

**STUDY OF HETEROSIS AND COMBINING ABILITY
IN CMS BASED RICE (*Oryza sativa* L.) HYBRIDS**

M. Sc. (Ag.) Thesis

by

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BREEDING
COLLEGE OF AGRICULTURE
INDIRA GANDHI KRISHI VISHWAVIDYALAYA
RAIPUR (Chhattisgarh)**

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**STUDY OF HETEROSIS AND COMBINING ABILITY
IN CMS BASED RICE (*Oryza sativa* L.) HYBRIDS**

Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.)

by

Divya Sahu

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FOR THE DEGREE OF**

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in

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CERTIFICATE – I

This is to certify that the thesis entitled “**Study of heterosis and combining ability analysis in CMS based rice (*Oryza sativa* L.) hybrids**” submitted in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture** of the Indira Gandhi Krishi vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Divya Sahu** under our guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instructions.

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


Chairman

Date: 19/7/19

THESIS APPROVED BY THE STUDENT’S ADVISORY COMMITTEE


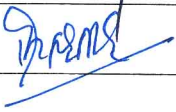

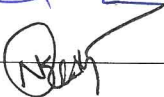
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CERTIFICATE – II

This is to certify that the thesis entitled “**Study of heterosis and combining ability analysis in CMS based rice (*Oryza sativa* L.) hybrids**” submitted by **Divya Sahu** to Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) in partial fulfillment of the requirements for the degree of **Master of Science in Agriculture** in the Department of **Genetics and Plant Breeding** has been approved by the external examiner and Student’s Advisory Committee after oral examination.

Date: 06/08/19


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Dated:


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TABLE OF CONTENTS

Chapters	Title	Page
	ACKNOWLEDGEMENT	v
	TABLE OF CONTENTS	vi
	LIST OF TABLES	viii
	LIST OF FIGURES	ix
	LIST OF NOTATIONS	x
	LIST OF ABBREVIATIONS	xi
	ABSTRACT	xiii
I	INTRODUCTION	1
II	REVIEW OF LITERATURE	6
	2.1 Combining ability	
	2.1.1 The general combining ability and specific combining ability	6
	2.1.2 Gene Action	10
	2.2 Quality parameters	14
	2.3 Heterosis	17
	2.4 Identification of maintainers and restorers	20
	2.5 Genetic purity of hybrids	23
III	MATERIALS AND METHODS	28
	3.1 Site of experiment	28
	3.2 Geography	28
	3.3 Climate and weather	28
	3.4 Experimental material	29
	3.5 Methods	29
	3.6 Biometrical analysis	38
	3.7 Combining ability analysis	39
	3.8 Heterosis	41
	3.9 Identification of maintainers and restorers	42
	3.10 Molecular studies	43
IV	RESULTS AND DISCUSSION	50
	4.1 Mean performance of genotypes	50
	4.2 Analysis of variance for R.B.D.	62
	4.3 Combining ability	63
	4.3.1 Analysis of variance for line \times tester	63
	4.3.2 Combining ability analysis for GCA and SCA effects	64
	4.4 Heterosis	87
	4.5 Identification of maintainers and restorers	119
	4.6 Genetic purity testing at molecular level	124

V	SUMMARY AND CONCLUSIONS	128
	SUGGESTIONS FOR FUTURE WORK	135
	REFERENCES	136
	APPENDICES	155
	RESUME	162

LIST OF TABLES

Table	Title	Page
3.1	Details of parents used in the study	31
3.2	The criteria for classifying the parental lines	43
4.1	Mean performance of parents for different characters	53
4.2	Mean performance of hybrids for different characters	57
4.3	Amylose percent with genotypes	61
4.4	Classification of genotypes on the basis of ASV and GT	62
4.5	Analysis of variance for RBD	66
4.6	Analysis of variance for line \times tester	67
4.7	General combining ability effects	72
4.8	Specific combining ability Effects	75
4.9	Mid parent Heterosis, Heterobeltiosis and Standard Heterosis for different characters	89
4.10	List of identified Maintainers and Restorers	122
4.11	Frequency of Maintainers and Restorers	122
5.1	Promising hybrids based on Mean performance, Heterosis and Combining Ability for Grain Yield per plant	131
5.2	HRR for the hybrids who gave best performance for grain yield per plant according to Mean Performance, Heterosis and Combining Ability	132
5.3	Promising hybrids based on Mean Performance, Heterosis and Combing Ability for HRR	133

LIST OF FIGURES

Figure	Title	Page
3.1	Graph showing weekly meteorological information during crop growth period of rice	30
3.2	Crossing Procedure	33
3.3	Test Cross Nursery	33
3.4	Different classes of pollen fertility	43
4.1	Frequency of Restorers and Maintainers	123
4.2	SSR marker RM 495 showing parental polymorphism between A and R lines	126
4.3	SSR marker RM 1 showing parental polymorphism between A and R lines	126

LIST OF NOTATIONS/ SYMBOLS

Notations	Description
%	Per cent
⁰ C	Degree Celsius
Cm	Centimeter
df	Degree of freedom
<i>et al.</i>	And co-worker/ and others
Fig.	Figure
g	Gram
h ²	Heritability
ha	Hectare
<i>i.e.</i>	That is
Kg	Kilogram
m ²	Square meter
mm	Millimetre
qt	Quintal
<i>viz.,</i>	Namely
/	Per
<	Lesser than
>	More than

LIST OF ABBREVIATIONS

Abbreviations	Descriptions
ANOVA	Analysis of Variance
ASV	Alkali spreading value
MP	Mid Parent
BP	Better parent
CD	Critical Difference
CK	Checks
CMS	Cytoplasmic male sterile
E	Environment
Fig.	Figure
HRR	Head Rice Recovery
GCA	General combining ability
GT	Gelatinization Temperature
L×T	Line × Tester
M	Maintainer
No.	Number
P	Parent
PM	Partial Maintainer
PR	Partial Restorer
R	Restorer
RBD	Randomized Complete Block Design
SCA	Specific combining ability
TGMS	Temperature sensitive genetic male sterility
WA	Wild Abortive
SSR	Simple Sequence Repeat

THESIS ABSTRACT

-
- a) Title of the thesis : Study of heterosis and combining ability in CMS based rice (*Oryza sativa* L.) hybrids
- b) Full name of the student : Divya Sahu
- c) Major subject : Genetics and Plant Breeding
- d) Name and address of the major advisor : Dr. S.S. Rao
Dean, IGKV, Raipur
- e) Degree to be awarded : M. Sc. (Agriculture, Genetics and Plant Breeding)


Signature of major advisor

Date 19/07/19


Signature of the student


Signature of head of the department

ABSTRACT

The experiment titled “Study of heterosis and combining ability in CMS based rice (*Oryza sativa* L.) hybrids” was supervised during *kharif* 2018 at “Research cum instructional Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.)” to evaluate GCA and SCA of parents and hybrids respectively, to evaluate the degree of heterosis, in three CMS lines, to find out the maintainers and restorers and to identify the true hybrids at molecular level, based on genetic diversity of the parents.

The materials used for experiment involved three CMS lines means female lines *i.e.*, IR58025A, IR79156A and IR68888A and ten testers *viz.*, Ganga Chur, Luchai, Pihu purple, Bathras, Pepri Luchai, Khura Bal, Sarojani, Kera Khadi, Luchai Red and Lajni Super-1 and their thirty F₁s were raised up in randomized complete

block design (RCBD) with three replications. And the obtained data was put into LxT analysis.

The observations recorded for yield and yield attributing traits and quality characters were, “Plant height (cm), Panicle length (cm), Flag leaf length and width (cm), Days to 50% flowering, Number of effective tillers per plant, Number of filled spikelet per panicle, Number of unfilled spikelet per panicle, Pollen fertility percentage, Spikelet fertility percentage, 1000 grain weight (g), Grain Yield per plant (g), Biological Yield per plant (g), Harvest index (%), Kernel length (mm), Kernel breadth (mm), Kernel L/B ratio, Cooked rice length (mm), Cooked rice breadth (mm), Cooked rice L/B ratio, Hulling percentage (%), Milling percentage (%), Head rice recovery (%), Amylose content (%), Alkali spreading value & Gelatinization temperature, Gel consistency.”

The prevalence of non-additive gene action for large portion of the characters were recorded in combining ability analysis. This recommend the probability of using heterosis in the materials.

The great general combiners distinguished for grain yield/ plant among the three lines was IR79156A because of its positive GCA impact. Among the testers, Luchai, Pepri luchai and Sarojini were distinguished as great combiner for the same trait and other related characteristics. Pihu purple was recognized as great general combiner for the greater part of the quality attributes.

The hybrids, IR 68888 A/ Kera khadi showed the highest SCA value followed by IR 58025 A/ Luchai red, IR 79156 A/ Sarojini and IR 79156 A/ Luchai for grain yield/ plant. Some hybrids *viz.* IR 58025 A/ Sarojini, IR 58025 A/ Pihu purple, IR 68888 A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Kera khadi and IR 68888 A/ Luchai red were recognized as promising hybrid for quality traits *viz.*, kernel length, kernel breadth cooked rice length, cooked rice breadth, hulling%, milling% and head rice recovery on the basis of SCA effect. IR 79156 A/ Luchai, IR 68888 A/ Sarojini, IR 58025 A/ Ganga chur were recognized as promising crosses for pollen fertility% and spikelet fertility% on the basis of SCA effect.

Six crosses named, IR 79156A/ Luchai, IR 79156A/ Sarojini, IR 58025 A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, and IR 58025 A/ Sarojini were recognized as favorable hybrids of “mean performance, degree of heterosis, GCA and SCA effects (of their corresponding parents)” for grain yield/ plant. Five hybrids, *viz.*, IR 79156A/ Luchai, IR 79156A/ Sarojini, IR 68888 A/ Sarojini, IR 68888 A/ Luchai and IR 58025 A/ Sarojini showed desired HRR among these six hybrids. Hence, for the commercial use, these hybrids were recognized as superior quality hybrid.

Crosses IR 58025 A/ Sarojini, IR-79156A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, IR 68888 A/ Luchai red and IR-79156A/ Bathras were recognized as favorable hybrids based on “mean performance, degree of heterosis, GCA effects and SCA effects (of their relating parents) for HRR.

Based on, “pollen and spikelet fertility per cent”, Sarojini was recorded as potential restorers for lines IR79156 A and IR 68888A. Other than this Lajni super-1, Luchai, Pepri luchai and Khura bal were also identified as potential restorers. The parents Kera khadi behaved as partial restorer for lines IR 58025 A and IR 79156 A while, Luchai and Pepri luchai acted as partial restorer for the lines IR58025A and IR 68888A. The parents Ganga chur, Pihu purple, Bathras and Luchai red were recognized as partial maintainers for all the CMS lines.

For fingerprinting of hybrids, total of two SSR markers were utilized for evaluation of variance within parents and genetic purity testing of hybrid seed in rice. To establish the hybrid, the polymorphism recognized among the parents was utilized. The 2 markers *i.e.*, “RM 495 and RM 1” are used. Parents used, based on polymorphic detection were “Ganga chur, Luchai, Pepri luchai, Sarojini and Kera khadi and the three CMS lines, IR 58025 A, IR 79156 A and IR 68888A”. Based on RM 495, all the hybrids were found true hybrid. Based on RM 1 all the hybrids were found true hybrid except “IR 58025 A/Ganga chur, IR 58025 A/ Pepri luchai, IR 68888 A/ Sarojini and IR 68888 A/Kera Khadi”.

शोध सारांश

क. शोध का शीर्षक	: सीएमएस आधारित संकर(ओरिज़ा सटाईवा एल.) धान में हेटेरोसिस और संयोजन क्षमता का अध्ययन
ख. छात्रा का पूरा नाम	: दिव्या साहू
ग. प्रमुख विषय	: आनुवंशिकी एवं पादप प्रजनन
घ. प्रमुख सलाहकार का नाम	: डॉ. एस.एस. राव (अधिष्ठाता, इंदिरा गांधी कृषि विश्वविद्यालय, रायपुर)
ड. पुरुस्कार से सम्मानित किया जाएगा	: एम. एससी. (कृषि, आनुवंशिकी एवं पादप प्रजनन)


प्रमुख सलाहकार के हस्ताक्षर


छात्रा के हस्ताक्षर

दिनांक 19/07/19


विभागाध्यक्ष के हस्ताक्षर

सार

शीर्षक "सीएमएस आधारित संकर (ओरिज़ा सटाईवा एल.) धान में हेटेरोसिस और संयोजन क्षमता का अध्ययन" का निरीक्षण खरीफ 2018 के दौरान अनुसंधान सह शिक्षण फ़ार्म "कृषि महाविद्यालय, इंदिरा कृषि विश्व विश्वविद्यालय, रायपुर (छत्तीसगढ़)" में किया गया था। जनक और आनुवंशिक विविधता के आधार पर आणविक स्तर पर सही संकरों की पहचान करने के लिए वशिष्ठ संयोजन क्षमता का अध्ययन, संकर ओज के परिमाण का मूल्यांकन एवं अध्ययन में शामिल तीन सीएमएस लाइनों के लिए मेंटेनर एवं रिस्टोरर की पहचान हेतु किया गया।

प्रयोग के लिए प्रयुक्त सामग्री में तीन सीएमएस लाइनों अर्थात् आई आर 58025ए, आई आर 79156ए और आई आर 68888ए और दस परीक्षक अर्थात्, गंगा चूर, लुचाई, पिहू पर्पल, बथरास, पेपरी लुचाई, खुरा बल, सरोजनी, केरा खादी, लुचाई रेड और लाजनी सुपर -1 और उनके तीस संकरों को

आर सी बी डी डिज़ाइन में तीन प्रतिकृत के साथ तथा चार चेक्स जैसे , इंदिरा सोना , के आर एच -4 , महामाया और अराइज़ 6444 के साथ लगाया गया।

प्रेक्षणों को भिन्न-भिन्न मात्रात्मक एवं गुणात्मक लक्षणों तथा सूक्ष्म पोषको जैसे, "पौधे की ऊँचाई (सेमी), पेनिकल की लंबाई (सेमी), फ्लैग लीफ की लंबाई और चौड़ाई (सेमी), 50% फूल खिलने के दिन, प्रति पौधे प्रभावी टिलर की संख्या, प्रति पैनिकल में भरे हुए स्पाइकलेट की संख्या, प्रति पैनिकलखाली स्पाइकलेट की संख्या, पराग की उर्वरता प्रतिशत, स्पाइकलेट की उर्वरता का प्रतिशत, 1000 अनाज का वजन (ग्राम), प्रति पौधा अनाज (ग्राम), प्रति पौधा जैविक उपज (ग्राम), हार्वेस्ट इंडेक्स (%) , कर्नेल लंबाई (मिमी), कर्नेल चौड़ाई (मिमी), कर्नेल एल / बी अनुपात, पकाया चावल की लंबाई (मिमी), पकाया चावल की चौड़ाई (मिमी), पकाया चावल एल / बी अनुपात, हल प्रतिशत (%), मिलिंग प्रतिशत (%) , हेड राइसरिकवरी (%), एमाइलोज कंटेंट (%), एल्कली स्प्रेडिंग वैल्यू और जिलेटिनाइजेशन तापमान, जेल स्थिरता।

सामान्य संयोजन क्षमता की तुलना में विशिष्ट संयोजन क्षमता के अधिक मानों के आधार पर संयोजन क्षमता विश्लेषण अधिकांश लक्षणों के लिए गैर योज्य जीन क्रिया की उपस्थिति दर्शाता है जो प्रायोगिक सामग्री में संकर ओज की उपयोगिता की सम्भावना प्रदर्शित करता है।

सकारात्मक एवं सार्थक सामान्य विश्लेषण क्षमताकेआधारपर तीनों लाइनों में सेआई आर 79156एको प्रति पौधे दानों की उपज एवं सम्बंधित लक्षणों के लिए अच्छे सामान्य संयोजक के रूप में पहचाना गयासाथ ही तीन टेस्टर्स लुचर्ड ,पेपरी लुचर्ड और सरोजिनी भीप्रति पौधे दानों की उपज एवं सम्बंधित लक्षणों के लिएअच्छे सामान्य संयोजक के रूप में पहचाने गए।

संकरआई आर 68888ए/ केरा खादी द्वारा प्रति पौधे दानों की उपज एवं सम्बंधित लक्षणों के लिए विशिष्ट संयोजन क्षमता के रूप में पहचाने गए।कुछ संकर अर्थातआईआर 58025ए/ सरोजिनी,आईआर 58025ए/ पिहू पर्पल, आई आर 68888ए/ लुचर्ड, आई आर 68888ए/ सरोजिनी, आई आर 68888ए/ केरा खादीऔर आई आर 68888ए / लुचर्ड रेड को गुणवत्ता गुण लक्षण अर्थात कर्नेल के लिए आशाजनक संकर के रूप में पहचाना गया। लंबाई, गिरी रोटी पके हुए चावल की लंबाई, पकाया चावल की चौड़ाई, पतवार%, मिलिंग% और सिर चावल की वसूली SCA प्रभाव के आधार पर। आईआर 79156 ए / लुचर्ड, आईआर 68888 ए / सरोजिनी, आईआर 58025 ए / गंगा चूर को एससीए प्रभाव के आधार पर पराग उर्वरता% और स्पाइकलेट प्रजनन क्षमता% के लिए आशाजनक क्रॉस के रूप में मान्यता दी गई थी।

आईआर 79156 ए/ लुचाई, आईआर 79156 ए/ सरोजिनी, आईआर 58025 ए/ लुचाई, आईआर 68888 ए/ सरोजिनी, आईआर 68888 ए/ लुचाई, और आईआर 58025 / सरोजिनी नाम के छह क्रॉस को "मीन प्रदर्शन" के अनुकूल संकर के रूप में मान्यता दी गई थी। अनाज की उपज / पौधे के लिए हेटेरोसिस, जीसीए और एससीए प्रभाव (उनके संबंधित जानको "केआधार पर। पांच संकर, अर्थात् आईआर 79156A / लुचाई, आईआर 79156A / सरोजिनी, आईआर 68888 ए / सरोजिनी, आईआर 68888 ए / लुचाई और आईआर 58025 ए / सरोजिनी ने इन छह संकरों के बीच वांछित एचआरआर दिखाया। इसलिए, व्यावसायिक उपयोग के लिए, इन संकरों को बेहतर गुणवत्ता वाले संकर के रूप में मान्यता दी गई थी।

पराग और स्पाइकलेट फर्टिलिटी% के आधार पर सरोजिनी को आईआर 79156 ए और आईआर 68888 ए की लाइनों के लिए संभावित रेस्टोरर के रूप में दर्ज किया गया था। इसके अलावा, लाजनी सुपर- 1, लुचाई, पेपरी लुचाई और खुरा बल को भी संभावित रेस्टोरर के रूप में पहचाना गया। जनक केरा खादी ने आईआर 58025 ए और आईआर 79156 एके लिए आंशिक रिस्टोरर के रूप में व्यवहार किया, जबकि लुचाई और पेपरी लुचाईने आईआर 58025 ए और आईआर 68888 एके लिए आंशिक रिस्टोरर के रूप में काम किया। जनक गंगा चूर, पिहू पर्पल, बथरास और लुचई रेड को सभी सीएमएस लाइनों के लिए आंशिक अनुचर के रूप में मान्यता दी गई थी।

संकरों के फिंगरप्रिंटिंग के लिए, जनकके भीतर विचरण के मूल्यांकन के लिए कुल दो एसएसआर मार्करों का उपयोग किया गया और चावल में संकर बीज के आनुवंशिक शुद्धता परीक्षण किया गया। संकर को स्थापित करने के लिए, जनकके बीच मान्यता प्राप्त बहुरूपता का उपयोग किया गया था। 2 मार्करों यानी, "आरएम 495 और आरएम 1" का उपयोग किया गया था। पॉलीमॉर्फिक डिटेक्शन पर आधारित जनक "गंगा चूर, लुचई, पेपरी लुचई, सरोजिनी और केरा खादी और तीन सीएमएस लाइनों, आईआर 58025 ए, आईआर 79156 ए और आईआर 68888 ए" का उपयोग करते थे। आरएम 495 के आधार पर, सभी संकर शुद्धसंकर पाए गए। RM 1 के आधार पर "आईआर 58025 A / गंगा चूर, आईआर 58025 A / पेपरी लुचाई, आईआर 68888 A / सरोजिनी और आईआर 68888 A / केरा खादी" को छोड़कर सभी संकर शुद्धसंकर पाए गए।

CHAPTER I INTRODUCTION

Agricultural sector will need to yield almost 50% additional food and biofuels till 2050 than it was in the year 2012, to satisfy the need of consistent developing population of human. According to FAO (2017) estimation, the population of world would achieve 9.74 billion in 2050 (Anon., 2017). Around 66% of the present human population relies upon rice (*Oryza sativa* L.) as their staple food (Talukdar *et al.* 2017).

India has a rich resource of rice germplasm at different ecological conditions. In India more than 40000 rice germplasm were recorded. Internationally, India ranks first in area of rice cultivation and second in production of rice. Approximately one-fourth means 43 million hectares of total rice cultivated area of the world is covered by India with a total production of 115.6 million tonnes in 2018-19, (The Economics Time 2019). Rice is mounting the biggest single utilization of land for production of food, which covers 9 per cent of the arable land of the earth. Rice gives 21% and 15% of global human per capita energy and protein respectively. (Anon., 2002). Calories from rice are especially significant, particularly between poor people in Asia where 50-80% of day by day caloric intake is represented by it (Anon., 2001).

Among cereal crops, rice is the most important and as a result of its utilization as prime staple food in numerous nations it has been referred as “Global Grain”. It is a self- pollinated crop which belongs to the genus *Oryza*, tribe Oryzeae, in the family Poaceae (Graminaeae).

Being a staple sustenance for the majority of the general people of nation, rice is considered as the most important crop of our country. This crop is the foundation of employment for many the provincial family units and the term “Rice is life” is best suitable in context of India since it assumes essential job in the nation's nourishment security. (Mahajan *et al.*, 2017).

The central eastern state, Chhattisgarh is also named as the “Rice bowl of India”. It has complete geological zone of 13.52 million hectares out of which 5.90 million hectare territory is cultivated land. Rice possesses a region of 3.65 million hectare with 7.65 million tons production and 1517 kg/ha productivity. The rice segment is a noteworthy wellspring of pay and work in rural regions, other than satisfying the local consumption demand (Anon., 2015).

In our country, for hybrid rice development, Chhattisgarh is presently identified as potential zone. At present, around 1.50 lakh hectares area under hybrid rice is covered by Chhattisgarh. In 2006, “Indira Sona”, the 1st public bred hybrid developed for shallow land in Chhattisgarh (Anon., 2010). Many other hybrids viz. “PAC 807, Ankur 7434, Arize Tej, PAC 8744, VNR 2355 and Arize 6129 gold” were also released as notified variety for Chhattisgarh state.

Rice is source of different essential minerals which is useful in assimilation and also rich in nutrient values. The eatable bit of rice consist of “27.9 gm carbohydrates, 2.66 gm protein, 0.28 gm fat, 365 gm sodium, 35 gm potassium per 100 gm.” Rice is also a rich source of Fe (7%), Zn (8%) and Ca (1%). For Asians, rice is a source of 20-80 % of dietary energy and 12-17 % of dietary protein on an average day by day intake. About a century back, serious crop development research was started by realizing that there was no choice to steady production of rice to keep pace with population developing at an alarming rate, (Chopra, 2001).

In the near future, supply shortage of a crop occurs because of the increase in demand, low gross domestic production of rice and saturation of cultivable field. To meet the growing demand, around 785.0 million tons of paddy (70 % more than the present production) will be required by the year 2025. (Manomani and Khan, 2003). Hence being the essential nourishment of the Indian population, productivity improvement of rice has transformed into an essential significance (Subbaiah *et al.*, 2011).

Since last two decades the productivity has come to stagnation and to offer substantial outcomes to break the genetic yield obstruction in rice, every efforts

have failed. Of the different methodologies planned to check the current yield hindrances in rice to feed the quickly expanding population and to increase the production, practically, hybrid rice technology is possible and promptly adoptable breeding alternative and is considered as one of the ideal, eco- friendly and sustainable technology (Virmani, 1996).

Hybrid rice technology has been adequately exhibited in China and India. Over the best inbred check varieties of corresponding duration, under irrigated ecosystem, the yield advantage were observed in the range of 15-20 per cent at field level (Virmani and Edwards, 1983) that has a good efficiency to recover the nutritional safety of poor nations where, there is a limitation of arable land and populations are increasing. China encouraged other rice developing nations to receive this innovation by its impressive progress. The present area of hybrid rice in our country is around three million hectare.

For building up the hybrids with better grain quality and high yield potential, the expected degree of “combining ability and heterosis” is required. In breeding, to overcome the frequent issues for choosing parents and crosses for high yield crop plants, analysis of combining ability is one of the effective methods (Faiz *et al.*, 2006).

Combining ability inspires the breeders to decide the degree of gene action engaged in the expression of yield and yield attributing characteristics of monetary significance. “General combining ability (GCA) and specific combining ability (SCA)” are the two kinds of combining ability. According to Sprague and Tatum (1942), the average performance of a line in a series of hybrid combinations is GCA and the deviation of a particular cross from the GCA is SCA. Means it is the parent’s performance in a specific cross. Higher frequency of heterotic hybrids were shown by the performance of good combining parents than poor combining parents (Jayasudha and Sharma, 2009). A parental line with good GCA and a hybrid with high SCA is ultimately the aim of a breeder in a hybrid breeding programme. All in all, GCA is less influenced by condition than SCA (Singh and Richharia, 1977).

For the heterotic exploitation of rice, test of diverse “cytoplasmic male sterile (CMS) lines and restorers for their combining ability” is an urgent need. To

evaluate nicking ability in self-pollinated crops and meanwhile to explain the nature and extent of gene action involved, the data of combining ability is useful. Kempthorne (1957) proposed the Line x Tester analysis of combining ability, is normally used to calculate general and specific combiners and study the gene action governing the characters' inheritance.

Jones (1926) first reported heterosis in rice who detected a noticeable increment in number of culm and grain yield in some F₁ hybrids in contrast to their parents. For choosing favorable recombinants in the successive generation, to release the best variety when it attained homozygosity, the F₁ hybrids can be utilized. Depending on the breeding objectives, both positive and negative heterosis is useful in improvement of crop. Generally, for yield, positive heterosis is required and for early maturity, negative heterosis is required (Nuruzzaman *et al.*, 2002). The per cent expansion or reduction in the average performance of crosses over the mid- parent (relative heterosis), better parent (heterobeltiosis) and the check variety (standard/useful heterosis) is known as hybrid vigour.

To meet the food requirements of people, the prime quick and long term objective of plant breeding stays expanded productivity/yield. But quality is also an essential component of the economic yield. A few parts of quality are clear to the purchasers, and their preference for a produce are significantly influenced by them. India is the 2nd largest exporter of quality rice in the world, hence, it is necessary to shift in the rice breeding strategies from quantity centered approach to quality oriented effort, (Sreedhar *et al.*, 2005). For the improvement of hybrids with high yield and better grain quality, desired nutritional quality and cooking quality, it is important to apply appropriate breeding techniques (Subbaiah *et al.*, 2011).

Because of use of cytoplasmic genetic male sterility (CGMS) and fertility restoration system, commercial exploitation of heterosis has been made possible. Among the lines, it is authoritative to identify locally adapted maintainers and restorers, to convert in to CMS lines for wider adaptability which can be developed by using conventional breeding procedures. It is fundamental to perceive the maintainers among the locally bread increasingly assorted lines

created through traditional breeding techniques. Two main observations *viz.*, “pollen fertility and spikelet fertility percentage”, are important to identify the maintainers and restorers.

To exploit the heterosis of rice at moderate level, it is essential to maintain the high level of genetic purity of hybrids. For achievement of hybrid technology, quality control is demanded by hybrid seed production in the term of observing genetic seed purity at both parental and hybrid seed production stage (Sudharani *et al.*, 2013). As indicated by an estimation, for each 1% impurity in the hybrid seed, the yield decrease is 100 kg for each ha (Mao *et al.*, 1996). As seed quality directly impacts the crop productivity, for successful commercialization of hybrids, assessment of genetic purity plays a vital role. As compared to other DNA markers, SSR has abundant polymorphism, co-dominant and large in quantity. Hence, in identification of plant variety, SSR has become an ideal molecular marker (Panaud *et al.*, 1996). Presently, the most widely utilized markers are, simple sequence repeat (SSR) markers (Sharopova *et al.*, 2002; Maccaferri *et al.*, 2007 and YU *et al.*, 2011) for quick assessment of hybrid and parental line seed purity. (Yashitola *et al.*, 2002 and Sundaram *et al.*, 2008).

Keeping the above facts under consideration, the present study entitled **“Study of heterosis and combining ability in CMS based rice (*Oryza sativa* L.) hybrids.”** was carried out with the following objectives:

1. Estimation of general combining ability and specific combining ability for grain yield
2. Identification of potential restorers and maintainers.
3. Estimation of heterosis for grain yield and quality traits.
4. Genetic purity testing of selected hybrids.

CHAPTER II

REVIEW OF LITERATURE

Hybrid rice technology seems to be the foremost possible and promptly adoptable to increase the level of yield in rice. Broad examination were go on all through India and abroad on totally various aspects of hybrid rice for example, “combining ability analysis, heterosis and identification of restorers and maintainers with conventional, classical and trendy approaches”.

For a complete understanding of the subject, the available related literature has been reviewed under following heads:

- 2.1 Combining ability analysis
- 2.2 Quality parameters
- 2.3 Heterosis
- 2.4 Identification of maintainers and restorer
- 2.5 Genetic purity of hybrids at molecular level

2.1 Combining ability analysis

The identification of parents with high general combining ability (GCA) effects and hybrids with high specific combining ability (SCA) effects is identified by combining ability analysis. Combining ability analysis can also estimate, additive and non-additive gene action and with the help of this possibility for commercial exploitation of heterosis would be determined. The general combining ability can be defined as the average performance of a parents or inbred in a series of cross combination and the specific combining ability can be defined as the performance of two specific inbreds during a particular cross combination. The literature on the combining ability in rice is reviewed here below the subsequent sub- heads:

2.1.1 The general combining ability (GCA) and specific combining ability (SCA)

Bagheri and Jelodar (2010) studied combining ability on 12 F₁ hybrids

along with their parents using line x tester analysis. And they concluded that IR62829A, within CMS parents, and IR50 and Poya, among male parents were observed to be good general combiners for many of the traits. And high significant SCA were observed for the hybrids IR62829A x Mosa-tarom, IR68899A x Poya, IR58025A x IR50 and IR58025A x Poya and considered as good specific cross combinations for grain yield and most of its related traits.

Tiwari *et al.* (2011) evaluate sixty F₁ hybrids along with their 13 parents, 3 CMS lines and 20 restorers. The result showed that the male lines *i.e.*, IR35454-18-1-1-2R, IET201108 and IR52256-9-2-2-1R were identified good general combiners for grain yield and almost all its major components. In the crosses NMS4A x IR633-76-1R, IR58025A x IR19058-107-1R, IR58025A x IR32419-28-3-1-3-3R, NMS4A x IR35454-18-1-1-2R and NMS4A x IR5226-9-2-2-1R, high sca effects was observed.

Bhadru *et al.* (2012) applied line x tester analysis and studied combining ability with four CMS (WA source) and well adapted seventeen elite diverse lines. They resulted that variances for the SCA were higher as compared to the variances of GCA for majority of the characters. IR-80555A x R-47, IR-79156A x R-43, IR-79156A x IR-13419, IR-68897A x R-48, IR-68897A x R-51 and IR-68897A x R-52 were identified as promising hybrids.

Ghosh *et al.* (2012) reported “high SCA variance as compared to the GCA variance for grain yield and yield components, suggesting the preponderance of dominance and epistatic gene action in expression of these traits using line x tester mating design with three CMS lines and seven elite testers. For head rice recovery per cent the line CRMS 31 A and IR 79156 A were observed as good combiners. Among the testers, NPT 80-1 was good general combiner for grain yield per plant and TOX 981-11-2-3 for both grain yield per plant and head rice recovery percent. The crosses APMS 6 A/ET 1-13, CRMS 31 A/ET 1-12, and IR 79156 A/ NP T 80-1 were found to be good with respect to grain yield per plant, head rice recovery per cent, and spikelets per panicle. The cross APMS 6 A/NPT 2-2-694- 1 was good combiner for head rice recovery per cent”.

Latha *et al.* (2013) conscious about nature and level of heterosis and joining capacity in 18 F1 crosses including three CMS lines and six testers and they utilized LxT examination. ANOVA for joining capacity of the considerable number of characters indicated exceptionally critical differences because of treatments, parents and crosses. They inferred that line CRMS 32A and analyzers viz. Super rice-8, R 1099-2569-1-1 and Jitpiti were recognized as great general combiners.

Sanghera and Waseem (2013) used 18 male parents with 2 CMS lines applied combining ability analysis through Line x Tester analysis of 36 hybrids developed by them. K-08-61-2 was found to be good general combiner among testers and SKAU 11A was observed to be a good general combiner among lines. The crosses, SKAU7A x K-08-61-2, SKAU7A x SR-2, SKAU11A x K08-60-2, SKAU11A x K-08-59-3 and SKAU11A x SKAU-389 were found to be good specific combiners.

Sharma *et al.* (2013) generated “75 hybrids from crossing three cytoplasmic male sterile lines with 25 testers were studied along with parents for combining ability and reported that amongst the parental lines, UPR-2080-24-1-R, IR-60076-1-R, PNR-165-10-6-R and IR-58025-A were found to be good general combiners. None of the crosses showed significant sca effects for all the characters. On the basis of *per se* performance and high sca effects, IR-58025-A x CSRC-50-2-1-4-BR, PMS-10-A x IR-42688-2-118-6-3, RPMS-100-A x UPRI-92-79-R and NMS-4-A x IR-32419-28-3-1-3-R were good specific combiners for grain yield/ plant”.

Upadhyay and Jaiswal (2015) reported that Jaya was found good general combiner for grain yield plant⁻¹, 100 grain weight, pollen fertility, kernel length, kernel breadth, kernel length after cooking, elongation ratio and alkali digestion value among the testers and IR68897A was good general combiner for days to maturity among the lines. In the analysis of Specific Combining Ability (SCA), cross IR67684A x Swetha was the best for grain yield plant⁻¹ and IR68897A x Sasyashree was the best for 1000 grain weight. IR80555A x Swetha was found the best for the characters days to maturity, seeds panicle⁻¹ and kernel breadth.

Khute *et al.* (2015) studied in New Plant Type (NPT) lines of rice about combining ability in line x tester mating design involving 3 CMS lines and 6 testers. “The analysis of variance for combining ability of all the traits showed that variances due to treatments, parents, hybrids were highly significant. Among the CMS lines IR 58025A was identified as a good general combiner for grain yield per plant. Among the testers NPT line HR 703 (3.09) was found to be good combiner for grain yield per plant followed by Jirashankar (NPT-Sel) (2.36) and IIRON N-1-114(0.79)”.

Mahto *et al.* (2015) evaluated three CMS lines and six testers using L x T mating design and concluded that among the CMS lines, CRMS31A was identified as a good general combiner for grain yield per plant and most attributing traits followed by CRMS32A. Among the testers R-1162-1667-1-1 was found to be good combiner for grain yield/plant followed by PUSABAS-6(P-1460) and INGER 1-114. Five cross combinations viz., IR79156A/Improved HMT, CRMS31A/BPT4358, CRMS32A/INGER-1114, CRMS 31A/R-1162-1667-1-1 and CRMS32A/Pusa Bas-6 (P-1460) were found to be outstanding with respect to grain yield per plant.

Sahu *et al.* (2016) conducted an experiment to study the combining ability and genetic behaviour of the parents on 21 hybrids which were generated in line x tester (L x T) fashion by using three CMS lines and seven testers. “IR 79156A was identified as a good general combiner for grain yield per plant because it exhibited the positive GCA effect with many desirable traits. Among the testers, Karmamahsuri, Suraksha, Bagdidhan and TOX981- 11-2-3 were found to be a good combiner for grain yield per plant and other related traits. Crosses IR 58025A/ Suraksha, IR 58025A/ Inger-2114, CRMS 32A/ Karmamahsuri, IR 79156A/ Karmamahsuri and IR 79156A/ RIL-62 showed the higher SCA value for grain yield per plant”.

Kishor *et al.* (2017) studied combining ability for yield and its components involving 3 indica and 5 tropical japonica rice. They concluded that, for all the characters, GCA and SCA were significant which indicated the significance of both additive and dominance genetic components. For grain yield per plant,

“Jaya/ IR 66738-118-1-2, Pant Dhan-12/ IR 66159-23-2-2-1, Pant Dhan-12/ IR 66155-2-1-1-2, Pant Dhan 12/ IR 66736-75-1-3 and Pant Dhan-12/ IR 66738-118-1-2” were good specific combiner among the hybrids.

Thorat *et al.* (2017) studied combining ability on grain yield and its components from line \times tester analysis of 12 rice hybrids produced by crossing three CMS lines and 4 testers. Among the female, IR58025A was the good general combiner parent and among male parent NPQ-49 was best general combiner. On the basis of SCA effects, the crosses IR58025A \times NPQ-49 and RTN12A \times NPQ-49 were identified as most promising for yield and desired traits.

Kumar and Singh (2017) recorded high gca in Sarjoo 52 and Narendra Usar 3 among the testers and among the female parental lines, IR 58025 A was observed as a good general combiner. The crosses, IR 688897A \times Sarjoo 52, IR 58025 A \times 21-2-5-B-1-1, IR 58025 A \times Narendra Usar 3 and IR 58025 A \times IR 71829-3R-73-1-2-B shown promising results in *per se* performance and highly significant positive sca effects in related to grain yield /plant.

Elshenawy *et al.* (2018) evaluate the performance of 21 F₁ hybrids along with their parents and resulted highly significant and positive GCA value of CMS line IR69625A and testers Giza178, Giza179 so considered as good parental lines combiner in hybrid combinations for high grain yield/plant.

Saikiran *et al.* (2018) developed thirty two hybrids from crossing four CMS lines with 8 restorers and studied among with parents for 14 yield and yield attributing characters and concluded that among the male parental lines, JGL 18047, IET 26264 and RNR 26060 appeared the best general combiners. The most promising specific cross combinations were JMS 13A \times RNR 26060 and CMS 64A \times WGL 14 for grain yield and most of the component characters.

2.1.2 Gene Action

The nature of gene action's knowledge involves within the expression of quantitative traits of economic importance. This can be useful in formulating a systematic breeding methodology for the genetic improvement of trait(s). Johannson (1909) gives the information about the genetic control of quantitative

traits. Fisher (1918) was the first to partition the genetic variance into three parts *i.e.*, additive, dominance and epistatic variance. Epistatic variance was further divided by Hayman and Mather (1955) into three components *i.e.* additive x additive, additive x dominance and dominance x dominance interactions. In the absence of epistasis, Line x tester analysis (Kempthorne, 1957) has been found to be the best in estimation of unbiased additive and dominance components. Review for The studies on estimation of genetic variance by line x tester analysis in rice are as under:

Satyanarayana *et al.* (2000) revealed higher SCA fluctuation than GCA changes for a considerable length of time to 50 per cent flowering, plant height, productive tillers per plant, panicle length, number of fertile grains per panicle, per cent spikelet fertility and test weight which demonstrate the transcendence of non-added substance quality activity overseeing for yields and related attributes.

Pradhan *et al.* (2006) generated 36 hybrids from crossing 3 lines with 12 testers and studied them along with parents. They found significant general combining ability (GCA) and specific combining ability (SCA) for all the characters, which indicate the importance of both additive and non-additive genetic components. But it is found that, for expression of different traits in the set of materials utilized there was predominance of non-additive genetic components.

Kumar (2008) saw most of non-added substance quality activity for every one of the characters under investigation *viz.*, days to 50% flowering, plant height, productive tiller per plant, panicle length, flag leaf area, filled grains per panicle, spikelets sterility percent, grain yield per plant and head rice recovery, respectively.

Jayasudha and Sharma (2009) contemplated 33 crosses delivered by intersection three lines and eleven testers alongside their parents for combining capacity and quality activity associated with the statement of characters in rice.

Bagheri and Jelodar (2010) studied on 12 F1 hybrids along with seven rice genotypes (three cytoplasmic male sterile lines and four restorer varieties) according to line x tester mating design. They recorded were higher SCA variances than the GCA variances for characters excluding plant height which showed

preponderance of non-additive gene action in the inheritance of the characters.

Ghosh *et al.* (2013) revealed most of +ve non-added substance quality activity for every one of the characteristics, while - ve for flag leaf length. All the seven testers displayed either minor or additive cytoplasmic gene action which influenced the fertility restoration behavior of different combinations of the same pollen parent.

Prasad (2014) conducted an experiment based on evaluation of a line x tester set of 36 hybrids and their 15 parents along with 2 checks. He concluded that “among the parents, best five genotypes were IR55179-3B-11-3, IR 11T159, Jaya, IR 58025 B and NDRK 50026 exhibited significant GCA effects, for grain yield/ plant, indicating the involvement of additive gene action for yield and component traits. Among the crosses, best five hybrids were Narendra Usar Dhan 2009 x NDRK 50026, Jaya x Narendra Usar Dhan 2008, IR11T164 x Narendra Usar Dhan 2008, CSR 28 x NDRK 50026 and Jaya x Narendra Usar Dhan 3 exhibited significant SCA effects for grain yield/ plant, indicating the preponderance of non-additive gene action for yield and components”.

Shrivastava *et al.* (2015) were found higher heritability attended with high genetic advance showed by tillers /plant, plant height, flag leaf length, flag leaf width, culm length, panicle weight/ plant, biological yield/ plant, seed yield/ plant, harvest index, spikelet density, total spikelets/ panicle, filled spikelets/ panicle, unfilled spikelets/ panicle, spikelet fertility and panicle index. This shows that by additive gene action these characters were governed and selection for these traits would be effective.

Singh *et al.* (2015) studied the combining ability of grain yield and its components from Line x Tester analysis, involving three CMS lines, 20 testers and resulting 60 rice hybrids. The analysis revealed the preponderance of non-additive gene action for all the characters under study. IR58025A x Mancha (14.42) and IR58025A x IR72164-352-2-5-5 (14.07) crosses were found to involve both parents with high GCA effect indicating the involvement of non-additive gene action operating in these crosses.

Gade *et al.* (2017) crossed three CMS lines with eight restorer lines in a

line \times tester mating design to obtain twenty four F_1 hybrids. Good specific crosses were obtained from high \times high, high \times low, low \times high and low \times low general combiner indicating predominance of non-additive gene action. The ratio of SCA and GCA variances was high for panicle length, spikelet fertility, number of productive tillers per plant which indicate the preponderance of non-additive gene action over the additive gene action.

Ramesh *et al.* (2017) studied on 24 hybrids along with their 11 parents and concluded that “in some characters like, days to 50% flowering, number of productive tillers per plant, number of unproductive tillers per plant, flag leaf length, flag leaf width, 1000 grain weight and grain length-breadth ratio variances of SCA were higher than GCA which indicates these traits are governed by Non-additive gene effect. The proportional contribution of lines and testers were more than the interactions of the line \times tester revealed the higher estimates of GCA variance that is additive gene action among the testers and lines”.

Thorat and Kunkerkar (2017) considered the nature and size of quality activity for example GCA and SCA of 12 yield and yield ascribing characters by utilizing seven rice genotypes and twelve F_1 s. Prevalence of non-added substance quality activities in the legacy of a large portion of the characters were indicated as a result of the higher SCA and GCA fluctuation proportion. NPQ-49 and Chedo Local among the male parents were seen to be great general combiners for the vast majority of the characters contemplated. For extent of quality activity, the crosses, IR 58025A/NPQ-49 and RTN12A/NPQ-49 were seen to be great explicit cross combinations.

Devi *et al.* (2018) studied the “gene action in rice resulting in predominance of non- additive gene action for most of the yield components and quality traits except straw yield/ plant, which was under the control of additive gene action. They found that the crosses Kavya/ HKR08-62, Gontrabidhan/ HKR08-62, Kavya/ MTU 1075 have shown significantly favorable SCA effects for grain yield, yield components and quality traits. Majority of the crosses with high SCA effects involved with high \times low combinations indicating additive \times dominance, dominance \times dominance type of gene interactions for expression of

traits”.

2.2 Quality Parameter

The quality characteristics of rice such as physical grain quality, cooking characteristics, taste and nutritional traits, determine acceptability at consumers's end.

These quality traits are controlled by many physico-chemical properties (Juliano, 1970).

Singh and Singh (2005) report about higher heritability with high genetic advance as percent of mean was more helpful than heritability alone for anticipating the gain in selection while taking a shot at 20 mutants of Pusa Basmati-1. In the present examination, HRR and ASV displayed high heritability with high hereditary development which demonstrate most of added substance quality activity and improvement of such characters through selection should be possible.

Kumar *et al.* (2006) studied on quality traits in 8 rice cultivars, 36 hybrids (F_1), and their 36 F_2 s. They found that, for grain length additive gene action was important, however for grain breadth and grain length: breadth ratio both additive and non-additive gene actions were important. For grain yield all the characters showed non significant result in association analysis. Hence, we can improve all characters without any opposing effect on grain yield plant^{-1} .

Shivani *et al.* (2007) recorded hulling % showed positive significant correlation with milling % and HRR indicating that the genotypes with higher hulling % also recorded higher estimates for milled and head rice. HRR also showed -ve but non significant correlation with grain L/B ratio.

Rajeshwari *et al.* (2010) studied on “association and path analysis for ten grain quality characters of 30 high yielding varieties of rice and revealed that head rice recovery had highly significant positive association ($r=0.86$) with milling percentage and significant negative association with elongation ratio (-0.39). The relationship between head rice recovery and kernel length after cooking was negative and significant (-0.41). Alkali spreading value exhibited positive and significant association with kernel length after cooking (0.40).

Grain quality characters *viz.*, kernel length, alkali spreading value and elongation ratio manifested positive correlation with kernel length after cooking. The quality characters *viz.*, alkali spreading value and elongation ratio also showed high positive direct effect on kernel length after cooking”.

Parikh *et al.* (2012) evaluated physio-chemical characters and cooking nature of 36 rice genotypes. It was reasoned that predominant genotypes were Rajm- 12 for grain yield, kernel length, L:B ratio and kernel length after cooking; Rajabhog for grain yield, kernel length after cooking, L:B of cooked rice and elongation index; Bikoni for HRR, elongation ratio, elongation index, and intermediate alkali values.

Gnamalar and Vivekanandan (2013) studied “seven high yielding rice genotypes *viz.*, ADT 41, ADT 46, CO 47, TKM 9, Jeeragasamba, ACM 98003 and AS 90033 and their 21 crosses subjected to combining ability studies for grain yield and grain quality analysis. Non-additive genetic variance was greater for grain yield, hulling percentage, milling percentage, head rice recovery, kernel breadth, linear elongation ratio, water uptake, volume expansion ratio, alkali spreading value, amylase content and gel consistency suggesting the postponement of selection to later generation from the segregating population. ADT 41 and AS 90033 were good general combiners for grain yield and grain quality traits. The hybrid combinations *viz.*, CO 47/ Jeeragasamba, ADT 41/ ACM 98003, TKM 9/ Jeeragasamba, ACM 98003/ AS 90033 and CO 47/ TKM 9 were identified as good specific combiners for grain yield and grain quality traits”.

Sao *et al.* (2015) studied on thirty five genotypes of rice and recorded small difference between GCV and PCV for the characters which indicate less influence of environment on these characters. They also concluded that the characters like, “head rice recovery, brown rice length and, brown rice L/B ratio, kernel length, kernel L/B ratio, cooked rice length, cooked rice L/B ratio and elongation ratio exhibited high heritability coupled with high genetic advance”.

Sreenivas *et al.* (2015) conducted an experiment in rice through Line \times Tester analysis of twenty four crosses developed by crossing four lines and six

testers. They concluded that among the crosses high sca values was registered by Samba Mahsuri \times Jagtial Samba for quality characters. The crosses Akshayadhan \times Cotton Dora Sannalu, Warangal Samba \times Early Samba, Akshayadhan \times Early Samba and Akshayadhan \times JGL-11727 exhibited positive values for some quality characters.

Abdala *et al.* (2016) studied on “eleven F₁ generation derived from crosses between aromatic and non-aromatic parental landraces genotypes. They resulted that high standard deviation was observed on head rice recovery (16.12) followed by gel consistence (13.81) and milling recovery (10.74) and correlation between brown rice length and paddy grain width ($r= 0.692$); paddy grain length and brown grain length ($r = 0.558$); head rice recovery and milling recovery ($r = 0.511$) and brown rice shape and grain rice length ($r = 0.404$) were positive highly significant, while correlation between brown rice shape and brown rice length were negative ($r = -0.497$)”.

Sahu *et al.* (2016) experimented on 21 crosses, generated in L \times T fashion by using three CMS lines and seven testers. They concluded that the L \times T interaction was significant for all 23 traits taken under study. The best general combiner identified was CRMS 32A for most of the quality traits *viz.*, hulling%, head rice recovery, milling% and elongation ratio. Genotypes TOX981-11-2-3, Karmamahsuri, Bagdidhan and Suraksha were identified as a good general combiner for HRR and other quality traits. The hybrids IR58025A/ Suraksha, IR58025A/ TOX981- 11-2-3, CRMS32A/ Inger-2-114 and IR58025A/ Kanakgopala were identified as promising hybrid based on SCA effect for head rice recovery and other quality traits.

Sahu *et al.* (2017) estimated the “components of genetic variability and associated statistical parameters for grain quality traits of 215 indigenous rice landraces of Chhattisgarh, India. All the genotypes were showed highly significant differences for all the studied grain quality traits and observed that sixty nine genotypes had short slender type grain characteristics whereas; forty seven genotypes have short bold type grains. Thirty genotypes showed more than 80% hulling per cent, fifty six genotypes showed more than 70% milling

percent and fourteen genotypes showed more than 65%”.

Gokulakrishnan (2018) used three lines *viz.*, “IR58025A, IR62829A and PUSA3A and ten testers as parents and obtain thirty F₁ hybrids. For heterosis studies majority of the crosses showed positive heterosis for the characters *viz.*, productive tillers, filled grains per panicle, spikelet fertility, thousand grain weight, grain yield per plant, grain length, grain breadth, grain L/B ratio, kernel L/B ratio, milling recovery, head rice recovery, and amylose content. Negative heterosis were recorded for the characters namely days to first flowering, plant height, panicle length, kernel length, kernel breadth and alkali digestion value”.

2.3 Heterosis

Heterosis is defined as the “superior performance in the growth, vigour, vitality, reproductive capacity, stress resistance, adaptability, grain yield, grain quality and other physiological traits of F₁ population of two genetically diverse parents (P) compared to either the mid- parent (MP) or better parent (BP) of the cross or to the check (CK) (Nanda and Virmani, 2000)”. In crop improvement, both positive and negative heterosis are useful, depending on the breeding objectives and nature of the trait.

It is a complex-biological phenomenon and to explain the cause of this, several theories have been proposed. Review related to heterosis is presented as under:

Faiz *et al.* (2006) crossed two CMS lines, IR69616A and JR70369 with testers 60001 and Basmati 385. The highest +ve heterosis, over better parents was observed for grain yield (41.83 %), no. of productive tillers per plant (11.04 %) and no. of filled grains per panicle (7.39 %) in the cross of IR69616A x Basmati 385.

Joshi (2007) studied heterosis (mid parent, better parent and standard) for 13 characters from 5 crosses and 3 WA, CMS lines. They estimated that the highest level of heterosis (62.60%), better parent heterosis (39.56%) and standard heterosis (19.38%) for height of plant was expressed by the hybrid IR58025A/Kanchan.

Kumar *et al.* (2008) observed that, “of the 72 hybrids and nine parental genotypes (ADT 37, Tulasi, IR 50, IR 64, Sasyasree, IR 20, ADT 38, ADT 44 and CR 1009) analyzed for combining ability, most of the crosses which exhibited high standard heterosis were endowed with high mean performance and specific combining ability (sca) effects. Several of the cross combinations that showed high sca effects had at least one of parent with high gca effects. Hence, they recognized the observed heterosis might be due to epitasis”.

Saravanan *et al.* (2008) estimated heterosis for days to 50 per cent flowering, plant height, productive tillers per plant, filled grains per panicle, 100-grain weight and grain yield per plant from seven lines, four testers and 20 hybrids. They resulted that “heterosis for grain yield per plant reached 76.37 and 64.95 per cent over mid parent and better parent, respectively. Two hybrids, i.e. IR 6331-1-B3R-B-24-3 x Jaya and CRAC 2221-67 x Jaya, were identified as favorable for grain yield and other desirable traits”.

Bagheri and Jelodar (2010) studied heterosis in 12 F₁ hybrids along with their parents in a line x tester fashion. The highest heterosis (106.60%) was observed in cross IR68899A x Poya followed by other eight crosses for yield and most of its related traits.

Devaraja (2009) recognized six hybrids blends from a line x tester contemplate with better explicit consolidating capacity and altogether elevated requirement heterosis for seed yield/plant over the check half breed KRH-2. He announced that the degree of percent heterosis was 46.35 in KCMS 31A/KMR-3, 29.58 in CRMS 31A/KMR-3 and 29.30 in KCMS 33A/KMR4.

Tiwari *et al.* (2011) studied 3 male sterile lines and 20 testers to estimate better parent heterosis for grain yield. More than 60% heterosis were found as well as for major components, significant sca were found, the NMS4A x IR633-76-1R, IR58025A x IR19058-107-1R and IR58025A x IR32419-28-3-1-3R were were significant combinations.

Latha *et al.* (2013) studied heterosis in 18 F₁ rice hybrids and observed that hybrid CRMS32A x R1099-2569-1-1 recorded a high degree of mid parent heterosis (62.02%), better parent heterosis (57.36%) and heterosis over checks

(15.06 and 25.52%) on, Mahamaya and Indirasona respectively.

Bhatti *et al.* (2015) conducted an experiment in which the F₁ hybrids of 30 crosses developed by crossing 10 lines with three testers were used in which the hybrid, HPR2529 X HPR1156 showed high heterosis over standard check for plant height, grain fertility, grain yield/plant biological yield/plant.

Ambati *et al.* (2016) crossed 3 male sterile lines viz., IR 58025A, IR 68902A and IR 72081A with 12 testers to produce 36 hybrids in 1 × t mating design and compared with the check, PA 6129. They concluded that significant standard heterosis for grain yield is observed, IR58025A × MTU1010 (18.26), IR68902A × RNR15038 (14.58) and IR72081A × RNR15038 (9.56). The best experimental hybrid IR58025A × MTU1010 recorded relative heterosis (78.27) and better parent heterosis (64.36).

Bedi *et al.* (2016) considered heterosis in rice contains three CMS lines viz., CRMS 31A, IR 58025A and IR79156A and five analyzers viz., NPT 453-2, NDR 8054 (IR 77768-25-NDR-B-108-14), CR 2330-3-3-2-1-1, NPT 76-8 and PR-115. Indira Sona (mixture) and Mahamaya (business cultivar) were utilized as check. The crosses were tried as line x tester mating plan with two replications. Cross IR 79156A/NPT 76-8 represented positive huge heterosis over checks for characters grain yield/plant, test weight, pollen fertility %, and HI.

Kumar and Adilakshmi (2016) concluded that out of twenty crosses, four crosses were exhibited highly significant standard heterosis for grain yield per plant which were APMS 9A × RM 83-19-3, CMS 12A × RM 83-19-3, APMS 10A × RM 89-12-3, APMS 10A × RM 80-55-2 which exhibited more than 20% standard heterosis.

Waza *et al.* (2016) were evaluate twenty F₁s from three male sterile lines and eight testers to study the heterosis. High grain yielding rice hybrids were IR68897A x Pusa Sugandh3, IR58025A x HURJM-59221 and IR58025A x Pusa Sugandh5. The hybrid, IR-68897A x Pusa Sugandh-3 was highest in yield/plant.

Devi (2017) studied about heterosis in a set of seven lines and three testers with 21 hybrids and reported that “among the parents, M1-10-29VL and

TM07280 were the best performing parents for seed yield per plant and its components traits. Cross combinations IR777629-72- 2-1-3/ IR64, Basmati 370/ CR2703, Sonam/ NDR118 and IR7734-4-0/ CR2703 exhibited high significant effects with high *per se* performance and standard heterosis over PHB71. Cross combinations M1-10-29 VL/ NDR118, Basmati 370/ CR2703, TM07280/ NDR118, IR77629 -72-2-1-3/ IR-64 and TM07280/ IR-64 exhibited highly significant heterosis over PHB71”.

Sahu *et al.* (2017) evaluated the heterotic expressions of 21 crosses for twenty traits. Indira Sona, first hybrid rice of Chhattisgarh was used to estimate the standard heterosis. They concluded that, IR-79156A/ RIL-62 perform significant for all the three type of heterosis in view of both, grain yield and grain quality together as well as for HRR and other quality characteristics in the desirable range.

Thorat *et al.* (2017) conducted an experiment in which 12 hybrids developed from crossing 3 male sterile lines and 4 testers were evaluated for all the three heterosis for yield and yield related traits in rice. They resulted that IR58025A x NPQ-49 and RTN12A x NPQ-49 were the top two heterotic combinations identified for grain yield plant-1 which exhibited >40% better parent heterosis and standard heterosis ranged from 3.65% to 53.15%.

Ramesh *et al.* (2018) conducted an experiment to estimate the degree of heterosis over better parent and standard check with three CMS lines and eight Rajendra Nagar lines. Better parent heterosis and standard heterosis were calculated by them in 24 crosses among 16 characters. Among 24 hybrids they found that the 3 hybrids *viz.*, IR 58025A x RNR 21301(34.46), JMS 13A x RNR 21604 (21.41) and JMS 13A x RNR 21218 (20.92) showed +ve standard heteosis in yield over the check DRRH-3.

2.4 Identification of Maintainer and Restorer lines

Cytoplasmic genetic male sterility was first discovered by Jones and Emsweller (1937) in onion crop and is controlled by the interaction of cytoplasmic and nuclear genes. By Sampath and Mohanty (1954) the role of

cytoplasm causing male sterility in rice was 1st reported. With the help of two breeding methods, Hybrid rice can be produced *viz.*, three line system of heterosis breeding (CGMS) and two line system of breeding. In India most of the hybrid varieties released were examples of three line breeding.

In three line breeding system, the sterility/fertility is due to interaction of nuclear gene with cytoplasm. Generally, Wild Abortive (WA) and Kalinga I were the two source of cytoplasm. In the three lines, the A line has sterile cytoplasm, hence A line is sterile and B is an isogenic line of A with the difference of only having fertile cytoplasm. The third line, R line is a restorer line which restores the fertility of A line. A line is crossed with R line in hybrid seed production. It is essential to identify effective restorer and maintainer lines in CMS line development programme for developing commercial rice hybrids. Some of the work related to identification of maintainers and restorer lines is as below:

Hariprasanna *et al.* (2005) identified 35 crosses, generated in a L x T mating design involving 7 CMS lines and five restorer genotypes. The genotype IR71604-4-4-3-8-7-3-3-3 was found to have wide fertility restoration capacity and restored 80% or above fertility in 4 CMS lines. Ranking of restorers in cross combinations for grain yield and yield components was also carried out taking into consideration the statistical significance difference between mean values.

Joshi *et al.* (2007) analyse pollen and spikelet in F₁ rice hybrids and their parents by using 9 improved cultivars, 6 landraces and 3 WA cytoplasmic-genetic male sterile (CMS) lines. They resulted that in hybrids, pollen fertility ranged from 0.5 to 82% and spikelet fertility from 0 to 87%. In pollen parents, pollen fertility varied from 28 to 97%, while spikelet fertility from 73 to 91%.

Jayashudha and Sharma (2010) identified ten genotypes as potential restorers based on the pollen fertility (%) and spikelet fertility (%). Genotypes RPHR203-3 and R1216-6 have been identified as potential restorers for all 3 lines. They also resulted higher frequency of potential restorers and absence of maintainers in the study.

Latha and Sharma (2012) studied on 3 lines and 6 testers. The two genotypes Super rice-8 for APMS6A and R1099-2569-1-1 for CRMS 32A were

identified as potential restorers and two genotypes SR-6-SW-8-1 for APMS6A and R-1557-1306-1-568-1 for CRMS32A were identified as maintainers based on pollen fertility (%) and spikelet fertility (%).

Hussain and Sanghera (2012) conducted an experiment to study 36 cross combinations developed by crossing 2 lines with 18 testers in LxT mating design to identify restorers and maintainers. 3 lines *viz.* K-08-61-2, K-08-60-2 and SR-2 were categorized as effective restorers and 5 lines *viz.* SKAU-405, Jhelum, SKAU-407, China-1007 and SKAU-391 were categorized as maintainers. The average ratio of restorers, partial restorers, partial maintainers and maintainers were 16:22:33:27, respectively.

Ali *et al.* (2014) crossed three CMS lines with 43 genotypes to create 129 crossovers. Out of 43 F₁s with IR 58025A, two were discovered completely sterile (IR 58025A/Kalijira-9 and IR 58025A/Sorukamini-2) and three as fully fertile (IR 58025A/Agali, IR 58025A/Benaful, and IR 58025A/Khasa). Kalijira-9 and Sorukamini-2 were recognized as maintainer for IR-68885. Aromatic line Benaful was distinguished as restorer for IR 58025A and IR 62829A.

Sahu *et al.* (2014) conducted an experiment with 7 rice genotype and three CMS lines to know about their restorer/maintainer behaviour. Genotypes Suraksha can be considered as potential restorers for the CMS line IR58025A on the basis of pollen fertility % and spikelet fertility %. RIL-62 were identified as potential restorers for the CMS line IR56A and CRMS32A. Karmamahsuri and TOX-981-11-2-3 can be considered as potential restorers for CMS line CRMS32A. Bagdidhan has been considered as potential restorer for all the 3 CMS lines.

Reddy *et al.* (2014) crossed 70 drought tolerant lines with two CMS lines and F₁s were analyzed for pollen fertility (1% I-KI solution) and spikelet fertility. 25 genotypes were restorers based on the fertility restoration in F₁'s. KMR3, IR 84891-B-112-CRA-15-1 and IR79906-B-192-2-2 produced F₁s with highest pollen fertility and spikelet fertility.

Dar *et al.* (2015) studied, "three cytoplasmic male sterile (CMS) lines with Wild Abortive (WA) CMS source were crossed with 9 rice genotypes to assess their restorer/maintainer behaviour. Out of 27 test crosses evaluated, 10 restorers, 8 partial restorers and 9 partial maintainer cross combinations were

categorized on the basis of pollen fertility and spikelet sterility. 3 genotypes K-08-61, K-08-60 and Pusa Sughand-5 were found as effective restorers for all the three CMS lines with spikelet fertility above 83% in F1s for data pooled over environments, besides one more genotype K-08-59 depicted restoration only with the introduced CMS line IR-68888A”.

Prasad *et al.* (2017) studied about “identification of maintainers and restorers for their utilization in hybridization programme as the parental lines. A Total of 38 rice genotypes of diverse source of origin were test crossed with CMS line IR 79156A for the evaluation of the genotypes in order to identify potential restorers and maintainers. The F1’s crossed between genotypes and CMS line expressed various degrees of fertility reactions. Among the tested cytoplasmic male sterile genotypes, 18 genotypes expressed restorer (R) reaction. Out of the remaining lines 17 genotypes were identified as partial restorers and 3 lines as partial maintainers”.

Hossain *et al.* (2018) crossed five CMS lines with 49 genotypes as ‘testers’ to get 245 hybrids. When they subjected this hybrids to pollen and spikelet fertility analysis, among the 245 hybrids 21 hybrids were expressed as restorers, 24 as maintainers, and 200 intermediate types. None of the testers were found to be restorer for all the five CMS lines. Except for D.ShanA, BAU581 was found to be maintainer for all the four lines. Purbachi was found to be maintainer for three lines except for IR73328A and D. ShanA. Out of 245 crosses only 45 crosses contributed directly to the identification of maintainer and restorer. Other crosses were of intermediate types which indicated neither maintainer nor restorer.

2.5 Genetic Purity of Hybrids at Molecular Level

The most important characteristics of good quality seed is the authenticity of a hybrid. For successful commercialization of hybrids, assessment of genetic purity plays a crucial role as the crop productivity is directly influenced by quality of seeds. As compared to most of the other markers, SSR has much more polymorphism, and is co-dominant and large in quantity. And for this reason, for the identification of plant variety, SSR is considered as an ideal marker for identifying the variety of plant and for genetic purity testing of hybrids.

Xin *et al.* (2005) used a total of 144 SSR primer pairs distributed on 12 rice chromosomes, out of which 47 detected polymorphism among the tested rice lines. “Among all these primers, RM337 and RM154 produced polymorphic patterns in four or more of the tested experimental materials respectively, and they could distinguish among most rice genotypes tested. Twenty-four primer pairs, two on each rice chromosome, were selected to make a reference SSR marker-based fingerprinting for the rice lines. For most of the primer pairs, F₁ hybrids mainly showed complementary pattern of both parents, which could be very useful to distinguish the F₁ from its parental lines. In addition, 5 primer pairs were selected as special primer pairs for five hybrid rice combinations respectively”.

Kumar *et al.* (2012) utilized 35 SSR markers for fingerprinting 2 prominent rice hybrids and their parental lines. 6 SSR markers were discovered polymorphic over the hybrids and delivered unique finger printing for the 2 crosses. A set of five markers (RM 206, RM 276, RM 204, RM234 and RM 228) separated the 2 crosses from one another, which can be utilized as referral markers for unambiguous distinguishing proof and protection of these hybrids. The investigation of plant-to-plant variety inside the parental lines of the mixture KRH-2 and DRRH-2, utilizing informative markers demonstrated lingering heterozygosity at two marker loci.

Rajendran *et al.* (2012) screened hundred SSR markers, out of which sixty two were found to be polymorphic. A total of 203 alleles were recorded as 0 to 1 data set (presence-1 and absence-0) with an average of 3.2 alleles per loci. “Commercial rice hybrid KRH-2 can be detected using its male parent KMR-3 specific markers RM297, RM442, RM541, RM584 and RM107 and female parent IR58025A specific markers RM529, RM489, RM589, RM533 and RM182 identified in this study”.

Deshmukh *et al.* (2013) employed “thirty simple sequence repeat microsatellite (SSR) markers for fingerprinting 18 rice hybrids and their parental lines. Twelve SSR markers were found polymorphic across the parents and produced unique fingerprint for the parents. Among the markers RM-17 and

RM-84 precisely distinguished between pure hybrids and mixture/off type. Cluster analysis based on Simple matching (SM) similarity coefficient using UPGMA grouped the hybrids into three clusters. The genetic similarity between the hybrids ranged from 0.43 to 0.81 with an average similarity index of 0.63”.

Sudharani *et al.* (2013) concluded that out of 50 markers used by them, only RM336 and RM 307 were found to be polymorphic to distinguish DRRH-2 and DRRH-3, respectively. Thus, these markers can be precisely used for assessment of seed purity.

Sahu *et al.* (2015) conducted an experiment in order to identify pure hybrid and pollen shedders/ off-types using ideal SSR marker (Microsatellite markers). The investigation was conducted using nine SSR markers on 21 rice hybrids and their corresponding 10 parental lines *i.e.*, three CMS lines and seven testers. RM 206 and RM 517, the two polymorphic markers were clearly distinguished all the parental lines used in the study while between pure hybrids and mixture/off type, only RM 206, alone is precisely distinguished. They found that all the hybrids were pure but highest purity was found in hybrid, CRMS-32A/ Suraksha for RM 206 under the investigation.

Kumar *et al.* (2015) concentrated to break down hereditary virtue in seed blend and assorted variety appraisal among various rice assortments. They utilized 6 primers (RM 1, RM 242, RM 276, RM285, RM 429, and RM 341) and discovered all are polymorphic, uncovering 28 allelic variations at 9 loci with a normal of 3.1 alleles per locus among the 7 rice assortments and their seed blend tried. A sum of 13 shared and 15 one of a kind allelic variations were created among the assortments and varietal blend tried. Considering the quantity of alleles related to the degree of polymorphism distinguished, 4 SSR markers (RM 1, RM 429, RM 242 and RM 341) gave off an impression of being progressively enlightening groundworks.

Bhaskaran and Umarani (2016) conducted an experiment in which they mix the seeds of two varieties in four different ratios and genotyping was carried out using polymorphic SSR markers. They resulted that the 24:1 ratio *i.e.* 5% admixtures or off types can be detected by this method. The results were further

confirmed in other set of varieties and pooling ratios. Results confirmed that this method can be used for detecting off type admixtures in seed lots using SSR markers.

Bora *et al.* (2016) played out an analysis to distinguish hereditary debasement in the seed heaps of CMS lines, restorers and half and halves. So as to assess variety inside parental lines and to test the hereditary immaculateness of the business seed parcels, 51 rice-explicit arrangement labeled microsatellite (STMS) preliminary sets conveyed all through the rice genome were utilized for fingerprinting of eight rice crossovers and their parental lines. What's more, they reasoned that among those, 51 markers, 28 microsatellite markers indicated polymorphism (54.90 %). An aggregate of 98 alleles were acquired with a normal of 1.92 alleles per preliminary pair and number of alleles intensified for every groundwork pair ran from 1 to 4.

Nataraj *et al.* (2016) employed “25 simple sequence repeats (SSR) markers for fingerprinting for newly release rice hybrid (KRH- 4) and their parental lines. Polymorphic primers viz., RM202, RM204, RM219, RM216, RM1385, RM21, RM336, RM209, RM7279 and RM206 could clearly distinguish KRH-4 from its parental lines. The polymorphic primer RM216 amplified an allele size of 160bp in CRMS32A (A) and 150bp in MSN36 (R). Similarly RM204 amplified an allele size of 110bp in CRMS-32A (A) and 120bp in MSN36 (R). RM7279 amplified an allele size of 190bp in CRMS32A (A) and 1800bp in MSN36 (R). Since the bands of RM204, RM216, and RM7279 of KRH-4 hybrid rice were complement type of their parents, clear and distinct that can be utilized for purity assessment of hybrid rice KRH-4”.

Singh *et al.* (2016) genotyped a lot of 729 Indian rice assortments utilizing 36 HvSSR markers to survey the genetic diversity and genetic relationship. An aggregate of 112 alleles was enhanced with a normal of 3.11 alleles per locus with mean Polymorphic Information Content (PIC) estimation of 0.29.

Koutu *et al.* (2017) used sixteen SSR markers for fingerprinting of three hybrids and their parental lines. They concluded that eight primers amplified a maximum of two alleles whereas, all other were detected as monomorphic. For

genetic purity of JRH 5, SSR marker RM 234, RM 228, RM 84, RM 279 and RM 237 were identified however for JRH 8 and JRH19, RM 234, RM 228, RM 279 and RM 510 were identified.

Ranjitha and Gowda (2017) employed (SSR) markers for two rice hybrids and their parental lines fingerprinting. The primers RM21, RM1385, RM 444 and RM 346 identified as unique markers for KRH-4 whereas, RM 206, RM 263, RM 164 and RM 276 for hybrid rice KRH-2 and also they were unique compared to SSR markers identified for other public bred hybrids to determine the genetic purity of seed lots and these markers can be used as referral markers for unambiguous identification and protection of these hybrids. These SSR markers demonstrated that the two alleles of the parental lines in unadulterated hybrids demonstrated the heterozygosity, could likewise recognize the off-types and the selfed seeds from its particular F₁ hybrid seeds.

Verma *et al.* (2017) revealed that “88.25 per cent genetic purity was assessed in 3 hybrids tested through statistical analysis of grow out test. Twelve out of 48 microsatellite used were found polymorphic and amplified a total of 29 alleles among the genotypes with an average polymorphic information content value of 0.45. Out of 12 informative markers, nine were found polymorphic across the genotypes and produced unique fingerprints. Five STMS markers (RM154, RM164, RM234, RM258 and RM519) showed polymorphism over all the genotypes and were identified as referral marker for use in unambiguous identification and protection of nine hybrids. Nevertheless, marker RM19 amplified allele was specific to the parental lines of CNRH 3 and APHR 2 (having common CMS line, IR62829). The results on genetic purity test through GOT had highly significant positive correlation ($r=0.96$) with molecular marker analysis”.

CHAPTER III

MATERIALS AND METHODS

The present study entitled “**Heterosis and combining ability Study in CMS based rice (*Oryza sativa* L.) hybrids**” was done during *Kharif* season 2017-18 and *Kharif* 2018 to creat information on “identification of restorer, magnitude of heterosis, combining ability, stability parameters for grain yield and yield contributing characters and quality characters”. Description of used materials and methods applied are given in this chapter. At two levels, the experiments were conducted–

(A) Field level

(B) Molecular level

(A) At field level

3.1 Site of experiment

The present research work was conducted at “Research Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.)”.

3.2 Geography

Raipur, the capital of C.G. (Rice Bowl of India) is situated in East Central part of the state which comes under 7th agro-climatic zone of India *i.e.*, Eastern Plateau and Hills region according to the planning commission. It is situated at 21°13’59” N latitude and 81°37’59” E longitude with an elevation of 298.50 meters above mean sea level.

3.3 Climate and weather information during crop season

The climate of Raipur is sub-humid with hot summer and cold winter. The most extreme temperature was 33.4°C and least 14.4°C during the crop growth period. The total rainfall got during crop growth stage was 772mm. The data relating to “weekly rainfall, minimum and maximum temperatures, relative humidity, evaporation and bright sunshine hours” of entire crop growing period have been presented in figure.3.1.

3.4 Experimental material

The research work comprises of three CMS lines *viz.*, IR-58025A, IR79156A, IR-68888A and ten rice varieties/ landraces *viz.*, Ganga Chur, Luchai, Pihu purple, Bathras, Pepri Luchai, Khura Bal, Sarojani, Kera Khadi, Luchai Red and Lajni Super- 1 as testers. Total 30 crosses are attempted by using Line x Tester design (Kempthorne, 1957). Four checks *viz.*, Indira Sona, KRH-4, Mahamaya and Arize-6444 Gold were also involved to estimate standard heterosis.

3.5 Methods

3.5.1 Nursery sowing

For the developing the F₁ hybrids, 3 male sterile lines *i.e.* CMS lines and ten testers were grown in *Rabi* 2017-18. In five rows of one meter length, the nursery of parents which were 21 days old were transplanted in crossing block keeping the spacing of “20 x 15 cm” and in separate blocks, three CMS lines were transplanted so that out crossing with other parents were avoid.

3.5.2 Hybridization

Crossing of selected ten male parents to all the three CMS lines was done to produce a set of hybrids in a line x tester fashion as proposed by Kempthorne (1957). One third portion of spikelets of CMS plant that were likely to flower the next day were clipped from the top in order to increase the seed settings.

The panicles which were clipped were fully covered with the help of butter paper bags, to avoid contamination with outer pollen grains to fertilize the CMS plants. Panicles from the testers were taken in the next morning (about 8:30 am) at the time of anthesis and in pollination room this panicles were kept at temperature of 2°C under high humidity in glass bottles. After the completion of anthesis, dusting of pollen grains was done over clipped spikelets with proper precaution.

Immediately, the panicles which are pollinated were again bagged and labelled properly with cross combination and date. In this way 30 crosses were attempted. After 30 days of hybridization, from the mother panicle, the bagged panicles were harvested and separated. From each cross, the hybrid seeds were separately collected and were sun dried. To take precaution against fungal attack, the seeds were also treated with bavistin before storage in paper bags.

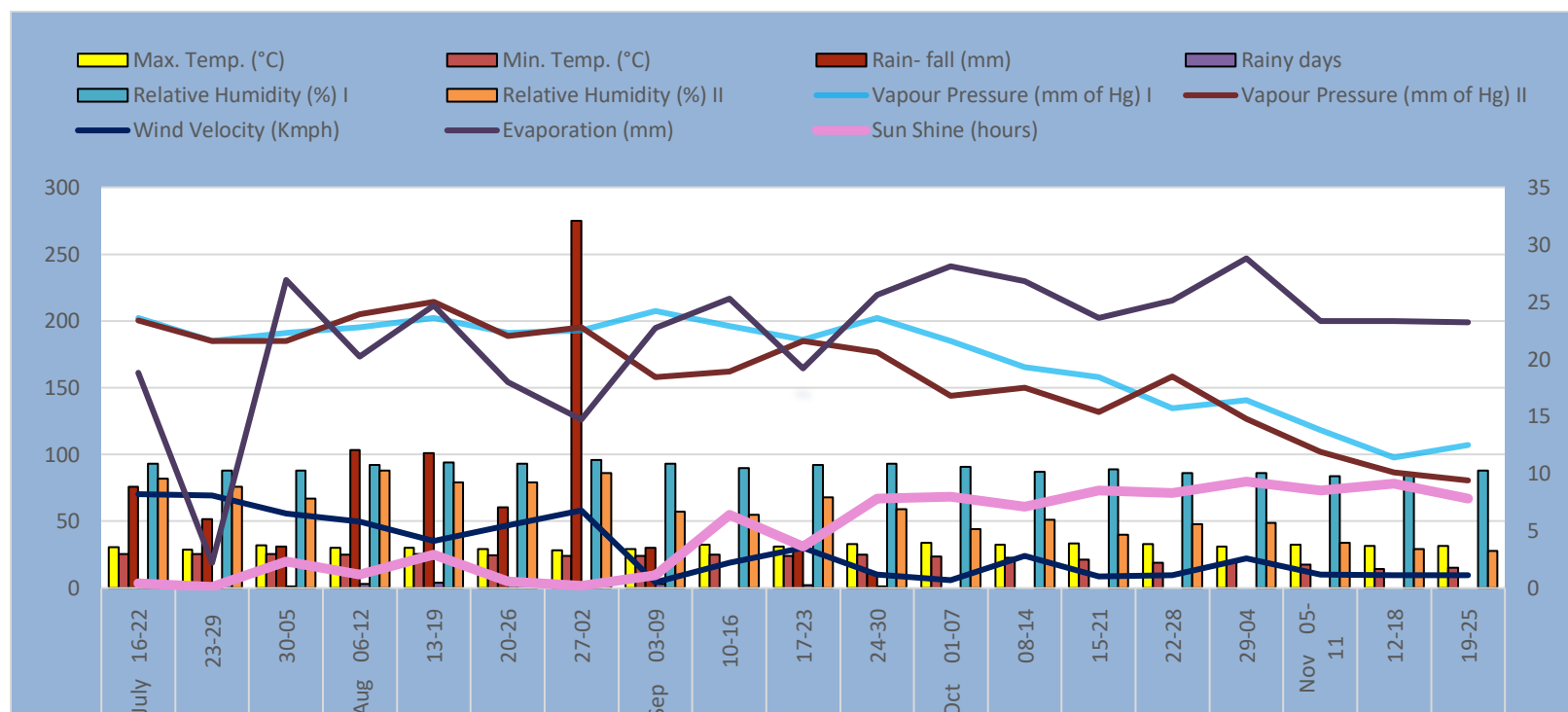


Fig 3.1: Graph showing the weekly meteorological information during crop growth period of rice.

Table 3.1 Detail of Genotypes used in the Investigation

Genotypes	Parentage	Source
Female Parents		
IR 58025A (WA)	IR 48483A/Pusa 167-120-3-2	IRRI, Manila, Philippines
IR 79156A (WA)	IR68897A/IR72798-42-1-2	IRRI, Manila, Philippines
IR 6888A (WA)	-	IRRI, Manila, Philippines
Male Parents		
Ganga Chur	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Luchai	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Pihu purple	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Bathras	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Pepri Luchai	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Khura Bal	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Sarojani	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Kera Khadi	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Luchai Red	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Lajni Super-1	Landrace/ Local Variety	IGKV, Raipur (C.G.)
Checks		
Indira Sona	IR 58025A × R-710-437-1-1	IGKV, Raipur (C.G.)
KRH-4	CRMS 32A x MSN 36	UAS, Bangalore
Mahamaya	Asha × Kranti	IGKV, Raipur (C.G.)
Arize -6444 Gold	-	Bayer Crop Science

3.5.3 Raising F₁'s and parents

In the nursery beds, carefully germinate the 30 hybrids during *Kharif* 2018 which are generated during the previous season. “Three CMS lines (A lines/ male sterile lines) and their isogenic lines (maintainer/B lines) and ten elite testers (pollen parents) along with four standard checks” were also sown in nursery beds.

3.5.4 Planting of F₁'s and parents in *Kharif* 2018

The twenty one days old seedlings of “13 parents (3 CMS lines along with their isogenic “B-line” / maintainer line and 10 testers), their 30 hybrids along with four standard checks *viz.*, Indira Sona, KRH-4, Mahamaya and 6444 Gold” were planted in “Randomized Complete Block Design (RCBD)” with three replications in the *kharif* 2018.

The row to row and plant to plant distance will be 20 and 15 cm. respectively. Transplanting of the seedlings was manually done, keeping single seedling per hill in a row of 1.8m. Standard agronomic package practices were implemented.

3.5.5 Observations recorded

In each treatment, five randomly selected plants were taken and observations were recorded in all the three replications for the traits taken under study which is shown in table number 3.2. For further statistical analysis, the mean values over five plants were considered.

3.5.5.1 Quantitative characters

3.5.5.1.1 Days to 50% flowering

From the sowing date to the date when primary panicles in 50% plants were in heading, the number of days were recorded.

3.5.5.1.2 Plant height (cm)

The plant height was measured in centimeters, from the ground level to the tip of primary panicles at the time of harvest.

3.5.5.1.3 Panicle length (cm)

The length of panicles of all the five selected plants were measured from the base to the tip of the panicle excluding awn if any at the time of harvest.



Fig: 3.2 Crossing Procedure



Fig: 3.3 Test Cross Nursery

3.5.5.1.4 Flag leaf length (cm)

The length of leaf blade of the flag leaf was recorded as flag leaf length.

3.5.5.1.5 Flag leaf width (cm)

The width of leaf blade of the flag leaf was recorded as flag leaf width.

3.5.5.1.6. Effective tillers per plant

At the time of harvesting, the total number of panicle bearing tillers in each plant was recorded.

3.5.5.1.7 Filled spikelets per panicle

The number of filled spikelets per panicle was recorded.

3.5.5.1.8 Unfilled spikelets per panicle

The number of unfilled spikelets per panicle was recorded.

3.5.5.1.9 Pollen fertility percent

By using a microscope, pollen grains were counted in this observation. By using 1:3 acetic acid and alcohol the florets were preserved first. Later on, by using 1% iodine potassium iodide (I₂-KI) solution as stain the pollen fertility counts were taken. The fertile pollen grains are stained ones. The total pollen grains in 5 microscopic fields were observed and counts of fertile pollen grains were seen in relation to the total. For calculating the pollen fertility percentage, fertile pollen's mean values (stained pollen) and total pollens were used.

$$\text{Pollen fertility percentage}(\%) = \frac{\text{No. of stained pollen grains}}{\text{Total no. of pollen grains}} \times 100$$

3.5.5.1.10 Spikelet fertility percent

The panicles were threshed after that sterile and fertile spikelets were counted. Spikelets fertility percentage was calculated as follows:

$$\text{Spikelet fertility percentage}(\%) = \frac{\text{Number of fertile spikelets}}{\text{Total Number of spikelets}} \times 100$$

3.5.5.1.11 1000 Grain weight (g)

Randomly, thousand seeds of each entry were taken and weighted in gram.

3.5.5.1.12 Grain yield per plant (g)

The weight of filled seeds of each plant in grams was recorded.

3.5.5.1.12 Biological yield per plant (g)

Excluding the root, weight of each plant was recorded and expressed in grams.

3.5.5.1.13. Harvest index (%)

The ratio of harvested grain to total shoot dry matter is harvest index was calculated and expressed in percentage:

$$\text{Harvest index (\%)} = \frac{\text{Grain yield}}{\text{Biological yield}} \times 100$$

3.5.5.2 Quality characters

3.5.5.2.1 Kernel length (mm)

The ten milled spikelet were randomly selected and their length was measured in terms of millimeters by graph method.

3.5.5.2.2 Kernel breadth (mm)

The ten milled spikelet were randomly selected and their breadth was measured in terms of millimeters by graph method.

3.5.5.2.3 Kernel L/B ratio

The ten milled spikelet were randomly selected and their length/breadth ratio was calculated by dividing respective length with breadth.

3.5.5.2.4 Cooked rice length (mm)

The ten cooked spikelet were randomly selected and their length was measured in terms of by millimeters graph method.

3.5.5.2.5 Cooked rice breadth (mm)

Randomly selected ten cooked spikelet's breadth was measured in terms of millimeters by graph method.

3.5.5.2.6 Cooked rice L/B ratio

Randomly selected ten cooked spikelet's length/breadth ratio was calculated by dividing respective length with breadth.

3.5.5.2.7 Hulling percentage

Before starting the de-hulling hundred gram of paddy sample was properly cleaned. The dehusking of rice was done by dehusker and weight of hulled rice was recorded.

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

3.5.5.2.8 Milling percentage

Milled rice weight was recorded by putting the brown rice into standard miller or polisher and later milled rice weight was recorded.

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

3.5.5.2.9 Head rice recovery (%)

The three fourth kernel was taken as whole grain from milled rice. Full and broken rice was sorted out and its weight was recorded.

$$\text{Head Rice Recovery} = \frac{\text{Weight of whole polished kernel}}{\text{Weight of paddy}} \times 100$$

3.5.5.2.10 Amylose content (%)

Weighing of 100 mg rice flour in a long test tube was done and 1 ml of rectified spirit and 9 ml of 1.0 N Sodium Hydroxide was added. After shaking it thoroughly test tubes was heated for 15 minutes on a pre heated water bath. Pour the sample in a 100 ml volumetric flask and then make the volume up to 100 ml with distilled water. From this, 5 ml sample in volumetric flask was taken and 1 ml of acetic acid and 2 ml of I₂– KI reagent was added and again make the volume up to 100 ml with distilled water. Cover all the flasks with black clothes for 20 minutes as I₂-KI loses colour when exposed to light. Finally at 620 nm on spectrophotometer the reading of the sample was recorded. The formula for calculating amylose (per cent), the formula used is given as under:

$$\text{Amylose (per cent)} = R \times 101.3$$

Where, R = reading at 620 nm on spectrophotometer.

Scale for Amylose test is given below:

S. No	Classification	Amylose %
1.	Waxy	1-2%
2.	Very low	2-9%
3.	Low	9-20%
4.	Intermediate	20-25%
5.	High	25-33%

3.5.5.2.11 Alkali Spreading Value and/ or Gelatinization Temperature

The alkali spreading value was measured in terms of alkali disintegration using a '7' point numerical spreading scale as suggested by Little *et al.*, (1958). In petri dishes six milled rice kernels were evenly placed and 1.7% KOH solution was poured in it and kept it at 30°C for 23 hours and the spreading scale was recorded.

The procedure to work out ASV & GT and spreading scale and classification of alkali spreading value and gelatinization temperature is given in Appendix-F.

Score	Spreading scale	
1	Kernel not affected	
2	Kernel swollen	
3	Kernel swollen, collar complete and narrow	
4	Kernel swollen, collar complete and wide	
5	Kernel split or dis-integration, collar complete and wide	
6	Kernel dispersed, merging with collar	
7	Kernel completely dispersed and intermingled	

Classification	Alkali spreaing value (ASV)	Gelatinization temperature (GT)
1-2	Low	High >74 °C
3	Low, intermediate	High, intermediate
4-5	Intermediate	Intermediate (70 °C – 74 °C)
6-7	High	Low (55 °C – 69 °C)

3.5.5.2.12 Gel consistency test

Gel consistency is a good index of cooked rice texture and measure of cold

paste viscosity of cooked milled rice flour. With hard gel consistency, the cooked rice hardens faster as compared to soft gel one. Rice with soft gel consistency tender soft, and remain soft even after cooling. For this reason, by most the rice consumers, rice with soft gel consistency are preferred (Sharma *et al.*, 2008). In gel consistency test, 0.2ml ethanol which contain 0.25% thymol blue as indicator and of 0.2 N Potassium hydroxide (2.0 ml) were added in 100mg of rice flour, then after alternatively boiling (90-100°C) and cooling (0-2°C) was done for 8 minute and 20 minutes respectively. Finally the length of the blue coloured gel was measured as gel consistency of the sample. The gel having more length was considered as soft while hard gel have less length.

Categories of gel consistency of rice are as follows:

S. No.	Length (mm)	Category
1.	26-40	Hard gel consistency
2.	41-60	Medium gel consistency
3.	61-100	Soft gel consistency

3.6 Biometrical analysis

The data recorded on 30 crosses and 13 parents for agronomic characters were subjected to the following analysis:

3.6.1 Mean

Mean is the average value of observation of genotypes of a series. It represents the standard average value over fluctuation in the environment. The formula for mean was calculated by:

$$\bar{X} = \frac{\sum X_i}{n}$$

Where,

$\sum X_i$ = Summation of all the observation

n = number of observation

3.6.2 Range

Range is the difference between the minimum and the maximum terms of a series of observation and hence provides the information about the variability present in the genotypes.

3.7 Combining ability analysis

Combining ability analysis was carried out by the method suggested by Kempthorne (1957). Mean sum of squares that arises due to different sources of variation were estimated and their expected genetic values were calculated. A model analysis of variance (ANOVA) table for Line \times tester analysis was given below :

ANOVA table for Line \times tester Analysis

Sources of Variation	Degree of Freedom	Sums of Squares	Mean sums of squares	Expected mean sums of Squares
Replication	(r-1)	SSR	-	-
Hybrids	(lt-1)	SS(h)	-	-
Lines	(l-1)	SS(l)	Ml	$Me+r[Cov.(FS)+rl(Cov.(HS)) - 2Cov.(HS)]$
Testers	(t-1)	SS(t)	Mt	$Me+r[Cov.(FS)+rl(Cov.(HS)) - 2Cov.(HS)]$
Line x testers	(l-1)(t-1)	SS (l \times t)	M(l \times t)	$Me+r[Cov.(FS) - 2Cov.(HS)]$
Error	(r-1)(t-1)	ESS	Me	-
Total	(rt-1)	-	-	-

Where,

r = number of replications l =

number of lines

t = number of testers

Estimation of full sib's and half sib's covariance was calculated from mean squares using following formula:

$$Cov.(HS)C = \frac{Ml + Mt - 2M(l \times t)}{r(l \times t)}$$

$$Cov.(FS) = \frac{Me + Mt + M(l \times t) - 3Me + 6r Cov.(HS) - r(l \times t) Cov.(HS)}{3r}$$

Cov. (HS) and Cov. (FS) were utilized to estimate variance due to General Combining Ability (GCA) and variance due to Specific Combining Ability (SCA) as under:

Variance of GCA = Cov. (HS)

Variance of SCA = Cov. (FS) -2 Cov. (HS)s

3.7.1 Estimation of GCA and SCA effects

The GCA and SCA effects of ijth observation were estimated by adopting the following model.

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

Where,

i = 1, 2 ...ith line

j = 1, 2 ...ith tester

k = Number of replications μ =

Mean

g_i = GCA effect of ith line

g_j = GCA effect of jth tester

s_{ij} = SCA effect of hybrid of ith line with jth tester

e_{ijk} = Error effect associated with the ijth observation

Significance of GCA effects of lines is tested as:

$$t = \frac{g_i}{SE(g_i)}$$

Significance of GCA effects of testers is tested as:

$$t = \frac{S_{ij}}{SE(S_{ij})}$$

The standard errors pertaining to GCA and SCA effects were worked out from the square root of error variance effects as given below:

1. Standard error for testing the GCA effects of lines:

$$SE(g_i) = \frac{\sqrt{Me}}{rt}$$

2. Standard error for testing the significance of difference between GCA effects of two lines:

$$SE(gi - gi) = \frac{\sqrt{2Me}}{rt}$$

3. Standard error for testing the GCA effects of tester:

$$SE(gi) = \frac{\sqrt{Me}}{rt}$$

3.8 Heterosis

Heterosis is calculated for each trait by utilizing the overall mean of each hybrid over replication for each trait.

Relative heterosis was when the heterosis is estimated over the mid parent *i.e.* mean value of the two parents is known as mid parent heterosis and it is calculated as:

$$d_i = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

Where,

d_i = Heterosis over mid parental value (relative heterosis)

$\overline{F_1}$ = Mean hybrid performance, and

\overline{MP} = Mid parental value *i.e.*, the arithmetic mean of two parents involved in the respective cross combination.

Heterobeltosis was calculated to describe the improvement of heterozygote over the better parent and is calculated as:

$$d_{ii} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where,

d_{ii} = Heterobeltosis *i.e.*, heterosis over better parent

$\overline{F_1}$ = Mean hybrid performance, and

\overline{BP} = Average performance of better parent in the respective cross combination

Standard heterosis was calculated at the deviation of hybrid from the checks or check varieties as under:

$$d_{iii} = \frac{\overline{F_1} - \overline{CK}}{\overline{CK}} \times 100$$

Where,

$\overline{d_{iii}}$ = Standard Heterosis i.e., heterosis over checks

$\overline{F_{ij}}$ = Mean hybrid performance, and

\overline{CK} = Average performance of checks in the respective cross combination

The significance of different types of heterosis was carried out by adopting 't' test as suggested by Nadarajan and Gunasekaran (2005):

$$t \text{ (relative heterosis)} = \frac{\overline{F_{ij}} - \overline{MP_{ij}}}{SE}$$

$$t \text{ (heterobeltiosis)} = \frac{\overline{F_{ij}} - \overline{BP_{ij}}}{SE}$$

$$t \text{ (standard heterosis)} = \frac{\overline{F_{ij}} - \overline{CK_{ij}}}{SE}$$

$\overline{F_{ij}}$ = Mean of ijth cross

$\overline{MP_{ij}}$ = Mid parental value for i, jth cross

$\overline{BP_{ij}}$ = Better parental value of i, jth cross

SE = Standard error of heterosis

$\overline{CK_{ij}}$ = Check variety mean value

3.9 Identification of Maintainer and Restorer Lines

During the year 2018, for fertility and sterility identification of F_1 plants, pollen studies were carried out. Randomly five plants were selected and from the just emerged panicles, 15-20 spikelet were collected in a vial which contain 70 % alcohol, for this purpose. With the help of a forceps, all the anthers from at least six spikelet were taken out and placed on a glass slide and pour a drop of 1 % iodine potassium iodide (I_2KI) stain. Crush the anther gently with the help of a needle to release the pollen grains. The debris were removed, after that place a cover slip and observe the slide under the microscope. To avoid foreign pollen contamination, cover 5 panicles of each test-cross with butter paper bags and were harvested at maturity for recording spikelet fertility/sterility observation.

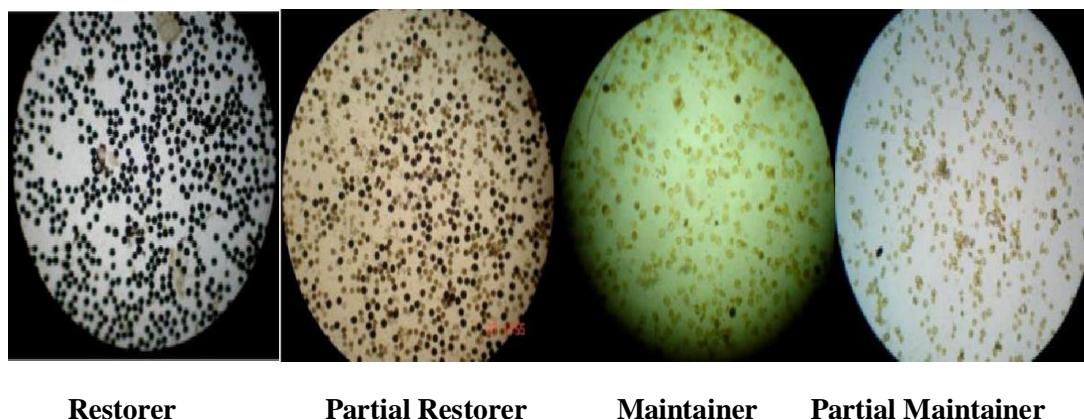


Fig 3.4 Different Classes of Pollen Fertility

The criteria for classifying the parental lines as “maintainers, partial maintainers, partial restorers and restorers” were used as proposed by Virmani *et al.* (1997). The categories of parental lines according to pollen fertility % and spikelet fertility % are given in Table 3.2 and their images are given in Fig. 3.3

Table 3.2 Criteria for classifying the parental lines as proposed by Virmani.

Pollen fertility (%)	Spikelet fertility (%)	Category
0-1	0	Maintainers
1.1-50	0.1-50	Partial maintainers
50.1-80	50.1-75	Partial restorers
> 80	>75	Restorers

B) At Molecular Level

3.10 Molecular Studies

Molecular work was carried out in “Plant Molecular Biology Laboratory, Department of Genetics and Plant Breeding, IGKV, Raipur (C.G.)”.

3.10.1 DNA Extraction

The genomic DNA of rice was extracted using CTAB method. In this method young leaves are collected from rice seedling and the standard protocol followed. Young leaves are preferred because it gives high quality of DNA in compared to old leaves. The protocol is given below:

Young leaves are cut very finely with scissors to get one gram of leaf sample and put it into a 2ml. of Eppendorf tube.

- To the Eppendorf tube 100µl of CTAB buffer is added along with 3 metal beads and place the tubes in the block.
- The block is fixed in the Tissue Lyser for minutes to grind the leaves finely.
- Remove the block from the Tissue Lyser and add 600 µl of CTAB extraction buffer to the tubes.
- Tubes are spun and vortexed for 1 minute to mix the contents properly.
- After vortex 700 µl of chloroform isoamyl alcohol (CIA) (24:1) was added into the tubes.
- Again vortex the samples and then centrifuge it at 14000 rpm for 10 minutes.
- The supernatant was transferred to a new Eppendorf tube of 1.5 ml.
- Repeat the above steps.
- After getting the supernatant 70 µl of Sodium acetate and 400 µl of pre-chilled isopropanol (equal volume of the supernatant transferred) was added to the tubes and they are kept in 4°C for 2 hr. or -20°C for overnight.
- The tubes are then centrifuged for 20 minutes at 14000 rpm. At the end of the process the pellets of DNA is seen at the bottom of the tube.
- The solution is then decanted and 50 µl of 70% ethanol is added for washing and the tubes are then centrifuged at 14000 rpm for 3 minutes.
- The solution is decanted and the tubes are left open for drying the pellets for 2 hours or till the smell of ethanol is completely evaporate.
- At last the pellets were dissolved 50 µl of TE buffer and stored at -20°C until use.

3.10.2 Dilution of DNA

DNA was diluted with DNAAs, RNAAs and protease free water, after quantification such that the final concentration of DNA would become 40 ng/µl for PCR amplification.

According to the following formula the dilution was carried out:

$$\text{Dilution} = \frac{\text{Required conc. of DNA } \left(\frac{\text{ng}}{\mu\text{l}}\right) \times \text{Total volume required}(\mu\text{l})}{\text{Available conc. of crude DNA } \left(\frac{\text{ng}}{\mu\text{l}}\right)}$$

For PCR amplification, the diluted DNA was subsequently used.

3.10.3 PCR amplification using SSR primers

Using a set of two random SSR (simple sequence repeat) markers, PCR analysis was done to identify the parental polymorphism between three lines “(IR 58025A, IR 79156A, IR 6888A) and ten testers *viz.*, Ganga Chur, Luchai, Pihu purple, Bathras, Pepri Luchai, Khura Bal, Sarojani, Kera Khadi, Luchai Red and Lajni Super-1”.

PCR analysis Protocol:

3.10.4 Visualization of amplified products in Polyacrylamide gel electrophoresis

Polyacrylamide gels give better resolution regarding the separation of the amplified fragments. Hence a five per cent polyacrylamide gels (vertical) are used before preparing the gel of the glass plate which are going to be used, washed thoroughly in detergent and distilled water. After this, structures for electrophoresis are prepared and gel is casted in the electrophoresis unit.

Table 3.5 List of SSR markers used to detect polymorphism among the

Primer	Tm °C	Amplicon Size	Chromosome No
RM 495	55	148-160	1
RM 1	55	72-113	1

3.10.5 Assembling and pouring the gel

The first step consists of fixing the gaskets on the sidewalls of the notch less glass and placing 1.5 mm thick spacers along the sides such that it will just touch the gasket of outer plate

In the next step the plate having notch is placed above the notch less

plate such that the spacers are present in between them. Later, clamps are put on the three sides of the plate and the plate were then checked for the leakage by pouring distilled water.

The casting process consists of pouring the 5% acrylamide solution of 65 ml which was made using 70 μ l of TEMED (N-N-N-N- Tetramethylethylene diamine) and 700 μ l of (freshly prepared) ammonium per sulphate (APS, 10%).

The next step is pouring the prepared solution by gently swirling the content so that no gas bubbles are formed inside the structure which is paced on the bench top. A 1.5 mm thick comb of 63 wells is then inserted in the gel then the assembly is kept for 20-30 min. for the process of polymerization.

3.10.6 Electrophoresis

- For the process of electrophoresis the gaskets were removed from the plate and the assembly is put inside the electrophoresis unit such that the notch less plate face towards the outer side while notched plate face inner side and the assembly is then placed tightly with the help of the clamps.
- Then in the upper tank, the TBE buffer (1x) is poured and rest was poured in bottom chamber and removal of the comb gently so that the wells formed in the gel won't be disturbed.
- In the last step, 4 μ l loading dye (10x) was added to PCR products and 5 μ l of each sample is loaded into the wells for facilitating the sizing of the various alleles. Ladder (50 bp) was loaded in the first well.
- Gel was run at 180 volts till the dye reached bottom of the gell.
- After electrophoresis, Ethidium bromide (10 μ l/100ml) used to stain the gel and after the treatment the gel are visualized in BIORAD Gel Doc XR+.

3.10.7 Visualization of bands

After electrophoresis, clamps were removed and glass plates were separated without damaging the gel.

- Water is poured over the gel for removal followed by flipping the gel with a spatula in a staining box.
- In the next step staining of the gel is done by adding Ethidium bromide solution (10 μ l of EtBr to 100 ml double distilled water) into the staining box and agitated for proper staining.
- After staining the gel is washed 2 times with double distilled water for rinse extra stain and then gel is scanned in BIO-RAD gel doc XR+ for visualization of the gel.
- Proper care is taken during handling of TEMED and ethidium bromide solution due to their cancer causing and mutagenic nature respectively.

3.10.2 Reagents and solutions

3.10.2.1 DNA extraction buffer

- 5 ml of Tris HCl (1M; pH-8)
- 5 ml of EDTA (1M; pH-8)
- 7.5 ml of NaCl (4M)
- SDS (20% W/V) 5 ml
- Adjustment of final volume up to 100 ml with distilled water.

3.10.2.2 TE buffer

- 1 ml of 1M Tris HCl (pH 8.0)
- 0.2 ml of 0.5M EDTA
- Adjustment of final volume up to 100 ml and autoclaved.

3.10.2.3 EDTA (1M; pH 8.0)

- 372.20 g of “disodium EDTA (disodium ethylene diamine tetra acetic acid, dehydrate; MW 372.2 g / mole)” was dissolved in 800

ml of distilled water.

- By using concentrated sodium hydroxide (NaOH), pH was set to 8.0 and adjust the final volume to 1000 ml with distilled water and sterilized by autoclaving.

3.10.2.4 4M NaCl

- 23.36 g of NaCl was dissolved in 80 ml of distilled water.
- Adjustment of final volume up to 100 ml and sterilized by autoclaving.

3.10.2.5 1M Tris HCl (pH 8.0 at 25° C)

- 121.1 g of Trizma base was dissolved in 800 ml of distilled water.
- By using concentrated HCL, the pH was set to 8.0.
- Before making the final pH adjustment, cool the solution at room temperature.
- Adjust the final volume to 1000 ml with distilled water and sterilized by autoclaving.

3.10.2.5 RNase solution (10 mg/ml)

- 10mg of RNase powder is dissolve in 1 ml of TE buffer by boiling.
- Allow to cool at room temperature and store in freezer.

3.10.2.6 70% Ethanol

- 70 ml of Absolute ethanol
- Addition of 30 ml double distilled water to make final volume 100 ml.

3.10.2.7 Reagents for PCR

- Primers: Highly variable Microsatellite markers from Invitrogen Life Technologies, USA.
- dNTPs: (dATP/dCTP/dGTP/dTTP) 2.5mM stock of dNTPs was used.
- Taq polymerase: 1unit/ μ l, 500 U (Banglore Genei) Taq were used for PCR amplification.

3.10.3 Solutions for electrophoresis

3.10.3.1 10X TBE buffer

- 216 g of Tris base
- 80 ml of EDTA (0.5M)
- 110 g of Boric Acid
- 500 ml of Distilled water. Final volume was adjusted to 2 liter.

3.10.3.2 Tank buffer (1X TBE)

- 100 ml of 10 X TBE + 900 ml of distilled water.

3.10.3.3 6X loading dye

- 4g of 40% Sucrose
- 0.025 g of Bromophenol Blue 0.25 % (w/v)
- Water: 10. ml.

3.10.3.4 5% PAGE Solution

- 47.5 g of Acrylamide
- 2.5 g of Bisacrylamide
- 100 ml of 10X TBE

3.10.3.5 Ethidium Bromide

- By using 10 mg ethidium bromide powder in ultrapure water, Ethidium bromide solution was prepared and the final volume was adjusted to 1 ml.

3.10.3.6 50bp DNA Ladder

- 0.5µg/ µl, 50 µg and 0.1 µg/ µl, 50 µg both are used at the time of sample loading on gel.

3.10.3.4 10% APS

- For the preparation of 10% APS, 1 gm APS (Ammonium per Sulphate) is dissolve in 8ml (approximately) of water and making the final volume 10.0 ml.

CHAPTER-IV

RESULTS AND DISCUSSION

The findings of the present investigation entitled “**Study of heterosis and combining ability in CMS based rice (*Oryza sativa* L.) hybrids.**” involving three CMS lines and ten testers along with thirty F₁s hybrids for their assessment of :

- 4.1 Mean performance of genotypes for different traits taken under study.
- 4.2 ANOVA for Randomized Complete Block Design
- 4.3 Combining ability estimates
- 4.4 Heterosis
- 4.5 Identification of maintainer(s) and restorer(s)
- 4.6 Genetic purity testing at molecular level.

4.1 Mean performance of genotypes for different characters taken under study

The observations were recorded for the forty seven genotypes i.e. thirteen parents, thirty hybrids and four checks in three replications for twenty six different characters and were used for calculation of the mean performance. The observations were first averaged for five plants taken randomly for each genotype in each replication and further were averaged over all the three replications. The mean performance of parents and hybrids for different quantitative and quality characters is presented in Table 4.1 and Table 4.2. The mean performance of different characters are described as below:

Quantitative characters

4.1.1 Plant height (cm)

The mean performance among the parents for plant height ranged from 77.93 cm (IR 68888A) to 147.52 cm (Kera khadi) with an overall average mean of 116.38 cm and in hybrids the plant height ranged from 78.81 cm (IR 68888 A/ Ganga chur) to 145.24 cm (IR 58025 A/ Pepri luchai) with an overall average of 116.10 cm. Considering the significant value of this trait among the entire cross combinations, three combinations *viz.*, IR 58025 A/ Bathras, IR-79156A/ Bathras and IR 68888 A/ Ganga chur were identified as good performing hybrids.

4.1.2 Panicle length (cm)

The mean of panicle length ranged from 22.01 cm (Lajni super- 1) to 27.16 cm (IR 58025 A) with an overall parental mean of 23.91 cm for parents and in hybrids, it ranged from 22.55 cm (IR 58025 A/ Ganga chur) to 28.83 cm (IR 58025 A/ Pepri luchai) with an overall average of 25.93 cm. Three cross combinations *viz.*, IR 58025 A/ Pepri luchai , IR-79156A/ Luchai red and IR 68888 A/ Pepri luchai were identified as good performing hybrids for panicle length, on the basis of high length of panicle.

4.1.3. Flag leaf length (cm)

The mean of flag leaf length ranged from 24.99 cm (Pihu purple) to 35.5 cm (Khura bal) with an overall parental mean of 28.86 cm. Among lines, IR 58025 A shows maximum flag leaf length (30.51) whereas IR 68888 A shown shortest flag leaf length (25.37) with an average mean of 27.66 cm. Among testers, Khura bal shows maximum flag leaf length (35.50 cm) whereas Pihu purple showed shortest flag leaf length (24.99 cm) with an average mean of testers being 29.22 cm. In hybrids the mean ranged from 26.11 (IR 68888 A/ Lajni super- 1) to 38.76 (IR-79156A/ Sarojini) with an overall average of 32.126.

4.1.4. Flag leaf width (cm)

The mean of flag leaf width ranged from 1.22 cm (Lajni super- 1) to 1.59 cm (Ganga chur) with an overall parental mean of 1.45 cm. In hybrids it ranged from 0.83 (IR 68888 A/ Lajni super- 1) to 1.64 (IR 68888 A/ Pepri luchai) with an overall average of 1.32. Three crosses *viz.*, IR 58025 A/ Luchai red, IR-79156A/ Luchai red and IR 68888 A/ Pepri luchai were identified as good for flag leaf width.

4.1.5. Days to 50% flowering

The mean performance of parents for days to 50% flowering ranged from 89.67days (Pihu purple) to 116.67 days (Luchai), with overall mean of 104.02 days. In the hybrids it ranged from 90.67 (IR 68888 A/ Bathras) to 112.33 days (IR 68888 A/ Luchai) with an overall average of 101.76 days. Considering the performance among the entire cross combinations, three combinations *viz.*, IR 58025 A/ Bathras, IR-79156A/ Pihu purple and IR 68888 A/ Bathras were identified as good performing hybrids for days to 50% flowering on the basis of early flowering.

4.1.6 Effective tillers per plant

The mean of effective tillers per plant for parents ranged from 5.77 (Khura bal) to 11.07 (IR 58025 A) with the overall parental mean of 8.79. The mean value of the hybrids ranged from 5.47 (IR 68888 A/ Luchai red) to 10.57 (IR 68888 A/ Ganga chur) with an overall average of 8.19. Three cross combinations *viz.*, IR 58025 A/ Lajni super- 1, IR-79156A/ Sarojini and IR 68888 A/ Ganga chur were identified as good performing hybrids for effective tillers per plant.

4.1.7. Filled spikelets per panicle

The mean value for filled spikelets per panicle among the parents ranged from 14.93 (IR 68888 A) to 177.77 (Luchai red) with an overall parental mean of 111.23. In hybrids it ranged from 23.27 (IR-79156A/ Ganga chur) to 176.07 (IR 68888 A/ Kera khadi) with an overall average of 71.452. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Sarojini and IR 68888 A/ Kera khadi were identified as good performing hybrids for fertile spikelets /panicle.

4.1.8. Unfilled spikelets per panicle

The mean of sterile spikelets per panicle for parents ranged from 21.33 (Khura bal) to 111.07 (IR 58025 A) with an overall parental mean of 54.36 while in the hybrids, it ranged from 40.33 (IR-79156A/ Luchai) to 169.33 (IR 68888 A/ Pepri luchai) with an overall average of 98.15. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Pihu purple, IR-79156A/ Luchai and IR 68888 A/ Sarojini were recorded as good performing hybrids for sterile spikelets/ panicle.

4.1.9 Pollen fertility percentage

The parental mean of pollen fertility percentage ranged from 0.02% (IR 79156 A) and (IR 58025 A) to 91.96% (Ganga chur) with an overall parental mean of 63.71%. The mean of the hybrids pollen fertility ranged from 13.59% (IR 68888 A/ Luchai red) to 93.23% (IR 68888 A/ Sarojini) with an overall average of 46.33% . Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Lajni super- 1, IR-79156A/ Pepri luchai and IR 68888 A/ Sarojini were identified as good performing hybrids for pollen fertility whereas cross combinations IR 58025 A/ Luchai red, IR 79156A/ Ganga chur and IR 68888 A/ Luchai red had low pollen fertility.

Table 4.1: Mean performance of parents for different characters

	Plant Height (cm)	Panicle Length (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	Days to 50% Flowering	Effective Tillers/ Plant	Filled Spikelets/ Panicle	Unfilled Spikelets/ Panicle	Pollen Fertility %	Spikelet Fertility %	1000 Grain Weight (g)	Grain Yield/ Plant (g)	Biological Yield/ Plant (g)
Parents	1	2	3	4	5	6	7	8	9	10	11	12	13
Lines/Females													
IR 58025 A	99.53	27.16	30.51	1.48	104.67	11.07	36	111.07	0.02	24.64	19.68	6	38.84
IR 79156 A	96.84	25.78	27.1	1.38	96.33	10.37	16.93	98.73	0.02	14.6	19.49	5.69	40.83
IR 68888 A	77.93	24.57	25.37	1.28	96.33	11.03	14.93	70.77	0.03	17.34	19.91	3.71	35.03
Average	91.43	25.84	27.66	4.14	99.11	10.82	22.62	93.52	0.02	18.86	19.69	5.13	38.23
Testers/Males													
Ganga chur	102.11	22.88	27.79	1.59	102.33	8.53	171.98	85.6	91.96	66.78	26.65	14.53	48.97
Luchai	127.32	20.23	27.51	1.52	116.67	10.8	209.4	38.4	83.75	84.59	16.86	15.77	42.43
Pihu purple	105.41	24.7	24.99	1.43	89.67	10.83	59.6	38.77	72.67	60.45	23.85	9.46	27.56
Bathras	113.99	23.02	26.2	1.49	98.33	8.1	116.67	31.4	84.32	78.68	32.56	16.85	36.43
Pepri luchai	136.09	24.52	28.71	1.59	115	7.37	124.6	30.6	78.81	80.78	20.13	16.89	57.93
Khura bal	143.18	26.84	35.5	1.59	97.67	5.77	85	21.33	87.14	79.88	30.02	10.49	31.83
Sarojini	121.02	22.43	33.22	1.29	103.67	6.4	138.07	42.67	91.4	76.39	18.94	12.31	32.26
Kera khadi	147.52	22.41	31.16	1.43	114.33	7.93	204.6	74.4	77.89	73.77	19.51	18.29	45.17
Luchai red	143.47	24.29	27.98	1.55	112	6.23	177.77	34.8	81.72	83.71	12.97	9.43	28.2
Lajni super- 1	98.55	22.01	29.11	1.22	105.33	9.93	90.53	28.13	78.53	76.53	12.43	7.16	27.67
Average	123.87	23.33	29.22	4.41	105.5	8.19	137.82	42.61	82.82	76.15	21.394	13.1	37.85
Checks													
Indira Sona	118.43	28.23	35.05	1.43	105	10.1	110.8	40.87	95.24	73.82	26.38	14.69	47.6
KRH 4	123.11	26.31	29.46	1.44	109.33	10.95	183.97	91.6	94.52	66.58	17.9	15.01	30.37
Mahamaya	111.27	26.95	26.85	1.39	109	8.77	117.47	16.47	96.55	87.84	32.77	18.99	43.2
6444 Gold	109.56	26.19	28.37	1.42	106.67	7.7	113.27	41.33	94.14	73.13	25.12	21.14	52.2
Average	115.59	26.92	29.93	1.42	107.5	9.38	131.37	47.57	95.11	75.34	25.54	17.45	43.34
Overall parental average	116.38	23.91	28.86	1.45	104.03	8.80	111.24	54.36	63.71	62.93	21.00	11.28	37.93
Lowest Range	77.93	22.01	24.99	1.22	89.67	5.77	14.93	21.33	0.02	14.60	12.43	3.71	27.56
Highest Range	147.52	27.16	35.50	1.59	116.67	11.07	177.77	111.07	91.96	84.59	32.56	18.29	57.93
Sem±	1.88	0.55	1.36	0.09	1.77	0.74	8.07	9.05	1.96	2.56	0.26	0.42	1.58
CD at 5%	5.28	1.54	3.83	0.26	4.97	2.08	22.67	25.42	5.51	7.20	0.73	1.18	4.43
CV%	2.80	3.74	7.60	11.87	2.98	15.14	15.97	19.18	6.14	9.07	2.12	8.17	6.59

Table 4.1: Mean performance of parents for different characters

Character	Harvest Index %	Kernal Length (mm)	Kernal Breadth (mm)	Kernal L/B Ratio	Cooked Rice Length (mm)	Cooked Rice Breadth (mm)	Cooked Rice L/B Ratio	Hulling %	Milling%	Head Rice Recovery %	Amylose Content %	Alkali spreading value	Gel consistency
Parents	14	15	16	17	18	19	20	21	22	23	24	25	26
Lines/Females													
IR 58025 A	15.4	6.17	1.67	3.7	9.33	2.17	4.31	71.2	56.13	50.5	17.63	7	72.92
IR 79156 A	13.79	6.17	1.57	3.94	9.16	2.57	3.57	69.44	54.92	49.6	20.91	7	31.81
IR 68888 A	10.38	5.9	1.47	4.02	8.53	2.8	3.05	63.56	33.03	28.4	17.3	6	32.04
Average	13.19	6.08	1.57	3.89	9.01	2.51	3.64	68.07	48.02	42.8	18.61	6.66	45.59
Testers/Males													
Ganga chur	30.01	6.03	2.2	2.74	10.5	3	3.5	67.45	63.36	53.4	26.02	5	34.53
Luchai	37.32	5.3	1.97	2.69	9.13	2.77	3.3	73.89	70.6	60.6	26.56	4	86.81
Pihu purple	34.4	6.37	2	3.19	10.06	2.83	3.55	72.54	65.36	60.7	11.55	6	56.86
Bathras	46.32	6.3	2.33	2.7	10.2	2.67	3.83	72.9	64.33	59.6	30.23	5	66.01
Pepri luchai	29.21	5.23	2.17	2.43	8.97	2.87	3.13	64.97	59.92	53.3	20.97	3	33.87
Khura bal	33.06	5.73	2.33	2.46	9.17	2.77	3.31	72.41	62.57	52.6	23.12	3	87.91
Sarojini	37.83	5.3	2	2.65	8.13	2.53	3.21	64.7	55.81	48.1	14.98	2	41.3
Kera khadi	40.81	5.47	2.17	2.54	9.1	2.63	3.46	72.53	68.02	62	12.79	3	43.32
Luchai red	33.83	4.7	1.8	2.62	8.63	2.13	4.05	75.55	64.54	59.5	18.39	3	34.93
Lajni super- 1	26.17	5	1.57	3.19	9.17	2.1	4.37	62.36	47.65	43	19.06	5	62.26
Average	34.9	5.54	2.05	2.72	9.3	2.63	3.57	69.93	62.25	55.3	20.36	3.9	54.78
Checks													
Indira Sona	30.85	6.6	1.77	3.74	9.8	2.9	3.38	72.58	66.33	53.3	25.08	3	38.97
KRH 4	49.48	5.37	1.83	2.92	8.73	3.13	2.79	72.3	67.45	59.8	26.59	5	55.26
Mahamaya	43.99	6.5	2.17	3	9.9	3.4	2.91	66.24	59.15	49.2	28.13	6	71.81
6444 Gold	40.55	6.07	2.03	2.98	10.4	3.17	3.28	71.54	67.52	59.5	24.57	6	48.66
Average	41.22	6.13	1.95	3.16	9.71	3.15	3.09	70.66	65.11	55.4	26.09	5	53.68
Overall parental average	29.89	5.67	1.94	2.99	9.24	2.60	3.59	69.50	58.94	52.41	19.96	4.69	52.66
Lowest Range	10.38	4.70	1.47	2.43	8.13	2.10	3.05	62.36	33.03	28.40	11.55	2.66	31.81
Highest Range	46.32	6.37	2.33	4.02	10.50	3.00	4.37	75.55	70.60	60.70	30.23	7.00	87.91
Sem±	1.41	0.15	0.06	0.10	0.18	0.06	0.10	0.41	0.58	0.65	0.31	0.31	0.54
CD at 5%	3.97	0.43	0.16	0.29	0.51	0.16	0.29	1.14	1.64	1.84	0.87	0.87	1.52
CV%	11.31	4.59	5.04	5.89	3.33	3.48	5.31	0.99	1.63	2.08	2.50	11.70	1.79

4.1.10 Spikelet fertility (%)

The mean value of parents for spikelet fertility percentage ranged from 14.6% (IR 79156 A) to 84.59% (Luchai) with overall parental mean of 62.93%. Among hybrids, spikelet fertility% ranged from 16.14% (IR 68888 A/ Luchai red) to 75.28% (IR-79156A/ Luchai) with an overall mean of 39.38%. Three cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Luchai and IR 68888 A/ Sarojini were identified as good performing hybrids for spikelet fertility% whereas three combinations IR 58025 A/ Bathras, IR-79156A/ Ganga chur and IR 68888 A/ Luchai red had low spikelet fertility.

4.1.11. Thousand seed weight (g)

The mean of 1000 seeds weight for parents ranged from 12.43 g (Lajni super-1) to 32.56 g (Bathras) with an overall parental average of 21.00 g. Among hybrids, thousand seed weight ranged from 16.52 g (IR 58025 A/ Luchai red) to 25.69 g (IR 58025 A/ Pihu purple) with an overall mean of 20.53 g. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Pihu purple, IR-79156A/ Pihu purple and IR 68888 A/ Pepri luchai were identified as good performing hybrids for test weight.

4.1.12. Grain yield per plant (g)

The mean parental value for the grain yield per plant, ranged from 3.71 g (IR 68888 A) to 18.29 g (Kera khadi) with overall parental mean of 11.27 g. Among hybrids, grain yield per plant ranged from 1.97 g (IR-79156A/ Ganga chur) to 17.2 g (IR-79156A/ Luchai) with an overall mean of 6.697 g. For this trait, three cross combinations *viz.*, IR 58025 A/ Luchai, IR-79156A/ Luchai, and IR 68888 A/ Sarojini were identified as good performing hybrids.

4.1.13 Biological yield per plant (g)

The mean value of biological yield for parents ranged from 27.56 g (Pihu purple) to 57.93 g (Pepri luchai) with an overall parental mean of 37.93 g. while in hybrids, biological yield per plant ranged from 24.8 g (IR 68888 A/ Lajni super-1) to 66.6 g (IR 68888 A/ Pepri luchai) with an overall mean of 42.71 g. Three cross combinations *viz.*, IR 58025 A/ Luchai, IR-79156A/ Sarojini and IR 68888 A/ Pepri luchai were identified as good performing hybrids for biological yield per plant.

4.1.14 Harvest Index (%)

The mean of harvest index in parents, ranged from 10.38% (IR 68888 A) to 46.32% (Bathras) with an overall average of 29.89%. Among hybrids, Harvest index ranged from 4.08% (IR 68888 A/ Luchai red) to 43.44% (IR 68888 A/ Sarojini) with an overall mean of 15.43%. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Luchai and IR 68888 A/ Sarojini were identified as good performing hybrids for harvest index.

4.1.15. Kernel length (mm)

The mean of kernel length in parents, ranged from 4.7mm (Luchai red) to 6.37 mm (Pihu purple) with an overall average of 5.66 mm. Among hybrids, Kernel length ranged from 5 mm (IR 58025 A/ Khura bal) to 6.77 (IR-79156A/ Luchai) with an overall mean of 5.74 mm. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Luchai and IR 68888 A/ Pihu purple were identified as good performing hybrids for kernel length.

4.1.16 Kernel breadth (mm)

The mean of kernel breadth in parents, ranged from 1.47 mm (IR 68888 A) to 2.33 mm (Bathras) with an overall average of 1.94 mm. Among hybrids, Kernel breadth ranged from 1.53 mm (IR 68888 A/ Lajni super- 1) to 2.27mm (IR 58025 A/ Luchai) with an overall mean of 1.90 mm. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Luchai, IR-79156A/ Ganga chur and IR 68888 A/ Bathras were identified as good performing hybrids for kernel breadth.

4.1.17. Kernel L/B Ratio

The mean of kernel L/B ratio in parents, ranged from 2.43 (Pepri luchai) to 4.02 (IR 68888 A) with an overall average of 2.99. Among hybrids, Kernel L/B ratio ranged from 2.43 (IR 58025 A/ Luchai) to 3.68 (IR-79156A/ Lajni super- 1) with an overall mean of 3.03. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Lajni super- 1, IR-79156A/ Lajni super- 1 and IR 68888 A/ Lajni super- 1 were identified with high kernel L/B ratio.

Table 4.2: Mean performance of hybrids for different characters

Character	Plant Height (cm)	Panicle Length (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	Days to 50% Flowering	Effective Tillers/Plant	Filled Spikelets/Panicle	Unfilled Spikelets/Panicle	Pollen Fertility %	Spikelet Fertility %	1000 Grain Weight (g)	Grain Yield / Plant (g)	Biological Yield /Plant (g)
Parents	1	2	3	4	5	6	7	8	9	10	11	12	13
IR 58025 A													
IR 58025 A/ Ganga chur	95.8	22.55	27.59	1.16	102	7.63	41.73	81.27	19.41	33.46	21.63	3.42	32.87
IR 58025 A/ Luchai	137.3	25.33	34.03	1.39	108.67	7.37	88.07	122.53	74.42	41.86	21.19	14.59	60.83
IR 58025 A/ Pihu purple	112.24	27.16	29.95	1.33	94.67	7.17	51	61.2	18.22	44.5	25.69	4.62	48.13
IR 58025 A/ Bathras	88.46	22.99	29.29	1.35	90.67	8.33	28.73	75.53	24.86	28.34	21.59	4.09	30.7
IR 58025 A/ Pepri luchai	145.24	28.83	33.05	1.52	109.67	12	101.2	85.93	58.94	54.06	19.6	8.68	55.2
IR 58025 A/ Khura bal	121.44	25.29	33.55	1.35	100.33	9.57	52.1	97.13	38.22	34.83	22.08	4.5	38.67
IR 58025 A/ Sarojini	127.36	27.17	34.22	1.41	99.33	7.57	172.13	76.6	65.67	69.19	22.16	12.61	32.93
IR 58025 A/ Kera khadi	127.75	25.34	36.01	1.44	101	6.97	114.73	101.87	59.88	52.98	21.02	4.4	41.84
IR 58025 A/ Luchai red	141.24	27.96	33.51	1.53	106.33	8.7	74.93	170.8	16.73	30.75	16.52	6.74	42.93
IR 58025 A/ Lajni super- 1	91.13	24.46	32.21	1.05	100.33	10.5	47.66	110.93	83.75	29.83	18.5	4.38	43.23
Average	118.8	25.71	32.34	1.35	101.3	8.58	77.23	98.38	46.01	41.98	20.99	6.8	42.73
IR-79156A													
IR-79156A/ Ganga chur	93.12	23.89	34.79	1.14	102.33	7.97	23.27	114.07	13.79	16.71	18.66	1.97	44.9
IR-79156A/ Luchai	140.68	27.33	34.65	1.45	107.67	7.57	122.07	40.33	87.7	75.28	21.1	17.2	61.13
IR-79156A/ Pihu purple	93.73	24.37	32.11	1.3	96.33	8.6	41.73	65.13	14.66	39.04	24.03	5.15	28.93
IR-79156A/ Bathras	85.16	23.18	32.13	1.32	102.33	8	28.53	87.8	15.02	27.57	20.1	2.53	32.5
IR-79156A/ Pepri luchai	144.87	27.03	34.93	1.5	110	6.9	81.73	118.27	91.97	41.13	19.62	8.46	47.9
IR-79156A/ Khura bal	122.23	26.76	33.91	1.19	105.33	7.07	18.13	82.27	82.12	17.67	21.31	3.45	26.93
IR-79156A/ Sarojini	127.65	26.92	38.76	1.48	101.67	9.03	133.87	50.93	86.96	72.42	21.61	16.6	64.37
IR-79156A/ Kera khadi	137.79	25.73	34.37	1.33	108.33	8.8	128.27	59.87	64.19	65.01	18.6	8.18	51.87
IR-79156A/ Luchai red	138.23	27.81	33.38	1.51	107	7.9	56.73	168.73	23.24	24.96	18.51	5.88	62.93
IR-79156A/ Lajni super- 1	86.26	24.79	32.45	1.07	98.67	8.8	56.73	105.73	35.88	34.73	19.68	4.73	37.27
Average	116.97	25.79	34.15	1.33	103.97	8.06	69.11	89.31	51.55	41.45	20.32	7.42	45.87
IR 68888 A													
IR 68888 A/ Ganga chur	78.81	26.27	28.33	1.25	95	10.57	24.67	109.33	15.16	18.4	16.93	2.88	42.9
IR 68888 A/ Luchai	132.25	25.37	32.53	1.34	112.33	7.8	136.47	123.27	51.74	52.64	19.44	13.64	49.13
IR 68888 A/ Pihu purple	88.8	27.46	28.35	1.31	93	8.83	27.6	69.4	25.07	28.72	21.39	3.18	35.7
IR 68888 A/ Bathras	87.28	23.35	28.37	1.3	90.67	8.97	18.67	88.87	16.05	17.06	20.65	2.55	25.5
IR 68888 A/ Pepri luchai	139.69	27.73	34.92	1.64	110.33	9.63	51.87	169.33	75.4	22.99	22.77	6.16	66.6
IR 68888 A/ Khura bal	124.88	27.63	31.38	1.21	99.33	6.47	51.4	112.07	57.75	32.13	21.33	2.89	26.03
IR 68888 A/ Sarojini	128.37	26.86	28.39	1.22	99.67	8.27	136.93	58.87	93.23	69.93	22.03	13.86	32.03
IR 68888 A/ Kera khadi	136.2	27	29.85	1.35	98.67	6	176.07	94.93	39.21	64.93	20.23	9.18	43.93
IR 68888 A/ Luchai red	129.67	27.29	30.66	1.47	110	5.47	31.47	167.07	13.59	16.14	18.46	1.99	48.7
IR 68888 A/ Lajni super- 1	79.57	24.06	26.11	0.83	91.33	7.37	25.07	74.47	27.3	24.17	19.64	2.42	24.8
Average	112.55	26.3	29.89	1.29	100.03	7.94	68.02	106.76	41.45	34.71	20.28	5.87	39.53
Overall average	116.11	25.93	32.13	1.32	101.77	8.19	71.45	98.15	46.34	39.38	20.54	6.70	42.71
Lowest Range	78.81	22.55	26.11	0.83	90.67	5.47	23.27	40.33	13.59	16.14	16.52	1.97	24.80
Highest Range	145.24	28.83	38.76	1.64	112.33	10.57	176.07	169.33	93.23	75.28	25.69	17.20	66.60
Sem±	1.88	0.55	1.36	0.09	1.77	0.74	8.07	9.05	1.96	2.56	0.26	0.42	1.58
CD at 5%	5.28	1.54	3.83	0.26	4.97	2.08	22.67	25.42	5.51	7.20	0.73	1.18	4.43
CV%	2.80	3.74	7.60	11.87	2.98	15.14	15.97	19.18	6.14	9.07	2.12	8.17	6.59

Table 4.2: Mean performance of hybrids for different characters

Character	Harvest Index %	Kernal Length (mm)	Kernal Breadth (mm)	Kernal L/B Ratio	Cooked Rice Length (mm)	Cooked Rice Breadth (mm)	Cooked Rice L/B Ratio	Hulling %	Milling %	Head Rice Recovery %	Amylose Content %	Alkali spreading value	Gel consistency
Parents	14	15	16	17	18	19	20	21	22	23	24	25	26
IR 58025 A													
IR 58025 A/ Ganga chur	10.39	5.67	1.93	2.93	10.13	2.6	3.9	70.39	66.13	59.8	22.52	3	53.16
IR 58025 A/ Luchai	23.97	5.4	2.27	2.43	9.13	2.7	3.39	70.05	61.36	51.4	18.65	3	81.24
IR 58025 A/ Pihu purple	9.57	6.5	1.87	3.48	9.6	2.8	3.43	69.86	54.62	49.6	21.88	5	45.61
IR 58025 A/ Bathras	13.15	5.97	2.03	2.94	10.07	2.87	3.51	71.88	56.85	49.5	27.21	3	21.07
IR 58025 A/ Pepri luchai	15.75	5.67	1.93	2.93	9.2	2.63	3.5	74.12	65.73	60.1	16.66	3	22.32
IR 58025 A/ Khura bal	11.57	5	2	2.48	9.2	2.57	3.59	68.14	64.52	59.5	22.86	6	74.07
IR 58025 A/ Sarojini	38.29	6.57	1.93	3.4	10.5	2.77	3.8	78.39	75.59	70.6	20.74	3	55.14
IR 58025 A/ Kera khadi	10.51	5.67	2.07	2.74	9.17	2.63	3.48	71.19	62.13	57.5	18.58	2	24.46
IR 58025 A/ Luchai red	15.62	5.3	1.83	2.89	9.33	2.77	3.4	69.31	61.39	52.4	17.23	6	78.81
IR 58025 A/ Lajni super- 1	10.06	5.7	1.6	3.56	9.37	2.73	3.43	73.47	61.28	50.3	10.8	6	72.76
Average	15.89	5.74	1.94	2.98	9.57	2.7	3.54	71.68	62.96	56.1	19.71	4	52.86
IR-79156A													
IR-79156A/ Ganga chur	4.37	5.87	2.03	2.88	9.33	2.77	3.38	72.07	52.82	47.5	23.06	5	22.07
IR-79156A/ Luchai	28.13	6.77	1.97	3.44	9.17	3.17	2.9	77.49	72.23	64.2	14.99	6	39.54
IR-79156A/ Pihu purple	17.82	6.5	1.9	3.43	9.67	2.9	3.34	68.8	55.5	48.2	17.64	5	48.92
IR-79156A/ Bathras	7.79	5.8	2.1	2.77	9.77	2.87	3.41	73.37	68.85	61.2	22.52	5	35.26
IR-79156A/ Pepri luchai	17.67	5.5	1.83	3	9.37	2.77	3.39	75.51	66.42	60.1	24.91	6	41.74
IR-79156A/ Khura bal	12.76	5.8	1.83	3.16	9.87	2.8	3.52	72.55	51.29	43.3	17.81	5	57.96
IR-79156A/ Sarojini	25.78	6.13	1.8	3.41	8.97	2.67	3.36	63.47	58.48	54.2	16.53	3	82.66
IR-79156A/ Kera khadi	15.78	5.13	1.9	2.71	9.27	3.1	2.99	69.06	63.21	58.5	24.98	5	75.7
IR-79156A/ Luchai red	9.34	5.5	1.83	3	8.97	3.07	2.92	73.66	68.53	60.5	21.91	2	89.87
IR-79156A/ Lajni super- 1	12.69	5.77	1.57	3.68	8.73	2.63	3.32	73.82	61.87	57.2	25.11	3	75.5
Average	15.21	5.87	1.87	3.15	9.31	2.87	3.25	71.98	61.92	55.5	20.95	4.5	56.92
IR 68888 A													
IR 68888 A/ Ganga chur	6.65	5.63	1.93	2.91	8.77	3.03	2.89	70.73	64.05	53.1	26.66	6	23.42
IR 68888 A/ Luchai	27.75	5.57	1.87	2.98	9.77	2.77	3.54	76.96	71.67	63	22.39	5	45.11
IR 68888 A/ Pihu purple	8.92	6.13	1.87	3.29	9.87	2.9	3.41	59.57	55.05	43.1	26.02	4	23.3
IR 68888 A/ Bathras	9.98	6	2.07	2.9	9.83	2.93	3.36	68.41	65.13	52.5	19.56	5	32.26
IR 68888 A/ Pepri luchai	9.25	5.33	2.03	2.62	9.27	2.9	3.2	73.38	58.77	49.4	27.13	6	47.86
IR 68888 A/ Khura bal	11.17	5.5	1.87	2.95	9.27	2.6	3.57	65.55	53.25	44.9	12.79	6	42.9
IR 68888 A/ Sarojini	43.44	5.43	1.97	2.76	8.77	2.63	3.33	78.64	71.91	63.6	22.79	3	75.14
IR 68888 A/ Kera khadi	20.94	5.5	1.9	2.9	9.87	3.07	3.22	69.76	66.49	59.2	22.39	7	32.91
IR 68888 A/ Luchai red	4.08	5.6	1.87	3	8.7	2.87	3.04	71.2	70.6	62.9	27.81	4	61.86
IR 68888 A/ Lajni super- 1	9.85	5.4	1.53	3.53	9.07	2.8	3.24	72.83	62.83	50.8	30.27	5	82.83
Average	15.2	5.61	1.89	2.98	9.31	2.85	3.28	70.7	63.97	54.2	23.78	5.1	46.76
Overall average	15.43	5.74	1.90	3.04	9.40	2.81	3.36	71.45	62.95	55.27	21.48	4.49	52.18
Lowest Range	4.08	5.00	1.53	2.43	8.70	2.60	2.89	59.57	51.29	43.10	10.80	2.33	21.07
Highest Range	43.44	6.77	2.27	3.68	10.50	3.17	3.59	78.64	75.59	70.60	30.27	6.67	89.87
Sem±	1.41	0.15	0.06	0.10	0.18	0.06	0.10	0.41	0.58	0.65	0.31	0.31	0.54
CD at 5%	3.97	0.43	0.16	0.29	0.51	0.16	0.29	1.14	1.64	1.84	0.87	0.87	1.52
CV%	11.31	4.59	5.04	5.89	3.33	3.48	5.31	0.99	1.63	2.08	2.50	11.70	1.79

4.1.18. Cooked rice length

The mean of cooked rice length in parents, ranged from 8.13 mm (Sarojini) to 10.5 mm (Ganga chur) with an overall average of 9.24 mm. Among hybrids, Cooked rice length ranged from 8.7 mm (IR 68888 A/ Luchai red) to 10.5 (IR 58025 A/ Sarojini) with an overall mean of 9.40 mm. Among the entire cross combinations, four cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Khura bal, IR 68888 A/ Kera khadi and IR 68888 A/ Pihu purple were identified as good performing hybrids for cooked rice length.

4.1.19. Cooked rice breadth

The mean of cooked rice breadth in parents, ranged from 2.1 mm (Lajni super- 1) to 3 mm (Ganga chur) with an overall average of 2.60 mm. Among hybrids, Cooked rice breadth ranged from 2.6 mm (IR 58025 A/ Ganga chur) to 3.17 mm (IR-79156A/ Luchai) with an overall mean of 2.81 mm. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Bathras, IR-79156A/ Luchai, and IR 68888 A/ Kera khadi were identified as good performing hybrids for cooked rice breadth.

4.1.20. Cooked rice L/B ratio

The mean of cooked rice L/B ratio in parents, ranged from 3.05 (IR 68888 A) to 4.37 (Lajni super- 1) with an overall average of 3.59. Among hybrids, Cooked rice L/B ratio ranged from 2.89 (IR 68888 A/ Ganga chur) to 3.59 (IR 58025 A/ Khura bal) with an overall mean of 3.36. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Khura bal, IR-79156A/ Khura bal, and IR 68888 A/ Luchai were identified as high cooked rice L/B ratio.

Quality Characters

4.1.21. Hulling (%)

The mean of hulling percentage in parents ranged from 62.36% (Lajni super- 1) to 75.55% (Luchai red) with an overall parental mean of 72.58%. Among hybrids, hulling% ranged from 59.57% (IR 68888 A/ Pihu purple) to 78.64% (IR 68888 A/ Sarojini) with an overall mean of 71.45%. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Luchai and IR 68888 A/ Sarojini were identified as good performing hybrids for hulling %.

4.1.22. Milling (%)

The parental mean of milling percentage ranged from 33.03% (IR 68888 A) to 70.6% (Luchai) with an overall parental mean of 58.94%. Among hybrids, milling % ranged from 51.29% (IR-79156A/ Khura bal) to 75.59% (IR 58025 A/ Sarojini) with an overall mean of 62.95% . Among the entire cross combinations, three combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Luchai and IR 68888 A/ Sarojini were identified as good performing hybrids for milling%.

4.1.23. Head rice recovery (%)

The mean of head rice recovery (HRR) for parents ranged from 28.4% (IR 68888 A) to 60.7% (Pihu purple) with an overall parental mean of 52.40%. Among hybrids, head rice recovery ranged from 43.1% (IR 68888 A/ Pihu purple) to 70.6% (IR 58025 A/ Sarojini) with an overall mean of 55.27%. Among the entire cross combinations, three cross combinations *viz.*, IR 58025 A/ Sarojini, IR-79156A/ Luchai and IR 68888 A/ Sarojini were identified as good performing hybrids for head rice recovery.

4.1.24 Amylose Content

The mean of amylose content ranged from 11.55% (Pihu purple) to 30.23% (Bathras) with an average parental value of 19.96%. Among hybrids, Amylose% ranged from 10.8% (IR 58025 A/ Lajni super- 1) to 30.27% (IR 68888 A/ Lajni super- 1) with an overall mean of 21.48%. Genotypes having intermediate Amylose content (20-25%) have considered as good genotype and are presented in Table 4.3.

4.1.16 Alkali spreading value/ Gelatinization temperature

“The general mean of Alkali spreading value/gelatinization temperature for parents ranged from 2.66 (Sarojini) to 7.00 (IR 79156 A) with an average parental mean of 4.69. Among hybrids, the scoring of alkali spreading value and gelatinization temperature ranged from 2.33 (IR-79156A/ Luchai red) to 6.67 (IR 68888 A/ Kera khadi) with an overall scoring mean of 4.49. The good quality rice grains have intermediate alkali spreading value of (4-5). Genotypes, having an intermediate alkali spreading value are presented in Table 4.4. The classification and spreading scale for scoring of alkali spreading value and gelatinization temperature is given in Appendix F”.

Table 4.3 Different crosses showing their amylose percent

Classification	Amylose (%)	Hybrids
Waxy	1-2%	None
Very low	2-9%	None
Low	9-20%	IR 58025 A/ Luchai, IR 58025 A/ Pepri luchai, IR 58025 A/ Kera khadi, IR 58025 A/ Luchai red, IR 58025 A/ Lajni super- 1, IR-79156A/ Luchai, IR-79156A/ Pihu purple, IR-79156A/ Khura bal, IR-79156A/ Sarojini, IR 68888 A/ Bathras, IR 68888 A/ Khura bal,
Intermediate	20-25%	IR 58025 A/ Ganga chur, IR 58025 A/ Pihu purple, IR 58025 A/ Khura bal, IR 58025 A/ Sarojini, IR-79156A/ Ganga chur, IR-79156A/ Bathras, IR-79156A/ Pepri luchai, IR-79156A/ Kera khadi, IR-79156A/ Luchai red, IR-79156A/ Lajni super- 1 IR 68888 A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Kera khadi,
High	25-33%	IR 58025 A/ Bathras, IR 68888 A/ Ganga chur, IR 68888 A/ Pihu purple, IR 68888 A/ Pepri luchai, IR 68888 A/ Luchai red, IR 68888 A/ Lajni super- 1

4.1.26 Gel Consistency

Mean value of Gel Consistency for parents ranged from 31.81 mm (IR 79156 A) to 87.91 mm (Khura bal) with an overall parental average of 52.66 mm. Among hybrids, gel consistency ranged from 21.07 mm (IR 58025 A/ Bathras) to 89.87 mm (IR-79156A/ Luchai red) with an overall mean of 52.18 mm. The good genotype of rice contains 40-60 mm gel consistency. The crosses IR 58025 A/ Ganga chur, IR 58025 A/ Pihu purple, IR 58025 A/ Sarojini, IR-79156A/ Pihu purple, IR-79156A/ Pepri luchai, IR-79156A/ Khura bal, IR 68888 A/ Luchai, IR 68888 A/ Pepri luchai and IR 68888 A/ Khura bal containing the intermediate gel consistency value.

Table 4.4 Classification of hybrids on the basis of ASV and GT

Classification	Alkali spreading value (ASV)	Gelatinization temperature (GT)	Hybrids
1-2	Low	High > 74°C	IR 58025 A/ Kera khadi, IR-79156A/ Luchai red
3	Low, Intermediate	High, Intermediate	IR 58025 A/ Ganga chur, IR 58025 A/ Luchai, IR 58025 A/ Bathras, IR 58025 A/ Pepri luchai, IR 58025 A/ Sarojini, IR-79156A/ Sarojini, IR-79156A/ Lajni super- 1, IR 68888 A/ Sarojini
4-5	Intermediate	Intermediate (70-74°C)	IR 58025 A/ Pihu purple, IR-79156A/ Ganga chur, IR-79156A/ Pihu purple, IR-79156A/ Bathras, IR-79156A/ Khura bal, IR-79156A/ Kera khadi, IR 68888 A/ Luchai, IR 68888 A/ Pihu purple, IR 68888 A/ Bathras, IR 68888 A/ Luchai red, IR 68888 A/ Lajni super- 1
6-7	High	Low (50-69°C)	IR 58025 A/ Khura bal, IR 58025 A/ Luchai red, IR 58025 A/ Lajni super- 1, IR-79156A/ Luchai, IR-79156A/ Pepri luchai, IR 68888 A/ Ganga chur, IR 68888 A/ Pepri luchai, IR 68888 A/ Khura bal, IR 68888 A/ Kera khadi

4.2 Analysis of variance (ANOVA) for R.B.D.

The analysis of variance (ANOVA) was performed in randomized complete block design (RBD) for 47 genotypes and the results are presented in Table 4.5. The analysis of variance (ANOVA) revealed the presence of highly significant differences among all the characters of rice taken under study. This indicates the existence of ample amount of variability among rice hybrids/genotypes for studied traits. Therefore, there is good opportunity to select the traits having good grain quality.

4.3 Combining ability

Data recorded on 30 hybrids, 3 lines and 10 testers was used for combining ability analysis using line x tester design proposed by Kempthorne (1957). The results of analysis are discussed under the following subheads:

4.3.1 ANOVA for line x tester

4.3.2 Combining ability analysis for GCA and SCA effects

4.3.1 Analysis of variance (ANOVA) for Line x Tester

The analysis of variance for combining ability of all the traits under study has been presented in the Table 4.6. The variance due to treatments was highly significant for all the characters under study. The variance due to parents was highly significant for all the characters under study except flag leaf breadth. The variance due to hybrids was also found highly significant for all of the characters. The variance due to parent vs. hybrids was also found highly significant for all of the characters. The variance due to lines was found significant for most of the traits under study except flag leaf breadth, effective tillers per plant, pollen fertility, 1000 grain weight, filled spikelets per panicle, grain yield per plant, biological yield and harvest index kernel length, kernel breadth, kernel L/B ratio, cooked rice length, alkali spreading value. The variance due to testers was found highly significant for all characters except flag leaf breadth. The variance due to line x tester was recorded highly significant for all the characters except flag leaf length, flag leaf breadth, biological yield/ plant and cooked rice L/B ratio. This suggested that sufficient variability is available in the material used for study.

Similar finding have been reported by “Saleem *et al.* (2010), Jarwar *et al.* (2012) for treatments, parents, parents vs. crosses and hybrids, Saidaiah *et al.* (2010) for treatments, parents, parents vs. crosses, Veerasha *et al.* (2013) for treatments and hybrids and testers except panicle length and lines vs. testers and Ghara *et al.* (2012), Shiva Prasad *et al.* (2013), Srikrishna Latha *et al.* (2013) for treatments, hybrids, testers and line x tester, Ghara *et al.* (2014) and Gahtyari *et al.* (2017) for genotypes, crosses, lines, testers and line x tester interactions for tiller number, plant height, days to 50% flowering, panicle length, number of spikelet per panicle, spikelet fertility and grain yield traits”.

4.3.2 Combining ability analysis for GCA and SCA effects

“The GCA effects of thirteen parentages *i.e.*, three lines and ten testers and the SCA effects of thirty hybrids combinations estimated according to procedure described by Kempthorne (1957, L x T mating design) and Singh and Chaudhary, (1985). The estimates of general combining ability (GCA) effects of lines and testers are presented in Table 4.7 and specific combining ability (SCA) effects of hybrids for different characters are presented in Table 4.8”. Character wise results of combining ability effects described below:

Quantitative characters

4.3.2.1 Plant height (cm)

Among the lines, IR 68888A (-3.55) showed negative highly significant GCA effect. Among the testers, Lajni super- 1 (-30.45), Bathras (-29.14), Ganga chur (-26.86), and Pihu purple (-17.85) showed negative highly significant GCA effects. Negative effects of these lines indicate their usefulness in breeding of developing dwarf and semi dwarf hybrids. The line IR 68888A and tester Lajni super- 1, Bathras, Ganga chur and Pihu purple were registered the good general combiners for plant height towards dwarfness.

Among the thirty hybrids, seven hybrids have shown significant SCA effects. Three hybrids have shown the positive significant SCA effects and four hybrids have shown the negative significant SCA effects. The highest negative significant SCA effects have shown by cross IR 58025 A/ Kera khadi (-8.85) followed by IR 68888 A/ Ganga chur (-6.88), IR 68888 A/ Pihu purple (-5.90) and IR 79156 A/ Pihu purple (-5.39).

GCA variance was higher than SCA variance indicating the additive gene action, therefore normal selection method is appropriate for this trait. Similar results also reported by El-Rewainy *et al.* (2011), Ghara, *et al.* (2012), Hasan *et al.* (2013) and Ali *et al.* (2017).

4.3.2.2 Penicle length (cm)

Among the parents, IR 68888A (0.37) shown significant positive GCA effects and in testers Pepri Luchai (27.16) showed positive highly significant GCA effect. Among the hybrids, IR 68888 A/ Ganga chur (1.66) have showed positive

significant SCA effect followed by IR 79156 A/ Luchai (1.47), IR 58025 A/ Pepri luchai (1.19) and IR 58025 A/ Pihu purple (1.05).

SCA variance was higher than GCA variance therefore heterosis breeding is appropriate for this trait. Similar results also reported by Zhu *et al.* (2009) and Ali *et al.* (2017).

4.3.2.3 Flag leaf length (cm)

Among the lines, IR 79156A (2.02) showed positive significant GCA effect. Among the testers, Pepri Luchai (2.17), Sarojini (1.66), Luchai (1.61) showed highly positive significant GCA effect.

Among the crosses, only four hybrids showed significant SCA effect. IR 79156 A/ Sarojini (2.95), IR 68888 A/ Pepri luchai (2.86) and IR 79156 A/ Ganga chur (2.53) showed positive significant SCA effect while only one hybrid, IR 68888 A/ Sarojini (-3.16) showed negative significant SCA effect.

4.3.2.4 Flag leaf width (cm)

Among the parents, none of the genotypes showed significant GCA effect.

Similarly among the hybrids, none of the hybrids has showed significant SCA effect.

4.3.2.5 Days to 50% flowering

Among the lines, IR 68888A (-1.73) showed negative highly significant effect. Among the testers, Bathras (-7.21), Pihu purple (-7.10) and Lajni super- 1 (-4.99) showed negative highly significant GCA effects. The negative GCA effects indicate their usefulness in breeding for early maturity.

Among the thirty hybrids, three hybrids have shown highly significant SCA effects. Two hybrids have shown the positive highly significant SCA effects and one hybrids have shown the negative highly significant SCA effects. The negative significant SCA effects have shown by cross IR 79156 A/ Luchai (-4.09). Negative values indicate that these are good combinations for early flowering.

SCA variance was higher than GCA variance resulting the presence of non additive gene action as the indicator of heterosis breeding for improvement

Table No. 4.5 Analysis of Variance for RBD

Source of Variations	df	Mean Squares							
		Plant Height (cm)	Panicle Length (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	Days to 50% Flowering	Effective Tillers/Plant	Filled Spikelets/Panicle	Unfilled Spikelets/Panicle
Replications	2	91.6700	2.0873	2.4167	0.0106	10.6453	40.2460	190.5962	446.8462
Treatments	46	1387.4500**	11.8955**	32.4886**	0.0767**	141.7163**	7.5594**	9634.2880**	4761.5620**
Error	92	10.6019	0.9070	5.5640	0.0263	9.3772	1.6414	195.4645	245.7422

Source of Variations	df	Mean Squares								
		Pollen Fertility %	Spikelet Fertility %	1000 Grain Weight (g)	Grain Yield/Plant (g)	Biological Yield/Plant (g)	Harvest Index %	Kernal Length (mm)	Kernal Breadth (mm)	Kernal L/B Ratio
Replications	2	35.0056	98.6181	1.3033	10.2733	59.7981	27.7063	0.1653	0.0094	0.0106
Treatments	46	3222.9600**	1723.2020**	47.8546**	93.8238**	388.6983**	505.1701**	0.6740**	0.1224**	0.4896**
Error	92	11.5356	19.7043	0.2000	0.5263	7.4672	5.9803	0.0698	0.0093	0.0319

Source of Variations	df	Mean Squares								
		Cooked Rice Length (mm)	Cooked Rice Breadth (mm)	Cooked Rice L/B Ratio	Hulling %	Milling%	Head Rice Recovery %	Amylose Content %	Alkali spreading value	Gel consistency
Replications	2	0.1368	0.0456	0.0206	1.1811	1.8673	20.7207	6.9204	2.3617	2.4297
Treatments	46	0.8838**	0.1904**	0.3272**	51.8388**	169.9155**	167.2262**	72.1785**	5.3179**	1303.9840**
Error	92	0.0976	0.0093	0.0325	0.4952	1.0239	1.2844	0.2867	0.2892	0.8779

Table No. 4.6 ANOVA for LxT

	df	Plant height (cm)	Penicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Days to 50 % flowering	Effective tillers per plant	Filled spikelet per penicle	Unfilled spikelet per penicle	pollen fertility percent
Characters		1	2	3	4	5	6	7	8	9
Replicates	2	89.007	2.251	1.338	0.024	9.171	39.056	119.724	545.534	37.279
Treatment	42	1510.973**	12.175**	32.468**	0.083**	147.649**	7.575**	9687.162**	4636.912**	3034.639**
Parents	12	1435.814**	11.906**	28.062**	0.047	213.137**	11.729**	13751.901**	2679.714**	4040.429**
Parents (Lines)	2	415.746**	4.999**	20.469*	0.029	69.444**	0.468	405.671	1279.165**	0.00
Parents (Testers)	9	1012.759**	9.939**	31.002**	0.049	237.352**	10.204**	8037.431**	1294.804**	113.898**
Parents (L vs T)	1	7283.443**	43.421**	16.787	0.057	282.585**	47.967**	91874.588**	17944.998**	47460.068**
Crosses	29	1594.069**	8.872**	25.387**	0.086**	120.854**	5.775**	6854.186**	3807.359**	2439.717**
Parents vs Crosses	1	3.077**	111.194**	290.671**	0.422**	138.848**	9.933**	43066.595**	52180.357**	8217.892**
Line Effect	2	309.289**	3.173**	137.08**	0.028	120.933**	3.484	759.925**	2284.05**	768.164**
Tester Effect	9	4890.473**	21.215**	28.428**	0.237**	299.048**	4.77*	19337.376**	8454.173**	6201.338**
Line * Tester Effect	18	88.621**	3.333**	11.456*	0.018	31.748**	6.532**	1289.73**	1653.208**	744.635**
Error	84	11.379	0.529	5.932	0.027	9.504	1.71	193.926	259.48	12.518
Total	128	504.645969	2.264305	14.56745	0.04543	54.82752	4.217641	3307.73471	1700.29481	1004.53861

*Significant at p=0.05% level, **Significant at p=0.01% level

cont.

Table No. 4.6 ANOVA for LxT

Characters	df	Spikelet fertility percent	1000 grain weight	Grain yield per plant	Biological yield per plant	Harvest index (%)	Kernel length (mm)	Kernel width (mm)	Kernel L/B ratio	Cooked rice length (mm)
		10	11	12	13	14	15	16	17	18
Replicates	2	129.683	1.329	12.416	61.852	39.874	0.164	0.0108	0.014	0.124
Treatment	42	1652.671**	38.256**	77.654**	405.666**	420.328**	0.626**	0.1266**	0.5**	0.829**
Parents	12	2035.129**	105.626**	70.932**	247.799**	354.474**	0.865**	0.2712**	0.959**	1.354**
Parents (Lines)	2	80.757*	0.139	4.625**	26.047*	19.71*	0.071	0.03	0.083	0.534
Parents (Testers)	9	170.169**	138.582**	44.758**	324.495**	105.651**	0.918**	0.1727**	0.213**	1.619**
Parents (L vs T)	1	22728.507**	19.997**	439.11**	1.039	3263.41**	1.977**	1.6397**	9.423**	0.605*
Crosses	29	1030.959**	11.494**	63.568**	463.569**	266.044**	0.543**	0.0698**	0.325**	0.617**
Parents vs Crosses	1	15092.799**	5.919**	566.806**	620.879**	5684.81**	0.161**	0.0364**	0.057**	0.699**
Line Effect	2	492.644**	4.814**	18.064**	301.456**	4.631	0.534**	0.0414*	0.283**	0.661**
Tester Effect	9	2694.456**	24.529**	186.89**	896.094**	715.818**	0.896**	0.1687**	0.648**	0.635**
Line * Tester Effect	18	259.024**	5.718**	6.963**	265.319**	70.203**	0.368**	0.0235**	0.169**	0.603**
Error	84	18.915	0.191	0.509	7.885	5.962	0.075	0.0099	0.034	0.106
Total	128	556.721906	12.6988	26.00808	139.2503	142.456	0.257414	0.0481953	0.1865625	0.34361719

*Significant at p=0.05% level, **Significant at p=0.01% level

cont.

Table No. 4.6 ANOVA for LxT

	df	Cooked rice width (mm)	Cooked rice L/B ratio	Hulling percent	Milling Percent	Head rice recovery percent	Amylose content (%)	Alkali spreading value	Gel consistency
Characters		19	20	21	22	23	24	25	26
Replicates	2	0.035	0.014	1.261	2.836	18.675	5.329	2.566	4.019
Treatment	42	0.157**	0.311**	54.859**	179.69**	177.191**	71.768**	5.443**	1386.789**
Parents	12	0.262**	0.559**	57.846**	297.439**	257.459**	90.128**	6.526**	1294.788**
Parents (Lines)	2	0.308**	1.202**	48.082**	506.973**	469.66**	11.95**	0.778	1680.768**
Parents (Testers)	9	0.27**	0.474**	63.786**	128.338**	119.151**	115.149**	4.015**	1287.94**
Parents (L vs T)	1	0.098**	0.036	23.92**	1400.281**	1077.834**	21.292**	40.619**	584.462**
Crosses	29	0.079**	0.17**	51.932**	122.239**	142.391**	64.482**	5.143**	1472.46**
Parents vs Crosses	1	1.171**	1.452**	103.891**	432.778**	223.176**	62.728**	1.126**	6.347**
Line Effect	2	0.244**	0.765**	13.268**	31.656**	25.871**	130.653**	9.411**	784.908**
Tester Effect	9	0.086**	0.149**	66.127**	190.088**	212.921**	36.191**	3.758**	2961.166**
Line * Tester Effect	18	0.057**	0.114**	49.131**	98.38**	120.073**	71.275**	5.362**	804.502**
Error	84	0.01	0.035	0.541	1.012	1.315	0.293	0.264	0.853
Total	128	0.0586	0.1255	18.3750	59.6691	59.2955	23.8243	1.9993	455.6626

*Significant at p=0.05% level, **Significant at p=0.01% level

of this trait. Similar results also reported by Sharma *et al.* (2012), Ghara, *et al.* (2012), Hasan *et al.* (2013), Dharwal *et al.* (2017) and Ramesh *et al.* (2018).

4.3.2.6 Productive tillers per plant

Among the lines none of them shown significant GCA effects whereas; among testers Pepri Luchai (1.32) and Kera khadi (-0.94) shown the positive and negative GCA effects respectively.

Among the thirty hybrids, five hybrids shown significant SCA effect. Three hybrids, IR 58025 A/ Pepri luchai (2.10), IR 68888 A/ Ganga chur (2.10) and IR 79156 A/ Kera khadi (1.67) shown positive significant SCA effect whereas IR 79156 A/ Pepri luchai (-2.48) and IR 68888 A/ Luchai red (-1.63) shown negative significant SCA effect.

Similar results also reported by Narasimman *et al.* (2007), Wang *et al.* (2009), Kumar *et al.* (2010), Satheesh *et al.* (2010), Sharma *et al.* (2012) and Ghara, *et al.* (2012) and Kishor *et al.* (2017).

4.3.2.7 Filled spikelets per panicle

Among the lines, IR 58025A (5.78) showed positive significant GCA effect. Among the testers, Sarojini (76.19), Kera khadi (68.24) and Luchai (44.08) showed positive highly significant GCA effects. The line IR 58025A and testers Sarojini, Kera khadi and Luchai were recorded good general combiners for fertile spikelets per panicle. The testers Ganga chur (-41.56), Pihu purple (-31.34), Khura bal (-30.91), Lajni super- 1 (-28.30) and Luchai red (-17.07) were recorded negative significant GCA effect, indicating their use in developing of new maintainers.

Among the hybrids, thirteen hybrids have shown significant SCA effects. Three hybrids have shown the positive highly significant SCA effects, four has shown positive significant SCA effects and five hybrid has shown the highly significant negative SCA effects and only one hybrid shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 68888 A/ Kera khadi (39.81) followed by IR 68888 A/ Luchai (24.37) and CRMS 332A/ Kadamphool (18.71).

GCA variance was higher than SCA variance hence normal selection method should be rewarded for improvement of such traits. Similar results were also

supported by Sao and Motiramani (2006), Mirarab *et al.* (2011) and Tiwari *et al.* (2011) and Ramesh *et al.* (2018).

4.3.2.8 Unfilled spikelets per panicle

Among the lines, IR 79156A (-10.63) showed highly negative significant GCA effect. Among the testers, Kera khadi (-14.39) showed negative significant while Sarojini (-37.81), Pihu purple (-16.75) and Bathras (-15.88) showed negative highly significant GCA effects. Parents, IR 79156A, Kera khadi, Sarojini, Pihu purple and Bathras were identified good general combiners and may be useful for developing new hybrid for less number of sterile spikelets per panicle.

Among the hybrids, nine hybrids have shown significant SCA effects. Three hybrids have shown the positive highly significant SCA effects, two have positive significant SCA effects while three hybrids have shown the negative highly significant SCA effects and one have negative significant SCA effects. The highest negative significant SCA effect has shown by cross IR 79156 A/ Luchai (-44.41) followed by IR 58025 A/ Pepri luchai (-37.01), IR 68888 A/ Lajni super- 1 (-34.78) and IR 58025 A/ Pihu purple (-20.43). These hybrids were recorded as best specific combiners for less number of sterile spikelets per panicle.

The SCA variance was found higher than the GCA variance, indicating the role of non-additive gene action and heterosis breeding. The present finding had also been supported by Jayashudha and Sharma (2009) and El-Rewainy *et al.* (2011) and Ramesh *et al.* (2018).

4.3.2.9 Pollen fertility percentage

The line IR 79156A (5.22) showed positive highly significant GCA effect. Among the testers, highly significant positive GCA effects shown by Sarojini (35.62), Pepri Luchai (29.10) Luchai (24.95), Khura bal (13.03) and Kera khadi (8.09) and these testers were identified as good general combiners for the trait and further used for developing new restorer line and hybrids. Whereas the line IR 68888A (-4.89) and testers, Ganga chur (-30.22), Luchai red (-28.49), Bathras (-27.69) and Pihu purple (-27.02) have shown highly negative GCA effect and these can be used in breeding program for developing new maintainers.

Among the hybrids, nineteen hybrids have shown significant SCA effect in which nine have shown positive whereas ten showed negative SCA effects.

Table 4.7 General combining ability effects of parents for different characters

Characters	Plant height (cm)	Penicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Days to 50 % flowering	Effective tillers per plant	Filled spikelet per penicle	Unfilled spikelet per penicle	pollen fertility percent
	1	2	3	4	5	6	7	8	9
IR 58025A	2.69 **	-0.22	0.22	0.03	-0.47	0.39	5.78 *	-1.57	-0.33
IR 79156A	0.87	-0.15	2.02 **	0.01	2.20 **	-0.13	-2.35	-10.63 **	5.22 **
IR 68888A	-3.55 **	0.37 **	-2.24 **	-0.03	-1.73 **	-0.26	-3.43	12.20 **	-4.89 **
Ganga chur	-26.86 **	-1.69 **	-1.89 *	-0.14 **	-1.99	0.53	-41.56 **	1.61	-30.22 **
Luchai	20.64 **	0.08	1.61 *	0.07	7.79 **	-0.62	44.08 **	-4.57	24.95 **
Pihu purple	-17.85 **	0.4	-1.99 **	-0.01	-7.10 **	0.01	-31.34 **	-16.75 **	-27.02 **
Bathras	-29.14 **	-2.76 **	-2.20 **	0	-7.21 **	0.24	-46.14 **	-15.88 **	-27.69 **
Pepri Luchai	27.16 **	1.94 **	2.17 **	0.23 **	8.23 **	1.32 **	6.81	24.56 **	29.10 **
Khura bal	6.74 **	0.63 *	0.82	-0.08	-0.1	-0.49	-30.91 **	-2.79	13.03 **
Sarojini	11.69 **	1.05 **	1.66 *	0.05	-1.54	0.1	76.19 **	-37.81 **	35.62 **
Kera khadi	17.81 **	0.09	1.29	0.05	0.9	-0.94 *	68.24 **	-14.39 *	8.09 **
Luchai red	20.28 **	1.76 **	0.39	0.18 **	6.01 **	-0.84	-17.07 **	68.92 **	-28.49 **
Lajni super- 1	-30.45 **	-1.49 **	-1.87 *	-0.34 **	-4.99 **	0.7	-28.30 **	-2.9	2.64

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.7 General combining ability effects of parents for different characters

Characters	Spikelet fertility percent	1000 grain weight	Grain yield per plant	Biological yield per plant	Harvest index (%)	Kernel length (mm)	Kernel width (mm)	Kernel L/B ratio	Cooked rice length (mm)
	10	11	12	13	14	15	16	17	18
IR 58025A	2.60 **	0.46 **	0.10	0.02	0.45	0.01	0.04 *	-0.06	0.17 **
IR 79156A	2.07 **	-0.21 *	0.72 **	3.16 **	-0.22	0.13 *	-0.03	0.11 **	-0.09
IR 68888A	-4.67 **	-0.25 **	-0.82 **	-3.18 **	-0.23	-0.13 *	-0.01	-0.05	-0.08
Ganga chur	-16.52 **	-1.46 **	-3.94 **	-2.49 **	-8.30 **	-0.02	0.06	-0.13	0.01
Luchai	17.21 **	0.04	8.45 **	14.32 **	11.18 **	0.17	0.13 **	-0.09	-0.04
Pihu purple	-1.96	3.17 **	-2.38 **	-5.12 **	-3.33 **	0.63 **	-0.03	0.36 **	0.31 **
Bathras	-15.05 **	0.24	-3.64 **	-13.15 **	-5.13 **	0.18	0.16 **	-0.17 *	0.49 **
Pepri Luchai	0.01	0.13	1.07 **	13.85 **	-1.21 *	-0.24 *	0.03	-0.18 **	-0.12
Khura bal	-11.17 **	1.04 **	-3.08 **	-12.17 **	-3.60 **	-0.31 **	0.01	-0.17 **	0.05
Sarojini	31.13 **	1.40 **	7.66 **	0.40	20.40 **	0.30 **	0.01	0.15 *	0.01
Kera khadi	21.59 **	-0.59 **	0.56 *	3.17 **	0.31	-0.31 **	0.05	-0.26 **	0.03
Luchai red	-15.43 **	-2.70 **	-1.83 **	8.81 **	-5.75 **	-0.28 **	-0.06	-0.07	-0.40 **
Lajni super- 1	-9.80 **	-1.26 **	-2.86 **	-7.61 **	-4.57 **	-0.12	-0.34 **	0.55 **	-0.34 **

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.7 General combining ability effects of parents for different characters

Characters	Cooked rice width (mm)	Cooked rice L/B ratio	Hulling percent	Milling Percent	Head rice recovery percent	Amylose content (%)	Alkali spreading value	Gel consistency
	19	20	21	22	23	24	25	26
IR 58025A	2.60 **	0.46 **	0.10	0.02	0.45	0.01	0.04 *	-0.06
IR 79156A	2.07 **	-0.21 *	0.72 **	3.16 **	-0.22	0.13 *	-0.03	0.11 **
IR 68888A	-4.67 **	-0.25 **	-0.82 **	-3.18 **	-0.23	-0.13 *	-0.01	-0.05
Ganga chur	-16.52 **	-1.46 **	-3.94 **	-2.49 **	-8.30 **	-0.02	0.06	-0.13
Luchai	17.21 **	0.04	8.45 **	14.32 **	11.18 **	0.17	0.13 **	-0.09
Pihu purple	-1.96	3.17 **	-2.38 **	-5.12 **	-3.33 **	0.63 **	-0.03	0.36 **
Bathras	-15.05 **	0.24	-3.64 **	-13.15 **	-5.13 **	0.18	0.16 **	-0.17 *
Pepri Luchai	0.01	0.13	1.07 **	13.85 **	-1.21 *	-0.24 *	0.03	-0.18 **
Khura bal	-11.17 **	1.04 **	-3.08 **	-12.17 **	-3.60 **	-0.31 **	0.01	-0.17 **
Sarojini	31.13 **	1.40 **	7.66 **	0.40	20.40 **	0.30 **	0.01	0.15 *
Kera khadi	21.59 **	-0.59 **	0.56 *	3.17 **	0.31	-0.31 **	0.05	-0.26 **
Luchai red	-15.43 **	-2.70 **	-1.83 **	8.81 **	-5.75 **	-0.28 **	-0.06	-0.07
Lajni super- 1	-9.80 **	-1.26 **	-2.86 **	-7.61 **	-4.57 **	-0.12	-0.34 **	0.55 **

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.8 Specific Combining Ability Effects of Hybrids for Different Characters

	Plant height (cm)	Penicle length (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Days to 50 % flowering	Effective tillers per plant	Filled spikelet per penicle	Unfilled spikelet per penicle	pollen fertility percent
	1	2	3	4	5	6	7	8	9
IR 58025 A/ Ganga chur	3.87	-1.47 **	-2.86	-0.05	2.69	-1.48	6.07	-18.72	3.62
IR 58025 A/ Luchai	-2.13	-0.46	0.08	-0.03	-0.42	-0.6	-33.24 **	28.72 **	3.46
IR 58025 A/ Pihu purple	11.29 **	1.05 *	-0.4	-0.01	0.47	-1.42	5.11	-20.43 *	-0.76
IR 58025 A/ Bathras	-1.2	0.04	-0.86	0.01	-3.42	-0.49	-2.36	-6.97	6.55 **
IR 58025 A/ Pepri luchai	-0.72	1.19 **	-1.47	-0.06	0.13	2.10 *	17.16 *	-37.01 **	-16.17 **
IR 58025 A/ Khura bal	-4.1	-1.04 *	0.39	0.07	-0.87	1.48	5.78	1.54	-20.82 **
IR 58025 A/ Sarojini	-3.12	0.41	0.22	0.01	-0.42	-1.11	18.71 **	16.03	-15.96 **
IR 58025 A/ Kera khadi	-8.85 **	-0.46	2.39	0.04	-1.2	-0.68	-30.73 **	17.88	5.78 *
IR 58025 A/ Luchai red	2.17	0.5	0.78	0.01	-0.98	0.96	14.78 *	3.5	-0.79
IR 58025 A/ Lajni super- 1	2.79	0.24	1.74	0.04	4.02	1.22	-1.27	15.46	35.10 **
IR 79156 A/ Ganga chur	3.01	-0.19	2.53 *	-0.05	0.36	-0.63	-4.28	23.14 *	-7.54 **
IR 79156 A/ Luchai	3.07	1.47 **	-1.11	0.05	-4.09 *	0.12	8.88	-44.41 **	11.20 **
IR 79156 A/ Pihu purple	-5.39 *	-1.81 **	-0.05	-0.02	-0.53	0.53	3.97	-7.43	-9.87 **
IR 79156 A/ Bathras	-2.67	0.16	0.18	-0.01	5.58 **	-0.3	5.57	14.37	-8.84 **
IR 79156 A/ Pepri luchai	0.74	-0.68	-1.39	-0.06	-2.2	-2.48 **	5.81	4.39	11.32 **
IR 79156 A/ Khura bal	-1.49	0.35	-1.06	-0.07	1.47	-0.5	-20.07 **	-4.26	17.54 **
IR 79156 A/ Sarojini	-1.01	0.09	2.95 *	0.11	-0.76	0.87	-11.43	-0.57	-0.21
IR 79156 A/ Kera khadi	3.01	-0.15	-1.07	-0.05	3.47	1.67 *	-9.08	-15.06	4.55
IR 79156 A/ Luchai red	0.99	0.27	-1.16	0.01	-2.98	0.67	4.7	10.5	0.17
IR 79156 A/ Lajni super- 1	-0.26	0.51	0.17	0.09	-0.31	0.04	15.92 *	19.32 *	-18.31 **
IR 68888 A/ Ganga chur	-6.88 **	1.66 **	0.33	0.1	-3.04	2.10 *	-1.79	-4.42	3.93
IR 68888 A/ Luchai	-0.94	-1.01 *	1.03	-0.02	4.51 *	0.48	24.37 **	15.69	-14.66 **
IR 68888 A/ Pihu purple	-5.90 **	0.76	0.46	0.03	0.07	0.89	-9.08	27.87 **	10.64 **
IR 68888 A/ Bathras	3.87	-0.19	0.68	0.01	-2.16	0.79	-3.21	-7.4	2.29
IR 68888 A/ Pepri luchai	-0.03	-0.51	2.86 *	0.12	2.07	0.38	-22.97 **	32.62 **	4.85 *
IR 68888 A/ Khura bal	5.59 *	0.69	0.67	-0.01	-0.6	-0.98	14.29 *	2.71	3.28
IR 68888 A/ Sarojini	4.13	-0.49	-3.16 *	-0.12	1.18	0.23	-7.28	-15.47	16.17 **
IR 68888 A/ Kera khadi	5.84 **	0.61	-1.32	0.01	-2.27	-1	39.81 **	-2.82	-10.33 **
IR 68888 A/ Luchai red	-3.15	-0.77	0.38	0.01	3.96	-1.63 *	-19.48 **	-14	0.62
IR 68888 A/ Lajni super- 1	-2.53	-0.75	-1.91	-0.12	-3.71	-1.27	-14.66 *	-34.78 **	-16.79 **

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.8 Specific Combining Ability Effects of Hybrids for Different Characters

	pollen fertility percent	Spikelet fertility percent	1000 grain weight	Grain yield per plant	Biological yield per plant	Harvest index (%)	Kernel length (mm)	Kernel width (mm)	Kernel L/B ratio	Cooked rice length (mm)
	9	10	11	12	13	14	15	16	17	18
IR 58025 A/ Ganga chur	3.62	8.01 **	2.09 **	0.56	-7.38 **	2.80 **	-0.06	-0.08	0.08	0.55 **
IR 58025 A/ Luchai	3.46	-17.33 **	0.15	-0.66	3.78 **	-3.11 **	-0.51 **	0.19 **	-0.47 **	-0.39 *
IR 58025 A/ Pihu purple	-0.76	4.48	1.53 **	0.2	10.52 **	-2.99 **	0.12	-0.05	0.14	-0.28
IR 58025 A/ Bathras	6.55 **	1.42	0.35	0.93 *	1.11	2.39 *	0.04	-0.08	0.13	0.01
IR 58025 A/ Pepri luchai	-16.17 **	12.06 **	-1.53 **	0.81 *	-1.39	1.07	0.17	-0.04	0.14	-0.25
IR 58025 A/ Khura bal	-20.82 **	4.02	0.04	0.78 *	8.10 **	-0.72	-0.43 *	0.06	-0.33 **	-0.42 *
IR 58025 A/ Sarojini	-15.96 **	-3.92	-0.24	-1.85 **	-10.20 **	2.00 *	0.52 **	-0.01	0.26 *	0.92 **
IR 58025 A/ Kera khadi	5.78 *	-10.59 **	0.61 *	-2.96 **	-4.06 **	-5.69 **	0.23	0.07	0.02	-0.44 *
IR 58025 A/ Luchai red	-0.79	4.2	-1.77 **	1.76 **	-8.61 **	5.49 **	-0.17	-0.05	-0.01	0.16
IR 58025 A/ Lajni super- 1	35.10 **	-2.34	-1.24 **	0.43	8.11 **	-1.25	0.08	-0.01	0.03	0.14
IR 79156 A/ Ganga chur	-7.54 **	-8.22 **	-0.2	-1.50 **	1.52	-2.54 **	0.01	0.09	-0.14	0.01
IR 79156 A/ Luchai	11.20 **	16.61 **	0.74 **	1.34 **	0.94	1.74	0.72 **	-0.04	0.38 **	-0.1
IR 79156 A/ Pihu purple	-9.87 **	-0.45	0.54 *	0.12	-11.82 **	5.94 **	-0.01	0.05	-0.08	0.04
IR 79156 A/ Bathras	-8.84 **	1.18	-0.47	-1.25 **	-0.23	-2.30 *	-0.26	0.06	-0.21	-0.03
IR 79156 A/ Pepri luchai	11.32 **	-0.34	-0.83 **	-0.03	-11.83 **	3.67 **	-0.13	-0.07	0.04	0.18
IR 79156 A/ Khura bal	17.54 **	-12.61 **	-0.04	-0.88 *	-6.77 **	1.15	0.23	-0.04	0.19	0.51 **
IR 79156 A/ Sarojini	-0.21	-0.16	-0.11	1.53 **	18.10 **	-9.83 **	-0.04	-0.07	0.11	-0.36
IR 79156 A/ Kera khadi	4.55	1.97	-1.14 **	0.2	2.83 *	0.26	-0.43 *	-0.03	-0.19	-0.08
IR 79156 A/ Luchai red	0.17	-1.06	0.89 **	0.29	8.25 **	-0.12	-0.1	0.02	-0.08	0.06
IR 79156 A/ Lajni super- 1	-18.31 **	3.08	0.62 *	0.17	-0.99	2.04 *	0.01	0.03	-0.02	-0.23
IR 68888 A/ Ganga chur	3.93	0.21	-1.89 **	0.95 *	5.86 **	-0.26	0.04	-0.02	0.06	-0.56 **
IR 68888 A/ Luchai	-14.66 **	0.71	-0.89 **	-0.68	-4.72 **	1.37	-0.21	-0.15 **	0.09	0.49 **
IR 68888 A/ Pihu purple	10.64 **	-4.03	-2.06 **	-0.31	1.29	-2.95 **	-0.11	0.01	-0.06	0.24
IR 68888 A/ Bathras	2.29	-2.59	0.12	0.31	-0.89	-0.09	0.21	0.01	0.09	0.03
IR 68888 A/ Pepri luchai	4.85 *	-11.73 **	2.35 **	-0.78 *	13.21 **	-4.74 **	-0.03	0.11 *	-0.18	0.07
IR 68888 A/ Khura bal	3.28	8.59 **	0.01	0.1	-1.33	-0.43	0.2	-0.02	0.14	-0.1
IR 68888 A/ Sarojini	16.17 **	4.09	0.35	0.32	-7.90 **	7.83 **	-0.48 **	0.08	-0.37 **	-0.56 **
IR 68888 A/ Kera khadi	-10.33 **	8.62 **	0.53	2.76 **	1.23	5.43 **	0.2	-0.04	0.17	0.52 **
IR 68888 A/ Luchai red	0.62	-3.14	0.88 **	-2.06 **	0.36	-5.37 **	0.27	0.04	0.09	-0.22
IR 68888 A/ Lajni super- 1	-16.79 **	-0.74	0.62 *	-0.6	-7.12 **	-0.79	-0.09	-0.02	-0.01	0.09

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.8 Specific Combining Ability Effects of Hybrids for Different Characters

	Cooked rice width (mm)	Cooked rice L/B ratio	Hulling percent	Milling Percent	Head rice recovery percent	Amylose content (%)	Alkali spreading value	Gel consistency
	19	20	21	22	23	24	25	26
IR 58025 A/ Ganga chur	-0.1	0.32 **	-0.90 *	5.33 **	5.55 **	0.21	-1.29 **	19.60 **
IR 58025 A/ Luchai	-0.07	-0.07	-5.01 **	-6.86 **	-8.97 **	1.74 **	-1.29 **	25.26 **
IR 58025 A/ Pihu purple	0.04	-0.14	3.56 **	-0.24	1.87 **	1.80 **	0.49	5.65 **
IR 58025 A/ Bathras	0.08	-0.1	0.44	-6.55 **	-5.66 **	5.88 **	-1.18 **	-9.14 **
IR 58025 A/ Pepri luchai	-0.03	-0.05	-0.44	0.17	2.74 **	-4.47 **	-0.4	-15.67 **
IR 58025 A/ Khura bal	0.01	-0.16	-0.83 *	8.37 **	9.48 **	6.80 **	0.82 *	15.08 **
IR 58025 A/ Sarojini	0.18 **	0.12	4.66 **	7.13 **	7.02 **	2.49 **	0.49	-16.52 **
IR 58025 A/ Kera khadi	-0.20 **	0.07	0.96 **	-1.60 **	-1.72 **	-1.64 **	-1.73 **	-20.57 **
IR 58025 A/ Luchai red	-0.03	0.1	-2.31 **	-5.25 **	-7.03 **	-3.32 **	2.04 **	1.28 *
IR 58025 A/ Lajni super- 1	0.11	-0.09	-0.13	-0.51	-3.29 **	-9.49 **	2.04 **	-4.95 **
IR 79156 A/ Ganga chur	-0.1	0.09	0.48	-6.93 **	-6.18 **	-0.49	0.68 *	-15.55 **
IR 79156 A/ Luchai	0.23 **	-0.27 **	2.13 **	5.05 **	4.47 **	-3.15 **	1.34 **	-20.49 **
IR 79156 A/ Pihu purple	-0.03	0.05	2.20 **	1.69 **	1	-3.67 **	0.46	4.90 **
IR 79156 A/ Bathras	-0.09	0.09	1.62 **	6.48 **	6.57 **	-0.04	0.79 *	0.99
IR 79156 A/ Pepri luchai	-0.06	0.13	0.65	1.90 **	3.34 **	2.55 **	0.57	-0.31
IR 79156 A/ Khura bal	0.08	0.07	3.28 **	-3.82 **	-6.18 **	0.52	-0.54	-5.09 **
IR 79156 A/ Sarojini	-0.09	-0.03	-10.55 **	-8.93 **	-8.85 **	-2.96 **	0.12	6.94 **
IR 79156 A/ Kera khadi	0.1	-0.14	-1.47 **	0.51	-0.07	3.53 **	0.23	26.60 **
IR 79156 A/ Luchai red	0.1	-0.09	1.74 **	2.94 **	1.69 **	0.13	-1.66 **	8.28 **
IR 79156 A/ Lajni super- 1	-0.15 *	0.1	-0.08	1.12 *	4.21 **	3.59 **	-1.99 **	-6.27 **
IR 68888 A/ Ganga chur	0.19 **	-0.42 **	0.42	1.60 **	0.63	0.28	0.61	-4.04 **
IR 68888 A/ Luchai	-0.15 *	0.34 **	2.88 **	1.81 **	4.50 **	1.41 **	-0.06	-4.76 **
IR 68888 A/ Pihu purple	-0.01	0.09	-5.76 **	-1.45 **	-2.87 **	1.87 **	-0.94 **	-10.55 **
IR 68888 A/ Bathras	0	0.02	-2.06 **	0.07	-0.9	-5.84 **	0.39	8.15 **
IR 68888 A/ Pepri luchai	0.09	-0.08	-0.2	-2.08 **	-6.07 **	1.93 **	-0.17	15.98 **
IR 68888 A/ Khura bal	-0.1	0.09	-2.44 **	-4.55 **	-3.30 **	-7.33 **	-0.28	-9.99 **
IR 68888 A/ Sarojini	-0.1	-0.09	5.89 **	1.80 **	1.83 **	0.47	-0.61	9.58 **
IR 68888 A/ Kera khadi	0.09	0.07	0.51	1.10 *	1.79 **	-1.89 **	1.50 **	-6.03 **
IR 68888 A/ Luchai red	-0.07	-0.01	0.56	2.31 **	5.33 **	3.19 **	-0.39	-9.56 **
IR 68888 A/ Lajni super- 1	0.04	-0.01	0.21	-0.61	-0.92	5.91 **	-0.06	11.23 **

*Significant at p=0.05% level, **Significant at p=0.01% level

The highly significant positive SCA effects were recorded by cross, IR 58025 A/ Lajni super- 1 (35.10), IR 79156 A/ Khura bal (17.54), IR 68888 A/ Sarojini (16.17), IR 79156 A/ Pepri luchai (11.32), IR 79156 A/ Luchai (11.20), IR 68888 A/ Pihu purple (10.64) and IR 58025 A/ Bathras (6.55) indicating their use in hybridization programme for development of new restorers. On the other hand, negatively highly significant specific combining ability (SCA) effect was recorded by IR 58025 A/ Khura bal (-20.82), IR 79156 A/ Lajni super- 1 (-18.31), IR 68888 A/ Lajni super- 1 (-16.79), IR 58025 A/ Pepri luchai (-16.17), IR 58025 A/ Sarojini (-15.96), IR 68888 A/ Luchai (-14.66), IR 68888 A/ Kera khadi (-10.33), IR 79156 A/ Pihu purple (-9.87), IR 79156 A/ Bathras (-8.84) and IR 79156 A/ Ganga chur (-7.54) indicating their use in hybridization programme for development of new maintainers.

The SCA variance was found higher than the GCA variance, indicating the role of non-additive gene action. Similar finding was also supported by Sao and Motiramani (2006), Srikrishna Latha *et al.* (2013) and Ghosh *et al.* (2013) for pollen fertility per cent and Devi *et al.* (2018).

4.3.2.10 Spikelet fertility (%)

Among the lines, IR 58025A (2.60) and IR 79156A (2.07) has showed positive highly significant GCA effect. Among the testers, Sarojini (31.13), Kera khadi (21.59) and Luchai (17.21) showed positive highly significant GCA effects.

Among the hybrids, ten hybrids have shown significant SCA effects. Five hybrids have shown the positive highly significant while five hybrids have shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 79156 A/ Luchai (16.61) followed by, IR 58025 A/ Pepri luchai (12.06), IR 68888 A/ Khura bal (8.59) and IR 68888 A/ Kera khadi (8.62) and IR 58025 A/ Ganga chur (8.01). These hybrids were registered as best specific combiner for spikelet fertility percentage.

The SCA variance was found higher than the GCA variance, indicating the role of non-additive gene action. Similar results were also reported by Jayasudha and Sharma (2009), Ghara *et al.* (2012), Ghosh *et al.* (2013) and Thorat and Kunkerkar (2017).

4.3.2.11 Test Weight/ thousand seed weight (g)

Among the lines, IR 58025A (0.46) showed positive highly significant GCA effect whereas, among the testers, Pihu purple (3.17) Sarojini (1.40) and Khura bal (1.04) showed positive highly significant GCA effects. Along with IR 58025A, Pihu purple, Sarojini and Khura bal were identified as good general combiner for the trait.

Among the thirty hybrids, eighteen hybrids have shown significant SCA effects. Six hybrids have shown the positive highly significant and four hybrids shown positive significant SCA effects and eight hybrids have shown the negative highly significant SCA effects. The highest positive significant SCA effects have shown by cross IR 68888 A/ Pepri luchai (2.35) followed by IR 58025 A/ Ganga chur (2.09), IR 58025 A/ Pihu purple (1.53), IR 79156 A/ Luchai red (0.89), IR 68888 A/ Luchai red (0.88) and IR 79156 A/ Luchai (0.74). These hybrids were registered as best specific combiner for test weight.

The SCA variance was found higher than the GCA variance, indicating the role of non-additive gene action. Similar findings were also supported by Zhu *et al* (2009), Satheesh *et al.* (2010), El-Rewainy *et al.* (2011), Ghosh *et al.* (2013), Ali *et al.* (2018) and Ramesh *et al.* (2018).

4.3.2.12 Grain yield per plant (g)

Among the lines, IR 79156A (0.72) showed significant GCA effect. Among the testers, Luchai (8.45), Sarojini (7.66), Pepri Luchai (1.07) and Kera khadi (0.56) showed positive significant GCA effects.

Among the thirty hybrids, fifteen hybrids have shown significant SCA effects. Four hybrids have shown the positive highly significant SCA effects while four hybrids have shown the positive significant SCA effects and five hybrids have shown the negative highly significant SCA effects while two hybrids have shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 68888 A/ Kera khadi (2.76) followed by IR 58025 A/ Luchai red (1.76), IR 79156 A/ Sarojini (1.53) and IR 79156 A/ Luchai (1.34). These hybrids were identified as good specific combiner for the trait.

The SCA variance was found higher than the GCA variance, indicating the role of non-additive gene action therefore hetetrosis breeding will be

rewarded for improvement of this trait. Similar findings were also supported by “Singh *et al.* (2007), Satheesh *et al.* (2010), Mirarab *et al.* (2011), El-Rewainy *et al.* (2011), Srivastava *et al.* (2012), Ghara *et al.* (2012), Pratap *et al.* (2013), Utharasu and Anandakumar (2013), Ghosh *et al.* (2013), Hasan *et al.* (2013), Gahtyari *et al.* (2017) and Kishor *et al.* (2017)”.

4.3.2.13 Biological yield per plant (g)

Among the lines, IR 79156A (3.16) showed positive highly significant GCA effect. Among the testers, Luchai (14.32), Pepri Luchai (13.85), Luchai red (8.81) and Kera khadi (3.17) showed positive highly significant GCA effects.

Among the hybrids, eight hybrids have shown the positive highly significant SCA effects and one have positive significant SCA effects whereas, ten hybrids have shown negative highly significant SCA effects. The highest positive significant SCA effect has shown by IR 79156 A/ Sarojini (18.10) followed by IR 68888 A/ Pepri luchai (13.21).

The SCA variance was found higher than the GCA variance, indicating the role of non-additive gene action and heterosis breeding. Similar findings were also supported by Kumar *et al.* (2007), Tiwari *et al.* (2011), Ghosh *et al.* (2013) and Belhekar *et al.* (2017).

4.3.2.14 Harvest Index (%)

Among the lines, no one showed significant GCA effects. Among the testers, Sarojini (20.40), and Luchai (11.18) showed positive significant GCA effects.

Among the hybrids, eighteen hybrids have shown significant SCA effects. Eight hybrids have shown the negative highly significant and one has negative significant SCA effects. Six hybrids IR 68888 A/ Sarojini (7.83), IR 79156 A/ Pihu purple (5.94), IR 58025 A/ Luchai red (5.49), IR 68888 A/ Kera khadi (5.43), IR 79156 A/ Pepri luchai (3.67) and IR 58025 A/ Ganga chur (2.80) have shown the positive highly significant SCA effect while only three have shown the positive significant SCA effect.

SCA variance was higher than GCA variance resulting the non additive gene action and heterosis breeding programme. Similar findings were also

supported by Panwar (2005), Kumar *et al.* (2007), Malik and Singh (2013) and Srijan *et al.* (2016).

4.3.2.15 Kernel length (mm)

Among the lines, IR 79156A (0.13) positive significant GCA effects while. Among the testers, Pihu purple (0.63), and Sarojini (0.30) showed positive highly significant GCA effects. Among the parents, IR 79156A with Pihu purple (0.63), and Sarojini were identified as good general combiner for trait.

Among the hybrids, six hybrids have shown significant SCA effects. Two hybrids have shown the positive highly significant SCA effects and two hybrids have shown the negative highly significant SCA effects while two hybrids have shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 79156 A/ Luchai (0.72) followed by IR 58025 A/ Sarojini (0.52). These two hybrids were identified as good specific combiner for kernel length.

The sca variance was greater than the gca variance indicating the predominance of non-additive gene action for this trait. The result is similar to the findings of Sharma and Mani (2005) and Saravana *et al.* (2006).

4.3.2.16 Kernel breadth (mm)

Among the lines IR 58025 (0.04) have shown positive significant GCA effect. Among the testers Bathras (0.16) and Luchai (0.13) showed positive highly significant GCA effect.

Among the hybrids, only three hybrid showed significant SCA effect. The two hybrids (0.19) and IR 68888 A/ Pepri luchai (0.11) showed positive significant SCA effect.

The SCA variance was greater than the GCA variance indicating the predominance of non-additive gene action for this character.

Similar findings were also supported by Sharma and Mani (2005) and Veni *et al.* (2005).

4.3.2.17 Kernel L/B ratio

Among the lines, IR 79156A (0.11) showed positive highly significant GCA effects. Among the testers, Lajni super- 1 (0.55) and Pihu purple (0.36) showed positive significant GCA effects. Among the parents, line IR 79156A

with testers Lajni super- 1 and Pihu purple were identified as good general combiner for trait.

Among the hybrids, five hybrids has shown significant SCA effects. Only one hybrids have shown the positive highly significant SCA effects while one have shown the positive significant SCA effects and three hybrids have shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 79156 A/ Luchai (0.38). This hybrid was identified as good specific combiner for the trait.

The sca variance was greater than the gca variance indicating predominance of non-additive gene action. Similar result was supported by Sharma and Mani (2005).

4.3.2.18 Cooked rice length (mm)

Among the lines, IR 58025A (0.17) showed positive highly significant GCA effects. Among the testers, Bathras (0.49) and Pihu purple (0.31). Line IR 58025A with Bathras and Pihu purple were identified as good general combiner for trait.

Among the hybrids, ten hybrids have shown significant SCA effects. Five hybrids have shown the positive significant SCA effects and two hybrids have shown the negative highly significant SCA effects. The highest positive significant SCA effect has shown by cross IR 58025 A/ Sarojini (0.92) followed by IR 58025 A/ Ganga chur (0.55), IR 68888 A/ Kera khadi (0.52), IR 79156 A/ Khura bal (0.51) and IR 68888 A/ Luchai (0.49) .

The sca variance was greater than the gca variance indicating the predominance of non-additive gene action for this character. Similar findings were also supported by Nayak and Reddy (2005) and Chandirakala *et al.* (2012).

4.3.2.19 Cooked rice breadth (mm)

Among the lines, IR 79156A (0.06) shown positive highly significant GCA effects and IR 68888A (0.04) shown positive significant GCA effects. Among the testers, Kera khadi (0.12) showed positive highly significant GCA effects while Luchai red (0.09) and Bathras (0.08) shown positive significant GCA effects. Kera khadi were identified as good general combiner for this trait.

Among the hybrids, six hybrids have shown significant SCA effects. Three hybrids have shown the positive highly significant SCA effects and three hybrids have shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 79156 A/ Luchai (0.23) followed by IR 68888 A/ Ganga chur (0.19) and IR 58025 A/ Sarojini (0.18). These three hybrids were identified as good specific combiner for this trait.

The sca variance was greater than the gca variance indicating the predominance of non-additive gene action for this character. Similar findings were also supported by Nayak and Reddy (2005) and Chandirakala *et al.* (2012).

4.3.2.20 Cooked rice L/B ratio

Among the lines, IR 58025 (0.18) shown significant positive GCA effects. Among the testers, Khura bal (0.20) showed positive highly significant GCA effects while Sarojini (0.14) showed positive significant GCA effects.

Among the hybrids, four hybrids have shown significant SCA effects. Two hybrids have shown the positive highly significant SCA effects and two hybrids have shown the negative highly significant SCA effects. The highest positive significant SCA effect has shown by cross IR 68888 A/ Luchai (0.34) followed by IR 58025 A/ Ganga chur (0.32), CRMS32A/RIL-62 (0.19).

The sca variance was greater than the gca variance indicating the predominance of non-additive gene action for this character. Similar findings were also supported by Nayak and Reddy (2005).

4.3.2.21 Hulling (%)

Among the lines, IR 79156A (0.52) showed positive highly significant GCA effects while IR 58025 (0.23) showed positive significant GCA effects and among testers, Luchai (3.38), Pepri Luchai (2.88), Sarojini (2.04) and Lajni super- 1 (1.92) showed positive highly significant GCA effect. Line IR 79156A with tester Luchai, Pepri Luchai, Sarojini and Lajni super- 1 were identified as good general combiner for hulling percent.

Among the hybrids, nineteen hybrids have shown significant SCA effects. Ten hybrids have shown the positive highly significant SCA effects and seven hybrids have shown the negative highly significant SCA effects and two hybrids have shown negative significant SCA effects. The positive highly significant

SCA effect has shown by cross IR 68888 A/ Sarojini (5.89) followed by IR 58025 A/ Sarojini (4.66), IR 58025 A/ Pihu purple (3.56), IR 79156 A/ Khura bal (3.28), IR 68888 A/ Luchai (2.88), IR 79156 A/ Luchai (2.13), IR 79156 A/ Pihu purple (2.20), IR 79156 A/ Luchai red (1.74), IR 79156 A/ Bathras (1.62) and IR 58025 A/ Kera khadi (0.96) cross was identified as good specific combiner for hulling percent.

The SCA variance was greater than the GCA variance indicating the predominance of non-additive gene action for this character. Similar findings were also supported by EL-Hissewy (2004), Tyagi *et al.* (2010) and Sahu *et al.* (2016).

4.3.2.22 Milling (%)

Among the lines, IR 68888A (1.45) showed positive highly significant GCA effect. Among the testers, Sarojini (5.50), Luchai (5.26), Luchai red (3.68), Pepri Luchai (2.60) and Kera khadi (0.78) showed positive highly significant GCA effect. Line IR 68888A with testers Sarojini, Luchai, Luchai red, Pepri Luchai and Kera khadi were identified as good general combiner for milling percent.

Among the hybrids, twenty four hybrids have shown significant SCA effects. Twelve hybrids have shown the positive highly significant SCA effects while two have shown the positive significant SCA effects and ten hybrids have shown the negative significant SCA effects. The highest positive significant SCA effect has shown by cross IR 58025 A/ Khura bal (8.37) followed by IR 58025 A/ Sarojini (7.13), IR 79156 A/ Bathras (6.48), IR 58025 A/ Ganga chur (5.33), IR 79156 A/ Luchai (5.05), IR 79156 A/ Luchai red (2.94), IR 68888 A/ Luchai red (2.31), IR 79156 A/ Pepri luchai (1.90), IR 68888 A/ Luchai (1.81), IR 68888 A/ Sarojini (1.80), IR 79156 A/ Pihu purple (1.69), IR 68888 A/ Ganga chur (1.60)

The SCA variance was greater than the GCA variance indicating the predominance of non-additive gene action for this character. Similar findings were also supported by Tyagi *et al.* (2010) and Sahu *et al.* (2016).

4.3.2.23 Head rice recovery (%)

Among the lines, IR 58025 (0.80) showed positive highly significant GCA effect. Among the testers, Sarojini (7.51), Luchai (4.27), Luchai red (3.35), Kera khadi (3.12) and Pepri Luchai (1.27) showed positive highly significant GCA effect. IR 58025 with Sarojini, Luchai, Luchai red, Kera khadi and Pepri Luchai were identified as good general combiner for trait.

Among the hybrids, total twenty five hybrids have shown significant SCA effects. Fourteen hybrids have shown the positive highly significant SCA effects and eleven hybrids have shown the negative highly significant SCA effects. The highest positive significant SCA effect has shown by cross IR 58025 A/ Khura bal (9.48) followed by IR 58025 A/ Sarojini (7.02), IR 79156 A/ Bathras (6.57) IR 58025 A/ Ganga chur (5.55), IR 68888 A/ Luchai red (5.33) IR 68888 A/ Luchai (4.50) IR 79156 A/ Luchai (4.47), IR 79156 A/ Lajni super- 1 (4.21) IR 79156 A/ Pepri luchai (3.34) IR 58025 A/ Pepri luchai (2.74), IR 58025 A/ Pihu purple (1.87), IR 68888 A/ Sarojini (1.83), IR 68888 A/ Kera khadi (1.79) and IR 79156 A/ Luchai red (1.69).

The SCA variance was greater than the GCA variance indicating the predominance of non-additive gene action for this character. Similar findings were also supported by Tyagi *et al.* (2010), Ghosh *et al.* (2013) and Sahu *et al.* (2016).

4.3.2.24 Amylose %

Among the lines, IR 68888A (2.30) showed the significant GCA value. Among the testers, Ganga chur (2.60), Bathras (1.62), Pepri Luchai (1.42), Luchai red (0.84), Lajni super- 1 (0.58) and Kera khadi (0.50) have shown the positive highly significant GCA effects.

Among the hybrids, twenty three hybrids have shown significant SCA effects. Thirteen hybrids have shown positive highly significant SCA effects, and ten hybrids have shown negative highly significant SCA effects. Highest positive significant SCA effect have shown in cross IR 58025 A/ Khura bal (6.80) followed by IR 68888 A/ Lajni super- 1 (5.91), IR 58025 A/ Bathras (5.88), IR 79156 A/ Lajni super- 1 (3.59) IR 79156 A/ Kera khadi (3.53), IR 68888 A/ Luchai red (3.19) IR 79156 A/ Pepri luchai (2.55) IR 58025 A/ Sarojini (2.49), IR 68888 A/ Pepri luchai (1.93) IR 68888 A/ Pihu purple (1.87) IR 58025 A/ Pihu purple (1.80), IR 58025 A/ Luchai (1.74) and IR 68888 A/ Luchai (1.41) which are considered as good hybrids for this trait.

SCA variance was higher than GCA variance indicating the presence of non additive gene action. Therefore heterosis breeding will be rewarded for improvement of this trait.

4.3.2.25 Alkali spreading value

Among the lines, IR 68888A (0.61) showed the significant GCA value. Among the testers, Khura bal (0.84), and Pepri Luchai (0.73) have shown the positive highly significant GCA effects.

Among the hybrids, fourteen hybrids have shown significant SCA effects. Four hybrids have shown positive highly significant SCA effects, while three hybrids have shown positive significant SCA effects and seven hybrids have shown negative highly significant SCA effects. Highest positive significant SCA effect have shown in cross IR 58025 A/ Khura bal (6.80) followed by IR 68888 A/ Lajni super- 1 (5.91) ,IR 58025 A/ Bathras (5.88), IR 79156 A/ Lajni super- 1 (3.59) IR 79156 A/ Kera khadi (3.53), IR 68888 A/ Luchai red (3.19) IR 79156 A/ Pepri luchai (2.55) IR 58025 A/ Sarojini (2.49), IR 68888 A/ Pepri luchai (1.93) IR 68888 A/ Pihu purple (1.87) IR 58025 A/ Pihu purple (1.80), IR 58025 A/ Luchai (1.74) and IR 68888 A/ Luchai (1.41) which are considered as good hybrids for this trait.

SCA variance was higher than GCA variance indicating the presence of non additive gene action. Similar results were reported by Patil *et al.* (2003), Choudhary *et al.* (2004) and Singh *et al.* (2017).

4.3.2.26 Gel consistency

Among lines, IR 79156A (4.74) and IR 58025 (0.68) showed positive highly significant GCA effect whereas among testers, Lajni super- 1 (24.85), Luchai red (24.66), Sarojini (18.80), Khura bal (6.13) and Luchai (3.11) have shown the positive highly significant GCA effects. IR 79156A and IR 58025 with Lajni super- 1, Luchai red, Sarojini, Khura bal and Luchai can be good combiners for this trait.

Among hybrids, twenty eight hybrids have shown the significant SCA effects. Twelve hybrids showed positive highly significant SCA effects while one hybrid showed positive significant SCA effects and similarly fifteen hybrids showed negative highly significant SCA effects. Highest SCA effects have shown in IR 79156 A/ Kera khadi (26.60) followed by IR 58025 A/ Luchai (25.26), IR 58025 A/ Ganga chur (19.60), IR 58025 A/ Khura bal (15.08), IR 68888 A/ Pepri luchai (15.98), IR 68888 A/ Lajni super- 1 (11.23), IR 68888 A/ Sarojini (9.58) IR 79156 A/ Luchai red (8.28), IR 68888 A/ Bathras (8.15), IR 79156 A/ Sarojini (6.94),

IR 58025 A/ Pihu purple (5.65), IR 79156 A/ Pihu purple (4.90). These hybrids are considered as good hybrids.

SCA variance was higher than GCA variance indicating the non additive gene action.

4.4 Heterosis

Investigations on heterosis provides fundamental information regarding the utility of the cross combinations and its use for commercial exploitation. The magnitude of heterosis for yield, yield components and quality traits depends to a large extent on genetic variation, genetic base and adaptability of parents. The presence of significant amount of non additive gene action is a prerequisite for the commercial exploitation of heterosis in rice.

A programme to produce hybrid population may be initiated for a number of reasons. A partial listing of these would include: existence of a significant amount of dominance variance, a requirement for high degree of uniformity in the harvested product, a need for flexibility in the programme and the availability of cytoplasmic sterility. The demonstration of heterosis in crop is not adequate justification for the establishment of a programme to produce hybrids. The existence of heterosis demonstrates two things: some degree of genetic diversity between parents and some degree of dominance. Heterosis can arise when many loci are involved, if for each locus, the heterozygote is slightly superior to the mid-parental value. The existence of therefore, provides no guide as to the degree of dominance. Such information must be derived from specifically designed experiments.

The Heterosis over mid parent (Relative heterosis), over better parent (heterobeltiosis) and over standard check (standard heterosis/useful heterosis) was estimated for all the characters under study. The estimates of mid parent, better parent and standard heterosis are given in Table 4. The results of heterosis are described below.

4.4.1 Plant height (cm)

The mid parent heterosis ranged from -19.21 % (IR 79156 A/ Bathras) to 30.54 % (IR 68888 A/ Pepri luchai). Among hybrids, sixteen hybrids showed highly significant positive relative heterosis and nine hybrids showed highly significant

negative relative heterosis and one hybrid show significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -25.29 % (IR 79156 A/ Bathras) to 10.94 % (IR 79156 A/ Luchai). Among hybrids, sixteen hybrids showed highly significant negative better heterosis, one hybrid have shown significant negative better heterosis, five hybrids showed highly significant positive and three showed positive significant better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -33.45 % (IR 68888 A/ Ganga chur) to 22.63 % (IR 58025A/ Pepri luchai). Among hybrids, eleven hybrids showed highly significant negative heterosis and one hybrid show significant negative heterosis whereas fifteen hybrids showed highly positive significant heterosis and one hybrid show positive significant heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -35.98 % (IR 68888 A/ Ganga chur) to 17.98 % (IR 58025A/ Pepri luchai). Among hybrids, twelve hybrids showed highly significant negative heterosis and ten hybrids showed significant highly positive heterosis and one hybrid showed significant positive heterosis for this trait.

The negative heterotic effects indicating that the hybrids were shorter than their mid parents and positive heterotic effects showed that hybrids were taller with their mid parents. Cross IR 79156 A/ Bathras and 68888 A/ Ganga chur showed highest significant negative estimates of relative, better parent and for both the standard checks which indicate that this cross can be used for breeding dwarf hybrid. The testers Ganga chur, Pihu purple, Bathras, Khura bal, Kera khadi, Luchai red and Lajni super- 1 showed significant negative estimate for all heterosis.

Similar results have also been reported by “Issac (2007), Gawas *et al.* (2007), Saidaiah *et al.* (2010), Patil *et al.* (2012), Jarwar *et al.* (2012), Srikrishna Latha *et al.* (2013), Huang *et al.* (2015) and Sahu *et al.* (2016)”.

4.4.2 Panicle length (cm)

The mid parent heterosis ranged from -9.87 % (IR 58025A/ Ganga chur) to 18.79 % (IR 79156A/ Luchai). Among hybrids, fifteen hybrid showed highly significant positive relative heterosis and two hybrid showed highly significant negative relative heterosis. Two hybrids showed significant positive

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Plant height (cm)				Penicle length (cm)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-4.98 *	-6.18 *	-19.11**	-22.18**	-9.87 **	-16.97 **	-20.12**	-14.29**
IR 58025 A/ Luchai	21.05 **	7.84 **	15.93**	11.53**	6.94 *	-6.70 *	-10.25**	-3.7
IR 58025 A/ Pihu purple	9.53 **	6.48 *	-5.23*	-8.83**	4.76	0.02	-3.78	3.24
IR 58025 A/ Bathras	-17.14 **	-22.39 **	-25.31**	-28.14**	-8.37 **	-15.34 **	-18.56**	-12.62**
IR 58025 A/ Pepri luchai	23.28 **	6.72 **	22.63**	17.98**	11.60 **	6.19 *	2.15	9.60**
IR 58025 A/ Khura bal	0.07	-15.19 **	2.54	-1.36	-6.30 *	-6.85 *	-10.39**	-3.85
IR 58025 A/ Sarojini	15.49 **	5.24 *	7.54**	3.45	9.57 **	0.05	-3.76	3.27
IR 58025 A/ Kera khadi	3.42	-13.40 **	7.87**	3.77	2.26	-6.68 *	-10.23**	-3.67
IR 58025 A/ Luchai red	16.25 **	-1.55	19.26**	14.73**	8.74 **	3	-0.92	6.31*
IR 58025 A/ Lajni super- 1	-7.98 **	-8.43 **	-23.05**	-25.97**	-0.49	-9.92 **	-13.34**	-7.02*
IR 79156 A/ Ganga chur	-6.39 **	-8.81 **	-21.37**	-24.36**	-1.79	-7.32 *	-15.35**	-9.17**
IR 79156 A/ Luchai	25.52 **	10.49 **	18.78**	14.27**	18.79 **	6	-3.19	3.88
IR 79156 A/ Pihu purple	-7.32 **	-11.09 **	-20.86**	-23.87**	-3.46	-5.48	-13.68**	-7.37*
IR 79156 A/ Bathras	-19.21 **	-25.29 **	-28.09**	-30.82**	-5	-10.09 **	-17.88**	-11.89**
IR 79156 A/ Pepri luchai	24.39 **	6.45 **	22.32**	17.68**	7.49 **	4.86	-4.23	2.76
IR 79156 A/ Khura bal	1.85	-14.63 **	3.2	-0.71	1.72	-0.27	-5.2	1.72
IR 79156 A/ Sarojini	17.19 **	5.48 *	7.78**	3.69	11.67 **	4.42	-4.63	2.33
IR 79156 A/ Kera khadi	12.77 **	-6.60 **	16.34**	11.92**	6.78 *	-0.21	-8.86**	-2.2
IR 79156 A/ Luchai red	15.05 **	-3.65	16.72**	12.29**	11.08 **	7.86 *	-1.49	5.7
IR 79156 A/ Lajni super- 1	-11.71 **	-12.47 **	-27.17**	-29.93**	3.77	-3.83	-12.16**	-5.75
IR 68888 A/ Ganga chur	-12.45 **	-22.82 **	-33.45**	-35.98**	10.73 **	6.92 *	-6.92*	-0.13
IR 68888 A/ Luchai	28.87 **	3.87	11.66**	7.42**	13.27 **	3.26	-10.11**	-3.55
IR 68888 A/ Pihu purple	-3.13	-15.76 **	-25.02**	-27.87**	11.46 **	11.17 **	-2.72	4.38
IR 68888 A/ Bathras	-9.04 **	-23.43 **	-26.30**	-29.10**	-1.86	-4.96	-17.26**	-11.23**
IR 68888 A/ Pepri luchai	30.54 **	2.64	17.95**	13.47**	12.98 **	12.86 **	-1.75	5.42
IR 68888 A/ Khura bal	12.96 **	-12.78 **	5.45*	1.44	7.48 **	2.96	-2.13	5.02
IR 68888 A/ Sarojini	29.05 **	6.07 **	8.39**	4.27	14.28 **	9.31 **	-4.84	2.1
IR 68888 A/ Kera khadi	20.83 **	-7.67 **	15.00**	10.64**	14.94 **	9.88 **	-4.35	2.64
IR 68888 A/ Luchai red	17.14 **	-9.61 **	9.49**	5.33*	11.72 **	11.07 **	-3.31	3.75
IR 68888 A/ Lajni super- 1	-9.83 **	-19.27 **	-32.82**	-35.37**	3.31	-2.09	-14.76**	-8.54**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Flag leaf length (cm)				Flag leaf breadth (cm)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-5.36	-9.57	-21.29**	-6.37	-24.27 **	-26.89 **	-18.88*	-19.63*
IR 58025 A/ Luchai	17.32 **	11.56	-2.89	15.51*	-7.45	-8.77	-3.03	-3.93
IR 58025 A/ Pihu purple	7.93	-1.84	-14.55**	1.64	-8.59	-9.93	-6.99	-7.85
IR 58025 A/ Bathras	3.29	-4	-16.44**	-0.6	-9.09	-9.6	-5.59	-6.47
IR 58025 A/ Pepri luchai	11.62 *	8.33	-5.71	12.16	-0.76	-4.2	6.29	5.31
IR 58025 A/ Khura bal	1.67	-5.48	-4.26	13.88*	-12.27	-15.48	-5.83	-6.7
IR 58025 A/ Sarojini	7.4	3.01	-2.36	16.14*	1.81	-4.51	-1.4	-2.31
IR 58025 A/ Kera khadi	16.80 **	15.58 *	2.76	22.23**	-0.8	-2.48	0.7	-0.23
IR 58025 A/ Luchai red	14.60 *	9.86	-4.38	13.75*	1.21	-1.08	6.99	6
IR 58025 A/ Lajni super- 1	8.07	5.59	-8.08	9.33	-22.37 *	-29.12 **	-26.81**	-27.48**
IR 79156 A/ Ganga chur	26.74 **	25.16 **	-0.74	18.07**	-23.15 **	-28.15 **	-20.28*	-21.02*
IR 79156 A/ Luchai	26.88 **	25.93 **	-1.14	17.59**	-0.23	-4.82	1.17	0.23
IR 79156 A/ Pihu purple	23.28 **	18.47 *	-8.39	8.97	-7.58	-9.3	-9.09	-9.93
IR 79156 A/ Bathras	20.55 **	18.55 *	-8.33	9.04	-7.89	-11.38	-7.46	-8.31
IR 79156 A/ Pepri luchai	25.19 **	21.69 **	-0.32	18.57**	1.35	-5.25	5.13	4.16
IR 79156 A/ Khura bal	8.35	-4.47	-3.23	15.10*	-20.18 *	-25.52 **	-17.02	-17.78
IR 79156 A/ Sarojini	28.51 **	16.68 **	10.6	31.55**	10.97	7.49	3.73	2.77
IR 79156 A/ Kera khadi	17.98 **	10.29	-1.94	16.64*	-5.23	-6.78	-6.99	-7.85
IR 79156 A/ Luchai red	21.21 **	19.30 **	-4.76	13.29*	3.19	-2.37	5.59	4.62
IR 79156 A/ Lajni super- 1	15.48 *	11.5	-7.4	10.15	-17.44	-22.22 *	-24.94**	-25.64**
IR 68888 A/ Ganga chur	6.56	1.92	-19.17**	-3.86	-12.56	-21.01 *	-12.35	-13.16
IR 68888 A/ Luchai	23.01 **	18.22 *	-7.19	10.4	-4.05	-11.62	-6.06	-6.93
IR 68888 A/ Pihu purple	12.6	11.74	-19.10**	-3.77	-3.69	-8.84	-8.62	-9.47
IR 68888 A/ Bathras	10.02	8.28	-19.05**	-3.71	-6.01	-12.72	-8.86	-9.7
IR 68888 A/ Pepri luchai	29.14 **	21.64 **	-0.36	18.52**	14.42	3.36	14.69	13.63
IR 68888 A/ Khura bal	3.1	-11.61 *	-10.46	6.51	-16.01	-24.27 **	-15.62	-16.4
IR 68888 A/ Sarojini	-3.11	-14.55 *	-19	-3.65	-5.44	-5.93	-14.92	-15.7
IR 68888 A/ Kera khadi	5.61	-4.19	-14.82	1.32	-0.49	-5.61	-5.83	-6.7
IR 68888 A/ Luchai red	14.93 *	9.58	-12.52	4.06	4.25	-4.74	3.03	2.08
IR 68888 A/ Lajni super- 1	-4.16	-10.31	-25.51**	-11.39	-33.87 **	-35.42 **	-42.19**	-42.73**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Days to 50 % flowering				Effective tillers per plant			
	Mid	Better	Standerd		Mid	Better	Standerd	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-1.45	-2.55	-2.86	-6.71**	-22.11 *	-31.02 **	-24.42*	-30.29**
IR 58025 A/ Luchai	-1.81	-6.86 **	3.49	-0.61	-32.62 **	-33.43 **	-27.06*	-32.72**
IR 58025 A/ Pihu purple	-2.57	-9.55 **	-9.84**	-13.41**	-34.55 **	-35.24 **	-29.04**	-34.55**
IR 58025 A/ Bathras	-10.67 **	-13.38 **	-13.65**	-17.07**	-13.04	-24.70 *	-17.49	-23.90*
IR 58025 A/ Pepri luchai	-0.15	-4.64 *	4.44	0.3	30.20 **	8.43	18.81	9.59
IR 58025 A/ Khura bal	-0.82	-4.14	-4.44	-8.23**	13.66	-13.55	-5.28	-12.63
IR 58025 A/ Sarojini	-4.64 *	-5.10 *	-5.40*	-9.15**	-13.36	-31.63 **	-25.08*	-30.90**
IR 58025 A/ Kera khadi	-7.76 **	-11.66 **	-3.81	-7.62**	-26.67 **	-37.05 **	-31.02**	-36.38**
IR 58025 A/ Luchai red	-1.85	-5.06 *	1.27	-2.74	0.58	-21.39 *	-13.86	-20.55*
IR 58025 A/ Lajni super- 1	-4.44 *	-4.75 *	-4.44	-8.23**	0.01	-5.12	3.96	-4.11
IR 79156 A/ Ganga chur	3.02	-0.01	-2.54	-6.40**	-15.7	-23.15 *	-21.12*	-27.25**
IR 79156 A/ Luchai	1.1	-7.71 **	2.54	-1.52	-28.50 **	-29.94 **	-25.08*	-30.90**
IR 79156 A/ Pihu purple	3.58	-0.01	-8.25**	-11.89**	-18.87 *	-20.62 *	-14.85	-21.46*
IR 79156 A/ Bathras	5.14 *	4.07	-2.54	-6.40**	-13.36	-22.83 *	-20.79*	-26.94**
IR 79156 A/ Pepri luchai	4.10 *	-4.35 *	4.76*	0.61	-22.18 *	-33.44 **	-31.68**	-36.99**
IR 79156 A/ Khura bal	8.59 **	7.85 **	0.32	-3.66	-12.4	-31.83 **	-30.03**	-35.46**
IR 79156 A/ Sarojini	1.67	-1.93	-3.17	-7.01**	7.75	-12.86	-10.56	-17.5
IR 79156 A/ Kera khadi	2.85	-5.25 *	3.17	-0.91	-3.83	-15.11	-12.87	-19.63*
IR 79156 A/ Luchai red	2.72	-4.46 *	1.9	-2.13	-4.82	-23.79 *	-21.78*	-27.85**
IR 79156 A/ Lajni super- 1	-2.15	-6.33 **	-6.03*	-9.76**	-13.3	-15.11	-12.87	-19.63*
IR 68888 A/ Ganga chur	-4.36 *	-7.17 **	-9.52**	-13.11**	8.01	-4.23	4.62	-3.5
IR 68888 A/ Luchai	5.48 **	-3.71	6.98**	2.74	-28.55 **	-29.31 **	-22.77*	-28.77**
IR 68888 A/ Pihu purple	0.01	-3.46	-11.43**	-14.94**	-19.21 *	-19.94 *	-12.54	-19.33*
IR 68888 A/ Bathras	-6.85 **	-7.80 **	-13.65**	-17.07**	-6.27	-18.73	-11.22	-18.11
IR 68888 A/ Pepri luchai	4.42 *	-4.06	5.08*	0.91	4.71	-12.69	-4.62	-12.02
IR 68888 A/ Khura bal	2.41	1.71	-5.40*	-9.15**	-23.02 *	-41.39 **	-35.97**	-40.94**
IR 68888 A/ Sarojini	-0.33	-3.86	-5.08*	-8.84**	-5.16	-25.08 *	-18.15	-24.51*
IR 68888 A/ Kera khadi	-6.33 **	-13.70 **	-6.03*	-9.76**	-36.73 **	-45.62 **	-40.59**	-45.21**
IR 68888 A/ Luchai red	5.60 **	-1.79	4.76*	0.61	-36.68 **	-50.45 **	-45.87**	-50.08**
IR 68888 A/ Lajni super- 1	-9.42 **	-13.29 **	-13.02**	-16.46**	-29.73 **	-33.23 **	-27.06*	-32.72**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Filled spikelet per panicle				Unfilled spikelet per panicle			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-59.87 **	-75.73 **	-62.33**	-77.31**	-17.36	-26.83 *	98.86**	-11.28
IR 58025 A/ Luchai	-28.23 **	-57.94 **	-20.52*	-52.13**	63.96 **	10.32	199.84**	33.77*
IR 58025 A/ Pihu purple	6.69	-14.43	-53.97**	-72.28**	-18.31	-44.90 **	49.76	-33.19*
IR 58025 A/ Bathras	-62.36 **	-75.37 **	-74.07**	-84.38**	6.04	-31.99 **	84.83**	-17.54
IR 58025 A/ Pepri luchai	26.03 *	-18.78 *	-8.66	-44.99**	21.32	-22.63	110.28**	-6.19
IR 58025 A/ Khura bal	-13.88	-38.71 **	-52.98**	-71.68**	46.73 **	-12.55	137.68**	6.04
IR 58025 A/ Sarojini	97.78 **	24.67 **	55.35**	-6.43	-0.35	-31.03 *	87.44**	-16.38
IR 58025 A/ Kera khadi	-4.63	-43.92 **	3.55	-37.63**	9.85	-8.28	149.27**	11.21
IR 58025 A/ Luchai red	-29.89 **	-57.85 **	-32.37**	-59.27**	134.19 **	53.78 **	317.94**	86.46**
IR 58025 A/ Lajni super- 1	-24.66	-47.35 **	-56.98**	-74.09**	59.39 **	-0.12	171.45**	21.11
IR 79156 A/ Ganga chur	-75.37 **	-86.47 **	-79.00**	-87.35**	23.76	15.53	179.12**	24.53
IR 79156 A/ Luchai	7.86	-41.71 **	10.17	-33.65**	-41.18 *	-59.15 **	-1.31	-55.97**
IR 79156 A/ Pihu purple	9.06	-29.98	-62.33**	-77.31**	-5.26	-34.03 *	59.38	-28.89*
IR 79156 A/ Bathras	-57.29 **	-75.54 **	-74.25**	-84.49**	34.94 *	-11.07	114.85**	-4.15
IR 79156 A/ Pepri luchai	15.5	-34.40 **	-26.23*	-55.57**	82.89 **	19.78	189.40**	29.11*
IR 79156 A/ Khura bal	-64.42 **	-78.67 **	-83.63**	-90.14**	37.03	-16.68	101.31**	-10.19
IR 79156 A/ Sarojini	72.73 **	-3.04	20.82*	-27.23**	-27.96	-48.41 **	24.63	-44.40**
IR 79156 A/ Kera khadi	15.8	-37.31 **	15.76	-30.28**	-30.84 *	-39.37 **	46.49	-34.64**
IR 79156 A/ Luchai red	-41.72 **	-68.09 **	-48.80**	-69.16**	152.72 **	70.90 **	312.89**	84.21**
IR 79156 A/ Lajni super- 1	5.58	-37.33 **	-48.80**	-69.16**	66.68 **	7.09	158.73**	15.43
IR 68888 A/ Ganga chur	-73.61 **	-85.66 **	-77.74**	-86.59**	39.84 **	27.73	167.54**	19.36
IR 68888 A/ Luchai	21.66 *	-34.83 **	23.16**	-25.82**	125.83 **	74.19 **	201.63**	34.57*
IR 68888 A/ Pihu purple	-25.94	-53.69 **	-75.09**	-85.00**	125.08 **	74.19 **	69.82*	-24.24
IR 68888 A/ Bathras	-71.63 **	-84.00 **	-83.15**	-89.85**	73.96 **	25.58	117.46**	-2.98
IR 68888 A/ Pepri luchai	-25.66	-58.37 **	-53.19**	-71.81**	234.10 **	139.28 **	314.36**	84.86**
IR 68888 A/ Khura bal	2.87	-39.53 **	-53.61**	-72.06**	143.36 **	58.36 **	174.23**	22.34
IR 68888 A/ Sarojini	79.00 **	-0.82	23.59*	-25.57**	3.79	-16.82	44.05	-35.74**
IR 68888 A/ Kera khadi	60.40 **	-13.95 *	58.90**	-4.29	30.79	27.6	132.30**	3.64
IR 68888 A/ Luchai red	-67.34 **	-82.30 **	-71.60**	-82.90**	216.51 **	136.08 **	308.81**	82.39**
IR 68888 A/ Lajni super- 1	-52.47 **	-72.31 **	-77.38**	-86.37**	50.59 *	5.23	82.22*	-18.7

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Pollen fertility percent				Spikelet fertility percent			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-57.80**	-78.89 **	-79.62**	-79.46**	-26.80 **	-49.90 **	-54.68**	-49.74**
IR 58025 A/ Luchai	77.66**	-11.14 **	-21.85**	-21.26**	-23.35 **	-50.52 **	-43.30**	-37.13**
IR 58025 A/ Pihu purple	-49.86**	-74.92 **	-80.86**	-80.72**	4.59	-26.39 **	-39.73**	-33.17**
IR 58025 A/ Bathras	-41.04**	-70.51 **	-73.89**	-73.69**	-45.13 **	-63.98 **	-61.61**	-57.43**
IR 58025 A/ Pepri luchai	49.53**	-25.21 **	-38.11**	-37.64**	2.56	-33.08 **	-26.78**	-18.81**
IR 58025 A/ Khura bal	-12.31*	-56.14 **	-59.87**	-59.57**	-33.36 **	-56.40 **	-52.82**	-47.69**
IR 58025 A/ Sarojini	43.64**	-28.16 **	-31.05**	-30.53**	36.98 **	-9.42 *	-6.28	3.92
IR 58025 A/ Kera khadi	53.69**	-23.13 **	-37.13**	-36.65**	7.68	-28.18 **	-28.23**	-20.43**
IR 58025 A/ Luchai red	-59.07**	-79.53 **	-82.43**	-82.30**	-43.25 **	-63.27 **	-58.35**	-53.82**
IR 58025 A/ Lajni super- 1	113.10**	6.59	-12.06**	-11.39**	-41.02 **	-61.02 **	-59.59**	-55.19**
IR 79156 A/ Ganga chur	-70.02**	-85.00 **	-85.52**	-85.41**	-58.93 **	-74.98 **	-77.36**	-74.90**
IR 79156 A/ Luchai	109.37**	4.72	-7.91**	-7.21*	51.78 **	-11.01 *	1.97	13.06*
IR 79156 A/ Pihu purple	-59.67**	-79.83 **	-84.61**	-84.49**	4.05	-35.41 **	-47.11**	-41.36**
IR 79156 A/ Bathras	-64.38**	-82.19 **	-84.23**	-84.11**	-40.88 **	-64.96 **	-62.65**	-58.59**
IR 79156 A/ Pepri luchai	133.34**	16.70 **	-3.43	-2.69	-13.76 *	-49.08 **	-44.29**	-38.22**
IR 79156 A/ Khura bal	88.44**	-5.75	-13.77**	-13.11**	-62.61 **	-77.89 **	-76.07**	-73.47**
IR 79156 A/ Sarojini	90.24**	-4.86	-8.69**	-7.99**	59.20 **	-5.19	-1.9	8.78
IR 79156 A/ Kera khadi	64.76**	-17.59 **	-32.60**	-32.09**	47.14 **	-11.87 *	-11.93*	-2.35
IR 79156 A/ Luchai red	-43.14**	-71.56 **	-75.60**	-75.41**	-49.23 **	-70.19 **	-66.19**	-62.52**
IR 79156 A/ Lajni super- 1	-8.7	-54.34 **	-62.33**	-62.04**	-23.78 **	-54.62 **	-52.96**	-47.84**
IR 68888 A/ Ganga chur	-67.05**	-83.52 **	-84.09**	-83.96**	-56.25 **	-72.45 **	-75.08**	-72.36**
IR 68888 A/ Luchai	23.50**	-38.23 **	-45.68**	-45.26**	3.28	-37.78 **	-28.70**	-20.94**
IR 68888 A/ Pihu purple	-31.03**	-65.50 **	-73.68**	-73.48**	-26.16 **	-52.49 **	-61.10**	-56.87**
IR 68888 A/ Bathras	-61.94**	-80.96 **	-83.15**	-83.02**	-64.46 **	-78.31 **	-76.89**	-74.37**
IR 68888 A/ Pepri luchai	91.29**	-4.32	-20.83**	-20.22**	-53.12 **	-71.53 **	-68.85**	-65.46**
IR 68888 A/ Khura bal	32.50**	-33.72 **	-39.36**	-38.90**	-33.90 **	-59.78 **	-56.48**	-51.74**
IR 68888 A/ Sarojini	103.94**	2	-2.1	-1.36	49.23 **	-8.45	-5.27	5.04
IR 68888 A/ Kera khadi	0.63	-49.66 **	-58.83**	-58.52**	42.53 **	-11.98 *	-12.05*	-2.48
IR 68888 A/ Luchai red	-66.76**	-83.37 **	-85.73**	-85.63**	-68.06 **	-80.72 **	-78.14**	-75.76**
IR 68888 A/ Lajni super- 1	-30.54*	-65.26 **	-71.33**	-71.12**	-48.49 **	-68.41 **	-67.26**	-63.69**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	1000 grain weight				Grain yield per plant			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-6.63 **	-18.85 **	-18.01**	20.86**	-66.72 **	-76.49 **	-76.74**	-77.23**
IR 58025 A/ Luchai	15.98 **	7.69 **	-19.66**	18.42**	34.01 **	-7.48 *	-0.68	-2.8
IR 58025 A/ Pihu purple	18.03 **	7.70 **	-2.6	43.56**	-40.30 **	-51.22 **	-68.57**	-69.24**
IR 58025 A/ Bathras	-17.34 **	-33.69 **	-18.16**	20.64**	-64.14 **	-75.68 **	-72.11**	-72.70**
IR 58025 A/ Pepri luchai	-1.56	-2.67	-25.71**	9.50**	-24.18 **	-48.62 **	-40.90**	-42.16**
IR 58025 A/ Khura bal	-11.16 **	-26.46 **	-16.31**	23.36**	-45.39 **	-57.07 **	-69.34**	-69.99**
IR 58025 A/ Sarojini	14.75 **	12.58 **	-16.01**	23.80**	39.08 **	3.96	-14.14**	-15.97**
IR 58025 A/ Kera khadi	7.29 **	6.83 **	-20.31**	17.47**	-63.78 **	-75.94 **	-70.04**	-70.68**
IR 58025 A/ Luchai red	1.21	-16.04 **	-37.36**	-7.67**	-12.68	-28.54 **	-54.13**	-55.11**
IR 58025 A/ Lajni super- 1	15.20 **	-6.01 *	-29.88**	3.35	-33.50 **	-38.87 **	-70.20**	-70.84**
IR 79156 A/ Ganga chur	-19.13 **	-30.00 **	-29.28**	4.25*	-80.51 **	-86.44 **	-86.59**	-86.87**
IR 79156 A/ Luchai	16.10 **	8.30 **	-20.00**	17.92**	60.35 **	9.11 *	17.14**	14.64**
IR 79156 A/ Pihu purple	10.87 **	0.71	-8.92**	34.25**	-31.98 **	-45.54 **	-64.91**	-65.66**
IR 79156 A/ Bathras	-22.77 **	-38.28 **	-23.82**	12.29**	-77.52 **	-84.96 **	-82.75**	-83.12**
IR 79156 A/ Pepri luchai	-0.96	-2.55	-25.63**	9.63**	-25.11 **	-49.94 **	-42.42**	-43.65**
IR 79156 A/ Khura bal	-13.90 **	-29.00 **	-19.21**	19.09**	-57.35 **	-67.11 **	-76.51**	-77.01**
IR 79156 A/ Sarojini	12.47 **	10.88 **	-18.09**	20.73**	86.34 **	36.88 **	13.05**	10.64**
IR 79156 A/ Kera khadi	-4.64 **	-4.70 *	-29.52**	3.89	-31.80 **	-55.29 **	-44.33**	-45.51**
IR 79156 A/ Luchai red	14.06 **	-5.01 **	-29.83**	3.43	-22.21 **	-37.62 **	-59.96**	-60.82**
IR 79156 A/ Lajni super- 1	23.33 **	1.01	-25.39**	9.98**	-26.33 **	-33.89 **	-67.77**	-68.46**
IR 68888 A/ Ganga chur	-27.28 **	-36.47 **	-35.81**	-5.38**	-68.43 **	-80.18 **	-80.39**	-80.81**
IR 68888 A/ Luchai	5.72 **	-2.38	-26.30**	8.64**	40.04 **	-13.49 **	-7.13	-9.11*
IR 68888 A/ Pihu purple	-2.25	-10.33 **	-18.90**	19.54**	-51.73 **	-66.40 **	-78.35**	-78.81**
IR 68888 A/ Bathras	-21.30 **	-36.58 **	-21.72**	15.38**	-75.19 **	-84.86 **	-82.64**	-83.01**
IR 68888 A/ Pepri luchai	13.69 **	13.08 **	-13.70**	27.21**	-40.21 **	-63.54 **	-58.06**	-58.95**
IR 68888 A/ Khura bal	-14.59 **	-28.96 **	-19.16**	19.17**	-59.31 **	-72.45 **	-80.32**	-80.74**
IR 68888 A/ Sarojini	13.42 **	10.63 **	-16.48**	23.11**	74.92 **	14.23 **	-5.65	-7.66
IR 68888 A/ Kera khadi	2.64	1.59	-23.30**	13.06**	-16.50 **	-49.77 **	-37.45**	-38.78**
IR 68888 A/ Luchai red	12.26 **	-7.31 **	-30.02**	3.15	-69.76 **	-78.93 **	-86.47**	-86.76**
IR 68888 A/ Lajni super- 1	21.44 **	-1.37	-25.54**	9.76**	-55.55 **	-66.25 **	-83.55**	-83.90**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Biological yield per plant				Harvest index (%)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-25.14 **	-32.88 **	-30.95**	8.23	-54.22 **	-65.37 **	-66.31**	-78.99**
IR 58025 A/ Luchai	49.71 **	43.36 **	27.80**	100.33**	-9.1	-35.80 **	-22.34**	-51.57**
IR 58025 A/ Pihu purple	44.97 **	23.94 **	1.12	58.51**	-61.59 **	-72.20 **	-69.00**	-80.67**
IR 58025 A/ Bathras	-18.43 **	-20.95 **	-35.50**	1.1	-57.40 **	-71.62 **	-57.39**	-73.43**
IR 58025 A/ Pepri luchai	14.08 **	-4.72	15.97**	81.78**	-29.37 **	-46.07 **	-48.95**	-68.16**
IR 58025 A/ Khura bal	9.43	-0.44	-18.77**	27.33**	-52.26 **	-65.01 **	-62.50**	-76.62**
IR 58025 A/ Sarojini	-7.36	-15.20 *	-30.81**	8.45	43.86 **	1.21	24.09**	-22.62**
IR 58025 A/ Kera khadi	-0.39	-7.37	-12.11*	37.77**	-62.61 **	-74.25 **	-65.95**	-78.77**
IR 58025 A/ Luchai red	28.09 **	10.55	-9.80*	41.38**	-36.52 **	-53.82 **	-49.36**	-68.42**
IR 58025 A/ Lajni super- 1	30.02 **	11.32	-9.17	42.37**	-51.57 **	-61.54 *	-67.38**	-79.66**
IR 79156 A/ Ganga chur	-0.01	-8.31	-5.67	47.86**	-80.03 **	-85.43 **	-85.82**	-91.16**
IR 79156 A/ Luchai	46.84 **	44.07 **	28.43**	101.32**	10.06	-24.64 **	-8.84	-43.16**
IR 79156 A/ Pihu purple	-15.40 **	-29.14 **	-39.22**	-4.72	-26.05 **	-48.21 **	-42.26**	-63.99**
IR 79156 A/ Bathras	-15.88 **	-20.41 **	-31.72**	7.03	-74.10 **	-83.20 **	-74.77**	-84.26**
IR 79156 A/ Pepri luchai	-3.00	-17.32 **	0.63	57.74**	-17.80 *	-39.50 **	-42.72**	-64.28**
IR 79156 A/ Khura bal	-25.87 **	-34.04 **	-43.42**	-11.31	-45.52 **	-61.40 **	-58.64**	-74.21**
IR 79156 A/ Sarojini	76.11 **	57.63 **	35.22**	111.96**	-0.12	-31.86 **	-16.45*	-47.90**
IR 79156 A/ Kera khadi	20.62 **	14.83 **	8.96	70.80**	-42.20 **	-61.34 **	-48.87**	-68.12**
IR 79156 A/ Luchai red	82.33 **	54.12 **	32.21**	107.24**	-60.79 **	-72.41 **	-69.74**	-81.13**
IR 79156 A/ Lajni super- 1	8.81	-8.73	-21.71**	22.72**	-36.53 **	-51.55 *	-58.89**	-74.36**
IR 68888 A/ Ganga chur	2.14	-12.40 **	-9.87*	41.27**	-67.08 **	-77.85 **	-78.46**	-86.57**
IR 68888 A/ Luchai	26.85 **	15.79 **	3.22	61.80**	16.35 *	-25.65 **	-10.06	-43.92**
IR 68888 A/ Pihu purple	14.06 *	1.9	-25.00**	17.56*	-60.17 **	-74.08 **	-71.10**	-81.98**
IR 68888 A/ Bathras	-28.64 **	-30.01 **	-46.43**	-16.03*	-64.80 **	-78.46 **	-67.66**	-79.83**
IR 68888 A/ Pepri luchai	43.28 **	14.96 **	39.92**	119.32**	-53.25 **	-68.32 **	-70.02**	-81.30**
IR 68888 A/ Khura bal	-22.13 **	-25.69 **	-45.31**	-14.27	-48.55 **	-66.20 **	-63.78**	-77.42**
IR 68888 A/ Sarojini	-4.80	-8.56	-32.70**	5.49	80.21 **	14.82 **	40.78**	-12.21**
IR 68888 A/ Kera khadi	9.56	-2.73	-7.70	44.68**	-18.20 **	-48.70 **	-32.14**	-57.69**
IR 68888 A/ Luchai red	54.03 **	39.01 **	2.31	60.37**	-81.53 **	-87.93 **	-86.77**	-91.75**
IR 68888 A/ Lajni super- 1	-20.89 **	-29.21 **	-47.90**	-18.33*	-46.11 **	-62.37 *	-68.08**	-80.10**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Kernel length (mm)				Kernel breadth (mm)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-7.10 *	-8.11 *	-14.14**	5.59	-0.01	-12.12 **	9.43*	5.45
IR 58025 A/ Luchai	-5.81	-12.43 **	-18.18**	0.62	24.77 **	15.25 **	28.30**	23.64**
IR 58025 A/ Pihu purple	3.72	2.09	-1.52	21.12**	1.82	-6.67	5.66	1.82
IR 58025 A/ Bathras	-4.28	-5.29	-9.60**	11.18**	1.67	-12.86 **	15.09**	10.91*
IR 58025 A/ Pepri luchai	-0.58	-8.11 *	-14.14**	5.59	0.87	-10.77 **	9.43*	5.45
IR 58025 A/ Khura bal	-15.97 **	-18.92 **	-24.24**	-6.83	-0.01	-14.29 **	13.21**	9.09*
IR 58025 A/ Sarojini	14.53 **	6.49	-0.51	22.36**	5.45	-3.33	9.43*	5.45
IR 58025 A/ Kera khadi	-2.58	-8.11 *	-14.14**	5.59	7.83 *	-4.62	16.98**	12.73**
IR 58025 A/ Luchai red	-2.45	-14.05 **	-19.70**	-1.24	5.77	1.85	3.77	0.012
IR 58025 A/ Lajni super- 1	2.09	-7.57 *	-13.64**	6.21	-1.03	-4	-9.43*	-12.73**
IR 79156 A/ Ganga chur	-3.83	-4.86	-11.11**	9.32*	7.96 *	-7.58 *	15.09**	10.91*
IR 79156 A/ Luchai	18.02 **	9.73 **	2.53	26.09**	11.32 **	0.01	11.32*	7.27
IR 79156 A/ Pihu purple	3.72	2.09	-1.52	21.12**	6.54	-5	7.55	3.64
IR 79156 A/ Bathras	-6.95 *	-7.94 *	-12.12**	8.07*	7.69 *	-10.00 **	18.87**	14.55**
IR 79156 A/ Pepri luchai	-3.51	-10.81 **	-16.67**	2.48	-1.79	-15.38 **	3.77	0.017
IR 79156 A/ Khura bal	-2.52	-5.95	-12.12**	8.07*	-5.98	-21.43 **	3.77	0.002
IR 79156 A/ Sarojini	6.98 *	-0.54	-7.07*	14.29**	0.93	-10.00 *	1.89	-1.82
IR 79156 A/ Kera khadi	-11.75 **	-16.76 **	-22.22**	-4.35	1.79	-12.31 **	7.55	3.64
IR 79156 A/ Luchai red	1.23	-10.81 **	-16.67**	2.48	8.91 *	1.85	3.77	0.01
IR 79156 A/ Lajni super- 1	3.28	-6.49	-12.63**	7.45	-0.01	-0.01	-11.32*	-14.55**
IR 68888 A/ Ganga chur	-5.59	-6.63	-14.65**	4.97	5.45	-12.12 **	9.43*	5.45
IR 68888 A/ Luchai	-0.6	-5.65	-15.66**	3.73	8.74 *	-5.08	5.66	1.82
IR 68888 A/ Pihu purple	0.01	-3.66	-7.07*	14.29**	7.69	-6.67	5.66	1.82
IR 68888 A/ Bathras	-1.64	-4.76	-9.09**	11.80**	8.77 *	-11.43 **	16.98**	12.73**
IR 68888 A/ Pepri luchai	-4.19	-9.60 *	-19.19**	-0.62	11.93 **	-6.15	15.09**	10.91*
IR 68888 A/ Khura bal	-5.44	-6.78	-16.67**	2.48	-1.75	-20.00 **	5.66	1.82
IR 68888 A/ Sarojini	-2.98	-7.91 *	-17.68**	1.24	13.46 **	-1.67	11.32*	7.27
IR 68888 A/ Kera khadi	-3.23	-6.78	-16.67**	2.48	4.59	-12.31 **	7.55	3.64
IR 68888 A/ Luchai red	5.66	-5.08	-15.15**	4.35	14.29 **	3.7	5.66	1.82
IR 68888 A/ Lajni super- 1	-0.92	-8.47 *	-18.18**	0.62	1.1	-2.13	-13.21**	-16.36**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Kernel L/B ratio				Cooked rice length (mm)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-9.04 *	-20.79 **	-21.56**	0.16	0.55 **	-3.49	3.4	16.03**
IR 58025 A/ Luchai	-24.17 **	-34.47 **	-35.07**	-17.10**	-0.39 *	-2.14	-6.80*	4.58
IR 58025 A/ Pihu purple	1.11	-5.94	-6.82	18.97**	-0.28	-4.64	-2.04	9.92**
IR 58025 A/ Bathras	-8.32 *	-20.70 **	-21.45**	0.29	0.01	-1.31	2.72	15.27**
IR 58025 A/ Pepri luchai	-4.35	-20.79 **	-21.56**	0.16	-0.25	-1.43	-6.12*	5.34
IR 58025 A/ Khura bal	-19.57 **	-33.03 **	-33.65**	-15.28**	-0.42 *	-1.43	-6.12*	5.34
IR 58025 A/ Sarojini	6.81	-8.28 *	-9.10*	16.07**	0.92 **	12.50 **	7.14**	20.23**
IR 58025 A/ Kera khadi	-12.12 **	-25.92 **	-26.61**	-6.29	-0.44 *	-1.79	-6.46*	4.96
IR 58025 A/ Luchai red	-8.44 *	-21.87 **	-22.62**	-1.2	0.16	0.01	-4.76	6.87*
IR 58025 A/ Lajni super- 1	3.33	-3.78	-4.71	21.68**	0.14	0.36	-4.42	7.25*
IR 79156 A/ Ganga chur	-13.70 **	-26.80 **	-22.79**	-1.41	0.01	-11.11 **	-4.76	6.87*
IR 79156 A/ Luchai	3.71	-12.68 **	-7.93*	17.56**	-0.1	-0.01	-6.46*	4.96
IR 79156 A/ Pihu purple	-3.79	-13.02 **	-8.27*	17.12**	0.04	-3.97	-1.36	10.69**
IR 79156 A/ Bathras	-16.75 **	-29.84 **	-25.99**	-5.5	-0.03	-4.25	-0.34	11.83**
IR 79156 A/ Pepri luchai	-5.75	-23.84 **	-19.68**	2.56	0.18	2.18	-4.42	7.25*
IR 79156 A/ Khura bal	-1.14	-19.70 **	-15.35**	8.09	0.51 **	7.64 **	0.68	12.98**
IR 79156 A/ Sarojini	3.43	-13.44 **	-8.67*	16.62**	-0.36	-2.18	-8.5	2.67
IR 79156 A/ Kera khadi	-16.50 **	-31.36 **	-27.60**	-7.55	-0.08	1.09	-5.44*	6.11*
IR 79156 A/ Luchai red	-8.54 *	-23.92 **	-19.70**	2.53	0.06	-2.18	-8.50**	2.67
IR 79156 A/ Lajni super- 1	3.32	-6.51	-1.48	25.80**	-0.23	-4.73	-10.88**	0
IR 68888 A/ Ganga chur	-13.84 **	-27.51 **	-22.03**	-0.44	-0.56 **	-16.51 **	-10.54**	0.38
IR 68888 A/ Luchai	-11.21 **	-25.85 **	-20.22**	1.86	0.49 **	6.93 *	-0.34	11.83**
IR 68888 A/ Pihu purple	-8.83 *	-18.31 **	-12.04**	12.32*	0.24	-1.99	0.68	12.98**
IR 68888 A/ Bathras	-13.68 **	-27.84 **	-22.30**	-0.79	0.03	-3.59	0.34	12.60**
IR 68888 A/ Pepri luchai	-18.70 **	-34.80 **	-29.84**	-10.41*	0.07	3.35	-5.44*	6.11*
IR 68888 A/ Khura bal	-9.04 *	-26.68 **	-21.14**	0.70	-0.1	1.09	-5.44*	6.11
IR 68888 A/ Sarojini	-17.27 **	-31.32 **	-26.07**	-5.60	-0.56 **	2.73	-10.54**	0.38
IR 68888 A/ Kera khadi	-11.73 **	-28.00 **	-22.48**	-1.01	0.52 **	8.42 **	0.68	12.98**
IR 68888 A/ Luchai red	-9.54 *	-25.35 **	-19.65**	2.60	-0.22	0.77	-11.22**	-0.38
IR 68888 A/ Lajni super- 1	-2.26	-12.34 **	-5.68	20.44**	0.09	-1.09	-7.48**	3.82

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Cooked rice width (mm)				Cooked rice L/B ratio			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	0.65	-13.33 **	-10.34**	-17.02**	-0.26	-9.59 **	15.34**	39.86**
IR 58025 A/ Luchai	9.46 **	-2.41	-6.90*	-13.83**	-10.95 **	-21.35 **	0.19	21.49**
IR 58025 A/ Pihu purple	12.00 **	-1.18	-3.45	-10.64**	-12.71 **	-20.34 **	1.54	23.13**
IR 58025 A/ Bathras	18.62 **	7.50 *	-1.15	-8.51**	-13.69 **	-18.56 **	3.9	26.00**
IR 58025 A/ Pepri luchai	4.64	-8.14 **	-9.20**	-15.96**	-5.87	-18.79 **	3.44	25.44**
IR 58025 A/ Khura bal	4.05	-7.23 *	-11.49**	-18.09**	-5.94	-16.78 **	6.05	28.60**
IR 58025 A/ Sarojini	17.73 **	9.21 **	-4.6	-11.70**	0.98	-11.91 **	12.26**	36.13**
IR 58025 A/ Kera khadi	9.72 **	-0.01	-9.20**	-15.96**	-10.34 **	-19.18 **	2.98	24.88**
IR 58025 A/ Luchai red	28.68 **	27.69 **	-4.6	-11.70**	-18.77 **	-21.19 **	0.44	21.79**
IR 58025 A/ Lajni super- 1	28.13 **	26.15 **	-5.75*	-12.77**	-21.07 **	-21.65 **	1.39	22.95**
IR 79156 A/ Ganga chur	-0.6	-7.78 **	-4.6	-11.70**	-4.57	-5.5	-0.18	21.05**
IR 79156 A/ Luchai	18.75 **	14.46 **	9.20**	1.06	-15.75 **	-18.94 **	-14.37**	3.83
IR 79156 A/ Pihu purple	7.41 **	2.35	0.01	-7.45**	-6.5	-6.72	-1.33	19.66**
IR 79156 A/ Bathras	9.55 **	7.50 *	-1.15	-8.51**	-7.80 *	-10.81 **	0.83	22.27**
IR 79156 A/ Pepri luchai	1.84	-3.49	-4.6	-11.70**	1.09	-5.22	0.12	21.41**
IR 79156 A/ Khura bal	5	1.2	-3.45	-10.64**	2.27	-1.4	4.23	26.40**
IR 79156 A/ Sarojini	4.58	3.9	-8.05**	-14.89**	-0.84	-5.88	-0.54	20.60**
IR 79156 A/ Kera khadi	19.23 **	17.72 **	6.90**	-1.06	-14.98 **	-16.32 **	-11.54**	7.27
IR 79156 A/ Luchai red	30.50 **	19.48 **	5.75*	-2.13	-23.34 **	-27.88 **	-13.54**	4.84
IR 79156 A/ Lajni super- 1	12.86 **	2.6	-9.20**	-15.96**	-16.44 **	-24.09 **	-1.87	19.00**
IR 68888 A/ Ganga chur	4.6	1.11	4.6	-3.19	-11.70 **	-17.41 **	-14.43**	3.77
IR 68888 A/ Luchai	-0.6	-1.19	-4.6	-11.70**	11.54 **	7.27	4.78	27.06**
IR 68888 A/ Pihu purple	2.96	2.35	0	-7.45**	3.13	-4.22	0.7	22.12**
IR 68888 A/ Bathras	7.32 **	4.76	1.15	-6.38**	-2.04	-11.94 **	-0.48	20.68**
IR 68888 A/ Pepri luchai	2.35	1.16	0	-7.45**	3.62	2.35	-5.4	14.72**
IR 68888 A/ Khura bal	-6.59 *	-7.14 *	-10.34**	-17.02**	12.25 **	7.74	5.66	28.13**
IR 68888 A/ Sarojini	-1.25	-5.95 *	-9.20**	-15.96**	6.39	3.74	-1.5	19.44**
IR 68888 A/ Kera khadi	12.88 **	9.52 **	5.75*	-2.13	-1.08	-6.94	-4.74	15.51**
IR 68888 A/ Luchai red	16.22 **	2.38	-1.15	-8.51**	-14.59 **	-25.16 **	-10.23*	8.86
IR 68888 A/ Lajni super- 1	14.29 **	0.01	-3.45	-10.64**	-12.71 **	-25.91 **	-4.15	16.23**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Hulling percent (%)				Milling Percent (%)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	1.53 *	-1.15	-3.02**	-2.64**	10.68 **	4.37 **	-0.31	-1.96
IR 58025 A/ Luchai	-3.45 **	-5.20 **	-3.49**	-3.11**	-3.16 **	-13.09 **	-7.49**	-9.02**
IR 58025 A/ Pihu purple	-2.79 **	-3.69 **	-3.74**	-3.37**	-10.09 **	-16.44 **	-17.66**	-19.02**
IR 58025 A/ Bathras	-0.24	-1.39	-0.96	-0.58	-5.84 **	-12.04 **	-14.29**	-15.71**
IR 58025 A/ Pepri luchai	8.86 **	4.09 **	2.12**	2.52**	13.28 **	9.70 **	-0.9	-2.55*
IR 58025 A/ Khura bal	-5.11 **	-5.90 **	-6.12**	-5.75**	8.72 **	3.12 *	-2.73*	-4.34**
IR 58025 A/ Sarojini	15.36 **	10.08 **	8.00**	8.42**	35.06 **	34.68 **	13.96**	12.07**
IR 58025 A/ Kera khadi	-0.94	-1.85 *	-1.92*	-1.53	0.1	-8.65 **	-6.33**	-7.88**
IR 58025 A/ Luchai red	-5.54 **	-8.26 **	-4.51**	-4.13**	1.74	-4.89 **	-7.45**	-8.98**
IR 58025 A/ Lajni super- 1	10.02 **	3.18 **	1.23	1.63*	18.10 **	9.18 **	-7.61**	-9.14**
IR 79156 A/ Ganga chur	5.30 **	3.79 **	-0.7	-0.31	-10.68 **	-16.64 **	-20.37**	-21.69**
IR 79156 A/ Luchai	8.12 **	4.87 **	6.76**	7.18**	15.09 **	2.3	8.89**	7.09**
IR 79156 A/ Pihu purple	-3.09 **	-5.16 **	-5.21**	-4.84**	-7.71 **	-15.09 **	-16.33**	-17.71**
IR 79156 A/ Bathras	3.09 **	0.64	1.08	1.48	15.18 **	6.52 **	3.79**	2.08
IR 79156 A/ Pepri luchai	12.36 **	8.74 **	4.04**	4.44**	15.68 **	10.85 **	0.14	-1.52
IR 79156 A/ Khura bal	2.28 **	0.18	-0.05	0.35	-12.69 **	-18.02 **	-22.67**	-23.95**
IR 79156 A/ Sarojini	-5.36 **	-8.60 **	-12.55**	-12.21**	5.64 **	4.79 **	-11.83**	-13.29**
IR 79156 A/ Kera khadi	-2.72 **	-4.79 **	-4.85**	-4.48**	2.83 *	-7.08 **	-4.71**	-6.29**
IR 79156 A/ Luchai red	1.61 *	-2.50 **	1.49	1.89*	14.74 **	6.18 **	3.32**	1.61
IR 79156 A/ Lajni super- 1	12.02 **	6.31 **	1.71*	2.11**	20.64 **	12.66 **	-6.72**	-8.27**
IR 68888 A/ Ganga chur	7.98 **	4.87 **	-2.54**	-2.16**	32.90 **	1.09	-3.44**	-5.04**
IR 68888 A/ Luchai	11.98 **	4.15 **	6.03**	6.45**	38.33 **	1.52	8.06**	6.27**
IR 68888 A/ Pihu purple	-12.46 **	-17.88 **	-17.93**	-17.60**	11.91 **	-15.77 **	-17.00**	-18.38**
IR 68888 A/ Bathras	0.27	-6.15 **	-5.75**	-5.38**	33.38 **	0.77	-1.81	-3.43**
IR 68888 A/ Pepri luchai	14.19 **	12.96 **	1.11	1.5	40.14 **	8.69 **	-11.40**	-12.87**
IR 68888 A/ Khura bal	-3.58 **	-9.47 **	-9.68**	-9.33**	11.41 **	-14.89 **	-19.71**	-21.04**
IR 68888 A/ Sarojini	22.63 **	21.55 **	8.34**	8.77**	61.89 **	28.85 **	8.42**	6.62**
IR 68888 A/ Kera khadi	2.53 **	-3.81 **	-3.88**	-3.50**	31.59 **	-2.25	0.24	-1.42
IR 68888 A/ Luchai red	2.37 **	-5.75 **	-1.89*	-1.51	44.70 **	9.38 **	6.43**	4.67**
IR 68888 A/ Lajni super- 1	15.68 **	14.58 **	0.34	0.74	55.75 **	31.86 **	-5.28**	-6.84**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Head rice recovery percent				Amylose content (%)			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	15.19 **	12.06 **	12.12**	0.02	3.18	-13.45 **	-10.21**	-15.32**
IR 58025 A/ Luchai	-7.51 **	-15.25 **	-3.69*	-14.08**	-15.58 **	-29.77 **	-25.62**	-29.86**
IR 58025 A/ Pihu purple	-10.72 **	-18.25 **	-6.96**	-17.00**	50.01 **	24.13 **	-12.75**	-17.71**
IR 58025 A/ Bathras	-10.04 **	-16.96 **	-7.14**	-17.16**	13.68 **	-10.01 **	8.48**	2.31
IR 58025 A/ Pepri luchai	15.83 **	12.79 **	12.63**	0.47	-13.68 **	-20.55 **	-33.57**	-37.35**
IR 58025 A/ Khura bal	15.54 **	13.23 **	11.61**	-0.43	12.18 **	-1.14	-8.86**	-14.05**
IR 58025 A/ Sarojini	43.18 **	39.89 **	32.36**	18.08**	27.18 **	17.62 **	-17.32**	-22.02**
IR 58025 A/ Kera khadi	2.18	-7.34 **	7.76**	-3.87*	22.16 **	5.39 *	-25.92**	-30.13**
IR 58025 A/ Luchai red	-4.75 **	-12.02 **	-1.77	-12.37**	-4.32 *	-6.29 *	-31.30**	-35.21**
IR 58025 A/ Lajni super- 1	7.62 **	-0.36	-5.72**	-15.89**	-41.15 **	-43.36 **	-56.95**	-59.40**
IR 79156 A/ Ganga chur	-7.74 **	-11.01 **	-10.96**	-20.56**	-1.73	-11.38 **	-8.05**	-13.29**
IR 79156 A/ Luchai	16.58 **	5.98 **	20.43**	7.44**	-36.83 **	-43.55 **	-40.22**	-43.62**
IR 79156 A/ Pihu purple	-12.64 **	-20.64 **	-9.68**	-19.43**	8.70 **	-15.64 **	-29.67**	-33.67**
IR 79156 A/ Bathras	12.03 **	2.59	14.72**	2.34	-11.93 **	-25.51 **	-10.21**	-15.32**
IR 79156 A/ Pepri luchai	16.86 **	12.83 **	12.67**	0.51	18.97 **	18.80 **	-0.66	-6.32**
IR 79156 A/ Khura bal	-15.24 **	-17.65 **	-18.83**	-27.58**	-19.10 **	-22.97 **	-28.99**	-33.03**
IR 79156 A/ Sarojini	10.82 **	9.21 **	1.54	-9.42**	-7.90 **	-20.96 **	-34.10**	-37.85**
IR 79156 A/ Kera khadi	4.91 **	-5.61 **	9.77**	-2.07	48.23 **	19.45 **	-0.41	-6.08**
IR 79156 A/ Luchai red	10.94 **	1.66	13.51**	1.26	11.51 **	4.78 *	-12.64**	-17.61**
IR 79156 A/ Lajni super- 1	23.59 **	15.37 *	7.26**	-4.31**	25.63 **	20.09 **	0.12	-5.58**
IR 68888 A/ Ganga chur	29.83 **	-0.58	-0.53	-11.26**	23.10 **	2.47	6.31**	0.26
IR 68888 A/ Luchai	41.65 **	3.97 *	18.14**	5.40**	2.11	-15.69 **	-10.71**	-15.79**
IR 68888 A/ Pihu purple	-3.31	-29.06 **	-19.27**	-27.98**	80.43 **	50.42 **	3.76*	-2.14
IR 68888 A/ Bathras	19.24 **	-12.02 **	-1.63	-12.24**	-17.70 **	-35.30 **	-22.01**	-26.45**
IR 68888 A/ Pepri luchai	21.14 **	-7.17 **	-7.31**	-17.31**	41.78 **	29.38 **	8.17**	2.02
IR 68888 A/ Khura bal	11.01 **	-14.55 **	-15.77**	-24.86**	-36.70 **	-44.67 **	-48.99**	-51.89**
IR 68888 A/ Sarojini	66.21 **	32.06 **	19.22**	6.36**	41.20 **	31.73 **	-9.13**	-14.30**
IR 68888 A/ Kera khadi	30.89 **	-4.62 **	10.92**	-1.05	48.84 **	29.44 **	-10.71**	-15.79**
IR 68888 A/ Luchai red	43.17 **	5.69 **	18.00**	5.27**	55.86 **	51.25 **	10.89**	4.58**
IR 68888 A/ Lajni super- 1	42.49 **	18.26 *	-4.69**	-14.97**	66.47 **	58.77 **	20.68**	13.81**

*Significant at p=0.05% level, **Significant at p=0.01% level

Table 4.9 Mid parent Heterosis, Heterobeltiosis and Standard Heterosis

Crosses	Alkali spreading value				Gel consistency			
	Mid	Better	Standard		Mid	Better	Standard	
			Indira Sona	KRH-4			Indira Sona	KRH-4
IR 58025 A/ Ganga chur	-55.56 **	-60.00 **	-20	-50.00**	-1.05	-27.10 **	36.42**	-3.79**
IR 58025 A/ Luchai	-51.52 **	-60.00 **	-20	-50.00**	1.72 *	-6.42 **	108.46**	47.01**
IR 58025 A/ Pihu purple	-26.32 **	-30.00 **	40.00**	-12.5	-29.72 **	-37.46 **	17.03**	-17.47**
IR 58025 A/ Bathras	-55.56 **	-60.00 **	-20	-50.00**	-69.66 **	-71.10 **	-45.92**	-61.87**
IR 58025 A/ Pepri luchai	-13.33	-35.00 **	30.00**	-18.75**	-58.21 **	-69.40 **	-42.73**	-59.62**
IR 58025 A/ Khura bal	17.24 *	-15.00 *	70.00**	6.25	-7.89 **	-15.74 **	90.08**	34.05**
IR 58025 A/ Sarojini	-35.71 **	-55.00 **	-10	-43.75**	-3.46 **	-24.39 **	41.48**	-0.22
IR 58025 A/ Kera khadi	-53.33 **	-65.00 **	-30.00*	-56.25**	-57.91 **	-66.45 **	-37.23**	-55.73**
IR 58025 A/ Luchai red	13.33	-15.00 *	70.00**	6.25	46.13 **	8.07 **	102.22**	42.61**
IR 58025 A/ Lajni super- 1	11.76	-5	90.00**	18.75*	7.65 **	-0.22	86.72**	31.67**
IR 79156 A/ Ganga chur	-16.67 **	-25.00 **	50.00**	-6.25	-33.46 **	-36.08 **	-43.37**	-60.06**
IR 79156 A/ Luchai	3.03	-15.00 *	70.00**	6.25	-33.32 **	-54.45 **	1.47	-28.44**
IR 79156 A/ Pihu purple	-21.05 **	-25.00 **	50.00**	-6.25	10.34 **	-13.97 **	25.52**	-11.48**
IR 79156 A/ Bathras	-16.67 **	-25.00 **	50.00**	-6.25	-27.91 **	-46.59 **	-9.53**	-36.20**
IR 79156 A/ Pepri luchai	13.33	-15.00 *	70.00**	6.25	27.10 **	23.22 **	7.11**	-24.47**
IR 79156 A/ Khura bal	-3.45	-30.00 **	40.00**	-12.5	-3.17 **	-34.07 **	48.74**	4.89**
IR 79156 A/ Sarojini	-35.71 **	-55.00 **	-10	-43.75**	126.13 **	100.13 **	112.11**	49.58**
IR 79156 A/ Kera khadi	-6.67	-30.00 **	40.00**	-12.5	101.52 **	74.74 **	94.24**	36.98**
IR 79156 A/ Luchai red	-53.33 **	-65.00 **	-30.00*	-56.25**	169.31 **	157.26 **	130.61**	62.63**
IR 79156 A/ Lajni super- 1	-52.94 **	-60.00 **	-20	-50.00**	60.52 **	21.27 **	93.74**	36.63**
IR 68888 A/ Ganga chur	0.01	-5.56	70.00**	6.25	-29.65 **	-32.18 **	-39.91**	-57.62**
IR 68888 A/ Luchai	-3.23	-16.67 *	50.00**	-6.25	-24.09 **	-48.03 **	15.76**	-18.37**
IR 68888 A/ Pihu purple	-27.78 **	-27.78 **	30.00*	-18.75*	-47.58 **	-59.02 **	-40.20**	-57.83**
IR 68888 A/ Bathras	-5.88	-11.11	60.00**	0.01	-34.20 **	-51.13 **	-17.22**	-41.62**
IR 68888 A/ Pepri luchai	21.43 **	-5.56	70.00**	6.25	45.22 **	41.30 **	22.82**	-13.39**
IR 68888 A/ Khura bal	25.93 **	-5.56	70.00**	6.25	-28.47 **	-51.20 **	10.09**	-22.36**
IR 68888 A/ Sarojini	-30.77 **	-50.00 **	-10	-43.75**	104.87 **	81.91 **	92.81**	35.97**
IR 68888 A/ Kera khadi	42.86 **	11.11	100.00**	25.00**	-12.68 **	-24.04 **	-15.56**	-40.45**
IR 68888 A/ Luchai red	-7.14	-27.78 **	30.00*	-18.75*	84.72 **	77.09 **	58.75**	11.95**
IR 68888 A/ Lajni super- 1	-0.01	-11.11	60.00**	0.01	75.68 **	33.05 **	112.57**	49.90**

*Significant at p=0.05% level, **Significant at p=0.01% level

relative heterosis and only one hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -16.97 % (IR 58025A/ Ganga chur) to 12.86 % (IR 68888 A/ Pepri luchai). Among hybrids, five hybrids showed highly significant positive better heterosis and three hybrids showed significant positive better heterosis while four hybrids showed highly significant negative and four hybrids showed significant negative better parent heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -20.12% (IR 58025A/ Ganga chur) to 2.15% (IR 58025A/ Pepri luchai). Among hybrids, none of the hybrids showed significant positive standard heterosis and fourteen hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -14.29% (IR 58025A/ Ganga chur) to 9.60% (IR 58025A/ Pepri luchai). Among hybrids, six hybrids showed highly significant negative standard heterosis and two have significant negative standard heterosis whereas only one hybrid show highly significant positive relative heterosis and one shows significant positive relative heterosis for this trait.

Hybrids are generally characterized by having larger panicles indicating their efficiency in partitioning of assimilates to reproductive parts. Panicle length is one of the important attributes for higher yields in hybrids hence positive heterotic effects are desired for such traits. Highest significant positive heterotic effects were shown in crosse IR 79156 A/ Luchai.

Similar findings reported by Sreedhar *et al.* (2012), Patil *et al.* (2012), Utharasu and Anandakumar (2013), Veerasha *et al.* (2013), Srikrishna Latha *et al.* (2013), Ghara *et al.* (2014), Shinde and Patel (2014) and Nayak *et al.* (2015).

4.4.3. Flag leaf length (cm)

The mid parent heterosis ranged from -5.36 % (IR 58025 A/ Ganga chur) to 29.14% (IR68888A/Pepri luchai). Among 30 hybrids, twelve hybrids showed highly significant positive relative heterosis while four shows significant positive relative heterosis and none of the hybrid showed negative relative heterosis for this trait.

The Heterobeltiosis ranged from -14.55% (IR68888A/Sarojini) to 21.69% (IR79156A/ Pepri luchai). Among 30 hybrids, six hybrids showed highly significant positive better heterosis while four hybrids showed significant positive better heterosis and two hybrids showed negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -25.51% (IR68888A/Lajni super- 1) to 10.6% (IR79156A/Sarojini). Among 30 hybrids, none of the hybrids showed significant positive heterosis and seven hybrids showed significant negative heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -11.39% (IR68888A/Lajni super- 1) to 31.55% (IR79156A/ Sarojini). Among 30 hybrids, six hybrids showed highly significant positive heterosis while seven shows significant positive heterosis and none of the hybrids showed significant negative heterosis for this trait.

4.4.4. Flag leaf width (cm)

The mid parent heterosis ranged from -33.87% (IR68888A/Lajni super- 1) to 14.42% (IR68888A/Pepri luchai). Among 30 hybrids, none of the hybrids showed significant positive relative heterosis and six hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -35.42% (IR68888A/Lajni super- 1) to 7.49% (IR79156A/ Sarojini). Among 30 hybrids, none of the hybrids showed significant positive better heterosis and eight hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -42.19% (IR68888A/Lajni super- 1) to 14.69% (IR68888A/Pepri luchai). Among 30 hybrids, none of the hybrids showed significant positive heterosis and five hybrids showed negative significant heterosis for this trait.

The standard heterosis (over KRH- 4) ranged from -42.73% (IR68888A/Lajni super- 1) to 13.63% (IR68888A/Pepri luchai). Among 30 hybrids, none of the hybrids showed significant positive heterosis and five hybrids showed negative significant heterosis for this trait.

Similar result has been reported by Wang *et al.* (2010).

4.4.5 Days to 50% flowering

The relative heterosis for this trait ranged from -10.67 % (IR 58025A/ Bathras) to 8.59% (IR79156A/ Khura bal). Among hybrids, five hybrids showed highly significant negative heterosis while three hybrids showed significant negative heterosis and three hybrids showed highly significant positive heterosis while three hybrids showed significant positive heterosis for this trait.

The heterobeltiosis ranged from -13.70 % (IR68888A / Kera khadi) to 7.85% (IR79156A/ Khura bal). Among hybrids, only one hybrid showed highly significant positive heterosis and ten hybrids showed highly significant negative heterosis while seven hybrids showed significant negative heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -13.65% (IR 58025A/ Bathras and IR68888A/Bathras) to 6.98% (IR68888A / Luchai). Among hybrids, seven hybrids showed highly significant negative heterosis, five hybrids showed significant negative heterosis and four hybrids showed positive heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -17.07% (IR 58025A/ Bathras and IR68888A/ Bathras) to 2.74% (IR68888A/Luchai). Among hybrids, nineteen hybrids showed highly significant negative heterosis and none of the hybrids showed highly significant positive heterosis for this trait.

Negative heterosis is desirable for days to flowering because this will make the hybrids to mature earlier as compared to parents. Testers Bathras and Lajni super- 1 showed highest significant negative estimates for all heterosis.

Heterosis in both negative and positive direction for days to flowering has also been reported by Peng and Virmani (1991) and Murthy and Kulkarni (1996).

4.4.6 Effective tillers per plant

The mid parent heterosis ranged from -36.68% (IR68888A/ Luchai red) to 30.20% (IR 58025A/ Pepri luchai). Among hybrids, eight hybrids showed highly significant negative relative heterosis while five hybrids showed significant negative relative heterosis and only one hybrid showed significant positive relative heterosis for this trait.

The heterobeltiosis ranged from -50.45% (IR68888A/ Luchai red) to 8.43% (IR 58025A/ Pepri luchai). Among hybrids, none of the hybrids showed significant positive better heterosis and thirteen hybrids showed highly significant negative better heterosis while eight hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -45.87% (IR68888A/ Luchai red) to 18.81% (IR 58025A/ Pepri luchai). None of the hybrid showed positive highly significant standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -50.08% (IR68888A/ Luchai red) to 9.59% (IR 58025A/ Pepri luchai). Among hybrids, none of the hybrids shown significant positive standard heterosis for this trait while seventeen hybrids showed highly significant negative standard heterosis.

Number of productive tillers per plant is known to contribute directly towards grain yield can be exploited. Hence, heterosis over better parent and standard check in the positive direction is desirable for this trait.

Similar results have been reported by “Jarwar *et al.* (2012), Sreedhar *et al.* (2012), Patil *et al.* (2012), Utharasu and Anandakumar (2013), Srikrishna Latha *et al.* (2013), Ghara *et al.* (2014), Shinde and Patel (2014) and Sahu *et al.* (2016)”.

4.4.7 Filled spikelets per panicle

The mid parent heterosis ranged from -75.37% (IR79156A / Ganga chur) to 97.78% (IR 58025A /Sarojini). Among hybrids, four hybrids showed highly significant positive relative heterosis, two hybrids showed significant positive heterosis, twelve hybrids showed highly significant negative heterosis for this trait.

The heterobeltiosis ranged from -86.47% (IR79156A / Ganga chur) to 24.67% (IR 58025A/ Sarojini). Among hybrids, only one hybrid showed significant positive better heterosis while twenty four hybrids showed highly significant negative better heterosis and two have shown significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -83.63% (IR79156A/ Khura bal) to 58.90% (IR68888A/Kera khadi). Among hybrids, three hybrids showed highly significant positive standard heterosis, two hybrids showed

significant positive standard heterosis and twenty hybrids showed highly significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -90.14% (IR79156A/ Khura bal) to -4.29% (IR68888A/Kera khadi). Among hybrids, none of the hybrids showed significant positive standard heterosis while twenty eight hybrids showed highly significant negative standard heterosis for this trait.

The number of fertile spikelets directly contributes to seed yield hence positive heterotic effect would be highly desirable. In the present study, more number of fertile spikelets is closely associated with high yield per plant resulting high productivity. Therefore, the main interest is to find out the cross combinations with more number of long and heavy panicle bearing tillers. The tester Sarojini with line IR 58025A, tester Luchai and Kera khadi with line IR 68888A, tester Sarojini with IR 79156 A recorded higher values of heterotic expression for better parent, mid parent and both checks. Virmani *et al.* (1981 and 1982) reported that heterosis in yield was primarily due to increased number of spikelets panicle-1 further supported by Patel *et al.* (1994) and Reddy (1996) that confirms the present trend in this traits.

Significant positive heterosis for number of fertile spikelets per panicle was reported by “Tiwari *et al.* (2011), Saidaiah *et al.* (2012), Sreedhar *et al.* (2012), Patil *et al.* (2012), Issac (2007), Premkumar *et al.* (2017) and Ramesh *et al.* (2018)”.

4.4.8 Unfilled spikelets per panicle

The mid parent heterosis ranged from -41.18% (IR 79156A/Luchai) to 234.10% (IR68888A/ Pepri luchai). Among hybrids, fourteen hybrids showed highly significant positive relative heterosis while two hybrids showed significant positive relative heterosis and two hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -59.15% (IR 79156A/Luchai) to 139.28% (IR68888A/ Pepri luchai). Among hybrids, seven hybrids showed highly significant positive better heterosis, five hybrids showed highly significant negative better heterosis while three hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -1.31% (IR 79156A/Luchai) to 317.94% (IR 58025A/ Luchai red). Among hybrids, twenty two hybrids showed highly significant positive standard heterosis, one have shown significant positive standard heterosis and one hybrid showed significant positive standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -55.97% (IR 79156A/Luchai) to 86.46% (IR 58025A/ Luchai red). Among hybrids, four hybrids showed highly significant positive standard heterosis, three have shown significant positive standard heterosis and four hybrid showed highly significant negative standard heterosis, two hybrid showed significant negative standard heterosis for this trait.

Result revealed that promising crosses were IR 79156A/Luchai, IR 58025A/Pihu purple, showed heterosis in negative direction over mid parent and better parent. IR 79156A/ Luchai showed heterosis in negative direction over standard checks *viz.*, KRH-4.

Similar results have been reported by and Ramesh *et al.* (2018).

4.4.9 Pollen fertility percentage

The mid parent heterosis ranged from -70.02% (IR 79156A / Ganga chur) to 133.34% (IR 79156A / Pepri luchai). Among hybrids, fourteen hybrids showed significant positive relative heterosis and twelve hybrids showed highly significant negative relative heterosis and two hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -85.00% (IR 79156A / Ganga chur) to 16.70% (IR 79156A / Pepri luchai). Among hybrids, only one hybrid showed highly significant positive better heterosis, twenty three hybrids showed highly significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -85.73% (IR68888A/ Luchai red) to -2.10% (IR68888A/ Sarojini). Among 30 hybrids, twenty eight hybrids showed highly significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -85.63% (IR68888A/ Luchai red) to -1.36% (IR68888A/ Sarojini). Among 30 hybrids, twenty

seven hybrids showed highly significant negative significant standard heterosis and one hybrid showed significant negative significant standard heterosis for this trait.

The pollen fertility is responsible for yield therefore positive significant heterotic estimates are desirable. The testers Pepri luchai, Sarojini, Kera khadi and Lajni super-1 with IR 58025A showed positive significant heterotic values over relative heterosis. Similarly Luchai, Sarojini and Khura bal with lines CRMS 31A and CRMS 32A showed positive significant heterosis.

Similar findings reported by Jayasudha and Sharma (2009), Srikrishna Latha *et al.* (2013) and Bedi *et al.* (2016).

4.4.10 Spikelet Fertility (%)

The mid parent heterosis ranged from -68.06% (IR68888A/ Luchai red) to 59.20% (IR 79156A/ Sarojini). Among hybrids, six hybrids showed highly significant positive relative heterosis and eighteen hybrids showed highly significant negative relative heterosis and one hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -80.72% (IR68888A/ Luchai red) to -5.19% (IR 79156A/ Sarojini). Among hybrids, none of the hybrids showed positive better heterosis and twenty four hybrids showed highly significant negative better heterosis while four hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -78.14% (IR68888A/ Luchai red) to 1.97% (IR 79156A/ Luchai). Among hybrids, none of the hybrid showed significant positive standard heterosis and twenty four hybrids showed highly significant negative standard heterosis and two hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -75.76% (IR68888A/ Luchai red) to 13.06% (IR 79156A/ Luchai). Among hybrids, only one hybrid showed significant positive standard heterosis and twenty four hybrids showed highly significant negative standard heterosis for this trait.

“Most of the hybrids had negative heterosis due to the problem of spikelet sterility, as reported by Virmani *et al.* (1982). Standard heterosis of both positive and negative nature was observed by Panwar *et al.* (2002) whereas; similar

nature for heterobeltiosis was reported by Hari ramakrishnan *et al.* (2009) and Belhekar *et al.* (2017). Positive heterosis over batter parent and standard variety was reported by Virmani *et al.* (1981) they concluded that heterosis in yield was primarily due to increased fertile spikelets per panicle”.

4.4.11 Thousand Seed weight (g)

The mid parent heterosis ranged from -27.28% (IR 68888A / Ganga chur) to 23.33% (IR 79156A / Lajni super-1). Among hybrids, fifteen hybrids showed significant positive relative heterosis and ten hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -38.28% (IR 79156A/ Bathras) to 13.08% (IR 68888A/ Pepri luchai). Among hybrids, eight hybrids showed significant positive better heterosis and thirteen hybrids showed highly significant negative better heterosis while two hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -37.36% (IR 58025A/ Luchai red) to -2.60% (IR 58025A/ Pihu purple). Among hybrids, all hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -7.67% (IR 58025A/ Luchai red) to 43.56% (IR 58025A/ Pihu purple). Among hybrids, twenty two hybrids showed highly significant positive standard heterosis while only one showed significant positive standard heterosis and two hybrids showed significant negative standard heterosis for this trait.

“The trait thousand grains weight is an important yield component in the final yield, as the bold grained varieties normally out yield the other types. In the present study positive significant values are reported which were in agreement with the earilier findings by Rahimi *et al.* (2010), Krishna *et al.* (2011), Kumar *et al.* (2012), Pratap *et al.* (2013), Singh *et al.* (2013), Latha *et al.* (2013) and Sahu *et al.* (2017)”.

4.4.12 Grain yield per plant (g)

The mid parent heterosis ranged from -80.51% (IR 79156A/ Ganga chur) to 86.34% (IR 79156A/ Sarojini). Among hybrids, six hybrids showed

significant positive relative heterosis and twenty three hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -86.44% (IR 79156A/ Ganga chur) to 36.88% (IR 79156A/ Sarojini). Among hybrids, most of the hybrids showed significant negative better heterosis except IR 79156A/ Sarojini and IR 79156A/ Luchai that showed positive significant better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -86.59% (IR 79156A/ Ganga chur) to 17.14% (IR 79156A/ Luchai). Among hybrids, only two hybrids showed significant positive standard heterosis while twenty five hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -86.87% (IR 79156A/ Ganga chur) to 14.64% (IR 79156A/ Luchai). Among hybrids, most of the hybrids showed significant negative standard heterosis for this trait except IR 79156A/ Luchai and 79156A/ Sarojini.

Grain yield is a complex trait that is multiplicative end product of several attributes of yield. Hybrid showing high heterosis for grain yield per plant, also manifested heterotic effects for productive tillers per plant, panicle length, number grains per panicle and 1000 grain weight. Increased yield in rice due to various component traits as observed in the present investigation is in close conformity the finding observed by the other workers Issac (2007), Li *et al.* (2008), Vaithiyaligan and Nandarajan (2010), Tiwari *et al.* (2011), Patil *et al.* (2012), Sreedhar *et al.* (2012), Pratap *et al.* (2013), Srikrishna Latha *et al.* (2013), Veerasha *et al.* (2013), Ghara *et al.* (2014), Shinde and Patel (2014), Seesang *et al.* (2014), Sahu *et al.* (2017) and Thorat *et al.* (2017).

4.4.13 Biological yield per plant (g)

The mid parent heterosis ranged from -28.64% (IR 68888A/ Bathras) to 82.33% (IR 79156A/ Luchai red). Among hybrids, twelve hybrids showed highly significant positive relative heterosis while only one showed significant positive relative heterosis and seven hybrids showed highly significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -34.04% (IR 79156A/ Khura bal) to 57.63% (IR 79156A/ Sarojini). Among hybrids, eleven hybrids showed highly

significant negative better heterosis and nine hybrids showed highly significant positive better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -47.90% (IR 68888A/ Lajni super- 1) to 39.92% (IR 68888A/ Pepri luchai). Among hybrids, six hybrids showed highly significant positive standard heterosis while thirteen hybrids showed highly significant negative standard heterosis and only three showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -18.33% (IR 68888A/ Lajni super- 1) to 119.32% (IR 68888A/ Pepri luchai). Among hybrids, nineteen hybrids showed highly significant positive standard heterosis and only two hybrids showed significant negative standard heterosis for this trait.

Crosses having high grain yield per plant (economic yield per plant) and high biological yield per plant indicate that these crosses may be utilized in developing high yield potential hybrids (Akinwale *et al.*, 2011). The tester Luchai showed higher positive significant estimates with all the CMS lines for all heterosis. Similar results have been reported by Issac (2007), Tiwari *et al.* (2011), Kumar *et al.* (2012), Pratap *et al.* (2013) and Srikrishna Latha *et al.* (2013).

4.4.14 Harvest Index (%)

The mid parent heterosis ranged from -81.53% (IR 68888A/ Luchai red) to 80.21% (IR 68888A/ Sarojini). Among hybrids, three hybrids showed significant positive relative heterosis and twenty four hybrids showed highly significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -87.93% (IR 68888A/ Luchai red) to 14.82% (IR 68888A/ Sarojini). Among hybrids, twenty eight hybrids showed significant negative better heterosis for this trait and only one hybrid showed positive heterosis.

The standard heterosis (over Indira sona) ranged from -86.77% (IR 68888A/ Luchai red) to 40.78% (IR 68888A/ Sarojini). Among hybrids, only two hybrids showed significant positive standard heterosis while twenty six hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -91.75% (IR 68888A/ Luchai red) to -12.21% (IR 68888A/ Sarojini). Among hybrids, none of the

hybrids showed significant positive standard heterosis while all the hybrids showed significant negative standard heterosis for this trait.

Hybrid IR 68888A/ Sarojini had shown high standard heterosis for grain yield, biological yield and for harvest index which further support the concept that high biological yield leads to high economical yield and finally high harvest index.

Similar results have been reported by Bansal *et al.* (2000), Issac (2007), Tiwari *et al.* (2011), Kumar *et al.* (2012), Pratap *et al.* (2013), Utharasu and Anandakumar (2013) and Bedi *et al.* (2016).

4.4.15. Kernel length (mm)

The mid parent heterosis ranged from -15.97% (IR58025A/Khura bal) to 18.02% (IR79156A/Luchai). Among 30 hybrids, two hybrids showed highly significant positive relative heterosis while one showed significant positive relative heterosis and two hybrids showed highly significant negative relative heterosis and two showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -18.92% (IR58025A/Khura bal) to 9.73% (IR79156A/Luchai). Among 30 hybrids, only one hybrid showed significant positive better heterosis while fourteen hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -24.24% (IR58025A/Khura bal) to 2.53% (IR79156A/Luchai). Among 30 hybrids none of the hybrids showed significant positive standard heterosis while twenty six hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -6.83% (IR58025A/Khura bal) to 26.09% (IR79156A/Luchai). Among 30 hybrids, 11 hybrids showed significant positive standard heterosis while none of the hybrids showed significant negative standard heterosis for this trait.

Similar results have been reported by Shivani *et al.* (2009), Gnanamalar and Vivekanandan (2013) and Pratap *et al.* (2013).

4.4.16. Kernel breadth (mm)

The mid parent heterosis ranged from -5.98% (IR79156A/ Khura bal) to 24.77% (IR58025A/Luchai). Among 30 hybrids, five hybrids showed highly

significant positive relative heterosis, six hybrids showed significant positive relative heterosis and none of the hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -21.43% (IR79156A/ Khura bal) to 15.25% (IR58025A/Luchai). Among 30 hybrids, only one hybrid showed significant positive better heterosis while fourteen hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -13.21% (IR 68888A/ Lajni super-1) to 28.30% (IR58025A/Luchai). Among 30 hybrids, fourteen hybrids showed significant positive standard heterosis while three hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -16.36% (IR 68888A/ Lajni super-1) to 23.64% (IR58025A/Luchai). Among 30 hybrids, eight hybrids showed significant positive standard heterosis while three hybrids showed significant negative standard heterosis for this trait.

Similar results have been reported by Shivani *et al.* (2009), Gnanamalar and Vivekanandan (2013) and Pratap *et al.* (2013).

4.4.17. Kernel L/B ratio

The mid parent heterosis ranged from -24.17% (IR58025A/Luchai) to 6.81% (IR58025A/Sarojini). Among hybrids, none of the hybrids showed significant positive relative heterosis and nineteen hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -34.47% (IR58025A/Luchai) to -3.78% (IR58025A/Lajni super-1). Among hybrids, none of the hybrids showed significant positive better heterosis while twenty seven hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -35.07% (IR58025A/Luchai) to -1.48% (IR 79156A/ Lajni super-1). Among hybrids, none of the hybrids showed significant positive standard heterosis while twenty six hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -17.10% (IR58025A/Luchai) to 25.80% (IR 79156A/ Lajni super-1). Among hybrids, nine

hybrids showed significant positive standard heterosis while only two hybrids showed significant negative standard heterosis for this trait.

Similar results have been reported by Shivani *et al.* (2009), Gnanamalar and Vivekanandan (2013) and Pratap *et al.* (2013).

4.4.18. Cooked rice length (mm)

The mid parent heterosis ranged from -0.56% (IR 68888A/Ganga chur and IR 68888A/ Sarojini) to 0.92% (IR58025A/Sarojini). Among hybrids, five hybrids showed significant positive relative heterosis and five hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -16.51% (IR 68888A/Ganga chur) to 12.50% (IR58025A/Sarojini). Among hybrids, four hybrids showed significant positive better heterosis while only two hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -11.22% (IR 68888A /Luchai red) to 7.14% (IR58025A/Sarojini). Among hybrids, only one hybrid showed significant positive standard heterosis while fourteen hybrid showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -0.38% (IR 68888A /Luchai red) to 20.23% (IR58025A/Sarojini). Among hybrids, none of the hybrids showed significant positive standard heterosis while seventeen hybrids showed significant negative standard heterosis for this trait.

Similar results have been reported by Shivani *et al.* (2009) and Gnanamalar and Vivekanandan (2013).

4.4.19. Cooked rice breadth (mm)

The mid parent heterosis ranged from -6.59% (IR 68888A/Khura bal) to 30.50% (IR79156A/Luchai red). Among hybrids, seventeen hybrids showed significant positive relative heterosis while only one hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -13.33% (IR58025A/Ganga chur) to 27.69% (IR58025A/Luchai red). Among hybrids, nine hybrid showed significant positive better heterosis while six hybrids showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -11.49% (IR58025A /Khura bal) to 9.20% (IR79156A/Luchai). Among hybrids, four hybrids showed significant positive standard heterosis while ten hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -18.09% (IR58025A /Khura bal) to 1.06% (IR79156A/Luchai). Among hybrids, none of the hybrids showed significant positive standard heterosis while twenty five hybrids showed significant negative standard heterosis for this trait.

4.4.20. Cooked rice L/B ratio

The mid parent heterosis ranged from -23.34% (IR79156A/Luchai red) to 12.25% (IR68888A/Khura bal). Among hybrids, only two hybrids showed significant positive relative heterosis and fourteen hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -27.88% (IR79156A/Luchai red) to 7.74% (IR68888A/Khura bal). Among hybrids, none of the hybrids showed significant positive better heterosis while nineteen hybrid showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -14.43% (IR68888A /Ganga chur) to 15.34% (IR 58025A/Ganga chur). Among hybrids, only two hybrids showed significant positive standard heterosis while five hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -3.77% (IR68888A /Ganga chur) to 39.86% (IR 58025A/Ganga chur). Among hybrids, twenty five hybrids showed significant positive standard heterosis while none of the hybrids showed significant negative standard heterosis for this trait.

4.4.21. Hulling (%)

The mid parent heterosis ranged from -12.46% (IR 68888A/ Pihu purple) to 22.63% (IR 68888A/ Sarojini). Among hybrids, sixteen hybrids showed highly significant positive relative heterosis while two hybrids showed significant positive relative heterosis and nine hybrids showed highly significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -17.88% (IR 68888A/ Pihu purple) to 21.55% (IR 68888A/ Sarojini). Among hybrids, twelve hybrids showed highly significant positive better heterosis while thirteen hybrids showed highly significant negative better heterosis and one hybrid showed significant negative better heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -17.93% (IR 68888A/ Pihu purple) to 8.34% (IR 68888A/ Sarojini). Among hybrids, six hybrids showed highly significant positive standard heterosis and one hybrid showed significant positive standard heterosis while thirteen hybrids showed highly significant negative standard heterosis and two hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -17.60% (IR 68888A/ Pihu purple) to 8.77% (IR 68888A/ Sarojini). Among hybrids, seven hybrids showed significant positive standard heterosis while thirteen hybrids showed highly significant negative standard heterosis for this trait.

In the present investigation hybrid IR 68888A/ Sarojini exhibited highest significant heterosis over better parent, mid parent and standard heterosis over both the checks for hulling recovery percent.

“Higher yielding hybrids found in present study with no reduction in hulling % may be considered better. Similar results have been reported by Pandya and Tripathi (2006), Shivani *et al.* (2009) and Gnanamalar and Vivekanandan (2013), Sharma *et al.* (2013)”.

4.4.22. Milling (%)

The mid parent heterosis ranged from -12.69% (IR 79156 A/ Khura bal) to 61.89% (IR 68888A/ Sarojini). Among hybrids, twenty one hybrids showed significant positive relative heterosis while only one hybrids showed significant positive relative heterosis and five hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -18.02% (IR 79156 A/ Khura bal) to 34.68% (IR 58025/ Sarojini). Among hybrids, thirteen hybrids showed significant positive relative heterosis while only one hybrids showed significant positive

relative heterosis and eleven hybrids showed significant negative relative heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -22.67% (IR 79156 A/ Khura bal) to 13.96% (IR 58025/ Sarojini). Among hybrids, seven hybrids showed highly significant positive standard heterosis while seventeen hybrids showed highly significant negative standard heterosis and only one hybrid showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -23.95% (IR 79156 A/ Khura bal) to 12.07% (IR 58025/ Sarojini). Among hybrids, five hybrids showed highly significant positive standard heterosis while nineteen hybrids showed highly significant negative standard heterosis for this trait.

Similar results have been reported by Pandya and Tripathi (2006), Shivani *et al.* (2009) and Gnanamalar and Vivekanandan (2013).

4.4.23. Head Rice Recovery (%)

The mid parent heterosis ranged from -15.24% (IR 79156 A/ Khura bal) to 66.21% (IR 68888A/ Sarojini). Among hybrids, twenty one hybrids showed significant positive relative heterosis and seven hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -29.06% (IR 68888A / Pihu purple) to 39.89% (IR 58025/ Sarojini). Among hybrids, nine hybrids showed highly significant positive relative heterosis while three hybrids showed significant positive relative heterosis and fourteen hybrids showed significant negative relative heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -19.27% (IR 68888A / Pihu purple) to 32.36% (IR 58025/ Sarojini). Among hybrids, fifteen hybrids showed highly significant positive standard heterosis while ten hybrids showed highly significant negative standard heterosis and only one hybrid showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -27.98% (IR 68888A / Pihu purple) to 18.08% (IR 58025/ Sarojini). Among hybrids, five hybrids showed significant positive standard heterosis while sixteen hybrids showed highly

significant negative standard heterosis and only one hybrid showed significant negative standard heterosis for this trait.

Similar results have been reported by Singh (2005), Shivani *et al.* (2009) and Gnanamalar and Vivekanandan (2013).

4.4.24. Amylose content%

The mid parent heterosis ranged from -41.15% (IR 58025A/ Lajni super-1) to 80.43% (IR 68888A / Pihu purple). Among hybrids, seventeen hybrids showed highly significant positive relative heterosis and nine hybrids showed highly significant negative relative heterosis and only one hybrid showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -44.67% (IR 68888A/ Khura bal) to 58.77% (IR 68888A/ Lajni super-1). Among hybrids, eleven hybrids showed highly significant positive relative heterosis and two hybrids showed significant positive relative heterosis while fourteen hybrids showed highly significant negative heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -56.95% (IR 58025A/ Lajni super-1) to 20.68% (IR 68888A/ Lajni super-1). Among hybrids, five hybrids showed significant positive standard heterosis and only one hybrid showed significant positive standard heterosis while twenty hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -59.40% (IR 58025A/ Lajni super-1) to 13.81% (IR 68888A/ Lajni super-1). Among hybrids, only two hybrids showed highly significant positive standard heterosis while twenty four hybrids showed highly significant negative standard heterosis for this trait.

4.4.25 Alkali Spreading Value

The mid parent heterosis ranged from -55.56% (IR 58025 A/ Ganga chur) to 42.86% (IR 68888 A/ Kera khadi). Among hybrids, four hybrids showed significant positive relative heterosis and fourteen hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -65.00% (IR 58025 A/ Kera khadi and IR 79156 A/ Luchai red) to -5% (IR 58025 A/ Lajni super- 1). Among hybrids, twenty three hybrids showed significant negative relative heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -30.00% (IR 58025 A/ Kera khadi and IR 79156 A/ Luchai red) to 100.00% (IR 68888 A/ Kera khadi). Among hybrids, twenty one hybrids showed significant positive standard heterosis while none of the hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -56.25% (IR 58025 A/ Kera khadi and IR 79156 A/ Luchai red) to 25.00% (IR 68888 A/ Kera khadi). Among hybrids, only two hybrids showed significant positive standard heterosis while thirteen hybrids showed significant negative standard heterosis for this trait.

4.4.26. Gel Consistency

The mid parent heterosis ranged from -69.66% (IR 58025 A/ Bathras) to 169.31% (IR 79156 A/ Luchai red). Among hybrids, thirteen hybrids showed significant positive relative heterosis and fifteen hybrids showed significant negative relative heterosis for this trait.

The heterobeltiosis ranged from -71.10% (IR 58025 A/ Bathras) to 157.26% (IR 79156 A/ Luchai red). Among hybrids, ten hybrids showed significant positive relative heterosis and nineteen hybrids showed significant negative relative heterosis for this trait.

The standard heterosis (over Indira sona) ranged from -45.92% (IR 58025 A/ Bathras) to 130.61% (IR 79156 A/ Luchai red). Among hybrids, twenty hybrids showed significant positive standard heterosis while nine hybrids showed significant negative standard heterosis for this trait.

The standard heterosis (over KRH-4) ranged from -61.87% (IR 58025 A/ Bathras) to 62.63% (IR 79156 A/ Luchai red). Among hybrids, twelve hybrids showed significant positive standard heterosis while seventeen hybrids showed significant negative standard heterosis for this trait.

4.5 Identification of Maintainer and Restorer Lines

For three line breeding systems, identification of restorers and maintainers are the necessary. The identification of new restorers and maintainers were essential for production of potentially high yielding and widely adopted hybrid rice by using diverse source of cytoplasmic sterile lines from different origin.

The specific genotypes which produce higher fertile (above 75% spikelet fertility and above 80% pollen fertility) progeny after the crossing with the CMS lines can be used as male parent and are called potential restorers. Similarly those specific genotypes which produce completely male sterile progeny (0-0.1 spikelet fertility% and 0-1% pollen fertility%) after crossing with CMS line, can be converted into female parent (CMS line) are called maintainers. Partial restorers are not useful for developing the hybrids. Thus potential restorer can be utilized in further hybrid rice breeding programme to develop location specific hybrids.

Identification of restorers and maintainers was carried out by considering observations on pollen fertility and spikelet fertility percentage as per the classification is given by Virmani *et al.*, (1997). The findings of the present investigation are discussed here in under:

The restorers and maintainers identified in the present investigation are presented in the Table 4.10. In the present study, the frequency of maintainers appears to be quite high as compared to restorers for cytoplasmic male sterile lines IR 58025A, IR 79156A and IR 68888A. Frequency table (Table 4.11) and Figure 4.1 illustrated that percentage of partial maintainers are highest followed by partial restorer, restorers and maintainer (lowest) respectively, based on pollen fertility. Similar results were found, based on spikelet fertility.

The studies on pollen and spikelet fertility percentages indicated that none of the hybrids possessed complete i.e. 100% pollen and spikelet sterility. So, none of the parent could be identified as maintainer, of course partial maintainers were identified. Ganga chur, Pihu purple, Bathras, Khura bal, Luchai red were identified as partial maintainer for the CMS line IR58025A. The parent Ganga chur, Pihu purple, Bathras, Luchai red, Lajni super- 1 were identified as partial maintainer for the line IR79156A. The genotypes Ganga chur, Pihu purple, Bathras, Kera khadi, Luchai red, Lajni super- 1 were identified as partial maintainers in relation to line IR68888A. The lines identified as partial maintainers can be further multiplied and back crossed with their respective F₁'s to look for completely sterile back cross progenies so that these can be developed as new CMS lines.

Similarly work plan was reported by Durai and Nadarajan (2007), Umadevi *et al.* (2010), Jayashudha and Sharma (2010), Sharma *et al.* (2012), Sri Krishnalatha and Sharma (2012), Veerasha *et al.* (2013) and Sahu *et al.* (2014).

The parents Luchai, Pepri luchai, Sarojini, Kera khadi can be considered as partial restorers for the CMS line IR58025A. Parent Kera khadi was identified as partial restorers for the CMS line IR79156A. Whereas the parents, Luchai, Pepri luchai, Khura bal can be considered as partial restorers for CMS line IR68888A. Lajni super- 1 has been considered as potential restorer for CMS line IR 58025A and Luchai, Pepri luchai, Khura bal, Sarojini has been identified as potential restorer for IR79156A and Sarojini has been identified as potential restorer for CMS line IR68888A.

Hybrid IR 68888 A/ Sarojini showed highest pollen fertility (93.23%) and spikelet fertility (75.23%) followed by cross IR-79156A/ Pepri luchai (91.97% and 72.13%). Therefore these parents involved in the crosses can be effectively utilized as good restorer lines to develop high yielding rice hybrids.

Findings of similar nature have been reported by Durai and Nadarajan (2007), Akhter *et al.* (2008), Babu *et al.* (2010), Jayasudha and Sharma (2010), Umadevi *et al.* (2010), Sanghera *et al.* (2010), Waghmode and Ingale (2011), Sri Krishnalatha and Sharma (2012), Khan *et al.* (2012), Veerasha *et al.* (2013), and Sahu *et al.* (2014).

The genotypes, Luchai, Pepri luchai, Sarojini, Kera khadi were recorded as partial restorers for the line IR58025A, while the genotype Kera khadi acted as partial restorers for the line IR 79156A . The Genotypes Luchai, Pepri luchai, Khura bal was observed as partial restorers for CMS line IR 68888A.

Similar types of results were reported by Bisne and Motiramani (2005), Jayasudha and Sharma (2010), Sri Krishnalatha and Sharma (2012), Khan *et al.* (2012), Veerasha *et al.* (2013) and Sahu *et al.* (2014).

In some cases, the same genotype behaved as a restorer for one CMS line and as partial maintainer or partial restorer for the other CMS line. Tester Khura bal behaved as partial maintainer for CMS line IR58025A and partial restorer for both CMS line IR68888A and IR 79156A based on pollen and spikelet fertility

Table No. 4.10 List of Identified Restorers and Maintainers

CMS Line	Potential Maintainer (pollen fertility % 0 to 1 and spikelet fertility % 0-0.1)	Partial Maintainer (pollen fertility % 1.1 to 50 and spikelet fertility % 0.1 to 50)	Partial Restorer (pollen fertility % 50.1 to 80 and spikelet fertility % 50.1 to 75)	Potential Restorer (pollen fertility % >80 and spikelet fertility % >75)
IR58025A	–	Ganga chur, Pihu purple, Bathras, Khura bal, Luchai red	Luchai, Pepri luchai, Sarojini, Kera khadi	Lajni super- 1
IR79156A	–	Ganga chur, Pihu purple, Bathras, Luchai red, Lajni super- 1	Kera khadi	Luchai, Pepri luchai, Khura bal, Sarojini
IR68888A	–	Ganga chur, Pihu purple, Bathras, Kera khadi, Luchai red, Lajni super- 1	Luchai, Pepri luchai, Khura bal	Sarojini

Table No. 4.11 Frequency of Restorers and Maintainers (Based on pollen and spikelet fertility)

S.N.	CMS LINES	CLASSIFICATION BASED ON															
		POLLEN FERTILITY								SPIKLET FERTILITY							
		R	%	PR	%	PM	%	M	%	R	%	PR	%	PM	%	M	%
1.	IR58025A	1	3.33	4	13.33	5	16.66	0	0	1	3.33	4	13.33	5	16.66	0	0
2.	IR79156A	4	13.33	1	3.33	5	16.66	0	0	3	13.33	3	3.34	4	16.67	0	0
3.	CRMS32A	1	3.33	3	10.00	6	20.00	0	0	2	3.33	3	10.00	5	20.00	0	0
	TOTAL	6	19.99	8	26.66	16	53.32	0	0	6	19.99	8	26.67	16	53.33	0	0

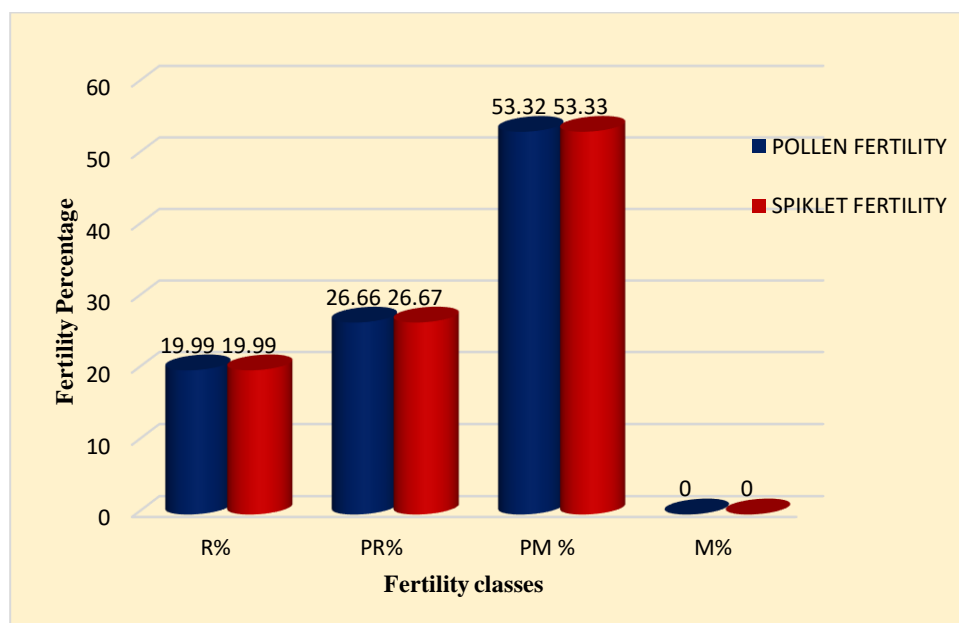


Fig. 4.1 Frequency of Restorers and Maintainers

respectively. Genotype Lajni super- 1 behaved as potential restorer for IR58025A and partial maintainer for IR79156A and IR68888A.

Genotype Ganga chur, Pihu purple, Bathras and Luchai red behaved as partial maintainer for all the CMS lines IR 58025A, IR 79156A and IR68888A. Genotype Sarojini behaved as partial restorer for line IR 58025A and potential restorer for lines IR 79156A and IR68888A. Tester Luchai behaved as partial restorer for lines IR 58025A and IR68888A and partial maintainer for both line IR 79156A. Tester Kera khadi behaved as partial maintainer for line IR68888A and behaved as partial restorer for line IR 58025A and IR 79156A.

The variations in behaviour of fertility restoration indicate that either the fertility-restoring genes are different or that their penetrance and expressivity varied with the genotypes of the parents or the modifiers of female background. This could be due to differential nuclear cytoplasmic interactions between the testers and CMS lines. This kind of the differential reaction of the same genotype in restoring the fertility of different CMS lines of same cytoplasmic source was reported by Murugan and Ganesan (2006), Umadevi *et al.* (2010) and Jayasudha and Sharma (2010), Sri Krishnalatha and Sharma (2012), Sharma *et al.* (2012) and Veerasha *et al.* (2013) and Sahu *et al.* (2014).

4.6 Genetic purity testing at molecular level

In rice, cytoplasmic male sterile (CMS) based three-line breeding system has become the most popular method of hybrid rice production which has helped to evaluate more rice hybrids. Selection of diverse parents with desirable characters can be done based on analysis of morphological, biochemical and DNA based markers. DNA based molecular markers have been used effectively to assess the genetic variability in several crop species. It also facilitates identifying of parental line specific molecular markers (Nandakumar *et al.*, 2004; Sarao *et al.*, 2010), that are useful in detecting hybrids derived from them as well as genome mapping of economically important traits.

Earlier the genetic divergence among the parents has been assessed by using morphological traits which are often influenced by environment and require special experimental designs to distinguish genotypic and phenotypic variations. But the recent developments in the field of molecular marker technology have provided tools for in depth analysis of the relationship between genetic divergence at molecular level and the performance of hybrids. The hybrids showing strong heterosis were usually developed from parental lines diverse in relatedness, ecotype, geographic origin, etc. Among the vast array of molecular markers, microsatellite markers also known as simple sequence repeats (SSR) have been extensively used to study the genetic diversity and its relationship to heterosis .

4.6.1 Identification of SSR markers for parental polymorphism

The present study was conducted to determine the genetic diversity of thirteen genotypes. Three rice cytoplasmic male sterile lines (CMS lines) and ten restorer lines were analyzed by microsatellite markers. Four SSR markers with known sequences were taken for the study, out of which two polymorphic markers were identified namely, RM-1 and RM-495 for parental polymorphism study.

4.6.2 Genetic purity of hybrid at molecular level

“Maintenance of high level of genetic purity of hybrids is essential to exploit the moderate level of heterosis observed in rice crop because there is always a chance of contamination in the hybrid seed production plot due to pollen shedders, out crossing and physical mixtures during the subsequent handling of the harvested material (Sudharani *et al.*, 2013). It is estimated that for every one per cent impurity

in the hybrid seed, the yield reduction is 100 kg/ha (Mao *et al.*, 1996). Assessment and maintenance of genetic purity of the parental lines and hybrids is crucial in delivering the pure hybrid seed for the successful adoption of this technology (Deshmukh *et al.*, 2013). Genetic purity of hybrids is generally assessed by conducting grow out test (GOT) where morphological and floral characters are analyzed, however results may be influenced by environment. Further, it is expensive and time consuming. DNA based markers are rapid reliable and cost effective for hybrid purity assessment (Yadav *et al.*, 2013)".

Molecular markers, in contrast, being based on DNA sequence variation, provide an unbiased means of identifying crop varieties (Nandakumar *et al.*, 2004, Tamilkumar *et al.*, 2009). Among the various DNA based markers currently available, genetically mapped simple sequence repeat (SSR) markers are most widely used for rapid assessment of hybrid and parental line seed purity in rice (Yashitola *et al.*, 2002, Maccaferri *et al.* 2007 and YU *et al.*, 2011) because of their multi-allelic nature, high reproducibility, co-dominant inheritance, abundance and extensive genome coverage (Sundaram *et al.*, 2008). SSR marker gives authentic result with high accuracy, high reliability and low cost (Yadav *et al.*, 2013). A large number of SSR markers have been developed and mapped in rice, which vary in the degree of polymorphism depending on their position in the coding or non-coding segments, nature of their repeat motifs and the genome wide abundance.

Total of thirty rice hybrids and their thirteen parental lines were analysed using four microsatellite markers. The parental polymorphism survey indicated that out of four markers, two SSR markers namely, RM 1 and RM495 showed parental polymorphism where band size varied from 100 bp to 200 bp. The profile of SSR primer RM 495 is depicted in (Figure 4.6.1) which clearly shows polymorphism between the parents and some hybrids. The band size varies from 100 to 200 bp. Similar profile was also observed with the marker RM 1 which also showed polymorphism between the parents and some hybrids (Figure 4.6.2). The band size for RM 1 varies from 70 to 150 bp.

Figure 4.2: SSR marker RM 495 showing parental polymorphism between A and R lines

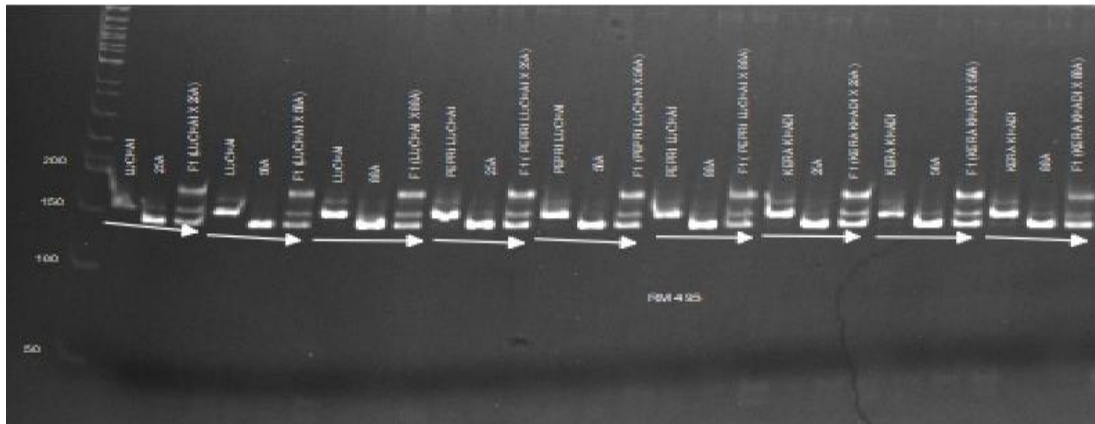
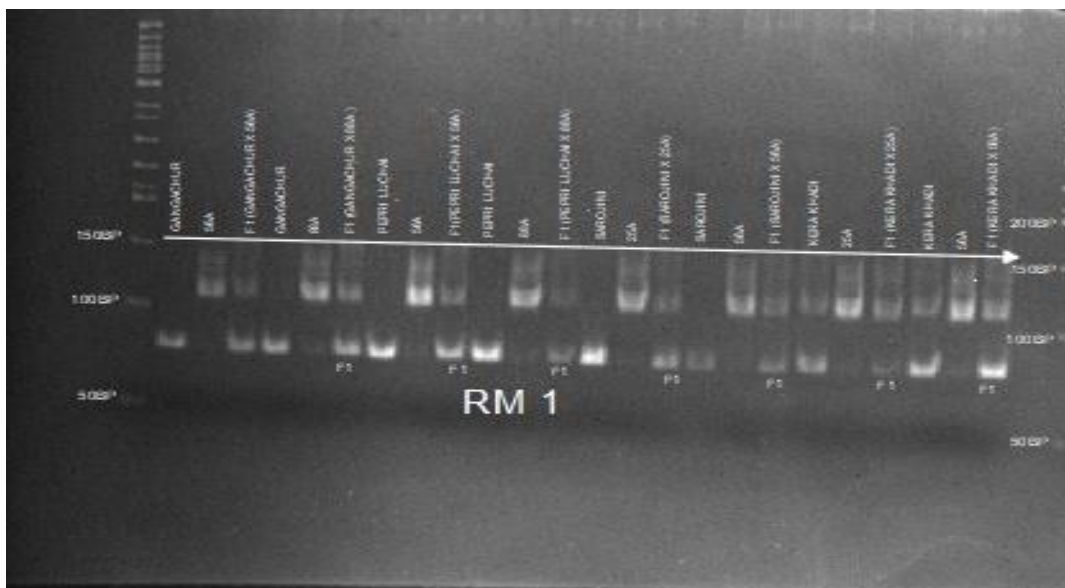


Figure 4.3: SSR marker RM 1 showing parental polymorphism between A and R lines



To determine the purity of hybrids, banding pattern of hybrid plants and their parental lines were studied and found that pure hybrid gives two bands corresponds to their parental lines bands. Off types or mixtures shows differential banding pattern than the parental bands. The SSR primer RM-495 gave significant result for total of nine hybrids (cross combinations) namely, IR-58025A/Luchai, IR-79156A /Luchai, IR-68888A/Luchai, IR-58025A/ Pepri luchai, IR-79156A / Pepri luchai, IR-68888A / Pepri luchai, IR-58025A/ Kera khadi IR-79156A/Kera khadi and IR-68888A / Kera khadi. All nine hybrids shows two bands, each from their corresponding parent for RM-497 and rest of all were monomorphic or the F1 resemble like female parent. Similarly RM-1 gave significant result for, IR-58025A/ Ganga chur, IR-79156A/ Ganga chur, IR-68888A / Ganga chur, IR-58025A/ Pepri luchai, IR-79156A / Pepri luchai, IR-68888A / Pepri luchai, IR-58025A/ Kera khadi IR-79156A/Kera khadi and IR-68888A / Kera khadi .

To determine the purity of hybrids; banding pattern of eight individual plant of each hybrid were taken and their parental lines were studied. The band size in the parents and the population ranged between 70 to 200 bp. This result was confirmed using field observations. Rest of all hybrids identified for RM 495 and RM 1 were not shown similar banding pattern for all plants.

In the present study two polymorphic markers clearly distinguish all the parental lines. Out of these markers RM-495 distinguishes pure hybrids and mixture/off types very precisely. However, both the polymorphic markers are still relevant and can be used to determine the purity of rice hybrids. Therefore, it is concluded that genetic purity analysis through SSR marker will be a useful tool for resolving the problem arises in seed certification programme as well as the rapid determination of genetic purity of the rice hybrids.

CHAPTER V

SUMMARY AND CONCLUSIONS

For more than one third population of world, rice is the most essential food crop and a chief source for food of world. For millions of mankind, it is a staple food from the beginning of civilization. Hybrid rice technology offers a prospect to increment in the production and productivity of rice among the obtainable advanced and because of the technologies that are immediately adoptable, and thereby guaranteed a balanced supply of food as per projected estimate made for 2025.

The present investigation “**Study of heterosis and combining ability in CMS based rice (*Oryza sativa* L.) hybrids.**” was directed at “Research cum Instructional Farm of Department of Genetics and Plant Breeding, IGKV, Raipur, Chhattisgarh during *kharif* 2017 and *kharif* 2018” and this study under taken with the objectives given below:

1. Estimation of general combining ability and specific combining ability for grain yield
2. Identification of potential restorers and maintainers.
3. Estimation of heterosis for grain yield and quality traits.
4. Genetic purity testing of selected hybrids.

The experimental material which are used were, three lines *viz.*, “IR-58025A, IR79156A, IR-6888A and ten rice varieties/ landraces *viz.*, Ganga Chur, Luchai, Pihu purple, Bathras, Pepri Luchai, Khura Bal, Sarojani, Kera Khadi, Luchai Red and Lajni Super-1 as tester and their thirty hybrids. The hybrids were generated in line x tester pattern for the estimation of combining ability effects and magnitude of heterosis. The hybrids were evaluated along with their parents in Randomized Complete Block Design (RCBD) with three replications under rainfed conditions. Twenty one days old seedlings of total 18 hybrids and their parents were transplanted

in the field. A standard spacing of 20 x 15 cm was adopted for the planting. Single seedling per hill was planted. Recommended package of practices were followed”.

As the positive GCA value is significant for IR 79156A (among lines) for grain yield/ plant, it is considered as good general combiner. And for the same trait, Luchai, Pepri luchai and Sarojini were also good combiners (among the testers).

IR 68888 A/ Kera khadi showed highest SCA value followed by IR 58025 A/ Luchai red, IR 79156 A/ Sarojini and IR 79156 A/ Luchai for grain yield per plant. Some hybrids *viz.*, IR 58025 A/ Sarojini, IR 58025 A/ Pihu purple, IR 68888 A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Kera khadi and IR 68888 A/ Luchai red were identified as favorable hybrids for quality traits *viz.*, kernel length, kernel breadth cooked rice length, cooked rice breadth, hulling%, milling% and head rice recovery based on SCA effects. IR 79156 A/ Luchai, IR 68888 A/ Sarojini, IR 58025 A/ Ganga chur were found to be favorable hybrids for pollen fertility% and spikelet fertility% on the basis of SCA effects.

Six hybrids *viz.*, IR 79156A/ Luchai, IR 79156A/ Sarojini, IR 58025 A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, and IR 58025 A/ Sarojini were found as favorable crosses on the basis of “mean performance, heterosis estimation, SCA effects and GCA effects (of their corresponding parents) for grain yield per plant”. In Table 5.1 favorable crosses are listed. Among these six hybrids, five hybrids *viz.*, IR 79156A/ Luchai, IR 79156A/ Sarojini, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, and IR 58025 A/ Sarojini showed desired HRR with intermediate amylose content Table 5.2 showed the HRR performance of the same hybrids which are mentioned above:

Crosses IR 58025 A/ Sarojini, IR-79156A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, IR 68888 A/ Luchai red and IR-79156A/ Bathras were identified as favorable crosses based on good performance in HRR. List of favorable crosses for HRR are listed in Table 5.3.

On the basis of spikelet and pollen fertility % the genotype, Sarojini was found to be potential restorer for lines IR 79156 A and IR 68888A. Besides, Lajni super- 1, Luchai, Pepri luchai and Khura bal were also identified as potential restorers. This study indicated that “none of the testers could be identified as potential maintainer but Ganga chur, Pihu purple, Bathras, Khura bal and Luchai red have been identified as partial maintainers for the CMS line IR58025A. Ganga chur, Pihu purple, Bathras, Luchai red and Lajni super- 1 have been identified as partial maintainers for the CMS line IR 79156 A and Ganga chur, Pihu purple, Bathras, Kera khadi, Luchai red, and Lajni super- 1 have been identified as partial maintainers for the CMS line IR 68888A. The parents Ganga chur, Pihu purple, Bathras and Luchai red have been identified as partial maintainers for all the three lines. The parents Kera khadi performed as partial restorers for lines IR 58025A and IR 79156 A whereas, Luchai and Pepri luchai acted as partial restorers for the lines IR58025A and IR 68888A”.

Table 5.1 Promising hybrids based on Mean performance, Heterosis and Combining Ability for Grain Yield per plant

Hybrids	Heterosis					GCA Effects		SCA Effects
	Mean Value (g)	MP	BP	Indira sona	KRH- 4	Lines	Testers	Hybrids
IR-79156A/ Luchai	17.2	60.35 **	9.11 *	17.14**	14.64**	0.72 **	8.45 **	1.34 **
IR-79156A/ Sarojini	16.6	86.34 **	36.88 **	13.05**	10.64**	0.72 **	7.66 **	1.53 **
IR 58025 A/ Luchai	14.59	34.01 **	-7.48 *	-0.68	-2.8	0.1	8.45 **	-0.66
IR 68888 A/ Sarojini	13.86	74.92 **	14.23 **	-5.65	-7.66	-0.82 **	7.66 **	0.32
IR 68888 A/ Luchai	13.64	40.04 **	-13.49 **	-7.13	-9.11*	-0.82 **	8.45 **	-0.68
IR 58025 A/ Sarojini	12.61	39.08 **	3.96	-14.14**	-15.97**	0.1	7.66 **	-1.85 **

Table 5.2 HRR for the hybrids who gave best performance for grain yield per plant according to Mean Performance, Heterosis And Combining Ability

Hybrids	Heterosis					GCA Effects		SCA Effects
	Mean Value (g)	MP	BP	Indira sona	KRH- 4	Lines	Testers	Hybrids
IR-79156A/ Luchai	64.2	16.58 **	5.98 **	20.43**	7.44**	0.22	4.27 **	4.47 **
IR-79156A/ Sarojini	54.2	10.82 **	9.21 **	1.54	-9.42**	0.22	7.51 **	-8.85 **
IR 58025 A/ Luchai	51.4	-7.51 **	-15.25 **	-3.69*	-14.08**	0.80 **	4.27 **	-8.97 **
IR 68888 A/ Sarojini	63.6	66.21 **	32.06 **	19.22**	6.36**	-1.02 **	7.51 **	1.83 **
IR 68888 A/ Luchai	63	41.65 **	3.97 *	18.14**	5.40**	-1.02 **	4.27 **	4.50 **
IR 58025 A/ Sarojini	70.6	43.18 **	39.89 **	32.36**	18.08**	0.80 **	7.51 **	7.02 **

Table 5.3 Promising hybrids based on Mean Performance, Heterosis and Combing Ability for HRR

Hybrids	Heterosis					GCA Effects		SCA Effects
	Mean Value (g)	MP	BP	Indira sona	KRH- 4	Lines	Testers	Hybrids
IR 58025 A/ Sarojini	70.6	43.18 **	39.89 **	32.36**	18.08**	0.80 **	7.51 **	7.02 **
IR-79156A/ Luchai	64.2	16.58 **	5.98 **	20.43**	7.44**	0.22	4.27 **	4.47 **
IR 68888 A/ Sarojini	63.6	66.21 **	32.06 **	19.22**	6.36**	-1.02 **	7.51 **	1.83 **
IR 68888 A/ Luchai	63	41.65 **	3.97 *	18.14**	5.40**	-1.02 **	4.27 **	4.50 **
IR 68888 A/ Luchai red	62.9	43.17 **	5.69 **	18.00**	5.27**	-1.02 **	3.35 **	5.33 **
IR-79156A/ Bathras	61.2	12.03 **	2.59	14.72**	2.34	0.22	-0.87 *	6.57 **

*Significant at p=0.05% level, **Significant at p=0.01% level

“Total of two microsatellite markers (SSR markers) were used for fingerprinting of hybrids, assessing variation within parental lines and testing the genetic purity of hybrid seed in rice. The polymorphism detected between the parental lines was used to establish hybridity. The two polymorphic markers i.e., RM 495 and RM 1 were clearly distinguished all the parental lines used in the study”. The parents used on the basis of polymorphic detection were Ganga chur, Luchai, Pepri luchai, Sarojini and Kera khadi and the three CMS lines, IR 58025 A, IR 79156 A and IR 68888A. Based on RM 495, all the hybrids were found true hybrid. Based on RM 1 all the hybrids were found true hybrid except IR 58025 A/Ganga chur, IR 58025 A/ Pepri luchai, IR 68888 A/ Sarojini and IR 68888 A/Kera khadi.

The parents used on the basis of polymorphic detection were Ganga chur, Luchai, Pepri luchai, Sarojini and Kera khadi and the three CMS lines, IR 58025 A, IR 79156 A and IR 68888A. Based on RM 495, all the hybrids were found true hybrid. Based on RM 1 all the hybrids were found true hybrid except IR 58025 A/Ganga chur, IR 58025 A/ Pepri luchai, IR 68888 A/ Sarojini and IR 68888 A/Kera khadi.

CONCLUSION

- “The analysis of variance (ANOVA) for RBD for 47 genotypes showed the presence of highly significant differences among all the traits of rice taken under study. This indicates the existence of ample amount of variability among rice hybrids/ genotypes for studied traits.
- The predominance of specific combining ability (SCA) variance for most of the characters suggested the predominance of non-additive or dominant and epistatic gene action, which is very important for controlling expression of these traits. Hence, the phenomenon of heterosis can be inferred to be playing important role in determining seed yield in case of rice hybrids and can be exploited commercially”.

- Total of 24 traits are governed by dominance and epistatic gene action. This suggests that, it is possible to exploit heterosis in 24 characters whereas simple selection would be choose for others characters for improvement.
- “CMS line IR 79156A was found to be the good general combiner for most of the yield and component traits. Among the testers, Luchai, Pepri luchai and Sarojini were found to be good combiner for grain yield per plant and other related traits.”
- Crosses, IR 68888 A/ Kera khadi ,IR 58025 A/ Luchai red, IR 79156 A/ Sarojini and IR 79156 A/ Luchai are good specific combiners for grain yield.
- Among these six crosses selected for grain yield, five were *viz.*, IR 79156A/ Luchai, IR 79156A/ Sarojini, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, and IR 58025 A/ Sarojini showed desired HRR. Hence, these hybrids were good for commercial use.
- Crosses IR 79156 A/ Luchai and IR 79156 A/ Sarojini showed significant heterosis yield of grain.
- Sarojini were found to be potential restores for lines IR 79156 A and IR 68888A. Other than this Lajni super- 1, Luchai, Pepri luchai and Khura bal were also identified as potential restorers.
- Effective maintainers were not found.
- On the basis of molecular testing Pepri luchai and Kera khadi gave significant result on both the markers *i.e.* RM 495 and RM 1.

SUGGESTIONS FOR FUTURE RESEARCH WORK

- More number of lines and testers should be incorporated in the hybrid rice breeding programme.
- There is good opportunity to select the traits having good grain quality.
- The testers, Luchai, Pepri luchai and Sarojini were identified as good general combiners for most of the traits and may be used in further research to develop better hybrids.
- The testers, Pihu purple was identified as good general combiner for most of the quality traits may be used for developing good quality hybrids of rice.
- The superior crosses viz., IR 79156A/ Luchai, IR 79156A/ Sarojini, IR 58025 A/ Luchai, IR 68888 A/ Sarojini, IR 68888 A/ Luchai, and IR 58025 A/ Sarojini should be retested next year in retestcross nursery for confirmation of results. These promising hybrids offer greater scope for further commercial exploitation of hybrid vigour.
- Partial maintainers identified in this study should be recurrently backcrossed to develop locally adapted CMS lines.
- The best potential restorers identified viz., Sarojini Lajni super- 1, Luchai, Pepri luchai and Khura bal should be again retest. These restorers will also be crossed with other cytoplasmic male sterile (CMS) lines to develop good heterotic hybrids.
- The genotype identified as partial maintainer will be further improved by attempting B x B crosses and converted into locally adapted similar grain type CMS line.
- Characterization of more number of parents at molecular level should be done which is useful for hybrid breeding programme.

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Appendix A- Weekly meteorological data of Rice during kharif 2018

No.	Date	Max. Temp. (°C)	Min. Temp. (°C)	Rain-fall (mm)	Rainy days	Relative Humidity (%)		Vapour Pressure (mm of Hg)		Wind Velocity (Kmph)	Evaporation (mm)	Sun Shine (hours)
						I	II	I	II			
29	July 16-22	30.4	25.4	75.8	4	93	82	23.6	23.4	8.2	18.8	0.4
30	23-29	28.6	25.4	51.4	3	88	76	21.6	21.6	8.1	2.2	0.1
31	30-05	31.9	25.4	31	1	88	67	22.3	21.6	6.5	26.9	2.3
32	Aug 06-12	30	24.8	103.4	3	92	88	22.8	23.9	5.8	20.2	1.2
33	13-19	30.3	25.3	101.2	4	94	79	23.6	25	4.1	24.7	2.9
34	20-26	29	24.6	60.4	3	93	79	22.3	22	5.5	18	0.6
35	27-02	28.3	24.1	275	4	96	86	22.5	22.8	6.8	14.7	0.2
36	Sep 03-09	29.2	23.9	30.2	3	93	57	24.2	18.4	0.5	22.7	1.1
37	10-16	32.6	25.1	0	0	90	55	22.9	18.9	2.2	25.3	6.4
38	17-23	31	24.1	32.8	2	92	68	21.7	21.6	3.5	19.2	3.6
39	24-30	32.9	25	11	1	93	59	23.6	20.6	1.2	25.6	7.8
40	Oct 01-07	34	23.8	0	0	91	44	21.6	16.8	0.7	28.1	8
41	08-14	32.4	22.8	0	0	87	51	19.3	17.5	2.8	26.8	7.1
42	15-21	33.4	21.3	0	0	89	40	18.4	15.4	1	23.6	8.5
43	22-28	32.9	18.9	0	0	86	48	15.7	18.5	1.1	25.1	8.3
44	29-04	31	19.6	0	0	86	49	16.4	14.8	2.6	28.8	9.3
45	Nov 05-11	32.3	17.7	0	0	84	34	13.8	11.9	1.2	23.3	8.5
46	12-18	31.5	14.4	0	0	86	29	11.4	10.1	1.1	23.3	9.1
47	19-25	31.4	15.3	0	0	88	28	12.5	9.4	1.1	23.2	7.8

Appendix- B
Preparation of iodine potassium iodide (IKI) solution for
pollen testing

Take 100 ml distilled water + 1 gm iodine



Dissolve by heating



Take 200 ml distilled water in another flask and 2 gm potassium
iodide dissolve it, by stirring



Mix both solutions in equal proportion



Filter and store the final solution in dark bottle

Appendix-C

Procedure to workout Hulling Percentage

Weight desired amount of paddy (minimum 100 g)



Dehusking in a standard dehusker/sheller



After cleaning dehusked kernels (brown rice) is weighted.



Percentage is determined by using the following formula.

Formula:

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

Appendix-D

Procedure to workout Milling Percentage

Dehusked kernels (brown rice) are put into a standard polisher/miller.



Time of the polisher is adjusted in such a way that percent polishing is 5% (approx).



Total polished kernels (white rice) are weight.



Then milling percentage is calculated by the following formula.

Formula:

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

Appendix-E

Procedure to work out the Head Rice Recovery percentage

The polished kernels are passed through rice grader/rice sizing devices which having different (mm) grooves



The whole grains are separated from the broken grains in order to qualify the head rice recovery



Full grains and $\frac{3}{4}$ size grains are considered and weighted as head rice recovery



The percentage of the head rice recovery and broken grains are calculated as per the following formula

Formula:

$$\text{Head Rice Recovery} = \frac{\text{Weight of whole polished kernel}}{\text{Weight of paddy}} \times 100$$

Appendix-F

Procedure to work out the Alkali Spreading Value or Gelatinization Temperature

Reagents:

Potassium Hydroxide (KOH): Preparation dissolve 19.54 gm KOH pellets(85%) in 1000 ml of distilled water store at least 24 hours and filter it before use.

Procedure:

Select duplicate sets of six whole milled kernels without cracks and put them in plastic boxes. Broken kernels can also used if whole grains are not available. Add 10 ml of 1.7% Potassium hydroxide to the sample. Provide enough space between kernels to allow spreading. Keep the sample undisturbed in an incubator at 27-30°C for 23 hours. A standard variety or hybrid is used as a check and all samples are evaluated at least in two replications. The spreading and clearing of kernels noted on a 7 point scale is expressed as average of six values.

Scoring is done as follows:

S. No.	Spreading Scale
1	Kernel not affected
2	Kernel swollen
3	Kernel swollen, collar incomplete and Narrow
4	Kernel swollen, collar complete and wide
5	Kernel split or segmented, collar complete and wide
6	Kernel dispersed, merging with collar
7	All kernel dispersed and inter mingled

Classification	Alkali spreading value (ASV)	Gelatinization temperature (GT)
1-2	Low	High > 74°C
3	Low, Intermediate	High, intermediate
4-5	Intermediate	Intermediate (70-74°C)
6-7	High	Low (50-69°C)

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