, L5T2, L5T4 and L6T3 showed significant standard heterosis for L/B ratio over standard check. Three cross combinations *viz.*, L2T2, L3T3 and L5T2 exhibited significant positive standard heterosis at all locations as well as in pooled analysis. Based on overall performance the top 3 specific cross combinations were L3T3 (20.34), L2T2 (17.50) and L5T2 (11.90).Standard heterosis of positive and negative was observed by Krishna Veni *et al. (*2005) and Singh (2005).

4.4.11 Bran oil content

Range of standard heterosis at Jagitial location, for bran oil content was from -44.13 (L3T2) to 2.89 (L1T3) and at Warangal location, this trait exhibited standard heterosis from -44.05 (L6T1) to 0.89 (L1T3).

At Hyderabad location standard heterosis for bran oil content was from -39.47 (L4T1) to 0.89 (L1T2). In pooled analysis it varied from -42.12 (L6T1) to -1.61 (L1T3). None of the cross combinations exhibited significant positive heterosis over superior check (Keshari) at all the locations and over locations.

4.4.12 Milling percent

At Jagitial location, the cross combination L2T1 (-10.83) recorded lowest milling percent and L1T5 (9.21) recorded highest milling percent. Nineteen cross combinations exhibited significant positive standard heterosis. The range of standard heterosis at Warangal location, varied from -6.41 (L2T3) to 6.70 (L3T4 and L5T1). Eighteen cross combinations recorded significant positive standard heterosis.

Milling percent at Hyderabad location, exhibited a range from -5.87 (L5T2) to 7.62 (L4T1).Sixteen cross combinations revealed significant positive standard heterosis over standard check.

In pooled analysis milling per cent recorded a range from -5.55 (L2T3) to 6.56 (L6T1). Nineteen cross combinations showed significantly greater standard heterosis over standard check MTU 1010. The cross combinations L1T5, L3T4, L3T5, L4T4, L5T1 and L6T1 displayed significant positive standard heterosis for milling per cent at all locations and also in pooled analysis. The top 3 performing hybrids identified based on *per se* and *sca* effects were L6T1 (6.56), L1T5 (6.15) and L4T4 (6.07). These results were in agreement with the early findings of Singh and Lal (2005), and Shivani *et al*. (2009).

4.4.13 Head rice recovery

Range of standard heterosis at Jagitial location for head rice recovery was from -13.61 (L2T1) to 10.12 (L4T3) and seven cross combinations recorded significant positive standard heterosis. Among the 30 cross combinations evaluated against standard check, L1T2 (-11.99) recorded lowest standard heterosis and L3T4 (2.08)

recorded highest standard heterosis at Warangal location. None of the cross combinations showed significant positive standard heterosis at this location. Standard heterosis at Hyderabad location was ranged from -12.36 (L2T1) to 2.60 (L4T1 and L6T1) and three cross combinations *viz.*, L4T1, L4T4 and L6T1recorded significant positive standard heterosis over standard check.

Standard heterosis for head rice recovery ranged from -9.92 (L2T5) to 6.33 (L5T4) in pooled analysis and four cross combinations *viz.*, L1T5, L4T4, L5T4 and L6T1 registered significant positive standard heterosis. None of the cross combinations registered significant positive standard heterosis over standard check at all locations and also in pooled analysis. Based on *per se* performance and positive *sca* effects superior combinations identified were L6T1 (3.66), L4T4 (2.08) and L1T5 (1.55).

Head rice recovery is most important among milling indices, as the economic value of the rice is determined by percentage of unbroken rice kernels. Negative to positive heterosis over standard check reported by Singh (2005), Singh and Lal (2005), and Shivani *et al*. (2009).

4.4.14 Alkali spreading value

Among the cross combinations at Jagitial location, standard heterosis effects ranged from -30.89 (L5T4) to 48.44 (L6T4) and fourteen cross combinations recorded significant positive standard heterosis. At Warangal location, standard heterosis varied from -29.80 (L5T1) to 46.35 (L6T4). Among the cross combinations, thirteen cross combinations showed significant positive standard heterosis at this location.

Standard heterosis for alkali spreading value at Hyderabad location ranged from -15.18 (L5T4) to 57.22 (L6T4) and 23 cross combinations exhibited significant positive standard heterosis.

A range of standard heterosis from -25.46 (L5T4) to 50.54 (L6T4) was observed in pooled analysis. Twenty cross combinations showed significant standard heterosis for alkali spreading value over standard check. Ten cross combinations *viz.*, L1T3, L2T2, L3T2, L3T3, L3T4, L3T5,L4T3, L4T5,L5T2, L6T2 and L6T4 exhibited significant positive standard heterosis at all locations as well as in pooled analysis. Based on overall performance the top 3 specific cross combinations were L6T4 (50.42), L6T2(45.86) and L4T3 (37.42).Standard heterosis of positive was observed by Krishna Veni *et al.* (2005) and Singh (2005).

High alkali spreading value corresponded to low gelatinization temperature. Most of the cross combinations possessed Intermediate gelatinization temperature (alkali spreading value between 4-5) which is a desirable feature. Intermediate gelatinization temperature (alkali spreading value >4-5.4) was desirable for cross combinations exhibited by eleven cross combinations *viz.,* L1T1(4.78), L1T2(4.61), L1T4(4.30), L2T1(4.68), L2T3 (4.47), L2T5 (4.51), L3T1 (4.91), L3T4 (5.38), L4T2(5.10), L4T4 (5.10), L5T2 (5.40), L5T3(5.24), L5T5 (4.70), L6T1 (4.07), L6T3 (5.32), L6T5 (5.31) and check MTU 1010 (4.41).

4.4.15 Water uptake

Among the cross combinations at Jagitial location standard heterosis ranged from -12.50 (L3T2) to 33.33 (L2T2). Fifteen cross combinations noticed significant positive heterosis over superior check. At Warangal location it varied from -12.59 (L3T2) to 52.45 (L2T4) and 22 cross combinations showed significant positive standard heterosis.

The range of standard heterosis at Hyderabad location was from -23.31 (L3T4) to 43.56 (L5T4) and fourteen cross combinations recorded significant positive heterosis over standard check.

Water uptake is an important factor that indicates the amount of water and time required for cooking. A range of -10.89 (L3T2) to 36.44 (L5T4) was observed for water uptake in pooled analysis. Twenty two cross combinations recorded significant positive standard heterosis over standard check. Eight cross combinations, namely, L1T2, L2T1, L2T3, L2T4, L3T1, L4T2, L5T4 and L6T2 possessed significant positive standard heterosis at all locations and also in pooled analysis. The top 3 heterotic cross combinations identified were L5T4 (36.44), L2T4 (32.22) and L2T1 (29.11) based on *per se* performance and *sca* effects. Shivani *et al*. (2009) reported negative heterosis in her studies.

4.4.16 Gel consistency

At Jagitial location, gel consistency of cross combinations showed standard heterosis over standard check from -26.32 (L2T1) to 9.65 (L6T5). Out of 30 cross combinations only two cross combinations (L6T5 and L6T1) possessed significant positive standard heterosis. Estimates of standard heterosis at Warangal location varied

from -15.66 (L6T4) to 19.70 (L2T1). Thirteen cross combinations recorded significant positive heterosis over standard check.

Gel consistency at Hyderabad location, exhibited standard heterosis ranging from -30.17 (L4T3) to -0.43 (L2T5) and among cross combinations, none of the cross combinations revealed significant positive standard heterosis over check MTU 1010.

In pooled analysis, a range from -15.20 (L4T3) to -0.61 (L2T5) was recorded for gel consistency and none of the cross combinations exhibited significant positive standard heterosis over standard check MTU 1010.

Rice with soft to medium gel consistency is preferred one by most of the rice consumers. High flaky rice generally have a gel consistency of 40 mm or less, soft to medium soft rice have gels in the range of 41 to 60 mm and soft gel types have gels measuring 61 to 100 mm in the length. Soft gel consistency was exhibited by all the two checks and cross combinations in the study over locations.

4.4.17 Amylose content

Among the cross combinations at Jagitial location, standard heterosis effects ranged from -16.97 (L1T2) to 25.08 (L2T2) and ten cross combinations recorded significant negative standard heterosis. At Warangal location, standard heterosis varied from -21.36 (L1T5) to 16.47 (L2T2). Among cross combinations, ten cross combinations showed significant negative standard heterosis at this location.

Standard heterosis for amylose content at Hyderabad location ranged from -18.36 (L3T1) to 14.35 (L2T1) and 17 cross combinations exhibited significant negative standard heterosis.

A range of standard heterosis from -14.91 (L1T5) to 16.05 (L2T2) was observed in pooled analysis. Eleven cross combinations *viz.*, L1T2, L1T5, L3T1, L3T2, L2T4, L4T1, L4T3, L4T5, L5T4, L6T2 and L6T3 showed significant standard heterosis for amylose content over standard check. Based on overall performance the best three specific cross combinations were L1T5 (-14.91), L6T2 (13.73) and L1T2(-13.33)

Amylose content of rice determines the hardness or stickiness of cooked rice. Higher amylose content (>25%) gives non sticky soft or hard cooked rice. Rice varieties having 20-25% (Intermediate) amylose give soft and flaky cooked rice. Most of the

cross combinations studied exhibited intermediate amylose content over locations. Cross combinations *viz.*, L2T1, L2T2, L4T4and L5T3recorded high amylose content while two checks showed intermediate amylose content over locations.

Among the cross combinations studied, all the cross combinations exhibited greater than 55% of head rice recovery. Cross combinations possessed medium to slender (L1T2, L2T2, L3T3, L4T2, L4T4, L4T5, L5T2, L5T4, L5T5, L6T2, L6T3) kernels with intermediate gelatinization temperature (L1T1, L1T2, L1T4, L2T1, L2T3 L2T5, L3T1 , L3T4, L4T2, L4T4 , L5T2 ,L5T3, L5T5 , L6T1 , L6T3, L6T5), intermediate amylose content (except L2T1, L2T2, L4T4 and L5T3) and soft gel consistency.

Table 4.4.2. Most promising cross combinations for yield and quality characters based on *sca* effects, *per se* performance and heterosis

Cross	Characters
Keshari× MTU1010	Grain yield per plant, 1000-grain weight, number of productive tillers per plant, kernel length, milling per cent, head rice recovery, water uptake and amylose content
MandhyaVijaya×Swarna	Grain yield per plant, Number of grains per panicle, kernel length, kernel breadth and L/B ratio
Phalguna × NDR359	Grain yield per plant, 1000-grain weight, panicle length, milling per cent and head rice recovery
MandhyaVijaya× NDR359	Grain yield per plant, kernel length and amylose content
Phalguna ×Swarna	Grain yield per plant, kernel breadth L/B ratio and milling per cent
Kandhagiri× RPBio226	Grain yield per plant, L/B ratio, water uptake and amylose content.

Table 4.4.3. Most promising cross combinations for bran oil content based on *per se* performance correlating with optimum grain yield per plant.

Cross	Bran oil content (%)	Grain yield per plant (g)
Keshari× IR64	16.20	22.20
Kandagiri× RP Bio226	14.10	24.80
Keshari× NDR359	13.70	25.70
Phalguna × MTU1010	13.70	26.00
Kandagiri× MTU1010	13.30	26.40

4.5 Stability Analysis

4.5.1 Eberhart and Russell's Stability model

The presently cultivated varieties and hybrids though having high seed yield potential they are unpredictable in their performance even under less varied conditions of cultivation. Lack of varieties and hybrids suitable to specific location accounts for the decline in the area and productivity of rice, apart from the yield losses due to biotic and abiotic stresses. This warrants the attention of the plant breeders to evolve superior varieties that would sustain well in different environmental conditions.

The results of pooled analysis of variance for stability as devised by Eberhart and Russell (1966) were presented in (Tables 4.5.1 and 4.5.2). The genotypes showed significant differences for all the characters when tested against Pooled error. Environments showed highly significant differences for all the characters under study except 1000-grain weight and kernel length whereas genotype × environment interaction components showed significant differences for all the characters when tested against pooled error, indicating wide differential behavior of genotypes in changing environments. Significance of environment (linear) component for all the characters except test weight and kernel length, when tested against pooled deviation indicated that the genotypes responded linearly for most of the characters under study.

The Genotype × Environment (linear) interaction was significant for number of productive tillers per plant, number of grains per panicle, kernel length and bran oil content when tested against pooled deviation, which suggested that the performance of genotypes across the environments could be predicted for these traits with great precision, as reported by Waghmode *et al.* (2011) and Lal and Singh (2012). Both linear and non-linear components were significant for number of productive tillers per plant, number of grains per panicle, kernel length and bran oil content indicating the importance of both the components in determining the stability of these traits and these results were confirmed by Gourishankar *et al.* (2008), Panwar *et al.* (2008) and Dushyanthakumar *et al.* (2010). Significance of pooled deviations for all the characters indicated that the performance of genotypes is entirely unpredictable in nature as such, importance of non–linear component in determining interaction of genotypes with environments has to be considered. Biswas *et al*. (2011) and Subudhi *et al.* (2012) also reported similar findings. Early flowering, dwarfness and less kernel breadth are desirable in rice, negative values were treated on favourable side and for rest of the traits positive values were considered as desirable. Environmental index for different characters at three locations were given in table 4.5.3.

Stability parameters for bran oil content, yield and quality characters under investigation were presented in Table 4.5.4.

4.5.1.1 Days to 50 % flowering

The pooled analysis of variance for this character indicated significant differences among genotypes and environments and further partitioning of MSS due to G × E into linear and non-linear revealed predominant role of non-linear component. Similar results were obtained by Dushyanthakumar *et al.* (2010) and Ahmad Ramezanil *et al.* (2011) earlier.

The mean value for this trait varied from 80.89 (L1T2) to 122.56 (L1T3). Environment 3 (-9.70) was found to be favourable for this trait. Among the cross combinations L3T1(μ=103.33, b_i=1.03, S^2d_i=-0.90), LIT1 (μ=92.78, b_i=1.05, S^2d_i=2.30) and L1T2(μ=80.89, b_i =1.13, S^2d_i=-0.68) were identified as a stable one's having low mean than grand mean with regression coefficient near 'unity' and non–significant deviation from regression. The cross combinations L2T2 (μ = 95.44, b_i = 1.37, S^2d_i = -0.44) and L3T5 (99.89, b_i =1.54, S^2d_i=1.67) having low mean, regression coefficient greater than 'unity' and non-significant deviation from regression were

found to be suitable for better environment. Regression coefficient less than one (b_i<1) with low mean than general mean and non-significant deviation from regression were observed in L5T5 (μ = 86.89, b_i = 0.83, S^2d_i = -0.70), L5T2 (μ = 102.22, b_i = 0.65, S^2d_i = -0.75) and L6T1 (μ = 104.67, b_i = 0.82, S^2d_i = 1.33). These cross combinations perform better in unfavorable environments with early flowering.

In cross combinations *viz.*, L1T5 (μ=98.67, b_i =0.82, S^2di=6.34**), L2T4 (μ=99.00, b_i =1.40, S^2di=14.10**) , L2T5 (μ=103.22, b_i =1.19, S^2di=6.55**) , L5T1 (μ=97.22, b_i =0.65, S^2di=38.51**), L5T3 (μ=105.67,b_i =0.97, S^2di=26.96**) and L6T2 (μ =104.78, b_i =0.92, S^2di=22.61**)the performance has been found to be highly unpredictable because of their significant deviation from regression values and low mean than gran mean. Lavanya *et al.* (2005), Saidaiah *et al.* (2010c), Umadevi *et al.* (2010a) and Waghmode and Mehta (2011) also identified stable hybrids for days to 50% flowering.

4.5.1.2 Plant height

The significant pooled deviation for this character indicated that the performance of genotypes is highly unpredictable.

The mean values for this trait ranged from 93.59 (L1T2) to 129.60 (L2T1). Environment 1 (-16.65) was favourable for this trait. The cross combinations L2T4 (μ= 105.34, b_i =1.19, S^2di=-0.69), L3T3 (μ=107.28, b_i =1.25*, S^2di=-0.97) and L4T2 (μ=104.24, b_i=1.27, S^2di=-0.99) with low mean, regression coefficient greater than 'unity' and non–significant deviation from regression were suitable for favourable environment. For poor environment, the cross combination, L5T2 (μ=103.52, b_i =0.19*, S^2di=-0.97) with low mean and regression coefficient less than 'unity' was suitable.

. The cross combinations with unpredictable performance having significant deviation from regression values and mean lower than gran mean were L1T2 (38.99**), L1T3 (93.04**), L1T4 (55.29**), L2T2 (59.35**), L2T5 (7.68**), L3T2 (86.85**), L4T3 (9.25**), L4T5 (7.45**), L5T1 (16.77**), L5T3 (152.74**), L5T4 (10.21**), L5T5 (20.17**) and L6T4 (23.01**). Stable cross combinations for plant height were also reported by Lavanya *et al.* (2005) and Waghmode and Mehta (2011).

4.5.1.3 Panicle length

The mean value for this trait ranged from 16.47 (L5T4) to 26.33 (L6T1). Among all the environments, Environment 2 (E.I. = 2.201) was found to be most favourable for this trait. Among 30 cross combinations, 24 cross combinations exhibited non-significant deviation from the regression (S^2d_i) values *i.e.* the F_1s are within the range of minimum deviation from regression and whose performance can be predicted.

The stable cross combinations identified were L1T1 (μ= 26.26, b_i=0.91, S^2di=-0.23), L4T4 (μ=22.54, b_i=0.89, S^2di=0.01), and L6T3 (μ=22.31, b_i=1.07, S^2di=1.27) having high mean than grand mean, regression coefficient near to'unity' and non–significant deviation from regression. For better environment, the cross combinations *viz.*, L2T5 (μ=23.26, b_i=1.50, S^2di=-0.03), L3T3 (μ=22.15, b_i=1.20, S^2di=-0.09), L3T5 (μ=24.08, b_i=1.20, S^2di=0.72) and L5T1 (μ=24.71, b_i=1.29, S^2di=-0.34) with high mean, regression coefficient greater than 'unity' and non-significant deviation from regression were identified. The cross combinations *viz.*, L4T5, L5T2 , L6T1 and L6T5 were suitable for poor environments as they recorded high mean (23.54, 23.15,26.33,24.22) with regression coefficient (0.55, 0.75,0.74, 0.74) less than 'unity' and non–significant (0.02,0.41,0.23,-0.45) deviation from regression.

In case of two cross combinations, L1T5 (3.31**) and L2T1 (1.71*) the performance was un-predictable, due to significant deviations from regression. Lavanya *et al.* (2005), Umadevi *et al.* (2010) and Waghmode and Mehta (2011) also identified stable hybrids for panicle length.

4.5.1.4 Productive tillers per plant

Productive tillers per plant is an important yield contributing character in rice. Highly significant MSS due to G × E interaction for this character revealed that the genotypes interacted considerably with all environments. The significant pooled deviation for this character indicated that the performance of genotypes is highly unpredictable. Such results were also reported previously by Subhudhi *et al.* (2012).

The mean character for this trait varied from 7.56 (L2T1) to 13.11 (L6T5) and the environment 2 (EI: 0.611) was observed to be most favourable for this trait. The $_C$ross combinations *viz.*, L2T5 (μ=11.33, b_i=1.01, S^2di=-0.17) and L6T5 (μ=13.11, b_i=1.14, S^2di=-0.09) which have recorded high mean than grand mean (10.54) , regression

coefficient near 'unity' and non–significant deviation from regression were considered as stable for this trait.

Whereas three cross combinations, L1T5, L3T4 and L3T5 with high mean (12.78, 10.67, 12.44), regression coefficient (1.85, 2.72, 2.71) greater than unity and non–significant deviation from regression (0.26, 0.10, 0.27) were found suitable for better environment. In poor environment the cross combinations L2T2 (μ=10.56, b_i=0.62, S^2di=0.21), L6T1 (μ=11.89, b_i=0.52, S^2di=-0.07), L6T2 (μ=12.11, b_i= 0.74, S^2di=-0.05) and L6T4 (μ=11.89, b_i=0.62, S^2di=0.21) were suitable. Further, in case of L3T2 (1.68**), L4T1 (4.93**) and L5T3 (2.26**) the performance was found to be highly unpredictable, as they recorded significant deviations from regression. Earlier findings of Shanmuganathan and Ibrahim (2005), Saidaiah *et al.* (2010c), Umadevi *et al.* (2010) and Sreedhar *et al.* (2011) also recorded stable hybrids for this trait.

4.5.1.5 Number of grains per panicle

The pooled analysis of variance of three locations revealed that G × E interactions were significant for this character implying differantial response of genotypes. Arumugan *et al.*(2007), Panwar *et al.*(2008), Ramya and Senthilkumar (2008) also reported significant G x E interaction for this trait as observed in the present study.

The observed range was from 91.89 (L3T4) to 195.11 (L3T3) and environment 2 (11.159) was favourable for this trait. Among the cross combinations tested, 28 crosses exhibited significant deviations from the regression (S^2d_i) as such their performance cannot be predicted in the varying environments.

None of the cross combinations found stable for number of grains per panicle as they recorded significant deviations from the regression (S^2d_i).

4.5.1.6 1000- grain weight

Pooled analysis of variance indicated presence of significant G × E interaction for 1000-grain weight also (Sreedhar et al., 2011). Good amount of variation was found for this trait with a lowest value of 15.06 (L5T2) and highest value of 31.08 (L2T1). With regard to environments, environment 2 (0.349) was highly favourable for this trait. Twenty six cross combinations exhibited non-significant deviations from the regression (S^2d_i) values as such, their performance could be highly predicted. The cross combinations with high mean than grand mean, regression coefficient near to 'unity' and non-significant deviation from regression are L5T5 (μ=24.48, b_i=0.93, S^2di=-0.49)

and L6T1 (μ=30.09, b_i=1.01, S^2di= -0.47) were considered as stable for 1000 grain weight.

Only one cross combination, L1T2 (μ=21.94, b_i=0.04, S^2di=0.19) was identified for poor environment. In better environment, the cross combinations, L1T4 (μ=22.71, b_i=2.05, S^2di=0.09), L2T3 (μ=21.69, b_i=1.93, S^2di=1.06), L3T5 (μ=22.77, b_i=4.06, S^2di=-0.25), L4T1 (μ=25.67, b_i=3.53, S^2di=0.00), L4T5 (μ=24.51, b_i=1.67, S^2di=-0.48), L5T1(μ=27.70, b_i=1.37, S^2di=-0.30) and L6T5 (μ=23.78, b_i=1.33, S^2di= -0.28) with high mean, regression coefficient greater than 'unity' and non–significant S^2di fared better. Where as in case of certain cross combinations, L3T1 (5.24**) and L3T2 (12.96**) which had significant deviations from regression, 1000-grain weight was highly unpredictable. Stable hybrids for 1000-grain weight also reported by Babu *et al.* (2005), Lavanya *et al.* (2005), Shanmuganathan and Ibrahim (2005), Sreedhar *et al.* (2011) and Waghmode and Mehta (2011).

4.5.1.7 Grain yield per plant

High grain yield is the ultimate objective for any breeder to tackle the hunger problem of growing population. The component of G × E interaction was significant for grain yield which indicated that the grain yield per plant is highly variable with the changing environments. Earlier, Nayak A.R. (2008), Bhakta and Das *(*2008), Dushyantha Kumar *et al.*(2010), Biswas *et al.*(2011) and Subudhi *et al.*(2012) also reported similar results.

The mean values ranged from 13.74 (L1T3) to 34.13 (L3T1) with the grand mean of 24.55 and the environment 2 (2.563) was most favourable for this trait. Among the cross combinations studied, 12 cross combinations revealed non-significant deviations from the regression (S^2d_i) values, which implies that the genotypes were within the range of minimum deviation from regression and performance could be predicted with respect to these cross combinations.

The cross combinations are L3T1, L6T1, L4T1 and L6T5 were considered stable as they recorded high mean than grand mean (34.13, 32.81, 30.76, 26.00) with regression coefficient (1.12,1.11, 1.04, 0.92) near 'unity' and non–significant (-1.17,-1.22, 0.23,-1.18) deviation from regression. The cross combinations, L1T1 (μ=25.68, b_i=2.06*, S^2di=-1.17), L2T1 (μ=25.97, b_i=1.94, S^2di=-0.06) and L5T1 (μ=27.61, b_i=1.87*, S^2di=-1.21) with high mean, regression coefficient greater than 'unity' and non–significant deviation from regression performed well under better environment. The cross combination L5T5 which exhibited high mean (26.40) with regression

coefficient (-1.55) less than 'unity' and non–significant (0.21) deviation from regression were identified for unfavorable environments. The cross combinations showing unpredictable performance with highly significant deviation from regression were L1T5 (14.68**), L3T2 (46.42**), L3T3 (28.59**), L3T5 (30.24**), L4T5 (30.34**), L6T3 (8.92**) and L6T4 (13.43**).

4.5.1.8 Kernel length

Pooled analysis of variance for this character revealed highly significant differences among genotypes and environments and significant G X E interactions.

The mean value for this trait ranged from 4.55 (L1T3) to 7.02 (L4T1) and expression of the character was good in environment 1 (0.034). The cross combinations, L1T1(μ=6.34, b_i=2.53,S^2di=0.01), L1T5 (μ=6.19, b_i=5.24*, S^2di=-0.01), L2T1 (μ=6.79, b_i=4.27, S^2di=0.00), L2T2 (μ=6.75, b_i=4.26, S^2di=0.00), L3T3 (μ=6.20, b_i=2.09, S^2di=0.01), L5T2 (μ=6.59, b_i=2.08, S^2di=0.00), L5T5 (μ=6.02, b_i=1.58, S^2di=0.00), L6T4 (μ=6.24, b_i=2.02, S^2di=-0.01), L3T1 (μ=6.74, b_i=1.48, S^2di=-0.01) and L6T2 (μ=6.68, b_i=1.41, S^2di=0.00) were suitable for favourable environment because of high mean, regression coefficient greater than 'unity' in addition to non–significant deviation from regression.

With respect to poor environment, the cross combinations, L4T1 (μ=7.02, b_i=-0.64, S2di=-0.01) and L6T5 (μ=6.55, b_i=0.61, S2di=0.02) which recorded high mean with less than 'unity' regression coefficient and non–significant deviation from linearity were considered suitable. Un-predictable nature of variation was observed with the cross combination L4T5 (0.06**). Nayak A.R. (2008) also reported significant deviations in prediction of the performance of certain cross combinations for kernel length as observed in the present investigation.

4.5.1.9 Kernel breadth

The mean values for this trait ranged from 1.73 (L3T3) to 2.71 (L6T1) and environment 2 (0.032) was found to be favourable for this trait. Most of the cross combinations exhibited non-significant S^2d_i values whose performance could be predicted. Among the cross combinations, L1T3 (μ=1.84, b_i=0.79, S^2di=0.00) and L3T3 (μ=1.73, b_i=1.09, S^2di=0.00) were considered as stable because of low (desirable) mean, regression coefficient around 'unity' and non–significant deviation from regression.

Further, the cross combinations, L2T2 (μ=1.93, b_i=1.37, S^2di=0.00), L3T2 (μ=1.99, b_i=1.35, S^2di=0.00), L3T4 (μ=1.96, b_i=1.90, S^2di=0.00), L5T2 (μ=1.98, b_i=1.37, S^2di=0.00), L5T4 (μ=1.81, b_i=1.54, S^2di=0.00) and L6T3 (μ=1.84, b_i=1.39, S^2di=0.00) were observed to be suitable for better environment as they recorded low mean with greater than 'unit' regression and non–significant deviation from linearity.

In poor environment, the cross combinations, L2T5 (μ=1.99, b_i=0.42, S^2di=0.00), L4T2 (μ=1.92, b_i=0.34, S^2di=0.00), L4T4 (μ=1.91, b_i= 0.28, S^2di=0.00), L5T1 (μ=1.83, b_i= -0.68, S^2di=0.00) and L5T5 (μ=1.99, b_i=0.27, S^2di=0.00) were suitable. The cross combinations *viz.,* L1T2 (0.08**), L1T4 (0.02*), L2T3 (0.03**) and L2T4 (0.01*) showed significant deviation from regression.

4.5.1.10 L/B ratio

Higher L/B ratio is most desirable trait in rice from trade and consumers point of view. Kernel with L/B ratio more than 3.0 is considered as slender. Analysis of variance for this character pooled over 3 environments showed highly significant differences among genotypes and environments.

High amount of variability was observed for this character with lowest mean value of 2.22 (L4T3) to highest value of 3.58 (L3T3) and environment 1 (0.070) was found to be most favourable for expression of this trait. The cross combination *viz.,* L1T5 (μ=2.90, b_i=0.94, S^2di=-0.01) which recorded high mean than grand mean, regression coefficient near 'unity' in addition to non–significant deviation from regression was considered as stable for this trait. The cross combinations, L2T2 (μ=3.50, b_i=2.29*, S^2di=-0.01), L3T3 (μ=3.58 b_i=1.60, S^2di=0.00), L3T5 (μ=2.74, b_i=1.90,S^2di=0.00), L4T4 (μ=3.07,b_i=1.85, S^2di=0.01), L5T2 (μ=3.33, b_i=1.72, S^2di=0.00), L5T4 (μ=3.29,b_i=2.27,S^2di=0.01), L6T2 (μ=3.08, b_i=1.52, S^2di=-0.01 and L6T4 (μ=2.92, b_i=1.33, S^2di=-0.01) with high mean and b_i valuemore than 'unity' and non–significant deviation from regression were highly suitable for favorable environment. Whereas, cross combinations *viz.,* L2T5 and L5T5 were identified for poor environment in view of high mean (2.94, 3.02), regression coefficient (0.14, 0.52) less than 'unity' and non–significant S^2di estimate (0.01,-0.01).

Among cross combinations viz., L1T2 (0.32**), L4T2 (0.04*) and L6T3 (0.05**) the performance has been found to be highly unpredictable because of their significant deviation from regression values.

4.5.1.11 Bran oil content

Pooled analysis of variance for this character revealed highly significant differences among genotypes and environments and also the G x E interaction and further partitioning of MSS due to G × E into linear, non-linear revealed predominant role of non-linear component.

Bran oil content ranged from 9.92 (L6T1) to 16.86 (L1T3) in the present study and among the three environments, environment 3 (0.439) was found to be favourable for this trait. Among thirty cross combinations studied, 20 cross combinations showed non-significant deviation from the regression (S^2d_i) values. As the cross combinations were within the range of minimum deviation from regression, there was a scope to predict the variation in their performance.

The cross combination, L5T3 (μ=13.98, b_i=0.90, S^2di=-0.13), has recorded high mean than grand mean, regression coefficient near 'unity' and non–significant deviation from regression, as such, they were considered as stable for this trait. The cross combinations, L1T2 (μ= 16.23, b_i=1.66, S^2di=-0.30), L5T2 (μ= 14.83, bi=2.60, S^2di=0.02) and L6T5 (μ= 12.88, bi=3.49*, S^2di=0.31) were identified for better environment based on stability parameters.

The cross combinations, L1T1, L1T3, L5T4 and L5T5 were suitable for poor environment as they recorded high mean (13.72, 16.86, 14.05, 13.31), with regression coefficient less than 'unity' (-1.65,-2.59,-0.21, -4.09,) and non–significant deviations (0.02, 0.74,-0.31,-0.13) from regression. The cross combinations *viz.,* L1T4 (1.94**), L3T4 (1.28*) and L6T2 (1.44*) with significant deviations from regression exhibited unpredictable performance. Balalic *et al*. (2011) also reported stable hybrids for oil content as results of present study.

4.6 Character Association

Grain yield is a complex character and is dependent on its contributing traits. A study was envisaged on character association, to assess the relationships among bran oil content, yield and its components to have an insight into the causes for higher yield and bran oil in cross combinations. Further, location wise analysis helps understand the

variation in association under different environments and to identify a stable character influencing the yield for further concentration and emphasis in breeding programmes.

Simple correlations were worked out on bran oil content, yield and its contributing characters at Jagitial, Warangal and Hyderabad locations and also finally on pooled data (Table 4.6).

4.6.1 Days to 50 % flowering

This trait showed non-significant positive correlation with grain yield per plant in all the locations while it had significant positive correlation with grain yield per plant, panicle length, number of grains per panicle and L/B ratio over locations. In pooled analysis, this trait exhibited negative significant correlation with plant height, number of productive tillers per plant, 1000 grain weight, kernel length, kernel breadth and bran oil content. At Jagitial and Warangal, this trait had significant positive correlation with the plant height and number of grains per panicle but negative with bran oil content. Negative non-significant association observed for this trait with panicle length, number of productive tillers per panicle, 1000-grain weight, kernel length and kernel breadth whereas positive non-significant correlation with L/B ratio at Jagitial. At Warangal, days to 50% flowering was positively and non-significantly correlated with number of productive tillers per plant and kernel breadth but it showed negative non-significant association with panicle length, 1000 grain weight, kernel length and L/B ratio. Whereas at Hyderabad, this trait had a positive significant correlation with plant height and number of grains per panicle and non-significant with plant height, panicle length, kernel breadth and negative non-significant with number of productive tillers per plant, 1000- grain weight, kernel length, L/B ratio and bran oil content. Similar type of associations was reported by Krishna *et al.* (2008) and Abdul Fiyyaz *et al*. (2011) for grain yield per plant and Ravindra Babu *et al*. (2012) for panicle length.

4.6.2 Plant height (cm)

It associated positively with grain yield per plant, 1000–seed weight, kernel length and kernel breadth but negatively with bran oil content in all the locations and over locations. The pooled analysis indicated a negative significant association with panicle length, L/B ratio and a positive significant relation with number of productive tillers per plant but negative non-significant with number of grains per panicle. At Jagitial, this trait showed positive significant association with panicle length and non-significant

with number of grains per panicle while negatively correlated with number of productive tillers per plant. Plant height (Warangal location) exhibited significant positive association with panicle length, number of grains per panicle and non-significant with number of productive tillers per plant. At Hyderabad, this trait had positive non-significant association with panicle length and number of grains per panicle while negative with productive tillers per plant. In all the locations this trait showed negative non-significant association with L/B ratio.

The similar association with Krishna *et al.* (2008) for 1000 grain weight, kernel length and kernel breadth Sebesan *et al.* (2009) and Abdul Fiyyaz *et al.* (2011) for grain yield per plant.

4.6.3 Panicle length (cm)

Panicle length had positive and significant association with 1000–grain weight, kernel length, kernel breadth and grain yield per plant whereas negative significant association with bran oil content in all locations and in pooled analysis. In addition to this, at Jagitial, panicle length had positive significant correlation with number of grains per panicle while negative significant association with L/B ratio. At Hyderabad, this trait showed positive significant correlation with number of grains per panicle. In pooled analysis, negative significant association was observed with productive tillers per plant but non-significant with L/B ratio. Similar results were reported by Rajamadhan *et al.* (2011), Bhadru *et al.* (2012) and Ravindra Babu *et al.* (2012) for grain yield per plant and Krishna *et al.* (2008) for kernel length and 1000 grain weight.

4.6.4 Number of productive tillers per plant

This trait exhibited positive and significant association with grain yield per plant in Jagitial and pooled analysis. At Jagitial, this trait also showed positive significant correlation with number of grains per panicle, 1000-grain weight, kernel length, kernel breadth but negative association with bran oil content. In pooled analysis, number of productive tillers per plant had significant positive correlation with kernel length and kernel breadth while negative with L/B ratio.

Rajamadhan *et al.* (2011), Bhadru *et al.* (2012) and Ravindra Babu *et al.* (2012) also reported a strong association between productive tillers and grain yield per plant and Sakthivel (2001) for 1000 grain weight.

4.6.5 Number of grains per panicle

Number of grains per panicle had significant positive association with grain yield per plant and kernel breadth in all locations and pooled analysis. This trait showed positive significant correlation with kernel length in Warangal, Hyderabad and pooled analysis whereas significant negative association with bran oil content in Jagitial, Hyderabad and pooled analysis. In addition to this, this trait also exhibited significant positive association with 1000-grain weight, L/B ratio at Hyderabad and Warangal respectively.

Padmaja *et al*. (2011) and Zulqarnain *et al*. (2012) reported positive significant correlation with grain yield per plant as observed in the present study.

4.6.6 1000–grain weight (g)

It associated positively and significantly with kernel length, kernel breadth and grain yield in all locations and pooled analysis. Long bold grains have more length and breadth with increased 1000 seed weight, which results in higher yields. This trait showed negative significant association with L/B ratio (in Jagitial) and bran oil content (in all locations).

Krishna *et al.* (2008) also observed a positive correlation for 1000 grain weight among kernel length and kernel breadth and Yadav *et al.* (2011) and Zulqarnain *et al*. (2012) for grain yield per plant.

4.6.7 Kernel length (mm)

Kernel length had significant positive association with kernel breadth, L/B ratio and grain yield per plant while negative significant association with bran oil content in all locations and pooled analysis except Warangal. Krishna *et al.* (2008) reported a positive association between kernel length and kernel breadth and Mareker and Siddiqui (1996) for grain yield per plant.

4.6.8 Kernel breadth (mm)

This trait had a negative significant association with L/B ratio, bran oil content and positive significant association with grain yield per plant in all locations and pooled analysis. Kernel breadth and L/B ratio were negatively correlated as observed by Pankaj Garge *et al.* (2010) and Rajeswari *et al.* (2010).

4.6.9 L/B ratio

Higher L/B ratio is desirable, as grains with high L/B ratio will be classified as fine and fetch higher premium in the market. This trait exhibited negative correlation with bran oil in Jagitial and pooled analysis. In the present investigation positive and negative significant correlation was observed with grain yield at Jagitial and in pooled analysis respectively. L/B ratio had no significance with grain yield in Warangal and Hyderabad. Tara Satyavathi *et al.* (2001) and Pankaj Garge *et al.* (2010) were also reported that L/B ratio positively correlated with grain yield per plant.

4.6.10 Bran oil content (%)

This trait exhibited a negative significant association with grain yield per plant in all locations and over locations. The results were in agreement in with the findings of Ravindra Babu (2002), Satyanarayana *et al.* (2003) and Mijice *et al.* (2009).

4.6.11 Grain yield per plant (g)

The grain yield per plant had a significant positive association with days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000- grain weight, kernel length, kernel breadth whereas negative significant association with L/B ratio and bran oil content on overall basis. Variation was observed in the association between bran oil, grain yield and other components over different environments.

At Jagtial this trait had significant positive association with the plant height, panicle length, productive tillers per plant, number of grains per panicle, 1000 grain weight, kernel length, kernel breadth and length/breadth ratio and negatively correlated with bran oil content. At Warangal, it was positively associated with plant height, panicle length, number of grains per plant, 1000-grain weight, kernel length and kernel breadth but negatively with bran oil content. At Hyderabad, this trait had significant positive association with the plant height, panicle length, number of grains per panicle, 1000 grain weight, kernel length, kernel breadth and negatively correlated with bran oil content.

Similar kind of association with this trait was observed in finding of Krishna *et al.* (2008) and Abdul Fiyyaz *et al.*(2011) for plant height, Rajamadhan *et al.*(2011), Bhadru*et al.* (2012) and Ravindra Babu *et al.*(2012) for number of productive tillers per plant, Pankaj Garge *et al.*(2010), Padmaja *et al.*(2011), Zulqarnain *et al.*(2012) for

number of grains per panicle, Yadav *et al.* (2010), Zulqarnain *et al*. (2012) for 1000 seed weight and Ravindra Babu (2002), Satyanarayana *et al*. (2003) and Mijice *et al.* (2009) for oil content**.**

4.7 Path Coefficient Analysis

Correlation gives only the relation between two variables whereas, path coefficient analysis helps us to know the direct and indirect effect through other components by partitioning the correlations on grain yield. Hence, the path coefficient analysis was done to know the direct and indirect effects of different yield components and bran oil content on yield for 3 locations separately and in pooled analysis. This type of location wise and pooled analysis helps us to know the stable associations among the traits for use in future selections by plant breeders (Table 4.7.).

4.7.1 Days to 50 % flowering

Days to 50 percent flowering showed a positive direct effects on grain yield per plant at Hyderabad and in pooled analysis while negative direct effect at Jagitial and Warangal. It had indirect positive effects on yield through panicle length, 1000-grain weight, kernel length and bran oil content at Jagitial and Warangal. In pooled analysis, it had high positive indirect effect on grain yield through panicle length and number of grains per panicle whereas it expressed negative indirect effects mainly through plant height, number of productive tillers per plant and kernel breadth.

The direct negative effect of days to 50 per cent flowering on grain yield per plant was reported by Pankaj *et al*. (2010), Yadav *et al.* (2010), Rajamadhan *et al*. (2011), Panday (2012) and Ravindra Babu *et al*. (2012).

4.7.2 Plant height (cm)

Plant height had positive direct effect on grain yield per plant at all locations and over locations. It showed positive low indirect effects *via* days to 50% flowering, panicle length, number of grains per panicle, 1000-grain weight, kernel length and kernel breadth at Jagitial and Warangal. This trait recorded low positive indirect effects on grain yield through number of productive tillers per plant, 1000-grain weight, kernel length and kernel breadth in pooled analysis.

Similar results were reported by Mulugeta *et al.* (2012), Pandey *et al*. (2012) and Ravindrababu *et al*. (2012).

4.7.3 Panicle length (cm)

Panicle length had direct positive effect on grain yield per plant in all locations and over locations. In pooled analysis, this trait showed positive indirect effect on grain yield mainly through number of grains per panicle, 1000-grain weight, kernel length and kernel breadth and it had negative indirect effects through days to 50% flowering, plant height, productive tillers per plant and bran oil content. Results reported by Kole and Hasib (2008), Sathish Chandra *et al.*(2009) and Pankaj *et al*. (2010) were in agreement with the results obtained in the present investigation.

4.7.4 Number of productive tillers per plant

The direct contribution of this character to grain yield was positive and high at Jagitial and Warangal whereas negative low direct effect on grain yield was observed at Hyderabad and in pooled analysis. The indirect effects through other characters were found to be very low.The indirect effect *via* bran oil content was negative, not at higher magnitudes. Basavaraja *et al.* (2011), Padmaja *et al.* (2011), Bhadru *et al.*(2012), Pandey *et al*.(2012) and Ravindra Babu *et al.*(2012) reported a high positive direct effect of number of productive tillers per plant on grain yield per plant as was observed in the present investigation.

4.7.5 Number of grains per panicle

This trait had positive direct effect on grain yield per plant at Jagitial, Warangal and over locations but at Hyderabad negative effects were observed.

It had high indirect positive contribution mainly through plant height, kernel length and kernel breadth at Warangal while through bran oil content at Hyderabad and in pooled analysis. This trait also showed negative indirect effect on yield through kernel length and kernel breadth at Hyderabad location. Its contribution to yield was attributed to indirect effect through plant height as was reported by Rajamadhan *et al*. (2011) and Bhadru *et al.* (2012).

4.7.6 1000–grain weight (g)

The yield component, 1000-grain weight exhibited the direct positive effect on grain yield per plant at all the locations and also in pooled analysis. However, it revealed high indirect positive influence through plant height, panicle length, kernel length and kernel breadth in all locations.

It also had indirect negative influence on grain yield per plant through days to 50%flowering, L/B ratio and bran oil content in all locations while through plant height, panicle length, number of productive tillers per plant, kernel length and kernel breadth over locations. The results reported by Sathish Chandra *et al.* (2009), Padmaja *et al.* (2011), Bhadru *et al.*(2012) and Yadav *et al.*(2012) also indicated that 1000 -grain weight plays greater role for higher grain yield per plant. This component had very high impact on grain yield per plant, which is evident from highly significant correlation coefficients followed by direct effects at all the locations.

4.7.7 Kernel length (mm)

Kernel length had direct positive influence on grain yield at all the locations and over locations. The similar results were reported by Pankaj Garge *et al.* (2010) and Rajamadhan *et al.* (2011).

While it had indirect positive influence through panicle length, number of productive tillers per plant, number of grains per panicle, 1000-grain weight, kernel breadth and L/B ratio at Jagitial location , days to 50 per cent flowering, productive tillers per plant, kernel breadth and bran oil content at Warangal location, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000-grain weight, kernel breadth and L/B ratio at Hyderabad and over locations. This character appeared to play an important role in yield contribution directly.

4.7.8 Kernel breadth (mm)

Kernel breadth had direct positive influence on grain yield at all the locations and over locations. While it had high indirect positive influence mainly through panicle length, 1000-grain weight and kernel length at Warangal and *via* 1000-grain weight and kernel length at Hyderabad.

This trait also had some indirect negative contribution mainly through 1000- grain weight and kernel length at Jagitial location. However, it also had indirect negative effect through days to 50% flowering, kernel length, L/B ratio and bran oil content on over all basis. These results are in conformity with the finding of Krishna *et al.* (2008) and Yadav *et al.* (2012).

4.7.9 L/B ratio

L/B ratio had direct positive influence on grain yield at all the locations except over locations. While it had indirect positive influence through days to 50 % flowering,

number of productive tillers per plant and kernel length at Jagitial, number of grains per panicle, kernel length and bran oil content at Warangal location, kernel length and bran oil content at Hyderabad and plant height, panicle length, productive tillers per plant, number of grains per panicle, 1000-grain weight, kernel breadth and bran oil content over the locations.

It also had indirect negative contribution through plant height, panicle length, 1000- grain weight and kernel breadth in all the location while through days to 50% flowering and kernel length over locations. The similar results were reported by Krishna *et al.* (2008) and Nandeshwar *et al.* (2010).

4.7.10 Bran oil content (%)

This trait expressed negative direct effect on grain yield in all the locations as well as in pooled analysis. The results are in agreement with the findings of Siddiquey, M. N. H *et al*. (2006).

Its indirect effect through days to 50% flowering and panicle length was positive in all locations. Contrastingly, indirect effect of bran oil content was negative through productive tillers per plant, number of grains per panicle, kernel length, kernel breadth and L/B ratio at Hyderabad and through plant height, 1000-grain weight and L/B ratio at Warangal. In pooled analysis, it expressed negative indirect effects through all the characters except number of productive tillers per plant.

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

Path coefficient analysis revealed that kernel breadth exerted highest positive

direct effect on grain yield followed by panicle length, 1000-grain weight, number of grains per panicle, days to 50 % flowering, plant height and kernel length in over all locations. The negative direct effect was noticed on grain yield by number of productive tillers per plant, L/B ratio and bran oil content. The results were in conformity Bhadru *et al.*(2012), Pandey *et al.* (2012) and Ravindra Babu *et al.* (2012) for plant height, Rajamadhan *et al.* (2011) for kernel length, Krishna *et al.* (2008), Yadav *et al.* (2012) for kernel breadth, Siddiquey M. N. H *et al*. (2006) for oil content, Basavaraja *et al*. (2011), Ravindra Babu *et al*. (2012) for 1000 grain weight, Mulugeta seyoum *et al*. (2012) for number of productive tillers per plant and Rajamadhan *et al*. (2011), Ravindra Babu *et al*. (2012) for number of grains per panicle.

4.8.Estimation of Genetic Parameters in F2 Generation for Bran Oil Content

In F_2 generation of the cross combination Keshari×Swarna, the estimated value of PCV (28.03) is higher than GCV (20.50), it means that the apparent variation is not only due to genotypes but also due to the influence of environment. Selection for this trait sometimes may be misleading (Phundan Singh and Narayanan, 2000). Medium heritability (53.48) coupled with high genetic advance as per cent of mean (41.39) was observed for this trait indicating the presence of additive gene action. Hence this trait can be improved through simple selection procedures (Table 4.8.1 and 4.8.2).

4.9 Mapping of Gene(s) for Bran Oil Content in Rice using SSR Markers

Rice bran is considered as a waste that is normally discarded during rice processing. It is well known that it is a nature source of vitamins, minerals and anti-oxidants. Besides, it contains 18-23% of oil which contains significant amounts of essential fatty acids, and linoleic acid that are necessary in order to maintain full health as well as a broad range of nutraccutial compounds that have been demonstrated to have remarkable therapeutic properties. It is a popular as cookinig oil in several Asian countries including Japan, China, and India. Oil content vis-a-vis seed yield per unit area remains the most important breeding objective in this crop. The oil content is known to be quantitatively inherited and therefore, only limited success has been achieved in the improvement of the trait through conventional breeding in other oil seed

crops also. Genetic markers have allowed researchers to systematically map and characterize the loci affecting quantitative traits.

Recent developments in quantitative genetics making use of molecular markers allow the determination of the map positions and the relative contribution of the different loci to observed trait variation. An important application of this knowledge is *via* Marker Assisted Selection (MAS), where molecular markers linked to the loci determining variation for the trait can be used to select the most favourable genotype without a need of determining oil content by relatively complex and expensive assays in the breeding generations. For MAS, ultimately the genes underlying the variation of the trait are the best suited markers.

Till now there are no reports about the markers related to bran oil , but an attempt has been made to find out the bran oil related markers, For this study 30 SSR markers covering the twelve chromosomes in Rice was taken . The present investigation mapping of gene(s)for bran oil content is a step forward for identification of markers, and that can be used in marker assisted breeding for development of new cultivars with high bran oil.

4.9.1 Selection of Parents

Based on the phenotypic data of bran oil content, Keshari (High bran oil content) and Swarna (High yielding but low bran oil content) were used as parents for the development of mapping population.

4.9.2 Development of Mapping Population

Crosses were affected between the chosen Keshari and Swarna parents and F_1s was developed. The F_1 of the cross was selfed to generate F_2 and F_2 generation was further sown to carry out the genotyping.

4.9.3 Parental polymorphism studies:

Parental polymorphism survey between Keshari and Swarna was studied using 30 markers. Among, Keshari and Swarna 2 (6.6%) were polymorphic, 22 markers were monomorphic and 6 were not amplified.(Table 4.9.1).

Table.4.9.1. Parental polymorphism survey between Keshari and Swarna

Polymorphism	No. of markers	Markers
Polymorphic	2	RM1, RM5140
Monomorphic	22	RM5, RM154, RM630, RM3763, RM15337, RM15580, RM16343, RM16757, RM18857, RM20672, RM283, RM11, RM455, RM118, RM125, RM447, RM22622, RM2252, RM6543, RM560, RM144, RM852, RM19
Not amplified	6	RM16343, RM18888, RM20096, RM271, RM484, RM277

4.9.4 Screening of F_2 population with SSR markers

The two polymorphic markers identified in parental polymorphism . i.e RM1 present on the chromosome 1 and RM5140 on the chromosome 5 were used to screen the 132 F_2 plants derived from Keshari ×Swarna, to identify the bran oil associated regions in the chromosomes. The genotypic and phenotypic data was analyzed using Single Marker Analysis and R2 values values for this trait were presented in the Table 4.9.2.

Table: 4.9.2. R2 values for RM1 and RM5140 Markers

Trait	Marker	R_2 %	Probability
High Bran oil Content	RM1	0.59	0.72
	RM5140	14.40	0.006
Low Bran oil Content	RM1	0.11	0.84
	RM5140	3.00	0.001

RM1 (Chromosome-1) with high bran oil content (**R_2 %**= 0.59) and low bran oil content (**R_2%**=0.11), RM5140 (Chromosome-5) with high bran oil content (**R_2 %**=14.40) and low bran oil content (**R_2 %**=3.00). Two markers, RM1 and RM5140 showed association but RM5140 shows the highest F value (Probability less than 0.005) and therefore most likely linked to the bran oil content. These results were in conformity with Lang *et al.* (2013)

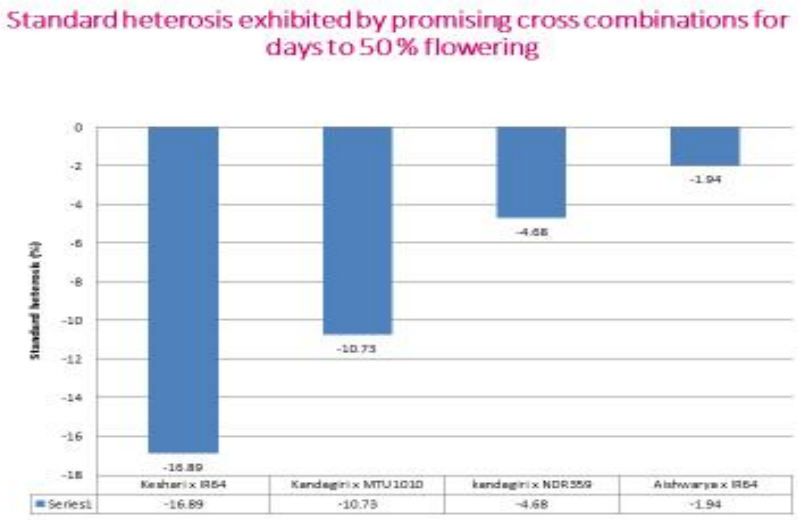


ILLUSTRATION No. 1

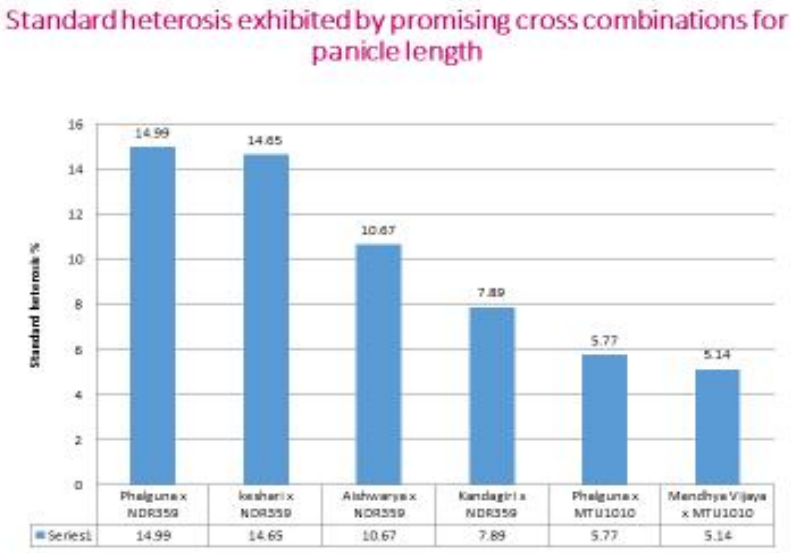


ILLUSTRATION No.2

Standard heterosis exhibited by promising cross combinations for 1000 grain weight (g)

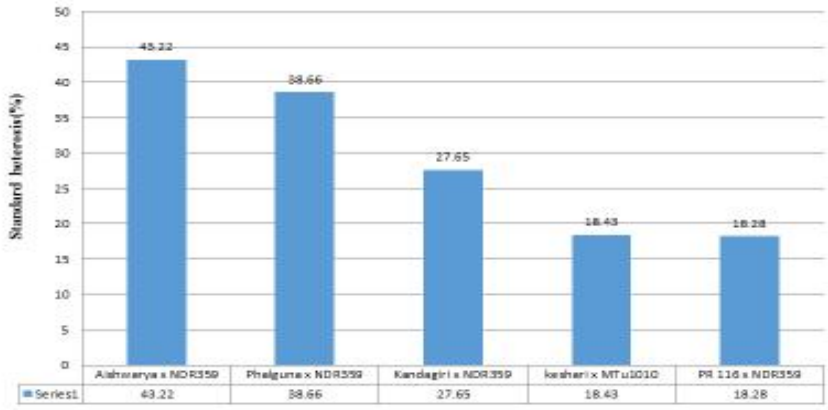
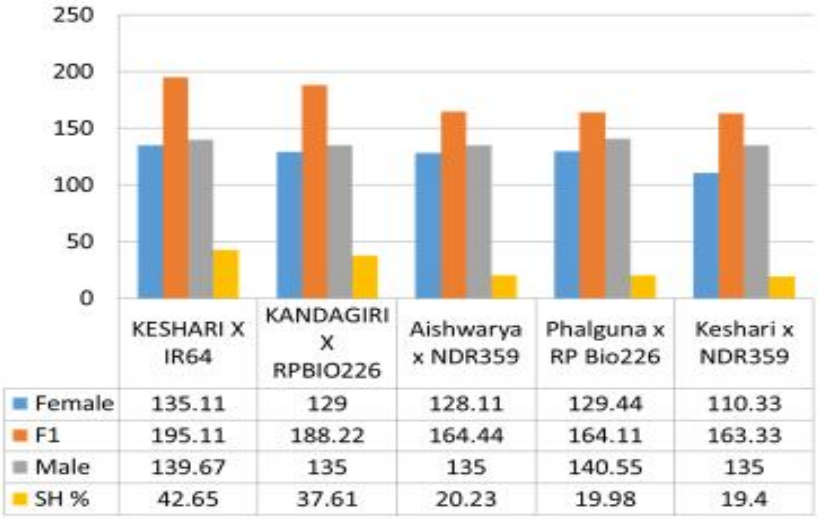


ILLUSTRATION No.3

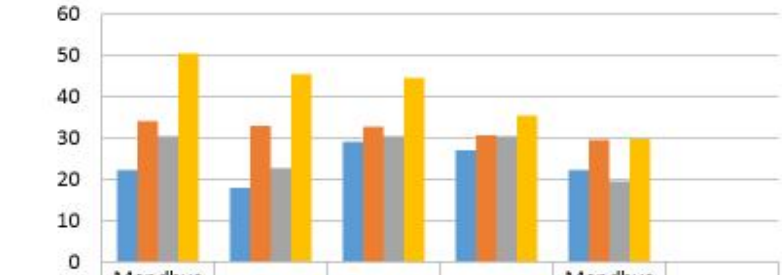
Comparison of parents, F1s and heterosis for number of grains per panicle



	KESHARI X IR64	KANDAGIRI X RPBIO226	Aishwarya x NDR359	Phalguna x RP Bio226	Keshari x NDR359
Female	135.11	129	128.11	129.44	110.33
F1	195.11	188.22	164.44	164.11	163.33
Male	139.67	135	135	140.55	135
SH %	42.65	37.61	20.23	19.98	19.4

ILLUSTRATION No.4

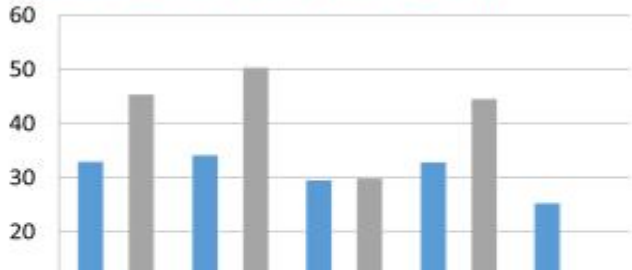
Comparison of parents, F1s and standard heterosis for grain yield per plant (g)



	Mandhya Vijaya x NDR359	Keshari x MTU1010	Phalguna x NDR359	PR116 x NDR359	Mandhya Vijaya x Swarna
Female	22.26	17.83	29.06	26.97	22.26
F1s	34.13	33	32.81	30.76	29.48
Male	30.55	22.7	30.55	30.55	19.42
SH %	50.37	45.37	44.54	35.49	29.86

ILLUSTARION No.5

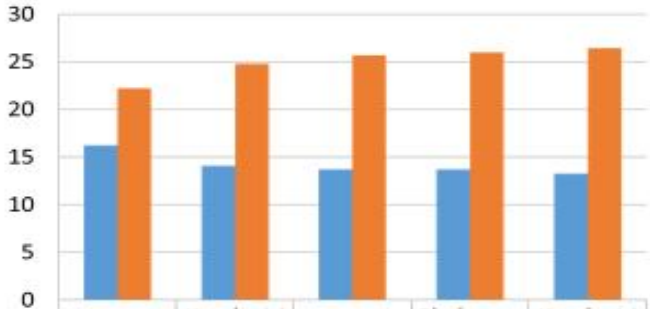
Mean performance, *sca* effect and standard heterosis in promising cross combinations for grain yield per plant (g)



	Keshari x MTU1010	Mandhya Vijaya x NDR359	Mandhya Vijaya x Swarna	Phalguna x NDR359	Phalguna x Swarna
Mean Performance	33	34.13	29.48	32.81	25.25
SCA Effects	7.7	3.16	6	1.41	1.34
SH %	45.37	50.37	29.86	44.54	11.26

ILLUSTRATION No.6

Most promising cross combinations for bran oil content based on per se performance correlating with optimum grain yield per plant



	Keshari x IR64	Kandagiri x RP Bio226	Keshari x NDR359	Phakguna x MTU1010	Kandagiri x MTU1010
Bran oil percent	16.2	14.1	13.7	13.7	13.3
Grain yield (g)	22.2	24.8	25.7	26	26.4

ILLUSTRATION No.7

Table 4.1. Analysis of variance (mean sum of squares) for bran oil content, yield, its component and quality traits in three different locations

Source of variation	d.f.	Location	Days to 50% flowering	Plant height	Panicle length	Number of tillers per plant	Number of grains per panicle	1000-grain weight	Grain yield per Plant	Kernel length	Kernel breadth
Replications	2	I	7.10 **	6.18	1.33	0.32	4.25	3.70 *	7.62	0.008	0.007
		II	2.45	3.96	0.85	2.27 *	13.56	0.80	7.58	0.002	0.002
		III	0.42	2.67	1.45	1.98 *	0.11	0.13	4.92	0.001	0.01
Genotypes	40	I	380.71 **	358.71 **	21.35**	5.72 **	2573.98 **	53.03 **	110.33 **	1.67**	0.19 **
		II	352.00 **	646.87 **	16.57 **	6.47 **	1518.76 **	48.35 **	73.97 **	1.50 **	0.15 **
		III	371.42**	524.24 **	17.13 **	9.75 **	2098.88 **	50.48 **	94.53 **	1.73 **	0.18 **
Error	80	I	2.00	3.39	1.43	0.52	8.11	1.01	4.08	0.02	0.004
		II	3.30	2.29	1.31	0.52	8.46	1.43	3.61	0.03	0.002
		III	3.26	2.77	1.15	0.46	6.70	1.43	3.54	0.01	0.004

I – Jagtial, **II – Warangal,** **III –Hyderabad**

**** Significant at 0.01 level of probability** *** Significant at 0.05 level of probability**

Table 4.1. Contd…

Source of variation	d.f.	Location	L/B Ratio	Bran oil content	Milling percentage	Head rice recovery	Alkali spreading value	Water uptake	Gel consistency	Amylose content
Replications	2	I	0.01	0.38	3.71	1.27	0.08	90.24	3.72	0.37
		II	0.03	0.19	19.06 **	25.39 **	0.04	64.23 *	0.30	0.73
		III	0.002	1.49	13.16**	24.08 **	0.02	55.49	0.74	2.59 **
Genotypes	40	I	0.29 **	13.63 **	24.75**	58.39 **	2.31 **	3865.67 **	148.35 **	17.60**
		II	0.22 **	13.62 **	17.76**	25.52 **	2.43 **	4677.87 **	105.14**	14.31**
		III	0.31 **	11.96**	16.70 **	23.76 **	2.38 **	6534.84 **	99.10 **	10.69**
Error	80	I	0.02	0.73	1.17	1.26	0.10	30.24	2.52	0.64
		II	0.02	0.74	0.47	0.87	0.06	19.44	2.68	0.45
		III	0.02	0.95	0.51	0.66	0.03	19.03	2.16	0.45

I – Jagtial, **II – Warangal,** **III –Hyderabad**

**** Significant at 0.01 level of probability** *** Significant at 0.05 level of probability**

Table 4.3.1. Analysis of variance of combining ability for different characters in rice at Jagitial location

	df.	Days to 50% flowering	Plant height	Panicle length	No. of productive tillers per plant	No. of grains per panicle	1000-grain weight	Grain yield per plant	Kernel length	Kernel breadth
Replications	2	18.41**	2.61	1.74	0.41	3.34	5.04*	5.26	0.003	0.01
Treatments	40	380.71**	358.71**	21.35**	5.72**	2573.98**	53.03**	110.33**	1.67**	0.19**
Parents	10	644.34**	431.55**	14.88**	3.67**	295.76**	45.80**	69.28**	1.19**	0.10**
Parents vs crosses	1	692.04**	64.77**	27.39**	0.35	20054.64**	14.26**	153.72**	2.18**	0.13**
Crosses	29	279.07**	343.73**	22.97**	6.61**	2756.79**	56.85**	122.99**	1.54**	0.22**
Line effect	5	317.08	239.56	15.83	13.34*	1477.34	4.56	125.74	1.52	0.18
Tester effect	4	652.31*	970.79	67.82*	13.32*	5255.54	232.18**	308.55*	4.0*	0.92**
Line × Tester effect	20	194.91**	244.37**	15.78**	3.58**	2576.91**	34.86**	85.19**	1.05**	0.09**
Error	58	2.01	3.47	1.73	0.52	6.94	1.12	3.52	0.02	0.01

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

Table 4.3.1.contd…….

	df.	L/B ratio	Bran oil content	Milling percent	Herd rice recovery	Alkali spreading value	Water uptake	Gel consistency	Amylose content
Replications	2	0.004	0.21	0.01	0.69	0.06	36.94	0.21	0.16
Treatments	40	0.29**	13.63**	24.75**	58.39**	2.31**	3865.67**	148.35**	17.60**
Parents	10	0.12**	19.19**	8.72**	79.85**	2.79**	6854.09**	194.42**	11.13**
Parents vs crosses	1	0.14**	6.02**	36.57**	131.30**	0.11	634.53**	86.24**	6.13**
Crosses	29	0.35**	11.97**	29.86**	48.49**	2.22**	2946.60**	134.61**	20.23**
Line effect	5	0.32	32.44**	63.78*	102.43*	3.20	7141.61*	58.06	26.19
Tester effect	4	0.68	9.63	26.06	85.39*	4.83*	3717.36	104.26	6.76
Line × Tester effect	20	0.30**	7.32**	22.15**	27.62**	1.45**	1743.69**	159.81**	21.43**
Error	58	0.02	0.91	0.86	1.34	0.10	29.19	2.02	0.69

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

Table 4.3.2. Analysis of variance of combining ability for different characters in rice at Warangal location

	df.	Days to 50% flowering	Plant height	Panicle length	No. of productive tillers per plant	No. of grains per panicle	1000-grain weight	Grain yield per plant	Kernel length	Kernel breadth
Replications	2	0.58	2.99	0.12	1.58	10.98	1.05	4.34	0.006	0.002
Treatments	40	352.00**	646.87**	16.57**	6.47**	1518.76**	48.35**	73.97**	1.50**	0.15**
Parents	10	583.20**	528.71**	15.12**	4.52**	497.49**	44.39**	35.71**	1.90**	0.07**
Parents vs crosses	1	148.24**	8589.40**	35.46**	1.13	56.06**	26.29**	111.02**	1.22**	0.37**
Crosses	29	279.30**	413.73**	16.42**	7.33**	1729.98**	50.45**	85.88**	1.36**	0.17**
Line effect	5	279.61	1126.70**	7.14	9.64	1487.58	11.35	75.92	1.12	0.17
Tester effect	4	756.63*	417.19	54.12**	13.43	1920.83	214.33**	286.53**	3.95*	0.60**
Line × Tester effect	20	183.76**	234.79**	11.20**	5.53**	1752.41**	27.54**	48.25**	0.19**	0.09**
Error	58	2.52	2.35	1.06	0.52	8.05	1.61	4.02	0.03	0.003

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

Table 4.3.2.contd……..

	df.	L/B ratio	Bran oil content	Milling percent	Herd rice recovery	Alkali spreading value	Water uptake	Gel consistency	Amylose content
Replications	2	0.01	0.40	12.78**	27.22**	0.007	34.44	0.54	0.72
Treatments	40	0.22**	13.62**	17.76**	25.52**	2.43**	4647.87**	105.14**	14.31**
Parents	10	0.14**	17.23**	14.71**	30.54**	2.43**	4039.09**	91.21**	17.40**
Parents vs crosses	1	0.05	3.93**	26.17**	59.25**	0.12	15994.84*	66.91**	7.20**
Crosses	29	0.6**	12.71**	18.52**	22.63**	2.51**	4507.89**	111.26**	13.49**
Line effect	5	0.13	33.42**	6.33	8.95	3.72	6052.44	129.88	15.63
Tester effect	4	0.27	20.96*	42.95	59.52	4.58	8187.08	24.60	10.83
Line × Tester effect	20	0.29**	5.58**	16.69**	18.67**	1.79**	3385.92**	123.94**	13.49**
Error	58	0.02	0.80	0.59	0.63	0.05	21.80	2.17	0.50

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

Table 4.3.3. Analysis of variance of combining ability for different characters in rice at Hyderabad location

	df.	Days to 50% flowering	Plant height	Panicle length	No. of productive tillers per plant	No. of grains per panicle	1000-grain weight	Grain yield per plant	Kernel length	Kernel breadth
Replications	2	5.28	1.55	1.81	2.23**	0.74	0.04	6.48	0.005	0.01
Treatments	40	371.42**	524.24**	17.13**	9.75**	2098.88**	50.48**	94.53**	1.72**	0.18**
Parents	10	536.34**	656.64**	12.63**	5.12**	546.27**	18.58**	90.63**	1.80**	0.09**
Parents vs crosses	1	171.45**	4115.43**	76.66**	10.54**	1809.01**	127.84**	16.75*	2.24**	0.20**
Crosses	29	321.45**	354.75**	16.63**	11.32**	2644.26**	58.82**	98.57**	1.68**	0.22**
Line effect	5	130.71	444.95	17.17	8.35	4329.67	3.01	65.22	1.26	0.15
Tester effect	4	653.52	817.80*	38.37*	7.90	2762.32	283.68**	215.47	4.66*	0.86**
Line × Tester effect	20	302.72**	239.59**	12.14**	12.75**	2199.30**	27.80**	83.51**	1.19**	0.10**
Error	58	3.17	3.15	1.29	0.43	5.65	1.66	3.70	0.02	0.004

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

Table 4.3.3.contd……..

	df.	L/B ratio	Bran oil content	Milling percent	Herd rice recovery	Alkali spreading value	Water uptake	Gel consistency	Amylose content
Replications	2	0.001	1.93	7.41**	21.06**	0.03	40.00	1.14	1.48*
Treatments	40	0.31**	11.95**	16.70**	23.76**	2.38**	6534.84**	99.10**	10.69**
Parents	10	0.11**	16.96**	6.32**	18.01**	3.20**	10582.37**	109.13**	4.57**
Parents vs crosses	1	0.07	1.07	0.02	0.09	1.01	1214.10**	30.41**	1.20
Crosses	29	0.38**	10.60**	20.85**	26.56**	2.15**	5322.64**	98.01**	13.13**
Line effect	5	0.36	15.90*	48.16*	65.33*	4.17*	6769.33*	116.36*	24.91
Tester effect	4	1.17*	27.91**	7.42	19.34	3.96*	5162.78	46.96	3.99
Line × Tester effect	20	0.31**	5.81**	16.71**	18.31**	1.28**	4992.94**	103.64**	12.01**
Error	58	0.03	1.13	0.40	0.40	0.03	19.89	1.50	0.43

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

4.5 CHARACTER ASSSOCIATION

4.5.1 Among yield, its components and bran oil percentage

Grain yield is a complex character and is dependent on its contributing traits. A study was envisaged on character association, to assess the relationships among yield, its components and bran oil content to have an insight into the causes for higher yield and bran oil in cross combinations. Further, location wise analysis helps understand the variation in association under different environments and to identify a stable character influencing the yield for further concentration and emphasis in breeding programmes.

Simple correlations were worked out on yield, its contributing characters and bran oil percentage jointly at Jagtial, Warangal and Rajendranagar locations and also finally on pooled data (Table 4.8.1).

4.5.1.1 Days to 50 % flowering

This trait showed non-significant positive correlation with grain yield per plant in three locations and significant positive correlation with grain yield per plant, panicle length, number of grains per panicle and L/B ratio in pooled. In pooled analysis, this trait exhibited negative significant correlation with plant height, number of productive tillers per plant, 1000 grain weight, kernel length, and kernel breadth and bran oil content. At Jagitial and Warangal, this trait had significant positive correlation with the plant height and number of productive tillers per plant but negative with bran oil content. Negative non-significant association observed for this trait with panicle length, no.of productive tillers per panicle, kernel length and kernel breadth whereas positive non-significant with L/B ratio. At Warangal days to 50% flowering was positively correlated with no. of productive tillers per plant and kernel breadth but negative with panicle length, 1000 grain weight, kernel length and L/B ratio.This trait had a positive significant correlation with total no. grains per panicle and non-significant with plant height, panicle length, kernel breadth whereas negative non-significant with no.of productive tillers per plant,1000 grain weight,, kernel length, L/B ratio and bran oil content at Rajendranagar location. Similar type of associations were reported byKrishna *et al.*(2008) and Abdul Fiyaz*et al*. (2011)for grain yield per plant,Ravindra Babu *et al.*(2012) for panicle length and Badhru*et al.*(2012) for 1000 seed weight.

4.5.1.2 Plant height

It associated positively with grain yield per plant, 1000–seed weight, kernel length, kernel breadth but negatively with bran oil content in three locations and pooled. The pooled analysis indicated a negative significant association with panicle length, L/B ratio and a positive significant relation with no. of productive tillers per plant but negative non-significant with no. of grains per panicle. At Jagitial, this trait showed positive significant association with panicle length and non-significant with no.of grains per panicle while negatively correlated with no.of productive tillers per plant. Plant height (Warangal location) exhibited significant positive association with panicle length, no.of grains per panicle and non-significant with effective tillers per plant. At Rajendranagar, this trait had positive association with panicle length and no. of grains per panicle but negative with effective tillers per plant. In all 3 locations this trait showed negative non-significant association with L/B ratio.This revealed that plant height is an important trait for realizing more yield, as tallness is associated with problem of lodging. Plants having sturdy and medium height culms should be preferred.

The similar association with height reported by Abdul Fiyaz*et al*. (2011) for grain yield for plant and Krishna *et al.*(2008) for 1000 grain weight, kernel length and kernel breadth.

4.5.1.3 Panicle length

Panicle length had positive and significant association with 1000–grain weight, kernel length, kernel breadth and grain yield per plant whereas negative significant association with bran oil content in three locations and pooled. In addition to this, at Jagitial panicle length `had positive significant correlation with no. of grains per panicle while negative significant association with the L/B ratio. At Rajendranagar,this trait showed positive significant correlation with no.of grains per panicle and in pooled analysis, negative significant association was observed with productive tillers per plant but non-significant with L/B ratio.. Similar results were reported by Rajamadhan*et al.* (2011), Bhadru*et al.* (2012) and Ravindra Babu *et al.* (2012) for grain yield per plant and Padmaja*et al*.(2011) for number of grains per panicle.

4.5.1.4 Number of productive tillers per plant

This trait exhibited positive and significant association with grain yield per plant in Jagitial and pooled analysis. At Jagitial, this trait showed positive significant correlation with no.of grains per panicle, 1000-grain weight, kernel length, kernel breadth but negative association with bran oil content. In pooled analysis, no. of productive tillers per plant had significant positive correlation with kernel length, kernel breadth while negative with L/B ratio.

Padmaja*et al.*(2011), Rajamadhan*et al.*(2011), Bhadru*et al.*(2012) and Ravindra Babu *et al.*(2012) also reported a strong association between productive tillers and grain yield per plant andTara Satyavathi*et al.* (2001) for L/B ratio.

4.5.1.5 Total number of grains per panicle

Total no. of grains per panicle had significant positive association with grain yield per plant and kernel breadth in three locations and pooled analysis. This trait showed positive significant correlation with kernel length in Warangal, Rajendranagar and pooled analysis whereas significant negative association with bran oil content in Jagitial, Rajendranagar and pooled analysis.In addition to this, this trait exhibited significant positive association with 1000-grain weight, L/B ratio at Rajendranagar and Warangal respectively.

Bhadru*et al.*(2012) reported positive significant correlation with 1000 grain weight, Yadhav*et al.*(2010) for 1000 grain weight and grain yield per plant and Nandeshwar*et al.*(2010), Ravindra babu *et al.*(2012) for grain yield per plant as observed in the present study.

4.5.1.6 1000–seed weight

It associated positively and significantly with kernel length, kernel breadth and grain yield in three locations and pooled analysis. Long bold grains have more length and breadth with increased 1000 seed weight, which results in higher yields. This trait showed negative significant association with L/B ratio (in Jagitial) and bran oil content (in three locations).

Krishna *et al.*(2008), Nandan *et al.* (2010) andPankaj Garge*et al.* (2010) also observed a positive correlation among kernel length, kernel breadth and grain yield per plant.

4.5.1.7 Kernel length

Kernel length had significant positive association with kernel breadth, L/B ratio, grain yield per plant but negative significant association withbran oil content in three locations and

pooled analysis.Krishna *et al.* (2008) reported a positive association between kernel length and kernel breadth,

4.5.1.8 Kernel breadth

This trait had a negative significant association with L/B ratio, bran oil content and positive significant association with grain yield per plant in three locations and pooled analysis. Kernel breadth and L/B ratio were negatively correlated as observed by Pankaj Garge*et al.* (2010) and Rajeswari*et al.* (2010).

4.5.1.9 L/B ratio

Higher L/B ratio is desirable, as grains with high L/B ratio will be classified as fine and fetch higher premium in the market. This trait exhibited negative correlation with bran oil in Jagitial and pooled analysis. In the present investigation positive and negative significant correlation was observed with grain yield in Jagitial and pooled analysis respectively. L/B ratio had no significance with grain yield in Warangal and Rajendranagar.Tara Satyavathi*et al.* (2001) and Pankaj Garge*et al.* (2010) were also reported that L/B ratio also positively correlated with grain yield per plant.

4.5.1.10 Bran oil content

This trait exhibited a negative significant association with grain yield per plant in all locations and over locations.The results were in agreement in with the findings of Ravindra Babu (2002),Satyanarayana*et al.* (2003) andMijice*etal.* (2009).

4.5.1.11 Grain yield per plant

The seed yield per plant had a significant positive association with days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000- grain weight, kernel length, kernel breadth whereas negative significant association with bran oil content on overall basis. Variation was observed in the association between grain yield, bran oil and other components over different environments.

At Jagtial this trait had significant positive association with the plant height, panicle length, productive tillers per plant, numberof grains per panicle, 1000 grain weight, kernel length, kernel breadth and length/breadth ratio and negatively correlated with bran oil

content. At Warangal, it was positively associated with plant height, number of grains per plant, 1000-grain weight, kernel length and kernel breadth but negatively with bran oil content.At Rajendranagar this trait had significant positive association with the plant height, panicle length, numberof grains per panicle, 1000 grain weight, kernel length, kernel breadth and negatively correlated with bran oil content

Pooled analysis revealed a significant positive association with days to 50% flowering, plant height, number productive tillers per plant, panicle length, number of grains per panicle, 1000–grain weight,kernel length and kernel breadth. However, a negative significant correlation was recorded with L/B ratio and bran oil content

Similar kind of association with this trait was observed in finding of Krishna *et al.* (2008) and Abdul Fiyaz*et al.*(2011) for plant height, Rajamadhan*et al.*(2011), Bhadru*et al.* (2012) and Ravindra Babu *et al.*(2012) for number of productive tillers per plant, Pankaj Garge*et al.*(2010), Padmaja*et al.*(2011),Zulqarnain*et al.*(2012) for number of grains per panicle, Yadav *et al.* (2010), Zulqarnain*et al.* (2012)for 1000 seed weight andRavindra Babu (2002),Satyanarayana*et al.* (2003) and Mijice*etal.* (2009) for oil content**.**

Table 4.5.3. Environment indices for bran oil content, yield and quality components for three locations

Characters		Locations		
		Jagitial	**Warangal**	**Hyderabad**
Days to 50% flowering	**Ij**	7.50	2.20	-9.70
Plant height (cm)	**Ij**	-16.65	9.02	7.63
Panicle length (cm)	**Ij**	1.00	2.20	-3.20
Number of productive tillers per plant	**Ij**	-1.00	0.61	0.39
Total no. of grains per panicle	**Ij**	7.39	11.16	-19.05
1000 -grain weight (g)	**Ij**	-0.16	0.35	-0.19
Grain yield per plant (g)	**Ij**	0.36	2.56	-2.92
Kernel length (mm)	**Ij**	0.03	-0.05	0.01
Kernel breadth (mm)	**Ij**	-0.04	0.03	0.005
L/B ratio	**Ij**	0.07	-0.07	0.003
Bran oil content (%)	**Ij**	-0.04	-0.40	0.42

Ij- environment index

Table 4.7. Direct and Indirect effects for yield and its component characters for three different locations and pooled

Character	Location	Days to 50% flowering	Plant height	Panicle length	Effective tillers /plant	Total no. grains/ panicle	1000 Seed weight	Kernel length	Kernel breadth	L/B ratio	Bran oil	"r" value
Days to 50% flowering	**I**	**-0.0179**	-0.0046	0.0002	0.0012	-0.0047	0.0007	0.0740	0.0016	-0.0018	0.0039	0.0538
	II	**-0.1967**	-0.0686	0.1276	-0.0015	-0.0437	0.1144	0.0058	-0.0205	0.0067	0.0432	0.0177
	III	**0.1775**	0.0229	0.0064	-0.0244	0.0564	-0.0008	-0.0191	0.0228	-0.029	-0.0270	0.1150
	P	**0.4670**	-0.2550	0.2786	-0.2001	0.2347	-0.0719	-0.0574	-0.1321	0.0795	-0.0950	0.3882
Plant height	**I**	0.0225	**0.1097**	0.0042	-0.0001	0.0009	0.1039	0.0244	0.0053	-0.0006	-0.0020	0.2785
	II	0.0713	**0.2043**	0.0902	0.0066	0.0588	0.0803	0.0423	0.0681	-0.0159	-0.0990	0.5155
	III	-0.0189	**0.2464**	-0.0250	0.0196	-0.0157	-0.0737	-0.0367	-0.0569	0.1136	0.1440	0.3054
	P	-0.0697	**0.1276**	-0.0175	0.0792	-0.0103	0.0274	0.0176	0.0518	-0.0336	-0.0570	0.1215
Panicle length	**I**	0.0015	-0.0526	**0.3204**	-0.0027	-0.0370	0.0614	-0.0356	-0.0560	0.0232	0.0267	0.2589
	II	-0.064	-0.0283	**0.3009**	-0.0023	-0.0090	-0.0386	-0.0229	-0.0280	0.2013	0.0117	0.3914
	III	0.0023	0.0108	**0.2632**	-0.0062	0.0196	0.0191	0.0260	0.0294	-0.0003	-0.0170	0.3527
	P	-0.4624	-0.2264	**0.7753**	-0.1142	0.4412	0.3369	0.1104	0.1365	-0.0380	-0.2020	0.7659
Effective tillers /plant	**I**	-0.0180	-0.0019	0.0058	**0.2599**	0.0596	0.0611	0.0684	0.0678	0.0084	-0.0570	0.5111
	II	0.0010	0.0042	0.0047	**0.1306**	-0.0173	0.0046	-0.0024	0.0046	-0.0090	-0.0003	0.0874
	III	0.0030	0.0029	0.0021	**-0.0217**	0.0001	-0.0017	-0.0008	-0.0039	0.0038	-0.0020	-0.0169
	P	0.0241	-0.0349	0.0083	**-0.0563**	-0.0053	-0.0033	-0.0119	-0.0313	0.0200	-0.0030	0.2592
Total no. grains/panicle	**I**	0.0442	0.0152	0.0515	0.0385	**0.1678**	0.0262	0.0163	0.0350	-0.0618	-0.0390	0.3147
	II	0.0958	0.1239	0.0603	-0.3572	**0.4309**	0.0254	0.1715	0.1248	0.0983	-0.3523	0.5220
	III	-0.0813	-0.0274	-0.0794	-0.0001	**-0.2558**	-0.0507	-0.1011	-0.1148	0.2215	0.1040	0.2009
	P	-0.2439	0.0392	-0.2761	-0.0454	**0.4852**	0.0151	-0.0595	-0.1074	0.3448	0.2425	0.4298
1000 grain weight	**I**	-0.2188	0.1843	0.2302	0.1061	0.0705	**0.4512**	0.1857	0.2863	-0.3111	-0.4400	0.6064
	II	-0.2198	0.1065	0.1632	0.0096	0.0160	**0.2709**	0.1218	0.1601	-0.2302	-0.0980	0.5270
	III	-0.2019	0.2169	0.1303	0.0344	0.0854	**0.4311**	0.1727	0.2301	-0.2382	-0.3800	0.5489
	P	0.3696	-0.0970	-0.1963	-0.0265	0.2141	**0.5519**	-0.2187	-0.2718	0.0348	0.0816	0.5213

*** Significant at 5% level, Bold values – Direct effect, I – Jagtial, II – Warangal Residual effect: I =0.540**

****Significant at 1% level, Normal values – Indirect effect, III – ICRISAT, P – Pooled II =0.5876**

Contd…….

Table 4.7. contd….

Character	Location	Days to 50% flowering	Plant height	Panicle length	Effective tillers/ plant	Total No. grains/ panicle	1000 Seed weight	Kernel length	Kernel breadth	L/B ratio	Bran oil	Seed yield/plant
Kernel length	**I**	-0.2066	-0.1686	0.1096	0.0977	0.0360	0.1528	**0.3711**	0.2489	0.1881	-0.2360	0.5929
	II	0.0038	-0.0267	-0.0461	0.0024	-0.0513	-0.0579	**0.3688**	0.2855	-0.0751	0.0153	0.4725
	III	-0.0142	0.0331	0.0544	0.0050	0.0522	0.0529	**0.1322**	0.0831	0.0743	-0.032	0.4601
	P	-0.0156	0.0175	0.0181	0.0268	0.1156	0.0614	**0.1269**	0.0885	0.0717	-0.038	0.5331
Kernel breadth	**I**	0.0143	-0.0881	-0.0743	-0.0417	-0.0333	-0.1013	-0.1071	**0.6597**	0.0554	0.1406	0.4883
	II	0.0007	-0.1340	0.1103	0.0088	0.0730	0.1490	0.1673	**0.2521**	-0.1713	-0.1610	0.5172
	III	0.0030	0.0755	0.0905	0.0347	0.0872	0.1038	0.1223	**0.1944**	-0.0651	-0.1960	0.4541
	P	-0.3323	0.4053	0.1757	0.5544	0.2208	0.4000	-0.6959	**0.7976**	-0.3705	-0.4280	0.7577
L/B ratio	**I**	0.0004	-0.0003	-0.0008	0.0001	-0.0003	-0.0011	0.0022	-0.0015	**0.0043**	-0.0009	0.2060
	II	-0.0151	-0.0116	-0.0031	-0.0102	0.0339	-0.1166	0.0867	-0.0421	**0.0786**	0.0201	0.0179
	III	-0.0181	-0.0103	-0.0005	-0.0194	-0.0007	-0.0098	0.0623	-0.0671	**0.1108**	0.0029	0.0603
	P	-0.0492	0.0297	0.0055	0.0401	0.0104	0.0087	-0.0638	0.0306	**-0.2128**	0.0167	-0.2072
Bran oil	**I**	0.0523	0.0482	0.0530	0.0519	0.0552	0.0742	-0.2872	-0.0806	0.0521	**-0.5390**	-0.5420
	II	0.0577	-0.1277	0.0482	0.0006	0.0307	-0.0954	0.0313	0.0636	-0.0955	**-0.3630**	-0.4820
	III	0.0636	0.1272	0.1106	-0.0388	-0.1722	0.0787	-0.1024	-0.1269	-0.0113	**-0.4240**	-0.4880
	P	-0.0044	-0.0045	-0.0056	0.0013	-0.0063	-0.0010	-0.0064	-0.0049	-0.0032	**-0.3713**	-0.3920

*** Significant at 5% level, Bold values – Direct effect, I – Jagitial, II –Warangal Residual effect: III = 0.6737**

****Significant at 1% level, Normal values – Indirect effect, III – ICRISAT, P – Pooled P =0.5**

Table 4.5.4. Mean performance and stability parameters for brain oil content, yield, its components and other quality traits

Cross combinations	Days to 50% flowering			Plant height (cm)			Panicle length (cm)		
	Mean	b_i	S^2di	Mean	b_i	S^2di	Mean	b_i	S^2di
L1T1	92.78	1.05	2.30	109.89	0.47	624.5 ***	26.26	0.91	-0.23
L1T2	80.89	1.13	-0.68	93.59	0.50	38.99 ***	19.40	0.64	0.99
L1T3	122.56	0.66	-0.18	102.63	1.10	93.0 4***	21.93	1.08	-0.43
L1T4	115.33	1.04	-0.78	102.03	1.46	55.29 ***	20.64	1.04	0.23
L1T5	98.67	0.82	6.34**	108.07	0.92	14.11 ***	23.90	1.12	3.31**
L2T1	109.45	0.69	5.18*	129.60	1.07	45.07 ***	25.34	0.94	1.71*
L2T2	95.44	1.37	-0.44	105.11	1.10	59.35 ***	22.09	0.59*	-0.44
L2T3	119.78	1.12	-0.82	116.71	1.59*	-0.97	20.66	0.84	0.02
L2T4	99.00	1.40	14.10**	105.32	1.19	-0.69	21.74	2.03*	-0.44
L2T5	103.22	1.19	6.55**	105.96	1.49	7.68 **	23.26	1.50	-0.03
L3T1	103.33	1.03	-0.90	122.95	1.36*	-0.99	21.45	1.19	3.00**
L3T2	108.22	1.10	-0.76	97.53	1.36	86.85 ***	20.02	1.12	3.02**
L3T3	115.11	1.11	6.89**	107.28	1.25*	-0.97	22.15	1.20	-0.09
L3T4	112.56	0.96	20.37**	113.17	1.20	5.7 4**	20.76	1.44	0.03
L3T5	99.89	1.54	1.67	123.46	1.24	6.26 **	24.08	1.20	0.72
L4T1	117.78	0.97	4.78*	112.45	-0.16	152.32 ***	22.04	1.22	-0.44
L4T2	104.11	1.20	3.93*	104.24	1.27*	-0.99	18.92	1.02	0.75
L4T3	112.78	1.06	9.30*	99.02	1.23	9.25 **	21.23	1.18	0.72
L4T4	105.67	1.09	-0.08	114.04	1.06	-0.91	22.54	0.89	0.01
L4T5	109.00	0.71	2.34	105.22	0.81	7.45 **	23.54	0.55	0.02
L5T1	97.22	0.65	38.51**	107.17	1.30	16.77 ***	24.71	1.29	-0.34
L5T2	102.22	0.65	-0.75	103.52	0.19*	-0.97	23.15	0.75	0.41
L5T3	105.67	0.97	26.96**	95.73	0.39	152.74 ***	19.72	1.16	0.40

L5T4	114.11	0.72	3.59*	96.94	0.88	10.21 ***	16.47	-0.11	6.32***
L5T5	86.89	0.83	-0.70	100.37	1.27	20.17 ***	20.00	1.52	0.05
L6T1	104.67	0.82	1.33	128.32	0.97	5.42 *	26.33	0.74	0.23
L6T2	104.78	0.92	22.61**	110.30	0.80	0.01	21.00	0.66	2.18*
L6T3	113.78	1.10	2.50	114.90	0.82	0.45	22.31	1.07	1.27
L6T4	107.00	1.28	80.10**	103.53	1.25	23.01 ***	20.21	0.47	0.33
L6T5	116.45	0.79	0.25	109.30	0.63	-0.44	24.22	0.74*	-0.45
Grand Mean	105.94			108.28			22.00		

Table 4.5.4. contd……

Cross combinations	**Productive tillers per plant**			**No.of grains per panicle**			**1000 grain weight (g)**		
	Mean	**b_i**	**S^2di**	**Mean**	**b_i**	**S^2di**	**Mean**	**b_i**	**S^2di**
L1T1	9.67	-1.06	0.12	163.33	1.63	7.05*	21.70	-0.23	-0.36
L1T2	10.44	1.04	0.24	138.78	1.84	153.01***	21.94	0.04	0.19
L1T3	10.89	1.43	1.21**	133.89	2.44	284.15***	17.06	2.64	-0.31
L1T4	10.11	2.55	0.87*	132.00	1.68	147.7***	22.71	2.05	0.09
L1T5	12.78	1.85	0.26	114.89	0.18	219.66***	25.70	-1.60	0.22
L2T1	7.56	0.62	0.21	164.44	-0.79	195.24***	31.08	-2.72*	-0.48
L2T2	10.56	0.62	0.21	124.22	1.49	-0.87	20.87	0.98	-0.45
L2T3	9.22	1.02	1.43**	147.56	1.41	14.07**	21.69	1.93	1.06
L2T4	9.56	3.66	4.86***	135.89	0.18	205.95***	15.61	7.34	-0.24
L2T5	11.33	1.01	-0.17	151.22	0.55	14.12**	19.43	2.93	0.48
L3T1	8.78	0.53	0.58*	155.11	1.70	47.73**	22.86	-5.39	5.24***
L3T2	12.56	1.08	1.68**	137.89	0.37	118.66***	22.63	3.29	12.96***
L3T3	9.56	0.22*	-0.17	195.11	2.15	197.86***	18.58	-8.68	5.35***
L3T4	10.67	2.72	0.10	91.89	1.11	132.37***	16.76	0.56	0.97
L3T5	12.44	2.71	0.27	150.11	1.23	44.32***	22.77	4.06	-0.25
L4T1	11.33	0.77	4.93***	188.22	-0.93	36.10**	25.67	3.53	0.00
L4T2	10.00	-1.26	0.28	132.00	1.91	625.70***	21.12	3.03	0.56
L4T3	10.44	0.90	4.00***	133.89	-0.68	325.42***	18.63	-0.42	-0.42
L4T4	9.44	1.29	2.71***	126.56	0.20	100.10***	17.29	7.56	-0.10

L4T5	8.22	0.32	0.64*	138.11	0.19	50.69***	24.51	1.67	-0.48
L5T1	11.00	0.56	0.91*	124.45	2.57	1906.62***	27.70	1.37	-0.30
L5T2	10.44	1.19	0.41	131.56	-0.21	41.21**	15.06	3.17	-0.49
L5T3	10.67	2.16	2.26***	118.56	1.41	2583.07***	20.04	0.24	-0.15
L5T4	8.89	0.36	1.70**	122.33	1.87	997.68***	16.08	0.00	-0.27
L5T5	10.78	0.64	1.49**	116.67	1.70	241.88***	24.48	0.93	-0.49
L6T1	11.89	0.52	-0.07	163.33	2.09	15.64**	30.09	1.01	-0.47
L6T2	12.11	0.74	-0.05	124.67	-0.10	697.12***	20.78	-1.37	3.61**
L6T3	10.00	0.05	0.05	143.00	0.38	134.17***	17.36	2.22	0.06
L6T4	11.89	0.62	0.21	164.11	2.55	17.47**	16.14	-1.47	1.11
L6T5	13.11	1.14	-0.09	138.11	-0.10*	-2.27	23.78	1.33	-0.28
Grand Mean	10.54			140.06			21.34		

Table 4.5.4. contd…….

Cross combinations	**Grain Yield per plant (g)**			**Kernal Length (mm)**			**Kernal breadth (mm)**		
	Mean	**b_i**	**S^2di**	**Mean**	**b_i**	**S^2di**	**Mean**	**b_i**	**S^2di**
L1T1	25.68	2.06*	-1.17	6.34	2.53	0.01	2.45	-0.34	0.04***
L1T2	22.21	1.81	-0.99	5.90	-6.28	0.10***	1.98	2.05	0.08***
L1T3	13.74	0.16	-1.05	4.55	-12.88*	0.00	1.84	0.79	0.00
L1T4	23.87	1.11	8.97**	5.18	-1.14	0.00	1.91	2.52	0.02***
L1T5	33.00	-0.30	14.68***	6.19	5.24*	-0.01	2.14	-0.71	0.00
L2T1	25.97	1.94	-0.06	6.79	4.27	0.00	2.43	0.48	0.00
L2T2	23.34	2.18	-0.16	6.75	4.26	0.00	1.93	1.37	0.00
L2T3	22.88	0.75	106.22***	4.69	-0.02	-0.01	1.84	3.53	0.03***
L2T4	18.34	2.27	20.85***	5.31	1.94	0.01	1.93	3.91	0.01*
L2T5	19.62	1.89	9.22**	5.85	-1.07	0.01	1.99	0.42	0.00
L3T1	34.13	1.12	-1.17	6.74	1.48	-0.01	2.50	1.10	0.00
L3T2	25.18	2.87	46.42***	5.61	1.82	-0.01	1.99	1.35	0.00
L3T3	29.48	0.53	28.59***	6.20	2.09	0.01	1.73	1.09	0.00
L3T4	15.63	1.93	9.96**	5.40	3.89	0.03*	1.96	1.90	0.00
L3T5	25.70	1.75	30.24***	5.66	2.48	-0.01	2.07	1.70	0.00

L4T1	30.76	1.04	0.23	7.02	-0.64	-0.01	2.64	-0.09*	0.00
L4T2	24.04	1.85	105.91***	5.88	6.57	0.05**	1.92	0.34	0.00
L4T3	18.82	-0.22	10.00**	4.88	8.78	0.00	2.20	0.47	0.00
L4T4	23.54	-0.33	40.55***	5.85	6.02	0.01	1.91	0.28	0.00
L4T5	26.13	-0.64	30.34***	6.64	-2.73	0.06**	2.11	0.81	0.00
L5T1	27.61	1.87*	-1.21	4.80	-3.15	0.17***	1.83	-0.68	0.00
L5T2	21.40	1.05	-1.19	6.59	2.08	0.00	1.98	1.37	0.00
L5T3	21.84	-0.68	8.39***	5.37	1.02	0.01	2.09	-0.70	0.00
L5T4	24.77	0.39	6.81*	5.93	1.86	0.03*	1.81	1.54	0.00
L5T5	26.40	-1.55	0.21	6.02	1.58	0.00	1.99	0.27	0.00
L6T1	32.81	1.11	-1.22	6.85	-2.66	0.00	2.71	-0.26	0.00
L6T2	23.49	-0.09	13.10***	6.68	1.41	0.00	2.18	1.95	0.00
L6T3	25.26	1.66	8.92**	5.83	-1.48	0.10***	1.84	1.39	0.00
L6T4	24.71	1.78	13.43***	6.24	2.02	-0.01	2.14	1.17	0.00
L6T5	26.00	0.92	-1.18	6.55	0.61	0.02	2.28	0.98	0.00
Grand Mean	24.55			5.94			2.08		

Table 4.5.4. contd…….

Cross combinations	**L/B ratio**			**Bran oil content (%)**		
	Mean	**b_i**	**S^2di**	**Mean**	**bi**	**S^2di**
L1T1	2.59	-0.05	0.01	13.72	-1.65	0.02
L1T2	3.00	-0.08	0.32***	16.23	1.66	-0.30
L1T3	2.49	-3.51	0.01	16.86	-2.59	0.74
L1T4	2.71	1.68	0.01	14.28	3.05	1.94**
L1T5	2.90	0.94	-0.01	10.97	-0.29	0.60
L2T1	2.80	1.32	-0.01	11.49	3.60	-0.23
L2T2	3.50	2.29*	-0.01	12.27	3.23	-0.26
L2T3	2.56	2.17	0.06**	11.33	1.04	2.99**

L2T4	2.77	3.14	0.00	10.84	1.89	-0.09
L2T5	2.94	0.14	0.01	11.60	0.64	2.22**
L3T1	2.70	0.84	-0.01	11.44	1.80	-0.23
L3T2	2.83	1.55	0.00	12.04	5.43	6.63***
L3T3	3.58	1.60	0.00	11.59	-2.27	1.58*
L3T4	2.76	2.26	0.02**	13.43	3.72	1.28*
L3T5	2.74	1.90	0.00	11.23	0.83	-0.31
L4T1	2.65	-0.19*	-0.01	10.42	-0.02	0.08
L4T2	3.08	2.32	0.04*	11.33	2.82	2.70**
L4T3	2.22	2.65	-0.01	12.36	1.42	1.18*
L4T4	3.07	1.85	0.01	11.31	-1.17	0.29
L4T5	3.14	-0.50	-0.01	10.25	0.66	-0.29
L5T1	2.62	-0.91	0.03	12.36	4.87	-0.24
L5T2	3.33	1.72	0.00	14.83	2.60	0.02
L5T3	2.57	-0.03	0.00	13.98	0.90	-0.13
L5T4	3.29	2.27	0.01	14.05	-0.21	-0.31
L5T5	3.02	0.52	-0.01	13.31	-4.09	-0.13
L6T1	2.53	-0.71	-0.01	9.92	0.93	-0.27
L6T2	3.08	1.52	-0.01	14.62	-1.23	1.44*
L6T3	3.18	1.01	0.05**	12.14	-0.67	-0.20
L6T4	2.92	1.33	-0.01	11.59	1.38	1.76*
L6T5	2.87	0.97	-0.01	12.88	3.49*	0.31
Grand Mean	2.90			12.50		

Table .4.6. Simple correlation coefficients for bran oil, yield and its component characters for 3 locations and pooled analysis

Characters	Location	Days to 50% flowering	Plant height	Panicle length	Effective tillers /plant	Total no. grains/ panicle	1000 Seed weight	Kernel length	Kernel breadth	L/B ratio	Branoil	Seed yield/plant
Days to 50% flowering	I	1.0000	0.2545**	-0.0125	-0.0694	0.2632**	-0.0416	-0.0178	-0.0893	0.1017	-0.219*	0.0538
	II	1.0000	0.3489**	-0.1401	0.0077	0.2223*	-0.073	-0.0295	0.0026	-0.0342	-0.22*	0.0177
	III	1.0000	0.1293	0.036	-0.1376	0.3176**	-0.0043	-0.1078	0.0156	-0.1632	-0.150	0.1150
	P	1.0000	-0.546**	0.5964**	-0.4286**	0.5026**	-0.1539*	-0.1229*	-0.283**	0.1702**	-0.204**	0.3882**
Plant height	I		1.0000	0.4367**	-0.0072	0.0904	0.4086**	0.4544**	0.5518**	-0.0636	-0.202*	0.2785**
	II		1.0000	0.4418**	0.0323	0.2876**	0.3931**	0.207*	0.3333**	-0.0781	-0.486**	0.5155**
	III		1.0000	0.1705	-0.1337	0.107	0.5033**	0.2507**	0.3885**	-0.0932	-0.30**	0.3054**
	P		1.0000	-0.1372**	0.6207**	-0.0808	0.2146**	0.1383**	0.4063**	-0.2634**	-0.212**	0.1215*
Panicle length	I			1.0000	0.0222	0.307**	0.5103**	0.2953**	0.4655**	-0.1927*	-0.222*	0.2589**
	II			1.0000	0.0363	0.1398	0.6023**	0.3577**	0.4377**	-0.0205	-0.183*	0.3914**
	III			1.0000	-0.0983	0.3103**	0.3023**	0.4119**	0.4654**	-0.0042	-0.261**	0.3527**
	P			1.0000	-0.1473**	0.5691**	0.4345**	0.1424**	0.1761**	-0.049	-0.261**	0.7659**
Effective tillers /plant	I				1.0000	0.2294*	0.2351**	0.2633**	0.2608**	0.0321	-0.218*	0.5111**
	II				1.0000	-0.1327	0.0354	-0.0187	0.035	-0.0689	-0.002	0.0874
	III				1.0000	0.0004	0.0798	0.0379	0.1786*	-0.175	0.0916	-0.0169
	P				1.0000	0.0936	0.0585	0.2113**	0.5557**	-0.3552**	0.0589	0.2592**
Total no. grains per panicle	I					1.0000	0.1563	0.0969	0.2088*	-0.0701	-0.231**	0.3147**
	II					1.0000	0.059	0.398**	0.2897**	0.2281*	-0.117	0.522**
	III					1.0000	0.1981*	0.3952**	0.4485**	-0.0059	-0.407**	0.2009*
	P					1.0000	-0.0312	0.1226*	0.2213**	-0.0924	-0.294**	0.4298**
1000 grain Weight	I						1.0000	0.4117**	0.6346**	-0.2463**	-0.311**	0.6064**
	II						1.0000	0.4494**	0.591**	-0.1115	-0.363**	0.527**
	III						1.0000	0.4005**	0.5338**	-0.0886	-0.186*	0.5489**
	P						1.0000	0.484**	0.6014**	-0.0771	-0.048	0.5213**

I – Jagtial , II – Warangal *Significant at 5% level **Significant at 1% level

III – Hyderabad, P – Pooled

Contd…

Table.4.6 (Contd…).

Characters	Location	Days to 50% flowering	Plant height	Panicle length	Effective tillers/ plant	Total no. grains/ panicle	1000 Seed weight	Kernel length	Kernel breadth	L/B ratio	Bran oil	Seed yield/plant
Kernel length	**I**							**1.0000**	0.6708**	0.5068**	-0.366**	0.5929**
	II							**1.0000**	0.6637**	0.5832**	-0.119	0.4725**
	III							**1.0000**	0.6291**	0.5622**	-0.242**	0.4601**
	P							**1.0000**	0.6975**	0.5651**	-0.302**	0.5331**
Kernel breadth	**I**								**1.0000**	-0.3467**	-0.254**	0.4883**
	II								**1.0000**	-0.283**	-0.242**	0.5172**
	III								**1.0000**	-0.3348**	-0.30**	0.4541**
	P								**1.0000**	-0.2711**	-0.229**	0.7577**
L/B ratio	**I**									**1.0000**	-0.218*	0.206*
	II									**1.0000**	0.1349	0.0179
	III									**1.0000**	0.0266	0.0603
	P									**1.0000**	-0.148**	-0.2072**
Bran oil	**I**										**1.0000**	-0.542**
	II										**1.0000**	-0.482**
	III										**1.0000**	-0.488**
	P										**1.0000**	-0.392**
Seed yield/plant	**I**											**1.0000**
	II											**1.0000**
	III											**1.0000**
	P											**1.0000**

I – Jagtial , II – Warangal *Significant at 5% level **Significant at 1% level

III – Hyderabad , P – Pooled

Table 4.5.1. Analysis of variance for yield and yield components for stability in rice (*Oryza sativa* L.)

Source	d.f.	Days to 50% flowering	Plant height	Productive tillers per plant	Panicle length	Number of grains per panicle	1000-grain weight	Grain yield per plant
Replication within environment	6	2.70	0.83	0.41	0.47	1.67	0.68	1.45
Genotypes	29	275.08 **	251.63 **	14.93 **	5.55 **	1409.51 **	52.08 **	66.10 **
Environment +(Genotype × Environment)	60	86.38 **	265.96 **	9.86 **	2.15 *	744.41 *	1.69	25.18
Environment	2	2327.65 **	6251.82 **	241.50 **	22.87 **	8303.37 **	2.76	228.07 **
Genotype × Environment	58	12.10**	59.55**	1.97**	1.74**	537.75**	1.95**	23.19**
Environment (linear)	1	4655.30 **	12503.65 **	483.01 **	45.74 **	16606.74 **	5.52	456.13 **
Genotype × Environment (linear)	29	8.50	68.85	2.49 **	1.62	601.30**	1.88	17.71
Pooled Deviation	30	6.37 **	48.58 **	1.11 **	0.91 **	300.00 **	1.07 **	13.04 **
Pooled Error	174	0.86	1.00	0.45	0.16	2.29	0.49	1.25
Total	89	147.87	261.29	11.51	3.26	961.13	18.11	38.52

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

Table 4.5.2. Analysis of variance for Kernel characters and Bran oil content for stability in rice (*Oryza sativa* L.)

Source	d.f.	Kernel length	Kernel breadth	L/B ratio	Bran oil
Replication within environment	6	0.002	0.003	0.002	0.28
Genotypes	29	1.44 **	0.19 **	0.29 **	8.86 **
Environment +(Genotype × Environment)	60	0.04	0.01	0.03	1.58
Environment	2	0.05	0.04 *	0.15 **	5.26 *
Genotype × Environment	58	0.05**	0.01**	0.02**	1.60**
Environment (linear)	1	0.11	0.07 **	0.31 **	10.52 **
Genotype × Environment (linear)	29	0.06 **	0.003	0.02	1.81**
Pooled Deviation	30	0.02 **	0.01 **	0.02 **	0.91 **
Pooled Error	174	0.01	0.001	0.008	0.32
Total	89	0.50	0.07	0.11	3.95

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

4.3.5. Estimates of gca effects for yield, its components and quality characters in rice (O.*sativa*L.*)* in 3 locations

Parents	Days to 50% flowering			Plant height (cm)			Panicle length (cm)		
	I	II	III	I	II	III	I	II	III
	Lines								
L1	-3.64**	-5.01**	-3.04**	-3.41***	-9.49**	-2.21**	0.53	0.21	0.53
L2	1.56**	-1.61**	-1.64**	-0.45	7.43**	5.81**	1.24**	0.68*	-0.07
L3	4.02**	0.72	0.89	-0.02	8.41**	5.41**	0.53	-0.28	-1.18**
L4	4.02**	3.86**	3.89**	1.50**	-0.13	-5.22**	-0.39	-0.39	-0.26
L5	-7.44**	-3.88**	-2.84**	-4.42***	-11.48**	-6.69**	-1.73**	-1.01*	-0.83**
L6	1.49**	5.92**	2.76**	6.80***	5.27**	2.91**	-0.17	0.79**	1.81**
Testers									
T1	-2.83**	-1.87**	-0.52	12.76***	7.18**	10.41**	2.69**	2.23**	2.13**
T2	-6.39**	-6.26**	-7.36**	-3.63***	-5.71**	-8.35**	-1.57**	-1.58**	-0.56*
T3	8.44**	9.86**	8.70**	-3.28***	-1.50**	-1.92**	-0.58*	-0.47	-0.96**
T4	3.89**	2.80**	2.31**	-5.36***	-1.76**	-0.19	-1.83**	-1.56**	-1.44**
T5	-3.11**	-4.53**	-3.13**	-0.49	1.79**	0.04	1.29**	1.38**	0.82**

I-Jagitial, II- Warangal, III- Hyderabad

*** Significance at 0.01 level of probability ** Significance at 0.05 level of probability**

Table 4.3.5.Contd…….

Parents	Productive tillers per plant			Number of grains per plant			1000 -grain Weight		
	I	II	III	I	II	III	I	II	III
	Lines								
L1	0.06	0.24	0.40*	1.34	2.34**	-14.14**	0.43	0.35	0.68*
L2	-1.28**	-0.62**	-0.80**	-1.86*	2.34**	13.32**	0.21	0.78**	0.20
L3	-0.21	0.44*	0.53**	9.08**	8.88**	-0.08	-0.19	-1.40**	-0.26
L4	-0.08	-1.16**	-0.73**	7.94**	-15.52**	18.66**	-0.43	0.85**	-0.09
L5	-0.14	-0.02	-0.40*	-18.39**	-8.06**	-25.61**	-0.74**	-0.61	-0.64*
L6	1.66**	1.11**	1.00**	1.88	10.01**	7.86**	0.72**	0.04	0.12
Testers									
T1	0.12	-1.21**	-0.43**	26.38**	14.83**	18.04**	5.02**	4.71**	5.81**
T2	0.90**	0.18	0.34*	-13.51**	-6.39**	-5.73**	-0.54*	-0.79**	-1.49**
T3	-0.38*	-0.43*	-0.43**	7.77**	6.44**	1.60*	-2.48**	-2.90**	-1.96**
T4	-1.27**	0.40*	-0.49**	-13.18**	-4.83**	-15.79**	-4.00**	-3.33**	-4.38**
T5	0.62**	1.07**	1.01**	-7.46**	-10.06**	1.88**	2.00**	2.30**	2.02**

I-Jagitial, II- Warangal, III- Hyderabad

*** Significance at 0.01 level of probability ** Significance at 0.05 level of probability**

Table 4.3.5.Contd……..

Parents	Grain yield per plant			Kernel length			Kernel breadth		
	I	II	III	I	II	III	I	II	III
	Lines								
L1	-0.93	-0.88	-0.72	-0.47**	-0.16**	-0.31**	0.002	-0.002	-0.04*
L2	-5.21**	1.33**	-3.67**	-0.04	-0.11*	-0.05	-0.11**	-0.05**	0.001
L3	2.17**	2.55**	-0.28	-0.02	-0.10*	0.06	-0.03	0.002	-0.05**
L4	1.77**	-2.71**	1.28*	0.14**	-0.03	0.23**	0.11**	0.06**	0.07**
L5	-0.26	-2.25**	2.09**	-0.12**	-0.15**	-0.33**	-0.12**	-0.16**	-0.13**
L6	2.45**	1.97**	1.31*	0.50**	0.55**	0.40**	0.15**	0.15**	0.15**
	Testers								
T1	4.72**	6.42**	3.70**	0.49**	0.52**	0.43**	0.38**	0.31**	0.37**
T2	1.83**	-1.42**	-4.22**	0.25**	0.24**	0.40**	-0.08**	-0.04**	-0.12**
T3	-2.19**	-4.51**	-0.93*	-0.69**	-0.61**	-0.77**	-0.17**	-0.17**	-0.13**
T4	-5.97**	-0.28	-1.97**	-0.26**	-0.37**	-0.25**	-0.16**	-0.09**	-0.15**
T5	1.60**	-0.22	3.42**	0.21**	0.21**	0.20**	0.03*	0.004	0.02

I-Jagitial, II- Warangal, III- Hyderabad

*** Significance at 0.01 level of probability** Significance at 0.05 level of probability**

Table 4.3.5. Contd……..

Parents	L/B ratio			Bran oil content			Milling %		
	I	II	III	I	II	III	I	II	III
	Lines								
L1	-0.26**	-0.09*	-0.08*	2.30**	2.11**	1.36**	1.66**	-0.46*	0.34
L2	0.13**	0.01*	-0.04	-0.48*	-1.73**	-0.74**	-4.12**	-0.49**	-2.79**
L3	0.05	-0.04	0.11**	-1.06**	-0.62**	0.06	0.63**	0.25	1.67**
L4	-0.07	-0.10**	0.02	-1.62**	-1.09**	-1.35**	0.45	-0.73**	1.95**
L5	0.11**	0.14**	0.006	1.20**	1.45**	0.99**	0.72*	0.86**	-1.24**
L6	0.05	0.07	-0.015	-0.33	-0.12	-0.32	0.65*	0.57**	0.079
Testers									
T1	-0.27**	-0.14**	-0.28**	-0.86**	-1.22**	-0.71**	-1.61**	1.88**	0.91**
T2	0.24**	0.17**	0.36**	0.11	1.02**	2.07**	-0.20	-1.70**	-0.19
T3	-0.10**	-0.05	-0.20**	0.55**	1.25**	-0.14	-0.49	-1.50**	0.37*
T4	0.10***	-0.06	0.07*	0.83**	-0.52*	-0.03	1.52**	0.59**	-0.34*
T5	0.03	0.08*	0.05	-0.63**	-0.54*	-1.18**	0.78**	0.73**	-0.73**

I-Jagitial, II- Warangal, III- Hyderabad

* Significance at 0.01 level of probability ** Significance at 0.05 level of probability

Table 4.3.5.Contd ……..

Parents									
	Head rice recovery			Alkali spreading value			Water uptake		
	I	II	III	I	II	III	I	II	III
	Lines								
L1	2.02**	0.20	0.06	-0.31**	-0.28**	-0.39**	-11.28**	-4.89**	3.00**
L2	-5.05**	-1.41**	-2.82**	-0.36**	-0.39**	-0.45**	39.72**	37.11**	21.00**
L3	-0.43	0.82**	2.18**	0.52**	0.57**	0.53**	-16.61**	-21.89**	-40.33**
L4	1.66**	-0.04	2.61**	0.11	0.13*	0.17**	-11.28**	-11.22**	-0.67
L5	0.83**	-0.10	-1.30**	-0.51**	-0.60**	-0.53**	11.39**	2.78*	12.67**
L6	0.97**	0.52*	-0.74**	0.55**	0.56**	0.67**	-11.94**	-1.89	4.33**
Testers									
T1	-1.98**	1.94**	1.37**	-0.76**	-0.74**	-0.61**	-10.56**	-24.50**	20.33**
T2	-2.67**	-1.94**	-0.10**	0.46**	0.58**	0.46**	18.33**	12.44**	-1.33
T3	1.67**	-1.94**	0.67**	0.46**	0.26**	0.48**	-17.78**	-19.22**	8.11**
T4	0.89**	1.11**	-1.19**	-0.26**	-0.23**	-0.22**	7.50**	25.78**	-1.33
T5	2.09**	0.84**	-0.75**	0.10	0.13*	-0.13*	2.50	5.50**	-25.78**

I-Jagitial, II- Warangal, III- Hyderabad

*** Significance at 0.01 level of probability ** Significance at 0.05 level of probability**

Table 4.3.5. Contd …….

Parents	Gel consistency			Amylose content		
	I	II	III	I	II	III
Lines						
L1	1.39**	1.58**	1.19**	-0.76**	-1.44**	-0.35*
L2	-2.94**	0.84	1.39**	1.69**	1.10**	1.70**
L3	-0.88*	-2.69**	-0.01	-1.32**	0.19	-1.11**
L4	-0.94*	3.58**	-5.54**	0.48*	-0.35	0.40*
L5	0.86*	1.04*	1.12**	1.24**	1.16**	1.04**
L6	2.52**	-4.36**	1.86**	-1.34**	-0.66**	-1.68**
Testers						
T1	0.60	1.74**	0.34	0.55**	-0.47***	0.01
T2	-2.01**	0.08	1.57**	-0.22	-0.13	0.10
T3	0.21	-1.53**	-1.88**	0.41*	0.93**	0.33*
T4	-2.40**	-0.03	-1.49**	0.23	0.63**	0.36*
T5	3.60**	-0.26	1.46**	-0.96**	-0.96**	-0.80**

I-Jagitial, II- Warangal, III- Hyderabad

*** Significance at 0.01 level of probability ** Significance at 0.05 level of probability**

Table 4.3.6. Estimates of gca effects for yield, its components and quality characters in pooled analysis.

Parents	Days to 50 % flowering	Plant height	Panicle length	Productive tillers per plant	Number of grains per panicle	1000-grain weight	Grain yield per plant
Lines							
L1	-3.90**	-5.04**	0.42*	0.23*	-3.49**	0.49**	-0.85**
L2	-0.57*	4.26**	0.62**	-0.90**	4.60**	0.40*	-2.52**
L3	1.88**	4.60**	-0.31	0.26*	5.96**	-0.62**	1.48**
L4	3.92**	-1.28**	-0.35*	-0.66**	3.69**	0.11	0.11
L5	-4.72**	-7.53**	-1.19**	-0.19	-17.35**	-0.67**	-0.14
L6	3.39**	4.99**	0.81**	1.26*	6.58**	0.29	1.91**
Testers							
T1	-1.74**	10.12**	2.35**	-0.51**	19.75**	5.18**	4.95**
T2	-6.67**	-5.90**	-1.24**	0.47**	-8.54**	-0.94**	-1.27**
T3	9.00**	-2.23**	-0.67**	-0.42**	5.27**	-2.45**	-2.54**
T4	3.00**	-2.44**	-1.61**	-0.45**	-11.27**	-3.91**	-2.74**
T5	-3.59**	0.45	1.16**	0.90**	-5.21**	2.11**	1.60**

*** Significance at 0.01 level of probability** **** Significance at 0.05 level of probability**

Table 4.3.6. Contd …….

Parents	Kernel length	Kernel breadth	L/B ratio	Bran oil content	Milling %	Head rice recovery	Alkali spreading value
Lines							
L1	-0.31**	-0.01	-0.14**	1.92**	0.51**	0.76**	-0.33**
L2	-0.07 **	-0.05**	0.03	-0.98**	-2.47**	-3.09**	-0.40**
L3	-0.02	-0.03**	0.04	-0.54**	0.85**	0.86**	0.54**
L4	0.11 **	0.08**	-0.05*	-1.35**	0.56**	1.41**	0.14**
L5	-0.20 **	-0.14**	0.09**	1.22**	0.11	-0.19	-0.54**
L6	0.48 **	0.15**	0.03	-0.26	0.43**	0.25	0.59**
Testers							
T1	0.48 **	0.35**	-0.23**	-0.93**	0.39**	0.44**	-0.70**
T2	0.29 **	-0.08**	0.26**	1.07**	-0.70**	-1.57**	0.50**
T3	-0.69 **	-0.16**	-0.11***	0.55**	-0.54**	0.13	0.40**
T4	-0.29**	-0.13**	0.04	0.10	0.59**	0.27*	-0.24**
T5	0.21**	0.02*	0.05*	-0.78**	0.26*	0.73**	0.04

*** Significance at 0.01 level of probability** **** Significance at 0.05 level of probability**

Table 4.3.6. Contd …….

Parents	Water uptake	Gel consistency	Amylose content
Lines			
L1	-4.39**	1.39**	-0.85**
L2	32.61**	0.24	1.50**
L3	-26.28**	-1.19**	-0.75**
L4	-7.72**	-0.97**	0.18
L5	8.94**	1.01**	1.14**
L6	-3.17**	0.007	-1.22**
Testers			
T1	-4.91**	0.90**	0.03
T2	9.82**	-0.12	-0.09
T3	-9.63**	-1.07**	0.56**
T4	10.65**	-1.31**	0.41**
T5	-5.93**	1.60**	-0.91**

*** Significance at 0.01 level of probability** **** Significance at 0.05 level of probability**

Table 4.8.1.Variance of parents, F_1 and F_2 generations for the character bran oil in Keshari × Swarna cross combination

S.No	Keshari	Swarna	F_1 generation	F_2 generation
1	4.31	3.35	7.83	11.22

Table 4.8.2. PCV, GCV, Heritability and GA for bran oil content in F_2 generation

Cross combination	Bran oil content
Keshari × Swarna	
PCV	28.03
GCV	20.50
Heritability (%)	53.48
GA	4.93
GAM	41.39

$\bar{X}$ = mean of F2 population= 11.91

Table 4.4.1. Standard heterosis for bran oil content, yield and quality characters in rice (*Oryza sativa* L.) at different locations and in pooled analysis

	Days to 50 % flowering				Plant height (cm)				Panicle length (cm)			
	JGL	**WGL**	**HYD**	**Pooled**	**JGL**	**WGL**	**HYD**	**Pooled**	**JGL**	**WGL**	**HYD**	**Pooled**
L1T1	0.33	-5.39**	-9.45**	-4.68**	16.99**	-0.78	25.08**	13.93**	10.90 **	13.68 **	20.58 **	14.65 **
L1T2	-11.51**	-16.16**	-23.64**	-16.89**	-1.54	-4.09**	-3.10*	-2.97**	-20.94 **	-14.21 **	-9.61 *	-15.27 **
L1T3	26.32**	24.58**	26.91**	25.91**	-1.93	21.96**	-1.20	6.40**	-5.24	-2.86	-4.80	-4.25
L1T4	21.71**	18.52**	14.91**	18.49**	-10.27**	12.55**	12.67**	5.78**	-7.61	-10.62 **	-11.66 *	-9.86 **
L1T5	4.93**	-0.67	-0.36	1.37	7.68**	21.72**	6.62**	12.04**	9.79 *	0.40	2.74	4.37
L2T1	14.47**	10.10**	12.73**	12.44**	29.23**	37.64**	35.53**	34.36**	13.52 **	5.71	13.55 **	10.67 **
L2T2	3.95**	0.00	-10.45**	-1.94*	0.97	23.08**	2.44	8.97**	-5.82	-7.04	3.77	-3.55
L2T3	26.64**	23.23**	18.91**	23.06**	4.56*	33.92**	22.48**	21.00**	-8.83 *	-11.95 **	-8.23	-9.80 **
L2T4	10.20**	0.00	-5.82**	1.71*	-0.85	19.09**	8.26**	9.19**	-1.93	4.65	-21.44 **	-5.05 *
L2T5	12.17**	4.71**	0.73	6.05**	-5.83**	24.17**	9.40**	9.85**	4.55	4.25	-5.66	1.55
L3T1	9.54**	6.73**	1.82	6.16**	16.14**	28.25**	26.73**	27.46**	-0.36	-8.63 *	-10.81 *	-6.34 **
L3T2	15.13**	11.45**	6.55**	11.19**	-12.82**	18.89**	-3.96**	1.12	-6.51	-14.87 **	-17.15 **	-12.58 **
L3T3	23.36**	16.50**	14.55**	18.26**	0.12	21.17**	11.08**	11.22**	-1.41	-2.66	-6.35	-3.26
L3T4	20.72**	12.12**	13.82**	15.64**	7.92**	24.96**	17.95**	17.33**	-5.93	-6.37	-17.50 **	-9.36 **
L3T5	10.86**	3.03*	-6.91**	2.63**	19.19**	39.62**	24.41**	27.99**	1.10	9.03 *	5.15	5.14 *
L4T1	24.67**	19.19**	18.91**	21.00	33.90**	22.23**	-2.88*	16.58**	-4.11	-1.20	-6.69	-3.77
L4T2	12.83**	6.06**	1.45	6.96**	-3.67*	18.31**	8.20**	8.08**	-20.97 **	-12.99 **	-18.52 **	-17.36 **
L4T3	17.43**	18.86**	10.91**	15.87**	-8.84**	14.87**	0.76	2.66**	-3.81	-7.70 *	-11.15 *	-7.31 **
L4T4	12.83**	8.42**	4.00*	8.56**	11.62**	26.66**	15.83**	18.24**	-0.83	-3.98	0.69	-1.55
L4T5	11.84**	13.13**	10.91**	11.99**	6.37**	17.15**	3.83**	9.09**	-2.51	0.27	12.69 **	2.80
L5T1	-2.63*	4.71**	-2.55	-0.11	-0.77	24.58**	8.33**	11.10**	8.63 *	8.90 *	5.66	7.89 **
L5T2	5.92**	14.38**	4.73**	5.02**	16.33**	7.71**	-0.41	7.33**	1.88	-3.45	6.00	1.10
L5T3	8.55**	13.13**	3.64*	8.56**	2.74	-7.16**	2.34**	-0.75	-16.55 **	-9.03 *	-16.81 **	-13.88 **
L5T4	19.08**	15.15**	17.45**	17.24**	-4.86**	4.94**	0.79	0.51	-40.69 **	-29.08 **	-11.15 *	-28.09 **
L5T5	-7.89**	-10.77**	-13.82**	-10.73**	-8.38**	11.11**	7.69**	4.05**	-13.21 **	-5.31	-21.44 **	-12.65 **
L6T1	8.55**	8.75**	5.09**	7.53**	30.00**	42.00**	27.20**	33.04**	9.38 *	13.41 **	24.01 **	14.99 **
L6T2	7.57**	11.78**	3.27*	7.65**	12.32**	20.93**	9.91**	14.35**	-15.59 **	-6.64	-1.37	-8.30 **
L6T3	19.41**	18.86**	12.00**	16.89**	17.37**	25.91**	14.25**	19.12**	-7.45	1.46	-1.72	-2.57
L6T4	10.20**	18.18**	0.73	9.93**	-4.02*	20.90**	4.05**	7.34**	-17.30 **	-13.28 **	-2.92	-11.76 **
L6T5	21.38**	18.52**	18.91**	19.63**	14.36**	17.12**	8.93**	13.32**	3.45	2.92	12.35 **	5.77 *

Table 4.4.1. contd …..

	Number of productive tillers per plant				Number of grains per panicle				1000-grain weight (g)			
	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled
L1T1	-3.03	-35.00 **	-19.44 **	-20.18 **	44.84 **	19.16 **	-3.18 *	19.42 **	0.76	-6.63	6.79	0.00
L1T2	-15.15 **	-20.00 **	-5.56	-13.76 **	16.58 **	11.23 **	-22.98 **	1.46	-2.29	-4.90	11.75 *	1.13
L1T3	-15.15 **	-17.50 **	2.78	-10.09 **	34.24 **	0.00	-37.16 **	-2.11 *	-25.19 **	-22.19 **	-16.39 **	-21.40 **
L1T4	-30.30 **	-7.50	-13.89 **	-16.51 **	25.27 **	-5.07 **	-27.63 **	-3.49 **	0.00	1.44	13.41 **	4.66
L1T5	0.00	7.50	8.33	5.50 *	-14.40 **	-16.30 **	-17.11 **	-16.00 **	21.68 **	8.50 *	26.32 **	18.43 **
L2T1	-36.36 **	-37.50 **	-38.89 **	-37.61 **	20.65 **	8.59 **	32.76 **	20.23 **	43.97 **	30.26 **	57.28 **	43.22 **
L2T2	-9.09	-15.00 **	-13.89 **	-12.84 **	9.51 **	-5.95 **	-29.58 **	-9.18 **	-4.43	-8.36	1.99	-3.84
L2T3	-24.24 **	-20.00 **	-27.78 **	-23.85 **	31.25 **	6.61 **	-11.74 **	7.88 **	2.14	-3.60	1.66	-0.05
L2T4	-48.48 **	-22.50 **	5.56	-21.10 **	2.99	-2.64	-1.71	-0.65	-35.42 **	-21.33 **	-27.81 **	-28.06 **
L2T5	-6.06	-10.00 *	-2.78	-6.42 *	29.08 **	2.42	2.93	10.56 **	-16.43 **	-11.38 **	-2.98	-10.48 **
L3T1	-24.24 **	-27.50 **	-30.56 **	-27.52 **	41.03 **	12.56 **	-10.51 **	13.40 **	0.55	-8.79 *	26.82 **	5.36 *
L3T2	3.03	-7.50	16.67 **	3.67	7.88 **	-1.32	-3.18 *	0.81	13.59 **	2.02	-3.15	4.30
L3T3	-15.15 **	-27.50 **	-19.44 **	-21.10 **	80.71 **	39.43 **	11.98 **	42.65 **	-16.79 **	-32.28 **	8.77	-14.39 **
L3T4	-27.27 **	-5.00	-5.56	-11.93 **	-25.54 **	-25.77 **	-47.19 **	-32.82 **	-19.57 **	-26.95 **	-21.36 **	-22.74 **
L3T5	-12.12 *	2.50	16.67 **	2.75	33.97 **	5.73 **	-7.58 **	9.75 **	3.05	4.47	7.55	4.95
L4T1	-6.06	-22.50 **	11.11 *	-6.42 *	51.63 **	14.54 **	50.61 **	37.61 **	12.67 **	16.43 **	26.49 **	18.28 **
L4T2	3.03	-27.50 **	-25.00 **	-17.43 **	34.51 **	-8.81 **	-31.78 **	-3.49 **	-8.85 *	-3.89	5.46	-2.66
L4T3	-15.15 **	-27.50 **	2.78	-13.76 **	27.45 **	-32.38 **	4.89 **	-2.11 *	-15.27 **	-20.03 **	-6.13	-14.13 **
L4T4	-24.24 **	-15.00 **	-27.78 **	-22.02 **	10.60 **	-19.16 **	-10.76 **	-7.47 **	-24.12 **	-13.98 **	-23.51 **	-20.33 **
L4T5	-27.27 **	-32.50 **	-36.11 **	-32.11 **	9.24 **	-4.19 **	-0.73	0.97	10.69 **	8.50 *	20.53 **	12.95 **
L5T1	-6.06	-20.00 **	0.00	-9.17 **	43.75 **	-16.74 **	-47.92 **	-9.02 **	24.43 **	21.90 **	37.75 **	27.65 **
L5T2	-15.15 **	-12.50 **	-13.89 **	-13.76 **	1.90	-11.89 **	0.00	-3.82 **	-33.59 **	-30.12 **	-27.98 **	-30.62 **
L5T3	-21.21 **	-2.50	-13.89 **	-11.93 **	-26.09 **	11.01 **	-28.85 **	-13.32 **	-6.41	-13.11 **	-2.65	-7.63 **
L5T4	-21.21 **	-25.00 **	-33.33 **	-26.61 **	-8.42 **	8.81 **	-33.99 **	-10.56 **	-27.94 **	-30.40 **	-18.54 **	-25.91 **
L5T5	-9.09	-22.50 **	0.00	-11.01 **	14.95 **	-16.52 **	-39.36 **	-14.70 **	11.60 **	7.20	20.53 **	12.80 **
L6T1	3.03	-10.00 *	2.78	-1.83	48.37 **	22.25 **	-9.78 **	19.42 **	37.56 **	31.56 **	48.01 **	38.66 **
L6T2	3.03	-7.50	5.56	0.00	-15.22 **	-7.05 **	-5.13 **	-8.85 **	2.93	-12.68 **	-2.32	-4.24
L6T3	-9.09	-22.50 **	-19.44 **	-17.43 **	4.58 *	2.42	0.49	4.55 **	-24.58 **	-21.47 **	-13.41 **	-20.02 **
L6T4	3.03	-5.00	-2.78	-1.83	38.37 **	26.21 **	-15.65 **	19.98 **	-20.76 **	-32.71 **	-22.68 **	-25.60 **
L6T5	9.09	5.00	11.11 *	8.26 **	11.96 **	-9.47 **	2.69	0.97	6.41	4.90	18.38 **	9.58 **

	Grain yield per plant (g)				Kernel length (mm)				Kernel breadth (mm)			
	JGL	**WGL**	**HYD**	**Pooled**	**JGL**	**WGL**	**HYD**	**Pooled**	**JGL**	**WGL**	**HYD**	**Pooled**
L1T1	29.97 **	22.60 **	-12.54	13.12 **	8.66 **	6.29 **	9.48 **	8.15 **	22.49**	18.78**	32.04**	24.45**
L1T2	11.42	6.83	-24.34 **	-2.15	-6.10 **	5.20 *	2.88	0.66	2.21	11.17**	-11.30**	0.68
L1T3	-33.28 **	-43.36 **	-40.56 **	-39.45 **	-29.00 **	-11.21 **	-26.73 **	-22.34 **	-8.01**	-6.09**	-5.56*	-6.55**
L1T4	7.62	11.43	-4.13	5.14	-11.57 **	-10.06 **	-13.42 **	-11.69 **	-4.77	4.57*	-8.09**	-2.77
L1T5	79.47 **	19.45 **	44.10 **	45.37 **	8.89 **	1.94	5.98 **	5.61 **	10.05**	6.60**	8.94**	8.53**
L2T1	27.98 **	24.05 **	-8.55	14.39 **	19.15 **	13.15 **	14.95 **	15.75 **	23.51**	24.53**	22.09**	23.38**
L2T2	24.01 **	12.09	-26.40 **	2.84	16.98 **	12.01 **	16.36 **	15.12 **	-4.26	-0.34	-0.51	-1.69
L2T3	-26.82 **	17.61 **	6.49	0.78	-20.11 **	-19.67 **	-20.42 **	-20.07 **	-15.67**	-5.25**	0.84	-6.66**
L2T4	-23.84 **	4.20	-41.30 **	-19.19 **	-9.34 **	-10.92 **	-8.07 **	-9.44 **	-10.39**	2.03	2.02	-2.09
L2T5	-12.25	2.63	-32.89 **	-13.56 **	0.85	1.72	-3.21 *	-0.23	0.34	0.85	2.36	1.19
L3T1	69.37 **	41.00 **	43.95 **	50.37 **	15.84 **	14.35 **	14.78 **	14.99 **	25.55**	28.43**	27.66**	27.22**
L3T2	57.95 **	15.11 *	-35.69 **	10.92 **	-3.36	-5.32 *	-4.06 *	-4.24 **	-0.34	4.06*	-0.84	0.96
L3T3	69.37 **	11.17	15.63 *	29.86 **	5.87 **	4.17	7.11 **	5.72 **	-13.46**	-10.15**	-12.48**	-12.03**
L3T4	-32.45 **	-12.48 *	-50.88 **	-31.13 **	-7.41 **	-11.21 **	-5.08 **	-7.88 **	-2.56	3.89*	-2.53	-0.40
L3T5	8.11	29.70 **	-0.74	13.22 **	-1.42	-4.80 *	-4.17 *	-3.47 **	3.92	9.81**	2.19	5.31**
L4T1	49.67 **	34.03 **	24.48 **	35.49 **	19.54 **	20.93 **	18.84 **	19.77 **	35.26**	34.01**	33.90**	34.39**
L4T2	64.40 **	-6.31	-32.45 **	5.92	1.94	-5.26 *	4.34 **	0.36	-1.87	-1.02	-4.38	-2.43
L4T3	6.62	-34.43 **	-18.73 **	-17.08 **	-10.42 **	-23.04 **	-16.69 **	-16.71 **	11.75**	12.86**	10.12**	11.58**
L4T4	-9.74	1.84	17.70 *	3.68	2.22	-5.03 *	1.92	-0.28	-2.39	-1.86	-4.22	-2.82
L4T5	51.32 **	-14.19 *	15.78 *	15.12 **	9.40 **	15.27 **	15.12 **	13.27 **	5.79*	7.61**	8.60**	7.34**
L5T1	39.57 **	28.12 **	-1.62	21.63 **	-15.56 **	-13.66 **	-25.10 **	-18.14 **	-4.60	-7.45**	-8.26**	-6.78**
L5T2	7.12	-4.60	-18.44 **	-5.73	14.76 **	11.66 **	10.83 **	12.41 **	-2.04	1.86**	1.69	0.51
L5T3	19.80 *	-26.68 **	0.88	-3.79	-6.21 **	-8.23 **	-10.72 **	-8.39 **	7.84**	4.40*	6.91*	6.38**
L5T4	12.25	6.96	8.70	9.10 *	4.56 *	0.97	-1.86	1.21	-10.39**	-5.58**	-7.93**	-7.96**
L5T5	33.28 **	-13.92 *	35.10 **	16.30 **	3.30	1.77	2.82	2.63 *	1.02	1.18	1.18	1.13
L6T1	66.23 **	43.23 **	26.70 **	44.54 **	15.73 **	19.67 **	14.89 **	16.75 **	39.01**	37.06**	37.77**	37.94**
L6T2	31.79 **	-15.51 *	-0.44	3.48	14.02 **	13.04 **	14.50 **	13.85 **	7.33**	13.37**	10.96**	10.56**
L6T3	41.23 **	10.25	-14.31 *	11.26 **	2.05	2.29	-6.09 **	-0.61	-9.03**	-4.91*	-6.07*	-6.66**
L6T4	10.43	22.73 **	-8.11	8.86 *	8.09 **	5.43 *	5.58 **	6.37 **	7.33**	10.83**	7.93**	8.70**
L6T5	29.64 **	12.35 *	3.54	14.54 **	13.90 **	12.41 **	8.91 **	11.73 **	14.82**	17.60**	15.01**	15.81**

	L/ B ratio				Bran oil content (%)				Milling percent			
	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled
L1T1	-11.07**	-10.57 *	-17.06 **	-12.91**	-17.55 **	-18.25 **	-24.04 **	-19.91 **	-0.86	6.55 **	6.74 **	4.13 **
L1T2	-7.72 *	-5.85	16.16 **	0.90	-7.15	-9.37 *	0.89	-5.26	1.81*	-2.28 **	1.91 *	0.46
L1T3	-22.60 **	-5.51	-21.07 **	-16.42 **	2.89	0.89	-8.80	-1.61	5.92 **	-1.00	-2.93 **	0.69
L1T4	-6.82	-14.17 **	-6.02	-8.99 **	-11.19 **	-28.30 **	-10.39 *	-16.67 **	5.20 **	0.00	1.61	2.27 **
L1T5	-0.56	-4.50	-2.79	-2.61	-41.05 **	-33.13 **	-33.73 **	-35.99 **	9.21 **	4.56 **	4.64 **	6.15 **
L2T1	-3.36	-9.11 *	-5.57	-6.01 *	-35.85 **	-40.86 **	-21.86 **	-32.94 **	-10.83 **	6.13 **	-5.57 **	-3.39 **
L2T2	22.82 **	12.49 **	17.17 **	17.50 **	-31.03 **	-35.64 **	-18.30 **	-28.40 **	3.34 *	5.13 **	0.59	3.04 **
L2T3	-5.15	-15.52 **	-21.07 **	-13.92 **	-26.22 **	-41.63 **	-33.73 **	-33.85 **	-10.11 **	-6.41 **	0.00	-5.55 **
L2T4	1.68	-13.05 **	-10.03 *	-7.13 **	-35.60 **	-42.79 **	-31.75 **	-36.75 **	1.81*	1.00	-2.64 **	0.08
L2T5	1.01	0.67	-5.24	-1.19	-25.64 **	-38.54 **	-32.74 **	-32.30 **	-4.29 **	1.80 *	-3.37 **	-1.94 **
L3T1	-7.38	-10.91 *	-9.81 *	-9.37 **	-35.66 **	-36.99 **	-26.81 **	-33.20 **	-0.14	1.38	-1.12	0.05
L3T2	-2.57	-9.34 *	-3.01	-4.96 *	-44.13 **	-35.45 **	-9.00	-29.70 **	3.05 *	0.00	6.74 **	3.23 **
L3T3	22.71 **	15.86 **	22.41 **	20.34 **	-38.93 **	-23.85 **	-34.32 **	-32.36 **	1.86*	-0.43	6.89 **	2.74 **
L3T4	-4.59	-14.62 **	-2.56	-7.24 **	-17.36 **	-34.09 **	-13.16 **	-21.60 **	4.63 **	6.70 **	5.43 **	5.59 **
L3T5	-4.81	-13.27 **	-6.24	-8.10 **	-34.89 **	-36.99 **	-31.36 **	-34.44 **	4.48 **	5.27 **	3.81 **	4.53 **
L4T1	-11.30 **	-9.90 *	-11.48 **	-10.90 **	-36.81 **	-41.24 **	-39.47 **	-39.17 **	-0.38	2.14 **	7.62 **	3.09 **
L4T2	5.59	-4.61	8.92 *	3.32	-43.36 **	-36.03 **	-21.86 **	-33.85 **	-1.62	-1.99 *	3.81 **	0.03
L4T3	-19.69 **	-31.95 **	-24.53 **	-25.37 **	-34.69 **	-28.28 **	-20.47 **	-27.88 **	6.73 **	-2.33 **	4.40 **	2.91 **
L4T4	5.03	-3.04	6.80	2.95	-30.65 **	-33.84 **	-37.49 **	-33.96 **	7.49 **	5.27 **	5.43 **	6.07 **
L4T5	3.80	6.86	5.80	5.49 *	-41.71 **	-41.63 **	-37.09 **	-40.17 **	0.38	2.85 **	2.49 **	1.90 **
L5T1	-11.41 **	-6.86	-17.95 **	-12.09 **	-28.53 **	-40.28 **	-14.54 **	-27.89 **	3.24 *	6.70 **	4.94 **	4.96 **
L5T2	17.23 **	9.45 *	9.03 *	11.90 **	-17.68 **	-18.44 **	-4.06	-13.47 **	-0.86	1.99 *	-5.87 **	-1.54 **
L5T3	-12.64 **	-12.15 **	-16.39 **	-13.73 **	-21.02 **	-15.69 **	-18.46 **	-18.39 **	2.05*	6.55 **	1.47	3.38 **
L5T4	17.45 **	6.97	6.80	10.41 **	-18.30 **	-18.28 **	-17.35 **	-17.98 **	3.15 *	0.28	0.00	1.15 *
L5T5	2.35	0.45	1.78	1.53	-20.03 **	-14.65 **	-32.54 **	-22.33 **	6.97 **	1.71 *	-0.15	2.86 **
L6T1	-16.33 **	-12.49 **	-16.39 **	-15.07 **	-43.94 **	-44.05 **	-38.28 **	-42.12 **	6.39 **	6.55 **	6.74 **	6.56 **
L6T2	6.71	0.00	3.46	3.40	-21.40 **	-8.77 *	-13.71 **	-14.64 **	3.77 **	-3.99 **	2.49 **	0.74
L6T3	12.42 **	7.76	-0.22	6.64 **	-31.23 **	-27.14 **	-28.98 **	-29.12 **	0.62	4.13 **	4.79 **	3.17 **
L6T4	0.89	-4.95	-2.01	-2.01	-26.60 **	-39.89 **	-30.56 **	-32.36 **	2.00*	5.13 **	-1.47	1.92 **
L6T5	-0.78	-4.95	-5.02	-3.58	-26.80 **	-33.13 **	-14.34 **	-24.84 **	1.24	3.37 **	-2.49 **	0.74

	Head rice recovery (%)				Alkali spreading value				Water uptake (mm)			
	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled	JGL	WGL	HYD	Pooled
L1T1	-5.74 **	0.52	0.49	-1.50*	1.19	4.44	20.65 **	8.34**	-8.33 **	-2.80	4.91 **	-1.78
L1T2	-6.64 **	-11.99 **	-5.37 **	-8.07**	1.26	-4.80	18.94 **	4.58	10.42 **	11.89 **	6.13 **	9.33**
L1T3	9.34 **	-6.04 **	-5.20 **	-0.83	25.93 **	18.34 **	32.57 **	25.31**	-4.17 *	-2.80	7.98 **	0.67
L1T4	0.84	-4.48 **	-7.15 **	-3.66**	-7.41	-5.44	6.12	-2.54	8.33 **	30.07 **	-3.07 *	11.11**
L1T5	9.84 **	-2.92 *	-1.79	1.55*	-11.11	-11.10 *	-8.65 **	-10.35**	12.50 **	35.66 **	1.23	15.78**
L2T1	-13.61 **	-1.35	-12.36 **	-8.95**	-0.96	4.01	16.00 **	6.02*	25.00 **	30.77 **	31.29 **	29.11**
L2T2	-10.40 **	-6.04 **	-6.02 **	-7.43**	20.96 **	15.62 **	39.59 **	24.83**	33.33 **	34.97 **	-6.13 **	19.56**
L2T3	-11.02 **	-11.78 **	-3.90 **	-8.91**	0.96	-6.30	10.61 **	1.39	16.67 **	20.98 **	28.83 **	22.44**
L2T4	-5.57 **	-10.73 **	-9.27 **	-8.59**	-18.44 **	-18.62 **	-14.29 **	-17.22**	29.17 **	52.45 **	17.18 **	32.22**
L2T5	-11.42 **	-7.61 **	-10.89 **	-9.92**	2.44	-5.09	10.29 **	2.22	20.83 **	20.98 **	-20.86 **	5.78**
L3T1	-8.72 **	-9.02 **	-5.53**	-7.76**	3.70	6.38	24.90 **	11.18**	8.33 **	8.39 **	8.59 **	8.44**
L3T2	-2.36	-5.42 **	2.11	-1.93**	24.67 **	24.14 **	41.31 **	29.61**	-12.50 **	-12.59 **	-7.98 **	-10.89**
L3T3	-0.34	-7.97 **	1.14	-2.49**	25.85 **	14.83 **	37.80 **	25.66**	-8.33 **	14.69 **	-17.18 **	-4.22**
L3T4	-3.37 *	2.08	-0.49	-0.52	13.56 *	12.75 **	41.88 **	22.01**	3.47	3.50 *	-23.31 **	-6.22**
L3T5	1.74	0.21	0.98	0.96	34.59 **	34.74 **	35.84 **	35.03**	16.67 **	22.38 **	-22.70 **	4.22**
L4T1	-5.40 **	-4.48 **	2.60 *	-2.42**	-18.52 **	-25.79 **	-4.73	-16.82**	2.78	2.80	5.52 **	3.78**
L4T2	-9.00 **	-10.73 **	-1.14	-6.98**	8.59	15.40 **	23.84 **	15.69**	20.83 **	40.56 **	7.36 **	22.22**
L4T3	10.12 **	-10.73 **	0.65	-0.25	30.59 **	28.65 **	54.94 **	37.42**	-6.25 **	-4.90 **	7.36 **	-0.89
L4T4	3.60 *	0.36	2.38 *	2.08**	13.56 *	2.72	32.73 **	15.66**	0.00	17.48 **	-12.27 **	1.11
L4T5	5.23 **	-1.20	-2.76 *	0.34	22.22 **	24.28 **	31.67 **	25.86**	1.39	2.80	2.45	2.22*
L5T1	-4.72 **	-1.09	2.11	-1.19	-23.41 **	-29.80 **	-10.04 **	-21.53**	-6.25 **	-6.29 **	-3.68 **	-5.33**
L5T2	-5.96 **	-5.26 **	-11.22 **	-7.47**	18.52 **	18.91 **	30.29 **	22.29**	29.17 **	34.27 **	-6.13 **	18.00**
L5T3	-2.36	-9.17 **	-3.58 **	-5.12**	16.07 **	7.81	34.37 **	18.81**	8.33 **	23.08 **	-1.84	9.33**
L5T4	0.79	-7.45 **	-12.03 **	6.33**	-30.89 **	-29.23 **	-15.18 **	-25.46**	32.64 **	32.17 **	43.56 **	36.44**
L5T5	9.84 **	-4.33 **	-5.37 **	-0.13	7.41	-0.50	13.71 **	6.57*	2.08	4.90 **	3.07 *	3.33**
L6T1	6.81 **	1.77	2.60 *	3.66**	-9.93	-17.34 **	5.31	-7.83**	2.78	4.20 **	12.27 **	6.67**
L6T2	-3.94 *	-10.58 **	-2.76 *	-5.85**	40.74 **	42.55 **	55.27 **	45.86**	15.28 **	20.98 **	17.79 **	18.00**
L6T3	-0.17	-4.33 **	-6.02 **	-3.55**	14.81 *	7.81	41.71 **	20.65**	0.00	-0.70	6.75 **	2.22**
L6T4	1.41	-1.20	-8.46 **	-2.78**	48.44 **	46.35 **	57.22 **	50.42**	-4.17 *	27.97 **	-11.04 **	3.56**
L6T5	-5.40 **	-8.08 **	-10.89 **	-8.16**	11.04	11.82 **	40.24 **	20.32**	3.47	25.87 **	-6.13 **	7.11**

			Gel consistency (mm)			Amylose content (%)		
	JGL	**WGL**	**HYD**	**Pooled**	**JGL**	**WGL**	**HYD**	**Pooled**
L1T1	-3.95 *	0.00	-12.50 **	-5.78**	6.42*	-7.12**	-5.74*	-2.27
L1T2	-4.82 **	-3.03	-4.74 **	-4.26**	-16.97**	-12.31**	-10.90**	-13.33**
L1T3	-1.32	9.60 **	-20.26 **	-4.71**	3.21	7.12**	-1.29	2.96
L1T4	-20.61 **	3.03	-5.17 **	-8.05**	13.00**	-3.56	-0.57	2.81
L1T5	-6.14 **	10.61 **	-17.24 **	-5.02**	-13.76**	-21.36**	-9.76**	-14.91**
L2T1	-26.32 **	19.70 **	-4.31 **	-4.71**	21.56**	10.83**	14.35**	15.51**
L2T2	-12.28 **	-14.65 **	-7.76 **	-11.40**	25.08**	16.47**	7.17**	16.05**
L2T3	-7.02 **	-4.04	-21.12 **	--11.09**	-0.15	4.30	-5.74*	-0.59
L2T4	-14.47 **	9.09 **	-25.00 **	-11.09**	-9.48**	-8.46**	-1.43	-6.37**
L2T5	-5.26 **	4.55 *	-0.43	-0.61	11.01**	-3.86	1.58	2.81
L3T1	-0.44	-4.04	-21.12 **	-8.81**	-7.03**	-10.83**	-18.36**	-12.20**
L3T2	-12.72 **	9.60 **	-18.97 **	-8.21**	-15.14**	-7.12**	-16.07**	-12.79**
L3T3	-18.42 **	4.55 *	-6.90 **	-7.45**	11.31**	15.13**	-4.59	7.11**
L3T4	-3.07	-8.08 **	-12.07 **	-7.75**	-2.75	5.34*	-9.33**	-2.32
L3T5	-17.11 **	-14.14 **	-8.62 **	-13.22**	-7.49*	-3.56	3.73	-2.32
L4T1	-24.56 **	9.09 **	-20.26 **	-12.92**	-0.92	-13.06**	-5.31*	-6.47**
L4T2	-3.95 *	14.14 **	-15.95 **	-2.74**	12.84**	-1.48	1.58	4.20**
L4T3	-10.09 **	-3.54	-30.17 **	-15.20**	0.46	-7.27**	-4.73*	-3.90*
L4T4	-5.70 **	13.13 **	-17.24 **	-4.10**	20.80**	11.42**	11.05**	14.32**
L4T5	-7.89 **	2.53	-19.83 **	-8.97**	-12.84**	-2.52	-14.63**	-10.02**
L5T1	-2.63	13.13 **	-18.97 **	-3.65**	5.50	-2.37	0.72	1.23
L5T2	-12.28 **	2.02	-5.60 **	-5.62**	13.00**	6.68**	11.19**	10.27**
L5T3	-10.53 **	-5.05 *	-4.74 **	-6.84**	17.74**	13.26**	11.91**	14.24**
L5T4	-14.91 **	8.08 **	-18.53 **	-9.27**	-7.95*	2.37	-9.04**	-4.89**
L5T5	0.00	-2.02	-12.50 **	-5.02**	9.93**	0.59	-13.20**	-1.13
L6T1	7.46 **	-12.12 **	-1.29	-1.52**	0.76	3.86	-10.19**	-1.98
L6T2	-25.00 **	2.53	-15.95 **	-13.53**	-13.91**	-11.87**	-15.35**	-13.73**
L6T3	-6.14 **	-5.56 **	-12.50 **	-8.21**	-10.24**	-14.09**	-11.76**	-12.05**
L6T4	-15.35 **	-15.66 **	-14.66 **	-15.20**	3.67	3.41	-6.31**	0.15
L6T5	9.65 **	6.06 **	-11.21 **	1.22	-1.68	-1.19	-s13.20**	-5.48**

Table 4.2.1. Mean performance of days to 50% flowering, plant height and panicle length in 3 locations and over locations

Genotypes	Days to 50%flowering				Plant height (cm)				Panicle length (cm)			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG
	Lines											
L1	83.66	81.00	76.00	80.22	80.90	84.60	87.23	84.24	22.03	23.33	20.17	21.84
L2	123.00	120.00	113.0	118.67	109.16	114.46	119.63	114.42	22.20	23.77	19.27	21.74
L3	119.00	115.00	111.67	115.22	104.63	109.07	114.40	109.37	21.21	22.80	20.13	21.38
L4	118.00	116.00	107.33	113.78	79.13	80.03	86.57	81.91	21.49	23.10	20.60	21.73
L5	82.00	81.67	77.33	80.33	78.63	84.17	86.30	83.03	20.69	22.43	18.20	20.44
L6	116.33	115.00	105.67	112.33	102.53	107.73	110.53	106.93	23.10	24.27	22.13	23.17
	Testers											
T1	105.00	106.00	96.67	102.56	110.33	119.53	129.93	119.93	25.53	27.13	24.47	25.71
T2	102.00	99.00	91.33	97.44	86.87	88.83	89.20	88.30	20.13	21.57	23.67	21.79
T3	122.33	117.67	111.33	117.11	97.10	94.17	101.53	97.60	21.57	20.80	18.17	20.18
T4	116.33	112.00	106.00	111.44	90.30	102.47	100.77	97.84	16.93	18.60	20.17	18.57
T5	101.33	99.00	91.67	97.33	86.33	97.77	105.27	96.46	24.17	25.10	19.43	22.90
	Cross combinations											
L1T1	101.67	93.67	83.00	92.78	101.00	97.00	131.67	109.89	26.80	28.53	23.43	26.26
L1T2	89.67	83.00	70.00	80.89	85.00	93.77	102.00	93.59	19.11	21.53	17.57	19.40
L1T3	128.00	123.33	116.33	122.56	84.67	119.23	104.00	102.63	22.90	24.38	18.50	21.93
L1T4	123.33	117.33	105.33	115.33	77.47	110.03	118.60	102.03	22.33	22.43	17.17	20.64
L1T5	106.33	98.33	91.33	98.67	92.97	119.00	112.23	108.07	26.53	25.20	19.97	23.90
L2T1	116.00	109.00	103.33	109.45	111.57	134.57	142.67	129.60	27.43	26.53	22.07	25.34
L2T2	105.33	99.00	82.00	95.44	87.17	120.33	107.83	105.11	22.76	23.33	20.17	22.09
L2T3	128.33	122.00	109.00	119.78	90.27	130.93	128.93	116.71	22.03	22.10	17.83	20.66
L2T4	111.67	99.00	86.33	99.00	85.60	116.40	113.97	105.32	23.70	26.27	15.27	21.74
L2T5	113.67	103.67	92.33	103.22	81.30	121.40	115.17	105.96	25.27	26.17	18.33	23.26

Table 4.2.1.Contd…….

L3T1	111.00	105.67	93.33	103.33	100.27	135.17	133.40	122.95	24.08	22.93	17.33	21.45
L3T2	116.67	110.33	97.67	108.22	75.27	116.23	101.10	97.53	22.59	21.37	16.10	20.02
L3T3	125.00	115.33	105.00	115.11	86.43	118.47	116.93	107.28	23.83	24.43	18.20	22.15
L3T4	122.33	111.00	104.33	112.56	93.17	122.17	124.17	113.17	22.73	23.50	16.03	20.76
L3T5	112.33	102.00	85.33	99.89	102.90	136.50	130.97	123.46	24.43	27.37	20.43	24.08
L4T1	126.33	118.00	109.00	117.78	115.60	119.50	102.23	112.45	23.17	24.80	18.13	22.04
L4T2	114.33	105.00	93.00	104.11	83.17	115.67	113.90	104.24	19.10	21.84	15.83	18.92
L4T3	119.00	117.67	101.67	112.78	78.70	112.30	106.07	99.02	23.25	23.17	17.27	21.23
L4T4	114.33	107.33	95.33	105.67	96.37	123.83	121.93	114.04	23.97	24.10	19.57	22.54
L4T5	113.33	112.00	101.67	109.00	91.83	114.53	109.30	105.22	23.56	25.17	21.90	23.54
L5T1	98.67	103.67	89.33	97.22	85.67	121.80	114.03	107.17	26.25	27.33	20.53	24.71
L5T2	107.33	103.33	96.00	102.22	100.43	105.30	104.83	103.52	24.62	24.23	20.60	23.15
L5T3	110.00	112.00	95.00	105.67	88.70	90.77	107.73	95.73	20.17	22.83	16.17	19.72
L5T4	120.67	114.00	107.67	114.11	82.13	102.60	106.10	96.94	14.33	17.80	17.27	16.47
L5T5	93.33	88.33	79.00	86.89	79.10	108.63	113.37	100.37	20.97	23.77	15.27	20.00
L6T1	110.00	107.67	96.33	104.67	112.23	138.83	133.90	128.32	26.43	28.47	24.10	26.33
L6T2	109.00	110.67	94.67	104.78	96.97	118.23	115.70	110.30	20.40	23.43	19.17	21.00
L6T3	121.00	117.67	102.67	113.78	101.33	123.10	120.27	114.90	22.37	25.47	19.10	22.31
L6T4	111.67	117.00	92.33	107.00	82.87	118.20	109.53	103.53	19.99	21.77	18.87	20.21
L6T5	123.00	117.33	109.00	116.45	98.73	114.50	114.67	109.30	25.00	25.83	21.83	24.22
Mean	112.01	107.48	96.96	105.48	92.07	112.24	112.40	105.57	22.66	23.88	19.28	21.94
S.E.(d)	11.24	10.85	11.13	2.63	10.95	14.62	13.18	6.74	2.82	2.51	2.53	1.29
C.V.	1.26	1.69	1.86	3.05	2.00	1.35	1.48	7.82	5.27	4.79	5.55	7.20

JGL- Jagitial **WGL- Warangal** **HYD- Hyderabad**

AVG- Average (pooled)

Table 4.2.2. Mean performance of number of productive tillers per plant, number of grains per panicle and 1000-grain weight in 3 locations and over locations

Genotypes	Number of Productive tillers per plant				Number of grains per panicle				1000 grain weight (g)			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG
	Lines											
L1	8.33	10.33	9.33	9.33	109.00	123.00	99.00	110.33	16.74	17.53	15.30	16.53
L2	8.33	11.00	9.67	9.67	118.67	140.00	125.67	128.11	25.48	22.97	21.13	23.19
L3	8.67	10.00	9.33	9.33	123.33	143.67	138.33	135.11	18.40	17.47	19.20	18.36
L4	10.33	11.67	12.67	11.56	118.67	138.67	129.67	129.00	22.93	21.13	20.53	21.53
L5	9.33	11.67	10.33	10.44	102.33	110.00	115.33	109.22	17.55	18.20	17.50	17.75
L6	9.33	12.00	11.00	10.78	121.67	136.00	130.67	129.44	25.10	24.23	21.50	23.61
	Testers											
T1	10.00	9.67	11.33	10.33	117.33	148.33	139.33	135.00	25.93	28.43	22.47	25.61
T2	7.67	10.33	9.00	9.00	105.67	122.33	125.00	117.67	18.13	21.13	16.50	18.59
T3	9.67	9.00	8.67	9.11	131.00	140.00	148.00	139.67	16.01	16.43	17.20	16.55
T4	11.00	11.33	9.67	10.67	134.67	148.00	139.00	140.56	16.42	16.30	15.80	16.17
T5	11.00	13.33	12.00	12.11	122.67	151.33	136.33	136.78	21.83	23.13	20.13	21.70
	Cross combinations											
L1T1	10.67	8.67	9.67	9.67	177.67	180.33	132.00	163.33	22.00	21.60	21.50	21.70
L1T2	9.33	10.67	11.33	10.44	143.00	168.33	105.00	138.78	21.33	22.00	22.50	21.94
L1T3	9.33	11.00	12.33	10.89	164.67	151.33	85.67	133.89	16.33	18.00	16.83	17.06
L1T4	7.67	12.33	10.33	10.11	153.67	143.67	98.67	132.00	21.83	23.47	22.83	22.71
L1T5	11.00	14.33	13.00	12.78	105.00	126.67	113.00	114.89	26.57	25.10	25.43	25.70
L2T1	7.00	8.33	7.33	7.56	148.00	164.33	181.00	164.44	31.43	30.13	31.67	31.08
L2T2	10.00	11.33	10.33	10.56	134.33	142.33	96.00	124.22	20.87	21.20	20.53	20.87
L2T3	8.33	10.67	8.67	9.22	161.00	161.33	120.33	147.56	22.30	22.30	20.47	21.69
L2T4	5.67	10.33	12.67	9.56	126.33	147.33	134.00	135.89	14.10	18.20	14.53	15.61

Table 4.2.2.contd……..

L2T5	10.33	12.00	11.67	11.33	158.33	155.00	140.33	151.22	18.25	20.50	19.53	19.43
L3T1	8.33	9.67	8.33	8.78	173.00	170.33	122.00	155.11	21.95	21.10	25.53	22.86
L3T2	11.33	12.33	14.00	12.56	132.33	149.33	132.00	137.89	24.80	23.60	19.50	22.63
L3T3	9.33	9.67	9.67	9.56	221.67	211.00	152.67	195.11	18.17	15.67	21.90	18.58
L3T4	8.00	12.67	11.33	10.67	91.33	112.33	72.00	91.89	17.56	16.90	15.83	16.76
L3T5	9.67	13.67	14.00	12.44	164.33	160.00	126.00	150.11	22.50	24.17	21.65	22.77
L4T1	10.33	10.33	13.33	11.33	186.00	173.33	205.33	188.22	24.60	26.93	25.47	25.67
L4T2	11.33	9.67	9.00	10.00	165.00	138.00	93.00	132.00	19.90	22.23	21.23	21.12
L4T3	9.33	9.67	12.33	10.44	156.33	102.33	143.00	133.89	18.50	18.50	18.90	18.63
L4T4	8.33	11.33	8.67	9.44	135.67	122.33	121.67	126.56	16.57	19.90	15.40	17.29
L4T5	8.00	9.00	7.67	8.22	134.00	145.00	135.33	138.11	24.17	25.10	24.27	24.51
L5T1	10.33	10.67	12.00	11.00	176.33	126.00	71.00	124.45	27.17	28.20	27.73	27.70
L5T2	9.33	11.67	10.33	10.44	125.00	133.33	136.33	131.56	14.50	16.17	14.50	15.06
L5T3	8.67	13.00	10.33	10.67	90.67	168.00	97.00	118.56	20.43	20.10	19.60	20.04
L5T4	8.67	10.00	8.00	8.89	112.33	164.67	90.00	122.33	15.73	16.10	16.40	16.08
L5T5	10.00	10.33	12.00	10.78	141.00	126.33	82.67	116.67	24.37	24.80	24.27	24.48
L6T1	11.33	12.00	12.33	11.89	182.00	185.00	123.00	163.33	30.03	30.43	29.80	30.09
L6T2	11.33	12.33	12.67	12.11	104.00	140.67	129.33	124.67	22.47	20.20	19.67	20.78
L6T3	10.00	10.33	9.67	10.00	137.00	155.00	137.00	143.00	16.47	18.17	17.43	17.36
L6T4	11.33	12.67	11.67	11.89	186.33	191.00	115.00	164.11	17.30	15.57	15.57	16.14
L6T5	12.00	14.00	13.33	13.11	137.33	137.00	140.00	138.11	23.23	24.27	23.83	23.78
Mean	9.51	11.10	10.76	10.46	139.2	147.63	123.33	136.90	20.98	21.40	20.53	20.97
S.E.(d)	1.49	1.58	1.88	0.90	29.14	22.44	26.32	16.98	4.25	4.10	4.18	1.10
C.V	7.56	6.49	6.30	10.55	2.04	1.97	2.10	15.19	4.79	5.58	5.82	6.39

JGL- Jagitial **WGL- Warangal** **HYD- Hyderabad**

AVG- Average (pooled)

Table 4.2.3.Mean performance of grain yield per plant, kernel length and kernel breadth in 3 locations and over locations

Genotypes	Grain yield per plant (g)				Kernel length(mm)				Kernel breadth(mm)			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG
	Lines											
L1	17.70	20.90	14.90	17.83	4.90	4.96	4.83	4.90	1.84	1.81	1.92	1.86
L2	25.06	26.97	25.27	25.77	4.95	4.98	4.89	4.94	1.89	1.94	1.83	1.89
L3	20.23	24.97	21.57	22.26	5.76	5.53	5.61	5.63	1.90	1.93	1.89	1.91
L4	28.87	27.23	24.80	26.97	6.57	6.46	6.70	6.58	2.09	2.14	2.18	2.14
L5	16.92	23.43	19.37	19.91	4.93	4.91	4.87	4.90	1.95	1.98	1.86	1.93
L6	27.23	29.53	30.43	29.07	6.62	6.52	6.41	6.52	2.20	2.15	2.29	2.21
	Testers											
T1	29.47	30.07	32.13	30.56	6.93	7.01	6.83	6.92	2.31	2.25	2.27	2.28
T2	15.63	19.37	19.50	18.17	6.18	6.32	6.05	6.18	2.03	2.08	2.00	2.04
T3	21.75	21.43	15.10	19.43	4.67	4.72	4.82	4.74	1.68	1.75	1.78	1.74
T4	23.15	25.33	21.40	23.23	5.08	5.14	5.25	5.16	1.79	1.84	1.91	1.84
T5	20.13	25.37	22.60	22.70	5.85	5.83	5.91	5.86	1.96	1.97	1.98	1.97
	Cross combinations											
L1T1	26.17	31.10	19.77	25.68	6.36	6.20	6.47	6.34	2.40	2.34	2.61	2.45
L1T2	22.43	27.10	17.10	22.21	5.49	6.13	6.08	5.90	2.00	2.19	1.75	1.98
L1T3	13.43	14.37	13.43	13.74	4.15	5.18	4.33	4.55	1.80	1.85	1.87	1.84
L1T4	21.67	28.27	21.67	23.87	5.17	5.24	5.12	5.18	1.86	2.06	1.82	1.91
L1T5	36.13	30.30	32.57	33.00	6.37	5.94	6.26	6.19	2.15	2.10	2.15	2.14
L2T1	25.77	31.47	20.67	25.97	6.97	6.60	6.79	6.79	2.42	2.45	2.41	2.43
L2T2	24.97	28.43	16.63	23.34	6.84	6.53	6.88	6.75	1.87	1.96	1.97	1.93
L2T3	14.73	29.83	24.07	22.88	4.67	4.68	4.70	4.69	1.65	1.87	1.99	1.84
L2T4	15.33	26.43	13.27	18.34	5.30	5.19	5.43	5.31	1.75	2.01	2.02	1.93
L2T5	17.67	26.03	15.17	19.62	5.90	5.93	5.72	5.85	1.96	1.99	2.02	1.99
L3T1	34.10	35.77	32.53	34.13	6.78	6.67	6.78	6.74	2.46	2.53	2.52	2.50
L3T2	31.80	29.20	14.53	25.18	5.65	5.52	5.67	5.61	1.95	2.05	1.96	1.99
L3T3	34.10	28.20	26.13	29.48	6.19	6.07	6.33	6.20	1.69	1.77	1.73	1.73
L3T4	13.60	22.20	11.10	15.63	5.42	5.18	5.61	5.40	1.91	2.05	1.93	1.96

Table 4.2.3.contd…….

L3T5	21.77	32.90	22.43	25.70	5.77	5.55	5.66	5.66	2.03	2.16	2.02	2.07
L4T1	30.13	34.00	28.13	30.76	6.99	7.05	7.02	7.02	2.65	2.64	2.65	2.64
L4T2	33.10	23.77	15.27	24.04	5.96	5.52	6.17	5.88	1.92	1.95	1.89	1.92
L4T3	21.47	16.63	18.37	18.82	5.24	4.49	4.92	4.88	2.19	2.22	2.18	2.20
L4T4	18.17	25.83	26.60	23.54	5.98	5.54	6.02	5.85	1.91	1.93	1.89	1.91
L4T5	30.47	21.77	26.17	26.13	6.40	6.72	6.80	6.64	2.07	2.12	2.15	2.11
L5T1	28.10	32.50	22.23	27.61	4.94	5.03	4.43	4.80	1.87	1.82	1.81	1.83
L5T2	21.57	24.20	18.43	21.40	6.71	6.51	6.55	6.59	1.92	2.01	2.01	1.98
L5T3	24.12	18.60	22.80	21.84	5.49	5.35	5.28	5.37	2.11	2.06	2.11	2.09
L5T4	22.60	27.13	24.57	24.77	6.12	5.89	5.80	5.93	1.75	1.86	1.82	1.81
L5T5	26.83	21.84	30.53	26.40	6.04	5.93	6.08	6.02	1.98	1.99	2.00	1.99
L6T1	33.47	36.33	28.63	32.81	6.77	6.98	6.79	6.85	2.72	2.70	2.72	2.71
L6T2	26.53	21.43	22.50	23.49	6.67	6.59	6.77	6.68	2.10	2.23	2.19	2.18
L6T3	28.43	27.97	19.37	25.26	5.97	5.96	5.55	5.83	1.78	1.87	1.86	1.84
L6T4	22.23	31.13	20.77	24.71	6.32	6.15	6.24	6.24	2.100	2.18	2.13	2.14
L6T5	26.10	28.50	23.40	26.00	6.66	6.55	6.44	6.55	2.25	2.32	2.27	2.28
Mean	24.22	26.53	21.85	24.19	5.90	5.84	5.88	5.87	2.02	2.08	2.06	2.05
S.E.(d)	6.24	5.17	5.78	2.22	0.75	0.71	0.76	0.15	0.25	0.23	0.25	0.06
C.V.	8.33	7.16	8.61	15.91	2.39	2.72	1.95	3.15	3.17	2.24	3.06	3.26

JGL- Jagitial **WGL- Warangal** **HYD- Hyderabad**

AVG- Average (pooled)

Table 4.2.4. Mean performance of L/B ratio, bran oil content and milling percent in 3 locations and over locations

Genotypes	L/B Ratio				Bran oil content (%)				Milling %			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG
	Lines											
L1	2.66	2.74	2.52	2.64	17.30	17.25	16.85	17.13	71.67	70.00	68.40	70.02
L2	2.62	2.57	2.67	2.62	12.31	11.53	11.72	11.85	67.90	71.20	67.60	68.90
L3	3.03	2.90	2.97	2.97	13.96	11.60	13.80	13.12	70.03	73.20	69.50	70.91
L4	3.14	3.01	3.07	3.07	12.33	13.48	11.33	12.38	70.94	69.20	72.30	70.81
L5	2.53	2.48	2.62	2.54	15.09	13.93	14.86	14.63	72.20	72.43	69.30	71.31
L6	3.01	3.03	2.80	2.95	13.45	13.36	11.20	12.67	70.76	72.50	69.60	70.95
	Testers											
T1	3.00	3.16	3.01	3.06	11.09	10.67	10.53	10.76	69.37	70.30	68.40	69.36
T2	3.04	3.03	3.03	3.03	10.25	9.97	9.99	10.07	66.52	65.20	69.20	66.97
T3	2.78	2.70	2.71	2.73	11.05	11.11	11.30	11.16	71.32	72.20	70.83	71.45
T4	2.84	2.80	2.75	2.80	10.29	10.15	10.44	10.29	68.83	71.50	71.40	70.58
T5	2.98	2.96	2.99	2.98	11.26	10.41	11.07	10.92	69.87	70.20	68.20	69.42
	Cross combinations											
L1T1	2.65	2.65	2.48	2.59	14.27	14.10	12.80	13.72	69.27	74.80	72.80	72.29
L1T2	2.75	2.79	3.47	3.00	16.07	15.63	17.00	16.23	71.13	68.60	69.50	69.74
L1T3	2.31	2.80	2.36	2.49	17.80	17.40	15.37	16.86	74.00	69.50	66.20	69.90
L1T4	2.78	2.54	2.81	2.71	15.37	12.37	15.10	14.28	73.50	70.20	69.30	71.00
L1T5	2.96	2.83	2.91	2.90	10.20	11.53	11.17	10.97	76.30	73.40	71.37	73.69
L2T1	2.88	2.69	2.82	2.80	11.10	10.20	13.17	11.49	62.30	74.50	64.40	67.07
L2T2	3.66	3.33	3.50	3.50	11.93	11.10	13.77	12.27	72.20	73.80	68.60	71.53
L2T3	2.83	2.50	2.36	2.56	12.77	10.07	11.17	11.33	62.80	65.70	68.20	65.57
L2T4	3.03	2.58	2.69	2.77	11.14	9.87	11.50	10.84	71.13	70.90	66.40	69.48
L2T5	3.01	2.98	2.83	2.94	12.87	10.60	11.33	11.60	66.87	71.47	65.90	68.08
L3T1	2.76	2.64	2.70	2.70	11.13	10.87	12.33	11.44	69.77	71.17	67.43	69.46

Table 4.2.4.contd……

L3T2	2.90	2.69	2.90	2.83	9.67	11.13	15.33	12.04	72.00	70.20	72.80	71.67
L3T3	3.66	3.43	3.66	3.58	10.57	13.13	11.07	11.59	71.17	69.90	72.90	71.32
L3T4	2.84	2.53	2.91	2.76	14.300	11.37	14.63	13.43	73.10	74.90	71.90	73.30
L3T5	2.84	2.57	2.80	2.74	11.27	10.87	11.57	11.23	73.00	73.90	70.80	72.57
L4T1	2.64	2.67	2.65	2.65	10.93	10.13	10.20	10.42	69.60	71.70	73.40	71.57
L4T2	3.15	2.83	3.26	3.08	9.80	11.03	13.17	11.33	68.73	68.80	70.80	69.44
L4T3	2.39	2.02	2.26	2.22	11.30	12.37	13.40	12.36	74.57	68.57	71.20	71.44
L4T4	3.13	2.87	3.19	3.07	12.00	11.41	10.53	11.31	75.10	73.90	71.90	73.63
L4T5	3.09	3.17	3.16	3.14	10.09	10.07	10.60	10.25	70.13	72.20	69.90	70.74
L5T1	2.64	2.76	2.45	2.62	12.37	10.30	14.40	12.36	72.13	74.90	71.57	72.87
L5T2	3.49	3.24	3.26	3.33	14.24	14.07	16.17	14.83	69.27	71.60	64.20	68.36
L5T3	2.60	2.60	2.50	2.57	13.67	14.54	13.74	13.98	71.30	74.80	69.20	71.77
L5T4	3.50	3.17	3.19	3.29	14.14	14.09	13.93	14.05	72.07	70.40	68.20	70.22
L5T5	3.05	2.98	3.04	3.02	13.84	14.72	11.37	13.31	74.73	71.40	68.10	71.41
L6T1	2.49	2.59	2.50	2.53	9.70	9.65	10.40	9.92	74.33	74.80	72.80	73.98
L6T2	3.18	2.96	3.09	3.08	13.60	15.73	14.54	14.62	72.50	67.40	69.90	69.93
L6T3	3.35	3.19	2.98	3.18	11.90	12.57	11.97	12.14	70.30	73.10	71.47	71.62
L6T4	3.01	2.82	2.93	2.92	12.70	10.37	11.70	11.59	71.27	73.80	67.20	70.76
L6T5	2.96	2.82	2.84	2.87	12.67	11.53	14.43	12.88	70.73	72.57	66.50	69.93
Mean	2.93	2.82	2.87	2.87	12.58	12.20	12.87	12.43	70.85	71.48	69.50	70.61
S.E.(d)	0.33	0.30	0.34	0.11	2.23	2.23	2.13	0.91	2.98	2.54	2.46	1.80
C.V.	4.61	5.29	4.87	4.68	6.77	7.07	7.55	8.87	1.53	0.96	1.03	3.13

JGL- Jagitial **WGL- Warangal** **HYD- Hyderabad**

AVG- Average (pooled)

Table 4.2.5. Mean performance of head rice recovery, alkali spreading value and water uptake in 3 locations and over pooled

Genotypes	Head rice recovery (%)				Alkali spreading value				Water uptake(ml)			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG
	Lines											
L1	57.49	59.50	68.40	57.72	4.11	4.29	3.99	4.13	250.00	270.00	235.00	251.67
L2	48.20	54.67	67.60	53.69	3.78	3.98	3.66	3.81	340.00	306.67	350.00	332.22
L3	55.30	59.50	69.50	57.47	4.88	4.73	5.12	4.91	278.33	255.00	293.33	275.56
L4	63.73	58.50	72.30	61.58	5.78	5.89	5.61	5.76	245.00	235.00	275.00	251.67
L5	53.13	55.50	69.30	55.38	3.78	3.53	3.42	3.58	320.00	316.67	365.00	333.89
L6	53.92	58.10	69.60	56.61	6.67	6.37	6.58	6.54	260.00	243.33	290.00	264.44
	Testers											
T1	52.19	60.20	68.40	57.06	3.78	3.95	4.18	3.97	193.33	220.00	183.33	198.89
T2	48.66	54.47	69.20	53.21	5.00	5.40	5.17	5.19	280.00	263.33	306.67	283.33
T3	60.60	62.60	70.83	61.43	5.06	5.16	5.36	5.19	200.00	190.00	218.33	202.78
T4	61.50	62.10	71.40	62.23	5.83	5.66	6.06	5.85	200.00	231.67	191.67	207.78
T5	59.27	63.97	68.20	61.58	4.50	4.65	4.08	4.41	240.00	238.33	271.67	250.00
	Cross combinations											
L1T1	55.87	64.30	72.80	60.66	4.55	4.86	4.93	4.78	220.00	231.67	285.00	245.56
L1T2	55.33	56.30	69.50	56.61	4.56	4.43	4.86	4.61	265.00	266.67	288.33	273.33
L1T3	64.80	60.10	66.20	61.07	5.67	5.51	5.41	5.23	230.00	231.67	293.33	251.67
L1T4	59.77	61.10	69.30	59.32	4.17	4.40	4.33	4.30	260.00	310.00	263.33	277.78
L1T5	65.10	62.10	71.37	62.53	4.00	4.14	3.73	3.96	270.00	323.33	275.00	289.44
L2T1	51.20	63.10	64.40	56.07	4.46	4.84	4.74	4.68	300.00	311.67	356.67	322.78
L2T2	53.10	60.10	68.60	57.00	5.44	5.38	5.70	5.51	320.00	321.67	255.00	298.90
L2T3	52.73	56.43	68.20	56.09	4.54	4.36	4.52	4.47	280.00	288.33	350.00	306.11
L2T4	55.97	57.10	66.40	56.29	3.67	3.79	3.50	3.65	310.00	363.33	318.33	330.56
L2T5	52.50	59.10	65.90	55.47	4.61	4.42	4.50	4.51	290.00	288.33	215.00	264.44
L3T1	54.10	58.20	67.43	56.80	4.67	4.95	5.10	4.91	260.00	258.33	295.00	271.11

Table 4.2.5.contd……..

L3T2	57.87	60.50	72.80	60.39	5.61	5.78	5.77	5.72	210.00	208.33	250.00	222.78
L3T3	59.07	58.87	72.90	60.04	5.66	5.34	5.63	5.54	220.00	273.33	225.00	339.44
L3T4	57.27	65.30	71.90	61.26	5.11	5.25	5.79	5.38	248.33	246.67	208.33	334.44
L3T5	60.30	64.10	70.80	62.17	6.06	6.27	5.55	5.96	280.00	291.67	210.00	260.56
L4T1	56.07	61.10	73.40	60.09	3.67	3.45	3.89	3.67	246.67	245.00	286.67	259.44
L4T2	53.93	57.10	70.80	57.28	4.89	5.37	5.06	5.10	290.00	335.00	291.67	305.56
L4T3	65.27	57.10	71.20	61.42	5.88	5.99	6.33	6.06	225.00	226.67	291.67	247.78
L4T4	61.40	64.20	71.90	62.86	5.11	4.78	5.42	5.10	240.00	280.00	238.33	252.78
L4T5	62.37	63.20	69.90	61.79	5.50	5.78	5.38	5.55	243.33	245.00	278.33	255.56
L5T1	56.47	63.27	71.57	60.84	3.45	3.27	3.67	3.46	225.00	223.33	261.67	236.67
L5T2	55.73	60.60	64.20	56.98	5.33	5.53	5.32	5.40	310.00	320.00	255.00	295.00
L5T3	57.87	58.10	69.20	58.42	5.22	5.02	5.49	5.24	260.00	293.33	266.67	273.33
L5T4	59.73	59.20	68.20	57.68	3.11	3.29	3.46	3.29	318.33	315.00	390.00	341.11
L5T5	65.10	61.20	68.10	61.50	4.83	4.63	4.64	4.70	245.00	250.00	280.00	258.33
L6T1	63.30	65.10	72.80	63.83	4.05	3.85	4.30	4.07	246.67	248.33	305.00	266.67
L6T2	56.93	57.20	69.90	57.98	6.33	6.63	6.34	6.44	276.67	288.33	320.00	295.00
L6T3	59.17	61.20	71.47	59.39	5.17	5.02	5.79	5.32	240.00	236.67	290.00	255.56
L6T4	60.10	63.20	67.20	59.87	6.68	6.81	6.42	6.64	230.00	305.00	241.67	258.89
L6T5	56.07	58.80	66.50	56.56	5.00	5.20	5.73	5.31	248.33	300.00	255.00	267.78
Mean	57.52	60.16	59.12	62.39	4.88	4.93	4.99	4.93	258.90	270.65	276.10	268.55
S.E.(d)	4.47	3.06	2.94	2.21	0.91	0.91	0.89	0.17	35.90	39.34	46.43	22.12
C.V.	1.95	1.55	1.38	4.33	6.31	5.00	3.19	4.29	2.12	1.63	1.58	10.09

JGL- Jagitial **WGL- Warangal** **HYD- Hyderabad**

AVG- Average (pooled)

Table 4.2.6. Mean performance of gel consistency, amylose content and grain type in 3 locations and over pooled

Genotypes	Gel consistency(mm)				Amylose content(%)				Grain type			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG
	Lines											
L1	68.33	64.67	72.00	68.33	20.50	21.77	22.57	21.61	SB	SB	SB	SB
L2	52.67	54.00	65.67	57.44	25.97	26.33	24.23	25.51	SB	SB	SB	SB
L3	59.33	66.00	67.00	64.11	24.07	20.37	22.70	22.38	SS	MS	MS	MS
L4	64.00	71.67	57.00	64.22	22.47	19.47	22.53	21.49	LS	LS	LS	LS
L5	73.33	65.33	73.33	70.67	20.47	23.57	21.77	21.93	SB	SB	SB	SB
L6	65.33	59.33	67.00	63.89	25.03	26.17	24.63	25.28	LS	LS	LB	LB
	Testers											
T1	79.33	75.00	72.67	75.67	20.40	19.73	21.50	20.54	LS	LS	LS	LS
T2	63.33	66.33	71.00	66.89	24.13	25.00	22.60	29.91	LS	LS	LS	LS
T3	74.67	67.00	60.00	67.22	23.17	22.10	20.83	22.03	SB	SB	SB	SB
T4	62.00	64.33	65.00	63.78	21.77	23.60	20.83	22.07	SB	SB	SB	SB
T5	76.00	66.00	77.33	73.11	21.80	22.47	23.23	22.50	MS	MS	MS	MS
	Cross combinations											
L1T1	73.00	66.00	67.67	68.89	23.20	20.87	21.90	21.99	LB	LB	LB	LB
L1T2	72.33	64.00	73.67	70.00	18.10	19.70	20.70	19.50	SB	LB	LS	SS
L1T3	75.00	72.33	61.67	69.67	22.50	24.07	22.93	23.17	SB	SB	SB	SB
L1T4	60.33	68.00	73.33	67.22	24.63	21.67	23.10	23.13	SB	SB	SB	SB
L1T5	71.33	73.00	64.00	69.44	18.80	17.67	20.97	19.14	LB	MS	LB	LB
L2T1	56.00	79.00	74.00	69.67	26.50	24.90	26.57	25.99	LB	LB	LB	LB
L2T2	66.67	56.33	71.33	64.78	27.27	26.17	24.90	26.11	LS	LS	LS	LS
L2T3	70.67	63.33	61.00	65.00	21.77	23.43	21.90	22.37	SB	SB	SB	SB
L2T4	65.00	72.00	58.00	65.00	19.73	20.57	22.90	21.07	SS	SB	SB	SB
L2T5	72.00	69.00	77.00	72.67	24.20	21.60	23.60	23.13	SS	MS	MS	SB
L3T1	75.67	63.33	61.00	66.67	20.27	20.03	18.97	19.76	LB	LB	LB	LB

Table 4.2.6.contd…….

L3T2	66.33	72.33	62.67	67.11	18.50	20.87	19.50	19.62	MS	MS	MS	MS
L3T3	62.00	69.00	72.00	67.67	24.27	25.87	22.17	24.10	LS	LS	LS	LS
L3T4	73.67	60.67	68.00	67.44	21.20	23.67	21.07	21.98	SB	SB	MS	SB
L3T5	63.00	56.67	70.67	63.44	20.17	21.67	24.10	21.98	MS	MS	MS	MS
L4T1	57.33	72.00	61.67	63.67	21.60	19.53	22.00	21.04	LB	LB	LB	LB
L4T2	73.00	75.33	65.00	71.11	24.60	22.13	23.60	23.44	SS	SB	LS	SS
L4T3	68.33	63.67	54.00	62.00	21.90	20.83	22.13	21.62	SB	SB	SB	SB
L4T4	71.67	74.67	64.00	70.11	26.33	25.03	25.80	25.72	SS	MS	LS	SS
L4T5	70.00	67.67	62.00	66.56	19.00	21.90	19.83	20.24	LS	LS	LS	LS
L5T1	74.00	74.67	62.67	70.44	23.00	21.93	23.40	22.78	SB	SB	SB	SB
L5T2	66.67	67.33	73.00	69.00	24.63	23.97	25.83	24.81	LS	LS	LS	LS
L5T3	68.00	62.67	73.67	68.11	25.67	25.45	26.00	25.70	SB	SB	SB	SB
L5T4	64.67	71.33	63.00	66.33	20.07	23.00	21.13	21.40	LS	SS	SS	SS
L5T5	76.00	64.67	67.67	69.44	23.83	22.60	20.17	22.20	LS	MS	LS	LS
L6T1	81.67	58.00	76.33	72.00	21.97	23.33	20.87	22.06	LB	LB	LB	LB
L6T2	57.00	67.67	65.00	63.22	18.77	19.80	19.67	19.41	LS	LB	LS	LS
L6T3	71.33	62.33	67.67	67.11	19.57	19.30	20.50	19.79	SS	SS	SB	SS
L6T4	64.33	55.67	66.00	62.00	22.60	23.23	21.77	22.53	LS	LB	LB	LB
L6T5	83.33	70.00	68.67	74.00	21.43	22.20	20.17	21.27	LB	LB	LB	LB
Mean	68.50	66.64	67.18	67.44	22.34	23.38	22.33	22.35	------	-------	-------	--------
S.E.(d)	7.10	6.02	5.82	4.55	2.49	2.24	1.96	1.03	-------	-------	-------	------
C.V.	2.32	2.46	2.19	9.22	3.59	3.01	3.00	5.63	------	-------	-------	--------

JGL: JAGITIAL **WGL: WARANGAL** **HYD: HYDERABAD** **AVG: AVERAGE**

LS: LONG SLENDER **LB: LONG BOLD** **SB: SHORT BOLD** **SS: SHORT SLENDER** **MS: MEDIUM SLENDER**

Classified as per DDR procedure

Table 4.2.6. Mean performance of grain chalkiness in 3 locations and over pooled

Genotypes				
	JGL	WGL	HYD	AVG
	Lines			
L1	A	A	A	A
L2	OC	OC	OC	OC
L3	VOC	VOC	VOC	VOC
L4	VOC	A	VOC	VOC
L5	VOC	VOC	VOC	VOC
L6	VOC	VOC	A	A
	Testers			
T1	OC	OC	OC	OC
T2	VOC	OC	VOC	VOC
T3	OC	OC	OC	OC
T4	VOC	VOC	VOC	VOC
T5	A	A	A	A
	Cross combinations			
L1T1	VOC	OC	VOC	OC
L1T2	OC	P	OC	P
L1T3	OC	OC	OC	OC
L1T4	A	A	A	A
L1T5	VOC	VOC	VOC	VOC
L2T1	VOC	VOC	VOC	VOC
L2T2	VOC	VOC	VOC	VOC
L2T3	P	P	VOC	P
L2T4	VOC	VOC	VOC	VOC
L2T5	P	P	P	P
L3T1	OC	OC	OC	OC

L3T2	P	OC	P	OC
L3T3	VOC	VOC	VOC	VOC
L3T4	OC	OC	OC	OC
L3T5	A	A	A	A
L4T1	OC	OC	OC	OC
L4T2	VOC	VOC	VOC	VOC
L4T3	VOC	OC	VOC	OC
L4T4	VOC	VOC	VOC	VOC
L4T5	OC	VOC	OC	VOC
L5T1	VOC	VOC	VOC	VOC
L5T2	VOC	VOC	VOC	VOC
L5T3	A	A	A	A
L5T4	VOC	VOC	VOC	VOC
L5T5	A	A	A	A
L6T1	A	A	A	A
L6T2	VOC	VOC	VOC	VOC
L6T3	VOC	VOC	VOC	VOC
L6T4	OC	OC	OC	OC
L6T5	VOC	VOC	VOC	VOC

JGL: JAGITIAL **WGL: WARANGAL** **HYD: HYDERABAD** **AVG: AVERAGE**

A-Absent of chalkiness **VOC- very occasionally chalky,** **OC- occasionally chalky,** **P- present**

genotypes	Days to 50%flowering				Plant height				Panicle length			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG

genotypes	Days to 50%flowering				Plant height				Panicle length			
	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG	JGL	WGL	HYD	AVG

Table 4.3.4. Analysis of variance of combining ability for different characters in rice (*O. sativa* L.) in pooled analysis

	df	Days to 50% flowering	Plant height	Panicle length	No. productive tillers per plant	No. of grains per panicle	1000 grain weight	Grain yield	Kernel length	Kernel breadth
Replications	2	11.23*	8.78*	2.35	3.33**	5.77	2.12	0.21	0.004	0.01*
Locations	2	7331.82**	16819.47**	698.81**	85.63**	18895.81**	23.68**	673.94**	0.12**	0.10**
Replications ×environment	4	5.07	2.01	0.64	0.62	6.08	1.25	9.96*	0.03	0.05
Treatments	40	1041.95**	1120.58**	40.10**	14.64**	3597.81**	141.06**	189.39**	4.69**	0.494**
Parents	10	1753.09**	1555.30**	30.14**	9.48**	1119.78**	97.52**	170.65**	5.64**	0.25**
Parents Vs crosses	1	214.86**	7378.77**	3.97	8.00**	10086.99**	136.80**	118.35**	5.54**	0.67**
Crosses	29	829.25**	754.88**	44.78**	16.65**	4228.54**	156.23**	198.31**	4.33**	0.57**
Line effects	5	614.02	1331.62*	25.71	26.74	3842.02	11.80	116.07	3.49	0.46
Tester effects	4	2030.15*	2000.87**	154.67**	22.52	8707.68	720.31**	574.85*	12.43*	2.33**
L × T effect	20	637.07**	361.50**	27.57**	12.95**	3429.34**	79.51**	143.55**	2.92**	0.25**
Location Vs parents	20	5.40*	30.80**	6.25**	1.92**	109.87**	5.63**	12.48**	0.026	0.008**
Location × parent Vs cross	2	398.44**	2695.41**	73.63**	2.01*	8691.45**	16.04**	81.57**	0.049	0.02*
Location Vs crosses	58	27.28**	178.66**	5.62**	4.31**	1451.25**	4.95**	54.57**	0.13**	0.02**
Location ×line effect	10	56.69*	239.79	7.21	2.30	1726.29	73.56	75.41	0.21	0.02
Location × tester effect	8	16.15	102.45	2.82	6.06	615.50	4.94	117.85**	0.10	0.02
Environment × Line × Tester effect	40	22.16**	178.62**	5.78**	4.46**	1549.64**	5.30**	36.70**	0.12**	0.02**
Error	174	2.57	2.99	1.36	0.49	6.88	1.46	3.75	0.02	0.004
Total	269	148.61	261.33	12.33	3.58	958.54	18.96	40.75	0.51	0.07

Table 4.3.4. contd…….

	df	L/B ratio	Bran oil content	Milling %	Head rice recovery	Alkali spreading value	Water uptake	Gel consistency	Amylose content
Replications	2	0.04	2	0.29**	31.43**	0.09	117.95**	0.12	1.10
Locations	2	0.37**	13.86**	125.86**	216.15**	0.35**	9498.85**	112.96**	0.08
Replications ×environment	4	0.01	0.70	6.32**	9.66**	0.02	46.00	2.32	1.30*
Treatments	40	0.71**	32.03**	29.91**	64.53**	6.85**	10673.46**	121.08**	33.08**
Parents	10	0.34**	50.62**	15.87**	96.23**	8.19**	19306.16**	229.43**	22.39**
Parents Vs crosses	1	0.06	3.56*	40.56**	118.48**	0.94**	11594.65**	47.62**	13.04**
Crosses	29	0.86**	26.59**	34.38**	51.74**	6.59**	7664.90**	86.25**	37.47**
Line effects	5	0.30	74.98**	68.24	116.74*	10.99	17306.39*	48.18	57.27
Tester effects	4	1.85	39.57*	18.17	44.21	12.96*	4882.18	80.04	17.61
L × T effect	20	0.81**	11.90**	29.16**	36.99**	4.21**	5811.07**	96.21**	26.49**
Location Vs parents	20	0.02	1.38*	6.95**	16.07**	0.12*	1084.65**	82.67**	5.36**
Location × parent Vs cross	2	0.10**	3.58*	11.10**	36.08**	0.15	3124.41	67.97**	0.75
Location Vs crosses	58	0.07**	4.34**	17.43**	22.97**	0.14**	2556.12**	128.82**	4.69**
Location × line effect	10	0.10*	3.39	25.01	29.98*	0.04	1328.50	128.06	4.73
Location × tester effect	8	0.13**	9.47*	29.13*	60.02**	0.20	6092.52*	45.89	1.99
Environment × Line × Tester effect	40	0.04**	3.56**	13.19**	13.80**	0.15**	2155.75**	145.59**	5.22**
Error	240	0.02	0.81	0.72	0.93	0.06	22.90	2.45	0.51
Total	368	0.11	4.87	7.77	13.76	0.82	1706.66	40.56	4.99

***significance at 0.01 level of probability** ****significance at 0.05 level of probability**

Genotype	DF	PHT	PT	PL	GRNS	TW	GY	BO	KL	KB	L/B	MP	HRR	ASV	WU	GC	AC
LINES																	
Mandhya Vijaya					+		+			+		+	+				+
Phalguna			+	+	+		+		+			+		+			+
TESTERS																	
NDR359	+			+	+	+	+		+			+	+		+		
Swarna	+			+		+	+		+		+	+	+		+		

Table 4.3.7. Promising general combiners for yield, yield components and quality traits

Genotypes	Characters
LINES	
Mandhya Vijaya(L3)	Number of grains per panicle, grain yield per plant, kernel breadth, milling percent, head rice recovery and amylose content
Phalguna (L6)	Productive tillers per plant, panicle length, number of grains per panicle, grain yield per plant, kernel length, milling percentage, alkali spreading value and amylose content
TESTERS	
NDR359 (T1)	Days to 50% flowering, panicle length, number of grains per panicle, 1000-grain weight, grain yield per plant, kernel length, milling percentage, head rice recovery and water uptake.
Swarna (T3)	Days to 50% flowering, panicle length,1000-grain weight, grain yield per plant,, kernel length, L/B ratio, milling percentage, head rice recovery and water uptake.

General combiners identified for Bran oil contentwere **Keshari, Kandhagiri, IR64 and Swarna**

Table 4.3.11.Promising specific combiners for yield, yield components and quality traits

Cross Combinations	Characters
Keshari × RP Bio226	Grain yield per plant, Number of grains per panicle,1000 grain weight
Keshari × MTU1010	Grain yield per plant, productive tillers per plant,1000 grain weight, Kernel length, L/B ratio, Milling percent, Head Rice recovery, Water uptake, Amylose content
Ishwarya × IR64	Grain yield per plant, Days to 50 % flowering (Earliness), kernel length, L/B Ratio, Milling percent, Head Rice recovery, Alkali spreading value, Water uptake
Ishwarya × Swarna	Grain yield per plant,1000 grain weight, water uptake
Mandhya Vijaya × NDR359	Grain yield per plant, Days to 50% flowering, Kernel length, Water uptake, Amylose content
Mandhya Vijaya × Swarna	Grain yield per plant, Days to 50%flowering,plant height (Dwarfness), Panicle length, Number of grains per panicle, kernel length, kernel breadth, L/B ratio, Water uptake, Gel consistency
PR116 × RP Bio226	Grain yield per plant, Days to 50% flowering, panicle length, kernel breadth, L/B ratio, milling percent, head Rice recovery, alkali spreading value, gel consistency,
Kandhagiri × RP Bio226	Grain yield per plant, number of grains per panicle, kernel length, L/B ratio, Alkali spreading value, Water uptake, Amylose content.
Phalguna × NDR359	Grain yield per plant, Days to 50% flowering, Panicle length, Productive tillers per plant, 1000 grain weight, milling percent, Head Rice recovery, Gel consistency
Phalguna × Swarna	Grain yield per plant, Days to 50% flowering, Kernel breadth, L/B ratio, milling percent

Table 4.3.12.Promising specific combiners for bran oil content, yield contributing traits and quality characters

Cross combinations	Characters
Keshari × IR64	Bran oil content, Days to 50% flowering, Plant height, Number of grains per panicle, 1000 grain weight, Gel consistency and Amylose content.
Keshari × Swarna	Bran oil content, Number of productive tillers per plant, kernel breadth, head rice recovery, alkali spreading value and gel consistency.
Ishwarya × NDR 359	Bran oil content, 1000 grain weight, kernel length, L/B ratio, alkali spreading value, water uptake and gel consistency.
Ishwarya × MTU1010	Bran oil content, plant height, productive tillers per plant, number of grains per panicle, kernel breadth and gel consistency.
Mandhya Vijaya × RP Bio226	Bran oil content, milling percent, head rice recovery and gel consistency.
PR116 × Swarna	Bran oil content, Days to 50% flowering, Plant height, productive tillers per plant, milling percent, head rice recovery and amylose content.
Phalguna × IR64	Bran oil content, alkali spreading value, water uptake and amylose content.
Phalguna × MTU1010	Bran oil content, plant height and gel consistency.

Table 4.3.8. Estimates of *sca* effects for bran oil, yield, its components and quality characters in rice (*O. sativa* L.) at three locations

Cross combinations	Days to 50% flowering			Plant height (cm)			Panicle length (cm)		
	JGL	WGL	HYD	JGL	WGL	HYD	JGL	WGL	HYD
L1T1	-5.30**	-7.60**	-9.67**	0.02	-17.98**	7.55**	0.57	1.88**	1.97**
L1T2	-13.74**	-13.87**	-15.84**	0.40	-8.32**	-3.35**	-2.85**	-1.30	-1.19
L1T3	9.75**	10.34**	14.43**	-0.27	12.92**	-7.78**	-0.05	0.43	0.12
L1T4	9.64**	11.40**	9.82**	-5.39**	3.98**	5.09**	0.62	-0.42	-0.72
L1T5	-0.35	-0.26	1.26	5.23**	9.39**	-1.51	1.70*	-0.59	-0.18
L2T1	3.83**	4.33**	9.25**	7.62**	2.66**	10.54**	0.50	-0.57	1.20
L2T2	-3.27**	-1.27	-5.24**	-0.38	1.31	-5.53**	0.09	0.03	1.99**
L2T3	4.88**	5.61**	5.70**	2.36*	7.70**	9.13**	-1.62*	-2.30**	0.05
L2T4	-7.22**	-10.33**	-10.57**	-0.21	-6.56**	-7.55**	1.29	2.94**	-2.02**
L2T5	1.77*	1.66	0.86	-9.39**	-5.12**	-6.59**	-0.26	-0.09	-1.22
L3T1	-3.63**	-1.33	-3.27**	-4.10**	2.28*	1.67	-2.14**	-3.21**	-2.42**
L3T2	5.58**	7.72**	7.88**	-12.71**	-3.76**	-11.86**	0.63	-0.97	-0.95
L3T3	-0.91	-3.38**	-0.83	-1.89	-5.74**	-2.46*	0.87	0.98	1.53*
L3T4	0.97	-0.66	4.88**	6.92**	-1.77*	3.04**	1.02	1.13	-0.14
L3T5	-2.02*	-2.33*	-8.66**	11.78**	8.99**	9.61**	-0.39	2.06**	1.99**
L4T1	11.70**	7.86**	9.38**	9.70**	-4.84**	-18.86**	-2.12**	-1.24	-2.54**
L4T2	3.25**	-0.74	0.22	-6.33**	4.21**	11.55**	-1.93**	-0.39	-2.14**
L4T3	-6.91**	-4.18**	-7.16**	-11.15**	-3.36**	-2.70**	1.21	-0.17	-0.31
L4T4	-7.02**	-7.46**	-7.11**	8.59**	8.42**	11.43**	3.18**	1.84**	2.46**
L4T5	-1.02	4.53**	4.66**	-0.81	-4.42**	-1.43	-0.34	-0.02	2.53**
L5T1	-4.50**	1.26	-3.54**	-14.30**	8.80**	-5.59**	2.29**	1.91**	0.43
L5T2	7.72**	5.32**	9.95**	16.85**	5.19**	3.96**	4.92**	2.62**	3.19**
L5T3	-4.44**	-2.12*	-7.10**	4.77**	-13.55**	0.43	-0.52	0.11	-0.84
L5T4	10.77**	6.93**	11.95**	0.28	-1.45	-2.92**	-5.10**	-3.83**	0.73
L5T5	-9.55**	-11.40**	-11.26**	-7.61**	1.01	4.11**	-1.58*	-0.80	-3.52**
L6T1	-2.10*	-4.53**	-2.14*	1.04	9.08**	4.67**	0.90	1.24	1.35*
L6T2	0.45	2.85**	3.02**	2.16*	1.37	5.23**	-0.86	0.02	-0.88
L6T3	-2.37**	-6.25**	-5.03**	6.18**	2.02*	3.37**	0.11	0.94	-0.55
L6T4	-7.15**	0.13	-8.97**	10.19**	-2.61**	-9.09**	-1.02	-1.66*	-0.30
L6T5	11.17**	7.80**	13.13**	0.79	-9.86**	-4.19**	0.87	-0.54	0.39

Table 4.3.8. contd……..

Cross combinations	Productive tillers per plant			Number of grains per panicle			1000-grain weight (g)		
	JGL	WGL	HYD	JGL	WGL	HYD	JGL	WGL	HYD
L1T1	0.94*	-1.52**	-1.23**	2.48	11.43**	7.08**	-4.63**	-5.14**	-6.12**
L1T2	-1.16**	-0.91*	-0.34	7.71**	20.65**	3.86*	0.25	0.75	2.16**
L1T3	0.11	0.03	1.43**	8.10**	-9.17**	-22.80**	-2.79**	-1.13	-3.03**
L1T4	-0.66	0.53	-0.51	18.04**	-5.56**	7.58**	4.21**	4.76**	5.39**
L1T5	0.77	1.86**	0.65	-36.34**	-17.34**	4.25**	2.95**	0.76	1.59*
L2T1	-1.38**	-0.98*	-2.36**	-23.97**	-4.56**	28.62**	5.02**	2.95**	4.51**
L2T2	0.83*	0.62	-0.14	2.24	-5.34**	-32.60**	0.01	-0.48	0.67
L2T3	0.44	0.56	-1.03*	7.63**	0.82	-15.60**	3.39**	2.73**	1.07
L2T4	-1.33**	-0.60	3.02**	-6.08**	-1.90	15.45**	-3.29**	-0.93	-2.43**
L2T5	1.44**	0.40	0.52	20.18**	10.98**	4.12**	-5.14**	-4.26**	-3.83**
L3T1	-1.12**	-0.72	-2.70**	-9.91**	-5.10**	-16.97**	-4.05**	-3.90**	-1.15
L3T2	1.10*	0.55	2.18**	-10.68**	-4.87**	16.80**	4.34**	4.10**	0.10
L3T3	0.37	-1.50**	-1.36**	57.36**	43.95**	30.13**	-0.34	-1.72*	2.97**
L3T4	-0.66	0.66	0.35	-52.02**	-43.43**	-33.14**	0.56	-0.05	-0.66
L3T5	-0.28	1.00*	1.52**	15.25**	9.45**	3.18*	-0.49	1.57*	-1.25
L4T1	0.74	1.54**	3.56**	4.22*	22.30**	47.62**	-1.16*	-0.31	-1.39*
L4T2	0.96*	-0.51	-1.54**	23.11**	8.18**	-40.93**	-0.31	0.48	1.66*
L4T3	0.24	0.10	2.56**	-6.83**	-40.31**	1.73	0.24	-1.13	-0.19
L4T4	0.13	0.93*	-1.04**	-6.55**	-9.03**	-2.21	-0.18	0.69	-1.27
L4T5	-2.08**	-2.06**	-3.54**	-13.94**	18.85**	-6.21**	1.42*	0.26	1.19
L5T1	0.81	0.74	1.90**	20.88**	-32.50**	-42.44**	1.71**	2.41**	1.42*
L5T2	-0.96*	0.35	-0.54	9.44**	-3.94*	46.66**	-5.40**	-4.12**	-4.51**
L5T3	-0.35	2.30**	0.23	-46.16**	17.88**	0.00	2.47**	1.92**	1.05
L5T4	0.53	-1.53**	-2.04**	-3.55*	25.83**	10.38**	-0.70	-1.64*	0.28
L5T5	-0.02	-1.86**	0.45	19.38**	-7.27**	-14.61**	1.92**	1.42*	1.74*
L6T1	0.01	0.94*	0.83*	6.28**	8.43**	-23.91**	3.11**	3.99**	2.73**
L6T2	-0.76	-0.11	0.38	-31.82**	-14.67**	6.20**	1.10	-0.74	-0.10
L6T3	-0.82	-1.50**	-1.83**	-20.10**	-13.17**	6.53**	-2.95**	-0.66	-1.87**
L6T4	1.40**	0.00	0.22	50.17**	34.10**	1.92	-0.60	-2.82**	-1.31
L6T5	0.17	0.66	0.38	-4.54**	-14.67**	9.25**	-0.66	0.23	0.55

Table 4.3.8. contd……..

Cross combinations	Grain yield per plant (g)			Kernel length (mm)			Kernel breadth (mm)		
	JGL	WGL	HYD	JGL	WGL	HYD	JGL	WGL	HYD
L1T1	-2.52*	-1.54	-4.84**	0.35**	-0.06	0.39**	-0.02	-0.07**	0.19**
L1T2	-3.36**	2.29*	0.41	-0.26**	0.15	0.03	0.04	0.13**	-0.17**
L1T3	-8.34**	-7.35**	-6.54**	-0.66**	0.14	-0.55**	-0.07	-0.08**	-0.05
L1T4	3.66**	2.31*	2.72*	-0.07	-0.13	-0.28**	-0.02	0.04	-0.07*
L1T5	10.57**	4.29**	8.24**	0.64**	-0.01	0.40**	0.08*	-0.01	0.09*
L2T1	1.35	-3.39**	-0.99	0.54**	0.28**	0.46**	0.11**	0.09**	-0.04
L2T2	3.44**	1.41	2.89*	0.66**	0.50**	0.57**	0.02	-0.05	0.04
L2T3	-2.77*	5.90**	7.04**	-0.57**	-0.49**	-0.43**	-0.11**	-0.02	0.03
L2T4	1.60	-1.73	-2.72*	-0.37**	-0.22*	-0.21**	-0.02	0.05	0.08*
L2T5	-3.62**	-2.18	-6.21**	-0.25**	-0.06	-0.38**	-0.01	-0.07**	-0.08*
L3T1	2.30	-0.30	7.48**	0.32**	0.34**	0.34**	0.07	0.11**	0.12**
L3T2	2.89*	0.96	-2.59*	-0.55**	-0.51**	-0.73**	0.02	-0.02	0.05
L3T3	9.21**	3.05**	5.72**	0.92**	0.88**	1.09**	-0.14**	-0.17**	-0.17**
L3T4	-7.50**	-7.17**	-8.28**	-0.28**	-0.25**	-0.14*	0.06	0.03	0.04
L3T5	-6.90**	3.46**	-2.33*	-0.40**	-0.45**	-0.55**	-0.08	0.05	-0.03
L4T1	-1.25	3.18**	1.52	0.38**	0.66**	0.41**	0.12**	0.16**	0.12**
L4T2	4.59**	0.78	-3.42**	-0.39**	-0.57**	-0.41**	-0.15**	-0.18**	-0.14**
L4T3	-3.01*	-3.25**	-3.60**	-0.18*	-0.77**	-0.49**	0.21**	0.22**	0.15**
L4T4	-2.52*	1.70	5.66**	0.12	0.03	0.08	-0.07	-0.15**	-0.11**
L4T5	2.20	-2.41*	-0.15	0.07	0.64**	0.41**	-0.11**	-0.06*	-0.03
L5T1	-1.26	1.22	-5.18**	-1.41**	-1.23**	-1.62**	-0.44**	-0.43**	-0.51**
L5T2	-4.91**	0.76	-1.06	0.60**	0.52**	0.52**	0.07	0.10**	0.18**
L5T3	1.66	-1.74	0.02	0.31**	0.21*	0.42**	0.36**	0.28**	0.28**
L5T4	3.92**	2.55*	2.82*	0.51**	0.50**	0.42**	-0.01	0.01	0.02**
L5T5	0.59	-2.79*	3.40**	-0.03	-0.01	0.24**	0.02	0.04	0.03
L6T1	1.39	0.84	2.00	-0.20*	0.00	0.00	0.15**	0.13**	0.11**
L6T2	-2.65*	-6.22**	3.78**	-0.05	-0.09	0.01	-0.09	0.05	0.07*
L6T3	3.26**	3.40**	-2.63*	0.18*	0.12	-0.03	-0.24**	-0.21**	-0.25**
L6T4	0.84	2.33*	-0.20	0.10	0.06	0.13*	0.07	0.02	0.04
L6T5	-2.84*	-0.35	-2.95**	-0.02	-0.10	-0.12	0.02	0.05	0.06

Table 4.3.8. contd…….

Cross combinations	L/ B ratio			Bran oil content (%)			Milling %		
	JGL	WGL	HYD	JGL	WGL	HYD	JGL	WGL	HYD
L1T1	0.23**	0.06	-0.04	0.39	1.11*	-0.77	-1.96**	1.62**	2.06**
L1T2	-0.18*	-0.09	0.30**	1.22*	0.40	0.65	-1.50*	-1.01*	-0.14
L1T3	-0.28**	0.13	-0.25**	2.51**	1.94**	1.22*	1.65*	-0.30	-4.00**
L1T4	-0.01	-0.12	-0.06	-0.20	-1.32*	0.84	-0.86	-1.69**	-0.18
L1T5	0.24**	0.03	0.05	-3.91**	-2.13**	-1.94**	2.68**	1.37**	2.26**
L2T1	0.07	0.02	0.26**	0.01	1.05*	1.69**	-3.15**	1.34**	-3.21**
L2T2	0.34**	0.35**	0.30**	-0.13	-0.28	-0.49	5.34**	4.22**	2.09**
L2T3	-0.16*	-0.26**	-0.28**	0.25	-1.55**	-0.87	-3.77**	-4.07**	1.13**
L2T4	-0.15	-0.18*	-0.22**	-1.65**	0.02	-0.66	2.56**	-0.96*	0.04
L2T5	-0.11	0.08	-0.05	1.53**	0.77	0.33	-0.98	-0.53	-0.06
L3T1	0.03	0.01	-0.02	0.61	0.61	0.05	-0.43	-2.72**	-4.64**
L3T2	-0.33**	-0.25**	-0.46**	-1.83**	-1.36**	0.28	0.40	-0.12	1.83**
L3T3	0.75**	0.71**	0.86**	-1.37**	0.41	-1.77**	-0.15	-0.67	1.36**
L3T4	-0.25**	-0.18*	-0.15	2.08**	0.41	1.67**	-0.22	2.30**	1.08*
L3T5	-0.19*	-0.28**	-0.24**	0.51	-0.06	-0.24	0.41	1.16**	0.37
L4T1	0.03	0.10	0.03	0.97	0.35	-0.67	-0.42	-1.22**	1.05*
L4T2	0.03	-0.05	-0.01	-1.13*	-0.99	-0.48	-2.68**	-0.54	-0.45
L4T3	-0.39**	-0.64**	-0.45**	-0.08	0.11	1.96**	3.43**	-0.96*	-0.61
L4T4	0.15	0.21*	0.22**	0.34	0.92	-1.02	1.95**	2.28**	0.80
L4T5	0.18*	0.37**	0.21*	-0.11	-0.39	0.20	-2.28**	0.44	-0.81
L5T1	-0.14	-0.05	-0.15	-0.42	-2.02**	1.19*	1.84**	0.40	2.41**
L5T2	0.19*	0.13	0.01	0.48	-.50	0.18	-2.43**	0.67	-3.86**
L5T3	-0.36**	-0.29**	-0.19*	-0.54	-0.25	-0.03	-0.11	3.68**	0.58
L5T4	0.35**	0.28**	0.23**	-0.34	1.06*	0.03	-1.35*	-2.80**	0.29
L5T5	-0.04	-0.05	0.11	0.81	1.17**	-1.37*	2.05**	-1.95**	0.58
L6T1	-0.23**	-0.14	-0.08	-1.55**	-1.10*	-1.49**	4.12**	0.58	2.32**
L6T2	0.05	-0.08	-0.14	1.38**	2.74**	-0.14	0.88	-3.24**	0.52
L6T3	0.45**	0.36**	0.31**	-0.78	-0.65	-0.49	-1.04	2.24**	1.53**
L6T4	-0.08	-0.03	-0.01	-0.24	-1.08*	-0.87	-2.08**	0.89**	-2.03**
L6T5	-0.07	-0.14	-0.08	1.18*	0.10	3.01**	-1.88**	-0.49	-2.34**

Table 4.3.8. contd……..

Cross combinations	Head rice recovery (%)			Alkali spreading value			Water uptake (ml)		
	JGL	WGL	HYD	JGL	WGL	HYD	JGL	WGL	HYD
L1T1	-2.32**	1.58**	1.27**	0.72**	0.93**	0.88**	-18.44**	-16.50**	-16.33**
L1T2	-2.17**	-2.54**	-0.86	-0.49**	-0.81**	-0.26**	-2.33	-18.44**	8.67**
L1T3	2.96**	1.26*	-1.53**	0.62**	0.58**	0.28**	-1.22	-21.78**	4.22
L1T4	-1.29*	-0.78	-0.87	-0.16	-0.04	-0.09	3.50	11.55**	-16.33**
L1T5	2.84**	0.48	1.98**	-0.68**	-0.66**	-0.80**	18.50**	45.16**	19.78**
L2T1	0.08	1.99**	-3.75**	0.67**	1.02**	0.75**	10.55**	21.50**	37.33**
L2T2	2.66**	2.87**	1.62**	0.44*	0.25	0.64**	1.66	-5.44*	-42.67**
L2T3	-2.03**	-0.79	2.15**	-0.46*	-0.46**	-0.56**	-2.22	-7.11**	42.89**
L2T4	1.97**	-3.17**	0.71	-0.62**	-0.54**	-0.87**	2.50	22.88**	20.67**
L2T5	-2.69**	-0.91	-0.73	-0.03	-0.27	0.03	-12.50**	-31.83**	-58.22**
L3T1	-1.64*	-5.13**	-4.55**	0.01	0.17	0.14	26.88**	27.17**	37.00**
L3T2	2.81**	1.05	1.62**	-0.27	-0.32*	-0.26**	-52.00**	-59.78**	13.67**
L3T3	-0.32	-0.58	0.25	-0.21	-0.45**	-0.42**	-5.89	36.89**	-20.78**
L3T4	-1.34*	2.79**	1.11*	-0.05	0.04	0.45**	-2.83	-34.78**	-28.00**
L3T5	0.49	1.86**	1.57**	0.54**	0.63**	0.10	33.83**	30.50**	-1.89
L4T1	-1.76**	-1.38*	0.02	-0.58**	-0.88**	-0.72**	8.22*	3.17	-11.00**
L4T2	-3.21**	-1.50**	-0.82	-0.58**	-0.28	-0.62**	22.67**	56.22**	15.67**
L4T3	3.79**	-1.50**	-0.48	0.41*	0.65**	0.63**	-6.22	-20.44**	6.22*
L4T4	0.70	2.55**	2.44**	0.36*	-0.07	0.43**	-16.50**	-12.11**	-37.67**
L4T5	0.47	1.82**	-1.16*	0.39*	0.58**	0.28**	-8.16*	-26.83**	26.78**
L5T1	-0.53	0.86	3.63**	-0.18	-0.34*	-0.24*	-36.11**	-32.50**	-49.33**
L5T2	-.58	2.07**	-3.10**	0.48**	0.61**	0.34**	20.00**	27.22**	-34.33**
L5T3	-2.78**	-0.43	0.83	0.37*	0.41**	0.48**	6.11	32.22**	-32.11**
L5T4	-0.14	-2.38**	-2.51**	-1.02**	-0.83**	-0.83**	39.17**	8.89**	100.67**
L5T5	4.03**	-0.12	1.15*	0.34	0.15	0.25**	-29.17**	-35.83**	15.11**
L6T1	6.17**	2.06**	3.37**	-0.63**	-0.91**	-0.81**	8.89**	-2.83	2.33
L6T2	0.47	-1.96**	1.54**	0.43*	0.55**	0.16	10.00**	0.22	39.00**
L6T3	-1.61*	2.04**	-1.23*	-0.74**	-0.75**	-0.41**	9.44**	-19.78**	-0.44
L6T4	0.09	0.99	-0.87	1.49**	1.53**	0.92**	-25.83**	3.55	-39.33**
L6T5	-5.14**	-3.14**	-2.81**	-0.55**	-0.43**	0.13	-2.50	18.83**	-1.56

Table **4.3.8. contd…….**

Cross combinations	Gel consistency			Amylose content		
	JGL	WGL	HYD	JGL	WGL	HYD
L1T1	2.00*	-4.41**	-0.74	1.20*	0.54	-0.03
L1T2	**3.94****	-4.74**	4.03**	-3.12**	-0.96*	-1.32**
L1T3	4.34**	5.20**	-4.52**	0.64	2.35**	0.68
L1T4	-7.67**	-0.63	6.76**	2.96**	0.24	0.82*
L1T5	-2.67**	4.59**	-5.52**	-1.68**	-2.16**	-0.15
L2T1	-10.67**	9.32**	5.39**	2.05**	2.03**	2.58**
L2T2	2.61**	-11.68**	1.50	3.59**	2.96**	0.83*
L2T3	4.39**	-3.07**	-5.39**	-2.56**	-0.85*	-2.41**
L2T4	1.33	4.10**	-8.78**	-4.38**	-3.39**	-1.43**
L2T5	2.33*	1.32	7.28**	1.27**	-0.77	0.43
L3T1	6.93**	-2.81**	-6.21**	-1.17*	-1.92**	-2.21**
L3T2	0.21	7.86**	-5.76**	-2.16**	-1.43**	-1.76**
L3T3	-6.34**	6.13**	7.01**	2.98**	2.52**	0.67
L3T4	7.93**	-3.70**	2.62**	0.09	0.62	-0.45
L3T5	-8.73**	-7.48**	2.34**	0.25	0.21	3.74**
L4T1	-11.33**	-0.41	-0.01	-1.64**	-1.87**	-0.68
L4T2	6.94**	4.59**	2.10*	2.14**	0.37	0.83*
L4T3	0.06	-5.47**	-5.45**	-1.19*	-1.98**	-0.87*
L4T4	6.00**	4.03**	4.16**	3.42**	2.52**	2.77**
L4T5	-1.67	-2.74**	-0.78	-2.72**	0.97*	-2.04**
L5T1	3.53**	4.79**	-5.67**	-0.99*	-0.99*	0.08
L5T2	-1.19	-0.87	0.43**	1.42**	0.70	2.43**
L5T3	-2.08*	-3.93**	7.54**	1.82**	1.13**	2.36**
L5T4	-2.80**	3.23**	-3.51**	-3.60**	-1.01*	-2.53**
L5T5	2.53**	-3.21**	-1.79*	1.36**	0.17	-2.34**
L6T1	9.53**	-6.48**	7.26**	0.55	2.23**	0.26
L6T2	-12.52**	4.85**	-5.30**	-1.87**	-1.65**	-1.02*
L6T3	-0.41	1.13	0.81	-1.71**	-3.19**	-0.43
L6T4	-4.80**	-7.03**	-1.24	1.51**	1.03*	0.82*
L6T5	8.20**	7.52**	-1.52	1.53**	1.59**	0.37

*** Significance at 0.01 level of probability** *** * Significance at 0.05 level of probability**

JGL –Jagitial **WGL- Warangal** **HYD - Hyderabad**

Table 4.3.9. Estimates of *sca* effects for bran oil, yield, its components and quality traits in pooled analysis

Cross combinations	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Productive tillers per plant	No.of grains per panicle	1000-grains weight (g)	Grain yield per plant (g)	Kernel length (mm)	Kernel breadth (mm)
L1T1	-7.53**	-3.47**	1.48**	-0.60*	7.00**	-5.30**	-2.97 **	0.23 **	0.03
L1T2	-14.49**	-3.76**	-1.79**	-0.80**	10.74***	1.06**	-0.22	-0.02	-0.001
L1T3	11.51**	1.62**	0.17	0.53*	-7.96**	-2.32**	-7.41**	-0.39**	-0.07**
L1T4	10.29**	1.23*	-0.17	-0.22	6.69**	4.79**	2.90 **	-0.16**	-0.02
L1T5	0.22**	4.38**	0.31	1.10**	-16.48**	1.77**	7.70 **	0.35**	0.05*
L2T1	5.81**	6.94**	0.38	-1.58**	0.03	4.17**	-1.01	0.43 **	0.05*
L2T2	-3.27**	1.53**	0.70	0.44	-11.90**	0.07	2.581**	0.58**	-0.007
L2T3	5.4**	6.40**	-1.29**	-0.01	-2.38**	2.40**	3.39 **	-0.50**	-0.03
L2T4	-9.39**	-4.78**	0.74	0.36	2.49**	-2.22**	-0.95	-0.28 **	0.04
L2T5	1.44**	-7.03**	-0.53	0.79**	11.77**	-4.42**	-4.00 **	-0.24**	-0.05*
L3T1	-2.75 **	-0.047	-2.59**	-1.52**	-10.66**	-3.04**	3.16**	0.34 **	0.10**
L3T2	7.07 **	-9.45**	-0.43	1.28**	0.41	2.85**	0.421	-0.60 **	0.02
L3T3	-1.71 **	-3.37**	1.13**	-0.83**	43.82**	0.30	6.00 **	0.97 **	-0.16**
L3T4	1.74**	2.73**	0.67	0.32	-42.87**	-0.05	-7.66 **	-0.23**	0.04*
L3T5	-4.34 **	10.13**	1.22**	0.74**	9.30**	-0.05	-1.92**	-0.47**	0.002
L4T1	9.65 **	-4.67**	-1.97**	1.95**	24.72**	-0.96*	1.15	0.49 **	0.14**
L4T2	0.91	3.14**	1.49**	-0.36	-3.21**	0.62	0.65	-0.46**	-0.16**
L4T3	-6.09 **	-5.74**	0.24	0.97**	-15.14**	-0.37	-3.29 **	-0.48**	0.19**
L4T4	-7.20 **	9.49**	2.50**	0.007	-5.93**	-0.25	1.61 *	0.08	-0.11**
L4T5	2.73 **	-2.22**	0.72	-2.57**	-0.43	0.96*	-0.12	0.38**	-0.06**
L5T1	-2.26 **	-3.70**	1.55**	1.15**	-18.02**	1.85**	-1.74**	-1.42**	-0.46**
L5T2	7.67 **	8.68**	3.58**	-0.39	17.39**	-4.68**	-1.74 **	0.56**	0.12**
L5T3	-4.56 **	-2.78**	-0.42	0.73**	-9.43**	1.82**	-0.02	0.32 **	0.31**
L5T4	9.89**	-1.36*	-2.73**	-1.01**	10.89**	-0.69	3.09**	0.48**	0.004
L5T5	-10.74 **	-0.83	-1.97**	-0.48*	-0.83	1.70**	0.40	0.07	0.03
L6T1	-2.93 **	4.94**	1.17**	0.60*	-13.06**	3.28**	1.41 *	-0.06	0.13**
L6T2	2.11 **	2.92**	-0.58	-0.16	-13.43**	0.08	-1.70**	-0.05	**0.03**
L6T3	-4.56 **	3.86**	0.17	-1.39**	-8.92**	-1.83**	1.34*	0.09	-0.24**
L6T4	-5.33 **	-7.30**	0.10	0.54*	28.73**	-1.58**	0.99	0.10	0.04
L6T5	10.70**	-4.42**	0.24	0.41	-3.32**	0.04	-2.05**	-0.09	0.03

Table 4.3.9. contd……..

Cross combinations	L/B ratio	Bran oil content (%)	Milling %	Head rice recovery (%)	Alkali spreading value	Water uptake (ml)	Gel consistency (mm)	Amylose content (%)
L1T1	0.09	0.24	0.57*	0.18	0.85**	-17.09**	-1.05*	0.57*
L1T2	0.01	0.76*	-0.88**	-1.86**	-0.52**	-4.04*	1.08*	-1.80**
L1T3	-0.14**	1.89**	-0.88**	0.90**	0.49**	-6.26*	1.69**	1.22**
L1T4	-0.07	-0.23	-0.91**	-0.99**	-0.10	-0.43	-0.52	1.34**
L1T5	0.11*	-2.66**	2.10**	1.77**	-0.72**	27.82**	-1.20**	-1.34**
L2T1	0.12*	0.92**	-1.67**	-0.56	0.82**	23.13**	1.35**	2.22**
L2T2	0.33**	-0.30	3.89**	2.39**	0.44**	15.48**	-2.52***\	2.46**
L2T3	-0.24**	-0.73*	-2.24**	-0.22	-0.49**	11.19**	-1.36**	-1.92**
L2T4	-0.19**	-0.76*	0.55*	-0.16	-0.68**	15.35**	-1.12*	-3.07**
L2T5	-0.03	0.88**	-0.53*	-1.44**	-0.09	-34.19**	3.64**	0.31
L3T1	0.01	0.43	-2.60**	-3.77**	0.11	30.35**	-0.70	-1.76**
L3T2	-0.35**	-0.97**	0.70**	1.83**	-0.28**	-32.70**	0.77	-1.78**
L3T3	0.78**	-0.91**	0.20	0.22	-0.36**	3.41*	2.27**	2.06**
L3T4	-0.20**	1.39**	1.05**	0.85**	0.12	-21.87**	2.29**	0.08
L3T5	-0.24**	0.07	0.65*	1.30**	0.42**	20.82**	-4.62**	1.40**
L4T1	0.05	0.22	-0.19	-1.04**	-0.73**	0.13	-3.92**	-1.40**
L4T2	-0.01	-0.87**	-1.22**	-1.84**	-0.50**	31.52**	4.54**	1.11**
L4T3	-0.50**	0.67*	0.62*	0.60*	-0.56**	-6.82**	-3.62**	-1.35**
L4T4	0.20**	0.08	1.68**	1.90**	0.24**	-22.09**	4.73**	2.90**
L4T5	0.26**	-0.10	-0.88**	0.38	0.42**	-2.74	-1.73**	-1.26**
L5T1	-0.12*	-0.42	1.55**	1.32**	-0.25**	-39.32**	0.88	-0.63*
L5T2	0.11*	0.06	-1.87**	-0.54	0.48**	4.30**	0.46	1.52**
L5T3	-0.28**	-0.28	1.38**	-0.79**	0.42**	2.07	0.51	1.77**
L5T4	0.29**	0.25	-1.29**	-1.68**	0.90**	49.57**	-1.03*	-2.38**
L5T5	0.003	0.39	0.23	1.69**	0.25**	-16.63**	-0.82	-0.27
L6T1	-0.15**	-1.38**	2.34**	3.87**	-0.79**	2.80	3.44**	1.01**
L6T2	-0.09	1.33**	-0.61*	0.02	0.38**	16.40**	-4.32**	**-1.52****
L6T3	0.38**	-0.64	0.92**	-0.27	-0.63**	-3.59*	0.51	1.78**
L6T4	-0.03	-0.74*	-1.08**	0.07	1.32**	-20.54**	-4.36**	1.12**
L6T5	-0.10	1.43**	-1.57**	-3.70**	-0.28**	4.93**	4.73**	1.16**

***Significance at 0.01 level of probability** ****Significance at 0.01 level of probability**

Table 4.5.5. Classification ofcross combinations for different characters based on stability parameters

S.No.	Characters	Genotypes stable over all environments (b_i=1)	Genotypes suitable for favourable environments (b_i>1)	Genotypes suitable for poor environments (b_i< 1)
1	Days to 50% flowering	L3T1, L1T1, L1T2	L2T2, L3T5	L5T5, L6T1
2	Plant height	----------	L2T4, L2T3, L4T2	L5T2
3	Panicle length	L1T1, L4T4, L6T3	L2T5, L3T3, L3T5, L5T1	L4T5, L5T2, L6T1, L6T5
4	Productive tillers per plant	L2T5, L6T5	L1T5, L3T4, L3T5	L2T2, L6T1,L6T2, L6T4
5	Number of grains per panicle	--------	----------	----------
6	1000 grain weight	L5T5, L6T1	L1T4, L2T3, L3T5, L4T1, L4T5,L6T5, L5T1	L1T2
7	Grain yield per plant	L3T1, L4T1, L6T1, L6T5	L1T1, L5T1, L2T1	L5T5
8	Bran oil content	L5T3	L1T2, L5T2, L6T5	L1T1, L1T3, L5T4, L5T5
9	Kernel length	----------	L1T1, L1T5, L2T1, L2T2, L3T3, L5T2, L5T5, L6T4,L3T1, L6T2	L4T1, L5T1, L6T5
10	Kernel breadth	L1T3, L3T3	L3T4, L5T4,L2T2, L5T2,L6T3	L2T5, L4T2, L4T4, L5T1, L5T5
11	L/B ratio	L1T5	L2T2, L3T3, L3T5, L4T4, L5T2, L5T4, L6T2,L6T4	L2T5, L5T5

Table 4.3.10. Type of gene action for different characters based on GCA/ SCA variance ratio

S.No.	Characters	GCA variance	SCA variance	GCA/SCA ratio	Type of gene action
1	Days to 50% flowering	13.55	68.32	0.20	Non-additive
2	Plant height	26.51	20.32	1.30	Additive
3	Panicle length	1.28	2.42	0.53	Non-additive
4	Productive tillers per plant	0.24	0.94	0.26	Non -additive
5	Number of grains per panicle	65.14	208.86	0.31	Non-additive
6	1000- grain weight	5.81	8.21	0.71	Non-additive
7	Grain yield per plant	2.87	11.87	0.24	Non-additive
8	Bran oil content	0.86	0.93	0.92	Non-additive
9	Kernel length	0.10	0.31	0.32	Non-additive
10	Kernel breadth	0.023	0.026	0.88	Non-additive
11	L/B ratio	0.01	0.085	0.12	Non-additive
12	Milling percentage	0.18	1.77	0.10	Non-additive
13	Head rice recovery	0.25	2.58	0.10	Non-additive
14	Alkali spreading value	0.16	0.45	0.36	Non-additive
15	Water uptake	75.32	406.15	0.19	Non-additive
16	Gel consistency	0.58	0.10	5.80	Additive
17	Amylose content	0.10	3.47	0.03	Non-additive

Chapter IV

RESULTS AND DISCUSSION

The results obtained from the statistical analysis of the data from 6 lines, 5 testers and 30cross combinations of rice at three locations for bran oil content, yield, its components and quality characters are presented here under.

4.1 Analysis of Variance

The analysis of variance (ANOVA) of 41 genotypes (6 lines, 5 testers and 30 cross combinations) for bran oil content, yield, yield components and quality traits at 3 locations *viz*., Jagitial , Warangal and Hyderabad are presented in table 4.1. The results revealed the existence of significant differences among the genotypes studied for all the characters at different locations.In the present study the cross combinations were given with codes and discussed as per the table 4.1.2.

4.2 Mean Performance

Results on mean performance of parents and F_1 cross combinations for seventeen characters at different locations are presented character wise in tables 4.2.1 to 4.2.6.

4.2.1 Days to 50% Flowering

At Jagitial location, days to 50% flowering ranged from 82.00to 128.33 days with an overall mean value of 112.01days (Table 4.2.1). Among the lines, this trait ranged from 82.00 (L5) to 123.00 days (L2) and in testers it ranged from 101.33 (T5) to 122.33 (T3) days. This trait had mean values ranging from 89.67 (L1T2) and 128.33 (L2T3) in case of cross combinations.

Days to 50% flowering at Warangal location, exhibited variation from 81.00 to 123.33 days with a mean of 107.48days. The lines flowered between 81.00 (L1) to 120.00 (L2) days, whereas the testers flowered between 99.00 (T2 and T5) to 117.67 days (T3). Among the cross combinations this trait ranged from 83.00 (L1T2) to 123.33 (L1T3) days.

At Hyderabad location, this trait varied from 70.00 to 116.33 days with a mean of 96.96 days. The lines exhibited a range of 76.00 (L1) to113.00 days (L2) and the testers showed a range of 91.33(T2) to 111.33 days (T3). For cross combinations, it ranged from 70.00 (L1T2) to 116.33 days (L1T3).

4.2.2 Plant height (cm)

Plant height at Jagitial location, varied from 75.27 to 115.60 cm with a general mean 92.07cm. Among the lines, it ranged from 78.63 (L5) to 109.16 cm (L2) and in testers it varied from 86.33 (T5) to 110.33 cm (T1). The cross combinations exhibited a range from 75.27(L3T2) to 115.60 cm (L4T1).

At Warangal location, this character ranged from 80.03 to 138.83cm with a general mean of 112.24cm. The lines exhibited a range from 80.03 (L4) to 114.46 cm (L2) and for testers it ranged from 88.83(T2) to 119.53 cm (T1). In cross combinationsthis character ranged from 90.77 (L5T3) to 138.83 cm (L6T1).

Mean plant height at Hyderabad location, revealed a range from 86.30 to 142.67 cm with an average of 112.40cm. The range of this trait among the lines was from 86.30 (L5) to 119.63 cm (L2) and in testers, the range was from 89.2(T2) to 129.93 cm (T1). Among the cross combinations the plant height ranged from 101.10 (L3T2) to 142.67 cm (L2T1).

4.2.3 Number of productive tillers per plant

At Jagitial location, the genotypes manifested a mean number of productive tillers per plantof 9.51 with a range of 5.67 to 12.00 tillers per plant. The lines ranged from 8.33 (L1 and L2) to 10.33 (L4) tillers plant^{-1}, whereas the testers varied from 7.67 (T2) to 11.00 (T4 and T5) tiller number. Among the cross combinations, it ranged between 5.67 (L2T4) to 12.00 (L6T5) tillers plant^{-1}.

Number of productive tillers per plan at Warangal location, showed a variation from 8.33 to 14.33 with a mean of 11.10 tillers plant^{-1}. Estimates of tiller number in lines ranged from 10.00 (L3) to 12.00 (L6) and among testers it varied from 9.00 (T3) to 13.33 (T5). The cross combinations possessed tiller number from 8.33 (L2T1) to 14.33 (L1T5).

The genotypes at Hyderabad location, exhibited tillers range from 7.33 to 14.00 with a mean of 10.76 tillers plant^{-1}. Among lines, it varied from 9.33 (L1 and L3) to 12.67 (L4) tillers plant^{-1} whereas in testers, its range was from 8.67(T3) to 12.00 (T5). Tiller number in cross combinations varied from 7.33 (L2T1) to 14.00 (L3T2 and L3T5).

4.2.4 Panicle Length (cm)

Panicle length at Jagitial location, varied from 14.33 to 27.43 cm with a general mean of 22.66 cm. Among the lines it varied from 20.69 (L5) to 23.10 cm (L6) and among testers, it ranged from 16.93 (T4) to 25.53 cm (T1). The cross combinations exhibited a variation from 14.33 (L5T4) to 27.43 cm (L2T1). The cross combination L2T1 (27.43) registered highest panicle length followed by L1T1 (26.80) and L5T5 (26.53).

At Warangal location, it ranged from 17.80 to 28.53 cm with a general mean of 23.88cm. The lines exhibited a variation from 22.43 (L5) to 24.27 (L6) cm and for testers, it ranged from 18.60 (T4) to 27.13 cm (T1). In hybrids, it ranged from 17.80(L5T4) to 28.53 cm (L1T1).

The variation for panicle length at Hyderabad location, ranged from 15.27 to 24.47 cm with an average of 19.28 cm. It varied from 18.20 (L5) to 22.13 cm (L6) in lines while in testers, it ranged from 18.17 cm (T3) to 24.47 cm (T1). The hybrids possessed a range from 15.27 (L2T4 and L5T5) to 24.10 cm (L6T1).

4.2.5 Number of grains per panicle

The general mean of number of grains per panicle at Jagitial location was 139.72 with a range of 90.67 to 221.67 grains panicle^{-1}. The range of number of grains varied from 102.33 (L5) to 123.33 (L3) among the lines and from 105.67 (T2) to 134.67 (T4) among the testers. In hybrids number of grains ranged from 90.67 (L5T3) to 221.67 (L3T3). The hybrid L3T3 (221.67) registered highest number of grains followed by L6T4 (186.33) and L4T1 (186.00).

At Warangal location, the variation for number of grains panicle^{-1} ranged from 102.33to 211.00 with an overall mean of 147.63 grains panicle^{-1}. The lines exhibited a range of 110.00 (L5) to 143.67(L3) whereas the testers ranged between 122.33 (T2) to 151.33 (T5) grains panicle^{-1}. Among the hybrids, it varied from 102.33 (L4T3) to

211.00 (L3T3) filled grains panicle^{-1}. Highest number of grains were recorded in L3T3 (211.00) hybrid followed by L6T4 (191.00) and L6T1 (185.00).

Number of grains panicle^{-1} at Hyderabad location, exhibited variation from 71.00 to 205.33 with a mean of 123.33 grains panicle^{-1}. The lines varied between 99.00 (L1) to 138.33 (L3) grains panicle^{-1} while in testers, it ranged from 125.00 (T2) to 148.00 (T3). For this trait the hybrids showed a range of 71.00 (L5T1) to 205.33 (L4T1).Highest number of grains (205.33) was noted in L3T3 hybrid followed by L2T1(181.00) and L3T3(152.67).

4.2.61000 grain weight (g)

The genotypes at Jagitial location, exhibited a 1000-grain weight range from 14.10 to 31.43 g with an average weight of 20.98 g. The lines ranged from 16.74 (L1) to 25.48 g (L2) and the testers ranged from 16.01 (T3) to 25.93 g (T1). The hybrid L2T4 recorded the least test weight of 14.10 g and L2T1 showed a highest test weight of 31.43g.

1000-grain weight at Warangal location, displayed a variation from 15.57 to 30.43g with an overall mean of 21.40 g. Among the lines, it ranged from 17.47 (L3) to 24.23 g (L6), whereas the testers varied from 16.30 (T4) to 28.43 g (T1). The hybrids exhibited test weight range from 15.57 (L6T4) to 30.43 g (L6T1).

Among the genotypes at Hyderabad, the mean test weight ranged from 14.50 to 31.67g with a general mean of 20.53 g. The test weight among the lines varied from 15.30 (L1) to 21.50 g (L6) and among the testers it varied from 15.80(T4) to 22.47 g (T1). Hybrids showed test weight range from 14.50 (L5T2) to 31.67 g (L2T1).

4.2.7 Grain yield per plant (g)

The range of variation for grain yield plant $^{-1}$ at Jagitial location was from 13.43 to 36.13 g with a general mean of 24.22 g. The estimates of grain yield in lines ranged from 16.92 (L5) to 28.87 g (L4) whereas in testers, it varied from 15.63 (T2) to 29.47 g (T1). Among hybrids, it ranged from 13.43 (L1T3) to 36.13 g (L1T5).Out of 30 hybrids evaluated, the best among them were L1T5 (36.13), L3T1 (34.10) and L3T1(34.10).

The grain yield among the genotypes at Warangal location, ranged between 14.37and 36.33 g with a general mean of 26.53 g. The lines exhibited a range from 20.90 (L1) to 29.53 g (L6) and among the testers it recorded from 19.37 (T2) to 30.07g

(T1). In hybrids it varied from 14.37 (L1T3) to 36.33 g (L6T1). The hybrid L6T1 (36.33) recorded higher grain yield followed by L3T1 (35.77) and L4T1 (34.00).

At Hyderabad location, grain yield plant^{-1} varied from 11.10to 32.57 g with an average of 21.85g. In lines it ranged from 14.90 (L1) to 30.43 g (L6) while in testers, the range was from 15.10 (T3) to 32.13 g (T1). The hybrid L3T4 recorded the minimum grain yield of 11.10g and L1T5 hybrid exhibited maximum yield of 32.57 g. High yielding hybrids were L1T5 (32.57), L3T1 (32.53) and L5T5(30.53).

4.2.8 Mean Performance of Quality Characters

Quality in rice is quite complex in nature and it is determined by indices of milling, cooking, eating and nutritional quality characteristics. Market value is determined largely by grain size, shape, appearance and color, while percentage of milling and head rice recovery are the principal indices from trader's point of view. Physico-chemical properties of starch, like water uptake, gel consistency and amylose content constitute the cooking and eating qualities.

4.2.8.1 Kernel length (mm)

At Jagitial location, kernel length ranged from 4.15to 6.99 mm with an overall mean value of 5.90 mm. Among the lines, this trait ranged from 4.90 (L1) to 6.62 mm (L6) and in testers it ranged from 4.67 (T3) to 6.93 (T1) mm.Among the hybrids the kernel length ranged from 4.15 (L1T3) to 6.99 mm (L4T1).

Kernel length at Warangal location, showed a variation from 4.49 to 7.05 mm with a mean of 5.84 mm. Estimates of kernel length in lines ranged from 4.91 (L5) to 6.52 mm (L6) and among testers it varied from 4.72 (T3) to 7.01 mm (T1). The hybrids possessed kernel length from 4.49 (L4T3) to 7.05 mm (L4T1).

The genotypes at Hyderabad location, exhibited kernel length range from 4.33 to 7.02 with a mean of 5.88 mm. Among lines, it varied from 4.83 (L1) to 6.70 (L4) mm whereas in testers, its range was from 4.82 (T3) to 6.83mm (T1). Kernel length in hybrids varied from 4.33 (L1T3) to 7.02 (L4T1).

4.2.8.2 Kernel breadth (mm)

Kernel breadth at Jagitial location, varied from 1.65 to 2.72 mm with a general mean of 2.02 mm. Among the lines it varied from 1.84 (L1) to 2.20 mm (L6) and among testers, it ranged from 1.68 (T3) to 2.31 mm (T1). The hybrids exhibited a

variation from 1.65 (L2T3) to 2.72 mm (L6T1). The hybrid L2T3 (1.65) registered lowest kernel breadth followed by L3T3 (1.69) and L2T4 (1.75) desired direction.

At Warangal location, it ranged from 1.75 to 2.70 mm with a general mean of 2.08mm. The lines exhibited a variation from 1.81 (L1) to 2.15 mm (L6) and for testers, it ranged from 1.75 (T3) to 2.25 mm (T1). In hybrids, it ranged from 1.77 (L3T3) to 2.70 mm (L6T1).

The variation for kernel breadth at Hyderabad location, ranged from 1.73 to 2.72 mm with an average of 2.06 mm. It varied from 1.83 (L2) to 2.29 mm (L6) in lines while in testers, it ranged from 1.78 mm (T3) to 2.27 mm (T1). The hybrids possessed a range from 1.73 (L3T3) to 2.72 mm (L6T1).

4.2.8.3 L/B Ratio

At Jagitial location, the general mean for L /B ratio was 2.93 with a range of 2.31 to 3.66. The mean ranged from 2.53 (L5) to 3.14 (L4) in lines and from 2.78 (T3) to 3.04 (T2)among the testers. In hybrids this trait range varied from 2.31 (L1T3) to 3.66 (L2T2). The highest L/ B ratio was noted in L2T2 (3.66) hybrid followed by L3T2 (3.66) and L5T4 (3.50).

A range of 2.02 to 3.43 was observed for this trait at Warangal location, with a mean of 2.82. The mean of lines varied from 2.48 (L5) to 3.03 (L6), while in testers, its range was from 2.70 (T3) to 3.16 (T1). The hybrids exhibited a range of 2.02 (L4T3) to 3.43 (L3T3).

At Hyderabad location, the genotypes manifested a mean L / B ratio of 2.87 with a range of 2.26 to 3.66. In lines it was observed to range from 2.52 (L1) to 3.07 (L4) and among testers, it varied from 2.71(T3) to 3.03 (T2). The hybrids exhibited L /B ratio variation from 2.26 (L4T3) to 3.66 (L3T3).

4.2.4 Bran oil content (%)

The genotypes at Jagitial location, exhibited a bran oil content range from 9.67 to 17.80 % with an average bran oil content of 12.58%. The lines ranged from 12.31 (L2) to 17.30 (L1) % and the testers ranged from 10.25 (T2) to 11.26 (T5). The hybrid L3T2 recorded the least bran oil of 9.67 % and L1T3 showed a highest bran oil of 17.80 %. Only one hybrid (L1T3) was found superior to best check Keshari (17.30 %).

Bran oil content at Warangal location, displayed a variation from 9.65 to 17.40 with an overall mean of 12.20 %. Among the lines, it ranged from 11.53 (L2) to 17.25 % (L1), whereas the testers varied from 9.97 (T2) to 11.11% (T3). The hybrids exhibited bran oil range from 9.65 (L6T1) to 17.40 % (L1T3).

Among the genotypes at Hyderabad, the mean bran oil content ranged from 9.99 to 17.00 with a general mean of 12.87 %. The bran oil content among the lines varied from 11.72 (L2) to 16.85 % (L1) and among the testers it varied from 9.99 (T2) to 11.30 % (T3). Hybrids showed bran oil range from 10.20 (L4T1) to 17.00 % (L1T2).

4.2.8.5 Milling per cent

The genotypes at Jagitial location, exhibited a milling per cent range from 62.30 to 76.30 per cent with an average milling of 70.85 per cent. The lines ranged from 67.90 (L2) to 72.20 (L5) per cent and the testers ranged from 66.52 (T2) to 71.32 (T3) per cent. The hybrid L2T1 recorded the least milling per cent of 62.30 and L1T5 showed a highest milling per cent of 76.30 per cent.

Milling per cent at Warangal location, displayed a variation from 65.20 to 74.90 per cent with an overall mean of 71.48 per cent. Among the lines, it ranged from 69.20 (L4) to 73.20 (L3) per cent whereas the testers varied from 65.20 (T2) to 72.20 per cent (T3). The hybrids exhibited milling per cent range from 65.70 (L2T3) to 74.90 (L3T4 and L5T1) per cent.

Among the genotypes at Hyderabad, the mean milling per cent ranged from 64.20 to 73.40per cent with a general mean of 69.50 per cent. The milling per cent among the lines varied from 67.60 (L2) to 72.30 (L4) and among the testers it varied from 68.20 (T5) to 71.40 (T4) per cent. Hybrids showed milling per cent range from 64.20 (L5T2) to 73.40 (L4T1) per cent.

4.2.8.6 Head rice recovery (%)

At Jagitial location, the general mean for head rice recovery per cent was 57.52 per cent with a range of 48.20to 65.27 per cent. The mean ranged from 48.20 (L2) to 63.73 per cent (L4) in lines and from 48.66 (T2) to 61.50 (T4) per cent among the testers. In hybrids head rice recovery range varied from 51.20 (L2T1) to 65.27 (L4T3) per cent.

A range of 54.47 to 65.30 per cent was observed for this trait at Warangal location, with a mean of 60.16 per cent. The mean of lines varied from 54.67 (L2) to 59.50 (L1 and L3) per cent, while in testers, its range was from 54.47 (T2) to 63.97 (T5) per cent. The hybrids exhibited a range of 56.30 (L1T2) to 65.30 (L3T4) per cent.

At Hyderabad location, the genotypes manifested a mean head rice recovery of 59.12 per cent with a range of 64.20 to 73.40 per cent. In lines it was observed to range from 67.60(L2) to 72.30 (L4) per cent and among testers, it varied from 68.20 (T5) to 71.40 (T4) per cent. The hybrids exhibited head rice recovery variation from 64.20 (L5T2) to 73.40 (L4T1) per cent.

4.2.8.7 Alkali spreading value

Alkali spreading value at Jagitial location, varied from 3.11 to 6.68 with a general mean of 4.88. Among the lines it varied from 3.78 (L2 and L5) to 6.67 (L6) and among testers, it ranged from 3.78 (T1) to 5.83 (T4). The hybrids exhibited a variation from 3.11 (L5T4) to 6.68 (L6T4).

At Warangal location, it ranged from 3.27 to 6.81 with a general mean of 4.93. The lines exhibited a variation from 3.53 (L5) to 6.37 (L6) and for testers, it ranged from 3.95 (T1) to 5.66 (T4). In hybrids, it ranged from 3.27 (L5T1) to 6.81 (L6T4).

The variation for alkali spreading value at Hyderabad location, ranged from 3.42 to 6.58 with an average of 4.99. It varied from 3.42 (L5) to 6.58 (L6) in lines while in testers, it ranged from 4.08 (T5) to 6.06 (T4). The hybrids possessed a range from 3.46 (L5T4) to 6.42 (L6T4).

4.2.8.8 Water uptake (ml)

The general mean of water uptake at Jagitial location was 258.90 with a range of 193.33 to 340.00 ml. The range of water uptake varied from 245.00 (L4) to 340.00 ml (L2) among the lines and from 193.33 (T1) to 280.00 (T2) ml among the testers. In hybrids water uptake ranged from 210.00 (L3T2) to 320.00 ml(L2T2).The hybrid L2T2(320.00) registered highest water uptake followed by L5T4 (318.33) and L2T4(310.00).

At Warangal location, the variation for water uptake ranged from 190.00 to 363.33 with an overall mean of 270.65 ml. The lines exhibited a range of 235.00 (L4) to

316.67 (L5) whereas the testers ranged between 190.00 (T3) to 263.33 (T2) ml. Among the hybrids, it varied from 208.33 (L3T2) to 363.33 (L2T4) ml.

Water uptake at Hyderabad location, exhibited variation from 183.33 to 390.00 with a mean of 276.10. The lines varied between 235.00 (L1) to 365.0 ml (L5) while in testers, it ranged from 183.33 (T1) to 306.67 (T2) ml. The hybrids showed a range of 208.33 (L3T4) to 390.00 (L5T4) ml. Highest water uptake (390.00) was noted in L5T4 hybrid followed by L2T1 (356.67) and L2T3 (350.00).

4.2.8.9 Gel consistency (mm)

At Jagitial location, gel consistency ranged from 52.67 to 83.33 mm with an overall mean value of 68.50 mm. Among the lines, this trait ranged from 52.67 (L2) to 73.33 mm (L5) and in testers it ranged from 62.00 (T4) to 79.33 (T1) mm. Among the hybrids the gel consistency ranged from 56.00 (L2T1) to 83.33 mm (L6T5).

Gel consistency at Warangal location, showed a variation from 54.00 to 79.00 mm with a mean of 66.64 mm. Estimates of gel consistency in lines ranged from 54.00 (L2) to 71.67 mm (L4) and among testers it varied from 64.33 (T4) to 75.00 mm (T1). The hybrids possessed gel consistency from 55.67(L6T4) to 79.00 mm (L2T1).

The genotypes at Hyderabad location, exhibited gel consistency range from 54.00 to 77.33 with a mean of 67.18 mm. Among lines, it varied from 57.00 (L4) to 73.33 (L5) mm whereas in testers, its range was from 60.00 (T3) to 77.33 mm (T5). Gel consistency in hybrids varied from 54.00 (L4T3) to 77.00 (L2T5).

4.2.8.10 Amylose content (%)

Amylose content at Jagitial location, varied from 18.10 to 27.27% with a general mean of 22.34%. Among the lines it varied from 20.47 (L5) to 25.97 % (L2) and among testers, it ranged from 20.40 (T1) to 24.13 % (T2). The hybrids exhibited a variation from 18.10 (L1T2) to 27.27 % (L2T2).

At Warangal location, it ranged from 17.67 to 26.33 % with a general mean of 23.38 %. The lines exhibited a variation from 19.47(L4) to 26.33 %(L2) and for testers, it ranged from 19.73 (T1) to 25.00 (T2). In hybrids, it ranged from 17.67 (L1T5) to 26.17 % (L2T2).

The variation for amylose content at Hyderabad location, ranged from 18.97to 26.57 with an average of 22.33%. It varied from 21.77 (L5) to 24.63 (L6) % in lines while in testers, it ranged from20.83 (T3 and T4) to 23.23% (T5). The hybrids possessed a range from 18.97 (L3T1) to 26.57(L2T1).

4.2.8.11 Grain type

Based on kernel length and L/B ratio grains are classified long slender, long bold, short slender, short bold and medium slender as per DDR procedure. Among all these grains types long slender and medium slender grains are preferred by consumers.

Among lines, L5 had long slender grains in all locations and over locations while in L6 long slender grains observed at Jagitial and Warangal locations. In testers, T1 and T2 possessed long slender grains whereas T5 had medium slender grains at all locations and over locations.

Among 30 cross combinations, four crosses *viz.*, L2T2, L3T3, L4T5 and L5T2 recorded long slender grains and two crosses (L3T2 and L3T5) had medium slender grains in all locations and over locations.

4.2.8.12 Grain chalkiness

In lines L6 had no chalky grains at all locations as well as in pooled while in L4 and L6 grain chalkiness was absent at Warangal and Hyderabad and in pooled analysis respectively. Among testers, absence of grain chalkiness was observed in T5 at all locations and in pooled.

Grain chalkiness was absent in cross combinations L1T4, L3T5, L5T5 and L6T1 which is desirable in consumer point of view and also for fetching higher price for produce.

4.3 Combining Ability Analysis

Analysis of variance for combing ability was carried at different locations and presented in tables 4.3.1 to 4.3.3. The mean sum of squares of crosses was partitioned into lines, testers and line × tester effects.

Mean squares due to genotypes were highly significant for all the seventeen characters at all locations. Further, partitioning of the genotypes into parents and crosses

and comparison of parents *Vs* crosses showed significant differences among themselves for all the seventeen characters indicating that the crosses performed well compared to parents except for productive tillers per plant, alkali spreading value at Jagitial location, for productive tillers per plant, L/B ratio, alkali spreading value at Warangal, for L/B ratio, bran oil, milling recovery, head rice recovery and amylose content at Hyderabad location in case of parents vs crosses interaction. The differences among lines and testers were also significant. Line × tester mean sum of squares were found to be highly significant for yield, yield attributing traits and bran oil content studied at different locations.

4.3.1 Line × Tester Pooled Analysis for Combining Ability

The pooled analysis of variance for combining ability over three locations recorded significant differences for all the characters studied (Table 4.3.4). The differences among the parents, parents *Vs* crosses (except panicle length and L/B ratio) and crosses were observed to be significant for all the characters studied. Partitioning of crosses into lines, testers and line × tester revealed that the variance due to lines were significant for plant height, bran oil, head rice recovery and water uptake, whereas for testers 17 characters studied nine were found to be significant. The interaction due to lines x testers were significant for all the traits studied.

Interaction effect of parents *Vs* crosses× locations, crosses × locations were significant for all the characters, except for kernel length, alkali spreading value and amylose content in parents *Vs* crosses× locations interaction. Further, lines × locations interaction showed significant differences for days to 50% flowering, L/B ratio and head rice recovery. While, testers × locations were significant for grain yield per plant, L/B ratio, bran oil, milling recovery, head rice recovery and water uptake. Interaction effects of line ×tester × location were significant for all the characters studied.

4.3.2 Combining Ability Variances and Gene Action

The estimates of GCA and SCA variances in pooled analysis were presented in table 4.3.10. General combining ability is generally associated with additive gene action while specific combining ability is due to non-additive gene action. In the present investigation SCA variances were higher than GCA variances in pooled analysis for all the characters except plant height and gel consistency indicating the predominance of non-additive gene action for these characters.

4.3.3 Combining Ability Effects

General combining ability effects of parents at different locations and over locations (pooled) were estimated and presented in tables 4.3.5 and 4.3.6 whereas, specific combining ability effects of cross combinations were given in tables 4.3.8 and 4.3.9. The results are discussed character wise here under.

4.3.3.1 Days to 50% Flowering

***gca* effects**

At Jagitial, general combining ability effects for days to 50% flowering ranged from -7.44 (L5) to 4.02 (L3 and L4) in lines and from -6.39 (T2) to 8.44 (T3) in testers. Further, significant *gca* effects in desired direction was recorded for this trait in L1 (-3.64) and L5 (-7.44) lines and in testers *viz.*, T2 (-6.39), T5 (-3.11) and T1 (-2.83).

At Warangal location, the *gca* effects for this trait ranged from -5.01 (L1) to 5.92 (L6) in lines and from -6.26 (T2) to 9.86 (T3) in testers. Further, the lines L1 (-5.01), L5 (-3.88) and L2 (-1.61) and testers T2 (-6.26), T5 (-4.53) and T1 (-1.87) recorded significant *gca* effects in desired direction for this trait.

General combining ability effects for days to 50% flowering at Hyderabad location, varied from -3.04 (L1) to 3.89 (L4) in lines and from -7.36 (T2) to 8.70 (T3) in testers. Significant and negative *gca* effects desirable for the trait were noticed in L1 (-3.04), L5 (-2.84) and L2 (-1.64) lines and T2 (-7.36), T5 (-3.13) and T1 (-0.52) testers.

The estimated component of variance due to *sca* (68.32) was higher than *gca* (13.55) for days to 50% flowering in pooled analysis 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 e*t al.* (2011).

From the pooled analysis, among six lines involved three lines L5 (-4.72), L1 (-3.90) and L2 (-0.57) and three testers *viz.*, T2 (-6.67), T5 (-3.59) and T1 (-1.74) showed significant negative *gca* effects suggesting that they were good general combiners with favorable genes for earliness. The lines L1 and L5 and testers *viz.*, T1, T2 and T5 exhibited significant *gca* effects at different locations and as well as in pooled analysis.

***sca* effects**

Specific combining ability effects for days to 50% flowering at Jagitial location, varied from -13.74 (L1T2) to 11.70 (L4T1). Significant negative *sca* effects desirable for the trait were recorded by 14 cross combinations. The cross L1T2 (-13.74) recorded highest *sca* effect followed by L5T5 (-9.55) and L2T4 (-7.22).

At Warangal location, *sca* effects for this trait ranged from -13.87 (L1T2) to 11.40 (L1T4) and eleven cross combinations exhibited significant negative *sca* effects. The cross combinations L1T2 (-13.87) registered highest *sca* effect followed by L5T5 (-11.40) and L2T4 (-10.33).

Estimates of *sca* effects at Hyderabad location, ranged from -15.84 (L1T2) to 14.43 (L1T3). Fourteen crosses exhibited significant negative *sca* effects and the best among them were L1T2 (-15.84) followed by L5T5 (-11.26) and L2T4 (-10.57).

From the pooled analysis, out of thirty crosses fifteen cross combinations showed significant *sca* effects in desirable direction. The superior cross combinations identified among them were L1T2 (-14.49), L5T5 (-10.74), L2T4 (-9.39) and L1T1 (-7.53). Based on *per se* performance and negative *sca* effects L1T2 (high × high), L5T5 (high × high), L1T1 (high × high), L2T2 (high × high) and L5T1 (high × high) cross combinations were superior for days to 50% flowering. The cross combinations involving high × high general combiner revealed additive and additive × additive genetic component of variance where the characters can be easily improved through simple selection procedures in recombination breeding.

4.3.3.2 Plant height (cm)

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -4.42 (L5) to 6.80 (L6) among lines and from -5.36 (T4) to 12.76 (T1) among testers. The *gca* effects were significantly negative for L5 (-4.42) and L1 (-3.41) in lines while in testers, T4 (-5.36), T2 (-3.63) and T3 (-3.28) recorded significant negative *gca* effects for this trait.

Among the lines at Warangal location, *gca* effects ranged from -11.48 (L5) to 8.41(L3) and from -5.71 (T2) to 7.18 (T1) among testers. The estimates of *gca* effects

were significant and negative for L5 (-11.48) and L1 (-9.49) in lines and among testers T2 (-5.71), T4 (-1.76) and T3 (-1.50).

Range of *gca* effects at Hyderabad location, for plant height was from -6.69 (L5) to 5.81 (L2) among lines and from -8.35 (T2) to 10.41(T1) among testers. Lines L5 (-6.69), L4 (-5.22) and L1 (-2.21) recorded significant negative *gca* effects whereas in testers, T2 (-8.35) and T3 (-1.92) exhibited significant negative *gca* effects.

The variance due to specific combining ability (20.32) was lesser than the general combining ability (26.51) for this trait in pooled analysis indicating the influence of additive gene action. Conformity results were given by Ganasekaran *et al.* (2006) and Nadali Bagheri and Babaeian (2010).

In pooled analysis three lines L5 (-7.53), L1 (-5.04) and L4 (-1.28) recorded significant negative *gca* effect, while in testers T2 (-5.90), T4 (-2.44) and T3 (-2.23) registered significant *gca* effects in desired direction. These were found to be good combiners for producing dwarf plant types. The lines L1 and L5 and in testers *viz.*, T2 and T3 recorded significant negative *gca* effects at all locations as well as in pooled analysis.

***sca* effects**

At Jagitial location, estimates of *sca* effects for plant height varied from -14.30 (L5T1) to 16.86 (L5T2). Among cross combinations significant negative *sca* effects were recorded by 9 cross combinations. Top three crosses among them were L5T1 (-14.30), L3T2 (-12.71) and L4T3 (-11.15).

Range of *sca* effects at Warangal location was from -17.98 (L1T1) to 12.93 (L1T3).Thirteen cross combinations possessed significant negative *sca* effects at this location. The best among them were L1T1 (-17.98) followed by L5T3 (-13.55) and L6T5 (-9.87).

Among the cross combinations tested at Hyderabad location, *sca* effects ranged from-18.86 (L4T1) to 11.56 (L4T2). Thirteen cross combinations recorded significant negative *sca* effects. Highest *sca* effects were recorded by L4T1 (-18.86), L3T2 (-11.87) and L6T4 (-9.09).

In pooled analysis, fourteen cross combinations had recorded significant *sca* effects in desired direction. Some of the top specific combiners were L3T2 (-9.45), L6T4 (-7.30), L2T5 (-7.03), L4T3 (-5.74) and L4T1 (-4.67). The hybrids L2T5, L3T2, L4T3 and L6T4 exhibited significant negative *sca* effect at all locations and also in pooled analysis. Based on *per se* performance and negative *sca* effects cross combinations, L1T2 (High × high) and L5T3 (High × high) were identified as best specific cross combination for plant height. The cross combination involving high × high general combiner revealed additive and additive × additive genetic component of variance where the characters can be easily improved through simple selection procedures in recombination breeding

4.3.3.3 Panicle Length (cm)

***gca* effects**

Estimates of *gca* effects at Jagitial location, varied from -1.73 (L5) to 1.24 (L2) among the lines and from -1.83 (T4) to 2.69 (T1) among the testers. Highly significant positive *gca* effects were recorded by line L2 (1.24) and in testers, T1 (2.69) and T5 (1.29).

Among the lines at Warangal location, *gca* effects exhibited a range from -1.01 (L5) to 0.79 (L6) and among testers it varied from -1.58 (T2) to 2.23 (T1). The estimates of *gca* effects were positive and significant for lines L6 (0.79) and L2 (0.68) while, in testers T1 (2.23) and T5 (1.38).

At Hyderabad location, lines showed *gca* effects from -1.18 (L3) to 1.81 (L6) whereas testers ranged from -1.44 (T4) to 2.13 (T1). Significant positive *gca* effects were recorded by line L6 (1.81) whereas, in testers T1 (2.13) and T5 (0.82).

For this trait the estimated component of variance due to *sca* (2.42) was higher than *gca* (1.28) variance in pooled analysis. It indicates the predominance of non-additive gene action. This is in accordance with the earlier reports of Panwar (2005), Ganasekaran *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).

Among lines, L6 (0.81), L2 (0.62) and L1 (0.42) and among testers T1 (2.35) and T5 (1.16) revealed positive *gca* effects over pooled environments, implying that

they are good general combiners. For the character panicle length, T1 and T5 registered significant positive *gca* effects at all locations and also in pooled analysis.

***sca* effects**

For panicle length at Jagitial location exhibited *sca* effects for crosses from -5.10 (L5T4) to 4.92 (L5T2) and among hybrids evaluated four crosses registered significant positive *sca* effects. Some of the top specific crosses identified among them were L5T2 (4.92), L4T4 (3.18) and L5T1 (2.29).

At Warangal location, *sca* effects varied from -3.83 (L5T4) to 2.94 (L2T4) and significant positive *sca* effects were recorded by six cross combinations. The crosses L2T4 (2.94) recorded the highest *sca* effect followed by L5T2 (2.62) and L3T5 (2.06).

At Hyderabad location, crosses showed *sca* effects from -3.52 (L5T5) to 3.19 (L5T2). Out of 30 cross combinations tested only eight crosses recorded significant positive *sca* effects. The highest *sca* effect was recorded by cross L5T2 (3.19) followed by L4T5 (2.53) and L4T4 (2.47).

Seven cross combinations showed significant *sca* effects in positive direction and top four crosses among them were L5T2 (3.58), L4T4 (2.50), L5T1 (1.55) and L1T1 (1.48). Among the hybrids, 2crosses L4T4 and L5T2recorded significant positive *sca* effects at all locations as well as in pooled analysis. When compared over their *per se* performance and *sca* effects the crosses L6T1 (High × High), L1T1 (High × High), L5T1 (Low × High), L3T5 (Low × high) and L5T2 (Low × Low) found superior for this trait. 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 while 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 and the cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.4 Number of productive tillers per plant

***gca* effects**

Among the lines at Jagitial location, *gca* effects exhibited a range from -1.28 (L2) to 1.66 (L6) and in testers it recorded a range from -1.27 (T4) to 0.90 (T2). Line

L6 (1.66) showed significant positive *gca* effect and among testers, T2 (0.90) and T5 (0.62) recorded significant positive *gca* effects.

At Warangal location, *gca* effects for number of productive tillers per plant ranged from -1.16 (L4) to 1.11 (L6) in lines and from -1.21 (T1) to 1.07 (T5) among the testers. Further, significant and positive *gca* effects for this trait were noticed in L6 (1.11) in Lines and T5 (1.07) and T4 (0.40) in testers.

At Hyderabad location, *gca* effects for number of productive tillers varied from -0.80 (L2) to 1.00 (L6) in lines and from -0.49 (T4) to 1.01 (T5) in testers. Significant and positive *gca* effects were recorded in L6 (1.00), L3 (0.53) and L1 (0.40) among lines and T5 (1.01) and T2 (0.34) in testers.

The ratio of *gca* variance to *sca* variance was low (0.26) in pooled analysis 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 e*t al.* (2010a), Nadali Bagheri and Babaeian (2010), Saidaiah *et al.* (2010a) and Saidaiah e*t al.* (2011).

From the pooled analysis the lines L6 (1.26), L3 (0.26) and L1 (0.23) and two testers *viz*., T5 (0.90) and T2 (0.47) registered positive *gca* effects implying their good general combining ability. The line L6 and tester T5 recorded significant positive *gca* effect at all locations and also in pooled analysis. These parents may be involved in crossing programmes for improving this trait.

***sca* effects**

The *sca* effects at Jagitial location, ranged from -2.08 (L4T5) to 1.44 (L2T5). Further, significant positive *sca* effects displayed by six cross combinations. Top three specific combiners were L2T5 (1.44), L6T4 (1.40) and L3T2 (1.10).

At Warangal location, *sca* effects for tillers varied from -2.06 (L4T5) to 2.30 (L5T3) and only six cross combinations *viz.*,L5T3, L1T5, L4T1, L3T5, L6T1 and L4T4 exhibited significant positive *sca* effects. Among them L5T3 (2.30) followed by L1T5 (1.86) and L4T1 (1.54) were found superior.

Lowest and highest *sca* effects recorded at Hyderabad location, were -3.54 (L4T5) and 3.56 (L4T1). Among the crosses, eight hybrids recorded significant positive *sca* effects. The top performing ones were L4T1 (3.56), L2T4 (3.02) and L4T3 (2.56).

Among 30 cross combinations evaluated, 11 crosses showed significant positive *sca* effects over locations and top five specific cross combinations among them were L4T1 (1.95), L3T2 (1.28), L5T1 (1.15), L1T5 (1.10) and L4T3 (0.97) and none of the crosses revealed significant positive *sca* effects at all locations as well as in pooled analysis. However based on *per se* performance and *sca* effects the cross combinations L1T5 (high × high), L3T2 (high × high) and L3T5 (high × high) were detected as promising specific cross combination. The cross combination 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.

4.3.3.5 Number of grains per panicle

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -18.39 (L5) to 9.08 (L3) among the lines and from -13.51 (T2) to 26.38 (T1) among the testers. The estimates of *gca* effects were positive and significant for lines L3 (9.08), L4 (7.94) and L6 (1.88), and in testers, T1 (26.38) and T3 (7.77).

At Warangal location, *gca* effects for number of grains varied from -15.52 (L4) to 10.01 (L6) in lines and from -10.06 (T5) to 14.83 (T1) among testers. Further, significant and positive *gca* effects desirable for the trait were noticed in lines L6 (10.01), L3 (8.88), L1 and L2 (2.34) lines and the testers *viz.*, T1 (14.83) and T3 (6.44).

A range of -25.61 (L5) to 18.66 (L4) was observed for lines at Hyderabad location whereas, testers recorded a range from -15.79 (T4) to 18.04 (T1). The line L4 (18.66), L2 (13.32) and L6 (7.86) and the testers T1 (18.04), T5 (1.88) and T3 (1.60) exhibited significant positive *gca* effect.

Component of variance due to *sca* (208.86) was higher than *gca* (65.14) for number of grains panicle^{-1} in pooled analysis, indicating the prevalence of non-additive gene action. Similar results were observed by Panwar (2005), Ganasekaran *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).

From pooled analysis, L6 (6.58), L3 (5.96), L2 (4.60) and L4 (3.69) lines and two testers *viz.*,T1 (19.75) and T3 (5.27) registered significant positive *gca* effects indicating the good combining ability for grains panicle^{-1}.The line L6 and T1 and T3testers were identified as good general combiners at different locations as well as in pooled analysis. They may be utilized in future breeding programmers for improving the number of grains panicle^{-1}.

***sca* effects**

Among the crosses at Jagitial location, *sca* effects for number of grains per panicle ranged from -52.02 (L3T4) to 57.36 (L3T3) and significant positive *sca* effects were exhibited by fourteen hybrids. The top three promising crosses were L3T3 (57.37), L6T4 (50.17) and L4T2 (23.11).

Estimates of *sca* effects at Warangal location, ranged from -43.43 (L3T4) to 43.95 (L3T3). Among crosses, 12 crosses revealed significant positive *sca* effects for this trait. Top three superior crosses were L3T3 (43.95), L6T4 (34.10) and L5T4 (25.83).

Specific combining ability effects for grains panicle^{-1} at Hyderabad location ranged from -42.44 (L5T1) to 47.62 (L4T1). Significant positive *sca* effects were observed in sixteen hybrids. Highest performance was recorded by crosses L4T1 (47.62) followed by L5T2 (46.66) and L3T3 (30.13).

In pooled analysis, out of 30 crosses evaluated, 11 crosses showed significant *sca* effect in positive direction and some of the superior crosses among them were L3T3 (43.82), L6T4 (28.73), L4T1 (24.72) and L5T2 (17.39). The hybrids L1T2, L2T5, L3T3, L3T5 and L4T1displayed significant positive *sca* effect at all locations and also in pooled analysis. The superior cross combinations identified based on their *per se* performance and *sca* effects were L3T3 (High × High), L4T1 (High × High), L6T4 (High × Low), L2T5 (High × low), L3T5 (High × low) and L1T2 (Low × low). 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. The

crosses involving high × low *gca* effects resulted in superior combinations which may be due to complementary gene action and the crosses between two low combiners producing crosses with significant *sca* effect indicating the presence of non-additive inter allelic interaction. The cross between two low combiners revealed the presence of non-additive inter allelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.6 1000-grain weight (g)

***gca* effects**

Among the lines at Jagitial location, *gca* effects ranged from -0.74 (L5) to 0.72 (L6) and among testers, *gca* effects varied from –4.00 (T4) to 5.02 (T1). The line L6 (0.72) and testers *viz.*, T1 (5.02) and T5 (2.00) recorded significant positive *gca* effects.

Estimates of *gca* effects at Warangal location, varied from -1.40 (L3) to 0.85 (L4) among lines and from -3.33 (T4) to 4.71 (T1) in testers. The lines L4 (0.85) and L2 (0.78) and the testers T1 (4.71) and T5 (2.30) recorded significant positive *gca* effect.

For 1000-grain weight, *gca* effects at Hyderabad location, exhibited a range from -0.64 (L5) to 0.68 (L1) among lines whereas in testers, range was from -4.38 (T4) to 5.81 (T1). The line L1 (0.68) showed significant positive *gca* effects. Among testers T1 (5.81) and T5 (2.02) recorded significant *gca* effects in desired direction.

In pooled analysis the variance due to *gca* (5.81) was lesser than the *sca* (8.21) 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 Banumathy *et al.* (2003), Bhave *et al.* (2003), Swamy *et al.* (2003), Panwar (2005), Anand Kumar *et al.* (2006) and Kumar Babu e*t al*. (2010a).

For 1000-grain weight in pooled analysis, two lines L1 (0.49) and L2 (0.40) and two testers *viz.*, T1 (5.18) and T5 (2.11) were identified as potential general combiners based on their *gca* effects. The testers T1 and T5 were good general combiners at different locations and over locations. These may serve as useful source for improvement of this trait in hybridization programmes.

***sca* effects**

1000-grain weight *sca* effects at Jagitial location, exhibited a range from -5.40 (L5T2) to 5.03 (L2T1) among crosses. Ten cross combinations showed significant positive *sca* effects at this location. Top three specific crosses among them were L2T1 (5.02), L3T2 (4.34) and L1T4 (4.21).

At Warangal location *sca* effects ranged from -5.14 (L1T1) to 4.76 (L1T4) and nine crosses recorded significant positive *sca* effects. The top three crosses were L1T4 (4.76) followed by L3T2 (4.10) and L6T1 (3.99).

Estimates of *sca* effects at Hyderabad location, varied from -6.12 (L1T1) to 5.39 (L1T4) and nine crosses exhibited significant positive *sca* effects. Top three specific crosses were L1T4 (5.39), L2T1 (4.51) and L3T3 (2.97).

From pooled analysis 11 cross combinations showed significant *sca* effects in positive direction and the top five specific cross combinations identified among them were L1T4 (4.79), L2T1 (4.17), L6T1 (3.28), L3T2 (2.85) and L2T3 (2.40). Four hybrids *viz.*, L1T4, L2T1, L5T1 and L6T1 recorded significant positive *sca* effect at all locations and also in pooled analysis. The best specific cross combinations identified based on positive *sca* effect and *per se* performance were L2T1 (High × High), L6T1 (Low × High), L5T1 (Low × High), L1T2 (High × low), L1T4 (high × low), L4T5 (low × high), L5T5 (low × high), L1T5 (high × high) and L3T2 (low × low). 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. The crosses involving low × high *gca* effects resulted in superior combinations which may be due to complementary gene action and the crosses between two low combiners producing crosses with significant *sca* effect indicating the presence of non-additive interallelic interaction. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.7 Grain yield per plant (g)

***gca* effects**

Range of *gca* effects at Jagitial location, for grain yield was from -5.21(L2) to 2.45 (L6) among lines and from -5.97 (T4) to 4.72 (T1) among testers. Out of six lines,

L6 (2.45), L3 (2.17) and L4 (1.77) lines recorded significant positive *gca* effect whereas in testers T1 (4.72), T2 (1.83) and T5 (1.60).

General combining ability effects at Warangal location, varied from -2.71 (L4) to 2.55 (L3) in lines and in testers it ranged from -4.51 (T3) to 6.42 (T1). The lines L3 (2.55), L6 (1.97) and L2 (1.33) and in testersT1 (6.42) possessed significant positive *gca* effects.

At Hyderabad location, *gca* effects ranged from -3.67 (L2) to 2.09 (L5) among lines. Similarly, in testers it ranged from -4.22 (T2) to 3.70 (T1). Highly significant *gca* effects were recorded by L5 (2.09), L6 (1.31) and L4 (1.28) lines, and in testers, T1 (3.70) and T5 (3.42).

The estimated component of variance due to *sca* (11.87) was higher than the *gca* (2.87) for grain yield in pooled analysis. The ratio of *gca* variance to *sca* variance was low (0.24) indicating the presence of non-additive gene action. Comparable results were earlier reported by Panwar (2005), Rosamma and Vijayakumar (2005), Singh *et al.*(2005), Anand Kumar *et al.*(2006), Ganasekaran *et al.*(2006), Dalvi and Patel (2009), 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).

In pooled analysis, L6 (1.91) and L3 (1.48) lines and T1 (4.95) and T5 (1.60) testers showed significant positive *gca* effects and were considered to be good general combiners for grain yield plant^{-1}. The parent, L6 in lines and T1in testers recorded significant positive *gca* effects at different locations and also in pooled analysis.

sca effects

Range of *sca* effects at Jagitial location for grain yield was from -8.34 (L1T3) to 10.57 (L1T5). Among 30 hybrids evaluated, eight hybrids recorded significant positive *sca* effects for grain yield. The top three crosses were L1T5 (10.57) followed by L3T3 (9.21) and L4T2 (4.49).

At Warangal location, *sca* effects of grain yield varied from –7.35 (L1T3) to 5.90 (L2T3) and significant *sca* effects were noted by 10 hybrids. Top three specific crosses among them were L2T3 (5.90) followed by L1T5 (4.29) and L3T5 (3.46).

Among the cross combinations at Hyderabad location, *sca* effects ranged from -8.28 (L3T4) to 8.24 (L1T5) and ten crosses exhibited significant positive *sca* effects. Highest *sca* effect recorded by L1T5 (8.24) followed by L3T1 (7.48) and L2T3 (7.04).

In pooled analysis, ten crosses showed significant *sca* effects in positive direction out of 30 crosses evaluated. The crossesL1T5, L3T3 and L5T4recorded significant positive *sca* effect at all the locations and over all locations. The top five specific crosses among them were L1T5 (7.70), L3T3 (6.00), L2T3 (3.39), L3T1 (3.16) and L5T4 (3.10). The cross combinations L3T1 (High × High), L6T1 (High × High), L1T5 (Low× High), L3T2 (high × low), L6T3 (high × low), L1T4 (low × low), L2T2 (low × low), L2T3 (low × low), L4T4 (low × low) and L5T4 (low × low) were identified as good specific cross combinations based on positive *sca* effects and *per se* performance. 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 with low × high or high × low combiners resulted in superior combinations which may be due to complementary gene action. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents

4.3.3.8 Kernel length (mm)

***gca* effects**

At Jagitial, general combining ability effects for kernel length ranged from -0.47 (L1) to 0.50 (L6) in lines and from -0.69 (T3) to 0.49 (T1) in testers (Table). Further, significant *gca* effects in desired direction was recorded for this trait in L6 (0.50) and L4 (0.14) lines and in testers *viz.*, T1 (0.49), T2 (0.25) and T5 (0.21).

At Warangal location, the *gca* effects for this trait ranged from -0.16 (L1) to 0.55 (L6) in lines and from -0.61 (T3) to 0.52 (T1) in testers. Further, the line L6 (0.55) and testers T1 (0.52), T2 (0.24) and T5 (0.21) recorded significant *gca* effects in desired direction for this trait.

General combining ability effects for kernel length at Hyderabad location, varied from –0.33(L5) to 0.40 (L6) in lines and from -0.77 (T3) to 0.43 (T1) in testers.

Significant and positive *gca* effects desirable for the trait were noticed in L6 (0.40) and L4 (0.23) lines and T1 (0.43), T2 (0.40) and T5 (0.20) testers.

The estimated component of variance due to *sca* (0.31) was higher than *gca*(0.10) for kernel length in pooled analysis indicating the preponderance of non-additive gene action. Similar results were earlier reported by Bisne and Motiramani (2005) and Shivani *et al.* (2009).

From the pooled analysis, among six lines involved two lines L6 (0.48) and L4 (0.11) and three testers *viz.*, T1 (0.48), T2 (0.29) and T5 (0.21) showed significant positive *gca* effects suggesting that they were good general combiners with favorable genes for kernel length. The line L6 and testers *viz.*, T1, T2 and T5exhibited significant *gca* effects at different locations and as well as in pooled analysis.

***sca* effects**

Specific combining ability effects for kernel length at Jagitial location, varied from -1.41 (L5T1) to 0.92 (L3T3). Significant positive *sca* effects desirable for the trait were recorded by11 cross combinations. The cross L3T3 (0.92) recorded highest *sca* effect followed by L2T2 (0.66) and L1T5 (0.64).

At Warangal location, *sca* effects for this trait ranged from -1.23 (L5T1) to 0.88 (L3T3) and nine crosses exhibited significant positive *sca* effects. The cross L3T3 (0.88) registered highest *sca* effect followed by L4T1 (0.66) and L4T5 (0.64).

Estimates of *sca* effects at Hyderabad location, ranged from -1.62 (L5T1) to 1.09 (L3T3). Thirteencrosses exhibited significant positive *sca* effects and the best among them were L3T3 (1.09) followed by L2T2 (0.57) and L5T2 (0.52).

From the pooled analysis, out of thirty crosses, eleven cross combinations showed significant *sca* effects in desirable direction. The superior crosses identified among them were L3T3 (0.97), L2T2 (0.58), L5T2 (0.56), L4T1 (0.49), and L5T4 (0.48). The crosses *viz*., L2T1, L2T2, L3T1, L3T3, L4T1, L5T2, L5T3 and L5T4 showed significant positive *sca* effects at all locations and also in pooled analysis.

Based on *per se* performance and positive *sca* effects the crosses *viz*., L4T1 (High × High), L2T1 (Low × High) and L2T2 (Low × High), L1T1 (low × high), L1T5 (low × high), L3T1 (low × high), L3T3 (low × low), L4T5 (high × high), L5T2 (low ×

high) and L5T4 (low × low) were identified as superior for kernel length. The crosses between low × high resulted in superior cross combinations due to complementary gene action which had resulted out of both additive and non-additive gene action while 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. The cross between two low combiners revealed the presence of non-additive inter allelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents.

4.3.3.9 Kernel breadth (mm)

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -0.12 (L5) to 0.15 (L6) among lines and from -0.17 (T3) to 0.38 (T1) among testers. The *gca* effects were significantly negative for L5 (-0.12) and L2 (-0.11) in lines while in testers, T3 (-0.17), T4 (-0.16) and T2 (-0.08) recorded significant negative *gca* effects for this traits.

Among the lines at Warangal location, *gca* effects ranged from -0.16 (L5) to 0.15 (L6) and from -0.17 (T3) to 0.31 (T1) among testers. The estimates of *gca* effects were significant and negative for L5 (-0.16) and L2 (-0.05) in lines and among testers T3 (-0.17), T4 (-0.09) and T2 (-0.04).

Range of *gca* effects at Hyderabad location, for kernel length was from -0.13 (L5) to 0.15 (L6) among lines and from -0.15 (T4) to 0.37(T1) among testers. Lines L5 (-0.13), L3 (-0.05) and L1 (-0.04) recorded significant negative *gca* effects whereas in testers, T4 (-0.15), T3 (-0.13) and T2 (-0.12) exhibited significant negative *gca* effects.

The variance due to specific combining ability (0.026) was higher than the general combining ability (0.023) for this trait in pooled analysis indicating the influence of non-additive gene action. Conformity results were given by Bisne and Motiramani (2005) and Shivani *et al.* (2009).

In pooled analysis three lines L5 (-0.14), L2 (-0.05) and L3 (-0.03) recorded significant negative *gca* effect, while in testers T3 (-0.16), T4 (-0.13) and T2 (-0.08) registered significant *gca* effects in desired direction. These were found to be good

combiners for kernel breadth. The line L5 and in testers *viz.,* T3 and T4 recorded significant negative *gca* effects at all locations as well as in pooled analysis.

***sca* effects**

At Jagitial location, estimates of *sca* effects for kernel breadth varied from -0.44 (L5T1) to 0.36 (L5T3) among crosses and significant negative *sca* effects were recorded by7 hybrids. Top three crosses among them were L5T1 (-0.44), L6T3 (-0.24) and L4T2 (-0.15).

Range of *sca* effects at Warangal location was from -0.43 (L5T1) to 0.28 (L5T3). Nine crosses possessed significant negative *sca* effects at this location. The best among them were L5T1 (-0.43) followed by L6T3 (-0.21) and L4T2 (-0.18).

Among the crosses tested at Hyderabad location, *sca* effects ranged from-0.51 (L5T1) to 0.28 (L5T3). Eight cross combinations recorded significant negative *sca* effects. Highest *sca* effects were recorded by L5T1 (-0.51), L6T3 (-0.25) and L3T3 (-0.17).

In pooled analysis, eight cross combinations had recorded significant *sca* effects in desired direction. Some of the top specific combiners were L5T1 (-0.46), L6T3 (-0.24), L1T2 (-0.16), L3T3 (-0.16) and L4T4 (-0.11). The hybridsL3T3, L4T2, L4T4, L5T1 and L6T3exhibited significant negative *sca* effect at all locations and also in pooled analysis. Based on *per se* performance and *sca* effects L3T3 (High × High), L1T3 (low × high), L4T2 (low × high), L4T4 (low × high), L5T1 (high × low) and L6T3 low × high) were identified as best specific cross combination. The cross combination 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. The crosses between low × high or high × low resulted in superior cross combinations due to complementary gene action which had arised out of both additive and non-additive gene action.

4.3.3.10 L/B ratio

***gca* effects**

Among the lines at Jagitial location, *gca* effects exhibited a range from -0.26 (L1) to 0.13 (L2) and in testers it recorded a range from -0.27 (T1) to 0.24 (T2). Lines

L2 (0.13) and L5 (0.11) showed significant positive *gca* effect and among testers, T2 (0.24) and T4 (0.10) recorded significant positive *gca* effects.

At Warangal location, *gca* effects for L/B ratio ranged from -0.10 (L4) to 0.14 (L5) in lines and from -0.14 (T1) to 0.17 (T2) among the testers. Further, significant and positive *gca* effects for this trait were noticed in L5 (0.14) line and T2 (0.17) and T5 (0.08) in testers.

At Hyderabad location, *gca* effects for L/B ratio varied from -0.08 (L1) to 0.11 (L3) in lines and from -0.28 (T1) to 0.36 (T2) in testers. Significant and positive *gca* effects were recorded in L3 (0.11) line and T2 (0.36) and T4 (0.07) in testers.

The ratio of *gca* variance to *sca* variance was low (0.12) in pooled analysis 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 Bisne and Motiramani (2005), Shivani *et al.* (2009) and Kumar Babu *et al.* (2010)

From the pooled analysis the line L5 (0.09) and two testers *viz*., T2 (0.26) and T5 (0.05) registered positive *gca* effects implying their good general combining ability. The tester T2 recorded significant positive *gca* effect at all locations and also in pooled analysis. This parent may be involved in crossing programmes for improving this trait.

***sca* effects**

The *sca* effects at Jagitial location, ranged from -0.39 (L4T3) to 0.75 (L3T3). Further, significant positive *sca* effects displayed by eight crosses. Top three specific combiners were L3T3 (0.75), L6T3 (0.45) and L5T4 (0.35).

At Warangal location, *sca* effects for L/B ratio varied from -0.30 (L5T3) to 0.71 (L3T3) and only six crosses exhibited significant positive *sca* effects. Among them L3T3 (0.71) followed by L4T5 (0.37) and L6T3 (0.36) were found superior.

Range of *sca* effects at Hyderabad location was from -0.46 (L3T2) to 0.86 (L3T3). Among the crosses, eight hybrids recorded significant positive *sca* effects. The top performing ones were L3T3 (0.86), L6T3 (0.31) and L1T2 (0.30).

Among 30 cross combinations evaluated, nine crosses showed significant positive *sca* effects and top three specific cross combinations among them were

L3T3 (0.78), L6T3 (0.38), L2T2 (0.33), L5T4 (0.29) and L4T5 (0.26) and the crosses L2T2, L3T3, L5T4 and L6T3 revealed significant positive *sca* effects at all locations as well as in pooled analysis. However based on *per se* performance and *sca* effects the crosses L3T3 (Low × Low), L2T2 (Low × High), L4T4 (low × low), L4T5 (low × high), L5T4 (high × low), L6T3 (low × low) and L5T2 (High × High) were detected as promising specific cross combinations. The cross combinations involving high × high general combiner 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. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents. Low × high or high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.3.11Bran oil content (%)

***gca* effects**

At Jagitial location, estimates of *gca* effects varied from -1.62 (L4) to 2.30 (L1) among lines while in testers, range was from -0.86 (T1) to 0.83 (T4). Only two lines L1 (2.30) andL5 (1.20) showed significant positive *gca* effect and in testers T4 (0.83) and T3 (0.55).

Range of *gca* effects at Warangal location was from -1.73 (L2) to 2.11 (L1) in lines and from -1.22 (T1) to 1.25 (T3) in testers. Significant positive *gca* effects exhibited by L1 (2.11) and L5 (1.45) lines and in testers T3 (1.25) and T2 (1.02).

At Hyderabad location, estimates of *gca* effects varied from -1.35 (L4) to 1.36 (L1) in lines while in testers, range was from -1.18 (T5) to 2.07 (T2). Only two lines L1 (1.36) and L5 (0.99) and one tester T2 (2.07) showed significant positive *gca* effect.

In the present investigation, bran oil content seems to be mostly under the control of non -additive gene action in pooled analysis as the *gca* variance (0.86) was lower than *sca* variance (0.93).The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.92) revealing the preponderance of non- additive gene action in the inheritance of this trait.

The present findings are in accordance with the results of Sabaghnia N *et al*. (2010) and Amir Jose Klein Werle *et al*. (2013).

In pooled analysis, the estimates of *gca* effects revealed that L1 (1.92) and L5 (1.22) among lines and T2 (1.07) and T3 (0.55) among testers were good general combiners. Among the lines L1 and L5 were identified with significant positive *gca* effects at all locations as well as in pooled analysis. These lines can be utilized in basic breeding programmes for improvement of this trait.

***sca* effects**

At Jagitial location, estimates of *sca* effects varied from -3.91 (L1T5) to 2.51 (L1T3). Six hybrids recorded significant positive *sca* effects. Top performing crosses identified among them were L1T3 (2.51) followed by L3T4 (2.08) and L2T5 (1.53).

Range of *sca* effects at Warangal location, for bran oil was from -2.13 (L1T5) to 2.74 (L6T2). Six crosses possessed significant *sca* effects at this location. The superior crosses identified among them were L6T2 (2.74), L1T3 (1.94) and L5T5 (1.17).

For bran oil at Hyderabad location, *sca* effects ranged from -1.94 (L1T5) to 3.01 (L6T5). Among crosses, six crosses displayed significant positive *sca* effects. The top three crosses were L6T5 (3.01) followed by L4T3 (1.96) and L2T1 (1.69).

In pooled analysis, eight crosses recorded significant positive *sca* effects. The top performing three specific crosses among them were L1T3 (1.89), L6T5 (1.43), L3T4 (1.39), L6T2 (1.33) and L2T1 (0.92). Among the cross, L1T3exhibited significant positive *sca* effects at all locations and also in pooled analysis. From the above crosses, none of the cross was identified as best specific combiners as per their *per se* performance and *sca* effects.

4.3.3.12 Milling %

***gca* effects**

Among the lines at Jagitial location, *gca* effects ranged from -4.11 (L2) to 1.66 (L1) and among testers, *gca* effects varied from –1.61 (T1) to 1.52 (T4). The lines L1 (1.66), L5 (0.72), L6 (0.65) and L3 (0.63) and testers *viz.*, T4 (1.52) and T5 (0.78) recorded significant positive *gca* effects.

Estimates of *gca* effects at Warangal location, varied from -0.73 (L4) to 0.86 (L5) among lines and from -1.70 (T2) to 1.88 (T1) in testers. The lines L5 (0.86) and L6 (0.57) recorded significant positive *gca* effect and in testers T1 (1.88), T5 (0.73) and T4 (0.59).

gca effects at Hyderabad location, exhibited a range from -2.79 (L2) to 1.95 (L4) among lines whereas in testers, range was from -0.73 (T5) to 0.91 (T1). The lines L4 (1.95) and L3 (1.67) showed significant positive *gca* effects. Among testers T1 (0.91) and T3 (0.37) recorded significant *gca* effects in desired direction.

In pooled analysis the variance due to *gca* (0.18) was lesser than the *sca* (1.77) for milling recovery indicating the contribution of non-additive gene action in the inheritance of this trait. Results supporting the present investigation were put forth by Sharma and Mani (1998), Munhot *et al.* (2000) and Gonya Nayak (2011).

For milling percent in pooled analysis, four lines L3 (0.85), L4 (0.56), L1 (0.51) and L6 (0.43) and three testers *viz.*, T4 (0.59), T1 (0.39) and T5 (0.26) were identified as potential general combiners based on their *gca* effects. None of the lines and testers were good general combiners at different locations and over locations.

***sca* effects**

Milling percent *sca* effects at Jagitial location, exhibited a range from -3.77 (L2T3) to 5.34 (L2T2) among crosses. Nine hybrids showed significant positive *sca* effects at this location. Top three specific crosses among them were L2T2 (5.34), L6T1 (4.12) and L4T3 (3.43).

At Warangal location *sca* effects ranged from -4.07 (L2T3) to 4.22 (L2T2) and 10 crosses recorded significant positive *sca* effects. The top three crosses were L2T2 (4.22) followed by L5T3 (3.68) and L3T4 (2.30).

Estimates of *sca* effects at Hyderabad location, varied from -4.64 (L3T1) to 2.41 (L5T1) and ten crosses exhibited significant positive *sca* effects. Top three specific crosses were L5T1 (2.41), L6T1 (2.32) and L1T5 (2.27).

From pooled analysis 13 crosses showed significant *sca* effects in positive direction and the top three specific cross combinations identified among them were L2T2(3.89), L6T1(2.34), L1T5(2.10), L5T2 (1.87) and L4T4 (1.68). Two hybrids *viz.*,

L1T5 and L2T2 recorded significant positive *sca* effect at all locations and also in pooled analysis. The best specific cross combinations identified based on positive *sca* effect and *per se* performance were L6T1 (high × high), L1T5 (high × high), L4T4 (high × high), L1T1 (high × high), L3T5 (high × high), L2T4 (low × high), L3T2 (high × low), L3T4 (high × low), L4T3 (high × low), L5T1 (low × high), L5T5 (low × high), (L2T2 low × low) and (L5T3 low × low). 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. The cross between two low combiners revealed the presence of non-additive inter allelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents. Low × high or high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.3.13 Head rice recovery (%)

***gca* effects**

Estimates of *gca* effects at Jagitial location, varied from -5.05 (L2) to 2.02 (L1) among the lines and from -2.67 (T2) to 2.09 (T5) among the testers. Highly significant positive *gca* effects were recorded by lines L1 (2.02), L3 (1.66), L6 (0.97) and L4 (0.83) and in testers, T5 (2.09), T3 (1.67) and T4 (0.89).

Among the lines at Warangal location, *gca* effects exhibited a range from -1.41 (L2) to 0.82 (L3) and among testers it varied from -1.94 (T2 and T3) to 1.94 (T1). The estimates of *gca* effects were positive and significant for lines L3 (0.82) and L6 (0.52) while, in testers T1 (1.94), T4 (1.11) and T5 (0.84).

At Hyderabad location, lines showed *gca* effects from -2.82 (L2) to 2.61 (L4) whereas testers ranged from -1.19 (T4) to 1.37 (T1). Significant positive *gca* effects were recorded by lines L4 (2.61) and L3 (2.18) whereas, in testers T1 (1.37) and T3 (0.67).

For this trait the estimated component of variance due to *sca* (2.58) was higher than *gca* (0.25) variance in pooled analysis. It indicates the predominance of non-additive gene action. This is in accordance with the earlier reports of Sharma and Mani (1998), Munhot *et al.* (2000) and Gonya Nayak (2011).

Among lines, L4 (1.41), L3 (0.86) and L1 (0.76) and among testers T5 (0.73) T1 (0.44) and T4 (0.27) revealed positive *gca* effects, implying that they are good general combiners. For the character head rice recovery, line L3 registered significant positive *gca* effects at all locations and also in pooled analysis.

***sca* effects**

For head rice recovery at Jagitial location *sca* effects in crosses varied from -5.14 (L6T5) to 6.17 (L6T1) and among hybrids evaluated eight hybrids registered significant positive *sca* effects. Some of the top specific crosses identified among them were L6T1 (6.17), L5T5 (4.03) and L4T3 (3.79).

At Warangal location, *sca* effects varied from -5.13 (L3T1) to 2.87 (L2T2) and significant positive *sca* effects were recorded by 11 crosses. The crosses L2T2 (2.87) recorded the highest *sca* effect followed by L3T4 (2.79) and L4T4 (2.55).

At Hyderabad location, crosses showed *sca* effects from -4.55 (L3T1) to 3.63 (L5T1). Out of 30 hybrids tested 12 hybrids recorded significant positive *sca* effects. The highest *sca* effect was recorded by cross L5T1 (3.63) followed by L6T1 (3.37) and L4T4 (2.44).

Eleven cross combinations showed significant *sca* effects in positive direction and top 5 crosses among them were L6T1 (3.87), L2T2 (2.39), L4T4 (1.90), L3T2 (1.83) and L1T5 (1.77). Among the hybrids, L2T2 and L6T1 recorded significant positive *sca* effects at all locations as well as in pooled analysis. When compared over their *per se* performance and *sca* effects the crosses L6T1 (low × high) was found superior for this trait. The cross combinations involving 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.

4.3.3.14 Alkali spreading value

***gca* effects**

Estimates of *gca* effects at Jagitial location, ranged from -0.51 (L5) to 0.55 (L6) among the lines and from -0.76 (T1) to 0.46 (T2 and T3) among the testers. The estimates of *gca* effects were positive and significant for lines L6 (0.55) and L3 (0.52), and in testers, T2 and T3 (0.46).

At Warangal location, *gca* effects for alkali spreading value varied from -0.60 (L5) to 0.57 (L3) in lines and from -0.71 (T1) to 0.56 (T2) among testers. Further, significant and positive *gca* effects desirable for the trait were noticed in L3 (0.57), L6 (0.56) and L4 (0.13) among the lines and T2 (0.56), T3 (0.26) and T5 (0.13) among testers.

A range of -0.53 (L5) to 0.67 (L6) was observed for lines at Hyderabad location whereas, testers recorded a range from -0.61(T1) to 0.48 (T3). The lines L6 (0.67), L3 (0.53) and L4 (0.17) exhibited significant positive *gca* effect, whereas in testers T3 (0.48) and T2 (0.46).

Component of variance due to *sca* (0.45) was higher than *gca* (0.16) for alkali spreading value in pooled analysis, indicating the prevalence of non-additive gene action. Similar results were observed by Sharma and Mani (1998) and Munhot *et al.* (2000).

From pooled analysis, L6 (0.59), L3 (0.54) and L4 (0.14) lines and two testers *viz.*, T2 (0.50) and T3 (0.40) registered significant positive *gca* effects indicating the good combining ability for alkali spreading value. The lines L3, L6 and T2 and T3testers were identified as good general combiners at different locations as well as in pooled analysis. They may be utilized in future breeding programmers for improving this trait.

***sca* effects**

Among the crosses at Jagitial location, *sca* effects for alkali spreading value ranged from -1.02 (L5T4) to 1.49 (L6T4) and significant positive *sca* effects were exhibited by 12 hybrids. The top three promising crosses were L6T4 (1.49), L1T1 (0.72) and L2T1 (0.67).

Estimates of *sca* effects at Warangal location, ranged from -0.91 (L6T1) to 1.53 (L6T4) among crosses and 10 crosses revealed significant positive *sca* effects for this trait. Top three superior crosses were L6T4 (1.53), L1T1 (0.93) and L4T3 (0.65).

Specific combining ability effects for alkali spreading value at Hyderabad location ranged from -0.87 (L2T4) to 0.92 (L6T4). Significant positive *sca* effects were observed in 12 hybrids. Highest performance was recorded by cross L6T4 (0.92) followed by L1T1 (0.88) and L2T1 (0.75).

In pooled analysis, out of 30 crosses evaluated, 13 crosses showed significant *sca* effect in positive direction and some of the superior crosses among them were L6T4 (1.32), L1T1(0.85), L2T1 (0.82), L5T2 (0.48) and L2T2 (0.440). The hybrids L1T1, L1T3, L2T1, L4T5, L5T2 and L6T4 displayed significant positive *sca* effect at all locations and also in pooled analysis. The superior cross combinations identified based on their *per se* performance and *sca* effects were L6T2 (high × high), L4T5 (high × high). L4T4 (high × low), L3T5 (high × low), L6T4 (high × low), L1T3 (low × high), L2T2 (low × high), L5T2 (low × high), L5T3 (low × high), L1T1 (low × low), L2T1 (low × low) and L5T5 (low × low). 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. The cross between two low combiners revealed the presence of non-additive interallelic interaction. Superiority of low × low cross combination was mainly due to nicking ability/genetic diversity of their parents. Low × high or high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.3.15 Water uptake

***gca* effects**

Among the lines at Jagitial location, *gca* effects ranged from -16.61 (L3) to 39.72 (L2) and among testers, *gca* effects varied from –17.78 (T3) to 18.33 (T2). The lines L2 (39.72) and L5 (11.39) and testers *viz.*, T2 (18.33) and T4 (7.50) recorded significant positive *gca* effects.

Estimates of *gca* effects at Warangal location, varied from -21.89 (L3) to 37.11 (L2) among lines and from -24.50 (T1) to 25.78 (T4) in testers. The lines L2 (37.11) and L5 (2.78) recorded significant positive *gca* effect and in testers T4 (25.78), T2 (12.44) and T5 (5.50).

gca effects at Hyderabad location, exhibited a range from -40.33 (L3) to 21.00 (L2) among lines whereas in testers, range was from -25.78 (T5) to 20.33 (T1). The lines L2 (21.00), L5 (12.67), L6 (4.33) and L1 (3.00) showed significant positive *gca* effects. Among testers T1 (20.33) and T3 (8.11) recorded significant *gca* effects in desired direction.

In pooled analysis the variance due to *gca* (75.32) was lesser than the *sca* (406.15) for water uptake indicating the contribution of non-additive gene action in the

inheritance of this trait. Results supporting the present investigation were put forth by Sharma and Mani (1998).

For water uptake in pooled analysis, two lines L2 (32.61) and L5 (8.94) and two testers *viz.,* T4 (10.65) and T2 (9.82) were identified as potential general combiners based on their *gca* effects. The lines L2 and L5 were good general combiners at different locations and over locations. These may serve as useful source for improvement of this trait in hybridization programmes.

***sca* effects**

Water uptake *sca* effects at Jagitial location, exhibited a range from -52.00 (L3T2) to 39.17 (L5T4). Among crosses 11 hybrids showed significant positive *sca* effects at this location. Top three specific crosses among them were L5T4 (39.17), L3T5 (33.83) and L3T1 (26.88).

At Warangal location *sca* effects ranged from -59.78 (L3T2) to 56.22 (L4T2) and twelve crosses recorded significant positive *sca* effects. The top three crosses were L4T2 (56.22) followed by L1T5 (45.16) and L3T3 (36.89).

Estimates of *sca* effects at Hyderabad location, varied from -58.22 (L2T5) to 100.67 (L5T4) and 13 crosses exhibited significant positive *sca* effects. Top three specific crosses were L5T4 (100.67), L2T3 (42.89) and L6T2 (39.00).

From pooled analysis twelve crosses showed significant *sca* effects in positive direction and the top five specific cross combinations identified among them were L5T4 (49.57), L4T2 (31.52), L3T1 (30.35), L1T5 (27.82) and L2T1 (23.13). Hybrids *viz.,* L1T5, L2T1, L3T1, L4T2 and L5T4 recorded significant positive *sca* effect at all locations and also in pooled analysis. The best specific cross combinations identified based on positive *sca* effect and *per se* performance were L5T4 (high × high), L2T4 (high × high), L2T2 (high × high), L5T2 (high × high), L2T1 (high × low), L2T3 (high × low), L4T2 (low × high), L6T2 (low × high), L1T5 (low × low), L3T1 (low × low), L3T5 (low × low) and L6T5 (low × low). 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. The crosses involving high x low or low × high *gca* effects resulted in superior

combinations which may be due to complementary gene action. The cross between two low combiners revealed the presence of non-additive interallelic interaction.

4.3.3.16 Gel consistency

***gca* effects**

Range of *gca* effects at Jagitial location, for gel consistency was from -2.94 (L2) to 2.52 (L6) among lines and from -2.40 (T4) to 3.60 (T5) among testers. Out of six lines, L6 (2.52), L1 (1.39) and L5 (0.86) lines recorded significant positive *gca* effect whereas in testers T5 (3.60).

General combining ability effects at Warangal location, varied from -4.36 (L6) to 3.58 (L4) in lines and in testers it ranged from -1.53 (T3) to 1.74 (T1). The lines L4 (3.58), L1 (1.58) and L5 (1.04) and in testers T1 (1.74) possessed significant positive *gca* effects.

At Hyderabad location, *gca* effects ranged from -5.54 (L4) to 1.86 (L6) among lines. Similarly, in testers it ranged from -1.88 (T3) to 1.57 (T2). Highly significant *gca* effects were recorded by L6 (1.86), L2 (1.39), L1 (1.19) and L5 (1.12) lines and in testers, T2 (1.57) and T5 (1.46).

The estimated component of variance due to *sca* (0.10) was lesser than the *gca* (0.58) for gel consistency in pooled analysis. The ratio of *gca* variance to *sca* variance was high (5.80) indicating the presence of additive gene action.

In pooled analysis, L1 (1.39) and L5 (1.01) lines and T5 (1.60) and T1 (0.90) testers showed significant positive *gca* effects and were considered to be good general combiners for gel consistency. The parents, L1 and L5 recorded significant positive *gca* effects at different locations and also in pooled analysis.

***sca* effects**

Range of *sca* effects at Jagitial location for gel consistency was from -12.52 (L6T2) to 9.53 (L6T1). Among 30 hybrids evaluated, fourteen hybrids recorded significant positive *sca* effects for gel consistency. The top three crosses were L6T1 (9.53) followed byL6T5 (8.20) and L3T4 (7.93).

At Warangal location, *sca* effects of gel consistency varied from –11.68 (L2T2) to 9.32 (L2T1) and significant *sca* effects were noted by 12 hybrids. Top three specific crosses among them were L2T1 (9.32) followed by L3T2 (7.86) and L6T5 (7.52).

Among the hybrids at Hyderabad location, *sca* effects ranged from -8.78 (L2T4) to 7.54 (L5T3) and twelve crosses exhibited significant positive *sca* effects. Highest *sca* effect recorded by L5T3 (7.54) followed by L2T5 (7.28) and L6T1 (7.26).

In pooled analysis, ten hybrids showed significant *sca* effects in positive direction out of 30 crosses evaluated. The crossesL4T2 and L4T4recorded significant positive *sca* effect at all the locations and over all locations. The top 5 specific crosses among them were L4T4 (4.73), L6T5 (4.73), L4T2 (4.54), L2T5 (3.64) and L6T1 (3.44). The cross L6T5 (low × high) was identified as good specific cross combination based on positive *sca* effects and *per se* performance. The cross involving low x high *gca* effects resulted in superior combinations which may be due to complementary gene action

4.3.3.16 Amylose content

***gca* effects**

At Jagitial location, estimates of *gca* effects varied from -1.34 (L6) to 1.69 (L2) among lines while in testers, range was from -0.96 (T5) to 0.55 (T1). Three lines L6 (-1.34), L3 (-1.32) and L1 (-0.76) showed significant negative *gca* effect and in testers *viz.*, T5 (-0.96).

Range of *gca* effects at Warangal location was from -1.44 (L1) to 1.16 (L5) in lines and from -0.96 (T5) to 0.93 (T3) in testers. Significant negative *gca* effects exhibited by L1 (-1.44) and L6 (-0.66) lines and in testers T5 (-0.96) and T1 (-0.47).

At Hyderabad location, estimates of *gca* effects varied from -1.68 (L6) to 1.70 (L2) in lines while in testers, range was from -0.80 (T5) to 0.36 (T4).Three lines L6 (-1.68), L3 (-1.11) and L1 (-0.35) showed significant negative *gca* effect and in testers, T5 (-0.80).

In the present investigation, amylose content seems to be mostly under the control of non-additive gene action since in pooled analysis the *gca* variance (0.10) was less than *sca* variance (3.47).The present findings are in accordance with the results of Sharma and Mani (1998).

In pooled analysis, the estimates of *gca* effects revealed that L6 (-1.22), L1 (-0.85) and L3 (-0.75) among lines and T5 (-0.91) among testers were good general

combiners. Among the lines L1 and L6and in testers T5 were identified with significant negative *gca* effects at all locations as well as in pooled analysis. These lines can be utilized in basic breeding programmes for improvement of this trait.

***sca* effects**

At Jagitial location, estimates of *sca* effects varied from -4.38 (L2T4) to 3.59 (L2T2). Thirteen hybrids recorded significant negative *sca* effects. Top performing crosses identified among them were L2T4 (-4.38) followed by L5T4 (-3.60) and L1T2 (-3.12).

Range of *sca* effects at Warangal location, for amylose content was from -3.39 (L2T4) to 2.96 (L2T2). 12 crosses possessed significant *sca* effects at this location. The superior crosses identified among them were L2T4 (-3.40), L6T3 (-3.20) and L1T5 (-2.16).

For amylose content at Hyderabad location, *sca* effects ranged from -2.53 (L5T4) to 3.74 (L3T5). Among crosses, ten hybrids displayed significant negative *sca* effects. The top three crosses were L5T4 (-2.53) followed by L2T3 (-2.41) and L5T5 (-2.34).

In pooled analysis, twelve crosses recorded significant negative *sca* effects. The top performing three specific crosses among them were L2T4 (-3.07), L5T4 (-2.38) and L2T3 (-1.92). Among the crosses, L1T2, L2T3, L2T4, L3T1, L3T2, L4T3, L5T4 and L6T2exhibited significant negative *sca* effects at all locations and also in pooled analysis. From the above crosses LIT5 (high × high), L6T2 (high × low), L1T2 (high × low), L3T1 (high × low), L3T2 (high × low), L4T5 (low × high), L5T4 (low × high), L2T3 (low × low), L2T4 (low × low), L4T1 (low × low), L4T3 (low × low) and L5T4 (low × low) 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. The crosses involving high × low or low high effects resulted in superior combinations which may be due to complementary gene action. The cross between two low combiners revealed the presence of non-additive inter allelic interaction.

A perusal of *gca* effects from pooled analysis revealed that none of the parent recorded significant *gca* effects for all the characters studied. Among lines, L3

(MandhyaVijaya) and L6 (Phalguna) lines recorded significant positive *gca* effects for grain yield plant^{-1}. In addition to this, L6 had significant positive *gca* effect for productive tillers per plant, panicle length, number of grains per panicle, kernel length, milling per cent, alkali spreading value and it showed significant negative effect for amylose content. L3line exhibited significant positive *gca* effect for number of grains per panicle, milling recovery and head rice recovery while negative effects for kernel breadth and amylose content. In case of bran oil content, L1 (Keshari) and L5 (Kandagiri) lines exhibited significant positive gca effects.

Among testers T1(NDR359) and T5 (MTU1010) recorded significant positive *gca* effects for most of the characters *viz*., grain yield per plant, panicle length, 1000-grain weight, kernel length, milling percent, head rice recovery, water uptake while negative significant *gca* effects was recorded for days to 50 % flowering. In addition to these characters, T1 tester exhibited desirable significant positive *gca* effect for number of grains per panicle and the tester T5 possessed significant positive *gca* effect for L/B ratio whereas negative effects for amylose content. However, among testers, T2 (IR64) and T3 (Swarna) showed significant positive *gca* effects in desired direction for bran oil content.

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 transgressive segregants. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system. The crosses between two low combiners producing crosses with significant *sca* effect revealed the role of non-additive interallelic interaction. This may be due to high nicking ability/genetic diversity of parents involved. This component may be exploited through heterosis breeding. Similar findings were observed by Shivani *et al.* (2009).

4.4 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).

Commercial exploitation of heterosis in rice is profitable and it is important that the crosses are compared with released varieties rather than merely comparing with their mid / better parents. So in the present study the performance of the experimental crosses were compared with that of the most popular varieties 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 MTU1010 for yield and quality characters but over Keshari for bran oil content at different locations and in pooled analysis are presented in table 4.4.1. Based on overall performance (*per se* performance, positive *sca* effect and standard heterosis) the best heterotic cross combinations identified for yield, its components and quality characters were presented in table 4.4 .2 and were discussed character-wise hereunder.

4.4.1 Days to 50% Flowering

Standard heterosis for days to 50% flowering at Jagitial location ranged from -11.51 (L1T2) to 26.64 (L2T3). Three cross combinations recorded significant negative heterosis at this location. The range of standard heterosis at Warangal location was from -16.16 (L1T2) to 24.58 (L1T3) and three cross combinations exhibited significant negative standard heterosis over standard check.

At Hyderabad location, standard heterosis for this trait varied from -23.64 (L1T2) to 26.91 (L1T3) and six cross combinations exhibited significant negative standard heterosis.

From the pooled analysis, standard heterosis range for days to 50% flowering was from -16.89 (L1T2) to 25.91 (L1T3) and four hybrids recorded significant standard heterosis over standard check in desired direction. Two cross combinations exhibited significant negative standard heterosis at all locations and also in pooled analysis. Based on overall performance (*per se, sca* effect and standard heterosis) the top specific combiners identified for this trait were L1T2 (-16.89), L5T5 (-10.73), L1T1 (-4.68)and L2T2 (-1.94).

For this trait both positive and negative standard heterosis was observed by Singh *et al.* (2006), Gouri Shankar *et al.* (2010) and Tiwari *et al.* (2011).

4.4.2 Plant Height

Estimates of standard heterosis for plant height at Jagitial location was from -12.82 (L3T2) to 33.90 (L4T1). Significant negative heterosis was recorded by 7 cross

combinations. At Warangal location, estimates of standard heterosis varied from -16.16 (L5T3) to 24.58 (L1T3) among cross combinations. Further, significant negative heterosis was recorded by three cross combinations.

Standard heterosis for plant height at Hyderabad location, ranged from -3.96 (L3T2) to 35.83 (L2T1) and three cross combinations exhibited significant negative heterosis.

In pooled analysis, plant height range was from -2.97 (L1T2) to 34.36 (L2T1) and only one cross combination (L1T2) exhibited significant negative standard heterosis. None of the cross combinations recorded significant negative standard heterosis at different locations as well as pooled analysis. Highest significant negative heterosis was recorded by L1T2 (-2.97) and superiority of this cross combination confirmed by *per se* performance and high *sca* effects.

For the trait plant height, both positive and negative heterosis over standard check were recorded by Chaudhary *et al.* (2007), Rosamma and Vijayakumar (2007), Chandirakala *et al.* (2010), Gouri Shankar *et al.* (2010), Kumar Babu *etal*. (2010) and Tiwari *et al.* (2011).

4.4.3 Panicle length

At Jagitial location, panicle length showed standard heterosis over standard check from -40.69 (L5T4) to 13.52 (L2T1). Out of 30 cross combinations only five cross combinations possessed significant positive standard heterosis. Estimates of standard heterosis at Warangal location varied from -29.08 (L5T4) to 13.68 (L1T1). Four cross combinations recorded significant positive heterosis over standard check MTU1010.

Panicle length at Hyderabad location, exhibited standard heterosis ranging from -21.44 (L2T4 and L5T5) to 24.01 (L6T1) and among 30 cross combinations, five cross combinations revealed significant positive standard heterosis over check MTU1010.

In pooled analysis, a range from -28.09 (L5T4) to 14.99 (L6T1) was recorded for panicle length and six cross combinations exhibited significant positive standard heterosis over standard check MTU 1010. Out of 30 cross combinations evaluated only two cross combinations (L1T1 and L6T1) were found to have highly significant positive heterosis over standard check MTU 1010 at all locations and over locations. The

potential specific cross combinations identified as per *per se* performance and *sca* effects were L6T1 (14.99), L1T1 (14.65), L5T1 (7.89) and L3T5 (5.14). Earlier workers Seetaramaiah *et al.* (1999), Pandya and Tripathi (2006) and Chandirakala *et al.* (2010) reported positive standard heterosis for panicle length.

4.4.4 Number of productive tillers per plant

Among the cross combinations at Jagitial location standard heterosis ranged from -48.48 (L2T4) to 9.09 (L6T5) whereas at Warangal location, it varied from -37.50 (L2T1) to 7.50 (L1T5) and none of the cross combinations showed significant positive standard heterosis in both the locations.

The range of standard heterosis at Hyderabad location was from -38.89 (L2T1) to 16.67 (L3T2 and L3T5) and four cross combinations recorded significant positive heterosis over superior check MTU1010.

A range of -37.61 (L2T1) to 8.26 (L6T5) was observed for number of productive tillers per plant in pooled analysis. Two cross combinations *viz.*, L6T5 and L1T5 recorded significant positive standard heterosis over standard check. This trait directly contributes towards grain yield. None of the cross combinations possessed significant positive standard heterosis at all locations and also in pooled analysis. The best heterotic cross combination identified based on *per se* performance and *sca* effects was L1T5 (5.50).

Singh *et al.* (2006), Rosamma and Vijayakumar (2007), GouriSankar *et al.* (2010), Kumar Babu *et al.* (2010) and Tiwari *et al.* (2011) reported both positive and negative heterosis in their studies.

4.4.5 Number of grains per panicle

Among the cross combinations at Jagitial location, standard heterosis ranged from -26.09 (L5T3) to 80.71 (L3T3) and twenty three cross combinations recorded significant positive standard heterosis. At Warangal location, standard heterosis varied from -32.38 (L4T3) to 39.43 (L3T3). Among cross combinations, twelve cross combinations showed significant positive standard heterosis at this location.

Standard heterosis for grains per panicle at Hyderabad location ranged from -47.92 (L5T1) to 50.61 (L4T1) and four cross combinations exhibited significant positive standard heterosis.

A range of standard heterosis from -32.82 (L3T4) to 42.65 (L3T3) was observed in pooled analysis. Eleven cross combinations *viz.,* L1T1, L2T1, L2T3, L2T5, L3T1, L3T3, L3T5, L4T1, L6T1, L6T3 and L6T4 showed significant standard heterosis for number of grains per panicle over standard check. Three cross combinations *viz.*, L2T1, L3T3 and L4T1 exhibited significant positive standard heterosis at all locations as well as in pooled analysis. Based on overall performance the best specific cross combinations were L3T3 (42.65), L4T1(37.61), L6T4 (19.98), L1T1 (19.42), L2T5 (10.56) and L3T5 (9.75).Standard heterosis of both positive and negative was observed by Singh *et al*. (2006), Gouri Shankar *et al*. (2010), Kumar Babu e*t al.* (2010) and Tiwari *et al.* (2011).

4.4.6 1000-grain weight

At Jagitial location, the cross combination L2T4 (-35.42) recorded lowest test weight and L2T1 (43.97) recorded highest 1000-grain weight. Eight cross combinations exhibited significant positive standard heterosis. The range of standard heterosis at Warangal location, varied from – 32.71 (L6T4) to 31.56 (L6T1). Six cross combinations recorded significant positive standard heterosis over standard check.

1000-grain weight at Hyderabad location, exhibited a range from -27.98 (L5T2) to 57.28 (L2T1). Eleven cross combinations revealed significant positive standard heterosis over standard check.

In pooled analysis this trait recorded a range from -30.62 (L5T2) to 43.22 (L2T1). Nine cross combinations showed significantly greater standard heterosis over standard check MTU 1010. The cross combinations L1T5, L2T1, L4T1, L4T5, L5T1 and L6T1 displayed significant positive standard heterosis for 1000-grain weight at all locations and also in pooled analysis. The best performing cross combinations identified based on *per se* performance, heterosis and *sca* effects were L2T1 (43.22), L6T1 (38.66), L5T1 (27.65), L1T5 (18.43), L4T5 (12.95) and L5T5 (12.80).

Annadurai and Nadarajan (2001), Singh *et al.* (2006), Gouri Shankar *et al.* (2010), Kumar Babu e*t al*. (2010) and Tiwari *et al.* (2011) reported both positive and negative standard heterosis for this trait.

4.4.7 Grain yield per plant

Range of standard heterosis at Jagitial location for grain yield was from -33.28 (L1T3) to 79.47 (L1T5) and seventeen cross combinations recorded significant positive standard heterosis over check.

Among the 30 cross combinations evaluated against standard check, L1T3 (-43.36) recorded lowest standard heterosis and L6T1 (43.23) recorded highest standard heterosis at Warangal location. Significant positive standard heterosis was exhibited by twelve cross combinations *viz.,* L1T1, L1T5, L2T1, L2T3, L3T1, L3T2, L3T5, L4T1, L5T1, L6T1, L6T4 and L6T5.

Standard heterosis at Hyderabad location was ranged from -50.88 (L3T4) to 44.10 (L1T5) and eight cross combinations *viz.*, L1T5, L3T1, L3T3, L4T1, L4T4, L4T5, L5T5 and L6T1recorded significant positive standard heterosis over standard check.

Standard heterosis for grain yield ranged from -39.45 (L1T3) to 50.37 (L3T1) in pooled analysis and sixteen cross combinations *viz.,* L1T1, L1T5, L2T1, L3T1,L3T2, L3T3, L3T5, L4T1, L4T5, L5T1, L5T4, L5T5, L6T1, L6T3, L6T4 and L6T5 registered significant positive standard heterosis. The cross combination L3T1 exhibited the highest heterosis (50.37%) followed by L1T5 (45.37%), L6T1 (44.54%), L4T1 (35.49%) and L3T3 (29.86%).

The present investigation recorded a high order of standard heterosis for grain yield. Four cross combinations L1T5, L3T1, L4T1 and L6T1 registered significant positive standard heterosis over standard check at all locations and also in pooled analysis. Based on *per se* performance positive *sca* effects and heterosis superior combinations identified were L3T1 (50.37), L1T5 (45.37), L6T1 (44.54), L3T3 (29.86), L6T3 (11.26) and L5T4 (9.10).

Negative to positive heterosis over standard check reported by Singh *et al.* (2006), Rosamma and Vijayakumar (2007), Gouri Shankar *et al.* (2010), Kumar Babu e*t al.* (2010) and Tiwari *et al.* (2011).

The cross combinations L1T5 and L6T5 in pooled analysis showed significant positive standard heterosis for number of productive tillers per plant and 1000-grain

weight. This indicates that yield attributes helped the cross combinations to get high heterosis for grain yield per plant.

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

Based on *per se* performance, significant *sca* effects and heterosis for yield in pooled analysis the crossesL3T1, L1T5, L6T1, L3T3, L6T3 and L5T4 recorded high *per se* performance (34.13, 33.00, 32.81, 29.48, 25.26, 24.77 g), significant *sca* effects (3.16, 7.70, 1.41, 6.00, 1.34, 3.09 respectively) and standard heterosis (50.37%, 45.37%, 44.54%, 29.86% , 11.26%, 9.10%) over the standard check MTU 1010 for grain yield per plant.

4.4.8 Kernel length

At Jagitial location, kernel length showed standard heterosis over standard check from -29.00 (L1T3) to 19.54 (L4T1). Out of 30 cross combinations fourteen cross combinations possessed significant positive standard heterosis. Estimates of standard heterosis at Warangal location varied from -23.04 (L4T3) to 20.93 (L4T1). Twelve cross combinations recorded significant positive heterosis over standard check.

Kernel length at Hyderabad location, exhibited standard heterosis ranging from -26.73 (L1T3) to 18.84 (L4T1) and among cross combinations, fourteen cross combinations revealed significant positive standard heterosis over check MTU 1010.

In pooled analysis, a range from -22.34 (L1T3) to 19.77 (L4T1) was recorded for kernel length and fourteen cross combinations exhibited significant positive standard heterosis over standard check MTU 1010. Out of 30 cross combinations evaluated nine cross combinations *viz.*, L1T1, L2T1, L2T2, L3T1, L4T1, L4T5, L5T2, L6T1, L6T2, L6T4 and L6T5 were found to have highly significant positive heterosis over standard check MTU 1010 at all locations and over locations. The top 3 potential specific cross combinations identified as per *per se* performance and *sca* effects wereL4T1 (19.77), L2T1 (15.75) and L2T2 (15.12). Earlier workers Krishna Veni *et al. (*2005) and Singh (2005) reported both positive and negative standard heterosis for kernel length.

4.4.9 Kernel breadth

Estimates of standard heterosis for kernel breadth at Jagitial location was from -15.67 (L2T3) to 39.01 (L6T1). Significant negative heterosis was recorded by six cross combinations. At Warangal location, estimates of standard heterosis varied from -10.15

(L3T3) to 37.06 (L6T1) among cross combinations. Six cross combinations recorded significant negative heterosis.

Standard heterosis for kernel breadth at Hyderabad location, ranged from -12.48 (L3T3) to 37.77 (L6T1) and seven cross combinations exhibited significant negative heterosis.

In pooled analysis, kernel breadth range was from -12.03 (L3T3) to 37.94 (L6T1) and six cross combinations (L1T3, L2T3, L3T3, L5T1, L5T4, L6T3) exhibited significant negative standard heterosis. Highest significant negative heterosis was recorded by L3T3(-12.03), L5T1 (-6.78), L6T3 (-6.66) and L1T3 (-6.55) and superiority of these hybrids confirmed by *per se* performance and high *sca* effects.

For the trait kernel breadth, both positive and negative heterosis over standard check were recorded by Krishna Veni *et al. (*2005).

4.4.10 L/B ratio

Among the cross combinations at Jagitial location, standard heterosis effects ranged from -22.60 (L1T3) to 22.82 (L2T2) and five cross combinations recorded significant positive standard heterosis. At Warangal location, standard heterosis varied from -31.95 (L4T3) to 15.86 (L3T3). Among the cross combinations, only three cross combinations showed significant positive standard heterosis at this location.

Standard heterosis for L/B ratio at Hyderabad location ranged from -24.53 (L4T3) to 22.41 (L3T3) and five cross combinations exhibited significant positive standard heterosis.

A range of standard heterosis from -25.37 (L4T3) to 20.34 (L3T3) was observed in pooled analysis. Six cross combinations *viz.*, L2T2, L3T3, L4T5, L5T2, L5T4 and L6T3 showed significant standard heterosis for L/B ratio over standard check. Three cross combinations *viz.*, L2T2, L3T3 and L5T2 exhibited significant positive standard heterosis at all locations as well as in pooled analysis. Based on overall performance the top 3 specific cross combinations were L3T3 (20.34), L2T2 (17.50) and L5T2 (11.90).Standard heterosis of positive and negative was observed by Krishna Veni *et al. (*2005) and Singh (2005).

4.4.11 Bran oil content

Range of standard heterosis at Jagitial location, for bran oil content was from -44.13 (L3T2) to 2.89 (L1T3) and at Warangal location, this trait exhibited standard heterosis from -44.05 (L6T1) to 0.89 (L1T3).

At Hyderabad location standard heterosis for bran oil content was from -39.47 (L4T1) to 0.89 (L1T2). In pooled analysis it varied from -42.12 (L6T1) to -1.61 (L1T3). None of the cross combinations exhibited significant positive heterosis over superior check (Keshari) at all the locations and over locations.

4.4.12 Milling percent

At Jagitial location, the cross combination L2T1 (-10.83) recorded lowest milling percent and L1T5 (9.21) recorded highest milling percent. Nineteen cross combinations exhibited significant positive standard heterosis. The range of standard heterosis at Warangal location, varied from -6.41 (L2T3) to 6.70 (L3T4 and L5T1). Eighteen cross combinations recorded significant positive standard heterosis.

Milling percent at Hyderabad location, exhibited a range from -5.87 (L5T2) to 7.62 (L4T1).Sixteen cross combinations revealed significant positive standard heterosis over standard check.

In pooled analysis milling per cent recorded a range from -5.55 (L2T3) to 6.56 (L6T1). Nineteen cross combinations showed significantly greater standard heterosis over standard check MTU 1010. The cross combinations L1T5, L3T4, L3T5, L4T4, L5T1 and L6T1 displayed significant positive standard heterosis for milling per cent at all locations and also in pooled analysis. The top 3 performing hybrids identified based on *per se* and *sca* effects were L6T1 (6.56), L1T5 (6.15) and L4T4 (6.07). These results were in agreement with the early findings of Singh and Lal (2005), and Shivani *et al*. (2009).

4.4.13 Head rice recovery

Range of standard heterosis at Jagitial location for head rice recovery was from -13.61 (L2T1) to 10.12 (L4T3) and seven cross combinations recorded significant positive standard heterosis. Among the 30 cross combinations evaluated against standard check, L1T2 (-11.99) recorded lowest standard heterosis and L3T4 (2.08)

recorded highest standard heterosis at Warangal location. None of the cross combinations showed significant positive standard heterosis at this location. Standard heterosis at Hyderabad location was ranged from -12.36 (L2T1) to 2.60 (L4T1 and L6T1) and three cross combinations *viz.*, L4T1, L4T4 and L6T1recorded significant positive standard heterosis over standard check.

Standard heterosis for head rice recovery ranged from -9.92 (L2T5) to 6.33 (L5T4) in pooled analysis and four cross combinations *viz.*, L1T5, L4T4, L5T4 and L6T1 registered significant positive standard heterosis. None of the cross combinations registered significant positive standard heterosis over standard check at all locations and also in pooled analysis. Based on *per se* performance and positive *sca* effects superior combinations identified were L6T1 (3.66), L4T4 (2.08) and L1T5 (1.55).

Head rice recovery is most important among milling indices, as the economic value of the rice is determined by percentage of unbroken rice kernels. Negative to positive heterosis over standard check reported by Singh (2005), Singh and Lal (2005), and Shivani *et al*. (2009).

4.4.14 Alkali spreading value

Among the cross combinations at Jagitial location, standard heterosis effects ranged from -30.89 (L5T4) to 48.44 (L6T4) and fourteen cross combinations recorded significant positive standard heterosis. At Warangal location, standard heterosis varied from -29.80 (L5T1) to 46.35 (L6T4). Among the cross combinations, thirteen cross combinations showed significant positive standard heterosis at this location.

Standard heterosis for alkali spreading value at Hyderabad location ranged from -15.18 (L5T4) to 57.22 (L6T4) and 23 cross combinations exhibited significant positive standard heterosis.

A range of standard heterosis from -25.46 (L5T4) to 50.54 (L6T4) was observed in pooled analysis. Twenty cross combinations showed significant standard heterosis for alkali spreading value over standard check. Ten cross combinations *viz.*, L1T3, L2T2, L3T2, L3T3, L3T4, L3T5,L4T3, L4T5,L5T2, L6T2 and L6T4 exhibited significant positive standard heterosis at all locations as well as in pooled analysis. Based on overall performance the top 3 specific cross combinations were L6T4 (50.42), L6T2(45.86) and L4T3 (37.42).Standard heterosis of positive was observed by Krishna Veni *et al.* (2005) and Singh (2005).

High alkali spreading value corresponded to low gelatinization temperature. Most of the cross combinations possessed Intermediate gelatinization temperature (alkali spreading value between 4-5) which is a desirable feature. Intermediate gelatinization temperature (alkali spreading value >4-5.4) was desirable for cross combinations exhibited by eleven cross combinations *viz.,* L1T1(4.78), L1T2(4.61), L1T4(4.30), L2T1(4.68), L2T3 (4.47), L2T5 (4.51), L3T1 (4.91), L3T4 (5.38), L4T2(5.10), L4T4 (5.10), L5T2 (5.40), L5T3(5.24), L5T5 (4.70), L6T1 (4.07), L6T3 (5.32), L6T5 (5.31) and check MTU 1010 (4.41).

4.4.15 Water uptake

Among the cross combinations at Jagitial location standard heterosis ranged from -12.50 (L3T2) to 33.33 (L2T2). Fifteen cross combinations noticed significant positive heterosis over superior check. At Warangal location it varied from -12.59 (L3T2) to 52.45 (L2T4) and 22 cross combinations showed significant positive standard heterosis.

The range of standard heterosis at Hyderabad location was from -23.31 (L3T4) to 43.56 (L5T4) and fourteen cross combinations recorded significant positive heterosis over standard check.

Water uptake is an important factor that indicates the amount of water and time required for cooking. A range of -10.89 (L3T2) to 36.44 (L5T4) was observed for water uptake in pooled analysis. Twenty two cross combinations recorded significant positive standard heterosis over standard check. Eight cross combinations, namely, L1T2, L2T1, L2T3, L2T4, L3T1, L4T2, L5T4 and L6T2 possessed significant positive standard heterosis at all locations and also in pooled analysis. The top 3 heterotic cross combinations identified were L5T4 (36.44), L2T4 (32.22) and L2T1 (29.11) based on *per se* performance and *sca* effects. Shivani *et al*. (2009) reported negative heterosis in her studies.

4.4.16 Gel consistency

At Jagitial location, gel consistency of cross combinations showed standard heterosis over standard check from -26.32 (L2T1) to 9.65 (L6T5). Out of 30 cross combinations only two cross combinations (L6T5 and L6T1) possessed significant positive standard heterosis. Estimates of standard heterosis at Warangal location varied

from -15.66 (L6T4) to 19.70 (L2T1). Thirteen cross combinations recorded significant positive heterosis over standard check.

Gel consistency at Hyderabad location, exhibited standard heterosis ranging from -30.17 (L4T3) to -0.43 (L2T5) and among cross combinations, none of the cross combinations revealed significant positive standard heterosis over check MTU 1010.

In pooled analysis, a range from -15.20 (L4T3) to -0.61 (L2T5) was recorded for gel consistency and none of the cross combinations exhibited significant positive standard heterosis over standard check MTU 1010.

Rice with soft to medium gel consistency is preferred one by most of the rice consumers. High flaky rice generally have a gel consistency of 40 mm or less, soft to medium soft rice have gels in the range of 41 to 60 mm and soft gel types have gels measuring 61 to 100 mm in the length. Soft gel consistency was exhibited by all the two checks and cross combinations in the study over locations.

4.4.17 Amylose content

Among the cross combinations at Jagitial location, standard heterosis effects ranged from -16.97 (L1T2) to 25.08 (L2T2) and ten cross combinations recorded significant negative standard heterosis. At Warangal location, standard heterosis varied from -21.36 (L1T5) to 16.47 (L2T2). Among cross combinations, ten cross combinations showed significant negative standard heterosis at this location.

Standard heterosis for amylose content at Hyderabad location ranged from -18.36 (L3T1) to 14.35 (L2T1) and 17 cross combinations exhibited significant negative standard heterosis.

A range of standard heterosis from -14.91 (L1T5) to 16.05 (L2T2) was observed in pooled analysis. Eleven cross combinations *viz.*, L1T2, L1T5, L3T1, L3T2, L2T4, L4T1, L4T3, L4T5, L5T4, L6T2 and L6T3 showed significant standard heterosis for amylose content over standard check. Based on overall performance the best three specific cross combinations were L1T5 (-14.91), L6T2 (13.73) and L1T2(-13.33)

Amylose content of rice determines the hardness or stickiness of cooked rice. Higher amylose content (>25%) gives non sticky soft or hard cooked rice. Rice varieties having 20-25% (Intermediate) amylose give soft and flaky cooked rice. Most of the

cross combinations studied exhibited intermediate amylose content over locations. Cross combinations *viz.*, L2T1, L2T2, L4T4and L5T3recorded high amylose content while two checks showed intermediate amylose content over locations.

Among the cross combinations studied, all the cross combinations exhibited greater than 55% of head rice recovery. Cross combinations possessed medium to slender (L1T2, L2T2, L3T3, L4T2, L4T4, L4T5, L5T2, L5T4, L5T5, L6T2, L6T3) kernels with intermediate gelatinization temperature (L1T1, L1T2, L1T4, L2T1, L2T3 L2T5, L3T1 , L3T4, L4T2, L4T4 , L5T2 ,L5T3, L5T5 , L6T1 , L6T3, L6T5), intermediate amylose content (except L2T1, L2T2, L4T4 and L5T3) and soft gel consistency.

Table 4.4.2. Most promising cross combinations for yield and quality characters based on *sca* effects, *per se* performance and heterosis

Cross	Characters
Keshari× MTU1010	Grain yield per plant, 1000-grain weight, number of productive tillers per plant, kernel length, milling per cent, head rice recovery, water uptake and amylose content
MandhyaVijaya×Swarna	Grain yield per plant, Number of grains per panicle, kernel length, kernel breadth and L/B ratio
Phalguna × NDR359	Grain yield per plant, 1000-grain weight, panicle length, milling per cent and head rice recovery
MandhyaVijaya× NDR359	Grain yield per plant, kernel length and amylose content
Phalguna ×Swarna	Grain yield per plant, kernel breadth L/B ratio and milling per cent
Kandhagiri× RPBio226	Grain yield per plant, L/B ratio, water uptake and amylose content.

Table 4.4.3. Most promising cross combinations for bran oil content based on *per se* performance correlating with optimum grain yield per plant.

Cross	Bran oil content (%)	Grain yield per plant (g)
Keshari× IR64	16.20	22.20
Kandagiri× RP Bio226	14.10	24.80
Keshari× NDR359	13.70	25.70
Phalguna × MTU1010	13.70	26.00
Kandagiri× MTU1010	13.30	26.40

4.5 Stability Analysis

4.5.1 Eberhart and Russell's Stability model

The presently cultivated varieties and hybrids though having high seed yield potential they are unpredictable in their performance even under less varied conditions of cultivation. Lack of varieties and hybrids suitable to specific location accounts for the decline in the area and productivity of rice, apart from the yield losses due to biotic and abiotic stresses. This warrants the attention of the plant breeders to evolve superior varieties that would sustain well in different environmental conditions.

The results of pooled analysis of variance for stability as devised by Eberhart and Russell (1966) were presented in (Tables 4.5.1 and 4.5.2). The genotypes showed significant differences for all the characters when tested against Pooled error. Environments showed highly significant differences for all the characters under study except 1000-grain weight and kernel length whereas genotype × environment interaction components showed significant differences for all the characters when tested against pooled error, indicating wide differential behavior of genotypes in changing environments. Significance of environment (linear) component for all the characters except test weight and kernel length, when tested against pooled deviation indicated that the genotypes responded linearly for most of the characters under study.

The Genotype × Environment (linear) interaction was significant for number of productive tillers per plant, number of grains per panicle, kernel length and bran oil content when tested against pooled deviation, which suggested that the performance of genotypes across the environments could be predicted for these traits with great precision, as reported by Waghmode *et al.* (2011) and Lal and Singh (2012). Both linear and non-linear components were significant for number of productive tillers per plant, number of grains per panicle, kernel length and bran oil content indicating the importance of both the components in determining the stability of these traits and these results were confirmed by Gourishankar *et al.* (2008), Panwar *et al.* (2008) and Dushyanthakumar *et al.* (2010). Significance of pooled deviations for all the characters indicated that the performance of genotypes is entirely unpredictable in nature as such, importance of non–linear component in determining interaction of genotypes with environments has to be considered. Biswas *et al*. (2011) and Subudhi *et al.* (2012) also reported similar findings. Early flowering, dwarfness and less kernel breadth are desirable in rice, negative values were treated on favourable side and for rest of the traits positive values were considered as desirable. Environmental index for different characters at three locations were given in table 4.5.3.

Stability parameters for bran oil content, yield and quality characters under investigation were presented in Table 4.5.4.

4.5.1.1 Days to 50 % flowering

The pooled analysis of variance for this character indicated significant differences among genotypes and environments and further partitioning of MSS due to G × E into linear and non-linear revealed predominant role of non-linear component. Similar results were obtained by Dushyanthakumar *et al.* (2010) and Ahmad Ramezanil *et al.* (2011) earlier.

The mean value for this trait varied from 80.89 (L1T2) to 122.56 (L1T3). Environment 3 (-9.70) was found to be favourable for this trait. Among the cross combinations L3T1(μ=103.33, b_i=1.03, S^2d_i=-0.90), LIT1 (μ=92.78, b_i=1.05, S^2d_i=2.30) and L1T2(μ=80.89, b_i =1.13, S^2d_i=-0.68) were identified as a stable one's having low mean than grand mean with regression coefficient near 'unity' and non–significant deviation from regression. The cross combinations L2T2 (μ = 95.44, b_i = 1.37, S^2d_i = -0.44) and L3T5 (99.89, b_i =1.54, S^2d_i=1.67) having low mean, regression coefficient greater than 'unity' and non-significant deviation from regression were

found to be suitable for better environment. Regression coefficient less than one (b_i<1) with low mean than general mean and non-significant deviation from regression were observed in L5T5 (μ = 86.89, b_i = 0.83, S^2d_i = -0.70), L5T2 (μ = 102.22, b_i = 0.65, S^2d_i = -0.75) and L6T1 (μ = 104.67, b_i = 0.82, S^2d_i = 1.33). These cross combinations perform better in unfavorable environments with early flowering.

In cross combinations *viz.*, L1T5 (μ=98.67, b_i =0.82, S^2di=6.34**), L2T4 (μ=99.00, b_i =1.40, S^2di=14.10**) , L2T5 (μ=103.22, b_i =1.19, S^2di=6.55**) , L5T1 (μ=97.22, b_i =0.65, S^2di=38.51**), L5T3 (μ=105.67,b_i =0.97, S^2di=26.96**) and L6T2 (μ =104.78, b_i =0.92, S^2di=22.61**)the performance has been found to be highly unpredictable because of their significant deviation from regression values and low mean than gran mean. Lavanya *et al.* (2005), Saidaiah *et al.* (2010c), Umadevi *et al.* (2010a) and Waghmode and Mehta (2011) also identified stable hybrids for days to 50% flowering.

4.5.1.2 Plant height

The significant pooled deviation for this character indicated that the performance of genotypes is highly unpredictable.

The mean values for this trait ranged from 93.59 (L1T2) to 129.60 (L2T1). Environment 1 (-16.65) was favourable for this trait. The cross combinations L2T4 (μ= 105.34, b_i =1.19, S^2di=-0.69), L3T3 (μ=107.28, b_i =1.25*, S^2di=-0.97) and L4T2 (μ=104.24, b_i=1.27, S^2di=-0.99) with low mean, regression coefficient greater than 'unity' and non–significant deviation from regression were suitable for favourable environment. For poor environment, the cross combination, L5T2 (μ=103.52, b_i =0.19*, S^2di=-0.97) with low mean and regression coefficient less than 'unity' was suitable.

. The cross combinations with unpredictable performance having significant deviation from regression values and mean lower than gran mean were L1T2 (38.99**), L1T3 (93.04**), L1T4 (55.29**), L2T2 (59.35**), L2T5 (7.68**), L3T2 (86.85**), L4T3 (9.25**), L4T5 (7.45**), L5T1 (16.77**), L5T3 (152.74**), L5T4 (10.21**), L5T5 (20.17**) and L6T4 (23.01**). Stable cross combinations for plant height were also reported by Lavanya *et al.* (2005) and Waghmode and Mehta (2011).

4.5.1.3 Panicle length

The mean value for this trait ranged from 16.47 (L5T4) to 26.33 (L6T1). Among all the environments, Environment 2 (E.I. = 2.201) was found to be most favourable for this trait. Among 30 cross combinations, 24 cross combinations exhibited non-significant deviation from the regression (S^2d_i) values *i.e.* the F_1s are within the range of minimum deviation from regression and whose performance can be predicted.

The stable cross combinations identified were L1T1 (μ= 26.26, b_i=0.91, S^2di=-0.23), L4T4 (μ=22.54, b_i=0.89, S^2di=0.01), and L6T3 (μ=22.31, b_i=1.07, S^2di=1.27) having high mean than grand mean, regression coefficient near to'unity' and non–significant deviation from regression. For better environment, the cross combinations *viz.*, L2T5 (μ=23.26, b_i=1.50, S^2di=-0.03), L3T3 (μ=22.15, b_i=1.20, S^2di=-0.09), L3T5 (μ=24.08, b_i=1.20, S^2di=0.72) and L5T1 (μ=24.71, b_i=1.29, S^2di=-0.34) with high mean, regression coefficient greater than 'unity' and non-significant deviation from regression were identified. The cross combinations *viz.*, L4T5, L5T2 , L6T1 and L6T5 were suitable for poor environments as they recorded high mean (23.54, 23.15,26.33,24.22) with regression coefficient (0.55, 0.75,0.74, 0.74) less than 'unity' and non–significant (0.02,0.41,0.23,-0.45) deviation from regression.

In case of two cross combinations, L1T5 (3.31**) and L2T1 (1.71*) the performance was un-predictable, due to significant deviations from regression. Lavanya *et al.* (2005), Umadevi *et al.* (2010) and Waghmode and Mehta (2011) also identified stable hybrids for panicle length.

4.5.1.4 Productive tillers per plant

Productive tillers per plant is an important yield contributing character in rice. Highly significant MSS due to G × E interaction for this character revealed that the genotypes interacted considerably with all environments. The significant pooled deviation for this character indicated that the performance of genotypes is highly unpredictable. Such results were also reported previously by Subhudhi *et al.* (2012).

The mean character for this trait varied from 7.56 (L2T1) to 13.11 (L6T5) and the environment 2 (EI: 0.611) was observed to be most favourable for this trait. The $_C$ross combinations *viz.*, L2T5 (μ=11.33, b_i=1.01, S^2di=-0.17) and L6T5 (μ=13.11, b_i=1.14, S^2di=-0.09) which have recorded high mean than grand mean (10.54) , regression

coefficient near 'unity' and non–significant deviation from regression were considered as stable for this trait.

Whereas three cross combinations, L1T5, L3T4 and L3T5 with high mean (12.78, 10.67, 12.44), regression coefficient (1.85, 2.72, 2.71) greater than unity and non–significant deviation from regression (0.26, 0.10, 0.27) were found suitable for better environment. In poor environment the cross combinations L2T2 (μ=10.56, b_i=0.62, S^2di=0.21), L6T1 (μ=11.89, b_i=0.52, S^2di=-0.07), L6T2 (μ=12.11, b_i= 0.74, S^2di=-0.05) and L6T4 (μ=11.89, b_i=0.62, S^2di=0.21) were suitable. Further, in case of L3T2 (1.68**), L4T1 (4.93**) and L5T3 (2.26**) the performance was found to be highly unpredictable, as they recorded significant deviations from regression. Earlier findings of Shanmuganathan and Ibrahim (2005), Saidaiah *et al.* (2010c), Umadevi *et al.* (2010) and Sreedhar *et al.* (2011) also recorded stable hybrids for this trait.

4.5.1.5 Number of grains per panicle

The pooled analysis of variance of three locations revealed that G × E interactions were significant for this character implying differantial response of genotypes. Arumugan *et al.*(2007), Panwar *et al.*(2008), Ramya and Senthilkumar (2008) also reported significant G x E interaction for this trait as observed in the present study.

The observed range was from 91.89 (L3T4) to 195.11 (L3T3) and environment 2 (11.159) was favourable for this trait. Among the cross combinations tested, 28 crosses exhibited significant deviations from the regression (S^2d_i) as such their performance cannot be predicted in the varying environments.

None of the cross combinations found stable for number of grains per panicle as they recorded significant deviations from the regression (S^2d_i).

4.5.1.6 1000- grain weight

Pooled analysis of variance indicated presence of significant G × E interaction for 1000-grain weight also (Sreedhar et al., 2011). Good amount of variation was found for this trait with a lowest value of 15.06 (L5T2) and highest value of 31.08 (L2T1). With regard to environments, environment 2 (0.349) was highly favourable for this trait. Twenty six cross combinations exhibited non-significant deviations from the regression (S^2d_i) values as such, their performance could be highly predicted. The cross combinations with high mean than grand mean, regression coefficient near to 'unity' and non-significant deviation from regression are L5T5 (μ=24.48, b_i=0.93, S^2di=-0.49)

and L6T1 (μ=30.09, b_i=1.01, S^2di= -0.47) were considered as stable for 1000 grain weight.

Only one cross combination, L1T2 (μ=21.94, b_i=0.04, S^2di=0.19) was identified for poor environment. In better environment, the cross combinations, L1T4 (μ=22.71, b_i=2.05, S^2di=0.09), L2T3 (μ=21.69, b_i=1.93, S^2di=1.06), L3T5 (μ=22.77, b_i=4.06, S^2di=-0.25), L4T1 (μ=25.67, b_i=3.53, S^2di=0.00), L4T5 (μ=24.51, b_i=1.67, S^2di=-0.48), L5T1(μ=27.70, b_i=1.37, S^2di=-0.30) and L6T5 (μ=23.78, b_i=1.33, S^2di= -0.28) with high mean, regression coefficient greater than 'unity' and non–significant S^2di fared better. Where as in case of certain cross combinations, L3T1 (5.24**) and L3T2 (12.96**) which had significant deviations from regression, 1000-grain weight was highly unpredictable. Stable hybrids for 1000-grain weight also reported by Babu *et al.* (2005), Lavanya *et al.* (2005), Shanmuganathan and Ibrahim (2005), Sreedhar *et al.* (2011) and Waghmode and Mehta (2011).

4.5.1.7 Grain yield per plant

High grain yield is the ultimate objective for any breeder to tackle the hunger problem of growing population. The component of G × E interaction was significant for grain yield which indicated that the grain yield per plant is highly variable with the changing environments. Earlier, Nayak A.R. (2008), Bhakta and Das *(*2008), Dushyantha Kumar *et al.*(2010), Biswas *et al.*(2011) and Subudhi *et al.*(2012) also reported similar results.

The mean values ranged from 13.74 (L1T3) to 34.13 (L3T1) with the grand mean of 24.55 and the environment 2 (2.563) was most favourable for this trait. Among the cross combinations studied, 12 cross combinations revealed non-significant deviations from the regression (S^2d_i) values, which implies that the genotypes were within the range of minimum deviation from regression and performance could be predicted with respect to these cross combinations.

The cross combinations are L3T1, L6T1, L4T1 and L6T5 were considered stable as they recorded high mean than grand mean (34.13, 32.81, 30.76, 26.00) with regression coefficient (1.12,1.11, 1.04, 0.92) near 'unity' and non–significant (-1.17,-1.22, 0.23,-1.18) deviation from regression. The cross combinations, L1T1 (μ=25.68, b_i=2.06*, S^2di=-1.17), L2T1 (μ=25.97, b_i=1.94, S^2di=-0.06) and L5T1 (μ=27.61, b_i=1.87*, S^2di=-1.21) with high mean, regression coefficient greater than 'unity' and non–significant deviation from regression performed well under better environment. The cross combination L5T5 which exhibited high mean (26.40) with regression

coefficient (-1.55) less than 'unity' and non–significant (0.21) deviation from regression were identified for unfavorable environments. The cross combinations showing unpredictable performance with highly significant deviation from regression were L1T5 (14.68**), L3T2 (46.42**), L3T3 (28.59**), L3T5 (30.24**), L4T5 (30.34**), L6T3 (8.92**) and L6T4 (13.43**).

4.5.1.8 Kernel length

Pooled analysis of variance for this character revealed highly significant differences among genotypes and environments and significant G X E interactions.

The mean value for this trait ranged from 4.55 (L1T3) to 7.02 (L4T1) and expression of the character was good in environment 1 (0.034). The cross combinations, L1T1(μ=6.34, b_i=2.53,S^2di=0.01), L1T5 (μ=6.19, b_i=5.24*, S^2di=-0.01), L2T1 (μ=6.79, b_i=4.27, S^2di=0.00), L2T2 (μ=6.75, b_i=4.26, S^2di=0.00), L3T3 (μ=6.20, b_i=2.09, S^2di=0.01), L5T2 (μ=6.59, b_i=2.08, S^2di=0.00), L5T5 (μ=6.02, b_i=1.58, S^2di=0.00), L6T4 (μ=6.24, b_i=2.02, S^2di=-0.01), L3T1 (μ=6.74, b_i=1.48, S^2di=-0.01) and L6T2 (μ=6.68, b_i=1.41, S^2di=0.00) were suitable for favourable environment because of high mean, regression coefficient greater than 'unity' in addition to non–significant deviation from regression.

With respect to poor environment, the cross combinations, L4T1 (μ=7.02, b_i=-0.64, S2di=-0.01) and L6T5 (μ=6.55, b_i=0.61, S2di=0.02) which recorded high mean with less than 'unity' regression coefficient and non–significant deviation from linearity were considered suitable. Un-predictable nature of variation was observed with the cross combination L4T5 (0.06**). Nayak A.R. (2008) also reported significant deviations in prediction of the performance of certain cross combinations for kernel length as observed in the present investigation.

4.5.1.9 Kernel breadth

The mean values for this trait ranged from 1.73 (L3T3) to 2.71 (L6T1) and environment 2 (0.032) was found to be favourable for this trait. Most of the cross combinations exhibited non-significant S^2d_i values whose performance could be predicted. Among the cross combinations, L1T3 (μ=1.84, b_i=0.79, S^2di=0.00) and L3T3 (μ=1.73, b_i=1.09, S^2di=0.00) were considered as stable because of low (desirable) mean, regression coefficient around 'unity' and non–significant deviation from regression.

Further, the cross combinations, L2T2 (μ=1.93, b_i=1.37, S^2di=0.00), L3T2 (μ=1.99, b_i=1.35, S^2di=0.00), L3T4 (μ=1.96, b_i=1.90, S^2di=0.00), L5T2 (μ=1.98, b_i=1.37, S^2di=0.00), L5T4 (μ=1.81, b_i=1.54, S^2di=0.00) and L6T3 (μ=1.84, b_i=1.39, S^2di=0.00) were observed to be suitable for better environment as they recorded low mean with greater than 'unit' regression and non–significant deviation from linearity.

In poor environment, the cross combinations, L2T5 (μ=1.99, b_i=0.42, S^2di=0.00), L4T2 (μ=1.92, b_i=0.34, S^2di=0.00), L4T4 (μ=1.91, b_i= 0.28, S^2di=0.00), L5T1 (μ=1.83, b_i= -0.68, S^2di=0.00) and L5T5 (μ=1.99, b_i=0.27, S^2di=0.00) were suitable. The cross combinations *viz.,* L1T2 (0.08**), L1T4 (0.02*), L2T3 (0.03**) and L2T4 (0.01*) showed significant deviation from regression.

4.5.1.10 L/B ratio

Higher L/B ratio is most desirable trait in rice from trade and consumers point of view. Kernel with L/B ratio more than 3.0 is considered as slender. Analysis of variance for this character pooled over 3 environments showed highly significant differences among genotypes and environments.

High amount of variability was observed for this character with lowest mean value of 2.22 (L4T3) to highest value of 3.58 (L3T3) and environment 1 (0.070) was found to be most favourable for expression of this trait. The cross combination *viz.,* L1T5 (μ=2.90, b_i=0.94, S^2di=-0.01) which recorded high mean than grand mean, regression coefficient near 'unity' in addition to non–significant deviation from regression was considered as stable for this trait. The cross combinations, L2T2 (μ=3.50, b_i=2.29*, S^2di=-0.01), L3T3 (μ=3.58 b_i=1.60, S^2di=0.00), L3T5 (μ=2.74, b_i=1.90,S^2di=0.00), L4T4 (μ=3.07,b_i=1.85, S^2di=0.01), L5T2 (μ=3.33, b_i=1.72, S^2di=0.00), L5T4 (μ=3.29,b_i=2.27,S^2di=0.01), L6T2 (μ=3.08, b_i=1.52, S^2di=-0.01 and L6T4 (μ=2.92, b_i=1.33, S^2di=-0.01) with high mean and b_i valuemore than 'unity' and non–significant deviation from regression were highly suitable for favorable environment. Whereas, cross combinations *viz.,* L2T5 and L5T5 were identified for poor environment in view of high mean (2.94, 3.02), regression coefficient (0.14, 0.52) less than 'unity' and non–significant S^2di estimate (0.01,-0.01).

Among cross combinations viz., L1T2 (0.32**), L4T2 (0.04*) and L6T3 (0.05**) the performance has been found to be highly unpredictable because of their significant deviation from regression values.

4.5.1.11 Bran oil content

Pooled analysis of variance for this character revealed highly significant differences among genotypes and environments and also the G x E interaction and further partitioning of MSS due to G × E into linear, non-linear revealed predominant role of non-linear component.

Bran oil content ranged from 9.92 (L6T1) to 16.86 (L1T3) in the present study and among the three environments, environment 3 (0.439) was found to be favourable for this trait. Among thirty cross combinations studied, 20 cross combinations showed non-significant deviation from the regression (S^2d_i) values. As the cross combinations were within the range of minimum deviation from regression, there was a scope to predict the variation in their performance.

The cross combination, L5T3 (μ=13.98, b_i=0.90, S^2di=-0.13), has recorded high mean than grand mean, regression coefficient near 'unity' and non–significant deviation from regression, as such, they were considered as stable for this trait. The cross combinations, L1T2 (μ= 16.23, b_i=1.66, S^2di=-0.30), L5T2 (μ= 14.83, bi=2.60, S^2di=0.02) and L6T5 (μ= 12.88, bi=3.49*, S^2di=0.31) were identified for better environment based on stability parameters.

The cross combinations, L1T1, L1T3, L5T4 and L5T5 were suitable for poor environment as they recorded high mean (13.72, 16.86, 14.05, 13.31), with regression coefficient less than 'unity' (-1.65,-2.59,-0.21, -4.09,) and non–significant deviations (0.02, 0.74,-0.31,-0.13) from regression. The cross combinations *viz.,* L1T4 (1.94**), L3T4 (1.28*) and L6T2 (1.44*) with significant deviations from regression exhibited unpredictable performance. Balalic *et al*. (2011) also reported stable hybrids for oil content as results of present study.

4.6 Character Association

Grain yield is a complex character and is dependent on its contributing traits. A study was envisaged on character association, to assess the relationships among bran oil content, yield and its components to have an insight into the causes for higher yield and bran oil in cross combinations. Further, location wise analysis helps understand the

variation in association under different environments and to identify a stable character influencing the yield for further concentration and emphasis in breeding programmes.

Simple correlations were worked out on bran oil content, yield and its contributing characters at Jagitial, Warangal and Hyderabad locations and also finally on pooled data (Table 4.6).

4.6.1 Days to 50 % flowering

This trait showed non-significant positive correlation with grain yield per plant in all the locations while it had significant positive correlation with grain yield per plant, panicle length, number of grains per panicle and L/B ratio over locations. In pooled analysis, this trait exhibited negative significant correlation with plant height, number of productive tillers per plant, 1000 grain weight, kernel length, kernel breadth and bran oil content. At Jagitial and Warangal, this trait had significant positive correlation with the plant height and number of grains per panicle but negative with bran oil content. Negative non-significant association observed for this trait with panicle length, number of productive tillers per panicle, 1000-grain weight, kernel length and kernel breadth whereas positive non-significant correlation with L/B ratio at Jagitial. At Warangal, days to 50% flowering was positively and non-significantly correlated with number of productive tillers per plant and kernel breadth but it showed negative non-significant association with panicle length, 1000 grain weight, kernel length and L/B ratio. Whereas at Hyderabad, this trait had a positive significant correlation with plant height and number of grains per panicle and non-significant with plant height, panicle length, kernel breadth and negative non-significant with number of productive tillers per plant, 1000- grain weight, kernel length, L/B ratio and bran oil content. Similar type of associations was reported by Krishna *et al.* (2008) and Abdul Fiyyaz *et al*. (2011) for grain yield per plant and Ravindra Babu *et al*. (2012) for panicle length.

4.6.2 Plant height (cm)

It associated positively with grain yield per plant, 1000–seed weight, kernel length and kernel breadth but negatively with bran oil content in all the locations and over locations. The pooled analysis indicated a negative significant association with panicle length, L/B ratio and a positive significant relation with number of productive tillers per plant but negative non-significant with number of grains per panicle. At Jagitial, this trait showed positive significant association with panicle length and non-significant

with number of grains per panicle while negatively correlated with number of productive tillers per plant. Plant height (Warangal location) exhibited significant positive association with panicle length, number of grains per panicle and non-significant with number of productive tillers per plant. At Hyderabad, this trait had positive non-significant association with panicle length and number of grains per panicle while negative with productive tillers per plant. In all the locations this trait showed negative non-significant association with L/B ratio.

The similar association with Krishna *et al.* (2008) for 1000 grain weight, kernel length and kernel breadth Sebesan *et al.* (2009) and Abdul Fiyyaz *et al.* (2011) for grain yield per plant.

4.6.3 Panicle length (cm)

Panicle length had positive and significant association with 1000–grain weight, kernel length, kernel breadth and grain yield per plant whereas negative significant association with bran oil content in all locations and in pooled analysis. In addition to this, at Jagitial, panicle length had positive significant correlation with number of grains per panicle while negative significant association with L/B ratio. At Hyderabad, this trait showed positive significant correlation with number of grains per panicle. In pooled analysis, negative significant association was observed with productive tillers per plant but non-significant with L/B ratio. Similar results were reported by Rajamadhan *et al.* (2011), Bhadru *et al.* (2012) and Ravindra Babu *et al.* (2012) for grain yield per plant and Krishna *et al.* (2008) for kernel length and 1000 grain weight.

4.6.4 Number of productive tillers per plant

This trait exhibited positive and significant association with grain yield per plant in Jagitial and pooled analysis. At Jagitial, this trait also showed positive significant correlation with number of grains per panicle, 1000-grain weight, kernel length, kernel breadth but negative association with bran oil content. In pooled analysis, number of productive tillers per plant had significant positive correlation with kernel length and kernel breadth while negative with L/B ratio.

Rajamadhan *et al.* (2011), Bhadru *et al.* (2012) and Ravindra Babu *et al.* (2012) also reported a strong association between productive tillers and grain yield per plant and Sakthivel (2001) for 1000 grain weight.

4.6.5 Number of grains per panicle

Number of grains per panicle had significant positive association with grain yield per plant and kernel breadth in all locations and pooled analysis. This trait showed positive significant correlation with kernel length in Warangal, Hyderabad and pooled analysis whereas significant negative association with bran oil content in Jagitial, Hyderabad and pooled analysis. In addition to this, this trait also exhibited significant positive association with 1000-grain weight, L/B ratio at Hyderabad and Warangal respectively.

Padmaja *et al*. (2011) and Zulqarnain *et al*. (2012) reported positive significant correlation with grain yield per plant as observed in the present study.

4.6.6 1000–grain weight (g)

It associated positively and significantly with kernel length, kernel breadth and grain yield in all locations and pooled analysis. Long bold grains have more length and breadth with increased 1000 seed weight, which results in higher yields. This trait showed negative significant association with L/B ratio (in Jagitial) and bran oil content (in all locations).

Krishna *et al.* (2008) also observed a positive correlation for 1000 grain weight among kernel length and kernel breadth and Yadav *et al.* (2011) and Zulqarnain *et al*. (2012) for grain yield per plant.

4.6.7 Kernel length (mm)

Kernel length had significant positive association with kernel breadth, L/B ratio and grain yield per plant while negative significant association with bran oil content in all locations and pooled analysis except Warangal. Krishna *et al.* (2008) reported a positive association between kernel length and kernel breadth and Mareker and Siddiqui (1996) for grain yield per plant.

4.6.8 Kernel breadth (mm)

This trait had a negative significant association with L/B ratio, bran oil content and positive significant association with grain yield per plant in all locations and pooled analysis. Kernel breadth and L/B ratio were negatively correlated as observed by Pankaj Garge *et al.* (2010) and Rajeswari *et al.* (2010).

4.6.9 L/B ratio

Higher L/B ratio is desirable, as grains with high L/B ratio will be classified as fine and fetch higher premium in the market. This trait exhibited negative correlation with bran oil in Jagitial and pooled analysis. In the present investigation positive and negative significant correlation was observed with grain yield at Jagitial and in pooled analysis respectively. L/B ratio had no significance with grain yield in Warangal and Hyderabad. Tara Satyavathi *et al.* (2001) and Pankaj Garge *et al.* (2010) were also reported that L/B ratio positively correlated with grain yield per plant.

4.6.10 Bran oil content (%)

This trait exhibited a negative significant association with grain yield per plant in all locations and over locations. The results were in agreement in with the findings of Ravindra Babu (2002), Satyanarayana *et al.* (2003) and Mijice *et al.* (2009).

4.6.11 Grain yield per plant (g)

The grain yield per plant had a significant positive association with days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000- grain weight, kernel length, kernel breadth whereas negative significant association with L/B ratio and bran oil content on overall basis. Variation was observed in the association between bran oil, grain yield and other components over different environments.

At Jagtial this trait had significant positive association with the plant height, panicle length, productive tillers per plant, number of grains per panicle, 1000 grain weight, kernel length, kernel breadth and length/breadth ratio and negatively correlated with bran oil content. At Warangal, it was positively associated with plant height, panicle length, number of grains per plant, 1000-grain weight, kernel length and kernel breadth but negatively with bran oil content. At Hyderabad, this trait had significant positive association with the plant height, panicle length, number of grains per panicle, 1000 grain weight, kernel length, kernel breadth and negatively correlated with bran oil content.

Similar kind of association with this trait was observed in finding of Krishna *et al.* (2008) and Abdul Fiyyaz *et al.*(2011) for plant height, Rajamadhan *et al.*(2011), Bhadru*et al.* (2012) and Ravindra Babu *et al.*(2012) for number of productive tillers per plant, Pankaj Garge *et al.*(2010), Padmaja *et al.*(2011), Zulqarnain *et al.*(2012) for

number of grains per panicle, Yadav *et al.* (2010), Zulqarnain *et al*. (2012) for 1000 seed weight and Ravindra Babu (2002), Satyanarayana *et al*. (2003) and Mijice *et al.* (2009) for oil content**.**

4.7 Path Coefficient Analysis

Correlation gives only the relation between two variables whereas, path coefficient analysis helps us to know the direct and indirect effect through other components by partitioning the correlations on grain yield. Hence, the path coefficient analysis was done to know the direct and indirect effects of different yield components and bran oil content on yield for 3 locations separately and in pooled analysis. This type of location wise and pooled analysis helps us to know the stable associations among the traits for use in future selections by plant breeders (Table 4.7.).

4.7.1 Days to 50 % flowering

Days to 50 percent flowering showed a positive direct effects on grain yield per plant at Hyderabad and in pooled analysis while negative direct effect at Jagitial and Warangal. It had indirect positive effects on yield through panicle length, 1000-grain weight, kernel length and bran oil content at Jagitial and Warangal. In pooled analysis, it had high positive indirect effect on grain yield through panicle length and number of grains per panicle whereas it expressed negative indirect effects mainly through plant height, number of productive tillers per plant and kernel breadth.

The direct negative effect of days to 50 per cent flowering on grain yield per plant was reported by Pankaj *et al*. (2010), Yadav *et al.* (2010), Rajamadhan *et al*. (2011), Panday (2012) and Ravindra Babu *et al*. (2012).

4.7.2 Plant height (cm)

Plant height had positive direct effect on grain yield per plant at all locations and over locations. It showed positive low indirect effects *via* days to 50% flowering, panicle length, number of grains per panicle, 1000-grain weight, kernel length and kernel breadth at Jagitial and Warangal. This trait recorded low positive indirect effects on grain yield through number of productive tillers per plant, 1000-grain weight, kernel length and kernel breadth in pooled analysis.

Similar results were reported by Mulugeta *et al.* (2012), Pandey *et al*. (2012) and Ravindrababu *et al*. (2012).

4.7.3 Panicle length (cm)

Panicle length had direct positive effect on grain yield per plant in all locations and over locations. In pooled analysis, this trait showed positive indirect effect on grain yield mainly through number of grains per panicle, 1000-grain weight, kernel length and kernel breadth and it had negative indirect effects through days to 50% flowering, plant height, productive tillers per plant and bran oil content. Results reported by Kole and Hasib (2008), Sathish Chandra *et al.*(2009) and Pankaj *et al*. (2010) were in agreement with the results obtained in the present investigation.

4.7.4 Number of productive tillers per plant

The direct contribution of this character to grain yield was positive and high at Jagitial and Warangal whereas negative low direct effect on grain yield was observed at Hyderabad and in pooled analysis. The indirect effects through other characters were found to be very low.The indirect effect *via* bran oil content was negative, not at higher magnitudes. Basavaraja *et al.* (2011), Padmaja *et al.* (2011), Bhadru *et al.*(2012), Pandey *et al*.(2012) and Ravindra Babu *et al.*(2012) reported a high positive direct effect of number of productive tillers per plant on grain yield per plant as was observed in the present investigation.

4.7.5 Number of grains per panicle

This trait had positive direct effect on grain yield per plant at Jagitial, Warangal and over locations but at Hyderabad negative effects were observed.

It had high indirect positive contribution mainly through plant height, kernel length and kernel breadth at Warangal while through bran oil content at Hyderabad and in pooled analysis. This trait also showed negative indirect effect on yield through kernel length and kernel breadth at Hyderabad location. Its contribution to yield was attributed to indirect effect through plant height as was reported by Rajamadhan *et al*. (2011) and Bhadru *et al.* (2012).

4.7.6 1000–grain weight (g)

The yield component, 1000-grain weight exhibited the direct positive effect on grain yield per plant at all the locations and also in pooled analysis. However, it revealed high indirect positive influence through plant height, panicle length, kernel length and kernel breadth in all locations.

It also had indirect negative influence on grain yield per plant through days to 50%flowering, L/B ratio and bran oil content in all locations while through plant height, panicle length, number of productive tillers per plant, kernel length and kernel breadth over locations. The results reported by Sathish Chandra *et al.* (2009), Padmaja *et al.* (2011), Bhadru *et al.*(2012) and Yadav *et al.*(2012) also indicated that 1000 -grain weight plays greater role for higher grain yield per plant. This component had very high impact on grain yield per plant, which is evident from highly significant correlation coefficients followed by direct effects at all the locations.

4.7.7 Kernel length (mm)

Kernel length had direct positive influence on grain yield at all the locations and over locations. The similar results were reported by Pankaj Garge *et al.* (2010) and Rajamadhan *et al.* (2011).

While it had indirect positive influence through panicle length, number of productive tillers per plant, number of grains per panicle, 1000-grain weight, kernel breadth and L/B ratio at Jagitial location , days to 50 per cent flowering, productive tillers per plant, kernel breadth and bran oil content at Warangal location, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000-grain weight, kernel breadth and L/B ratio at Hyderabad and over locations. This character appeared to play an important role in yield contribution directly.

4.7.8 Kernel breadth (mm)

Kernel breadth had direct positive influence on grain yield at all the locations and over locations. While it had high indirect positive influence mainly through panicle length, 1000-grain weight and kernel length at Warangal and *via* 1000-grain weight and kernel length at Hyderabad.

This trait also had some indirect negative contribution mainly through 1000- grain weight and kernel length at Jagitial location. However, it also had indirect negative effect through days to 50% flowering, kernel length, L/B ratio and bran oil content on over all basis. These results are in conformity with the finding of Krishna *et al.* (2008) and Yadav *et al.* (2012).

4.7.9 L/B ratio

L/B ratio had direct positive influence on grain yield at all the locations except over locations. While it had indirect positive influence through days to 50 % flowering,

number of productive tillers per plant and kernel length at Jagitial, number of grains per panicle, kernel length and bran oil content at Warangal location, kernel length and bran oil content at Hyderabad and plant height, panicle length, productive tillers per plant, number of grains per panicle, 1000-grain weight, kernel breadth and bran oil content over the locations.

It also had indirect negative contribution through plant height, panicle length, 1000- grain weight and kernel breadth in all the location while through days to 50% flowering and kernel length over locations. The similar results were reported by Krishna *et al.* (2008) and Nandeshwar *et al.* (2010).

4.7.10 Bran oil content (%)

This trait expressed negative direct effect on grain yield in all the locations as well as in pooled analysis. The results are in agreement with the findings of Siddiquey, M. N. H *et al*. (2006).

Its indirect effect through days to 50% flowering and panicle length was positive in all locations. Contrastingly, indirect effect of bran oil content was negative through productive tillers per plant, number of grains per panicle, kernel length, kernel breadth and L/B ratio at Hyderabad and through plant height, 1000-grain weight and L/B ratio at Warangal. In pooled analysis, it expressed negative indirect effects through all the characters except number of productive tillers per plant.

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

Path coefficient analysis revealed that kernel breadth exerted highest positive

direct effect on grain yield followed by panicle length, 1000-grain weight, number of grains per panicle, days to 50 % flowering, plant height and kernel length in over all locations. The negative direct effect was noticed on grain yield by number of productive tillers per plant, L/B ratio and bran oil content. The results were in conformity Bhadru *et al.*(2012), Pandey *et al.* (2012) and Ravindra Babu *et al.* (2012) for plant height, Rajamadhan *et al.* (2011) for kernel length, Krishna *et al.* (2008), Yadav *et al.* (2012) for kernel breadth, Siddiquey M. N. H *et al*. (2006) for oil content, Basavaraja *et al*. (2011), Ravindra Babu *et al*. (2012) for 1000 grain weight, Mulugeta seyoum *et al*. (2012) for number of productive tillers per plant and Rajamadhan *et al*. (2011), Ravindra Babu *et al*. (2012) for number of grains per panicle.

4.8.Estimation of Genetic Parameters in F2 Generation for Bran Oil Content

In F_2 generation of the cross combination Keshari×Swarna, the estimated value of PCV (28.03) is higher than GCV (20.50), it means that the apparent variation is not only due to genotypes but also due to the influence of environment. Selection for this trait sometimes may be misleading (Phundan Singh and Narayanan, 2000). Medium heritability (53.48) coupled with high genetic advance as per cent of mean (41.39) was observed for this trait indicating the presence of additive gene action. Hence this trait can be improved through simple selection procedures (Table 4.8.1 and 4.8.2).

4.9 Mapping of Gene(s) for Bran Oil Content in Rice using SSR Markers

Rice bran is considered as a waste that is normally discarded during rice processing. It is well known that it is a nature source of vitamins, minerals and anti-oxidants. Besides, it contains 18-23% of oil which contains significant amounts of essential fatty acids, and linoleic acid that are necessary in order to maintain full health as well as a broad range of nutraccutial compounds that have been demonstrated to have remarkable therapeutic properties. It is a popular as cookinig oil in several Asian countries including Japan, China, and India. Oil content vis-a-vis seed yield per unit area remains the most important breeding objective in this crop. The oil content is known to be quantitatively inherited and therefore, only limited success has been achieved in the improvement of the trait through conventional breeding in other oil seed

crops also. Genetic markers have allowed researchers to systematically map and characterize the loci affecting quantitative traits.

Recent developments in quantitative genetics making use of molecular markers allow the determination of the map positions and the relative contribution of the different loci to observed trait variation. An important application of this knowledge is *via* Marker Assisted Selection (MAS), where molecular markers linked to the loci determining variation for the trait can be used to select the most favourable genotype without a need of determining oil content by relatively complex and expensive assays in the breeding generations. For MAS, ultimately the genes underlying the variation of the trait are the best suited markers.

Till now there are no reports about the markers related to bran oil , but an attempt has been made to find out the bran oil related markers, For this study 30 SSR markers covering the twelve chromosomes in Rice was taken . The present investigation mapping of gene(s)for bran oil content is a step forward for identification of markers, and that can be used in marker assisted breeding for development of new cultivars with high bran oil.

4.9.1 Selection of Parents

Based on the phenotypic data of bran oil content, Keshari (High bran oil content) and Swarna (High yielding but low bran oil content) were used as parents for the development of mapping population.

4.9.2 Development of Mapping Population

Crosses were affected between the chosen Keshari and Swarna parents and F_1s was developed. The F_1 of the cross was selfed to generate F_2 and F_2 generation was further sown to carry out the genotyping.

4.9.3 Parental polymorphism studies:

Parental polymorphism survey between Keshari and Swarna was studied using 30 markers. Among, Keshari and Swarna 2 (6.6%) were polymorphic, 22 markers were monomorphic and 6 were not amplified.(Table 4.9.1).

Table.4.9.1. Parental polymorphism survey between Keshari and Swarna

Polymorphism	No. of markers	Markers
Polymorphic	2	RM1, RM5140
Monomorphic	22	RM5, RM154, RM630, RM3763, RM15337, RM15580, RM16343, RM16757, RM18857, RM20672, RM283, RM11, RM455, RM118, RM125, RM447, RM22622, RM2252, RM6543, RM560, RM144, RM852, RM19
Not amplified	6	RM16343, RM18888, RM20096, RM271, RM484, RM277

4.9.4 Screening of F_2 population with SSR markers

The two polymorphic markers identified in parental polymorphism . i.e RM1 present on the chromosome 1 and RM5140 on the chromosome 5 were used to screen the 132 F_2 plants derived from Keshari ×Swarna, to identify the bran oil associated regions in the chromosomes. The genotypic and phenotypic data was analyzed using Single Marker Analysis and R2 values values for this trait were presented in the Table 4.9.2.

Table: 4.9.2. R2 values for RM1 and RM5140 Markers

Trait	Marker	R_2 %	Probability
High Bran oil Content	RM1	0.59	0.72
	RM5140	14.40	0.006
Low Bran oil Content	RM1	0.11	0.84
	RM5140	3.00	0.001

RM1 (Chromosome-1) with high bran oil content (**R_2 %**= 0.59) and low bran oil content (**R_2%**=0.11), RM5140 (Chromosome-5) with high bran oil content (**R_2 %**=14.40) and low bran oil content (**R_2 %**=3.00). Two markers, RM1 and RM5140 showed association but RM5140 shows the highest F value (Probability less than 0.005) and therefore most likely linked to the bran oil content. These results were in conformity with Lang *et al.* (2013)

CHAPTER VI

SUMMARY AND CONCLUSIONS

The research work entitled “Genetic characterization and molecular studies for bran oil using SSR markers in rice (*Oryza sativa* L.)” was carried out at the Directorate of Rice Research, Rajendranagar, Hyderabad with an aim to develop more heterotic hybrids of wider compatibility .The main objectives of the investigation were to screen the available germplasm for selection of parents with high bran oil content, study the combining ability of parents and crosses, estimate the magnitude of heterosis, assess the stability of experimental hybrids for the traits under study and to know the character association among yield, yield components along with bran oil content.

During Rabi, 2011 fifty genotypes were screened for bran oil content at the Research Farm, Directorate of Rice Research, Rajendranagar, Hyderabad out of which six genotypes which performed better (with high and medium oil content) were selected and crosses were made with 5 testers in Line × tester design during *kharif*, 2012. The resultant 30 cross combinations along with the parents were evaluated for combining ability, heterosis and stability (Eberhart and Russel, 1966) at three locations *viz.*, Jagtial, Warangal and Hyderabad of Telangana state during Rabi, 2012-13.

The pooled analysis of variance for combining ability revealed significant differences due to environments, parents, hybrids and various interactions indicating the existence of wider variability in the material under study. The ratios of GCA / SCA variances revealed that non-additive gene action was predominant in the inheritance of days to 50% flowering, panicle length, productive tillers, number of grains per panicle, 1000 grain weight, grain yield per plant, kernel length, kernel breadth, L/B ratio, bran oil content, milling recovery, head rice recovery, alkali spreading value, water uptake, amylose content whereas plant height and gel consistency showed additive gene action. For improvement of these characters except plant height and gel consistency heterosis breeding can be used while for remaining traits simple selection procedures could be followed.

The *gca* effects of the parents in pooled analysis revealed that Keshari (L1) and MTU1010 (L5) among lines and IR64 (T2) and Swarna (T3) among testers were good general combiners for bran oil content whereas lines Mandhya Vijaya (L3) and Phalguna

(L6) and testers NDR359 (T1) and MTU1010 (T5) were found to be promising general combiners for grain yield per plant and other traits.

Based on significant *sca* effects in pooled analysis, for bran oil content eight crosses recorded significant positive *sca* effects. The top performing three specific crosses among them were Keshari × Swarna (L1T3), Phalguna × MTU1010 (L6T5) and Mandhya Vijaya × RPBio226 (L3T4) while for grain yield ten hybrids showed significant *sca* effects in positive direction. Based on *sca* effects the cross combinations Keshari × MTU1010 (L1T5), Mandhya Vijaya × Swarna (L3T3), Ishwarya × Swarna (L2T3), Mandhya Vijaya × NDR359 (L3T1) and Kandhagiri × RPBio226 (L5T4) were identified as promising for grain yield per plant.

On the whole, six cross combinations *viz.,* Mandhya Vijaya × NDR359 (L3T1) , Keshari × MTU1010 (L1T5), Phalguna × NDR359 (L6T1), Mandhya Vijaya × Swarna (L3T3), Kandhagiri × RP Bio226 (L5T4) and Phalguna × Swarna (L6T3) have been identified as promising based on *per se* performance, *sca* effects and heterosis for yield and its attributes in pooled analysis. Besides yield these cross combinations also possessed desirable quality characters like milling per cent, head rice recovery per cent, kernel length, kernel breadth, L/B ratio, gel consistency and amylose content. But in case of bran oil content, none of the cross combination showed significant heterosis in desirable direction though Keshari × IR64 (L1T2), Kandhagiri × RPBIO226 (L5T4), Keshari × NDR359 (L1T1), Phalguna × MTU1010 (L6T5) and Kandhagiri × MTU1010 (L5T5), had high bran oil content among all cross combinations with optimum yield.

Pooled analysis of variance for stability revealed that genotypes showed significant differences for all the characters. Environments showed highly significant differences for xall the character under study except 1000-grain weight and kernel length whereas, genotype × environment interaction components showed significant differences for all the characters when tested against pooled error, indicating wide differential behavior of genotypes in changing environments. Significance of environment (linear) component for all the characters except test weight and kernel length indicated that the genotypes responded linearly for most of the characters under study.

The Genotype × Environment (linear) interaction was significant for number of productive tillers per plant, number of grains per panicle, kernel length and bran oil content which suggested that the performance of genotypes across the environments could be

predicted for these traits with great precision. Significance of pooled deviations for all the characters indicated that the performance of genotypes is entirely unpredictable in nature as such, importance of non–linear component in determining interaction of genotypes with environments has to be considered.

Environmental indices revealed that Warangal was found to be the most favourable location for panicle length, number of productive tillers per plant, number of grains per panicle, 1000 grain weight, grain yield per plant and kernel breadth while Hyderabad was the most favourable for days to 50% flowering and bran oil content and Jagitial location was the most favourable for plant height, kernel length and L/B ratio.

From the present studies on stability, four hybrids *viz* Mandhya Vijaya × NDR359 (L3T1), Phalguna × NDR359 (L6T1), PR116 × NDR359 (L4T1) and Phalguna × MTU1010 (L6T5) were identified as stable hybrids for grain yield per plant. Three hybrids, Keshari × NDR359 (L1T1), Ishwarya × NDR359 (L2T1) and Kandhagiri × NDR359 (L5T1) were identified as suitable for favourable environments and one hybrid, Kandhagiri × MTU1010 (L5T5) for unfavourable environments. In case of bran oil content the hybrid, Kandhagiri × Swarna (L5T3) was considered as stable cross combination whereas Keshari × IR64 (L1T2), Kandhagiri × IR64 (L5T2) and Phalguna × MTU1010 (L6T5) for better and Keshari × NDR359 (L1T1), Keshari × Swarna (L1T3), Kandhagiri × RPBio226 (L5T4) and Kandhagiri × MTU1010 (L5T5) were suitable for poor environment.

Correlation studies revealed that grain yield per plant had a negative significant association with bran oil content and significant positive association was observed with days to 50% flowering, plant height, panicle length, number of productive tillers per plant, number of grains per panicle, 1000- grain weight, kernel length, kernel breadth on overall basis whereas the study on path coefficient analysis revealed that kernel breadth per plant exerted highest positive direct effect on grain yield followed by panicle length, 1000-grain weight, number of grains per panicle, days to 50 % flowering, plant height and kernel length in over all locations..

Based on above character association studies, the attributes *viz.* kernel breadth, panicle length, 1000-grain weight, number of grains per panicle, days to 50 % flowering, plant height and kernel length showed a significant positive association along with direct effect on grain yield per plant suggesting selection of these traits will be useful for the improvement of grain yield.

During *Kharif, 2013,* F_2 generation of Keshari × Swarna was grown at DRR Farm, Directorate of Rice Research, Hyderabad, for the estimation of genetic parameters. The estimated value of PCV is higher than GCV, it means that the apparent variation is not only due to genotypes but also due to the influence of environment. Selection for this trait sometimes may be misleading. Medium heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the presence of additive gene action. Hence this trait can be improved through simple selection procedures.

Conclusion and future strategy:

Based on the present study, it can be emphasized that L3T1 (Mandhya Vijaya × NDR359) and L6T1 (Phalguna × NDR359) are stable with the desirable *sca* effects, heterosis and *per se* performance for grain yield and other important attributes. In case of bran oil content, none of the cross combination showed significant heterosis in desirable direction though Keshari × IR64 (L1T2) and Kandhagiri × RPBio226 (L5T4) had high bran oil content among all cross combinations with optimum yield. This is a preliminary study to know the genetics of bran oil content in rice. Hence, further study has to be made under this new concept to know the genetics and heterosis for bran oil content .These hybrids may be further tested over locations, seasons and years and recommended for commercial release.

Till now there are no reports about the markers related to bran oil. Attempt has been made with 30 SSR markers representing 12 chromosomes in cross Keshari × Swarna to find out the bran oil related markers and concluded that concluded that RM5140 marker –can be used as bran oil related marker in future studies as it showed the highest F value (Probability less than 0.005). The markers and the population size used in the present study was low in number. By increasing the number of markers covering the all chromosomes and population size we can go for further studies to give a linkage map. The knowledge and material generated in the investigation could be utilized in future hybrid rice breeding programmes.

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APPENDIX I

LIST OF CHEMICALS

1. Agarose (sigma)
2. Bromophenol blue (sigma)
3. Chloroform (Qualigens)
4. Cetyl Trymethyl Ammonium bromide (CTAB)
5. dNTP's (Deoxy NucleosideTriphosphate)
6. Ethylene Diamine Tetra Acetic Acid (EDTA)
7. Ethidium bromide (10 mg / ml)
8. Icecold isopropanol
9. Isoamyl alcohol
10. Liquid Nitrogen
11. 2- Mercaptoethanol GR
12. NaOH pellets
13. NaCl
14. Nitric Acid (HNO_3 65%)
15. Phenol
16. Poly vinyl pyrrolidone
17. Proteinase K
18. RNase H
19. Taq polymerase
20. Sodium acetate
21. Sodium chloride
22. Tris base
23. 100 bp ladder
24. 70 %Ethanol

APPENDIX II

BUFFERS AND STOCK SOLUTIONS

1. CTAB buffer 100ml

2.0 g CTAB (Hexadecetyl trimethyl- ammonium bromide)

10.0 ml M Tris pH 8.0

4.0 ml 0.5 M EDTA pH 8.0 (Ethylenediamine tetraacetic acid Di-sodium salt)

28.0 ml 5 M NaCl

40.0 ml H_20

1g PVP 40 (Polyvinyl pyrrolidone- vinyl pyrrolidine homopolymer,MW 40,000)

Adjust all to pH 8.0 with HCl and make up to 100 ml with H_2O

2. Ethidium Bromide

Stock 20mg / ml can be prepared by dissolving 1gm of ethidium bromide in 50 ml of water.

3. Chloroform: Isoamyl alcohol (24:1)

Chloroform: isoamyl alcohol (24:1) were mixed and stored at room temperature.

4. Phenol: Chloroform: Isoamyl alcohol (25:24:1)

Phenol: Chloroform: isoamyl alcohol (25:24:1) were mixed and stored at room temperature.

5. TAE buffer (Tris / acetate / EDTA) 50X stock solution

242 g Tris base

57.1 ml Glacial acetic acid

100 ml 0.5 M EDTA (pH 8.0)

Adjusted the pH to 8.3 with acetic acid and make up to the volume to 1 lit with distilled water. Sterilization is done by autoclaving.

6. TE buffer (pH 8.0)

10 mM Tris HCl

1 mM EDTA.

2 ml of 0.5 M Tris-Cl pH 8.0 was mixed with 0.2 ml of 0.5 EDTA, make up to the vol to 100 ml with sterile distilled water.

7. 6X Gel loading buffer

0.25% (W/V) Bromo phenol blue

40% (W/V) sucrose in water

Dissolved 0.25g of Bromo phenol blue was mixed with 40g of sucrose, make up the vol to 100ml with distilled water.

8. RNase preparation

RNase buffer

A.1M Tris (pH 7.5)

B. 5M NaCl

Take 0.5ml of 1M Tris (final concentration 10mM) and 75 µl of 5M NaCl (final concentration 15mM) and make up the volume to 50 ml. Weighed 25 mg of ribonuclease H into a tube and add RNase buffer to a final volume of 5 ml (so final concentration 5mg / ml). Kept the tube in a boiling water bath for 10 min, cool and made aliquots of 1 ml in 1.5 ml Eppendorf tubes and stored at -20^0C.

APPENDIX III

EQUIPMENTS USED

- Agarose gel electrophoresis system (CBS Scientific, USA)
- Autoclave
- Cuvettes
- Electronic balance
- Eppendorf tubes
- Freezer of -20^0 and -80^0C
- Gel Documentation System (Geneflash; SYNGENE, U.K)
- Glass hooks
- DNA Thermal Cycler (Eppendorf, Germany)
- Ice maker(Sanyo)
- Incubator(Sanyo)
- Incubator shaker 37^0C
- Microwave oven
- Microcentrifuge
- Microcentrifuge tubes
- Micropipettes
- Pasture pipettes
- pH meter
- Power supply unit
- UV-absorption spectrophotometer (Beckman DU 650 model)
- UV- transilluminator
- Vaccum centrifuge
- Vortex mixer
- Water bath