

**“COMBINING ABILITY FOR YIELD, COLD, HEAT AND
GRAIN QUALITY IMPPROVEMENT IN RICE
(*Oryza sativa* L.)”**

Ph.D. (Ag.) Thesis

by

LAXMI SINGH

**DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
INDIRA GANDHI KRISHI VISHWAVIDYALAYA
RAIPUR (Chhattisgarh)**

2019

**“COMBINING ABILITY FOR YIELD, COLD, HEAT AND
GRAIN QUALITY IMPPROVEMENT IN RICE
(*Oryza sativa* L.)”**

Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur

by

LAXMI SINGH

**IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE DEGREE OF**

**Doctor of Philosophy
in
Agriculture
(Genetics and Plant Breeding)**

Roll No.130116049

I.D. No. 20161725161

JULY, 2019

CERTIFICATE –I

This is to certify that the thesis entitled “Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)” submitted in partial fulfillment of the requirements for the degree of **Doctor of Philosophy in Agriculture** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Laxmi Singh** under my guidance and supervision. The subject of the thesis has been approved by Student’s Advisory Committee and the Director of Instructions.

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

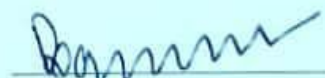

Chairman

Date: 22.7.19

THESIS APPROVED BY THE STUDENT’S ADVISORY COMMITTEE

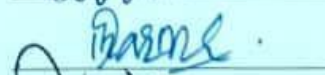
Chairman

(Dr. Prabharani Chaudhari)



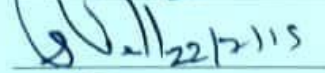
Member

(Dr. Deepak Sharma)



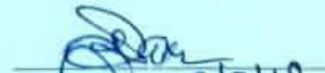
Member

(Dr. S. B. Verulkar)

 22/7/19

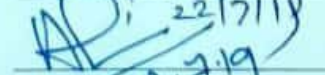
Member

(Dr. Ravi .R. Saxena)

 22/7/19

Member

(Dr. A. K. Sarawgi)

 22.7.19

CERTIFICATE – II

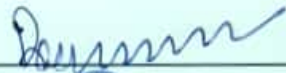
This is to certify that the thesis entitled “Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)” submitted by **Laxmi Singh** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur in partial fulfillment of the requirements for the degree of **Doctor of Philosophy 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: 27. 11. 2019


Signature External Examiner

(Name Satya Ranjan Das)

Major Advisor



Head of the Department


_____ 27.11.19

Faculty Dean

Approved/Not approved

Director of Instructions

ACKNOWLEDGEMENT

*At this moment of accomplishment, first of all with a sense of high resolve and reverence, I would like to give my sincerest thanks to my major advisor **Dr. Prabharani Chaudhari**, Associate Professor, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), for her support, kind guidance, precious instruction, sparing valuable time has given me a great inspiration and help at every step during my thesis work and pleasure to conduct this thesis under her supervision.*

*Most humbly and respectfully I wish to express my profound sense of gratitude to **Dr. A. K. Sarawgi**, Professor and Head, Department of Genetics and Plant Breeding, Indira Gandhi krishi Vishwavidyalaya, Raipur, for his untiring help, valuable suggestions and for providing necessary facilities during the course of my research work.*

*I am extremely indebted to **Dr. S. B. Verulkar**, Professor and Head, Department of Plant Molecular Biology and Biotechnology, Indira Gandhi krishi Vishwavidyalaya, Raipur, for his keen co-operation and kind help, valuble advice and providing necessary resources and facility, which have provided good and smooth basis for my Ph.D. tenure.*

*With great reverence, I express my sincere thanks to **Dr. Deepak Sharma**, for his valuable support and advice and providing field facilities during my thesis work.*

*I would like to express my sincere gratitude to **Dr. R. R. Saxena**, for her precious advice, encouragement and providing facilities during my academic and research work.*

*I greatly acknowledge **Dr. Toshiy mam**, for her keen observation, guidance, support and providing all facilities in laboratory during my molecular work.*

*I express my warmest gratitude to **Dr. R. R. Saxena**, for his valuable advice and extensive discussion around my research work.*

I would like to duly acknowledge **Dr. S. K. Patil**, Hon'ble Vice Chancellor, **Dr. S. S. Rao**, Dean, College of Agriculture, **Dr. M. P. Thakur**, Director of Instructions and **Dr. R. K. Vajpai** Director Research Services and **Dr. Madhav Pandey** Librarian, IGKV, Raipur for their help both administrative and technical issues which facilitated my research work.

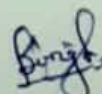
I would like to express my sincere gratitude to my all teachers of Genetics and Plant Breeding for their valuable support, advice and genuine guidance, whenever, I sought throughout my course work.

I am especially thankful to my senior **Dr. Madhulika Singh** for her helping nature and friendly attitude.

I am forever thankful to my friends **Uma, Prishila, Jai kisan, Avadhesh sir, Kiran, Anupama, Ashish, Arun** and **Namrata**. I would like to warm thanks to my batchmates **Suman, Sonal, Hema, Sopan, Ankur, Jayant** and **Jitendra** for providing a stimulating and fun filled environment. I would like to heartily thanks to my junior **Dipika, Bindiya, Priti, Varsha** and **Abhilasha**. My special thanks to **Helen** for her valuable help and support during my laboratory work.

I also thankful to Mr. **Shravan sir, Manish bhaiya, Mithlesh bhaiya, Moti Bhaiya, Bhedi Bhaia, Subhash Bhaiya** and all, who helped and supported in my field experiment.

Last but not the least, I would like to pay high regards to my beloved parents on this memorable moments. My deep and sincere gratitude to my elder sisters **Mrs. Mamta di** and **Neelam di** for their continous support and unparalleled love, my brother in laws **Mr. T. Singh** and **Mr. N. Singh**, for their vavluable support and suggestion. I am forever endebted to my uncle **Mr. Jitendra** , **Mr. T.N. Singh** and my aunti **Mrs. Sita Karma** and **Mrs Bhuneshila Singh** for their blessings, sincere encouragement and inspiration in my life.



(Laxmi Singh)

Raipur

Date: 22/07/19

Department of Genetics and Plant Breeding
College of Agriculture, IGKV, Raipur, Chhattisgarh

TABLE OF CONTENTS

Chapter	Title	PAGE
	ACKNOWLEDGEMENT	
	RESUME	
	TABLE OF CONTENTS	
	LIST OF TABLES	
	LIST OF FIGURES	
	LIST OF NOTATION /SYMBOLS	
	LIST OF ABBREVIATIONS	
	ABSTRACT	
I	INTRODUCTION	
II	REVIEW OF LITERATURE	
	2.1 Genetic variability parameters	
	2.1.1 Genetic variability and association analysis	
	2.1.2 Correlation analysis	
	2.2 Cold and heat tolerance	
	2.2.1 Cold tolerance screening	
	2.2.2 Heat tolerance screening	
	2.3 Combining ability	
	2.4 Heterosis	
	2.5 Stability analysis	
	2.6 Expression of sHSPs	
III	MATERIALS AND METHODS	
	3.1 Experimental site	
	3.2 Climatic and weather condition	
	3.3 Experimental materials	
	3.4 Experimental details	
	3.5 Nursery sowing and transplanting	
	3.6 Hybridization	
	3.6.1 Raising F ₁ and parents	
	3.7 Observations recorded	

Chapter	Title	PAGE
	3.7.1 Quantitative traits	
	3.7.2 Quality traits	
	3.7.4 Parameters for heat tolerance	
3.8	Molecular analysis	
	3.8.1 RNA isolation	
	3.8.2 Quantification of RNA	
	3.8.3 cDNA synthesis	
	3.8.4 Polymerase Chain Reaction (PCR) amplification using sHSP primer	
	3.8.4.1 Visualization of amplified products in Polyacrylamide gel electrophoresis	
	3.8.4.2 Development of genotypic data of the population	
	3.8.4.3 Scoring of data	
3.9	Statistical analysis	
	3.9.1 Analysis of variance	
	3.9.2 Parameters of variability	
	3.9.3 Character association analysis	
	3.9.4 Combining ability analysis	
	3.9.5 Stability analysis	
IV	RESULTS AND DISSCUSSION	
4.1	Genetic variability and association analysis for yield & yield contributing components	
	4.1.1 Analysis of variance	
	4.1.2 Mean performance of genotypes	
	4.1.3 GCV, PCV, Heritability (broad sense), Genetic advance, Genetic advance as percent of mean	
	4.1.4 Association analysis for yield & yield contributing components	

Chapter	Title	PAGE
4.2	The effect of cold and heat in selected rice genotypes	
4.2.1	Parameters for cold tolerance screening	
4.2.2	Parameters for heat tolerance screening	
4.3	Combining ability analysis for yield and quality traits	
4.3.1	Mean performance of parents and crosses	
4.3.2	Analysis of variance for combining ability	
4.3.3	GCA and SCA effects	
4.4	Heterosis for yield and quality traits	
4.5	Stability analysis for seed yield and its components	
4.6	Expression of small heat shock proteins	
V	SUMMARY AND CONCLUSIONS	
	REFERENCES	
	APPENDICES	
	APPENDIX –A	
	APPENDIX –B	
	APPENDIX –C	
	APPENDIX –D	
	APPENDIX –E	
	RESUME	

LIST OF TABLES

Table	Title	Page
3.1	List of rice genotypes used for current study	
3.2	Details of sowing and transplanting	
3.3	cDNA synthesis (reverse-transcription) reaction components	
3.4	PCR mix for one reaction	
3.5	Temperature profile used for PCR amplification using sHSP primer	
3.6	List of sHSP primers	
3.7	Skeleton of ANOVA for RBD design	
3.8	Analysis of variance for combining ability	
3.9	ANOVA to estimate stability parameters (Eberhart and Russell, 1966)	
4.1	Analysis of Variance (ANOVA) for quantitative traits (<i>Summer-2017</i>)	
4.2	Analysis of Variance (ANOVA) for quality traits (<i>Summer-2018</i>)	
4.3	Genetic parameters of variation for yield and its component traits (<i>Summer-2017</i>)	
4.4	Genetic parameters of variation for quality traits (<i>Summer-2018</i>)	
4.5	Estimation of genotypic and phenotypic correlation coefficient among yield and contributing traits in rice genotypes	
4.6	Selected rice genotypes/ varieties after cold screening	
4.7	Selected rice genotypes after heat screening	
4.8	Mean performance of quantitative traits of parents and crosses	
4.9	Mean performance of quality traits of parents and crosses	
4.10	Analysis of variance for combining ability of quantitative traits	
4.11	Proportional contribution to lines, testers and their interaction to total variance	

Table	Title	Page
4.12	Analysis of variance of combining ability for quality traits	
4.13	Proportional contribution to lines, testers and their interaction to total variance	
4.14	Estimates of general combining ability (GCA) effects for yield and yield traits	
4.15	Estimates of specific combining ability (SCA) effects for yield and yield traits	
4.16	Estimates of general combining ability (GCA) effects of parental lines for quality traits	
4.17	Estimates of specific combining ability (SCA) effects for quality traits	
4.18	Promising general combiner for yield and yield contributing traits and quality traits	
4.19	Selected desirable crosses for specific combining ability	
4.20	Estimation of Heterobeltiosis and standard heterosis for yield and yield contributing traits	
4.21	Estimation of Heterobeltiosis and standard heterosis for quality traits	
4.22	Analysis of variance of Eberhart and Russel model (1966)	
4.23	Selected genotypes on the basis of Eberhat and Russell stability model (1966)	
4.24	Gel score of genotypes in heat stress condition	

LIST OF FIGURES

Figure	Title	Page
3.1	Meteorological graph on <i>Summer</i> 2017	
3.2	Meteorological graph on <i>Summer</i> 2018	
3.3	Field view of experiment	
3.4	Crossing procedure in field	
3.5	Cold tolerance screening	
4.1	Expression of sHSPs in rice genotypes	

LIST OF NOTIONS/SYMBOLS

Abbreviations	Description
%	percent
<	Less than
>	More than
<i>et al.</i>	And other people
g	Gram (s)
ha	Hactare
<i>i.e.</i>	That is
m ²	Meter suare
max.	Maximum
min.	Minimum
mm	Milimeter
mt	Million tonns
No.	Number
<i>viz.</i>	For example
°C	Degree celcius
d.f.	Degree of freedom
µl	Micro litre
ng	Nano gram
cm	Centimeter

LIST OF ABBREVIATIONS

Abbreviations	Description
CD	Critical difference
cDNA	Complimentary DNA
DNA	Deoxy ribonucleic acid
Fig.	Figure
GAM	Genetic advance as percent of mean
gca	General combining ability
GCV	Genotypic coefficient of variation
Hsp	Heat shock protein
PCR	Polymerase chain reaction
PCV	Phenotypic coefficient of variation
RBD	Randomized Block Design
RT-PCR	Real time Polymerase chain reaction
sca	Specific combining ability
HI	Harvest index
Hull %	Hulling percent
Mill %	Milling percent
HRR %	Head rice recovery percent
PH	Plant hieght
GYP	Grain yield per plant

THESIS ABSTRACT

- a) Title of the Thesis : Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)
- b) Full Name of the Student : Laxmi Singh
- c) Major Subject : Genetics and Plant Breeding
- d) Name and Address of the Major Advisor : Dr. Prabharani Chaudhari
Associate Professor
Department of Genetics and Plant Breeding,
College of Agriculture, IGKV, Raipur,
Chhattisgarh-492012
- e) Degree to be Awarded : Doctor of Philosophy in Genetics and Plant Breeding

Signature of the Major Advisor

Date: 22/07/2019

Signature of the Student

Signature of Head of the Department

ABSTRACT

Rice (*Oryza sativa* L.) is the staple food for over half of the world's population. Population is growing at an alarming rate; so there is a need or challenge to meet the demand of rice with decreasing cultivation area and changing climatic condition. Rice cultivation has gradually changed in single season from double season, because the flowering phase of summer season rice occurs at the period with the high temperature stress that negatively affect the grain yield. Summer rice faces adverse climate condition in growth period i.e. low temperature during germination period and high temperature during flowering period. The low temperatures which occurs during the germination period, leads to delayed and lower percentage of germination and suppress the normal growth of seedlings. High temperature at flowering stage leads to lower spikelet fertility, low grain weight per panicle and low grain yield per plant. In quality traits, high temperature at flowering stage leads to breakage of grains during milling and drastically reducing the head rice recovery. Therefore, farmers are not interested in summer rice cultivation. Thus there is need to develop high yielding, early medium duration varieties with high head rice recovery.

Eighty seven rice genotypes were evaluated during Summer-2017 under managed field condition. On the basis of pollen fertility, spikelet fertility and grain

Eighty seven rice genotypes were evaluated during *Summer-2017* under managed field condition. On the basis of pollen fertility, spikelet fertility and grain yield per plant, thirty seven rice genotypes were selected and evaluated for cold, heat and quality parameters in *Summer-2018*. For combining ability analysis selected eight lines with four testers were crossed in Line x Tester mating design. Stability analysis was done by Eberhart and Russell model (1966) in selected thirty seven genotypes at three different dates of sowing on *Summer-2018*. Out of thirty seven, twelve rice genotypes were used for expression analysis of small heat shock proteins (sHSPs).

Among the eighty seven genotypes, the analysis of variance showed a wide range of variation, indicating the presence of sufficient amount of variability and possibility of manipulating these variations for rice improvement. The high heritability coupled with high genetic advance as percent of mean were reported for days to fifty percent flowering, flag leaf area, total grains per panicle, filled grain per panicle, 100 grain weight, spikelet fertility, grain yield per plant, biological yield per plant, effective tillers per plant, plant height, tillers per plant and harvest index, it indicates that these traits are under the influence of additive gene action with least environment influence. Grain yield per plant exhibited positive and highly positive significant correlation with biological yield per plant, filled grain per panicle, tillers per plant, effective tillers per plant, total grains per panicle, spikelet fertility and harvest index.

On the basis of cold tolerance screening eight genotypes viz., RJR:II , Banspatri, Ganga dhan, Tewan dhan, Digamber dhan, Barhasaal, Indira Barani Dhan-1 and Inbira Aerobic-1 and through heat tolerance screening thirteen genotypes viz., Dadbko, NPT 6, Gangtai, RJR:II, Ganga kali, NPT 19, NPT 6, Bega hundi, Kolhin khosa, Bega hundi, Ganga dhan, Safed Lalak and Ajam dhan were identified as cold and heat tolerant genotypes, respectively. Among these selected genotypes, three genotypes RJR:II, Banspatri and Ganga Kali identified as tolerance for both heat and cold stress.

In combining ability analysis three lines Ganga kali, Ajam dhan, Bega hundi, and one tester Indira Barani Dhan 1 for grain yield per plant and for head

rice recovery two lines Ajam dhan and Safed Lalak, two testers IR 64 and MTU 1010, identified as good general combiner. Among the thirty two crosses eight crosses viz. Bega hundi X Indira Barani Dhan 1, Ajam dhan X Indira Barani Dhan 1, Ganga kali X Indira Aerobic 1, RJR:II X IR-64, Banspatri X MTU 1010 were Safed Lalak X IR-64, NPT 19 X MTU 1010, NPT 6 X MTU 1010 showed highly positive significant and desirable sca effects for grain yield per plant. Therefore, these hybrids are recommended for heterosis breeding. The four crosses viz., RJR:II X Indira Barani Dhan 1, Banspatri X IR 64, Banspatri X MTU 1010 and NPT 6 X Indira Barani Dhan 1 showed highly positive significant sca effects for hulling, milling and head rice recovery. Banspatri X MTU 1010 showed positive and significant sca effects for grain yield per plant, hulling, milling and head rice recovery. Four cross combinations Ganga kali X IR 64, Ganga kali X Indira Aerobic 1, Ajam dhan X Indira Barani Dhan 1, Bega hundi and X Indira Barani Dhan 1 showed superior over better parent and check variety for grain yield per plant.

On the basis of stability analysis at three different dates Ajawain and Khurbal for early flowering, Indira Barani Dhan 1 for the plant height and Barhasal for the grain yield per plant found to be stable over the environment.

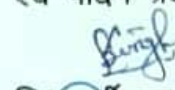
For expression analysis at flowering stage the three genotypes RJR:II, Ganga dhan, and Ajam dhan in most of the genes showed upregulation, when compare to tolerant and susceptible checks. So, these genotypes indicated as the tolerant in heat stress condition.

शोध सारांश

- अ) शोध शीर्षक : "चावल में उपज, ठंड, गर्मी और अनाज की गुणवत्ता में सुधार के लिए संयोजन क्षमता का विश्लेषण (ओराइजा सटाइवा एल)"
- ब) विध्यार्थी का पूरा नाम : लक्ष्मी सिंह
- स) प्रमुख विषय : आनुवंशिकी एवं पादप प्रजनन
- द) प्रमुख सलाहकार का नाम व पता : डॉ. प्रभारानी चौधरी (सह. प्राध्यापक)
आनुवंशिकी एवं पादप प्रजनन विभाग
कृषि महाविद्यालय, ई.गॉ.कृ.वि,
रायपुर(छ.ग.) 492012.
- इ) सम्मानित की जाने वाली उपाधि : पीएचडी. आनुवंशिकी एवं पादप प्रजनन


प्रमुख सलाहकार के हस्ताक्षर

दिनांक 22.07.2019


विध्यार्थी का हस्ताक्षर


विभागाध्यक्ष के हस्ताक्षर

शोध सारांश

चावल (ओराइजा सटाइवा एल) दुनिया की आधी से अधिक आबादी के लिए मुख्य भोजन है। बढ़ती जनसंख्या दर तक खतरनाक स्थिति में पहुँच गयी है। इसलिए घटती खेती के क्षेत्र तथा बदलते जलवायु स्थिति के साथ चावल की मांग को पूरा करना एक बड़ी चुनौती है। चावल की खेती धीरे-धीरे दो फसली से एक फसल समय में बदल गई है, क्योंकि गर्मियों के सीजन के चावल का पुष्पन अवस्था उच्च तापमान तनाव के साथ होता है जो अनाज की उपज को नकारात्मक रूप से प्रभावित करता है। ग्रीष्मकालीन चावल को विकास की अवधि में प्रतिकूल जलवायु की स्थिति का सामना करता पड़ता है यानी अंकुरण अवधि के दौरान कम तापमान और फूलों की अवधि के दौरान उच्च तापमान की स्थिति होती है। अंकुरण अवधि के दौरान कम तापमान से अंकुरण में देरी और कम अंकुरण के साथ अंकुरों की सामान्य वृद्धि को दबा देता है। पुष्पन की अवस्था में उच्च तापमान से स्पाइकलेट की उर्वरता कम हो जाती है एवं प्रति पौधा कम अनाज पैदा होता है। गुणवत्ता के लक्षणों को देखने पर पायगे की उच्च तापमान पुष्पन अवस्था के साथ मिलिंग के दौरान अनाज के टूटते हैं जिससे हेड राइस रिकवरी को काफी कम हो जाता है। इसलिए, गर्मीसहिष्णु- चावल को तैयार करना जलवायु

अवस्था के साथ मिलिंग के दौरान अनाज के टूटते हैं जिससे हेड राइस रिकवरी को काफी कम हो जाता है। इसलिए, गर्मीसहिष्णु- चावल को तैयार करना जलवायु परिवर्तन के प्रभावों को कम करने के लिए उपयोग की जाने वाली रणनीतियों में से एक है, विशेष रूप से उच्च तापमान वाले क्षेत्रों में जहां अधिकांश चावल उगाए जाते हैं वहां किसानों में ग्रीष्मकालीन चावल की खेती में कोई दिलचस्पी नहीं है। अतः इस प्रकार उच्च उपज, मध्यम अवधि एवं उच्च गुणवत्ता युक्त चावल की किस्मों को विकसित करने की आवश्यकता है।

सतासी चावल जीनोटाइप का मूल्यांकन ग्रीष्म ऋतु वर्ष -2017 के दौरान प्रबंधित क्षेत्र की स्थिति के तहत किया गया था। पराग की उर्वरता, स्पाइकलेट की उर्वरता और प्रति पौधे पर अनाज की पैदावार के आधार पर, ठंड, गर्मी और गुणवत्ता मानकों के लिए सैंतीस चावल के जीनोटाइप का चयन किया गया था। संयोजन क्षमता विश्लेषण के लिए लाइन X टेस्टर डिज़ाइन में आठ लाइनें और चार परीक्षक चुने गए। ग्रीष्म ऋतु वर्ष -2018 में बुवाई की तीन अलग-अलग -) तारीखों को चयनित कर सैंतीस जीनोटाइप्स में एबरट और रसेल मॉडल 1966) द्वारा स्थिरता विश्लेषण किया गया था। सताईस में से बारह चावल के जीनोटाइप छोटे ऊष्मा शॉक प्रोटीन (sHSPs) के अभिव्यक्ति विश्लेषण के लिए उपयोग किए गए थे।

सतासी जीनोटाइप्स के विविधता विश्लेषण ने विभिन्न प्रकार की भिन्नता दिखाई, जो चावल में सुधार के लिए इन विविधताओं की पर्याप्त मात्रा की उपस्थिति और इन विविधताओं में हेरफेर की संभावना को दर्शाती है। उच्च आनुवांशिक अग्रिम के साथ युग्मित उच्च आनुवांशिकता 50 प्रतिशत फूल, झंडे का पत्ती क्षेत्र, कुल दाना प्रति स्पाइकलेट, भरा दाना प्रति स्पाइकलेट, 100 अनाज वजन, स्पाइकलेट प्रजनन क्षमता, प्रति पौधा अनाज, प्रति पौधा जैविक उपज के लिए रिपोर्ट किया गया। पौधों के प्रति प्रभावी टिलर, पौधे की ऊँचाई, पौधों और फसल के सूचकांक के अनुसार टिलर, यह दर्शाता है कि ये लक्षण कम से कम पर्यावरणीय प्रभाव के साथ एडिटिव जीन क्रिया के प्रभाव में हैं। प्रति पौधा अनाज की पैदावार सकारात्मक और अत्यधिक महत्वपूर्ण सहसंबंध प्रति पौधे के साथ जैविक उपज, पूर्ण अनाज प्रति पौधा, प्रति पौधा कन्से की संख्या, प्रति पौधे प्रभावी कन्से की संख्या, कुल अनाज प्रति पौधा, स्पाइकलेट की प्रजनन क्षमता और फसल सूचकांक के साथ प्रदर्शित करता है।

ठंड सहिष्णुता के आधार पर आठ जीनोटाइपिंग स्क्रीनिंग आरजेआर :II, बंसपट्टी, गंगा धान, तेवन धान, दिगंबर धान, बरहासल, इंदिरा बारानी धान -1

और इंदिरा एरोबिक -1 और हीट टॉलरेंस स्क्रीनिंग तरह जीनोटाइप डब्बको, एनपीटी 6, गंगातई, आरजेआर :II, गंगा काली, NPT 19, NPT 6, बेगा हुंडी, कोल्हिन खोसा, बेगा हुंडी, गंगा धान, सफेद ललाक और अजम धान की पहचान क्रमशः ठंड और गर्मी सहिष्णु प्रोटोटाइप के रूप में की गई थी। इन चयनित जीनोटाइप्स में, तीन जीनोटाइप्स आरजेआर :II, बंसपात्री और गंगा काली को गर्मी और ठंडे तनाव दोनों के लिए सहिष्णुता के रूप में पहचाना गया।

क्षमता विश्लेषण के संयोजन में, गंगा काली, अजम धान, बेगा हुंडी, और एक परीक्षक इंदिरा बरानी धान-1 प्रति पौधा उपज के लिए और हेड राइस रिकवरी के लिए दो लाइनें अजम धान और सफेद ललाक, दो परीक्षक आईआर 64 और एमटीयू 1010, सामान्य संयोजन क्षमता के रूप में पहचान की गई। बेगा हुंडी X इंदिरा बरानी धान 1, अजम धान X इंदिरा बरानी धान 1, गंगा काली X इंदिरा एरोबिक 1, आरजेआर :II X आईआर 64, बंसपात्री X एमटीयू 1010, सफेद ललाक X 1 आईआरयू 64, एनपीटी 19 X एमटीयू 1010, एनपीटी 6 X MTU 1010 प्रति पौधा उपज के लिए अत्यधिक महत्वपूर्ण और वांछनीय विशिष्ट संयोजन क्षमता प्रभाव दिखाता है। इसलिए, इन संकरों को हेटरोसिस प्रजनन के लिए अनुशंसित किया जाता है। आरजेआर :II X इंदिरा बरानी धान 1, बंसपात्री X आईआर 64, बंसपात्री X एमटीयू 1010 और एनपीटी 6 X इंदिरा बरानी धान 1 पतवार, मिलिंग और हेड राइस रिकवरी के लिए अत्यधिक विशिष्ट संयोजन क्षमता प्रभाव दिखाते हैं। बंसपात्री X एमटीयू 1010 प्रति पौधा उपज, हलिंग, मिलिंग और हेड राइस रिकवरी के लिए सकारात्मक और महत्वपूर्ण विशिष्ट संयोजन क्षमता प्रभाव दिखाता है। चार क्रॉस कॉम्बिनेशन गंगा काली X आईआर 64, गंगा काली X इंदिरा एरोबिक 1, अजम धान X इंदिरा बरानी धान 1 और बेगा हुंडी X इंदिरा बरानी धान 1 बेहतर प्रति पौधा उपज के लिए बेहतर पैतृक और चैक किस्म से बेहतर है।

तीन अलगअलग तारीखों में स्थिरता के विश्लेषण के आधार पर-, अजवाईन और खुरबल को जल्दी फूल देने के लिए, पौधे की ऊंचाई के लिए इंदिरा बरानी धान 1 और प्रति पौधे अनाज की उपज के लिए बरहासल पर्यावरण उपयुक्त पाया गया है।

पुष्पन अवस्था में अभिव्यक्ति विश्लेषण के लिए तीन जीनोटाइप्स आरजेआर :II, गंगा धान, और अजम धान में से अधिकांश में सहिष्णुता और अतिसंवेदनशील जांच की तुलना में अपग्रंथन दिखाया गया है। तो, इन जीनोटाइप ने गर्मी तनाव की स्थिति में सहिष्णु के रूप में संकेत दिया।

CHAPTER-I

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food for over half the world's population. Rice is one of the world's largest cereal crop providing the caloric need for millions of people. Rice cultivation is the principal activity for the nutrition and source of income, especially in Asia. Asian countries produce 89 percent of world's rice and 50 percent of the people depends on rice for food (FAO, 2016). In India, rice farming is not just the major staple food but also very closely interwoven with the income and culture of millions of people and gained the status of major export commodity, so the term "rice is life" is most suitable in Indian context.

Rice is an excellent source of carbohydrates and rich in magnesium, thiamine, niacin, phosphorus, vitamin B₆, zinc and copper. Cooked, white, unenriched, long-grained rice contains 68% water, 28% carbohydrates, 3% protein, and negligible fat. In a 100 gram serving, it provides 130 calories and no micronutrients in significant amounts, with all less than 10% of the Daily Value (DV). Cooked, short-grained, white, rice also provides 130 calories and contains moderate amounts of B vitamins, iron, and manganese (10–17% DV) per 100 gram amount. Rice flour is rich in starch and used for making various food preparations.

Globally, rice is presently grown on 167 million hectare and the production is approximately 769 million tons of grain annually (Anonymous, 2017). India is considered to be one of the original centers of rice cultivation covering 42.9 million hectare area (38.8 million hectare in *Kharif* and 4.1 million hectare in *Rabi*) with an annual production of 111.0 million tons (96.4 million tons in *Kharif* and 14.5 million tons in *Rabi*) (Anonymous, 2018). Chhattisgarh is popularly famous as "Rice Bowl of India" because highest area is covered under rice cultivation. During *kharif* total estimated area of rice in C.G. is 3.71 million hectare area and productivity is 1967 kg/hac

and, during *rabi* season rice is grown on 1.85 million hectare area with productivity of 2950 kg/hac, in 2017-18 (Anonymous, 2019).

The average temperature of global earth/ocean in the past decade (2007-2016) was 0.90°C warmer than the baseline 1880-1937 (which is close to pre-industrial levels 1880-1910). In 2018 global temperature was 1.06°C (1.90°F) above that baseline (NOAA National Climatic Data Center, 2019). Global warming will expected rise to 1.5 °C above pre-industrial levels between 2030 and 2052, if warming continues to rise at the current rate (ICPP, 2018). It has been revealed 7-8% rice yield decline for each 1 °C increase in daytime temperature from 28 °C to 34 °C (Baker *et al.*, 1992). Rice yields are estimated to be reduced by 41% as a result of high temperature by the end of the 21st century (Ceccareli *et al.*, 2010). The decline in grain yield and quality of rice grown under heat stress condition has become a trouble for rice cultivation.

In recent years, rice production levels were unable to meet the demand, it leading to price instability and hunger riots. With the expected increasing of world's population towards 10 billion by 2050, the demand for rice will grow faster than the other crops. Population is growing an alarming rate, so there is a need or challenge to meet the demand of rice with decreasing cultivation area and changing climatic condition. Spikelet fertility, grain quality and yield increase in rice are challenged by heat stress.

India is second largest producer of rice after China. In India major share of rice is cultivated during *Kharif* season. A small area is grown in *rabi* or *summer* season with assured irrigation. Since 1970s, the rice cultivation pattern has gradually altered from double-season to single-season planting; because the blossoming phase of *rabi* or *summer* season rice occurs at the period with the high temperature stress that negatively affect the grain yield. Rice is a temperature responsive crop, during the germination stages of rice, the occurrence of low temperature stress inhibits seedling establishment and ultimately leads to non uniform crop germination. The optimum

temperature for rice cultivation is between 25°C and 35°C, and in temperate regions, rice growth is impressed by limited period that favors its growth (Zhao *et al.*, 2012). High temperature during flowering and grain filling stages lead to reductions in spikelet fertility and deterioration in rice quality, which adversely affect rice yield.

The summer rice nurseries are raised from second fortnight of November to end of December. The low temperatures are more prevalent for the period of the months of December and January. The nurseries raised during December usually fail due to adverse weather associated with prolonged low temperature. In germination phase, low temperature affect the delayed and lower percentage of germination. Prevalence of low temperatures during this month suppresses the normal growth of seedlings with respect to height, leaf emergence and dry matter production (Dacruz and Milach, 2000). The temperature lower than 20°C reduce both the speed and percentage of germination in rice. (Yoshida, 1981).

In summer rice high temperature occurs during flowering stage. In rice the most susceptible stages of development to temperature are flowering (anthesis and fertilization), and to a smaller extent booting (microsporogenesis). The seed set (spikelet fertility) is an important element of rice yield that is very responsive to high temperature. At high temperature cultivar difference and reduction in spikelet fertility were due mainly to decreased pollen production and pollen reception (pollen numbers on stigma). The lower spikelet fertility at high temperature resulted in lesser filled grains, low grain weight per panicle, and lower harvest index (Prasad *et al.*, 2006).

The major problem of growing rice in Chhattisgarh during summer season faces very low temperature at early growth stage and very high temperature at reproductive stage which leads to breakage of grains during milling drastically reducing the head rice recovery (HRR). Therefore, farmers are not interested in summer rice cultivation. Thus there is need to developed high yielding early medium duration varieties which can tolerate temperature stress with high head rice recovery. In Chhattisgarh state at Raipur the IGKV's rice germplasm collection is the largest

such in India and the second largest in the world. A total of 23,250 germplasm collection of rice accessions are being maintained and evaluated for biotic and abiotic stresses. So, in this large germplasm collection identification of better germplasm for heat tolerance is necessary for effective genetic manipulation. Screening for heat tolerance using suitable method have to be identified across different temperature regimes, and use breeding approaches to transfer the tolerance into desirable agronomic background. Breeding for heat tolerance in rice, the initial seeking for tolerant sources should be initiated among the advanced breeding lines, modern cultivars and landraces of the crop species.

The crucial requisite in plant breeding is the presence of genetic variation in breeding material. Importance of genetic variability is the selection of desired parents for use in crossing programme. For effective genetic improvement, knowledge on the magnitude and nature of the genetic variation governing the inheritance of quantitative characters like yield and its contributing traits is very important. Therefore, achievement on plant breeding activities depends on the presence of genetic variability in desired traits and selection ability of plant breeder (Adhikari *et al.*, 2018).

The success of plant breeding programme depends on the selection of appropriate genotypes as parents in the hybridization programme. The parent should have good combining ability and broad genetic diversity for different economic traits. Combining ability is an estimation of the value of genotypes on the basis of their offspring performance in specific mating design (Allard, 1960). Combining ability analysis provides information on two variance components viz., additive and dominance variance. It gives idea about choose parents, crosses and appropriate breeding procedures for the selection of desirable segregants (Salgotra *et al.* 2009). Among different biometrical techniques, Line x Tester (Kempthorne, 1957) methods appears to be best method to evaluate parents and crosses. It is the potent method for estimating the general combining ability (GCA) of parents and selection of desirable parents and crosses with high specific combining ability (SCA) for exploitation of heterosis. Line $\times$ tester analysis involves 'l' lines and 't' testers. A tester is a genotype that is used in detection of better germplasm in accordance with breeding objectives in

a hybrid breeding program. A tester line defined as that have simplicity in use, provide information that classifies relative performance of lines into heterotic groups or patterns, and exploit the expected mean yield. Combining ability analysis of the parentage to be utilized in breeding programme is essential for substantial maximization of the genetic gain and selection of efficient breeding methodology.

In food security programs development of high yielding varieties depends on crop yield potential and stability. The yield stability performance is one of the advantageous properties for a genotype for released as a variety for cultivation. Stability is a complex product of genetic yield potential to stress conditions. Yield stability of a cultivar as a consistency degree of its yield response function across environments to mean of all studied cultivar yield response function (Abeyasiriwardena *et al.*,1991). To meet these goals, estimation of genotype x environment (GxE) interaction is very crucial. A genotype considered as stable if its environmental variance is small, its response to environment is parallel to the mean response of all genotypes in trial or if the residual mean square from a regression model on the environmental index is small. Various statistical procedures have been proposed to find out the stability of cultivars.

High temperature generally induces the expression of heat shock proteins (HSPs). These HSPs helps in protecting with heat stress by increasing photosynthesis, partitioning of assimilate, nutrient and water use efficiency (WUE) and membrane thermal stability (Wahid *et al.* 2007). Such response allows crops to become tolerant in high temperature stress. They can be categorized into high molecular weight (ranges from 68 to 110kD) and low molecular weight groups (ranges from 15 to 27kD). The expression profiles of 23 rice sHSPs under vegetative, developmental and stress conditions were reported (Sarkar *et al.* 2009). High temperature stress induces several alteration in physiological, biochemical and molecular components in rice crop leads to decline in crop production. Development of heat tolerant rice requires about understanding of genetics, biochemical and physiological processes for identifying

and selecting traits for enhancing tolerance mechanism. Therefore, the present investigation was undertaken to select the heat tolerance and short duration variety with high grain yield.

Keeping in view the above points the present study entitled “Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)” was conducted with the following objectives:

1. To determine genetic variability and association analysis for yield & yield contributing components.
2. To understand the effect of cold and heat in selected rice genotypes.
3. To assess combining ability for yield and quality traits.
4. To determine the magnitude of heterosis for yield and quality traits.
5. To estimate stability parameters for seed yield and its components.
6. Expression analysis of sHSPs proteins and its relation to high temperature tolerance.

CHAPTER-II

REVIEW OF LITERATURE

The available literature on rice relevant to this study has been reviewed and summarized in this chapter. The review of literature is covered by the following points:

2.1 Genetic variability and association analysis

2.1.1 Genetic variability and association analysis parameters

2.1.2 Correlation analysis

2.2 Cold and heat tolerance

2.2.1 Cold tolerance screening

2.2.2 Heat tolerance screening

2.3 Combining ability

2.4 Heterosis, Heterobeltiosis and Standard heterosis

2.5 Stability analysis

2.6 Expression of sHSPs

2.1 Genetic variability parameters

2.1.1 Genetic variability and association analysis parameters

The most prerequisite of plant breeding is the presence of genetic variability in breeding materials. Presence of genetic variability in any breeding material provides not only a basis for selection but also provide information regarding selection of diverse parents for use in hybridization programme. The nature and extent of variability forms is the basis for all crop improvement programs.

The genetic variability is determined by certain genetic parameters viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) estimates and their partitioning into heritable and non heritable components, and genetic advance (GA). The GCV and PCV provide a measure to

compare the variability present in the traits. The GCV especially helps to compare the genetic variability in the traits. GCV and PCV were classified as suggested by Sivasubramanian and Madhavamenon (1973). Presence of small difference between GCV and PCV indicate the high genetic variability for the traits which may facilitate selection

Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance . Basic information on heritability is a prerequisite for any breeding programme. The presence of high heritability indicates that it should be easy to conduct effective selection for the trait.

Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population . Johnson *et al.* (1955) reported that though the heritable estimates give useful indication of relative values of selection based on phenotypic expression, the genetic gain should also be considered to arrive at a more reliable conclusion. The literature on the estimates of variance components of genetic parameters for yield and yield attributing traits in rice are reviewed here under:

Sumanth *et al.* (2007) evaluated twenty three rice genotypes and revealed that high GCV and PCV for seed yield per plant followed by flag leaf length, number of spikelets per panicle, biological yield per plant and panicles per plant. High estimates of heritability were observed for plant height, flag leaf length, biological yield per plant, spikelets per panicle, panicles per plant. High genetic advance was observed for plant height and number of spikelets per panicle.

Roy (2010) was evaluated fifty rice genotypes and revealed that moderate to high GCV with high heritability and genetic advance were observed for days to 50% flowering, plant height, number of filled grains per plant and grain yield per plant.

Subbaiah *et al.* (2011) evaluated sixteen parents and forty eight hybrids and reported that high GCV and PCV for total number of productive tillers per plant, harvest index, and gelatinization temperature in parents and for number of grains per panicle, total number of productive tillers per plant, amylose content and gelatinization temperature in hybrids. High heritability coupled with high genetic advance as per cent of mean was recorded for total number of productive tillers per plant, number of

grains per panicle, harvest index, gelatinization temperature, kernel length, kernel L/B ratio and grain yield per plant in parents and for total number of productive tillers per plant, total number of grains per panicle, harvest index, gelatinization temperature and amylose content in hybrids.

Fukrei *et al.* (2011) reported high GCV for plant height, number of tillers per plant, flag leaf area, number of ear bearing tillers, number of filled grains per panicle, panicle weight, straw weight, root length and area and grain yield. High heritability coupled with high genetic advance as percent of mean was observed for panicle weight and grain yield per plant.

Babu *et al.* (2012) evaluated twenty one rice hybrids and reported high GCV and PCV for number of filled grains per panicle, number of chaffy grains per panicle and iron content. The traits viz., number of filled grains per panicle and water uptake exhibited high heritability coupled with high genetic advance.

Sravan *et al.* (2012) evaluated thirty six exotic lines and reported high GCV for grain yield followed by harvest index and flag leaf length.

Pratap *et al.* (2012) evaluated one hundred high yielding rice genotypes and revealed that high heritability, genetic advance, PCV and GCV for flag leaf area, panicle per hill, and grain yield per hill.

Kumar *et al.* (2013) conducted experiment on Indian and exotic rice germplasm and reported that high genetic variability observed in plant height followed by days to 50 percent flowering, total biomass per plant and spikelets per panicle. High heritability coupled with high genetic advance as per cent of mean was observed for the traits, plant height, spikelets per panicle, 1000 grain weight, harvest index, grain yield per plant and total biomass per plant.

Aditya and Bhartiya (2013) evaluated eighteen rice genotypes under rainfed ecosystem. The high GCV and PCV was observed for grain yield per plot followed by fertile grains per panicle and grains per panicle. The broad sense heritability was highest for fertile grains per panicle (98.14%) and plant height followed by grains per panicle (97.74%), days to 50 per cent flowering (95.18) and days to maturity (94.71). The high estimate of genetic advance was observed for grains per panicle and fertile

grains per panicle. The number of grains per panicle and fertile grains per panicle had high heritability as well as high genetic advance.

Sivanath and Singh (2013) evaluated fifty rice genotypes and revealed low GCV and PCV for days to 50 per cent flowering, plant height and panicle length. While high heritability coupled with low genetic advance observed for days to 50 % flowering, panicle length and number of tiller per plant.

Lingaiah *et al.* (2014) measured variability in thirty three rice genotype. The GCV and PCV were moderate to high for test weight, number of grains per panicle and grain yield. High heritability coupled with high genetic advance as percent of mean was observed for number of grains per panicle, test weight and grain yield.

Patel *et al.* (2014) studied the genetic variation using forty four diverse genotypes of rice and revealed that high heritability coupled with high expected genetic advance as per cent of mean for grain yield per plant, number of grains per panicle and amylose content whereas, the highest GCV and PCV were observed for grain yield per plant and number of grains per panicle. While it was moderate for amylose content, 1000 grain weight, grain L/B ratio.

Rahman *et al.* (2014) studied in advanced breeding lines of fine grain rice and reported that high heritability coupled with high genetic advance for the number of effective tillers, number of filled spikelets and 1000 grain weight indicating that these traits may be under control of additive gene action.

Rukamanidevi *et al.* (2014) evaluated twenty nine genotypes and revealed that grain yield per plant, grains per panicle, test weight and effective tillers recorded high GCV and PCV. High heritability coupled with high genetic advance as percent of mean was recorded for yield per plant, grains per panicle, effective tillers, plant height, head rice recovery, L/B ratio, panicle length and days to 50 % flowering.

Sandhya *et al.* (2014) estimated genetic variability in thirty two rice genotypes and reported that high heritability coupled with high genetic advance for grain yield per plant, days to 50 per cent flowering, panicle length, panicles per plant and tillers per.

Ekka *et al.* (2015) estimated genetic variability in ninety six accessions of rice germplasm and reported that high GCV and PCV for number of effective tillers per plant, grain yield per plant and head rice recovery percentage. High heritability coupled with high genetic advance for number of effective tillers per plant, number of grains per panicle, head rice recovery percentage and grain yield.

Kishore *et al.* (2015) estimated genetic variability in seventy three rice genotypes and they observed high heritability coupled with high genetic advance as per cent mean for 1000 grain weight, days to 50 per cent flowering, and grain yield per plant.

Sameera *et al.* (2015) evaluated twenty five genotypes of rice and revealed that productive tillers per plant and number of grains per panicle showed high GCV and PCV. While, low GCV and PCV for days to 50 per cent flowering, plant height and panicle length. High heritability coupled with high genetic advance as per cent of mean was recorded for productive tillers per plant and number of grains per panicle.

Vijay Kumar (2015) was evaluated fifty seven genotypes of rice and revealed that high PCV for grain L/B ratio and the GCV estimates were moderate for L/B ratio, protein content and amylose content in land races and for amylose content in new plant types. High heritability with high genetic advance was reported for L/B ratio indicating preponderance of additive gene effect.

Chowdhary *et al.* (2016) evaluated sixty five rice genotypes and reported high heritability along with high genetic advance for amylose content and grain yield per plant.

Rukmanidevi *et al.* (2016) studied genetic variation in twenty seven rice genotypes and revealed that high heritability in broad sense coupled with high genetic advance as percent of mean for the traits like effective tillers, plant height, yield per plant, head rice recovery and length/breadth ratio, whereas the higher estimates of PCV and GCV were observed for yield per plant and filled seeds per panicle.

Sameera *et al.* (2016) evaluated twenty five rice varieties for assessing their variability for yield and yield component traits and reported that the traits like number

of grains per panicle, productive tillers per plant and grain yield per plant had high heritability coupled with high genetic advance.

Anis *et al.* (2016) observed higher estimates of GCV and PCV for number of filled grains per panicle. High heritability coupled with high genetic advance for growing period and plant height.

Bitew (2016) studied the genetic variability among twenty two selected upland rice varieties and recorded high GCV and PCV for biomass yield, grain yield per plant, number of fertile tillers per plant and unfilled grains per panicle. Similarly, high heritability coupled with high genetic advance as per cent of mean was observed for 1000 grain weight.

Devi *et al.* (2016) evaluated twenty seven rice genotypes and reported higher estimates of PCV and GCV for grain yield per plant and filled seeds per panicle. While, hulling percent, milling percent, kernel elongation ratio, day to 50 per cent flowering, panicle length, kernel length and kernel width showed low PCV and GCV values. High heritability in broad sense coupled with high genetic advance as per cent of mean were exhibited by effective tillers (88.8; 30.2), plant height (96.0; 35.3), flag leaf length (84.0; 32.8), filled seeds per panicle (96.0; 68.7) test weight (96.0; 39.1), grain yield per plant (98.0; 68.7), head rice recovery (94.0; 27.7) and L/B ratio (93.0; 20.4).

Karim *et al.* (2016) evaluated twenty five rice genotypes and revealed that effective tiller number per hill, number of unfilled grains per panicle, grain yield per plot and leaf area registered high variability estimates both at genotypic and phenotypic level as well. Further, low GCV was observed for number of effective tillers per hill, number of unfilled grains per panicle, grain yield per plot and grain L/B ratio.

Konate *et al.* (2016) evaluated seventeen recombinants inbred lines, their parents along with a check variety and observed lower GCV than PCV for all the characters studied. High heritability in broad sense estimates were obtained for biomass (68.77%), days to 50 per cent flowering (98.11%), plant height (81.94%), leaf area (82.90%), number of panicles (64.40%), leaf dry weight (72.91%), root weight

(67.43%) and yield per plant (62.23%). High estimates of heritability combined with moderate genetic advance as per cent mean recorded for biomass, day to 50 per cent flowering, leaf area, number of panicle and yield per plant.

Kumar and Uma (2016) studied the genetic variability in a set of fifty five local rice genotypes. High heritability coupled with high genetic advance was recorded for plant height, number of productive tillers per plant, panicle length, panicle weight, number of spikelets per panicle, test weight, grain and straw yield per plant, nitrogen use efficiency, grain quality traits and protein content at both low and no nitrogen conditions. High heritability with moderate to low genetic advance as per cent mean observed for SPAD value, number of tillers per plant and panicle fertility, respectively.

Abebe *et al.* (2017) reported higher PCV and GCV for plant height, culm length, number of unfilled grains per panicle, biomass yield and grain yield. High heritability was recorded for culm length followed by plant height, biomass yield and panicle length. Where, genetic advances as per cent of means was high for plant height, culm length, biomass yield, grain yield and number of unfilled grain per panicle.

Prasad *et al.* (2017) evaluated fifty boro rice genotypes and reported high GCV and PCV values for number of filled grains per panicle, number of unfilled grains per panicle, grain yield per plant. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of tillers per plant, number of productive tillers per plant, number of filled grains per panicle, number of unfilled grains per panicle, 1000- grain weight and grain yield per plant.

Bhinda *et al.* (2017) evaluated forty two genotypes of rice including three prominent checks. Alkali spreading value exhibited highest GCV (19.44%) and PCV (21.07%) followed by filled grains per panicle (GCV 14.83% and PCV 19.90%). High heritability coupled with high genetic advance was reported for gel consistency, plant height, filled grains per panicle, number of grains per panicle and days to 50 per cent flowering.

Nishanth *et al.* (2017) studied 525 germplasm lines and recorded high heritability for L/B ratio (0.98), harvest index (0.98) test weight (0.96) and yield per plant (0.94). Moreover, high to moderate genetic advance as per cent mean was noted for the characters viz., grain yield per plant (62.30), number of productive tillers per plant (42.33) and harvest index (23.90).

Rajpoot *et al.* (2017) reported high estimates of phenotypic and genotypic coefficient of variation for grains yield per plant. High heritability (broad sense) coupled with high genetic advance as per cent of mean for grain yield per plant, biological yield per plant, grains per panicle, panicle bearing tillers per plant, spikelets per panicle, L/B ratio and flag leaf area.

Shaikh *et al.* (2017) studied forty rice genotypes including two checks and reported high PCV and GCV for yield per plant followed by total number of grains per plant, effective tillers per square meter. High heritability along with high genetic advance as per cent of mean was registered for yield per plant, effective tillers per square meter, total number of grains per plant, effective tillers per plant and 1000 grain weight.

Srujana *et al.* (2017) evaluated twenty nine rice genotypes including one check. They recorded high to moderate estimates of GCV and PCV for grain yield per hill, harvest index, spikelets per panicle, tillers per hill, flag leaf length, panicles per hill. High estimates of heritability were observed for spikelets per panicle, days to maturity, biological yield, grain yield per hill, panicles per hill and tillers per hill. Further, they also noticed high estimates of heritability along with moderate to low estimates of genetic advance for spikelets per panicle, seed yield per plant, tillers per plant, panicles per plant and biological yield per hill.

Sumanth *et al.* (2017) observed highest GCV and PCV for seed yield per plant followed by flag leaf length, number of spikelets per panicle, biological yield per plant and panicles per plant. High estimates of heritability was observed for plant height, flag leaf length, biological yield per plant, spikelets per panicle, panicles per plant. High genetic advance was observed for number of spikelets per panicle and plant height.

Sreedhar (2017) was observed variability among thirty six rice genotypes. 1000-grain weight registered high heritability coupled with high genetic advance values. High heritability coupled with moderate genetic advance were recorded for days to 50 % flowering, plant height, panicle length and grain yield, whereas, low estimates of both parameters were observed for number of productive tillers per m².

Kalyan *et al.* (2017) evaluated seventy genotypes of rice and reported that characters like total tillers per plant, number of productive tillers per plant, number of filled grains per panicle and single plant yield showed high PCV and GCV estimates. High heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plant, followed by number of productive tillers per plant, number of filled grains per panicle, number of tillers per plant and plant height (cm). The high estimates of heritability coupled with moderate genetic advance as per cent of mean for days to 50 per cent flowering and days to maturity.

Jan *et al.*, (2017) studied among 35 rice (*Oryza sativa* L.) genotypes under temperate conditions of Kashmir valley. Harvest index showed the highest values of GCV (33.26) and PCV (33.59) and lowest for 1000 grain weight (6.66) and (7.08). High heritability together with high genetic advance was observed in biological yield (0.99) and (53.01). Number of spikelets per panicle (0.49). (46.50), denotes the number of filled grains per panicle (0.99) and (41.90). However, high heritability associated with low genetic advance as percentage of mean was observed for days to maturity (97.00) and (15.11) and 1000 seed weight (89.00) and (12.90).

Adhikari (2018) evaluated twenty six advance genotypes of lowland irrigated rice. High heritability was estimated for days to flowering (0.88), maturity (0.79), thousand grain weight (0.48) and plant height (0.43) suggesting these traits are under high genetic control. High phenotypic variation was observed for grain yield (24.87%), number of grains/panicle (22.45%), number of panicles/m² (20.95%) and straw yield (20.75%) while grain yield had medium (12.02%).

Pragnya *et al.* (2018) investigated seventy five soft rice genotypes. High GCV and PCV estimates were observed for seed yield per plant, number of tillers per plant and number of productive tillers per plant, moderate GCV and PCV for plant height,

panicle length, per cent filled grains per panicle and test weight, low for days to 50% flowering and days to maturity. High heritability coupled with high genetic advance as percent of mean was observed for plant height, number of tillers per plant, number of productive tillers per plant, per cent filled grains per panicle, seed yield per plant and test weight.

Anyaotha *et al.* (2018) noticed that grain yield per plant registered the highest PCV (41.72%) and genetic advance (41.08%). While, high heritability estimates were recorded by 1000 grain weight (88.71%), days to 50 per cent flowering (86.67%) and days to 85% maturity (71.98%).

Behera *et al.* (2018) conducted an experiment with forty nine elite slender grain rice genotypes and reported both PCV and GCV high for grain yield (PCV: 27.14%, GCV: 26.27%) and fertile grains per panicles (PCV: 20.61%, GCV: 20.52%). They also noticed high heritability coupled high genetic gain over mean for days to 50 per cent flowering, plant height, panicle length, flag leaf area, fertile grains per panicle, fertility percentage, 100 seed weight and grain yield per plant.

Kishore *et al.* (2018) observed that the characters viz., plant height, effective tillers per plant, flag leaf length, test weight and biological yield per plant showed higher estimates of heritability and genetic advance.

Singh *et al.* (2018) observed high heritability accompanied with high genetic advance for number of tillers per plant, biological yield per plant, panicle weight per plant, number of spikelets per panicle, fertile spikelets per panicle, spikelet density, grain yield per plant, panicle index, harvest index, head rice recovery and amylase content.

Acharya *et al.* (2018) evaluated eight rice genotypes and recorded higher value of GCV and PCV for grain per panicle, filled grain per panicle, harvest index and grain yield. High heritability along with high genetic advance as percent of mean was observed for grain per panicle, panicle length, harvest index and grain yield. However, high heritability along with moderate genetic advance as percent of mean was observed for days to 50% flowering, 1000 grain weight and plant height.

Hossain *et al.*, (2018) studied thirty three rice genotypes and found that highest phenotypic variation was found for number of grain per panicle and the lowest was observed in 100 grain weight. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) observed for number of unfilled grains per panicle, number of grains per panicle and grains yield per hill,

Subedi *et al.*, (2018) studied seven spring rice genotypes and found high heritability in broad sense and high genetic advance as percentage of mean found in flag leaf area, grain yield and test weight, whereas high heritability in broad sense and moderate or low genetic advance as percentage of mean found in plant height, maturity days, heading days, and chlorophyll.

2.1.2 Correlation analysis

Correlation is a bivariate analysis that measures the strength of association between two variables and the direction of the relationship. Correlation coefficient is used to measure the mutual relationship between various plant characters and to determine the component characters, on which selection can be based for genetic improvement in the yield. The correlation among the traits can be determined in terms of phenotypic correlation and genotypic correlation.

Chakraborty and Chakraborty (2010) evaluated forty seven bold grained rice genotypes with two locally recommended high yielding check varieties namely Ranjit and Monohar Sali of Barak Valley, and reported that significant positive genotypic correlation of grain yield per hill with sterility percentage, number of effective tillers per hill and panicle length.

Manonmani *et al.* (2010) assessed twenty rice genotypes and they observed no any quality characters were correlated with grain yield but milling per cent recorded highly significant positive correlation with head rice recovery and amylose content.

Rajeshwari *et al.* (2010) studied thirty pre-released cultures and high yielding varieties of rice and revealed that grain quality characters viz., kernel length, alkali spreading value and elongation ratio showed positive correlation with kernel length after cooking.

Wattoo *et al.* (2010) evaluated thirty genotypes and reported that grain yield per plant was significantly correlated with number of effective tillers per plant, number of grains per panicle and flag leaf area.

Selvaraj *et al.* (2011) evaluated twenty one rice genotypes and reported that plant height, number of tillers per plant, number of effective tillers per plant, panicle length, number of filled grains per panicle, test weight had significant positive correlation with grain yield.

Kiani G. (2012) studied twenty rice genotypes and observed that grains per panicle and filled grains per panicle were correlated significantly with grain yield.

Mohanty *et al.* (2012) observed strong positive association of kernel length, panicle length, plant height, number of productive tillers per plant, 1000-grain weight, days to maturity and number of grains per panicle with grain yield.

Nagesh *et al.* (2012) studied correlation in forty eight rice hybrids and revealed that grain yield per plant was highly significant positive correlation with number of productive tillers per plant followed by test -weight and number of grains per panicle.

Seyoum *et al.* (2012) evaluated fourteen upland rice genotypes and revealed that grain yield was positively and significantly associated with grains per panicle and spikelet per, whereas, had positive and non-significant association with tiller per plant, panicle length and panicles per plant both at genotypic and phenotypic level.

Arulmozhi and Muthuswamy (2013) carried out experiment with seventy four rice genotypes involving hybrids and their parental lines and revealed that grains per panicle, productive tillers per plant, panicle length and amylose content had significant positive association with grain yield at genotypic levels, however days to 50 per cent flowering and L/B ratio showed significant and negative association with yield at genotypic level.

Gande *et al.* (2013) observed that the grain yield per plant showed highly significant positive correlation with number of productive tillers and plant height.

Chakravorty *et al.* (2013) studied fifty one landraces of rice and found that leaf length was positively and significantly correlated with leaf breadth, plant height and culm length. Plant height was significantly correlated with leaf length.

Shabir *et al.* (2013) evaluated seventy nine rice genotypes and reported that highly positive significant association of grain yield with plant height, number of tillers per plant, panicle length, panicle weight, 1000-grain weight, number of grains per panicle and spikelet fertility.

Veni *et al.* (2013) studied seventy rice genotypes and reported that days to 50 per cent flowering, productive tillers per plant, panicle length, head rice recovery (HRR) and volume expansion ratio manifested significant positive association with grain yield.

Alam *et al.* (2014) studied seventy six rice genotypes and found that number of effective tillers plant and number of grain panicle were positively and significantly correlated with yield per plant.

Rukamanidevi *et al.* (2014) evaluated twenty nine genotypes of rice and revealed grain yield positively correlated with plant height, panicle length, grains per panicle and effective tillers. Whereas, plant height had significant and positive correlation with grains per panicle, panicle length. While, L/B ratio exhibited negative and significant correlation with head rice recovery and zinc content at both genotypic and phenotypic levels.

Patel *et al.* (2014) evaluated forty four diverse genotypes and reported that grain yield per plant was found positively and significantly associated with plant height, panicle length, number of total tillers per plant, number of effective tillers per plant, number of grains per panicle, harvest index and 1000-grain weight at both genotypic and phenotypic levels.

Kumar *et al.* (2014) reported that grain yield per plant had significant positive correlation with days to 50% flowering, days to maturity and tillers/plant while, it had significant negative correlation with plant height and flag leaf length.

Lakshmi *et al.* (2014) evaluated seventy genotypes of rice and revealed that grain yield per plant positively and significantly associated with days to maturity, number of productive tillers per plant, plant height and kernel length.

Lingaiah *et al.* (2014) carried out experiment in sixty four mid early group genotypes of rice. The correlation studies revealed that the genotypic correlation were

higher than the corresponding phenotypic correlations. Yield exhibited positive association with effective tillers per plant, panicle length and test weight. But negatively associated with days to 50% flowering and plant height.

Moosavi *et al.* (2015) evaluated 30 rice genotypes and reported that highest correlation between grain yield per plant and number of panicles.

Sarawgi *et al.* (2015) reported positive and significant correlation of leaf length and leaf width, effective tillers and plant height with grain yield.

Ekka *et al.* (2015) evaluated ninety six rice accession and indicated that grain yield per plant had positive significant correlation with leaf width, days to 50% flowering, plant height, panicle length, number of filled grains per panicle, 100 seed weight and paddy length. A positive and significant correlation of head rice recovery percentage was also observed with leaf length, leaf width, days to 50% flowering, number of filled grains per panicle and milling percentage.

Kishore *et al.* (2015) assessed seventy three rice and reported that grain yield per plant was positively and significantly associated with panicle bearing tillers per hill and number of grains per panicle indicated an increase in grain yield with an increase in these characters. However, significant and negative associations were observed for panicle bearing tillers per hill, number of filled grains per panicle with 1000 - seed weight.

Naseer *et al.* (2015) assessed twenty four asian rice genotypes and reported that single plant yield was positively and significantly correlated with number of grains per panicle and 1000 –grain weight at genotypic and phenotypic levels. While, positive and significant phenotypic correlation of tillers per plant was found with plant height and negative significant correlation with number of grains per panicle and yield per plant respectively.

Nirmaladevi *et al.* (2015) evaluated ninety two genotypes of rice and observed hulling percent significantly and positive correlation with milling percent, head rice recovery and grain yield per plant. While, hulling percent exhibited negative and significant with amylose content at both level and head rice recovery showed negative but non-significant correlation with grain L/B ratio.

Kumar (2015) was evaluated fifty seven rice genotypes and reported that grain length showed significant positive correlation with L/B ratio, 1000-grain weight and amylose content in both land races and new plant types.

Chowdhary *et al.* (2016) assessed sixty five genotypes of rice and they reported milling percentage shows a similar positive correlation with respect to head rice recovery whereas, yield per plant had non-significant association with all the quality parameters reflecting less influence of all these traits upon the final yield.

Dhurai *et al.* (2016) studied correlation in thirty two genotypes and found that significantly positive association of grain yield per plant with harvest index and number of grains per panicle. Whereas, a trait like days to 50 per cent flowering, number of effective tillers per plant, kernel L/B ratio and 1000-grain weight were non-significant positive association with grain yield per plant.

Sameera *et al.* (2016) studied correlation analysis in twenty five rice varieties and observed that grain yield per plant was positively and significantly associated with productive tillers per plant and number of grains per panicle also days to 50 per cent flowering with plant height, panicle length, productive tillers per plant, number of grains per panicle.

Santipriya *et al.* (2017) evaluated forty genotypes of rice and they revealed that the traits, productive tillers per plant, grains per panicle, panicle length, plant height and days to 50% flowering were found to possess significant positive association with grain yield per plant. While, the trait L/B ratio showed negative significant association with grain yield per plant at phenotypic levels.

Jan *et al.*, (2017) studied among 35 rice (*Oryza sativa* L.) genotypes under temperate conditions of Kashmir valley. Correlation studies revealed that harvest index (0.47) and (0.43) showed significant positive correlation with grain yield per hill at both genotypic and phenotypic level. While as days to 50% flowering (-0.31) and (-0.28) showed significant negative correlation with grain yield per hill.

Bhujel *et al.* (2018) studied in 24 rice genotypes at Rampur, Chitwan, Nepal during rainy season in 2017 and 2018 and they reported grain yield was negatively and significantly correlated with 50% flowering days.

Singh *et al.*, (2018) studied the correlation analysis in eighty four (including Check) rice (*Oryza sativa* L.) varieties and reported that biological yield per plant, harvest index, 1000-grain weight, panicle bearing tillers/plant and panicle length showed positive and significant correlation with grain yield per plant.

in rice. Crosses were made in line x tester analysis. The results revealed that grain yield per plant showed highly significant and positive correlation with plant height, flag leaf area, panicle bearing tillers per plant, panicle length, grains per panicle, 1000 grain weight and biological yield per plant.

Patra and Das (2018) studied on 17 elite rice hybrids along with 7 different checks. Grain yield per plant was positively correlated with plant height, panicle length, panicle number, grain number and harvest index.

Prakash *et al.*, (2018) investigated correlation analysis in 7 lines and 3 testers

Acharya *et al.*, (2018) evaluated eight rice genotypes for correlation analysis. The effective tiller per m², harvest index, grain per panicle and filled grain per panicle exhibited significant and positive correlation with grain yield. Plant height and ineffective tiller per m² exhibited negative correlation with grain yield.

Hossain *et al.*, (2018) studied thirty three rice genotypes and found that number of grains per panicle with grains yield per hill as well as length showed significant and positive correlation but number of tillers per hill showed highly significant and negative correlation with days to 50% flowering both at genotypic and phenotypic level.

Bitew *et al.*, (2018) evaluated twenty-two upland rice varieties for correlation analysis of grain yield and revealed that positive and significant associations with fertile tiller per plant ($r_g=0.792$), biomass yield ($r_g=0.789$), and plant height ($r_g=0.684$) at genotypic level.

Subedi *et al.*, (2018) studied seven spring rice genotypes and found grain yield was significantly correlated with flag leaf area ($r = 0.799^{**}$), fertility percentage ($r = 0.697^{**}$), effective tillers ($r = 0.665^*$), panicle length ($r = 0.587^*$) and leaf chlorophyll content ($r = 0.579^*$).

2.2 Cold and heat tolerance

2.2.1 Cold tolerance screening

Cold tolerance refers to the ability of genotypes to germinate, grow and produce satisfactory grain yields under conditions of relatively cold (but above-freezing) air and soil temperatures (Singh, 1985). The screening of genotypes for cold tolerance at seedling stage is the primary requirement of Rabi / summer season cultivars as seedlings are raised during the cold months of December and January. Greater and better synchronized germination is crucial for achieving an optimal seedling establishment and better productivity, however, environmental constraints such as freezing and low temperature are great impediments.

According to the methods of evaluation of rice genotypes for cold tolerance available in the literature, seeds are subjected to temperatures varying from 10 °C to 25 °C for periods of three to thirty five days and characteristics most commonly measured are germination percentage, speed of germination, coleoptile length and radicle length (Maya, 1988, Bertin *et al.*, 1996. Cruz and Milach (2004) proposed the following method for estimating the cold tolerance in two experiments. In experiment I, seeds were germinated under two conditions; 28 days in 13 °C and seven days in 28 °C and in experiment II, seeds were germinated at 72 hours with 28 °C, 96 hours at 13 °C and again 72 hours at 28 °C. In experiment I, percentage of reduction in radicle and coleoptile length and germination index were measured. In experiment II, radicle and coleoptile regrowth after the cold period were measured to identify tolerant genotypes.

Breeding cold tolerant varieties in rice is essential to reduce yield loss, for which information on various traits that contribute to tolerance is necessary. Identification of new genetic sources for cold tolerance is very important for which effective, low cost screening techniques are essential. The findings of earlier workers on cold screening in rice are summarized here:

da Cruz and Milach (2004) evaluated 24 rice genotypes of different origins. Cold tolerance was evaluated in experiment I, germination under two conditions: 13°C for 28 days and 28°C for seven days, and in experiment II, germination under 28°C for 72 hours, 13°C for 96 hours and again 28°C for 72 hours. In experiment I measured

characteristics were germination index, percentage of seeds with coleoptile length superior to 5 mm and percentage of reduction in coleoptile length due to cold. In experiment II the measured characteristic was coleoptile regrowth after the cold period. Among Japonica genotypes, Quilla 64117 and Diamante presented the highest cold tolerance, and among Indica, cultivars BR-IRGA 410 and IRGA 416 were the most cold tolerant at the germination stage.

Seema and Roy (2007) evaluated the impact of low temperature stress in six genotypes viz. Gautam, Richharia and Dhanlaxmi from cold tolerant group and Turauta, Jaya and Heera from susceptible group. A general decline in germination percentage, germination relative index and vigour index of germinating seeds in low temperature stress condition than under non stress condition was observed. Minimum values were recorded for Turanta, Jaya and Heera while the Gautam, Riccharia and Dhanlaxmi were affected relatively less.”

Ye *et al.* (2008) evaluated seventeen rice varieties from several countries for cold tolerance at the germination, seedling, booting and flowering stages. The seedling growth of Amaroo, B55, Bangjiemang, HSC55, Jyoudeki, Lijiangheigu and Quest were less affected by low temperature. Rice varieties B55, Bangjiemang, HSC55 and Lijiangheigu were consistently tolerant to low temperature at germination, seedling, booting and flowering stages.

Bosetti *et al.* (2012) examined 195 rice genotypes for cold tolerance. At 28°C, accession Kyuushuu showed the highest value for coleoptiles and Oiran showed the highest value for radicle length, whereas accessions Toga and Esojima Mochi showed the lowest values. At 13°C, the highest values for both traits were observed for the control genotype QUILLA 66304. Among the accessions, the highest value for CL13 was observed for Toga 1, whereas Sangoku displayed the highest value for RL13. The lowest values for both CL13 and RL13 were observed for accession Chousen.

Nanculao *et al.* (2013) were evaluated 20 experimental line of rice for cold tolerance. Germination under low temperatures induced a decrease in coleoptile length growth in all evaluated genotypes. Genotype ranking, principal component, and cluster analysis based on coleoptile length allowed us to find differences in cold tolerance

among rice genotypes. Of the Chilean varieties, 'Diamante-INIA' showed high cold tolerance, and 'Oro-INIA' and 'Brillante-INIA' showed an intermediate cold tolerance.

Sahu *et al.* (2014) evaluated 50 rice genotype for low temperature tolerance. The results of experiment explained that root length varies from 0.1cm to 0.8 cm. One of the genotype HHZ 5-DT1-DT1 had 0.8 cm root length at 15° C and its germination percentage is also 86.66 %, therefore this genotype is supposed to be good for summer paddy since it has cold tolerance. The maximum shoot length recorded was 9.3 cm in HHZ 12-SAL 8-Y1-SAL1 genotype. The genotypes which showed 100 per cent germination were IR 10C132 followed by IR 10C153, HHZ 8- SAL6-SAL3-Y2 and HHZ 17-DT6-Y1-DT1.

Pradhan *et al.* (2015) were used 220 germplasm lines for screening of tolerant genotypes, Genotypes namely Langma, Umleng-1 and Geetanjali showed survival up to 25 d, which were better than the positive check Kalinga-III surviving up to 20 d under chilling stress.

Dien and Yamakawa (2016) evaluated 186 rice varieties The average coleoptile length (mm) of varieties at 13°C was reduced by 98.41% compared to control condition. Under cold stress condition, ARC 13829 variety showed the longest coleoptile length (8.40 mm) and radicle length (14.20 mm) compared to other varieties. Tumo-Tumo variety expressed the highest germination index (95%) compared to other varieties.

Rahul *et al.* (2017) evaluated thirty seven rice genotypes among them HPR 1068, Himalaya-2216 and Vivek Dhan -82 showed lesser percentage of reduction for seedling vigour index at both temperatures and these genotypes can be used as cold tolerant donors in future breeding programs for development of seedling cold tolerant rice varieties.

Pradhan *et al.* (2017) evaluated nine rice genotypes and observation recorded for emergence of the plumule at the end of every 24 hrs from 3rd day to 10th day after sowing. Seedling length was measured at one week after transplanting. Seedling length was high in JGL 11118(30 cm), MTU 1075(29.5 cm) followed by RNR 15048 (27.8 cm) than checks.

Sales *et al.* (2017) conducted experiment with a pool of 200 traditional, landraces and modern elite and old cultivars of rice experiments. The highest mean growth rate when seeds were germinated at 15°C was determined for the cultivar Italica Livorno, The faster development coleoptile growth rate was observed in seeds of six varieties, two indica (IR-64 and IR-10198) and four japonica (Italica Livorno, Loto, Puita CL and Taichung-65), that showed coleoptile growth rates higher than 4.0 mm/d.

Lone *et al.* (2018) evaluated cold tolerance at the germination stage and identify the variability among 30 rice genotypes. Highest germination was achieved in SKAU-402 followed by SI-6, K-332, SI-5 and SI-3 with less percent decline in germination that is, 0.13, 0.17, 0.24 and 0.32 at 13°C. Percentage of coleoptiles growth by low temperature (13°C) was varied from 13.8 to 86.6%. In experiment II, radicle regrowth values varied from 2.0 to 12.0 mm, and SI-6,-SI-5, Kamad, SKAU-402 and K332, were the genotypes with high radicle regrowth.

2.2.2 Heat tolerance screening

Heat tolerance in plants is the ability of the plants to grow and produce economic yield when subjected to higher temperature condition. The tolerance of the plant to heat stress is characterized by minimal damage to photosynthetic machinery and increased biosynthesis of the protective compounds. Photosynthesis and reproductive phase of plant growth are highly sensitive to high temperature stress. So, a heat tolerant variety in this regard should have a better photosynthetic rate, membrane thermo stability and seed setting under high temperature (Nagarajan *et al.*, 2010). In rice breeding program, the heat tolerant materials for breeding can be selected from breeding germplasm (Singh, 2002).The findings of earlier workers on heat screening in rice are summarized here:

Agarie *et al.* (1995) evaluated rice cultivar and reported that electrolytic leakage was increased almost linearly with the time of leaf tissues submerged in test temperature (42°C) solution. EL increased from 8.1% to 71.6% with temperature increase from 40°C to 45°C. They found that membrane integrity and stability to the

stress as evaluated by electrolyte leakage correlate well with tolerance of other plant process to the stress.

Prasad *et al.* (2006) reported that based on decreases in spikelet fertility at high temperature, cultivar N-22 (25 and 9%) was most tolerant, while cultivars L-204, M-202, Labelle, Italica Livorna, WAB-12, CG-14 and CG17 were highly susceptible and cultivars M-103, S-102, Koshihikari, IR-8 and IR-72 were moderately susceptible to high temperature. flag leaf electrolyte leakage for different cultivars ranged between 44 and 56% The relative injury in cultivars Italica Livorna, M-103 and IR-72 were on par with each other but greater than other cultivars. Cultivars Koshihikari, N-22 and Labelle had the lowest relative injury.

Jagadish *et al.* (2007) studied the effect of high temperature at anthesis on spikelet fertility was studied on IR64 (lowland indica) and Azucena (upland japonica) at 29.6 °C (control), 33.7 °C, and 36.2 °C tissue temperatures. In IR64, there was no interaction between temperature and duration of exposure, and spikelet fertility was reduced by about 7% per °C > 29.6 °C. In Azucena there was a significant interaction and spikelet fertility was reduced by 2.4% °Cd⁻¹ above a threshold of 33 °C. The check cultivar N22 was the most heat tolerant genotype (64–86% fertility at 38°C) and cultivars Azucena and Moroberekan the most susceptible (<8%).

Ye *et al.* (2009) studied seventeen rice varieties in control environment (28°C) and stress environment (15°C). In control environment germination was observed 2 days after the commencement of treatments, with most seeds having germinated within 5 days. As no further germination was observed on Days 6 and 7, counts of ungerminated seeds were made on Day 7. Most varieties showed high levels of germination (GR >95%). Only the varieties Azucena, Pelde, and YRL39 (with 78.7%, 77.3%, and 84.7%, respectively) had slightly lower germination levels. In the low temperature treatment (15°C), germination was slower, with no germination observed until the 3rd day of treatment. The fastest germinating variety, HSC55, reached peak germination (the day germination rate was the highest) on Day 5, followed by Banjiemang, B55, Lijiangheigu, M103, and WAB38, which reached their peak

germination on Day 7. The slowest germinating varieties, Jyoudeki and YRL39, reached their peak germination Day 10.

Rang *et al.* (2011) revealed that better anther dehiscence, higher in vivo pollen germination and higher spikelet fertility were observed in both the N22 accessions compared with IR64, Apo and Moroberekan under high temperature, water stress and combined stress. N22 an aus rice cultivar is a good high temperature and water deficit stress tolerant donor.

Tenorio *et al.*, (2013) were evaluated 23 accessions for heat tolerance by exposing them to controlled high temperature during booting and flowering stages. High-temperature treatment of 39 °C is suitable for screening heat tolerance at booting stage, while 38 °C is suitable for flowering-stage evaluation. Dular and Todorokiwase are tolerant at the booting stage, while Milyang23 and IR2006-P12-12-2-2 are tolerant at the flowering stage. Giza178 is tolerant at both booting and flowering stages.

Maruyama *et al.* (2013) determined by the temperature (T_{75}) at which spikelet fertility becomes 75% of that of the control plants. They reported tolerance to spikelet sterility under high temperature was in the order of highest to lowest of; IR36, IR24, AKT, KSH, HTM, NPB, HNH, and NKM.

Reinoso *et al.* (2014) evaluated eight plants of each of the three cultivars on membrane stability based on the percentage of electrolyte leakage and revealed that 'F60' and 'F733' seemed to be the most susceptible. These cultivars exhibited respective electrolyte losses of ~ 20% and ~ 15% at both 35 and 40 °C. However, 'F473' plants did not exhibit changes in membrane stability throughout the heat stress treatment.

Smita *et al.*, (2014) were screened 40 rice genotype for heat tolerance. Based on spikelet fertility percentage and yield of grain per plant genotypes ZAKHA (ACC 86841), N22 (ACC 4819), PEH-KUH-TSAO-TU (ACC 8237), N22 (ACC 117273) and IR 64196-3B-23-3 was observed good performance to high temperature.

Naveen *et al.*, (2015) were screened 47 rice genotype against high temperature stress. Based on spikelet fertility percentage 26 genotypes were observed more than 80% spikelet fertility. Some genotypes viz., POORNIMA, BRRI DHAN 48,

PEHKUH-TSAO-TU (ACC 8237) were observed highly tolerant against high temperature.

Kumar *et al.* (2015) studied emphasizing the rise in temperature with respect to pollen viability was conducted with eleven rice genotypes. Reduction in grain yield was 8.6–54.5% in 2010 and 15.6–43.4% in 2011. The highest grain yield was observed in both years for IET 21577.

Kr *et al.* (2016) conducted experiment taking 10 rice genotypes including heat tolerant check N-22. Less decrease in pollen viability, spikelet fertility and panicle yield were recorded in N-22 and N-L-44 under heat stress. Vandana, Sahbhagi Dhanand CR-262-4 displayed a decrease of 30 to 35% in all three traits. But, Anjali, Swarna, PS-5, PB-1 and IR-64 were found to be very sensitive toward an increase in temperature during flowering with a decrease of more than 50% in yield. MSI of N-L-44 was almost similar to the check (N22) under heat stress. Vandana, S.Dhan and CR-262-4 showed a decrease of 12 To 13%. Whereas, Anjali, Swarna, PS-5, PB-1 and IR-64 showed a decrease of 16 to 21%.

Masuduzzaman *et al.* (2016) evaluated 1217 entries and screened heat tolerant lines based on yield, spikelet fertility and high grain filling under high temperature. Yield level and spikelet fertility ranged from 11.92 to 32.8 g/plant and 61% to 86%, respectively. The highest yield was found in IR 86991-146-2-1-1 (20.02 g/plant.) followed by IR 87606-109-2-2 (19.35 g/plant). Highest spikelet fertility was observed in IR 88268-107-1-1 (86%) followed by IR 88268-124-2-3 (84%). The lowest pollen sterility was found in IR 86991-146-2-1-1(0-20%). IR 86991-146-2-1-1 was found as more tolerant to heat at flowering stage having higher yield/plant, higher number of filled grains/panicle and lower pollen sterility (0-20%).

Mahantashivayogayya *et al.*, (2016) screened forty rice accessions for heat tolerance with Gangavati sona, IR-64, MTU 1010 and N-22 as checks. The check N-22 (66.00 days) was the earliest to days to 50 per cent flowering followed by the accessions EC792177 and EC792206. Number of tillers per plant at maturity was significantly highest (22.50) in the accession EC792195 followed by the accessions EC792203 and EC792178 (17.30). Significantly highest thousand grain weight was

recorded in the accessions EC792200 and EC792286 (25.00g). The significantly minimum per cent of chaffyness (0.40%) was recorded in the accession EC792183 followed by the accessions EC792179 (0.80%) and EC792216 (1.20%). The highest grain yield of 6167 kg/ha was recorded by accession EC792239 followed by EC792285 (5777 kg/ha) and EC792185 (5333 kg/ha), as against the checks MTU-1010(2520 kg/ha), N-22 (2400 kg/ha), IR-64 (2283 kg/ha) and local check Gangavati sona (1490 kg/ha).

Eswaran *et al.* (2017) screened fifty rice genotypes for heat tolerance. The genotype IR 10C172 (93.07%) recorded highly significant mean for spikelet fertility. This may be due to its tolerance nature of this genotype.

Rahul *et al.* (2017) evaluated thirty seven rice genotypes with reported cold tolerance at various phonological stages were used to evaluate for germination and seedling traits in laboratory conditions under three temperature regimes viz., normal (28°C), 8°C and 13°C respectively for identification of genotypes possessing seedling stage cold tolerance. On an overall basis HPR 1068, Himalaya-2216 and Vivek Dhan -82 showed lesser percentage of reduction for seedling vigour index at both temperatures and these genotypes can be used as cold tolerant donors in future breeding programs.

Hakata *et al.* (2017) evaluated nine cultivars and found at 35 °C/29 °C treatment the tolerance to spikelet sterility was in the order of highest to lowest of; IR36, IR24, Akitakomachi, Hitomebore, Nipponbar, Nikomaru, Koshihikari and Ninohikari.

Cheabu *et al.* (2018) Seed-setting rate, yield components and grain quality traits of 169 accessions from an exotic rice germplasm were tested under high temperatures from 40 °C to 45 °C for 6 h during the daytime at the vegetative and reproductive stages, respectively. The results showed that heat stress significantly decreased the seed-setting rate of all the accessions, but the heat stress effects diverse among accessions. Based on the decreases in seed-setting rate at high temperatures, N22 was the most tolerant, followed by AUS17, M9962, SONALEE and AUS16.

2.3 Combining ability

Combining ability measures the relative ability of a parental line to pass genetic information to its offspring. It helps in identifying parental lines to use in developing hybrids. Suitable inbred lines are used in crosses to develop hybrids whose performance level depends on the heritability of the traits and the combining ability of the parental lines. Therefore, knowledge of combining ability and genetic variances is pivotal in the development of high yielding hybrids. It is composed of general combining ability (GCA) and specific combining ability (SCA) which are important in partitioning total observed phenotype into parental genotype main effects and genotypic interaction effects respectively (Mohammadi *et al.*, 2010).

Characterization of inbred lines is important in hybrid development. A line X tester analysis evaluates a set of parents by crossing each to a common tester which is normally treated as a male (Motamedi *et al.*, 2014). The method helps in determining the ability of the parental lines to pass on heritable traits to the offspring. It was proposed by Kempthorne (1957) to investigate the interaction of genotypes of a tester with known performance and a line of unknown performance. It is based on the principles of a factorial experiment whereby the genotype of the tester is treated as one factor and the genotype of the line as the other factor.

General combining ability (GCA) was defined as the deviation of mean performance of a parent genotype in all its hybrid combinations from the population mean (Griffing, 1956). It is used as an indicator of the potential performance of a line when it is crossed to different genotypes. GCA of a line emanates from additive gene effects exerted by the genotype of that line (Marinkovic *et al.*, 2000). The gene effects of the lines involved in the cross should be neither dominant nor recessive to each other so that the observed phenotype in the offspring will be a sum total of parental effects. For a line to be selected it must have a positive and higher GCA for a particular trait. The application of GCA has been emphasized in a lot of studies although it is suggested to be more useful in yield estimates and in material that was not previously selected. It is also important for developing synthetic varieties (Ali *et al.*, 2014).

Specific Combining Ability (SCA) Specific combining ability is the deviation of the mean performance of a particular hybrid from the expected performance based on the GCA of its parents and the overall mean of the population (Griffing, 1956). SCA differs from GCA in that it is focused on a particular combination of one line and a tester hence it is specific. Since SCA is a result of interaction between line and tester genotypes, it takes into account dominance or epistatic gene effects. A desirable SCA means the genetic interactions between the genotypes involved in a particular hybrid are favourable. Although SCA is specific to a hybrid combination it can also be used to give an indication of how a genotype may perform in other crosses. It is expected that SCA will be positive when parents from distinctly different backgrounds are crossed and vice versa for related parents (Betran *et al.*, 2003) due to heterosis. In crosses involving more than two testers SCA provides useful information on the performance of individual lines.

Testers can be populations, inbred lines or single cross hybrids but the most widely used are inbred lines (Hallauer and Miranda, 1988). As a result of self pollination inbred lines are highly homozygous and of known characteristics. An expected mean can be calculated when a known tester line is crossed to an inbred line or hybrid. However, deviations from the expected mean often occur and they can be used to differentiate the combining abilities of the lines being tested (Makumbi *et al.*, 2011). The findings of earlier workers on combining ability in rice are summarized here:

Panwar (2005) studied combining ability of parents and crosses in rice and reported that the importance of non-additive gene action controlling all the traits under studied. The line IET 13846 and the testers Basmati 370, Kasturi, Taraori Basmati, Pusa Basmati-1 and IR 64 were good general combiners for grain yield per plant

Bisne and Motiramani (2005) reported that the predominance of non additive gene action over additive gene action for plant height, days to 50 per cent flowering, effective tillers per plant, panicle length, grain yield per plant, 100 grain weight, length and breadth of paddy. The lines DRR 2A and PMS 10A and testers R 827-287, BKP 232, R 1060-1674-2-103 and R 714-2-103 were good general combiners for grain

yield. The crosses, DRR 2A X R 827-287 and DRR 2A X R 1060-1674-1-1 exhibited higher SCA with high standard heterosis for grain yield.”

C. Issac Sunil (2006) studied for earliness and yield traits in rice and revealed that non-additive gene action for these characters. Based on the gca effects and per se performance AD 95128 and AD 95134 were identified as superior parents for earliness. TKM 9 and BTCE 23/ 99 for yield and AD 95157 for both earliness and yield potential. The hybrid AD 95134 x IR 64 was the earliest for improving yield and AD 95157 x TKM 9 identified as the best recombination for breeding.

Bagheri *et.al.* (2008) studied combining ability and gene action for yield and yield related traits viz., days to maturity, tillers per plant, panicle length and 1000 grain weight. The study indicated that both additive and non additive gene actions play key role in the inheritance of these traits.

Salgotra *et al.* (2009) studied combining ability among 15 basmati crosses and observed preponderance of dominant gene action for plant height, panicle length, effective tillers per plant, spikelet sterility, number of grains per panicle, 1000-grain weight and grain yield per plant. Sanwaal Basmati, Pusa 2517-2-51-1, Ranbir Basmati, Super Basmati, and Basmati 370 were found good general combiners and, Pusa 2517-2-51-1 X Pusa Basmati , Super Basmati X Ranbir Basmati were best crosses showing high specific combining ability effects.

Dwivedi and Pandey (2012) were evaluated forty five hybrid rice in which parent Sarjoo 52 and B4122 were found best general combiner for most of the characters, including grain yield per plant. The crosses BSI10xPant Dhan 12, B4116xSarjoo 52, BSI10xNarendra 359, B4122xGovind and B4122xManhar recorded the highest SCA effects for yield per plant.

Koli *et al.* (2013) studied of eighteen hybrids produced crossing between six genotypes with high yielding (IET 19695, IET 16310, IET 13846, IET 12016, IET 16320 and basmati 370) used as lines and three quality rice genotypes namely Pusa Sugandha-4, Pusa Sugandha-4 and Improved Pusa basmati-1 as testers. The estimates of GCA effects indicated that IET 12016 was found the best general combiner for grain yield per plant and milling percentage, IET 16320 for milling and head rice

recovery (HRR) percentage , whereas, IET 13846 was found superior general combiner for grain quality traits only. Pusa Sugandha-4 as tester was the best general combiner for grain length and Pusa Sugandha-5 for grain breadth and grain length breadth ratio, whereas Improved Pusa basmati-1 for HRR (%). High specific combining ability (SCA) effects were observed in the crosses IET 19695 x Pusa Sugandha-5 for grain yield per plant, IET 16310 x Pusa Sugandha-4, IET 13846 x Pusa Sugandha-4 and IET 16320 x Pusa Sugandha-5 for grain length and grain length breadth ratio and they were found the best combiner for grain yield and grain quality traits.

Prasad *et al.* (2013) experimented with four lines and four testers. Ujala Depama, IR-64, and MALIDA are identified as the good general combiners. IR64 X Malida, IR64 X Ujala Depama and MTU-1010 X Ujala Depama are good specific combinations . IR64 X Malida, IR64 X Ujala Depama, and Krishna Hamsa X Parwa Panki are identified as the best heterotic lines for the character under study.

Montazeri *et al.* (2014) studied with ten hybrids crossed with two lines and five testers. SCA variances were higher than the GCA variances for number of productive tillers per hill, 100-grain weight (gr) and panicle length (cm) and which indicated predominance of non-additive gene action. P35 tester produced the lowest height among testers, highest number of productive tillers and number of spikelets per panicle among parents and its hybrids produced highest number of productive tillers, highest panicle length (cm), highest number of spikelets per panicle (Tarom-Jelodar × P35) and lowest height (Danesh × P35) among hybrids. Also this variety was found as good general combiner for height (cm) and panicle length (cm).

Kolom *et al.* (2014) studied of forty five intervarietal crosses developed by crossing between three testers and fifteen lines along with parents and checks. Sca variance and non- additive variance components higher than genetic variance and additive variance for almost all the characters under study. The estimates of gca effects indicated that, Manchio Tsük, Koyapvu Tsok, among lines and Teke and RCM-5 among testers are good general combiners for grain yield per plant. The best

sca effects were observed in cross, Leikhumo (T) x Teke for plant height which also showed best sca effects for filled grains per panicle.

Rani *et al.* (2015) were carried out Line x tester analysis from seven lines and three testers which were selected on the basis of their grain number and grain weight. The line MTU 1075 was found as good general combiner for kernel length and the tester MTU 1010 found good general combiner for L/B Ratio and kernel length. Among 21 crosses, MTU 1075/ MTU 1010, NRI 003/ MTU 1010 and NRI 003/ MTU 3626 revealed wide scope for enhancing both grain dimensions and milling traits in order to develop promising rice varieties.

Devi and Lal (2015) studied about twenty one crosses developed by seven female and three male parents and reported that ML-10-29VL and TMO7280 showed good general combiners for seed yield per plant and most of the yield traits. The cross combinations IR77629-72XIR64, BASMATI370 X CR2703 and sonam X NDR1118 were the best specific combiners for seed yield per plant.

Rani and Satyanarayana (2015) studied with seven lines and three testers and twenty one crosses. Among ten parents the line MTU 1075 and the tester MTU 1010 found to be as good general combiners for most of the yield and yield related traits. The cross combinations viz., MTU 1075/MTU 1010, MTU II-118-24-4-1/MTU 3626, MTU 1121/TN1 and NRI 003/TN 1 showed significant and positive SCA effects for grain yield per plant.

Sultan *et al.* (2015) conducted experiment among the ten parents (four lines and six testers) in (2010) to produce (24) crosses. GCA were found as highly significant for all studied traits, except grain yield plant-1 and 1000 grain weight for regarding to number of tillers per plant, flag leaf area (cm²), number of panicle plant-1 and number of filled grains per panicle, the parental variety, Gz 9057-6-1-3-2 exhibited highly significant positive GCA effects for these traits. The rice variety Sakha 106 was found to be highly significant positive GCA effects for 1000-grain weight and grain yield plant-1. While, SKC 23819-192-2-2-1-1-2-1-2-2 proved to be excellent combiner for 1000-grain weight, while SKC 23819-192-2-2-1-1-2-2-1-2 was best combiner also for the grain yield per plant.

Nayak *et al.* (2016) studied with sixteen crossing between four aromatic lines and four non scented testers and reported that the heterotic crosses Yamini/MTU1010(Milling Recovery), Pusa1121/BM-71(Kernel Length), Ranbir Basmati/BM71(Kernel Breadth, kernel L/B ratio), Pusa 1121/MTU1081(Kernel Length after Cooking), RNR2354/BM71(Kernel Elongation Ratio), Yamini/Sye632003(Aroma, Alkali spreading value) and Pusa1121/BM71(Protein) were found to be superior, expressing heterosis, heterobeltiosis and standard heterosis in desirable direction.

Kumar *et al.* (2016) studied combining ability for yield through L X Tanalysis. The genotypes were used for crossing programme in 6 lines and 5 testers .Among the line AURC 14 and testers ADT 43 and IR 64 were considered as the best general combiners, while hybrids AURC 8 x ADT 36, AURC 1 x ADT 36, AURC 8 ADT 43, AURC 14 x ADT 36, AURC 10 x ADT 43, AURC 14 x TRY 1, AURC 22 x TRY 1, AURC 22 x IR 64, and AURC 25 x ADT 36 as good specific combiners for grain yield and other yield related and quality traits.

Rahaman *et al.* (2016) conducted experiment with 10 rice genotypes and 25 F₁s The variance of SCA were found significant for most of the characters. Higher ratio of SCA and GCA variances indicating preponderance of non-additive gene actions in the inheritance of all the characters except filled spikelet per panicle. Such results showed the higher estimates of GCA variances i. e. additive gene action but in case of days to flowering, 1000 grain weight and grain yield per hill higher estimates of SCA variance i.e. non-additive gene action were found. Among the male parents, SAU509R and SAU525R were observed as good general combiner for most of the character studied. IR62829A x SAU509R. IR62829A x SAU523R, Jin23A x SAU507R, Dakshahi A x SAU525R and Luhagura A x SAU523R were observed as good specific cross combinations.

Menaka and Ibrahim (2016) studied in forty eight crosses along with eight lines and six testers to find out their usefulness in improvement of quality traits. Analysis of variance revealed that ASD 16 line, Pusa Basmati 1, Basmati 370 testers were the good combiners for both yield and quality traits. The crosses ASD 16 / Pusa

Basmati 1, ADT 36 / GEB 24, ADT 43 / Jeeragasamba, MDU 5 / Improved White Ponni and MDU 2 / Pusa Basmati 1 were identified as the good specific combiners for grain yield and some other quality characters.

Thorat *et al.* (2017) conducted experiment with seven rice genotypes and twelve F_1 s. Higher ratio of SCA and GCA variances indicating preponderance of non-additive gene actions in the inheritance of all the characters except number of filled spikelets per panicle, days to 50 per cent flowering, and days to maturity results showed that the higher estimates of GCA variances i. e. additive gene action but in case of plant height, total number of spikelets per panicle, number of productive tillers per plant, panicle length, 1000 grain weight, spikelet fertility, grain yield per plant, harvest index and straw yield per plant higher estimates of SCA variance i.e. non-additive gene action were found. Among the male parents, NPQ-49 and Chedo Local were observed to be good general combiner. Cross combinations, IR58025A x NPQ-49 and RTN12 A x NPQ-49 were observed as good specific cross combinations.

Choudhary *et al.* (2017) studied of a set of three lines as females and ten testers as males of aerobic rice. The gca variances for females was found significant for plant height, days to maturity and panicle length while it was found non-significant for other traits, whereas gca variance for males were found highly significant for plant height, days to 50 % flowering, grains per panicle, panicle length, seed test weight, days to maturity and leaf area, while it was found non-significant for other traits. The study of sca variance and gca variance for all characters indicated the predominance of non additive gene action for all the studied traits except days to 50 % flowering, panicle length and days to maturity. For grain yield per plant and some of economic traits, male parents, KMP 128 and RCPR 7 were found good general combiners. The good specific combinations for grain yield and other attributing traits were GNR-3 x RCPR 6, AICRIP-1335 x RCPR 8 and NAUR-1 x NDR 1132-5.

Fahmi *et al.* (2017) evaluated 25 hybrid combinations of 10 line x 5 tester design. Giza 179 X Large Stigma and Sakha 105 X VNIRB 572 exhibited significant values of SCA effects for grain yield. Heritability estimates in narrow sense ranged from low to moderate. Sakha 101 X Novator, Sakha 106 X Novator and Giza 179 X

Large Stigma were the promising hybrid combinations for improving yield character according to results for mid and better parent heterosis.

Sreelakshmi and Babu (2018) evaluated twenty hybrids crossing between five females and four male lines along with parents and checks and indicated that among females, BPT 5204 and among males IR 64 were good general combiners for grain yield per plant. High sca effects were observed in the crosses, WGL 48684 x IR 36 and RNR 2465 x IR 36 found as the best combinations for grain yield per plant.

Saravanan *et al.* (2018) evaluated thirty two hybrids developed by crossing between eight lines and four testers General combining ability effects indicated that line K R 09009 as a good general combine for majority of the traits studied viz., 100 grain weight, high kernel length (KL), high kernel L/B ratio and moderate panicle exsertion and kernel breadth. Among the testers, ASD-19 was adjudged as good general combiner for all the traits viz., panicle exsertion, 100 grains weight, kernel breadth, kernel length, kernel L/B ratio and grain yield per plant.

2.4 Heterosis

Heterosis refers to the superior performance of hybrids relative to thier parents. It is an important approach for increasing rice production. It has not only contributed to food security, but also benefited the environment (Duvick, 1999). The different crop species in which hybrid varieties are used commercially, rice rank is very high. It has been commercially exploited in rice with a yield advantage of 20-25% over the best pure lines (Rather *et al.*, 2001). The findings of earlier workers on heterosis in rice are summarized here:

Tiwari *et al.* (2011) studied in LXT mating design crossing between three CMS lines and twenty elite restorers. The results indicated that the manifestation of heterobeltiosis for grain yield was significantly superiority of 43 hybrids ranging from 11.63 to 113.04% and 46 hybrids over standard variety (Sarjoo-52) ranging from 10.48 to 71.56%. Most of the crosses which exhibited superiority over better parent or

standard variety for grain yield also showed significant heterosis for number of spikelets per panicle and number of fertile spikelets.

Latha *et al.* (2013) studied in eighteen hybrids involving three CMS lines and six testers using LXTanalysis. The line 'CRMS 32A' and testers viz. R 1099-2569-1-1, Super rice-8 and Jitpiti were identified as good general combiners. The hybrid CRMS 32A X R 1099-2569-1-1 and 'APMS 6A X Super rice-8 were promising for grain yield

Kumar and Adilakshami (2016) evaluated twenty hybrids developed from crossing four CMS lines and five testers. Heterosis for grain yield was manifested due to the significant and positive heterosis for its components viz., effective tillers, test weight, number of fertile grains per panicle, harvest index, hulling%, milling%, kernel length after cooking kernel length, L/B ratio and elongation ratio. The top four heterotic combinations identified for grain yield per plant 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.

Thorat *et al.* (2017) evaluated twelve hybrids crossing between three CMS lines and four testers and reported significant and positive heterosis for grain yield per plant its components viz panicle length (cm), total productive tillers per plant, number of filled spikelets per panicle, 1000 grain weight (g), spikelet fertility (%), and harvest index (%). The heterotic combinations identified for grain yield per plant were IR58025A x NPQ-49 and RTN12A x NPQ-49 which exhibited more than 40% heterobeltosis and standard heterosis ranged from 3.64% to 53.14%.

Reddy *et al.* (2018) investigated three superior testers and twenty one hybrids were developed through line x tester mating design heterobeltiosis and standard heterosis for grain yield ranged from -38.71 to 32.96 % and -39.11 to 29.71%, respectively. A total of four hybrids viz., MTU 1010 x IR 50, ADT 39 x TRY 2, ADT 39 x IR 50 and PKM 3 x IR 50 were recorded maximum grain yield over better parent and standard parent and were identified as best hybrids for exploiting hybrid vigor.

2.5 Stability analysis

Varietal adaptability to environmental fluctuations is an important factor for the stabilization of crop production over the regions and years. An information on genotype x environment (GXE) interaction leads to successful evaluation of stable genotype, which could be used for the general cultivation. GXE interactions cause genotypes to perform differently in different environments. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations. The selection for superior genotypes based on yield per se at a single location in a year may not be very effective. Thus, evaluation of genotypes for stability performance under different environmental conditions for yield has become an essential component of breeding programme. Selection of superior genotypes is confounded by GXE interactions. A stable variety is one which has high mean than population mean, unit regression coefficient and minimum deviation from regression line (Eberhart and Russell, 1966). A breeder would usually want to develop a variety that have high yield performance in many locations and seasons. The findings of earlier workers on stability in rice are summarized here:

Sreedhar *et al.* (2011) studied eighty two genotypes and reported that pooled analysis of variance showed that G x E interactions were significantly difference for characters viz., number of productive tillers per plant, panicle weight, number of filled grains per panicle and 1000 seed weight and single plant yield ..

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

Rasyad *et al.* (2012) studied in four locally adapted and one high yielding cultivar of rice were evaluated at three environments in Riau, Indonesia. There were significant difference of environments on yield and yield components, except panicle number per plant. The cultivars Cisokan and IR64 were showed stable performance for all the environments.

Lal and Singh (2012) studied in fifteen genotypes of rice under six environments during *kharif* 2005-06. Pooled analysis indicated highly significant differences among the genotypes and environments for all the characters under study. Pusa Basumati-1, PR-114 and Sahib-140 were found promising with stable

Ajmera *et al.* (2017) evaluated thirty seven rice genotypes and reported that GXE interaction components showed highly significant differences for all the characters, when tested against pooled error and days to 50% flowering, total number of grains per panicle, plant height and 1000 grain weight showed significantly differences, when tested against pooled deviation. It indicates wide differential of genotypes in change environments. The environment + (Genotype x Environment) was significant for all the characters, when tested against pooled error and all the characters shown significant differences except number of filled grains, panicle length when tested against pooled deviation.

2.6 Expression of sHSPs

Small heat shock proteins (sHSPs) are a family of ATP-independent molecular chaperones which prevent cellular protein aggregation by binding to misfolded proteins. The sHsp gene family have different expression pattern depending on the tissue, organ and stage of development. There are at least seven different sHSP subfamilies in plant (Siddique *et al.* 2003; Ma *et al.* 2006). A sHSP subfamilies localize in cytosol mitochondria (MT), chloroplast (CP), peroxisome (PX) and endoplasmic reticulum (ER). The exact timing of the origin of the plant sHSP subfamilies is not yet known.

Rice is principal model for other monocotyledonous species and important staple food crop in the world and the (Lee *et al.*, 2011). Rice is considered a model plant species of the group monocots for small genome size and easy availability of large collection of full-length cDNAs (FL-cDNAs) and its whole genome is completely sequenced (IRGSP, 2005). In recent years, researchers have made great efforts on the functional analysis of individual sHsp family members in rice, however

sHsps still have not been fully characterized and little is known about their interactions.

Guan *et al.* (2004) studied about characterization and the expression profile of nine sHSP-CI gene family in rice (*Oryza sativa* Tainung No.67), of which Oshsp16.9B, Oshsp16.9A, Oshsp16.9D, Oshsp16.9C and Oshsp17.9B are clustered on chromosome 1, and Oshsp17.7, Oshsp17.3, Oshsp17.9A and Oshsp18.0 are clustered on chromosome 3. Oshsp18.0 and Oshsp17.3 are linked by a 356-bp putative bi-directional promoter. All sHSP-CI genes except Oshsp17.9B were induced strongly after a 2-h heat shock treatment. The genes on chromosome 3 whereas those on chromosome 1 were induced slowly by were induced rapidly at 32 and 41 °C, similar conditions.

Chang *et al.* (2007) reported class II sHSP isolated from rice (*Oryza sativa* L., cv. Tainong No. 67) seedlings heat shocked at 41 °C for 2 h. The obtained full-length cDNA clone, designated Oshsp18.0-CII.

Sarkar *et al.* (2009) reported that 19 sHsp genes were upregulated by high temperature stress through expression analysis based on microarray and RT-PCR. Besides heat stress, expression of sHsp genes was up or down regulated by the other biotic and abiotic stresses. Phylogenetic analysis showed that 23 out of these 40 genes constitute sHsps.

Chandel *et al.* (2013) reported the genes encoding small Hsps (OsHsp 16, OsHsp 17.7 and OsHsp 18), OsHsp 70 DnaK, OsHsp 100 and OsHsf A2a showed strong induction upon heat stress with varied pattern and degrees. Out of six rice genotypes, two R-1389-RF-42 and Nagina22 (check heat tolerant) showed higher gene expression levels for most of the Hsps and Hsf genes tested with prominently better way of regulation which contributed to their greater heat tolerance and surmount the stress.

Lee *et al.* (2013) studied gene expression profile of heat shock proteins and reported transcripts of chaperone 60, HSP70, HSP100, chloroplastic HSP26, and mitochondrial small HSP responded to heat stress rapidly and strongly.

Jung *et al.* (2014) analyzed that expression of the Oshsp16.9 gene was rapidly and strongly induced by stresses including stress (300 mM mannitol), high-salinity (250 mM NaCl), osmotic 100 μ M ABA, cold (4°C) and heat (45°C) through RT-PCR analysis.

Chen *et al.* (2014) studied about Hsp23.2, Hsp26.7, Hsp17.4, Hsp17.9A and Hsp16.9A were up-regulated in Nipponbare during seedling and anthesis stages in heat stress. The expressing levels of these sHsps in the heat-tolerant rice cultivar, Co39, were higher than the heat susceptible rice cultivar, Azucena. This indicated that the expressive level of these sHsps was positively related to avoid heat stress in rice crop.

Wang and Vinocur (2015) characterized HSPs gene OsHSP18.6 in rice. OsHSP18.6 could be induced by diverse stresses, such as salt, cold and drought, especially under heat. This gene was found expressed in leaf, stem, root, internode and spikelet.

Guo *et al.* (2016) reported that heat shock stress can induce high level expression of the two genes. Under normal growth conditions, Os16.9A and Os16.9B expressed in vegetative organs and young panicles. The β -glucuronidase staining combined with cytological observations showed that the two genes expressed mainly in the vascular tissues of roots, stems and young panicles, implicating that Os16.9A and Os16.9B play important roles not only for heat shock response, but also for normal development in rice.

Xiang *et al.* (2019) cloned gene encoding a SHSP (OsSHSP17.6) from *Oryza sativa* and the sequence assembly showed the encoding region of OsSHSP17.6 was 477 bp in length, encoding a polypeptide of 158 aa with a molecular weight of 17.6 kD. The protein appeared to be accumulated up to higher level under the condition of heat shock in western blotting assays.

CHAPTER-III

MATERIALS AND METHODS

The present study entitled “**Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)**” was conducted at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur (C.G.) during *Summer* -201, kharif 2017 and *Summer* -2018 and to generate the phenotypic data under managed field condition. The molecular work was conducted at R.H. Richharia research Laboratory (RRL) IGKV, Raipur (C.G.) to generate the genotypic data. The materials used, techniques and statistical tools that have helped in interpreting the data are briefly presented in this chapter:

3.1 Experimental site

The present research work was conducted at Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur (C.G.). Raipur is situated mid- eastern part of Chhattisgarh state and located at 21° 16’ N Latitude and 81° 36’ E longitude with an altitude of 289.60 meters above the mean sea level.

3.2 Climatic and weather condition

This region comes under dry and sub-humid climate. Weekly average meteorology data during the crop growing season were recorded at meteorological observatory, IGKV, Raipur (C.G.) are presented in fig 3.1 and fig 3.2, data in Appendices I and II.

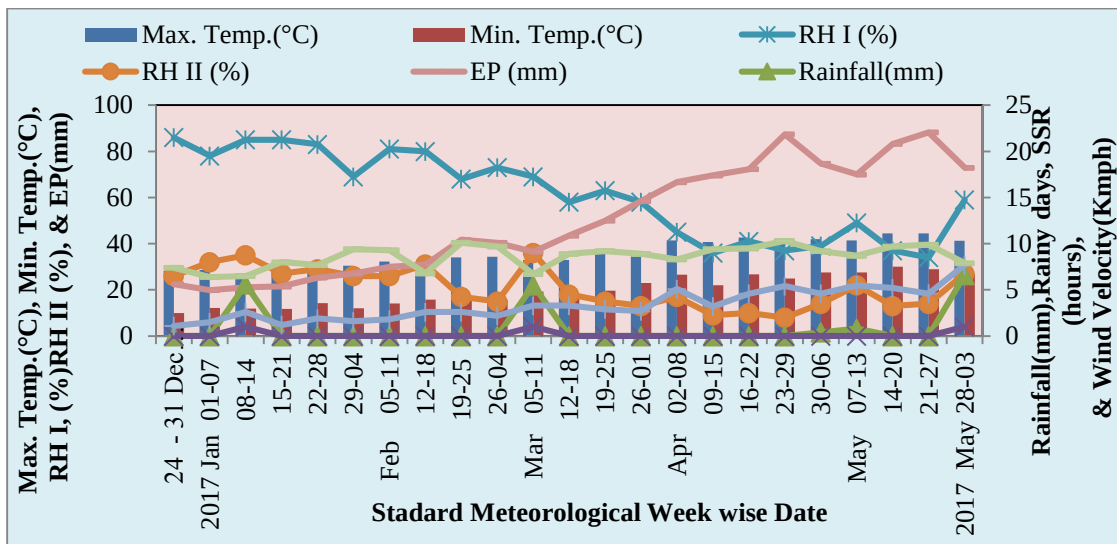


Fig 1: Meteorological observation during *Summer-2017*

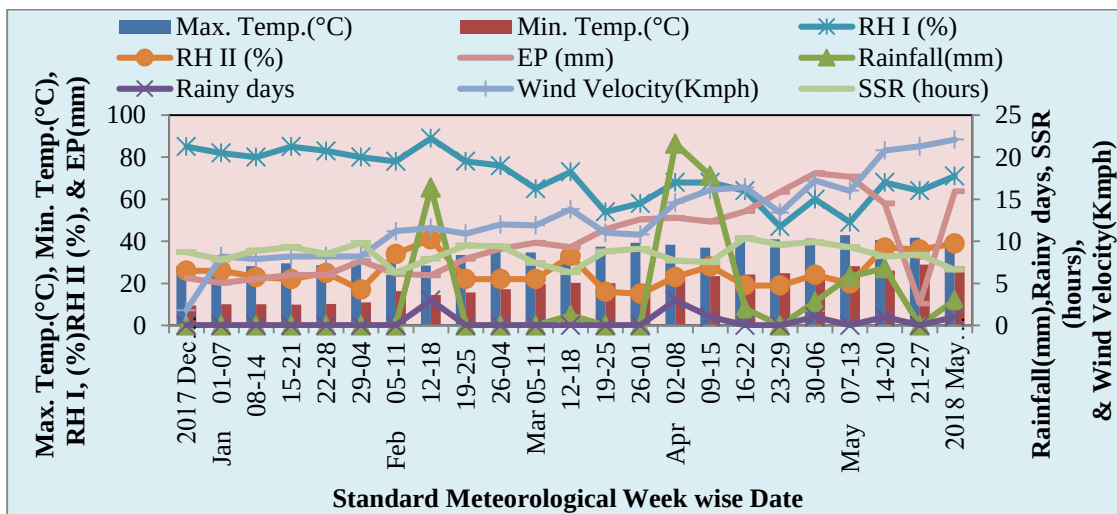


Fig 1: Meteorological observation during *Summer-2018*

3.3 Experimental material

The experimental material used in the present study comprised 80 rice genotypes/varieties and 7 checks (C). List of rice genotypes/varieties under study are described in table 3.1.

3.4 Experimental details

During *Summer*-2017, the set of genotype (87 rice genotypes) was evaluated in randomized block design (RBD) with two replications.

On the basis of pollen fertility, spikelet fertility and grain yield per plant thirty seven rice genotypes were selected and evaluated for cold, heat and quality parameters.

During *Kharif*-2017, on the basis of heat and cold tolerance parameters selected twelve parents (eight lines with four testers) were crossed in Line x Tester design

During *Summer*-2018, selected thirty seven genotypes were evaluated in three different dates for stability analysis. Thirty two F₁ and twelve parents were evaluated in RBD design with two replications.

On the basis of heat tolerance screening selected twelve rice genotypes were used for expression analysis.

3.5 Nursery Sowing and transplanting

The details of sowing and transplanting methods are given in table 3.2.

3.6 Hybridization

During *Kharif*- 2017 at flowering stage selected four male parents were crossed to each of the eight female lines to generate a set of hybrids in a line x tester manner as proposed by Kempthorne (1957). In order to increase the seed settings, the spikelet of female plant that were expected to flower the next day were clipped one third at the top, covered with butter paper bags to avoid outside pollen grains to fertilize the female plants. In the next morning (about 8:30 am) panicles from the male parents were collected at anthesis time and were kept in pollination room at

temperature of 40°C under high humidity in glass bottles, after complete anthesis the pollen grains were dusted over clipped spikelets with proper precaution. The pollinated panicles were immediately bagged and labeled properly with date and cross combination. In this way, 32 crosses were attempted for the present study (Fig: 3.3). The bagged panicles were harvested and separated from mother plants after thirty days of hybridization. The hybrid seeds of each cross were collected separately and sun dried. The seeds were treated with bavistin as a precautionary measure against fungal attack before storing in paper bags.

3.6.1 Raising F₁ and parents

During *Summer-18*, the treated seeds of total 32 F₁ generated during the previous season were carefully germinated in wooden trays. These wooden trays are kept in green house (Fig). Twelve parents (8 lines along with 4 tester lines) were also sown in nursery beds on the same day.

3.7 Observations recorded

In each treatment, observations were recorded on five randomly selected plants in both the replications for the traits given below. The mean value over five randomly selected plants was considered for further statistical analysis.

3.7.1 Quantitative traits

3.7.1.1 Days to 50% flowering

The number of days from sowing to the date when primary panicles in 50 per cent plant were in heading was recorded.

3.7.1.2 Plant height (cm)

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

3.7.1.3 Tillers per plant (No.)

Number of tillers per plant at maturity were counted and recorded.

Table 3.1: List of rice genotypes used for current study

S.No	Name	S.No	Name	S.No	Name	S.No	Name
1	Aerra Mindo	26	Bankal	51	Dadhmaini dhan	76	Bhejari
2	Aarmoti	27	Bakhiya	52	Digamber dhan	77	Ganga Puriha
3	Barhi	28	Banskupi	53	Harikhunta dhan	78	Khurabal
4	Batri (II)	29	Banspatri	54	Damru Baba-3	79	Nagbel
5	Dehura Baya	30	Bankari	55	Jeera Baba	80	P:357 III
6	Dokra Mechha	31	Bankadi	56	NPT 6	81	Nagina 22 (C-1)
7	Mal do kalam	32	Chingar Bnko	57	NPT 8	82	Swarna (C-2)
8	Hirikani	33	Shiv dharohar-4	58	NPT 9	83	Indira Barani Dhan 1 (C-3)
9	Jholar	34	Safri	59	NPT 11	84	MTU 1010 (C-4)
10	Jhular	35	Ganga kali	60	NPT 19	85	Samleshwari (C-5)
11	Kadam Phool	36	Bhurkund	61	NPT 26	86	IR-64 (C-6)
12	Kadam Phool	37	Gangtai	62	IR 42253	87	Indira Aerobic 1 (C-7)
13	Kakai	38	90 Number	63	NPT 12		
14	Kali Muchh	39	Dadbako	64	NPT 6		
15	Lallu	40	Gangtai dhan	65	NPT-27		
16	Lallu 14	41	Ganga dhan	66	CR dhan 40		
17	Local	42	Tendhumori dhan	67	R-1670-3269-2-3926-1		
18	No.16	43	Ajam dhan	68	Barhasal		
19	RJR:II	44	Bhatamokdo	69	Sitasaal Dhan		
20	OSSR: 181 III	45	Safed Lalak	70	Dan Banko		
21	Ajawain	46	Tewan dhan	71	Jodhari		
22	Vishun Bhog	47	Hajar Khunta	72	Jugsay		
23	Anjaniya	48	Sindursaal	73	Bega hundi		
24	Baikoni	49	Kolhin khosa	74	Anjaniya		
25	Baikoni	50	Neta Kalani	75	Banko		

C= Check

Table 3.2 Details of sowing and transplanting:

Conditions	Date of sowing	Date of transplanting	Spacing (cm)		No of rows/line	Length of row (m)	No. of replication	Design of experiment
			row to row	Plant to plant				
Summer 2016-17								
	27/12/2016	21/01/2017	20	15	2	2.5	2	RBD
Kharif- 2017								
Irrigated	30/06/2017	26/07/2017	20	15	2	2.5	2	RBD
Summer 2017-18								
1st date	23/12/2017	17/01/2018	20	20	2	2.5	2	RBD
2nd date	03/01/2018	29/01/2018	20	20	2	2.5	2	RBD
3rd date	13/01/2018	07/02/2018	20	20	2	2.5	2	RBD
F1 and parents	19/01/2018	14/02/2018	20	15	2	2	2	RBD



Nursery sowing



Seed germination



Fig 3.3: Field view after transplanting

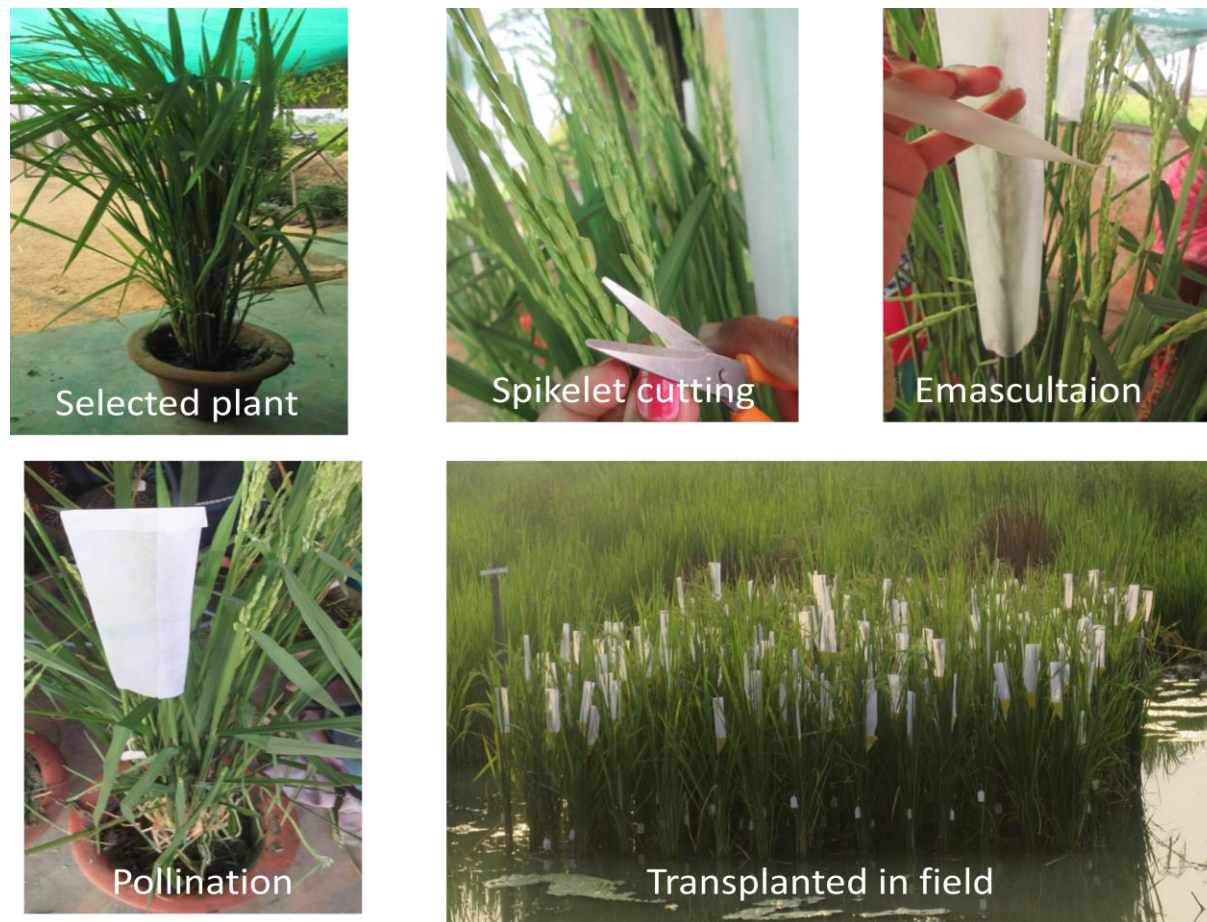


Fig 3.4: Crossing procedures in field

3.7.1.4 Effective tillers per plant (No.)

The total number of panicle bearing tillers in each plant was recorded at the time of harvest.

3.7.1.5 Flag Leaf Length (cm)

The leaf blade length of the flag leaf is called flag leaf length.

3.7.1.6 Flag Leaf Width (cm)

The leaf blade width of the flag leaf called flag leaf width.

3.7.1.7 Flag Leaf Area (cm²)

Flag leaf area was calculated by formula:

$$\text{Flag leaf area} = \text{Flag leaf length} \times \text{Flag leaf width} \times K$$

Where, K is the adjustment factor taken as 0.75.

3.7.1.8 Panicle length (cm)

The length of panicles was measured from the base to the tip of the panicle excluding awn if any at the time of harvest.

3.7.1.9 Total number of grains per panicle (No.)

At the time of harvest panicles from each plant were harvested separately. The total numbers of spikelets in these panicles were counted and recorded per plant wise.

3.7.1.10 Number of filled grains per panicle (No.)

It is ratio of fertile spikelet to the total no. of spikelet.

3.7.1.11 Grain yield per plant (g)

The matured panicles plants were harvested, threshed, cleaned and dried to 12-14% moisture level. The grain yield per plant was recorded in grams.

3.7.1.12 100 Grain weight (g)

The weights of well filled 100 grains were weighed and the mean weight expressed in grams.

3.7.1.13 Biological yield per plant (g)

Weight of each plant excluding root was recorded and expressed in grams

3.7.1.14 Harvest index (%)

The ratio of grain yield to the biological yield of each plant was calculated and expressed as percentage.

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

3.7.2 Quality characters

3.7.2.1 Hulling (%)

The mud lumps, rice stems, leaves and other foreign matter from the sample were removed and then 100 g of sample was weighed. The clean sample was shelled with the Satake Sheller. The samples were hulled and weights of dehulled grains were recorded.

$$\text{Hulling (\%)} = \frac{\text{Weight of dehulled grain or brown rice (g)}}{\text{Weight of paddy (g)}} \times 100$$

3.7.2.2 Milling (%)

The hulled samples were milled and weight of milled grains was recorded.

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

3.7.2.3 Head rice recovery (%)

After milling the whole and broken grains were separated and head rice recovery was calculated by the formula:

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

3.7.2.4 Paddy length (cm)

The length of randomly selected ten spiketets was measured in terms of millimeters by graph methods.

3.7.2.5 Paddy breadth (cm)

The breadth of randomly selected ten spiketets was measured in terms of millimeters by graph methods.

3.7.2.6 Paddy L/B ratio

The length/breadth of randomly selected ten spiketets was measured in terms of millimeters by dividing respective length and breadth graph methods.

3.7.2.7 Brown rice length (cm)

The length of randomly selected ten hulled spiketets was measured in terms of millimeters by graph methods.

3.7.2.8 Brown rice width (cm)

The width of randomly selected ten hulled spiketets was measured in terms of millimeters by graph methods.

3.7.2.9 Brown rice L/B ratio

The length/ width of randomly selected ten hulled spiketets was measured in terms of millimeters by dividing respective length and breadth ratio.

3.7.2.10 Kernel length (mm)

Ten milled grains were taken randomly and average length was recorded in millimeter.

3.7.2.11 Kernel breadth (mm)

Ten milled grains were taken randomly and average breadth was recorded in millimeter.

3.7.2.12 Kernel length/breadth (L/B) ratio

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

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

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

Designation	Length (mm)	Shape	L/B ratio
Extra long	>7.5	Slender	3.0
Long	6.61 – 7.5	Medium	2.1 - 3.0
Medium	5.51 – 6.60	Bold	1.1 – 2.0
Short	< 5.5	Round	1.1

3.7.2.13 Kernel length after cooking (mm)

After cooking the rice samples for 20 minutes, five cooked grains at random from each sample were taken and length was measured to nearest millimetre on a graph sheet.

3.7.2.14 Kernel breadth after cooking (mm)

Five cooked grains at random from each sample were taken and breadth was measured to nearest millimetre on a graph sheet.

3.7.2.15 Cooked Kernel Length: Breadth (CKL: CKB)

It was computed by the following formula:

$$\text{L/B ratio} = \frac{\text{Kernel Length after Cooking}}{\text{Kernel Breadth after Cooking}}$$

3.7.2.16 Elongation ratio

The length of rice grains of each sample was measured before and after cooking and kernel elongation ratio was worked out following standard method of Verghese (1950) as modified by Murthy (1965).

$$\text{Elongation ratio} = \frac{\text{Mean length of kernel after cooking (mm)}}{\text{Mean length of kernel before cooking (mm)}}$$

3.7.2.17 Elongation Index

It was computed by the following formula:

$$\text{Elongation index} = \frac{\text{L/B ratio of cooked rice}}{\text{L/B ratio of milled rice}}$$

3.7.2.18 Alkali spreading value (Gelatinization temperature)

It was estimated by the milled rice treated with a 1.7% solution of potassium hydroxide for 23 hrs at 30°C as per Jennings *et al* (1979).

Step:

1. Six milled kernels without cracks were selected and placed in plastic boxes of 4.6 x 4.6cm square and 1.9 cm high.
2. 10 ml of 1.7% KOH was added to the boxes which were maintained at 30°C for 23 hours.
3. A rating for spreading of 1-3 was classified as high, 4-5 as intermediate and 6-7 as low gelatinization temperature.

Classification	Alkali spreading 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)

3.7.2.19 Gel consistency (mm)

The gel consistency test is based on the consistency of the rice paste and following steps were followed in its estimation as per Jennings *et al* (1979).

Step I: 8-10 milled grains were finely ground and sieved through 100-mesh.

Step II: 100 mg of fine flour was weighed in duplicate and was placed in test tubes.

Step III:

a) 0.2 ml of 95% ethanol containing 0.025% thymol blue was added to the test tube

b) 2 ml of 0.2N KOH was added with a pipet.

c) The contents were thoroughly mixed and the tubes were covered with glass marbles.

d) The contents were heated on vigorously boiling water bath till the contents reached 2/3 the height of the tube.

e) Then the tubes were removed from water bath and allowed to stand for 5 minutes and cooled in ice water bath for 20 minutes.

Step IV: Then the tubes were laid horizontally on a table for 1 hour without any disturbance.

Step V: Total length of the gel from the bottom of the tube to the gel front was measured in mm.

Categorization of rice according to gel consistency:

i. Very flaky rice with hard gel consistency (length of gel, 40 mm or less).

ii. Flaky rices with medium gel consistency (length of gel, 41 to 60 mm).

iii. Soft rices with soft consistency (length of gel, more than 61 mm).

3.7.2.20 Amylose content (%)

Amylose content was determined by the method developed at International Rice Research Institute, Philippines (Jenning *et al.*, 1979).

Procedure for determining amylose content:

1. Weighing of 0.10 g of fine powdered rice grain in 100ml volumetric flask.
2. Add 4 ml methanol was added and kept for 2.30 hr.
3. After that methanol was extracted.
4. Add 9 ml of 1N NaOH and 1ml of 9.5% ethanol.
5. Then it was heated for 10 minutes in pre-heated water-bath.
6. Cool it and make up 100 ml volume with distilled water.
7. From this, 5 ml sample in volumetric flask was taken and 1ml of acetic acid and 2ml of potassium iodide (KI) reagent was added.
8. Again the volume was made up with 100 ml distilled water and kept for 20 minutes.
9. Finally the reading of the sample at 620 nm on spectrophotometer was recorded.

$$\text{Amylose (\%)} = R \times 76.92$$

R = Reading at 620nm on spectrophotometer.

Classification according to Kumar and Khush 1986):

waxy (0–2%), very low (3–9%), low (10– 19%), intermediate (20–25%), and high (>25%)

3.7.3 Parameters for cold tolerance

3.7.3.1 Germination (%)

The laboratory test for germination was conducted as per the ISTA rules (ISTA, 1985) by adopting between paper method. Four replications of hundred seeds each in a treatment were used for the germination test that were placed in seed germinator and maintained at constant temperature of 28 ± 0.5 °C and more than 90 per cent relative humidity. The first and the final counts were taken on fourth and seventh day, respectively. On the day of final count, the number of seeds germinated was counted and the per cent germination was calculated as follows:

$$\text{Germination \%} = \frac{\text{Number of normal seedlings}}{\text{Total number of seeds planted}} \times 100$$

This test was also done at temperature 13°C and 85 percent relative humidity.

3.7.3.2 Percentage of seeds with coleoptile superior to 5 mm (PERCOL)

This was obtained by considering all the germinated seeds 28 days after the beginning of the cold treatment and by verification of the percentage that presented coleoptile length superior to 5 mm, according to the formula given by Cruz and Milach (2004).

$$\text{PERCOL} = (\text{Number of seeds with coleoptile} > 5\text{mm}) \times 100/20$$

3.7.3.3 Percentage of reduction in coleoptile length (REDCOL)

This was obtained through comparison of average coleoptile length 28 days after germination at 13 °C (cold treatment) with that obtained 7 days after germination at 28 °C (control) and calculating the percentage of reduction in coleoptile length by germination under cold temperature, according to the formula given by Cruz and Milach (2004).



Coleoptile length 28 days after germination 13°C



Coleoptile length 7 days after germination 28°C

Fig: 3.5 cold tolerance screening

$$\text{REDCOL} = [(\text{coleoptile length under cold temperature} \times 100) / \text{coleoptile length under control}] - 100$$

Where, coleoptile length is the average of the 20 seeds evaluated per replication per genotype.

Cold reaction (Cruz and Milach, 2004):

- Highly tolerant - equal or less than 25 percent (= or <25%)
- Tolerant - between 25 to 50 percent (25-50%)
- Intermediate - equal 25 percent (= 25%)
- Sensitive - < 25 percent

3.7.3.4 Coleoptile regrowth

In Experiment II, seeds of the 24 rice genotypes were submitted to germination under the following conditions: 28°C for 72 hours, 13°C for 96 hours and again 28°C for 72 hours. This procedure was used to simulate field conditions, where temperature variation is ordinarily observed. The choice and sterilization of the seeds and conduction of the experiment were made according to Experiment I. Coleoptile length was measured in two occasions: after the period of 96 hours at 13°C (LENGTH 1) and after the second period of 72 hours at 28°C (LENGTH 2). Cold tolerance evaluation was performed through coleoptile regrowth (COLREG; mm), which consisted in the difference between the second and the first measurements.

$$\text{COLREG} = (\text{LENGTH 2}) - (\text{LENGTH 1}),$$

Where, coleoptile length is the average of the 20 seeds evaluated per replication.

Cold reaction (Cruz and Milach, 2004):

- Highly tolerant - equal or greater than 20mm (= or >20mm)
- Tolerant - between 8 to 20mm (8-20mm)
- Intermediate - equal to 8mm (= 8mm)
- Sensitive - < 8mm

3.7.3.5 Germination index (GI)

The germination index was calculated by using the formula given by Cruz and Milach (2004). For the calculation of GI only the seeds presenting coleoptile and radicle were considered.

$$GI = (N14 + N21/2) / 20 \times 100$$

Where, N14 = number of germinated seeds 14 days after the beginning of the cold treatment,

N21 = number of germinated seeds 21 days after the beginning of the cold treatment, 20 being the total number of seeds per genotype per replication.”

3.7.4 Parameters for heat tolerance

3.7.4.1 Canopy temperature

Canopy temperature was recorded during flowering stage by Infra red thermometer.

3.7.4.2 Membrane stability index (%)

Leaf membrane stability index (MSI) was determined according to the method of Premchandra *et al.*, (1990) as modified by Sairam (1994). To determine the MSI leaves were collected from both stressed and unstressed plants were taken to the lab. Leaf discs (100 mg) were thoroughly washed in running tap water followed by washing with double distilled water thereafter the discs were heated in 10 ml of double distilled water at 40°C for 30 min. Then electrical conductivity (C1) was recorded by EC (Electrical Conductivity) meter. Subsequently the same samples were placed in a boiling water bath at 100°C for 10 min and their electrical conductivity was also recorded (C2).

$$\text{Membrane Stability Index (MSI)} = 1 - \frac{C1}{C2} \times 100$$

3.7.4.3 Pollen fertility (%)

The observation was recorded by microscopic pollen grain count. The florets were first preserved in 70 percent alcohol in morning before anthesis. Later on the pollen fertility counts were taken by using 1% iodine potassium iodide (IKI) as stain. The stained pollen grains were counted as fertile and vice-versa (Virmani, 1997). The total counts of fertile pollen grains were observed in relation to the total pollen grains in the five microscopic fields. The mean of five microscopic fields was then calculated. These mean values for fertile pollens and total pollens were used for calculating the pollen fertility percentage. The pollen fertility percentage was calculated as follows:

$$\text{Pollen fertility (\%)} = \frac{\text{No. of darkly stained pollen grains under macroscopic field}}{\text{Total number of pollen grains}} \times 100$$

3.7.4.4 Spikelet fertility (%)

The ratio of total number of filled spikelets per panicle to the total number of spikelets per panicle for each panicle was calculated and expressed in percentage. The spikelet fertility percentage was calculated as follows:

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled spikelets per panicle}}{\text{Total number of spikelets per panicle (Filled spikelets + unfilled spikelets)}} \times 100$$

3.8 Molecular analysis

3.8.1 RNA isolation

Leaf samples from heat stressed (*Summer* 2018) and controlled (*Kharif* 2018) were collected from field at flowering stage for RNA isolation. Immediately after collection the leaves tissue were frozen in liquid nitrogen which was used for further gene expression studies. For gene expression studies extraction of RNA was done by trizol method. RNA was extracted as protocol given below:

Reagents for RNA isolation

1. Liquid nitrogen
2. Trizol reagent
3. Chloroform: IsoAmyl Alcohol (24:1, v:v)
4. Isopropanol
5. DEPC water
6. 70% Ethanol (with DEPC treated water)

Procedure:

1. All materials like pestle-mortar, microcentrifuge tubes and pipette tips required for RNA isolation were treated with 0.1 per cent DEPC water and further air dried and autoclaved before use.
2. Pestle and mortar was made chilled by pouring liquid Nitrogen into it.
3. ~200 mg leaf tissues were collected in mortar and pestle.
4. Tissues were grind in liquid nitrogen and collected in 2.0 ml micro centrifuge tube upto 500 µl mark.
5. 500 µl of Trizol was added and well vortex. It was allowed to sit for 10 minutes at room temperature.
6. 200 µl of chloroform: isoamyl alcohol was added and well vortex. Again the tubes were allowed to sit for 10 minutes at room temperature.
7. Then tubes were centrifuged at 4°C for 15 minutes at maximum speed on a desktop microcentrifuge.
8. The upper aqueous phase was carefully pipette out into clean 1.5 ml microcentrifuge tubes.
9. 500 µl of isopropanol was added and leave on bench for 10 minutes.
10. RNA pellet was collected by centrifuging the tubes at 4°C for 15 minutes at maximum speed and isopropanol was removed.
11. 500 µl of 70% Ethanol was added (DEPC treated) and the pellet was re-suspend with a pipette tip.
12. Again tubes were centrifuge as in step 5 for at least 5 minutes and decant the ethanol.

13. Tubes were kept in invert position on paper towel to make the pellet air-dry for 5-15 minutes until no droplets can be seen inside the tube.
14. The pellet was re-suspend in ~20 μ l of RNase free DEPC water and stored it at -20°C for further use.

3.8.2 Quantification of RNA

The isolated RNA was quantified using Nanodrop spectrophotometer (ND1000). 2 μ l of isolated RNA was placed over tip of Nanodrop to record absorbance at 260nm. The absorbance ratio (A230/A260) and (A230/A280) was recorded for each sample to estimate the purity of RNA. The acceptable absorbance ratio (A230/A260) for pure RNA should be more than 1.8.

3.8.3 cDNA synthesis

Once the RNA was isolated and quantified, used for cDNA synthesis using Thermo Scientific Verso™ cDNA Synthesis Kit as per manufacturer's instructions. The stepwise procedure as described in Thermo Scientific Verso™ cDNA Synthesis Kit was followed. The reaction must be set in ice all the time. The kit consisted of reaction components was given in table 3.3.

3.8.3.1 Protocol for cDNA synthesis:

1. Template RNA samples were thawed on ice then required amount of 1 μ l template RNA was dispensed in each tube.
2. Each component as primer solutions, 5x cDNA synthesis buffer, dNTP mix and water (PCR grade) were ice thawed and vortexed briefly to settle the contents.
3. Master Mix (except Verso Enzyme Mix and template RNA) was prepared on ice (Table 3.2).
4. The master mix was mixed by vortexing gently for not more than 5 sec.
5. RNA dependent DNA polymerase (Verso Enzyme Mix) was added to master mix and mixed by pipetting.
6. Master Mix was distributed in equal amount to each tube. (Master Mix = 10 μ l – amount of template RNA).

7. The 500µl PCR were then incubated at 42°C for 30 min. Followed by 95 °C for 2 min.
8. Stored at -20 °C till further use.

Table 3.3: cDNA synthesis (reverse-transcription) reaction Components

Components	Volume	Final Concentration
Master mix		
5x cDNA synthesis buffer		
dNTP Mix	4 µl	
RNA primer	2 µl	
RT Enhancer	1 µl	1x
Verso Enzyme Mix	1 µl	500 µM each
Water (PCR grade)	1 µl	
	Variable	
Template RNA	1-5 µl	1 ng
Total volume	20 l	

3.8.4 Polymerase Chain Reaction (PCR) amplification using sHSP primer

For PCR amplification, 1.5 µl of cDNA of each plant was dispensed in the bottom of PCR plates. Separately cocktail was prepared in an eppendorf tube as described in Table 3.4. 8.5µl of cocktail was added to each tube to make final volume 10 µl. Finally, the temperature profile (Table 3.5) was set on 96 wells Verti Thermal Cycler machine (Applied Biosystem, USA).

Table 3.4: PCR mix for one reaction

Reagent	Stock concentration	Volume (µl)
Nanopure H ₂ O	-	5.25
PCR buffer	10 X	1.0
dNTPs (Mix)	10 mM	1.0

Primer (forward)	5 pmol.	0.5
Primer (reverse)	5 pmol.	0.5
<i>Taq</i> polymerase	1 unit/ μ l	0.25
DNA template	40 ng/ μ l	1.5
Total		10

Table 3.5: Temperature profile used for PCR amplification using sHSP primer

Steps	Temperature (°C)	Duration	Cycles	Activity
1	95	5 min	1	Denaturation
2	95	30 sec	34 ↑ ↓	Denaturation
3	50	30 sec		Annealing
4	72	1 min		Extension
5	72	5 min	1	Final Extension
6	4	∞	1	Storage

3.8.4.1 Visualization of amplified products in Polyacrylamide gel electrophoresis

Five percent polyacrylamide gels (vertical) were used for better separation and visualization of PCR amplified microsatellite products, since polyacrylamide gels have better resolution. Gels were casted in *CBS-SCIENTIFIC* (Imperial Life Sciences, USA) electrophoresis unit and stained by using ethidium bromide and visualized on BIO-RAD Gel Doc XR⁺.

3.8.4.2 Development of genotypic data of the population

In expression analysis selected 10 rice genotypes with checks were used. A total of 17 sHSP primers were used in expression analysis (Table 3.6).

Table 3.6 List of sHSP primers

S. No	Primers	Sequence
1	Hsp16.9A-CI F	TGAAGATGTGATCGGTGAGG
	Hsp16.9A-CI R	GTTTGCAACCTGAAAAGCTC
2	Hsp17.9A-CI F	ATGTCGCTGATCCGCCGAG
	Hsp17.9A-CI R	AGGAGGCGCCGCGCGGAAG
	Hsp17.4-CI F	GCATTGGGCTAATCTAAAAC
3	Hsp17.4-CI R	AGTAGTAGAACATAATATAG
4	Hsp18.8-CX F	GAGCATGGACTGGAAGGAGA
	Hsp18.8-CX R	GTGAGGCTTCCTGTCGTTGT
5	Hsp23.6-MII F	GAGGTGAGGGACGGCGTGCT
	Hsp23.6-MII R	CAAAATTCATCAAGACTATG
6	Hsp26.2-MI F	ACCAACGGCCTCGCAACCGC
	Hsp26.2-MI R	CTACTCGACATTGACCTGGA
7	Hsp24.0-MI F	GGTCAACGTCGAGTAGGAGC
	Hsp24.0-MI R	AAGGACGCCTTGGCTTTAAT
8	Hsp26.7-P F	CGATGCGGACGATGCGGCAG
	Hsp26.7-P R	TCCAGAGTGATCGTTCAGTA
9	Hsp23.2-ER F	GTGGCAAGAAGAGCATCGGC
	Hsp23.2-ER R	CACAACGATGAAAGTGCGAT
10	Hsp21.8-ER F	GACGTGCGCGTGGAGGTGGA
	Hsp21.8-ER R	TCGCCGATCACTATTCACTG
11	Hsp18.6-CIII F	TCACCATCGCCTGAATCATA
	Hsp18.6-CIII R	TAATTTGCTTGATCCTCACA
12	Hsp16.0-Px F	CTCCAGCAAGCTCTGATCCT
	Hsp16.0-Px R	GCAGAAGACCCACCTTTATT
13	Hsp18.0-CII F	AGGAGGAGAGGCTGCTGGTG
	Hsp18.0-CII R	ATCACATCGCATAACGGCATA
14	Hsp19.0-CII F	ATGGGCAAGTTCATGAGGAG
	Hsp19.0-CII R	TCCAGGACCATCATGATGAT
15	Hsp17.8-CXI F	ATGTCTTTGGTGCTCTCGCG
	Hsp17.8-CXI R	TCACGGCCAGAAGCGGCAGC
16	Hsp22.3-CVI F	TGAGAATCCTAACCTCGCCG
	Hsp22.3-CVI R	GAATCGAATTTATGATCTCG

17	Hsp18.8-CV F	CCTGATTAGTGATTTCGATAT
	Hsp18.8-CV R	TCCTTCACGTTTTACTGCGA

3.8.4.3 Scoring of data

In order to evaluate gene expression pattern based on numerical values, the semi quantitative RT-PCR generated fluorescence data were digitalized using GelQuant.NET Analyzer software (www.biochemlabssolutiond.com). The relative expression of genes was expressed in terms of fold change for the samples under heat stress with respect to tolerant and susceptible checks.

3.8.5 Reagents and solutions

3.8.5.1 Primers:

3.8.5.2 dNTPs: (dATP/dCTP/dGTP/dTTP)

1 mM stock of dNTP (Genei™, Merck Biosciences, Bangalore) was used.

3.8.5.3 PCR buffer (10X)

10X (Genei™, Merck Biosciences, Bangalore) buffer was used.

3.8.5.4 *Taq* polymeras

1 unit/μl, *Taq* polymerase (Genei™, Merck Biosciences, Bangalore) was used for PCR.

3.8.5.5 RNA extraction buffer

Final volume was adjusted to 100ml with distilled water and the pH was maintained to 8.0.

3.8.5.6 TE buffer

1M Tris-Hcl (pH-8) = 1 ml

$$0.25 \text{ EDTA} = 0.4 \text{ ml}$$

Final volume was adjusted to 100 ml and autoclaved and the pH was maintained to 8.0.

3.8.5.7 EDTA (0.5M; pH-8)

186.12 g of EDTA was dissolved in 700 ml of distilled water. The pH was set to 8.0 using NaOH. Final volume was adjusted to 1000 ml with distilled water and sterilized by autoclaving.

3.8.5.8 4M NaCl

23.36 g of NaCl was dissolved in 80 ml of distilled water. Final volume was adjusted to 100 ml and sterilized by autoclaving.

3.8.5.9 1M Tris HCl (pH 8.3 at 25°C)

30.28 g of Trizma base was dissolved in 200 ml of distilled water. The pH was set to 8.0 using concentrated HCl. The final volume was adjusted to 250 ml with distilled water and sterilized by autoclaving.

3.8.5.10 10X TBE buffer

$$\text{Tris base} = 104 \text{ g}$$

$$\text{EDTA (0.5M)} = 40 \text{ ml}$$

$$\text{Boric Acid} = 55 \text{ g}$$

$$\text{Distilled water} = 500 \text{ ml}$$

Final volume was adjusted to 1 liter with distilled water.

3.8.5.11 1X TBE buffer

100 ml of 10 X TBE + 900 ml of distilled water were taken to make 1 lt of 1X TBE.

3.8.5.12 6X loading dye

Sucrose in water = 40% (W/V)

Bromophenol Blue = 0.25%

Store at 4°C

3.8.5.13 5% Acrylamide gel solution (1000ml)

47.5g of acrylamide and 2.5g of bis-acrylamide were weighed and dissolved in 500ml distilled water and then added to the beaker containing 100 ml of 10X TBE and the volume was made upto 1000ml by adding autoclaved double distilled water. The solution was sterilized by passing through 0.22 micron mesh and stored in amber colour bottle at 4°C.

3.8.5.14 10% Ammonium persulphate (APS) solution

10% Ammonium persulphate (APS) solution was prepared by adding 1.0g in 10ml of distilled water.

3.8.5.15 100bp DNA ladder

100bp DNA ladder of (Genei™, Merck Biosciences, Bangalore) was used as known marker.

3.9 Statistical analysis

The all data recorded for yield and yield contributing traits under all the growing season were tabulated and analyzed. The significance test was carried out by referring to F table values given by Fisher and Yates (1963).

3.9.1 Analysis of variance

Differences among eighty seven genotypes for various characters were tested for significance by using analysis of variance technique (Panse and Sukhatme, 1985). Skeleton of ANOVA for RBD design was depicted in table 3.4.

$$Y_{ij} = m + g_i + v_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation in i th genotype and j th replication

m = general mean

g_i = effect of i th genotype

v_j = effect of j th replication

e_{ij} = random error

Table 3.7: Skeleton of ANOVA for RBD design

: Source of variation	Degrees of freedom	Sum of Squares	Mean sum of squares	F-ratio
Replications	$r-1$	RSS	Mr	Mr/Me
Treatments	$t-1$	GSS	Mg	Mg/Me
Error	$(r-1)(t-1)$	ESS	Me	-
Total	$(rt-1)$	TSS		

Where,

r = number of replications

t = number of treatments

RSS = Replication Sum of Squares

GSS = Genotype Sum of Squares

ESS = Error Sum of Squares

TSS = Total Sum of Squares

Mr = Mean Sum of Squares due to replications

Mg = Mean Sum of Squares due to genotypes

Me = Mean Sum of Squares due to error

3.9.2 Parameters of variability

3.9.2.1 Mean (X)

Mean is the average value of observation of genotypes of a series. The mean value of each character was worked out by dividing the total sum of values with corresponding number of observations.

$$X = \Sigma X_i / n$$

Where,

X = Summation of all the observation

n = Number of observations

3.9.2.2 Range

Range is difference between highest and lowest series of the observation and provide information about the extent of variability present in the genotypes.

$$\text{Range} = \text{Highest value} - \text{Lowest value}$$

3.9.2.3 Standard deviation

Standard deviation is the root of sum of squares of deviation divided by there number, calculated by:

$$\text{Standard deviation} = \sqrt{\Sigma d^2 / n}$$

Where,

Σd^2 = Sum of squares of deviations

n = Total number of observation

3.9.2.4 Standard error of mean (SE_m)

Standard error of mean was calculated with the help of error mean squares from the analysis of variance table given as under:

$$SE_m = \sqrt{\frac{MSe}{r}}$$

The standard error of the difference between any two treatment is expressed by the following formula:

$$SE_d = \sqrt{\frac{2MSe}{r}}$$

Where,

SE = Standard error

MSe = Error mean sum of squares

r = Number of replications

3.9.3.5 Critical difference (CD)

For every character, the critical difference was the difference of any two mean values. In order to compare the critical difference the treatment means were calculated using the following formula:

$$CD \text{ (at 5\% or 1\%)} = SE_d \times t\text{-value (5\% or 1\%)} \text{ at error d.f.}$$

3.9.3.6 Coefficient of variation (%)

The coefficient of variation being a standardized form of variance is useful for comparing the extent of variance between different characters with different scales (Singh and Chaudhary, 1977) calculated by the following formula:

$$CV = \frac{\sqrt{MSe}}{\bar{X}} \times 100$$

3.9.4 Estimation of variability

According to Burton (1952), genotypic and phenotypic coefficients of variation were estimated by the following formula:

Genotypic coefficient of variation (GCV %)

$$GCV (\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Phenotypic coefficient of variation (GCV %)

$$PCV (\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = General mean of a particular character

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

The genotypic and phenotypic coefficients of variation were categorized as per the method suggested by Sivasubramanian and Madhavamenon (1973):

0-10% = Low

10-20% = Moderate

>20% = High

3.9.5 Heritability (broad sense)

Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance (total variance) and expressed as percentage (Burton and De Vane (1952).

$$h^2 (bs) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

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

The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955):

0-30% = Low

30-60% = Moderate

>60% = High

3.9.6 Expected genetic advance (GA)

Improvement in the mean genotypic value of progeny of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. Genetic advance was worked out by adopting the following formula given by Johnson *et al.* (1955):

$$GA = h^2 (bs) \times \sigma_p \times K$$

Where,

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

K = Selection differential, which is equal to 2.06 at 5% intensity of selection (Allard, 1960)

σ_p = Phenotypic standard deviation

3.9.7 Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean for each character was worked out as suggested by Johnson *et al.* (1955).

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

Where,

GA = Genetic advance

$\bar{X}$ = General mean

Genetic advance as per cent of mean was categorized as per the formula suggested by Johnson *et al.* (1955).

0-10 % = Low

10-20 = Moderate

>20 % = High

3.9.8 Character association analysis

3.9.8.1 Correlation coefficient (r)

The coefficient of correlation measure the degree of linear relationship between two variables. Correlation coefficient was computed as per the procedure outlined by Karl Pearson (1932)

3.9.8.2 Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1967) at (n-2) degrees of freedom at 5% and 1% level where, 'n' denotes the number of pairs of observations used in the calculation. If the observed value is more than the table value, the correlation coefficient is considered as significant.

3.9.9 Combining ability analysis

Combining ability analysis was done following Line x Tester approach developed by Kempthorne (1957) and emphasized by Arunachalam (1974) for estimating the combining ability effects and combining ability variances.

In the analyses of combining ability, hybrids were partitioned into male effects, female effects and male x female effects. Analyses of combining ability was based on the following statistical model by Singh and Chaudhary (1977):

$$Y_{ijk} = \mu + M_i + F_j + (M \times F)_{ij} + e_{ijk}$$

Where;

Y_{ijk} = kth observation on the ith and jth progeny

μ = general mean

M_i = effect of the ith male

F_j = effect of the jth female

$(M \times F)_{ij}$ = interaction effect and

e_{ijk} = error associated with each observation

3.9.9.1 Estimation of general and specific combining ability effects

The model used to estimate general combining ability (gca) and specific combining ability (sea) effects was:

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

Where,

μ = Population mean

g_i = gca effect of i^{th} female parent (line)

g_j = gca effect of j^{th} male parent (tester)

S_{ij} = sca effect of ij^{th} combination

e_{ijk} = Error associated with ij^{th} cross in k^{th} replication

i = Number of female parents

j = Number of male parents

k = Number of replications

Table 3.8 Analysis of variance for combining ability

Source	df	SS	MSS	EMS
Crosses	lt-1	CSS		
Line	l-1	LSS	MS1	
Tester	t-1	TSS	MS2	
Line X Tester	(l-1)(t-1)	LXTSS	MS3	
Error	(r-1)(lt-1)	ESS	MS4	
Total	rlt-1			

3.9.10 Stability analysis

The magnitude of G x E interaction was assessed for each character and each genotype. This was worked out as per the procedure suggested by Eberhart and Russell (1966). In Eberhart and Russell's model (1966), three parameters namely (i) overall mean of each genotype over a range of environments, (ii) the regression of each genotype on the environmental index and (iii) a function of the squared deviation

from the regression were estimated. Eberhart and Russell (1966) used to study the stability of genotypes under different environments.

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

Where,

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

μ_i = mean of i^{th} genotype over all the environments

b_i = regression coefficient of the i^{th} genotype on the environmental index
which measures the response of this genotype to varying environments

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

$\sum_j I_j = 0$ and

δ_{ij} = The deviation from regression of the i^{th} genotype at j^{th} environment

3.9.10.1 Analysis of variance for stability

The analysis of variance proposed by Eberhart and Russell (1966) is given below.

Table 3.9: ANOVA to estimate stability parameters (Eberhart and Russell, 1966)

Source of variation	Degree of freedom	Sum of square	Mean sum of square
Total	(ge-1)		
Varieties	(g-1)		MS1
Environment	g(e-1)		
Environment (Linear)	1		
Genotype x Environment (Linear)	(g-1)		MS2
Pooled deviation	g(e-2)		MS3
Deviation due to genotype 1	(e-2)		
Genotype g	(e-2)		
Pooled error	e(r-1)(g-1)		

Where,

g= Number of genotypes

e = Number of environments

r = Number of replications

3.9.10.2 Test of Significance

The mean sum of squares due to genotypes and environments were tested against G x E interaction. Whereas, mean sum of squares due to G x E interaction was tested against pooled error. Environment (linear) and G x E (linear) were tested against pooled deviation, if pooled deviation is non-significant both these linear components were tested against pooled error. Mean sum of squares due to pooled deviations were tested against pooled error.

A genotype with unit regression coefficient ($b_i=1$) and deviation not significantly different from zero ($S^2d_i=0$) was taken to be a stable genotype with unit response.

3.9.10.3 Computation of regression coefficient (b_i) for each genotype

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

Where,

b_i = regression coefficient of i_{th} genotype

$\sum I_j^2$ = the sum of squares of environmental indices which are common j to each value of b_i .

$\sum Y_{ij}^2$ = (for each genotype) = the sum of products of environmental j index (I_j) and the corresponding means (X) of that variety at each location.

3.9.11. Expression analysis of sHSPs

In order to evaluate gene expression pattern based on numerical values, the semi quantitative RT-PCR generated fluorescence data were digitalized using GelQuant.NET Analyzer software (www.biochemlabssolutiond.com). The relative expression of genes was expressed in terms of fold change for the samples under heat stress with respect to tolerant and susceptible checks.

CHAPTER - IV

RESULTS AND DISCUSSION

The present investigation entitled “**Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)**” was carried on eighty seven rice genotypes for grain yield and yield related characters viz., days to fifty percent flowering, plant height, total number of tillers per plant, number of effective tillers per plant, flag leaf area, panicle length, number of filled grains per panicle, total number of grains per panicle, spikelet fertility per cent, 100 grain weight grain yield per plant, biological yield per plant and harvest index. The results obtained are presented below under the following headings:

4.1 Genetic variability and association analysis for yield & yield contributing components:

4.1.1 Analysis of variance

4.1.2 Mean performance of genotypes

4.1.3 GCV, PCV, Heritability (broad sense), Genetic advance, Genetic advance as percent of mean

4.1.4 Association analysis for yield & yield contributing components

4.2 The effect of cold and heat in selected rice genotypes

4.2.1 Parameters for cold tolerance screening

4.2.2 Parameters for heat tolerance screening

4.3 Combining ability analysis for yield and quality traits

4.3.1 Mean performance of parents and crosses

4.3.2 Analysis of variance for combining ability

4.3.3 GCA and SCA effects

4.4 Heterosis for yield and quality traits

4.5 Stability analysis for seed yield and its components.

4.6 Expression of small heat shock proteins

4.1 Genetic variability and association analysis for yield and yield contributing traits

Eighty seven rice genotypes were studied for variability analysis on *Summer-2017*. On the basis of grain yield per plant, spikelet fertility percent and pollen fertility percent, thirty seven rice genotypes were selected for cold, heat and quality traits.

4.1.1 Analysis of variance

The analysis of variance for all the thirteen quantitative traits of eighty seven rice genotypes on *Summer-2017* and seventeen quality traits of selected thirty seven rice genotypes were studied. The analysis of variance showed a wide range of variation and significant differences for all the traits under study, indicating the presence of sufficient amount of variability. The quantitative and quality mean squares due to replications were non-significant for all the traits under studied. The results are presented in Table 4.1 (quantitative traits) and Table 4.2 (quality traits).

4.1.2 Mean performance and range of genotypes

The mean performance and range of eighty seven rice genotypes on *summer-2017* with respect to thirteen quantitative traits were studied and presented in Table 4.3.

4.1.2.1 Quantitative traits

Days to 50% flowering

It varied from 55 to 98 days with an average of 72 days. Swarna (55) had maximum and Dehura Baya (98) had minimum days to 50% flowering.

Plant height (cm)

It varied from 75.42 to 129.17 cm with an average of 72.29 cm. The tallest genotype was E/46-2602 (129.17cm) and shortest was RJR:II (75.42cm).

Tillers per plant (No.)

It varied from 6 to 19 with an average of 9. The maximum tiller was recorded in IR 64 (19) and minimum in Banko (6).

Effective tillers per plant (No.)

It varied from 5 to 16 with an average of 9. The maximum effective tiller was observed in IR 64 (16) and minimum tiller in Banko (5).

Flag leaf area (cm²)

It varied from 14.04 to 45.29 cm² with an average of 25.47 cm². The maximum flag leaf area was observed in Banko and minimum in Anjaniya (14.04 cm²).

Panicle length (cm)

Panicle length varied from 17.70 to 27.17 cm with an average of 22.28 cm. The longest panicle length was found in NPT 6 (27.17cm) and shortest in Lallu (17.70cm).

Filled grains per panicle (No.)

It varied from 3.45 to 181.65 with an average of 102.82. The maximum filled grains per panicle was observed in Tewan dhan (181.65) and minimum in Batri (II) (3.45).

Total number of grains per panicle (No.)

It varied from 47.04 to 210.80 with an average of 132.10. The maximum grains per panicle was found in MTU-1010 (210.80) and minimum in No.16 (47.04).

Spikelet fertility per panicle (%)

It varied from 33.15 to 97.30% with an average of 77.59%. The maximum spikelet fertility was observed in Nagina-22 (97.30%) and in Khurbal (33.15%).

100 grain weight (g)

It varied from 0.97 to 3.22 g with an average of 2.18 g. The maximum weight was found Banko (3.22 g) and minimum in Bhejari (0.97g).

Grain yield per plant (g)

It varied from 6.84 to 26.50 g with an average of 16.94 g. The high yield was found in Safed Lalak (16.94g) and low in Banko (6.84g).

Biological yield per plant (g)

It varied from 14.65 to 49.15 g with an average of 29.97 g. The highest biological yield per plant was observed in Ganga kali (49.15g) and lowest in Banko(14.65g).

Harvest index

It varied from 41.32 to 74.90% with an average of 56.83%. The maximum harvest index was found in Sitasaal Dhan (74.90%) and minimum in Juular (41.32%).

4.1.2.2 Quality traits

Out of eighty seven, selected thirty seven rice genotypes were used for quality observation of. The mean performance and range of thirty seven genotypes on *summer*-2018 with respect to seventeen quality traits were studied and presented in Table 4.4.

Hulling (%)

It varied from 36.54 (Khurabal) to 89.52%,(Indira Aerobic 1) with an average of 69.02%.

Milling (%)

It varied from 28.26 (Khurabal) to 76.90% (Indira Aerobic 1), with an average of 56.80%.

Head rice recovery (%)

It varied from 18.62 (Dadhbako) to 67.58% (Ganga kali), with an average of 43.03%.

Paddy length (cm)

It varied from 5.12 (Swarna) to 10.02cm (IR 64), with an average of 8.38cm.

Paddy breadth (cm)

It varied from 2.32 (Swarna) to 3.22 (Ganga kali) cm, with an average of 2.78cm.

Paddy L/B ratio

It varied from 2.21 (Swarna) to 4.17cm (IR 64), with an average of 3.04cm.

Brown rice length (cm)

It varied from 4.03(Swarn) to 7.71cm RJR:II), with an average of 6.67cm.

Brown rice width (cm)

It varied from 1.78 (Digamber dhan) to 2.62cm (Gangtai), with an average of 2.35cm.

Brown rice L/B ratio

It varied from 2.00 (Swarna) to 3.47cm (P:357 III), with an average of 2.85cm.

Kernel length (cm)

It varied from 5.08 (Nagina 22) to 7.20cm (P:357 III), with an average of 5.85cm.

Kernel breadth (cm)

It varied from 2.00(Ganga dhan) to 2.78cm (RJR:II), with an average of 2.39cm.

Kernel L/B (cm)

It varied from 1.89 (Baikoni) to 3.27cm (P:357 III), with an average of 2.46cm.

Elongation ratio

It varied from 1.11 (Chingar Bnko) to 2.16cm (Gangtai), with an average of 1.43cm.

Elongation index

It varied from 0.73 (Bega hundi) to 1.63cm (Gangtai), with an average of 1.02cm.

Alkali spreading value

It varied from 1.00 (Tewan dhan, Kolhin khosa) to 6.50 (RJR:II), with an average of 4.13.

Gel consistency (mm)

It varied from 36.40 (Ajam dhan) to 96.50mm (Khurabal), with an average of 64.64mm.

Amylose content

It varied from 14.98 (Tendhumori dhan) to 33.01 (Ajam dhan), with an average of 24.09.

4.1.3 Estimation of genetic variability parameters

4.1.3.1 Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

Quantitative traits

Information on the nature and magnitude of genetic variability is of immense significant for initiating any breeding programme. Further the presence of variability in the base material ensures better chances of selection for desirable plant types. In the present study estimates of phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the traits (Table 4.3), but the difference was relatively small for all traits, it indicating that these characters were less influenced by the environment. Similar findings were reported by Kalyan *et al.* (2017) and Pragnya *et al.* (2018).

In this study, the highest PCV and GCV was recorded for filled grains per panicle (35.52%, 34.58%), grain yield per plant (31.24%, 28.02%), total grains per panicle (27.24%, 26.59%), biological yield per plant (29.45%, 26.36%), total tillers per plant (28.59%, 24.96%), effective tillers per plant (26.19%, 23.29%) and flag leaf area (23.26%, 23.02%), indicating the presence of considerable genetic variability and less influence of environment on the expression on this traits. Similar findings were also reported by Sumanth *et al.* (2007), Fukrei *et al.* (2011), Sravan *et al.* (2012), Pragnya *et al.* (2018), Behera *et al.* (2018) for grain yield per plant, Babu *et al.* (2012) for filled grains per panicle, Pratap *et al.* (2012) for flag leaf area, Aditya and Bhartiya (2013) Rukmanidevi *et al.* (2016) for filled grains per panicle, Ekka *et al.* (2015) Sameera *et al.* (2015) for effective tillers per plant, Abebe *et al.* (2017) for biological yield per plant.

The moderate GCV was found for 100 grain weight (19.29%, 18.57%), spikelet fertility per panicle (19.10%, 17.84%), plant height (14.46%, 12.72%), harvest index (15.65%, 12.63%), days to 50% flowering (12.68%, 12.58%) and lowest was panicle length (9.79%, 8.00%). Similar findings were reported by Konate *et al.* (2016) for panicle length.

Quality traits

The present study, estimates of phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the traits (Table 4.4),

For quality traits, the highest PCV and GCV was recorded for Alkali spreading value (38.24%, 35.50%), head rice recovery (31.17%, 30.04%), gel consistency (24.97%, 21.04%), milling (24.35%, 23.32%). Moderate PCV and GCV were recorded for elongation index (18.97%, 18.93%), hulling percent (19.03%, 18.46%), Paddy L/B ratio (15.61%, 15.46%), amylase content (16.27%, 14.90%), elongation ratio (14.87%, 14.84%), Kernel L/B ratio (13.86%, 13.77%), brown rice L/B ratio (11.85%, 11.79%) and paddy length (11.44%, 11.36%) and brown rice length (10.63%, 10.53%). Low magnitude of PCV and GCV were found for paddy breadth (9.58%, 9.47%), kernel length (8.90%, 8.85%), brown rice width (7.84%, 7.77%) and kernel breadth (7.64%, 7.50%).

4.1.3.2 Heritability (broad sense)

Heritability is a measure of extent of phenotypic variation caused by the action of genes. The major function of heritability estimates is to provide information on transmission of characters from parents to their progeny.

Quantitative traits

High heritability was observed for all the thirteen traits under study viz. days to 50% flowering (98.48%) flag leaf area (97.96%), total grains per panicle (95.35%), filled grain per panicle (94.75%), 100 grain weight (92.66%), spikelet fertility per plant (87.24%) grain yield per plant (80.46%), biological yield per plant (80.11%), effective tillers per plant (79.10%), plant height (77.31%), total tillers per plant (76.25%), panicle length (66.65%) and harvest index (65.05%). Similar findings were reported by Singh *et al.* (2018), Subedi *et al.*, (2018) for grain yield per plant, Kishore *et al.* (2018), Sumanth *et al.* (2017) for flag leaf area and 100 seed weight.

Quality traits

The high heritability was observed for all the seventeen traits under study viz. elongation index (99.60%), elongation ratio (99.60%), brown rice L/B ratio (99.03), Kernel L/B ratio (98.73%), kernel length (98.92%), brown rice length (98.72%), paddy length (98.49%), brown rice width (98.23%), paddy L/B ratio (98.11%), paddy breadth (97.73%), kernel breadth (96.18%), hulling percent (94.12%), head rice recovery (92.87%), milling (91.72%), Alkali spreading value (86.21%), amylase content (83.82%) and gel consistency (70.97%).

4.1.3.3 Genetic advance as percent of mean

Quantitative traits

The genetic advance as percent of mean (GAM) was recorded high for the traits viz. filled grain per panicle (68.71), total grains per panicle (53.25), grain yield per plant (51.58), biological yield per plant (48.44), total tillers per plant (44.27), flag leaf area (46.94), effective tiller per plant (42.06), 100 grain weight (36.77), spikelet fertility per plant (34.18), days to 50% flowering (25.66), plant height (23.12), harvest index (20.97) and moderate value was recorded for panicle length (13.43).

Quality traits

The genetic advance as percent of mean (GAM) was recorded high for head rice recovery (59.64%), alkali spreading value (47.91%), milling (46.03%), elongation index (38.93%), hulling (36.90%), gel consistency (36.50%), paddy L/B ratio (31.55%), elongation ratio (30.51%), paddy length (23.22%), brown rice length (21.61%), kernel L/B ratio (28.19%), amylose content (28.10%). The moderate value was observed for paddy breadth (19.21%), kernel length (18.14%), brown rice width (15.83%), kernel breadth (15.15%).

4.1.3.4 Heritability (broad sense) and genetic advance s percent of mean (GAM)

Quantitative traits

Heritability and genetic advance as percent of mean are important selection parameters. Heritability estimates along with genetic advance as percent of mean are Heritability and genetic advance as percent of mean are important selection parameters. Heritability estimates along with genetic advance as percent of mean are more powerful for predicting the genetic gain under selection. From the result, high heritability coupled with high genetic advance as percent of mean was found in days to 50% flowering (98.48%,25.66), flag leaf area (97.96%,46.94), total grains per panicle (95.35%,53.25), filled grain per panicle (94.75%,68.71), 100 grain weight (92.66%, 36.77), spikelet fertility per plant (87.24%, 34.18), grain yield per plant (80.46%, 51.58), biological yield per plant (80.11%, 48.44), effective tillers per plant (79.10%, 42.06), plant height (77.31%, 23.12), total tillers per plant (76.25%, 44.27), and harvest index (65.05%, 20.97), it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effective for crop improvement. Similar results were reported by Ketan and Sarkar (2014), Sharma *et al.*, (2014) Kalyan *et al.* (2017) and Behera *et al.* (2018).

High heritability coupled with moderate genetic advance as percent of mean was reported in panicle length (66.65%, 13.43) indicating importance of both additive and non additive gene action. Sreedhar (2017) reported similar result for panicle length.

Table 4.1: Analysis of Variance (ANOVA) for quantitative traits (Summer-2017)

S. No.	Character	Replication (df=1)	Treatment (df=86)	Error (df=86)
1	Days to 50% flowering	3.89	166.71**	1.28
2	Plant height (cm)	112.23	357.45**	45.74
3	Tillers/plant (No.)	3.89	12.86**	1.73
4	Effective tiller/plant (No.)	3.45	9.63**	1.12
5	Flag leaf area(cm ²)	1.57	69.47**	0.72
6	Panicle length (cm)	0.36	7.94**	1.59
7	Number of filled grains/panicle (No.)	102.33	2598.52**	70.04
8	Total number of grains/panicle (No.)	72.46	2528.48**	60.36
9	Spikelet fertility/panicle (%)	72.36	411.17**	28.02
10	100 grain weight (g)	0.06	0.34**	0.01
11	Grain yield/plant (g)	12.84	50.51**	5.47
12	Biological yield/plant (g)	4.36	140.26**	15.49
13	Harvest index (%)	58	130.64**	27.67

* & ** represent significant levels at 5% (6.93) and 1% (1.65) respectively.

Table 4.2: Analysis of Variance (ANOVA) for quality traits (Summer-2018)

S. No.	Character	Replication	Treatment	Error
1	Hulling%	3.2963	325.7941**	17.3206
2	Milling%	91.9735	354.5902**	23.6211
3	Head rice recovery %	1.8848	344.6777**	26.3299
4	Paddy length (cm)	0.0026	1.8252**	0.0138
5	Paddy breadth (cm)	0.0059	0.1404**	0.0016
6	Paddy L/B ratio	0.0101	0.4466**	0.0043
7	Brown rice length (cm)	0.0014	0.9997**	0.0064
8	Brown rice width (cm)	0.0004	0.0676**	0.0006
9	Brown rice L/B ratio	0.0001	0.2265**	0.0011
10	Kernel length (cm)	0.0013	0.5389**	0.0029
11	Kernel breadth (cm)	0.0052	0.0658**	0.0013
12	Kernel L/B ratio	0.0054	0.2317**	0.0015
13	Elongation ratio	0.0001	0.0905**	0.0002
14	Elongation index	0.0006	0.0743**	0.0001
15	Alkali spreading value	0.1216	5.0818**	0.0938
16	Gel consistency (mm)	0.0164	319.7574**	7.5800
17	Amylose content	1.1284	28.2600**	2.4871

* & ** represent significant levels at 5% (6.93) and 1% (1.65) respectively.

Table 4.3: Genetic parameters of variation for yield and its component traits

S. No.	Character	Mean	Range	PCV(%)	GCV(%)	h^2 (bs) (%)	GA as % of mean
1	Days to 50% flowering	72.29	55-97.50	12.68	12.58	98.48	25.66
2	Plant height (cm)	98.18	75.42-129.17	14.46	12.72	77.31	23.12
3	Tillers/plant (No.)	9.45	5.50-17.25	28.59	24.96	76.25	44.27
4	Effective tiller/plant (No.)	8.86	5.50-16	26.19	23.29	79.10	42.06
5	Flag leaf area(cm ²)	25.47	14.04-45.29	23.26	23.02	97.96	46.94
6	Panicle length (cm)	22.28	17.70-27.17	9.79	8.00	66.67	13.43
7	Number of filled grains/panicle (No.)	102.82	36.45-181.65	35.52	34.58	94.75	68.71
8	Total number of grains/panicle (No.)	132.10	47.04-210.80	27.24	26.59	95.34	53.25
9	Spikelet fertility/panicle (%)	77.59	33.15-97.30	19.10	17.84	87.24	34.18
10	100 grain weight (g)	2.18	0.97-3.22	19.29	18.57	92.66	36.77
11	Grain yield/plant (g)	16.94	6.84-26.50	31.24	28.02	80.46	51.58
12	Biological yield/plant (g)	29.97	14.65-49.15	29.45	26.36	80.11	48.44
13	Harvest index (%)	56.83	41.32-74.90	15.65	12.63	65.05	20.97

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2 (bs)= Heritability in broad sense, GA= Genetic advance

Table 4.4: Genetic parameters of variation for quality traits (Summer-2018)

S. No.	Character	Mean	Range	PCV(%)	GCV(%)	h^2 (bs) (%)	GA as % of mean
1	Hulling%	68.31	39.37- 89.20	19.03	18.46	94.12	36.90
2	Milling%	56.84	28.19-76.55	24.35	23.32	91.72	46.05
3	Head rice recovery %	42.71	17.91-68.34	31.17	30.04	92.87	59.64
4	Paddy length (cm)	8.38	7.10-9.73	11.44	11.36	98.49	23.22
5	Paddy breadth (cm)	2.78	2.3-3.23	9.58	9.47	97.73	19.29
6	Paddy L/B ratio	3.04	2.36-3.86	15.61	15.46	98.11	31.55
7	Brown rice length (cm)	6.67	5.80-7.76	10.63	10.56	98.72	21.62
8	Brown rice width (cm)	2.35	1.76-2.63	7.84	7.77	98.23	15.83
9	Brown rice L/B ratio	2.85	2.44-3.32	11.85	11.79	99.03	24.17
10	Kernel length (cm)	5.85	5.20-6.43	8.90	8.85	98.92	18.14
11	Kernel breadth (cm)	2.39	2-2.80	7.64	7.50	96.18	15.15
12	Kernel L/B ratio	2.46	1.89-3.20	13.83	13.77	98.73	28.19
13	Elongation ratio	1.43	1.10-2.17	14.83	14.84	99.60	30.51
14	Elongation index	1.02	0.72-1.63	18.97	18.93	99.60	38.93
15	Alkali spreading value	4.13	1.00-7.00	38.24	35.50	86.21	47.91
16	Gel consistency	64.64	32.50-100	24.97	21.04	70.97	36.50
17	Amylose content	24.09	14.97-34.16	16.27	14.90	83.82	28.10

PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation,

h^2 (bs)= Heritability broad sense, GA= Genetic advance

Quality traits

The high heritability coupled with high genetic advance as percent of mean was recorded for elongation index (99.60%, 38.93), elongation ratio (99.60%, 30.51), brown rice L/B ratio (99.03, 21.61), Kernel L/B ratio (98.73%, 28.19), brown rice length (98.72%, 21.61), paddy length (98.49%, 23.22), paddy L/B ratio (98.11%, 28.19), paddy breadth (97.73%, 19.21), hulling percent (94.12%, 36.90), head rice recovery (92.87%, 59.64), milling (91.72%, 46.03), Alkali spreading value (86.21%, 47.91), amylase content (83.82%, 28.10) and gel consistency (70.97%, 36.50).

The high heritability coupled with moderate genetic advance as percent of mean was recorded for moderate value was observed for paddy breadth (19.21%), kernel length (98.21%, 18.14), brown rice width (98.21%, 15.83%), kernel breadth (96.18%, 15.15).

4.1.4 Association analysis for yield & yield contributing components

Yield is a complex polygenic traits has a large number of other contributing component traits. Correlation analysis reveals the relationship of dependent variable yield with its independent variables, thus association of various traits would determine their relative significance to improve yield. The correlation coefficients between grain yield per plant and its thirteen component traits and among themselves were estimated at genotypic and phenotypic levels (Table 4.5). In general, genotypic correlations were higher than phenotypic ones in magnitude for all the characters.

Days to 50% flowering

Days to 50% flowering exhibited positive and highly significant relationship with total grains per panicle ($r_g=0.523^{**}$, $r_p=0.507^{**}$), filled grain per panicle ($r_g=0.461^{**}$, $r_p=0.447^{**}$), panicle length ($r_g=0.472^{**}$, $r_p=0.388^{**}$), harvest index ($r_g=0.358^{**}$, $r_p=0.333^{**}$), biological yield per plant ($r_g=0.281^{**}$, $r_p=0.269^{**}$), effective tillers per plant ($r_g=0.234^*$, $r_p=0.215^*$) and flag leaf area ($r_g=0.230^*$, $r_p=0.227^*$). Similar results was finding by Aditya and Anuradha (2013) for panicle length.

Plant height (cm)

Plant height exhibited positive and highly significant and significant relationship with flag leaf area ($r_g = 0.329^{**}$, $r_p = 0.278^{**}$), 100 grain weight ($r_g = 0.235^*$, $r_p = 0.195$) and panicle length ($r_g = 0.279^*$, $r_p = 0.195$). Negative and highly significant relationship was found with filled grains per panicle ($r_g = -0.326^{**}$, $r_p = -0.268^{**}$), total tiller per plant ($r_g = -0.487^{**}$, $r_p = -0.345^{**}$), spikelet fertility ($r_g = -0.405^{**}$, $r_p = -0.291^{**}$) and effective tillers per plant ($r_g = -0.415^{**}$, $r_p = -0.315^{**}$).

Tillers per plant (No.)

Total tiller per plant exhibited positive and highly significant relationship with effective tiller per plant ($r_g = 0.977^{**}$, $r_p = 0.935^{**}$), biological yield per plant ($r_g = 0.576^{**}$, $r_p = 0.538^{**}$), filled grain per panicle ($r_g = 0.555^{**}$, $r_p = 0.465^{**}$), grain yield per plant ($r_g = 0.482^{**}$, $r_p = 0.438^{**}$), harvest index ($r_g = 0.420^{**}$, $r_p = 0.381^{**}$), total grain per panicle ($r_g = 0.416^{**}$, $r_p = 0.358^{**}$) and spikelet fertility ($r_g = 0.409^{**}$, $r_p = 0.327^{**}$) but negative and highly significant relationship with plant height ($r_g = -0.487^{**}$, $r_p = -0.345^{**}$).

Effective tillers per plant (No.)

Effective tiller per plant exhibited positive and highly significant and significant relationship with total tiller per plant ($r_g = 0.977^{**}$, $r_p = 0.935^{**}$), biological yield per plant ($r_g = 0.591^{**}$, $r_p = 0.551^{**}$), filled grain per panicle ($r_g = 0.579^{**}$, $r_p = 0.500^{**}$), total grain per panicle ($r_g = 0.476^{**}$, $r_p = 0.421^{**}$), grain yield per plant ($r_g = 0.470^{**}$, $r_p = 0.416^{**}$), harvest index ($r_g = 0.452^{**}$, $r_p = 0.422^{**}$), spikelet fertility ($r_g = 0.354^{**}$, $r_p = 0.289^{**}$) and days to fifty percent flowering ($r_g = 0.234^*$, $r_p = 0.215^*$), but negative and highly significant with the trait plant height ($r_g = -0.415^{**}$, $r_p = -0.315^{**}$). Similar findings were earlier reported by Yogameenakshi *et al.* (2004) by harvest index; Kalyan *et al.*, (2017) for effective tiller per plant and grain yield per plant.

Flag leaf area (cm²)

Flag leaf area exhibited positive and highly significant relationship with panicle length ($r_g = 0.424^{**}$, $r_p = 0.343^{**}$), plant height ($r_g = 0.329^{**}$, $r_p = 0.278^*$), total grain per panicle ($r_g = 0.242^*$, $r_p = 0.232^*$) and days to fifty percent flowering ($r_g = 0.230^*$, $r_p = 0.227^*$).

Panicle length (cm)

Panicle length exhibited positive and highly significant or significant relationship with days to fifty percent flowering ($r_g = 0.472^{**}$, $r_p = 0.388^{**}$), flag leaf area ($r_g = 0.424^{**}$, $r_p = 0.343^{**}$), total grain per panicle ($r_g = 0.306^{**}$, $r_p = 0.236^*$) and plant height ($r_g = 0.279^*$, $r_p = 0.195$).

Filled grains per panicle (No.)

Filled grain per panicle exhibited positive and highly significant relationship with total grain per panicle ($r_g = 0.855^{**}$, $r_p = 0.845^{**}$), biological yield per plant ($r_g = 0.704^{**}$, $r_p = 0.671^{**}$), harvest index ($r_g = 0.641^{**}$, $r_p = 0.589^{**}$), effective tiller per plant ($r_g = 0.579^{**}$, $r_p = 0.500^{**}$), spikelet fertility ($r_g = 0.591^{**}$, $r_p = 0.580^{**}$), grain yield per plant ($r_g = 0.483^{**}$, $r_p = 0.452^{**}$), total tiller per plant ($r_g = 0.555^{**}$, $r_p = 0.465^{**}$), days to fifty percent flowering ($r_g = 0.461^{**}$, $r_p = 0.447^{**}$), 100 grain weight ($r_g = -0.349^{**}$, $r_p = -0.325^{**}$), but negative and highly significant relationship with plant height ($r_g = -0.326^{**}$, $r_p = -0.268^*$). Whereas, positive and non-significant relationship with panicle length ($r_g = 0.193$, $r_p = 0.139$) and flag leaf area ($r_g = 0.109$, $r_p = 0.105$).

Total grains per panicle (No.)

Total grain per panicle exhibited positive and highly significant and significant relationship with filled grain per panicle ($r_g = 0.855^{**}$, $r_p = 0.845^{**}$), biological yield per plant ($r_g = 0.576^{**}$, $r_p = 0.553^{**}$), harvest index ($r_g = 0.541^{**}$, $r_p = 0.499^{**}$), days to 50% flowering ($r_g = 0.523^{**}$, $r_p = 0.507^{**}$), grain yield per plant ($r_g = 0.382^{**}$, $r_p = 0.364^{**}$), effective tiller per plant ($r_g = 0.476^{**}$, $r_p = 0.421^{**}$), total tiller per plant ($r_g = 0.416^{**}$, $r_p = 0.358^{**}$) panicle length ($r_g = 0.306^{**}$, $r_p = 0.236^*$) and flag leaf area ($r_g = 0.242^*$, $r_p = 0.232^*$).

Spikelet fertility per panicle (%)

Spikelet fertility exhibited highly significant and positive association with filled grain per panicle ($r_g = 0.591^{**}$, $r_p = 0.580^{**}$), biological yield per plant ($r_g = 0.456^{**}$, $r_p = 0.418^{**}$), total tiller per plant ($r_g = 0.409^{**}$, $r_p = 0.327^{**}$), harvest index ($r_g = 0.408^{**}$, $r_p = 0.364^{**}$), effective tiller per plant ($r_g = 0.354^{**}$, $r_p = 0.289^{**}$) and grain yield per plant ($r_g = 0.320^{**}$, $r_p = 0.277^{*}$), but negative and highly significant with 100 grain weight ($r_g = -0.315^{**}$, $r_p = -0.302^{**}$), plant height ($r_g = -0.405^{**}$, $r_p = -0.291^{**}$).

100 grain weight (g)

100 grain weight exhibited positive and significant correlation with plant height ($r_g = 0.235^{*}$, $r_p = 0.195$), but negative and highly significant and significant correlation with filled grain per panicle ($r_g = -0.349^{**}$, $r_p = -0.325^{**}$), spikelet fertility ($r_g = -0.315^{**}$, $r_p = -0.315^{**}$) and total grain per panicle ($r_g = -0.223^{*}$, $r_p = -0.204$).

Biological yield per plant (g)

Biological yield per plant exhibited positive and highly significant relationship with harvest index ($r_g = 0.844^{**}$, $r_p = 0.834^{**}$), filled grain per panicle ($r_g = 0.704^{**}$, $r_p = 0.671^{**}$), grain yield per plant ($r_g = 0.691^{**}$, $r_p = 0.658^{**}$), effective tiller per plant ($r_g = 0.591^{**}$, $r_p = 0.551^{**}$), total grain per panicle ($r_g = 0.576^{**}$, $r_p = 0.553^{**}$), total tiller per plant ($r_g = 0.576^{**}$, $r_p = 0.538^{**}$), spikelet fertility ($r_g = 0.456^{**}$, $r_p = 0.418^{**}$) and days to 50% flowering ($r_g = 0.281^{**}$, $r_p = 0.269^{*}$).

Harvest index (%)

Harvest index exhibited positive and highly significant and significant relationship with biological yield per plant ($r_g = 0.844^{**}$, $r_p = 0.834^{**}$), filled grain per panicle ($r_g = 0.641^{**}$, $r_p = 0.589^{**}$), total grain per panicle ($r_g = 0.541^{**}$, $r_p = 0.499^{**}$), effective tiller per plant ($r_g = 0.452^{**}$, $r_p = 0.422^{**}$), total tiller per plant ($r_g = 0.420^{**}$,

$r_p = 0.381^{**}$), spikelet fertility ($r_g = 0.408^{**}$, $r_p = 0.364^{**}$), days to 50% flowering ($r_g = 0.358^{**}$, $r_p = 0.333^{**}$) and grain yield per plant ($r_g = 0.219^*$, $r_p = 0.165$).

Grain yield per plant (g)

Grain yield per plant exhibited positive and highly significant correlation with biological yield per plant ($r_g = 0.691^{**}$, $r_p = 0.658^{**}$), filled grain per panicle ($r_g = 0.483^{**}$, $r_p = 0.452^{**}$), total tiller per plant ($r_g = 0.482^{**}$, $r_p = 0.438^{**}$), effective tiller per plant ($r_g = 0.470^{**}$, $r_p = 0.416^{**}$), total grain per panicle ($r_g = 0.382^{**}$, $r_p = 0.364^{**}$), spikelet fertility ($r_g = 0.320^{**}$, $r_p = 0.277^*$) and harvest index ($r_g = 0.219^*$, $r_p = 0.165$). This indicated that simultaneous selection of all these characters was important for yield improvement. So, they may be used as a selection criteria to improve the grain yield in rice. Similar findings were reported by Alam *et al.* (2014), Singh *et al.*, (2018) for filled grain per panicle, effective tiller per plant. Rangare *et al.*, (2012) for harvest index and biological yield per plant and Basavaraja *et al.*, (2011) reported that productive tillers per plant showed significant positive correlation with grain yield.

4.2 The effect of cold and heat in selected rice genotypes

4.2.1 Parameters for cold tolerance screening

Selected thirty seven genotypes in Summer-2017 were further evaluated for cold tolerance on germination stage at different temperature (13°C and 28°C) (Table 4.6). These experiments following the protocol established by da Cruz and Milach (2004).

4.2.1.1 Germination index (%)

Germination index expresses the germination speed under cold temperature. These results indicate that more seed of this genotype was germinated at 13°C on germinator after 14 and 21 days beginning of the experiment. The GI was varied between 96% (Tewan dhan) and 62% (Jeera Baba). Fifteen genotypes out of thirty seven rice genotypes showed more than 80% GI (Table 4.6), it indicates that these genotypes germination speed is high under cold condition. The highest GI was observed in Tewan dhan (96%) followed by Baikoni (93.50%), Digamber dhan (93%) and RJR:II (92.50%).

Table 4.5: Estimation of genotypic and phenotypic correlation coefficient among yield and contributing traits in rice genotypes

		PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	BYP	HI	GYP
DFP	g	-0.005	0.174	0.234*	0.230*	0.472**	0.461**	0.523**	0.082	-0.191	0.281**	0.358**	0.012
	p	0.003	0.154	0.215*	0.227*	0.388**	0.447**	0.507**	0.077	-0.176	0.269*	0.333**	0.014
PH	g		-0.487**	-0.415**	0.329**	0.279*	-0.326**	-0.136	-0.405**	0.235*	-0.208	-0.133	-0.163
	p		-0.345**	-0.315**	0.278*	0.195	-0.268*	-0.124	-0.291**	0.195	-0.174	-0.117	-0.133
TTP	g			0.977**	-0.108	0.118	0.555**	0.416**	0.409**	-0.083	0.576**	0.420**	0.482**
	p			0.935**	-0.099	0.055	0.465**	0.358**	0.327**	-0.047	0.538**	0.381**	0.438**
ETP	g				-0.042	0.162	0.579**	0.476**	0.354**	-0.093	0.591**	0.452**	0.470**
	p				-0.036	0.093	0.500**	0.421**	0.289**	-0.056	0.551**	0.422**	0.416**
FLA	g					0.424**	0.109	0.242*	-0.138	0.053	0.015	0.070	-0.039
	p					0.343**	0.105	0.232*	-0.125	0.045	0.012	0.063	-0.040
PL	g						0.193	0.306**	-0.102	-0.014	0.118	0.093	0.093
	p						0.139	0.236*	-0.097	-0.004	0.091	0.105	0.036
FGP	g							0.855**	0.591**	-0.349**	0.704**	0.641**	0.483**
	p							0.845**	0.580**	-0.325**	0.671**	0.589**	0.452**
TGP	g								0.090	-0.223*	0.576**	0.541**	0.382**
	p								0.074	-0.204	0.553**	0.499**	0.364**
SF	g									-0.315**	0.456**	0.408**	0.320**
	p									-0.302**	0.418**	0.364**	0.277*
TW	g										0.047	0.007	0.046
	p										0.056	0.017	0.059
BYP	g											0.844**	0.691**
	p											0.834**	0.658**
HI	g												0.219*
	p												0.165

* & ** represent significant levels at 5% and 1% respectively.

DFP-Days to 50% flowering, PH-Plant height, TTP-Total tillers per plant, ETP-Effective tillers per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grains per panicle, TGP- Total grains per panicle, TW-100 grain weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

4.2.1.2 Percent of seeds with coleoptiles length greater than 5mm (PERCOL5 %)

As per Cruz and Milach (2004), this characteristic reflects the coleoptiles elongation capacity under cold temperature. PERCOL5 after 28 days of germination at 13°C, seventeen genotype presented more than 70% of the seed (Table 4.6). The highest PERCOL5 was recorded in RJR:II (91%) followed by Ganga kali (85%), NPT 19 (81%), and lowest was Dhadhmaini dhan (62%) followed by Ajam dhan (62%) and IR 64 (64%).

4.2.1.3 Percent of reduction in coleoptile length (REDCOL%)

This characteristic expresses the amount of reduction in genotypes coleoptile length by germination under cold in relation to normal temperature. Range of reduction in coleoptiles length for genotypes varied between 35.52% (Tewan dhan) to 65.11% (Safed Lalak). The genotypes showed the less than 50% reduction in coleoptile length was RJR:II (47.66%), BANSPATRI (47.71%), Ganga dhan (44.46%), Digamber dhan (39.90%), Barhasal (48.08%) and Indira Barani Dhan-1 (49.04%) indicated cold tolerance genotypes. The REDCOL was one of the better methods to distinguish among tolerant and sensitive genotype, but case of GI and PERCOL5 however it was not possible. Reduction in coleoptiles length is one of the best characteristic for better distinguish between sensitive to cold stress (Meidema, 1982).

4.2.1.4 Coleoptile regrowth (COLREG mm)

Both REDCOL and COLREG seems to be the most adequate characteristics to be used to evaluate cold tolerance during the germination period in rice (Cruz and Milach, 2004). COLREG values were ranged between 2.50mm (Ajam dhan) to 10.85mm (Tewan dhan). The genotypes that showed the more than 8mm was RJR:II (8.70mm), Banspatri (10.45mm), Ganga dhan (9.75mm), Tewan dhan (10.82mm),

Digambar dhan (8.75mm), Barhasaal(9.05mm), Indira Barani Dhan-1 (10.00mm) and Indira Aerobic 1 (9.20mm), these genotype indicated as cold tolerant genotypes.

4.2.1.5 Radicle regrowth (REDREG mm)

Measurement of radical regrowth after a period of cold stress is an important indicator of crop resistance to cold stress (Rab and altveit, 1996). REDREG for all genotypes was varied from 3.35mm (Ajam dhan) to 10.65 mm (RJR:II). In this way, RJR:II (10.65mm), Barhasal (9.15mm), Ajawain (8.40mm), Ganga dhan (8.95mm), Tewan dhan (8.60mm), Digamber dhan (8.50mm), Indira Barani Dhan 1 (8.20mm) and Indira Aerobic 1(8.20 mm) had highest level of REDREG. It indicated that these genotypes perform as tolerance in cold condition. Priyanka *et al.* (2015) also evaluated cold tolerance of rice genotypes in terms of REDCOL.

4.2.2 Parameters for heat tolerance screening

Selected thirty seven genotypes in *Summer*-2017 were evaluated for heat tolerance at flowering condition for different heat parameters (Table 4.7).

Table 4.6: Selected rice genotypes/ varieties after cold screening

S. No.	Genotype/ Variety					REDR
		GI (%)	PERCOL5 (%)	REDCOL (%)	COLREG (mm)	EG (mm)
1	RJR:II	92.50	91.00	47.66	8.70	10.65
2	Banspatri	92.00	78.00	47.71	10.45	7.80
3	Ganga kali	85.00	85.00	44.46	9.75	8.95
4	Tewan dhan	96.00	75.00	35.52	10.85	8.60
5	Digamber dhan	93.00	81.00	36.90	8.75	8.50
6	Barhasal	76.00	72.00	48.04	9.05	9.15
7	Indira Barani Dhan 1	83.50	71.00	49.04	10.00	8.10
8	Indira Aerobic 1	81.00	79.00	39.91	9.20	8.20

GI= Germination index, PERCOL5%=Percent of coleoptiles length >5mm, REDCOL=Reduction in coleoptiles length, COLREG= Coleoptile regrowth, REDREG= Redicle regrowth.

4.2.2.1 Canopy temperature (°C)

Canopy temperature was measured by infrared thermometer at flowering stage of all rice genotypes from flag leaf area on the date 15 april 2018 to 5 may 2018. In this period the average atmospheric temperature was 41°C. The canopy temperature ranges from 32.90°C (Chingar Bnko) to 29.10°C (Swarna). The rice plant temperatures are not only depending on the organ position, shape, size and hull morphology but also influenced by the air temperature, air humidity, radiation, and plant type (Sheehy *et al.*, 1998; Yan *et al.*, 2008, 2010). The moderate heat stress of 40°C significantly decreased the spikelet fertility, whereas it caused little damage to the photosynthesis in flag leaves at anthesis because when the panicle temperature was above 38°C, the flag leaves were only approximately 34°C (Zhang *et al.*, 2016). This indicated that the damage degree induced by heat stress to rice plant organs mainly varied with their different temperatures.

4.2.2.2 Membrane stability index (%)

Cell membrane stability test has been used for identify the heat tolerance genotypes. When tissues are subjected to high temperature, electrical conductivity increases due to damage to the cell membrane and consequent solute leakage. Membrane stability indicated by electrolyte leakage was used in one study for screening thermal tolerance in crops (Saadalla *et al.*, 1990). In this study high membrane stability index at heat stress condition was found in Banko (81.25%) and low in Baikoni (52.38%). The comparison between control and stress condition, less reduction in membrane stability index was important parameter for heat tolerance. The result revealed that less reduction in membrane stability index was found in Dadbako (0.76%), NPT 6 (3.26%), P:357 III (4.31%), Gangtai (5.53%), RJR:II (5.56%) and Indira aerobic -1 (6.41%), so these genotypes indicated as heat tolerance.

4.2.2.3 Pollen fertility (%)

Pollen fertility was expressed as percentage of stained round shaped pollen grains. The pollen fertility percentage at high temperature was ranges between 93.71%

(IR 64) to 99.87% (NPT 6). All the genotypes were showed more than 90% pollen fertility. The pollen staining technique with IKI indicates only the formation of starch in pollen grains, thus indicates potentially viable pollen. However, it does not mean that the pollen will germinate on the stigma, grow pollen tube and fertilize the egg, whereas high temperatures at and soon after anthesis can result in poor anther dehiscence, poor pollen germination and retarded pollen tube growth. All of these can cause poor spikelet fertility (Prasad *et al.*, 2006).

4.2.2.4 Spikelet fertility (%)

High temperature during grain filling caused low spikelet sterility by shortening of the duration of grain filling. This might be due to unavailable supply with assimilates and the capacity of remobilizing carbohydrate reserves from vegetative organs to the grains under the stress (Li *et al.* 2013). Grain filling is also affected by impaired deposition of starch and protein under high temperature stress (Yamakawa and Hakata, 2010). High spikelet fertility percentage in heat stress condition shows as tolerance genotypes.

At high temperature spikelet fertility was varied from 40.40% (P:357 III) to 94.64 % (Tendhumori dhan). The genotypes which had high spikelet fertility (>90%) were Tendhumori dhan (94.64%), 90 Number (93.69%), Gangtai (93.41%), NPT 19 (92.53%), NPT 6 (92.14%), Dadhmaini dhan (92.00%), Bhatamokdo (91.57%), Digamber dhan (91.52%) and BAIKONI(90.52%), indicated as these genotypes could be perform better in high temperature. P:357 III (40.40%) had low (<50%) spikelet fertility.

4.3 Combining ability analysis for yield and quality traits

The line x tester design developed by Kempthorne (1957) which has been used in the present study to estimate combining ability. Line x tester is one of the technique where large number of genotype could be tested for their combining ability. It is necessary to assess the genetic potentiality of the parent in hybrid combination

through systematic studies in relation to general and specific combining ability which are due to additive and non additive gene action respectively (Griffings, 1956).

Table 4.7: Selected rice genotypes after heat screening

S. No.	Genotypes	Canopy temperature (°C)	MSI (%)			Pollen fertility (%)	Spikelet fertility (%)
			Control	Stress	Reduction		
1	Dadbako	30.5	75.76	75.00	0.76	95.5	90.14
2	NPT 6	31.83	78.26	75.00	3.26	99.87	92.14
3	Gangtai	29.17	78.26	72.73	5.53	98.19	93.41
4	RJR:II	30.77	72.22	66.67	5.56	99.08	89.12
5	Ganga kali	32.13	87.54	81.59	6.01	99.53	87.76
6	NPT 19	30.35	86.36	80.00	6.36	97.43	92.53
7	NPT 6	30.13	88.24	81.25	6.99	99.06	88.14
8	Bega hundi	31.03	84.21	76.67	7.54	99.03	90.07
9	Kolhin khosa	30.32	80.00	72.22	7.78	98.92	89.11
10	Banspatri	31.50	91.3	83.3	8.00	95.57	90.44
11	Ganga dhan	30.67	80.00	70.59	9.41	99.15	88.32
12	Safed Lalak	30.52	84.62	75.00	9.62	98.83	87.47
13	Ajam dhan	29.93	91.67	81.57	10.08	99.17	88.05

MSI= Membrane stability index

After cold and heat screening on thirty seven selected genotypes, eight lines selected for combining ability analysis. Out of eight lines, three lines (RJR:II, Banspatri and Ganga kali) showed tolerant in both cold and heat stress and five lines (Ajam dhan, Safed lalak, NPT-19, NPT 6 and Bega hundi) only showed tolerant in heat stress condition. Selected four testers (Indira Barani Dhan-1, Indira Aerobic-1, IR 64 and MTU 1010) were early maturity released variety. Thirty two crosses were derived by crossing eight lines with each of four testers and they were evaluated along with parents in randomized block design with two replications.

4.3.1 Mean performance of parents and hybrids

The mean performance of quantitative and quality traits of twelve parents (eight line and four testers) and thirty two crosses, were given in table 4.8 and 4.9, respectively.

4.3.1.1 Quantitative traits

Days to 50% flowering

Among the parental line, the maximum days to 50% flowering reported by Bega Hundi (96.00 days) and earlier by NPT 6 (89.50 days). In cross combination longest duration of 50% flowering was observed in RJR:II X IR 64 (109.00 days) and earlier in Banspatri X IR 64 (82.00 days) which was earlier than their parents.

Plant height (cm)

Among parental line, Ajam dhan (104.21 cm) was reported as tallest genotype and RJR:II (79.33 cm) was the shortest plant height, where shorter plant stature was desirable. In cross combination RJR:II X IR 64 (118.01 cm) was presented as tallest one and Bega Hundi X IR 64 (95.90 cm) was the shortest genotype.

Table 4.8 Mean performance of quantitative traits of parents and crosses

S. No	Parent /Cross Line	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
1	RJR:II	92.50	79.33	9.75	9.38	26.78	24.46	131.60	142.50	92.41	2.21	18.58	27.15	69.42
2	Banspatri	92.00	99.96	12.25	11.75	50.06	23.28	103.00	107.35	95.99	2.59	14.44	24.41	59.42
3	Ganga kali	95.00	93.91	11.50	11.13	28.10	21.43	142.95	149.10	95.90	1.92	12.94	23.42	56.41
4	Ajam dhan	97.50	104.21	8.88	8.13	33.81	20.79	162.55	172.60	94.25	2.66	17.45	30.26	57.51
5	Safed Lalak	98.50	87.74	18.25	17.63	52.37	23.58	142.70	151.00	94.52	2.38	23.16	38.38	60.40
6	NPT 19	92.50	86.60	12.75	12.38	29.60	23.37	206.30	223.15	92.49	2.01	19.35	29.00	67.49
7	NPT 6	89.50	82.18	15.63	14.25	35.61	22.22	127.30	132.40	96.12	2.68	20.09	35.65	56.71
8	Bega hundi	96.00	89.21	11.38	10.00	29.80	21.79	175.25	180.45	97.11	2.06	16.85	32.63	51.72
	Population mean	94.19	90.39	12.55	11.83	35.77	22.62	148.96	157.32	94.85	2.31	17.86	30.11	59.89
	SE(±)	3.07	8.51	3.07	3.01	9.98	1.25	31.90	34.94	1.74	0.31	3.23	5.25	5.52
Tester														
1	IBD-1	91.50	91.69	12.38	11.75	20.35	23.02	141.15	144.45	97.72	2.15	20.22	37.16	54.50
2	IA-1	93.00	87.40	15.63	15.13	27.80	26.71	190.75	203.45	93.79	2.35	16.84	29.50	57.07
3	IR-64	91.50	87.56	11.88	11.50	30.09	24.03	135.45	141.45	95.94	2.01	18.32	26.61	69.38
4	MTU 1010	94.50	86.76	15.13	13.88	30.58	21.10	149.15	151.15	98.67	2.25	18.41	29.48	62.39
	Population mean	92.63	88.35	13.76	13.07	27.21	23.72	154.13	160.13	96.53	2.19	18.45	30.68	60.83
	SE(±)	1.24	1.95	1.64	1.51	4.09	2.02	21.70	25.26	1.86	0.13	1.20	3.92	5.69

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Continue...

S. No	Parent /Cross	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
	Crosses													
1	RJR:II X Indir Barani Dhan 1	88.50	100.95	21.25	20.75	28.94	27.82	147.75	154.40	95.70	2.34	21.98	48.48	45.33
2	RJR:II X Indira Aerobic 1	90.50	116.63	26.50	24.50	36.61	26.82	149.40	157.65	94.77	2.72	22.21	60.59	36.57
3	RJR:II X IR-64	109.00	118.01	22.00	21.25	32.19	28.94	166.00	179.40	92.52	2.63	25.63	30.18	85.29
4	RJR:II X MTU 1010	102.20	110.98	24.50	23.63	32.28	27.40	148.50	161.30	92.05	2.06	14.14	29.19	48.43
5	Banspatri X Indir Barani Dhan 1	88.00	107.19	25.50	23.13	32.47	27.94	188.85	200.50	94.20	2.73	22.88	31.32	72.93
6	Banspatri X Indira Aerobic 1	87.50	113.79	20.25	19.13	28.20	30.13	148.60	160.15	92.78	2.47	22.09	28.75	76.87
7	Banspatri X IR-64	82.00	104.24	18.50	17.25	32.23	24.76	163.00	173.10	94.21	2.41	18.02	30.20	59.75
8	Banspatri XMTU 1010	99.50	102.82	23.50	22.75	36.87	26.29	199.25	216.55	92.06	2.00	23.44	28.18	83.10
9	Ganga kali X Indir Barani Dhan 1	101.50	112.65	20.75	19.88	32.43	27.20	149.50	160.35	93.22	1.78	21.52	34.13	63.01
10	Ganga kali X Indira Aerobic	93.00	103.47	18.00	17.63	31.82	30.90	216.80	228.10	95.04	2.02	34.70	39.75	87.76
11	Ganga kali X IR-64	94.50	103.05	28.63	27.13	41.20	28.63	144.60	157.90	91.60	2.29	29.35	71.54	41.03
12	Ganga kali XMTU 1010	94.00	100.29	16.88	15.50	32.82	29.47	146.15	154.75	94.44	2.67	23.05	29.10	79.26
13	Ajam dhan X Indir Barani Dhan 1	89.00	102.47	25.75	25.00	34.66	27.22	138.10	148.10	93.20	2.42	36.71	57.90	63.29
14	Ajam dhan X Indira Aerobic	87.50	99.01	23.25	22.50	38.36	26.94	135.65	147.75	91.81	2.25	26.18	37.70	69.42
15	Ajam dhan X IR-64	91.50	106.32	20.25	20.00	36.56	28.14	153.45	163.05	94.14	2.27	20.80	35.56	58.54
16	Ajam dhan XMTU 1010	92.50	103.28	19.75	19.13	37.89	28.48	185.10	192.90	95.96	1.99	21.95	35.53	61.77
17	Safed Lalak X Indir Barani Dhan 1	91.50	106.53	15.75	14.75	38.73	24.69	188.05	194.45	96.72	2.56	18.20	25.99	70.09
18	Safed Lalak X Indira Aerobic 1	88.50	101.79	18.75	18.25	34.03	26.62	160.50	168.60	95.21	2.39	17.24	34.04	50.68
19	Safed Lalak X IR-64	98.00	105.31	19.50	18.38	31.84	26.78	194.65	206.25	94.40	2.82	22.99	28.90	79.64
20	Safed Lalak XMTU 1010	94.50	98.01	14.00	13.38	35.68	26.92	198.55	208.90	95.05	2.85	18.52	26.10	70.93
21	NPT 19 X Indir Barani Dhan 1	89.50	100.27	12.88	12.13	38.62	27.66	136.65	144.45	94.63	2.46	20.70	31.36	66.04
22	NPT 19 X Indira Aerobic 1	98.50	99.90	15.13	14.00	42.88	28.07	130.90	147.95	88.49	2.58	17.44	25.22	69.03
23	NPT 19 X IR-64	90.50	98.85	16.25	14.88	36.28	25.53	135.95	151.25	89.92	2.14	14.36	24.14	59.53
24	NPT 19 XMTU 1010	92.00	100.91	12.50	12.13	37.80	24.74	146.75	172.50	85.08	2.02	18.87	27.69	68.12
25	NPT 6 X Indir Barani Dhan 1	89.50	108.51	12.25	11.38	37.43	23.28	139.10	151.45	91.83	2.40	16.22	27.07	59.86
26	NPT 6 X Indira Aerobic 1	87.50	103.66	15.50	15.00	35.88	29.26	110.45	133.10	83.33	2.70	17.97	26.45	68.00

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Conti...

S. No	Crosses	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
27	NPT 6 X IR-64	87.50	110.76	15.63	14.88	37.76	29.68	103.35	131.50	78.67	2.84	17.67	23.11	77.20
28	NPT 6 X MTU 1010	92.50	117.01	15.25	14.25	32.60	28.62	153.90	175.85	87.51	2.59	17.80	27.75	64.05
29	Bega hundi X Indira Barani Dhan 1	95.00	98.21	21.13	19.88	31.02	25.65	219.20	237.75	92.21	1.76	40.58	48.10	84.55
30	Bega hundi X Indira Aerobic 1	92.00	100.09	18.75	18.13	28.65	23.05	206.65	218.00	94.78	1.98	25.26	31.65	79.89
31	Bega hundi X IR-64	93.00	95.90	22.25	21.63	23.77	21.86	145.15	150.05	96.74	2.13	23.57	35.37	66.88
32	Bega hundi XMTU 1010	91.50	97.45	21.25	20.50	30.29	20.88	141.90	150.00	94.62	2.40	17.96	32.10	55.95
	Population mean	92.57	104.63	19.44	18.52	34.34	26.89	159.14	171.81	92.40	2.36	22.19	34.47	66.34
	SE(±)	5.34	6.06	4.28	4.13	4.10	2.36	29.19	28.34	3.99	0.31	6.08	11.26	12.91

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Table 4.9: Mean performance of quality traits of parents and crosses

S. no	Parent /Cross Line	H%	M%	HRR%	PL	PB	P L/B	BRL	BRW	B L/B	KL	KB	K L/B	ER	EI	ASV	GC	AC
1	RJR:II	83.36	53.03	37.68	9.16	2.78	3.29	8.08	2.42	3.35	7.32	2.42	3.03	1.23	0.70	5.50	78.00	16.19
2	Banspatri	85.88	64.74	56.30	9.00	2.81	3.20	6.48	2.42	2.69	6.02	2.37	2.54	1.58	0.99	4.00	99.00	16.81
3	Ganga kali	85.08	41.40	28.06	8.63	2.70	3.20	7.30	2.43	3.00	6.10	2.22	2.75	1.39	0.78	5.00	98.00	15.71
4	Ajam dhan	84.88	77.75	58.19	9.11	2.72	3.36	7.62	2.38	3.20	6.28	2.37	2.66	1.33	0.77	4.00	97.50	14.88
5	Safed Lalak	87.36	69.37	60.30	9.01	2.88	3.13	6.68	2.60	2.57	5.30	2.43	2.18	1.66	0.99	3.50	59.20	23.07
6	NPT 19	85.81	46.95	30.73	9.07	2.78	3.25	8.21	2.58	3.18	7.02	2.60	2.70	1.14	0.63	4.50	95.00	20.48
7	NPT 6	87.30	74.85	64.72	8.01	2.70	2.97	5.88	2.58	2.28	5.58	2.38	2.34	1.60	1.00	4.00	99.00	14.88
8	Bega hundi	89.95	70.84	61.20	9.05	2.81	3.22	6.80	2.60	2.62	5.00	2.62	1.91	1.86	1.22	5.00	78.50	23.00
	Population mean	86.20	62.37	49.65	8.88	2.77	3.20	7.13	2.50	2.86	6.08	2.43	2.51	1.47	0.89	4.44	85.88	18.13
	SE(±)	1.87	12.67	13.96	0.36	0.06	0.11	0.76	0.09	0.35	0.75	0.12	0.33	0.23	0.18	0.63	6.74	3.28
	Tester																	
1	Indira Barani Dhan-1	87.14	63.74	58.23	8.01	2.76	2.90	6.88	2.60	2.65	5.48	2.38	2.30	1.40	0.83	5.00	86.50	20.65
2	Indira Aerobic -1	90.50	73.68	58.26	7.84	2.80	2.80	6.68	2.43	2.75	5.33	2.42	2.21	1.48	0.96	6.00	58.50	21.92
3	IR-64	85.68	77.27	61.61	9.00	3.01	2.99	7.68	2.18	3.52	6.52	2.23	2.92	1.26	0.64	6.00	65.00	20.77
4	MTU 1010	88.93	68.01	56.30	8.01	3.00	2.67	6.80	2.58	2.64	5.83	2.20	2.65	1.31	0.67	3.50	68.50	20.49
	Population mean	88.06	70.68	58.60	8.22	2.89	2.84	7.01	2.45	2.89	5.79	2.31	2.52	1.36	0.78	5.38	72.13	20.96
	SE(±)	1.82	5.19	1.91	0.46	0.11	0.12	0.39	0.17	0.37	0.46	0.09	0.28	0.08	0.13	1.29	4.84	0.56

H%=hulling , M%=milling , HRR%=head rice recovery, PL=panicle length, PB=panicle breadth, PL/B=panicle length breadth ratio, BRL=brown rice length, BRW=brown rice width, KL=kernel length, KB=kernel breadth, KL/B=kernel length breadth ratio, ER=Elongation ratio, EI=Elongation index, ASV=Alkali spreading value, GC=Gel consistency, AC=Amylose content

Conti...

S. no	Parent /Cross	H%	M%	HRR%	PL	PB	P L/B	BRL	BRW	B L/B	KL	KB	K L/B	ER	EI	ASV	GC	AC
	Crosses																	
1	RJR:II X Indir Barani Dhan 1	83.87	74.19	58.89	9.12	2.37	3.86	7.48	2.42	3.10	6.62	2.23	2.97	1.12	0.58	5.00	96.00	28.35
2	RJR:II X Indira Aerobic 1	73.72	63.84	37.94	8.05	2.76	2.91	6.41	2.58	2.49	5.40	2.81	1.92	1.59	1.03	5.00	86.15	27.77
3	RJR:II X IR-64	86.02	75.97	64.91	7.62	2.55	2.99	6.48	2.58	2.51	5.45	2.58	2.11	1.34	0.83	5.00	75.45	25.04
4	RJR:II X MTU 1010	81.97	69.13	56.39	6.79	3.02	2.25	6.02	2.38	2.53	5.41	1.56	3.75	2.03	1.21	5.00	96.00	33.52
	Banspatri X Indir Barani Dhan 1															5.00		
5	1	65.64	56.62	27.27	9.31	2.81	3.31	6.78	2.43	2.79	6.02	2.50	2.41	1.25	0.66		64.00	27.96
6	Banspatri X Indira Aerobic 1	52.35	39.01	30.25	10.05	2.03	4.94	9.00	2.18	4.13	6.90	2.23	3.10	1.33	0.74	5.00	48.05	23.80
7	Banspatri X IR-64	87.73	74.69	66.06	7.77	3.01	2.57	6.03	2.18	2.76	5.30	2.40	2.21	1.57	0.82	6.00	57.50	27.81
8	Banspatri XMTU 1010	87.17	65.88	55.40	7.46	2.76	2.70	5.23	2.38	2.20	5.02	2.42	2.07	1.67	1.14	3.00	93.15	25.77
	Ganga kali X Indir Barani Dhan 1															3.00		
9	1	62.97	50.95	43.30	9.01	2.42	3.74	6.28	2.58	2.44	5.83	2.42	2.41	1.44	0.82		96.10	22.10
10	Ganga kali X Indira Aerobic	88.81	76.51	44.96	7.07	2.44	2.91	6.00	2.62	2.29	5.40	2.58	2.09	1.61	1.00	6.00	70.35	22.25
11	Ganga kali X IR-64	86.84	62.77	46.88	10.05	2.37	4.25	6.32	2.43	2.60	6.00	2.22	2.71	1.42	0.85	2.00	59.80	21.48
12	Ganga kali XMTU 1010	71.99	56.55	40.34	9.12	2.62	3.49	6.41	2.42	2.66	5.66	2.38	2.38	1.60	0.95	2.00	98.50	23.42
	Ajam dhan X Indir Barani Dhan 1															2.00		
13	1	81.38	68.88	55.75	9.15	2.55	3.59	7.23	2.43	2.98	6.21	2.43	2.55	1.61	0.95		60.00	10.91
14	Ajam dhan X Indira Aerobic	84.48	69.06	54.24	10.10	2.76	3.65	7.32	2.38	3.07	6.28	2.37	2.66	1.91	1.21	3.00	96.00	14.78
15	Ajam dhan X IR-64	84.36	64.25	58.24	9.08	2.75	3.29	6.07	2.62	2.32	5.20	2.42	2.16	1.87	1.17	2.00	60.60	18.41
16	Ajam dhan XMTU 1010	81.84	59.17	34.76	9.02	2.70	3.34	8.18	2.80	2.93	7.28	2.58	2.82	1.24	0.69	2.00	58.00	18.08
	Safed Lalak X Indir Barani Dhan 1															3.00		
17	1	88.81	69.95	55.71	8.75	2.62	3.35	6.09	2.58	2.36	5.38	2.58	2.08	1.54	0.94		100.00	20.98
18	Safed Lalak X Indira Aerobic 1	88.02	66.30	53.57	8.75	2.78	3.14	6.18	2.60	2.38	5.62	2.43	2.31	1.51	0.82	2.00	95.00	24.22
19	Safed Lalak X IR-64	90.93	65.04	59.83	8.80	2.80	3.14	7.13	2.43	2.94	6.03	2.40	2.51	1.56	0.96	4.00	100.00	21.20
20	Safed Lalak XMTU 1010	77.08	63.99	53.93	9.15	2.19	4.18	7.10	2.01	3.52	6.46	2.00	3.24	1.55	0.98	4.00	96.75	17.99
21	NPT 19 X Indir Barani Dhan 1	79.78	59.94	37.57	9.05	2.76	3.27	6.28	2.38	2.64	4.88	1.68	3.18	1.84	1.26	3.00	100.00	17.46
22	NPT 19 X Indira Aerobic 1	77.54	66.40	56.60	9.00	3.01	2.99	6.46	2.62	2.47	5.02	2.62	1.91	1.70	1.07	4.00	99.00	24.12
23	NPT 19 X IR-64	85.88	73.60	66.43	8.36	2.78	3.00	6.66	2.42	2.76	6.03	2.22	2.73	1.51	0.93	4.00	93.65	21.70
24	NPT 19 XMTU 1010	79.35	64.26	50.67	8.78	2.80	3.14	7.10	2.40	2.96	6.28	2.40	2.62	1.41	0.79	4.00	97.50	17.38
25	NPT 6 X Indir Barani Dhan 1	88.71	75.70	62.92	8.62	2.76	3.12	6.63	2.43	2.73	6.03	2.42	2.50	1.58	0.87	3.00	56.50	16.17
26	NPT 6 X Indira Aerobic 1	83.63	60.17	29.93	8.20	2.67	3.08	7.02	2.38	2.95	6.08	2.40	2.53	1.31	0.67	5.00	75.05	17.05
27	NPT 6 X IR-64	82.36	66.84	29.62	8.32	2.70	3.08	6.80	2.38	2.86	5.52	2.43	2.27	1.47	0.83	4.00	67.25	17.52
28	NPT 6 X MTU 1010	88.40	74.94	67.84	8.55	2.56	3.33	6.38	2.42	2.64	5.83	2.38	2.45	1.58	0.88	5.00	72.85	22.81
	Bega hundi X Indira Barani Dhan 1															5.00		
29	1	85.01	74.92	58.84	10.03	2.88	3.48	7.48	2.42	3.10	6.32	2.20	2.87	1.75	0.96		60.40	17.48
30	Bega hundi X Indira Aerobic 1	85.08	60.11	33.60	9.16	2.87	3.20	7.40	2.40	3.08	6.18	2.37	2.61	1.62	0.96	7.00	62.50	16.97
31	Bega hundi X IR-64	86.38	70.44	59.02	10.05	2.80	3.59	8.20	2.60	3.15	7.27	2.38	3.05	1.38	0.77	6.00	60.00	16.62
32	Bega hundi XMTU 1010	87.24	75.60	61.98	9.76	2.80	3.49	7.48	2.18	3.43	6.20	2.22	2.80	1.58	0.88	4.00	92.65	17.95
	Population mean	81.73	66.11	50.43	8.82	2.68	3.32	6.80	2.44	2.81	5.91	2.35	2.56	1.55	0.91	3.50	89.34	21.22
	SE(±)	8.47	8.29	12.31	0.85	0.23	0.51	0.77	0.16	0.41	0.61	0.25	0.42	0.20	0.17	1.75	11.68	4.85

Tillers per plant (No.)

Among parental line, Safed Lalak (18.25) had maximum number of tillers and genotype RJR:II (8.88) had lowest number of tillers. In cross combination, maximum tiller number was reported in Ganga kali X IR 64 (28.63), that is more than their both of the parents. Whereas, NPT 6 X Indira Barani Dhan 1 (12.25) was reported as minimum number of tillers.

Effective tillers per plant (No.)

Among parental line, Safed Lalak (17.63) had maximum number of effective tillers and lowest number of effective tillers was reported in Ajam dhan (8.13). In cross combination, maximum number of effective tillers was reported in Ganga kali X IR 64 (27.13), that is more than their both of the parents. Whereas, lowest number of effective tillers was reported in NPT 6 X Indira Barani Dhan 1 (11.38).

Flag leaf area (cm²)

Among parental line, the maximum flag leaf area was found in Banspatri (50.06 m²) and minimum in Indira Barani Dhan 1 (20.35c m²). In cross combination, maximum flag leaf area was found in NPT 19 X Indira Aerobic 1 (42.88 cm²) and minimum in Bega hundi X IR 64 (23.77cm²).

Panicle length (cm)

Among parental line, panicle length was presented at maximum in INDIRA Aerobic 1 (26.71c) and shortest panicle length in Ajam dhan (20.79cm). In cross combination, highest and shortest panicle length was found in Ganga kali X Indira Aerobic 1 (30.90cm) and Bega hundi X MTU 1010 (20.88cm), respectively.

Filled grains per panicle (No.)

Among parental line, the highest number of filled grains per panicle was found in NPT 19 (206.30) and lowest in Banspatri (103.00). In cross combination, maximum

number of filled grains per panicle was found in Bega hundi X Indira Barani Dhan 1 (219.20), that was more than both of their parents and minimum in NPT 6 X IR 64 (103.35).

Total grains per panicle (No.)

Among parental line, the maximum total grains per panicle was found in NPT 19 (223.15) and lowest in Banspatri (107.35). In cross combination, maximum number of total grains per panicle was found in Bega hundi X Indira Barani Dhan 1 (219.20), that was more than both of their parents and minimum in NPT 6 X IR 64 (103.35).

Spikelet fertility (%)

Among parental line, highest spikelet fertility was found in MTU 1010 (98.67%) and lowest in RJR:II (92.41%). In cross combination, highest spikelet fertility was found in Bega hundi X IR 64 (96.74%), that was more than their pollen parent and minimum in NPT 6 X IR 64 (78.67%).

100 grain weight (g)

Among parental line, maximum 100 grain weight was found in NPT 6 (2.68 g) and minimum in Ganga kali (1.92 g). In cross combination, maximum 100 grain weight was found in Safed Lalak X MTU 1010 (2.85 g) and minimum in Bega hundi X Indira Barani Dhan 1 (1.78 g).

Grain yield per plant (g)

Among parental line, the highest grain yield per plant was produced by safed Lalak (23.16 g) and the lowest by Ganga kali (12.94 g). In cross combination, highest grain yield per plant was produced by Ajam dhan X Indira Barani Dhan 1 (36.71 g), that was more than their both of the parents and lowest yield by RJR:II X MTU 1010 (14.14 g).

Biological yield per plant (g)

Among parental line, the biological yield per plant was ranged from 38.38 g (Safed Lalak) to 24.41 g (Banspatri). In cross combination, it is ranged from 71.54 g (Ganga kali X IR 64) to 23.11 g (NPT 6 X IR 64).

Harvest index (%)

Among parental line, the highest harvest index per plant was found in RJR:II (69.42%) and the lowest in Bega hundi (51.72%). In cross combination, highest harvest index was found in RJR:II X IR 64 (85.29%) , that was more than their both of the parents and lowest in RJR:II X Indira Aerobic 1 (36.57%).

4.3.1.2 Quality traits

The mean performance of twenty two quality traits of thirty two crosses, eight line and three testers were given in table 4.9.

Hulling (%)

Among parental line, the hulling percent was ranged from 83.36% (RJR:II) to 90.50% (Indira Aerobic -1). In cross combination, it is ranged from 52.35 % (Banspatri X Indira Aerobic 1) to 90.93% (Safed Lalak X IR 64).

Milling (%)

Among parental line, the milling percent was ranged from 41.40% (NPT 19) to 77.75% (Indira Aerobic -1). In cross combination, it is ranged from 39.01 % (Banspatri X Indira Aerobic 1) to 88.81% (Ganga kali X Indira Aerobic 1).

Head rice recovery (%)

Among parental line, the head rice recovery percent was ranged from 28.06% (Ganga kali) to 64.73% (IR 64). In cross combination, it is ranged from 27.27% (Banspatri X Indira Aerobic 1) to 66.06% (BanspatrI X IR 64).

Paddy length (mm)

Among parental line, the paddy length was ranged from 9.16 (RJR:II) to 7.84 cm (Indira Aerobic -1). In cross combination, it is ranged from 6.79 (RJR:II X MTU 1010) to 10.10cm (Ajam dhan X Indira Aerobic 1).

Paddy breadth (mm)

Among parental line, the paddy breadth was ranged from 2.70 (Ganga kali) to 3.01 mm (IR 64). In cross combination, it is ranged from 2.19 (Safed Lalak X MTU 1010) to 3.02 mm (RJR:II X MTU 1010).

Paddy L/B ratio (mm)

Among parental line, the paddy L/B ratio was ranged from 3.29 (RJR:II) to 2.67 mm (MTU 1010). In cross combination, it is ranged from 2.70 (Banspatri X MTU 1010) to 4.94 mm (Banspatri X Indira Aerobic 1).

Brown rice length (mm)

Among parental line, the brown rice length was ranged from 5.88 (NPT 6) to 8.21mm (NPT 19). In cross combination, it is ranged from 6.00 (Ganga kali X Indira Aerobic 1) to 8.21mm (Bega hundi X IR 64).

Brown rice width (mm)

Among parental line, the brown rice width was ranged from 2.18 (IR 64) to 2.60 mm (Safed Lalak, Bega hundi and Indira Barani Dhan-1). In cross combination, it is ranged from 2.18 (Bega hundi X MTU 1010) to 2.62 mm (NPT 19 X Indira Aerobic 1).

Brown rice L/B ratio

Among parental line, the brown rice L/B ratio was ranged from 2.28 (NPT 6) to 3.58mm (IR 64). In cross combination, it is ranged from 2.20 (Banspatri X MTU 1010) to 4.13mm (Banspatri X Indira Aerobic 1).

Kernel length (mm)

Among parental line, the kernel length was ranged from 5.00 (Bega Hundi) to 7.32 mm (RJR:II). In cross combination, it is ranged from 4.88 (NPT 19 X Indira Barani Dhan 1) to 7.28 mm (Ajm dhan X MTU 1010).

Kernel breadth (mm)

Among parental line, the Kernel breadth was ranged from 5.00 (Bega hundi) to 7.32 mm (RJR:II). In cross combination, it is ranged from 4.88 (NPT 19 X Indira Barani Dhan 1) to 7.27 mm (Bega hundi X IR 64).

Kernel L/B ratio

Among parental line, the Kernel L/B ratio was ranged from 1.91 (Bega hundi) to 3.03 mm (RJR:II). In cross combination, it is ranged from 1.91 (NPT 19 X Indira Aerobic 1) to 3.75 mm (RJR:II X MTU 1010).

Elongation ratio

Among parental line, the elongation ratio was ranged from 1.23 (RJR:II) to 1.86 mm (Bega hundi). In cross combination, it is ranged from 1.12 (RJR:II X Indira Barani Dhan 1) to 1.91 mm (Ajam dhan X Indira Aerobic 1).

Elongation index

Among parental line, the elongation index was ranged from 0.63 (NPT 19) to 0.99 mm (Banspatri). In cross combination, it is ranged from 0.58 (RJR:II X Indira Barani Dhan 1) to 1.21 mm (Ajam dhan X Indira Aerobic 1).

Alkali spreading value

Among parental line, the alkali spreading value was ranged from 3.50 (Safed Lalak and MTU 1010) to 6 (Indira Aerobic -1, IR 64). In cross combination, it is ranged from 1.50 (RJR:II X IR 64) to 7.00 (RJR:II X Indira Barani Dhan 1).

Gel consistency

Among parental line, the gel consistency was ranged from 58.00 (Indira Aerobic -1) to 99.00 (Banspatri and NPT 6). In cross combination, it is ranged from 48.05 (Banspatri X Indira Aerobic 1) to 100.00 (Safed Lalak X IR 64, NPT 19 X Indira Barani Dhan 1).

Amylose content

Among parental line, the amylase content was ranged from 14.88 (Ajam dhan) to 23.07 (Safed Lalak). In cross combination, it is ranged from 35.52 (RJR:II X MTU 1010) to 10.91 (Ajam dhan X Indira Barani Dhan 1).

4.3.2 Analysis of variance for combining ability

The analysis of variance for combining ability of quantitative and quality traits under study has been presented in table 4.10, 4.11, 4.12 and 4.13, respectively. The analysis of variance revealed that mean sum of square for all traits show highly significant difference between the genotypes. Highly significance due to line x testers indicate that they interacted and produced markedly different combining ability effects, this might be due to the wide genetic diversity of lines and testers. It was also found that mean squares due to lines were larger when compare to testers for all the traits indicating greater diversity among lines. This was in confirmation with ther results reported by Abuali *et al.*, (2012). The SCA variances were higher than the GCA variances for all the characters, revealed that expression of these characters were controlled by non-additive effects of genes. Predominance of non-additive gene action for grain yield and its components was also reported by Saidaiah *et al.* (2011) and Tiwari *et al.* (2011).

The proportional contribution to the total variance by lines, testers and interaction revealed that the line and line x tester interaction have contributed more than tester in respect of all the quantitative and quality traits. The results of analysis are discussed under following sub heads.

Table 4.10: Analysis of variance for combining ability of quantitative traits

Source	DF	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
Replication	1	0.64	0.05	1.00	0.61	1.22	1.88	44.22	23.04	1.19	0.11	21.09	58.29	16.90
Cross	31	57.01**	73.51**	36.61**	34.08**	33.60**	11.11**	1704.31**	1605.92**	31.89**	0.19**	74.14**	253.71**	333.51**
line	7	72.39**	179.01**	105.32**	101.86**	82.34**	27.06**	3342.53**	2409.42**	88.57**	0.35**	133.58**	434.65**	281.47**
tester	3	55.48**	5.87**	9.89**	8.53**	1.15**	5.30**	671.19**	641.55**	18.36**	0.06**	81.87**	209.06**	8.06**
line X Tester	21	52.11**	48.0	17.52**	15.14**	21.99**	6.63**	1305.83**	1475.86**	14.94**	0.16**	53.23**	199.78**	397.35**
Error	31	0.67	16.58	4.82	3.52	3.04	1.79	25.38	35.21	4.59	0.00	4.49	7.36	12.43
σ^2_l		8.96	20.30	12.56	12.29	9.91	3.16	414.64	296.78	10.50	0.04	16.14	435.96	18.39
σ^2_t		3.43	0.67	0.32	0.31	0.12	0.22	40.36	37.90	0.86	0.00	4.84	102.92	0.00
σ^2_{gca}		0.15	0.76	0.57	0.56	0.35	0.13	11.88	3.88	0.51	0.00	0.62	1.61	1.90
σ^2_{sca}		25.72	15.71	6.35	5.81	9.48	2.42	640.23	720.32	5.17	0.08	24.37	96.21	72.16
$\sigma^2_{gca}/\sigma^2_{sca}$		0.01	0.05	0.09	0.10	0.04	0.06	0.02	0.01	0.10	0.01	0.03	0.02	0.01

* at 5% level of significance, ** at 1% level of significance

Table 4.11: Proportional contribution to lines, testers and their interaction to total variance

Source	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
Due to lines	28.67	54.99	64.97	67.48	55.33	54.98	44.29	33.88	62.71	41.13	40.61	38.68	19.06
Due to testers	9.42	0.77	2.62	2.42	0.33	4.62	3.81	3.87	5.57	3.24	10.74	7.97	0.23
Due to line x testers	61.91	44.24	32.42	30.1	44.33	40.4	51.9	62.26	31.72	55.63	48.66	53.34	80.71

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, SF- Spikelet fertility, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Table 4.12: Analysis of variance of combining ability for quality traits

Source	df	H%	M%	HRR%	PL	PB	P L/B	BRL	BRW	B L/B	KL	KB	K L/B
Replication	1	2.508	5.676	7.791	0.003	0.009	0.010	0.000	0.000	0.000	0.041	0.038	0.139
Cross	31	143.453**	134.565**	298.633**	1.464**	0.104**	0.521**	1.194**	0.049**	0.329**	0.735**	0.120**	0.354**
line	7	166.833**	128.501**	160.247**	2.499**	0.124**	0.357**	1.458**	0.054**	0.346**	0.756**	0.043	0.168**
tester	3	172.317**	131.911**	561.915**	0.847**	0.016**	0.182**	0.226**	0.031**	0.063**	0.097**	0.161	0.444
line X Tester	21	131.536**	136.966**	307.149**	1.207**	0.110**	0.624**	1.245**	0.051**	0.361**	0.819**	0.140**	0.403*
Error	31	8.274	5.765	13.420	0.004	0.001	0.003	0.001	0.001	0.001	0.011	0.030	0.124
σ^2_{gca}		0.355	0.072	0.254	0.008	0.003	0.003	0.002	0.003	0.001	0.003	0.001	0.002
σ^2_{sca}		61.631	65.601	146.865	0.601	0.054	0.311	0.622	0.025	0.180	0.404	0.055	0.139
$\sigma^2_{gca}/\sigma^2_{sca}$		0.006	0.001	0.002	0.013	0.004	0.010	0.002	0.120	0.006	0.006	0.011	0.011

* at 5% level of significance, ** at 1% level of significance

Cont...

Source	df	ER	EI	ASV	GC	AC
Replication	1	0.003	2.049	0.250	0.640	0.757
Cross	31	0.081**	0.055**	6.129**	272.756**	46.959**
line	7	0.036**	0.040**	9.536**	404.400**	159.872**
tester	3	0.022**	0.014	0.500*	72.531**	10.218**
line X Tester	21	0.105**	0.066**	5.798**	257.478**	14.570**
Error	31	0.001	0.007	0.121	3.906	0.974
σ^2_{gca}		0.001	0.000	0.010	0.455	0.965
σ^2_{sca}		0.052	0.030	2.838	126.786	6.798
$\sigma^2_{gca}/\sigma^2_{sca}$		0.013	0.010	0.003	0.004	0.142

* at 5% level of significance, ** at 1% level of significance

Table 4.13: Proportional contribution to lines, testers and their interaction to total variance

Source	H%	M %	HR R%	PL	PB	P L/B	BR L	BR W	B L/B	KL	KB	K L/B	ER	EI	AS V	GC	AC
Due to lines	26.26	21.56	12.12	38.55	26.92	15.47	27.57	24.57	23.74	23.22	8.07	10.75	10.11	16.19	35.13	33.48	76.88
Due to testers	11.62	9.49	18.21	5.6	1.49	3.38	1.83	6.08	1.86	1.28	12.92	12.16	2.57	2.48	0.79	2.57	2.11
Due to line x testers	62.11	68.95	69.67	55.85	71.6	81.15	70.59	69.35	74.4	75.5	79.01	77.09	87.32	81.33	64.08	63.95	21.02

H%=hulling , M%=milling , HRR%=head rice recovery, PL=panicle length, PB=panicle breadth, PL/B=panicle length breadth ratio, BRL=brown rice length, BRW=brown rice width, KL=kernel length, KB=kernel breadth, KL/B=kernel length breadth ratio, ER=Elongation ratio, EI=Elongation index, ASV=Alkali spreading value, GC=Gel consistency, AC=Amylose content

:

4.3.3 General combining ability (GCA) and specific combining ability (SCA) effects

4.3.2.1 General combining ability (GCA) for yield traits

The breeders can utilize the good general combiner in specific breeding programme for obtaining desirable varieties. It provides information on the choice of parents in terms of expected performance of their progenies. High GCA effect are mostly due to additive gene effect or due to additive x additive interaction effects, hence it very important in maximization of genetic gain in rice. It is obvious that best cross combinations are not always found between high x high general combiners but may also occur in other types of parental combinations. Parents with highest gca effects will not necessarily generate top specific cross combinations as also reported by Ranganathan *et al.* (1973) and Rao *et al.* (1980). The good specific combinations for different traits involving good general combiners are expected to throw some useful transgressive segregants particularly for developing high yielding pure lines due to additive type of gene action. There are instances where low x low combiners produced the best combinations (Khalique *et al.*, 1977; Rahman *et al.*, 1981). General combining ability (GCA) effects for quantitative and quality traits are presented in table 4.14.

Days to 50% flowering

The estimates of GCA effect for days to fifty percent flowering showed negative and highly significant were the line Banspatri (-3.32 **), Ajam dhan (-2.44 **), NPT 6 (-3.32 **) and tester Indira Barani Dhan 1 (-1.01 **) and Indira Aerobic 1(-1.94 **). Hence, these genotypes considered as good general combiner for breeding early type in rice. The above findings are in general agreement with the findings of Montazeri *et al.* (2014) Satheeshkumar *et al.* (2016). On the contrary, positive and

highly significant were line RJR:II (4.98 **), Ganga kali (3.18 **) and tester IR 64 (0.68 **) and MTU 1010 (2.27 **)

Plant height (cm)

For plant height negative and highly significant GCA effect were found in line NPT 19 (-4.65 **), Bega hundi (-6.72 **). Hence, these genotypes considered as good for developing dwarf rice varieties. On the contrary, positive and highly significant GCA effect reported in line RJR:II (7.00 **) and NPT 6 (5.35 **). Similar findings were reported by Montazeri *et al.* (2014) and Devi *et al.* (2018),

Tillers per plant (No.)

For tillers per plant in result positive and highly significant GCA effect was found in line RJR:II (4.13 **), Banspatri (2.50 **), Ganga kali (1.63 *) and Ajam dhan (2.81 **), indicated as the best general combiner for maximum tillers. Whereas, negative and highly significant GCA effect was in line Safed Lalak (-2.44 **), NPT 19 (-5.25 **) and NPT 6 (-4.78 **).

Effective tillers per plant (No.)

For effective tillers per plant positive and highly significant GCA effect was found in parental line RJR:II (4.01 **), Banspatri (2.04 **), Ganga kali (1.51 *) and Ajam dhan (2.14 **), indicated as the best general combiner for the trait. The above findings are in general agreement with the findings of Satheeshkumar *et al.* (2016) and

Table 4.14: Estimates of general combining ability (GCA) effects for yield and yield traits

Parent	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
Line													
RJR:II	4.98 **	7.00 **	4.13 **	4.01 **	-1.83 **	0.86	-6.22 **	-8.63 **	1.36	0.07 **	-1.20	7.64 **	-12.43 **
Banspatri	-3.32 **	2.38	2.50 **	2.04 **	-1.89 **	0.39	15.79 **	15.76 **	0.91	0.04	-0.59	-4.86 **	6.83 **
Ganga kali	3.18 **	0.23	1.63 *	1.51 *	0.23	2.16 **	5.12 **	3.46	1.17	-0.17 **	5.02 **	9.16 **	1.43
Ajam dhan	-2.44 **	-1.87	2.81 **	3.14 **	2.53 **	0.81	-6.06 **	-8.86 **	1.37	-0.14 **	4.22 **	7.20 **	-3.08
Safed Lalak	0.56	-1.72	-2.44 **	-2.33 **	0.73	-0.63	26.30 **	22.74 **	2.94 **	0.29 **	-2.96 **	-5.71 **	1.50
NPT 19	0.06	-4.65 **	-5.25 **	-5.24 **	4.56 **	-0.38	-21.58 **	-17.77 **	-2.87 **	-0.06 **	-4.36 **	-7.37 **	-0.66
NPT 6	-3.32 **	5.35 **	-4.78 **	-4.64 **	1.58 *	0.82	-32.44 **	-23.84 **	-7.07 **	0.27 **	-4.78 **	-8.38 **	0.94
Bega hundi	0.31	-6.72 **	1.41	1.51 *	-5.91 **	-4.03 **	19.09 **	17.14 **	2.18 **	-0.30 **	4.65 **	2.33 *	5.48 **
SE (±)	0.29	1.44	0.78	0.66	0.62	0.47	1.78	2.10	0.76	0.02	0.75	0.959	1.6709
Tester													
Indira Barani Dhan 1	-1.01 **	-0.04	-0.03	-0.16	-0.05	-0.45	4.26 **	2.12	1.56 **	-0.06 **	2.66 **	3.57 **	-0.70
Indira Aerobic -1	-1.94 **	0.16	0.08	0.12	0.22	0.84 *	-1.77	-1.65	-0.38	0.02	0.69	1.05	0.94
IR-64	0.68 **	0.67	0.94	0.90	-0.36	-0.10	-8.37 **	-7.75 **	-0.88	0.08 **	-0.62	0.40	-0.36
MTU 1010	2.27 **	-0.79	-0.98	-0.86	0.19	-0.29	5.88 **	7.28 **	-0.31	-0.04 **	-2.73 **	-5.02 **	0.11
SE (±)	0.20	1.02	0.55	0.47	0.44	0.33	1.26	1.48	0.54	0.01	0.53	0.6781	1.1815

* at 5% level of significance, ** at 1% level of significance

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, SF- Spikelet fertility, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Table 4.15: Estimates of specific combining ability (SCA) effects for yield and yield traits

S. No.	Crosses	DFP	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
1	RJR:II X Indir Barani Dhan 1	-8.04 **	-10.66 **	-2.28	-1.62	-3.52 **	0.53	-9.43 *	-10.91 *	0.38	-0.04	-1.67	2.79	2.79
2	RJR:II X Indira Aerobic 1	-5.11 **	4.83	2.86	1.85	3.89 **	-1.76	-1.74	-3.89	1.39	0.25 **	0.53	17.44 **	17.44 **
3	RJR:II X IR-64	10.77 **	5.70	-2.50	-2.18	0.05	1.29	21.46 **	23.96 **	-0.36	0.12 **	5.26 **	-12.33	-12.33 **
													**	
4	RJR:II X MTU 1010	2.38 **	0.13	1.92	1.96	-0.41	-0.06	-10.29 **	-9.17 *	-1.41	-0.34 **	-4.12 **	-7.90 **	-7.90 **
5	Banspatri X Indir Barani Dhan 1	-0.24	0.22	3.59 *	2.72 *	0.08	1.11	9.66 **	10.81 *	-0.67	0.38 **	-1.39	-1.86	-1.86
6	Banspatri X Indira Aerobic 1	0.19	6.63 *	-1.77	-1.56	-4.46 **	2.01 *	-24.56 **	-25.77 **	-0.16	0.04	-0.21	-1.91	-1.91
7	Banspatri X IR-64	-7.93 **	-3.45	-4.38 **	-4.21 **	0.14	-2.42	-3.56	-6.73	1.78	-0.07	-2.97	0.19	0.19
							*							
8	Banspatri XMTU 1010	7.98 **	-3.40	2.55	3.05 *	4.24 **	-0.70	18.45 **	21.69 **	-0.95	-0.36 **	4.57 **	3.58	3.58
9	Ganga kali X Indir Barani Dhan 1	6.76 **	7.82 **	-0.28	0.00	-2.08	-1.40	-19.02 **	-17.04 **	-1.92	-0.35 **	-8.34 **	-13.07	-13.07 **
													**	
10	Ganga kali X Indira Aerobic	-0.81	-1.56	-3.14 *	-2.53	-2.96 *	1.02	54.31 **	54.47 **	1.84	-0.19 **	6.80 **	-4.93 *	-4.93 *
11	Ganga kali X IR-64	-1.93 **	-2.49	6.63 **	6.19 **	6.99 **	-0.33	-11.29 **	-9.62 *	-1.10	0.02	2.97	27.51 **	27.51 **
12	Ganga kali XMTU 1010	-4.02 **	-3.78	-3.20 *	-3.67 **	-1.94	0.71	-23.99 **	-27.81 **	1.17	0.52 **	-1.44	-9.51 **	-9.51 **
13	Ajam dhan X Indir Barani Dhan 1	-0.12	-0.26	3.53 *	3.50 *	-2.16	-0.02	-19.24 **	-16.97 **	-2.14	0.25 **	7.64 **	12.65 **	12.65 **
14	Ajam dhan X Indira Aerobic	-0.68	-3.92	0.92	0.72	1.28	-1.60	-15.66 **	-13.55 **	-1.59	-0.01	-0.93	-5.02 *	-5.02 *
15	Ajam dhan X IR-64	0.69	2.88	-2.94	-2.56	0.05	0.54	8.74 *	7.85	1.24	-0.04	-4.99 **	-6.51 **	-6.51 **
16	Ajam dhan XMTU 1010	0.11	1.30	-1.52	-1.67	0.83	1.07	26.15 **	22.67 **	2.49	-0.20 **	-1.73	-1.13	-1.13
17	Safed Lalak X Indir Barani Dhan 1	-0.62	3.66	-1.22	-1.28	3.71 **	-1.11	-1.65	-2.22	-0.18	-0.04	-3.69 *	-6.33 **	-6.33 **
18	Safed Lalak X Indira Aerobic 1	-2.68 **	-1.28	1.67	1.94	-1.26	-0.47	-23.17 **	-24.30 **	0.24	-0.29 **	-2.69	4.24 *	4.24 *
19	Safed Lalak X IR-64	4.19 **	1.73	1.56	1.29	-2.87 *	0.63	17.58 **	19.45 **	-0.07	0.09 *	4.37 **	-0.26	-0.26
20	Safed Lalak XMTU 1010	-0.89	-4.11	-2.02	-1.95	0.42	0.95	7.24 *	7.07	0.01	0.24 **	2.01	2.36	2.36

DFP-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, SF- Spikelet fertility, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Conti...

S. No	Crosses	DFF	PH	TTP	ETP	FLA	PL	FGP	TGP	SF	TW	GYP	BYP	HI
21	NPT 19 X Indir													
	Barani Dhan 1	-2.12 **	0.32	-1.28	-1	-0.22	1.61	-5.17	-11.71 **	3.54 *	0.22 **	0.2	0.69	0.69
22	NPT 19 X Indira													
	Aerobic 1	7.82 **	-0.24	0.86	0.6	3.76 **	0.73	-4.89	-4.44	-0.66	0.26 **	-1.09	-2.92	-2.92
23	NPT 19 X IR-64	-2.81 **	-1.8	1.13	0.69	-2.25	-0.87	6.76	4.96	1.27	-0.24 **	-2.86	-3.37	-3.37
24	NPT 19 XMTU 1010	-2.89 **	1.72	-0.7	-0.29	-1.29	-1.47	3.31	11.18 *	-4.14 **	-0.24 **	3.76 *	5.60 **	5.60 **
25	NPT 6 X Indir Barani													
	Dhan 1	1.26 *	-1.43	-2.38	-2.34	1.56	-3.97 **	8.14 *	1.36	4.93 **	-0.18 **	-3.85 *	-2.59	-2.59
26	NPT 6 X Indira													
	Aerobic 1	0.19	-6.48 *	0.77	1	-0.26	0.71	-14.48 **	-13.23 **	-1.63	0.04	-0.14	-0.70	-0.70
27	NPT 6 X IR-64	-2.43 **	0.11	0.03	0.1	2.2	2.06 *	-14.98 **	-8.73 *	-5.79 **	0.13 **	0.88	-3.39	-3.39
28	NPT 6 X MTU 1010	0.98	7.81 **	1.58	1.24	-3.51 **	1.2	21.33 **	20.59 **	2.49	0.01	3.11 *	6.68 **	6.68 **
29	Bega hundi X Indira													
	Barani Dhan 1	3.13 **	0.33	0.31	0	2.64 *	3.24 **	36.71 **	46.68 **	-3.94 *	-0.25 **	11.08 **	7.73 **	7.73 **
30	Bega hundi X Indira													
	Aerobic 1	1.07	2.02	-2.17	-2.03	0	-0.65	30.19 **	30.70 **	0.57	-0.11 *	-2.28	-6.20 **	-6.20 **
31	Bega hundi X IR-64	-0.56	-2.68	0.47	0.69	-4.31 **	-0.9	-24.71 **	-31.15 **	3.03	-0.02	-2.65	-1.83	-1.83
32	Bega hundi XMTU													
	1010	-3.64 **	0.33	1.39	1.33	1.67	-1.69	-42.20 **	-46.23 **	0.34	0.37 **	-6.15 **	0.31	0.31
	SE (±)	0.57	2.87	1.55	1.32	1.23	0.94	3.56	4.19	1.51	0.04	1.49	1.918	3.3417

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP-Total grain per panicle, SF- Spikelet fertility, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Devi *et al.* (2018), Whereas, negative and highly significant GCA effect was in parental line Safed Lalak (-2.33 **), NPT 19 (-5.24 **) and NPT 6 (-4.64 **).

Flag leaf area (cm²)

For flag leaf area positive and highly significant GCA effect was found in parental line Ajam dhan (2.53 **), NPT 19 (4.56 **) and significant in NPT 6 (1.58 *), indicated that these genotype had longer and wider leaves than the others and could be used as good combiner for increasing flag leaf area in crossing program. Whereas, negative and highly significant GCA effect was in parental line RJR:II (-1.83 **), Banspatri (-1.89 **) and Bega hundi (-5.91**).

Panicle length (cm)

For panicle length positive and highly significant GCA effect was found in parental line Ganga kali (2.16 **) and in tester Indira Aerobic 1 (0.84 *), indicated that these genotype used as good combiner for long panicle. Similar findings were reported by Montazeri *et al.* (2014). Whereas, negative and highly significant GCA effect was in parental line Bega hundi (-4.03**).

Filled grains per panicle (No.)

For filled grains per panicle positive and highly significant GCA effect was found in parental line Safed Lalak (26.30**), Bega hundi (19.09**) and Banspatri (15.79), indicated as the best general combiner for the trait. Whereas, negative and highly significant GCA effect was in parental line NPT 6 (-32.44**) and NPT 19 (-21.58 **). Similar findings were reported by Satheeshkumar *et al.* (2016)

Total grains per panicle (No.)

For total grains per panicle positive and highly significant GCA effect was found in parental line Safed Lalak (22.74**), Banspatri (15.76**) and Ajam dhan (22.71**), Bega hundi (17.14**) and tester MTU 1010 (7.28**), indicated as the best

general combiner for the trait. Whereas, negative and highly significant GCA effect was in parental line RJR:II (-8.63 **), Ajam dhan (-8.86 **), NPT 19 (-17.77**), NPT 6 (-23.84 **) and in tester IR 64 (-7.75**).

Spikelet fertility (%)

For spikelet fertility (%) positive and highly significant GCA effect was found in parental line Safed Lalak (2.94**), Bega hundi (2.18**) and tester Indir Barani Dhan 1 (1.56**), indicated as the best general combiner for the trait. Similar findings were reported by Thorat and Kunkerkar (2017). Whereas, negative and highly significant GCA effect was in parental line NPT 19 (-2.87**) and NPT 6 (-7.07**).

100 grain weight (g)

For 100 grain weight positive and highly significant GCA effect was found in parental line V/E 1644 (0.07**), Safed Lalak (0.29**), NPT 6 (0.27**) and tester IR 64 (0.08**), indicated as the best general combiner for the trait. The results are in accordance to Saravanan *et al.* (2008), Devi *et al.* (2018). Whereas, negative and highly significant GCA effect was in parental line Ganga kali (-0.17**), Ajam dhan (-0.14**), NPT 19 (-0.06**), Bega hundi (-0.30**) and in tester Indir Barani Dhan 1 (0.06**), MTU 1010 (-0.04**).

Grain yield per plant (g)

For grain yield per plant positive and highly significant GCA effect was found in parental line Ganga kali (5.02**), Ajam dhan (4.22**), Bega hundi (4.65**) and tester Indir Barani Dhan 1 (2.66**), indicated these genotypes considered as good parental combiner in crosses for increasing grain yield per plant. Whereas, negative and highly significant GCA effect was found in parental line Safed Lalak (-2.96**), NPT 19 (-4.36**), NPT 6 (-4.78**) and in tester MTU 1010 (-2.73**). These genotypes seems to be poor parental combiner in crosses. Present findings are in line with Kolom *et al.* (2014), Devi and Lal (2015) and Sreelakshmi and Babu (2018).

Biological yield per plant (g)

For biological yield per plant positive and highly significant GCA effect was found in parental line RJR:II (7.64**), Ganga kali (9.16**), Ajam dhan (7.20**) and significant in Bega hundi (2.33*) and tester Indir Barani Dhan 1 (3.57**), indicated as the good parental combiner in crosses. Whereas, negative and highly significant GCA effect was in parental line Banspatri (-4.86**), Safed Lalak (-5.71**), NPT 19 (-7.37**), NPT 6 (-8.38**) and in tester MTU 1010 (-5.02**).

Harvest index (%)

For harvest index per plant positive and highly significant GCA effect was found in parental line Banspatri (6.83**) and Bega hundi (2.33**), indicated as the good parental combiner in crosses. Whereas, negative and highly significant GCA effect was in parental line RJR:II (-12.43**). The above findings are in general agreement with the findings of Satheeshkumar *et al.* (2016).

4.3.2.3 Specific combining ability (SCA) effect for yield and yield contributing traits

Specific combining ability in plants is governed by dominant gene variances which is prerequisite for exploitation of heterosis. Specific combining ability (SCA) helps in identification of good hybrid combinations which may ultimately lead to the development of hybrids (Saleem *et al.*, 2008).

4.3.2.3.1 Quantitative traits

The specific combining ability effects of thirty two crosses for yield and yield contributing traits are presented in Table 4.15.

Days to 50% flowering

The specific combining ability effects for days to 50% flowering exhibited negative and highly significant in crosses RJR:II X Indira Barani Dhan 1 (-8.04**),

RJR:II X Indira Aerobic 1 (-5.11**), Banspatri X IR 64 (-7.93**), Ganga kali X IR 64 (-1.93**), Ganga kali X MTU 1010 (-4.02**), Safed Lalak X Indira Aerobic 1 (-2.68**), NPT 19 X Indira Barani Dhan 1 (-2.12**), NPT 19 X IR 64 (-2.81**), NPT 19 X MTU 1010 (-2.89**), NPT 6 X IR 64 (-2.43**) Bega hundi X MTU 1010 (-3.64**), indicated that these crosses combination were the best combination for early flowering. The positive and highly significant or significant SCA effects in crosses RJR:II X IR 64 (10.77**), RJR:II X MTU 1010 (2.38**), Banspatri X MTU 1010 (7.98**), Ganga kali X Indira Barani Dhan 1 (6.76**), Safed Lalak X IR 64 (4.19**), NPT 19 X Indira Aerobic 1 (7.82**), NPT 6 X Indira Barani Dhan 1 (1.26*), Bega hundi X INDIRA Barani Dhan 1 (3.13**), indicated that these crosses were undesirable type.

Plant height (cm)

For plant height SCA effects exhibited negative and highly significant or significant in crosses RJR:II X Indira Barani Dhan 1 (-10.66**), NPT 6 X Indira Aerobic 1 (-6.48*), indicated that these crosses may be useful for exploitation of heterosis due to their desirable stature. Similar finding were reported by Montazeri *et al.* (2014) and Kolom *et al.* (2014).

The positive and highly significant or significant SCA effects exhibited in crosses Banspatri X Indira Aerobic 1 (6.63*), Ganga kali X Indira Barani Dhan 1 (7.82**), NPT 6 X MTU 1010 (7.81**).

Tillers per plant (No.)

For tillers per plant positive and highly significant or significant SCA effects was recorded in crosses Banspatri X Indira Barani Dhan 1 (3.59*), Ganga kali X IR 64 (6.63**) and Ajam dhan X Indira Barani Dhan 1 (3.53*), indicated that these were best crosses with increasing total tillers per plant.

Effective tillers per plant (No.)

For effective tillers per plant positive and highly significant or significant SCA effects was recorded in crosses Banspatri X Indira Barani Dhan 1 (2.72*), Banspatri X MTU 1010 (3.05*), Ganga kali X IR 64 (6.19**) and Ajam dhan X Indira Barani Dhan 1 (3.53*), indicated that these were best crosses with increasing effective tillers per plant. Similar finding were reported by Montazeri *et al.* (2014).

Flag leaf area (cm²)

For flag leaf area positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Aerobic 1 (3.89**), Banspatri X MTU 1010 (4.24**), Ganga kali X IR 64 (6.99**), Safed Lalak X Indira Barani Dhan 1 (3.71**), NPT 19 X INDIRA AEROBIC 1 (3.76**), Bega hundi X Indira Barani Dhan 1 (2.64*), indicated that these crosses can be utilize for improving flag leaf area. The negative and highly significant or significant SCA effects exhibited in crosses RJR:II X Indira Barani Dhan 1 (-3.52**), Banspatri X Indira Aerobic 1 (-4.46**), Ganga kali X Indira Aerobic 1 (-2.96*), Safed Lalak X IR 64 (-2.87*), NPT 6 X MTU 1010 (-3.51**) and Bega hundi X IR 64 (-4.31**).

Panicle length (cm)

For panicle length positive and highly significant or significant SCA effects was recorded in crosses Banspatri X Indira Aerobic 1 (2.01 *), NPT 6 X IR 64 (2.06 *) and Bega hundi X Indira Barani Dhan 1 (3.24 **). Similar finding were reported by Montazeri *et al.* (2014). The negative and highly significant or significant SCA effects exhibited in crosses Banspatri X IR 64 (-2.42 *) and NPT 6 X Indira Barani Dhan 1 (-3.97 **).

Filled grains per panicle (No.)

For filled grains per panicle positive and highly significant or significant SCA effects was recorded in crosses RJR:II X IR 64 (21.46 **), Banspatri X Indira Barani Dhan 1 (9.66 **), Banspatri X MTU 1010 (18.45 **), Ganga kali X Indira Aerobic 1

(54.31 **), Ajam dhan X IR 64 (8.74 *), Ajam dhan X MTU 1010 (26.15 **), Safed Lalak X IR 64 (17.58 **), Safed Lalak X MTU 1010 (7.24 *), NPT 6 X Indira Barani Dhan 1 (8.14 *), (NPT 6) X MTU 1010 (21.33 **), Bega hundi X Indira Barani Dhan 1 (36.71 **) and Bega hundi X Indira Aerobic 1 (30.19 **). Similar findings were reported by Kolom *et al.* (2014) and Sultan *et al.* (2015).

Total grains per panicle (No.)

For total grains per panicle positive and highly significant or significant SCA effects was recorded in crosses RJR:II X IR 64 (23.96**), Banspatri X Indira Barani Dhan 1 (10.81 **), Banspatri X MTU 1010 (21.69 **), Ganga kali X Indira Aerobic 1 (54.47**), Ajam dhan X MTU 1010 (22.67 **), Safed Lalak X IR 64 (19.45 **), Safed Lalak X MTU 1010 (7.24 *), NPT 19 X MTU 1010 (11.18 *), NPT 6 X MTU 1010 (20.59 **), Bega hundi X Indira Barani Dhan 1 (46.68 **) and Bega hundi X Indira Aerobic 1 (30.70**).

Spikelet fertility per panicle (%)

For spikelet fertility positive and highly significant or significant SCA effects was recorded in crosses NPT 19 X Indira Barani Dhan 1 (3.54 *) and NPT 6 X Indira Barani Dhan 1 (4.93 **). The negative and highly significant or significant SCA effects exhibited in crosses NPT 19 X MTU 1010 (-4.14 **), NPT 6 X IR 64 (-5.79 **) and Bega hundi X Indira Barani Dhan 1 (-3.94 *).

100 grain weight (g)

For 100 grain weight positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Aerobic 1 (0.25 **), RJR:II X IR 64 (0.12 **), Banspatri X Indira Barani Dhan 1 (0.38 **), Ganga kali X MTU 1010 (0.52 **), Ajam dhan X Indira Barani Dhan 1 (0.25 **), Safed Lalak X IR 64 (0.09 *), Safed Lalak X MTU 1010 (0.24 **), NPT 19 X Indira Barani Dhan 1 (0.22 **), NPT 19 X

Indira Aerobic 1 (0.26 **), NPT 6 X IR 64 (0.13 **) and Bega hundi XMTU 1010 (0.37 **). Similar findings were reported by Sultan *et al.* (2015) and Saravanan *et al.* (2018).

Grain yield per plant (g)

For grain yield per plant positive and highly significant or significant SCA effects was recorded in crosses RJR:II X IR 64 (5.26 **), Banspatri X MTU 1010 (4.57 **), Ganga kali X Indira Aerobic 1 (6.80 **), Ajam dhan X Indira Barani Dhan 1 (7.64 **), Safed Lalak X IR 64 (4.37 **), NPT 19 X MTU 1010 (3.76 *), NPT 6 X MTU 1010 (3.11 *) and Bega hundi X Indira Barani Dhan 1 (11.08 **), indicated that these crosses can be utilize for increasing grain yield per plant. Similar findings were reported by Sultan *et al.* (2015), Choudhary *et al.* (2017), Sreelakshmi and Babu (2018) and Saravanan *et al.* (2018). The negative and highly significant or significant SCA effects exhibited in crosses RJR:II X MTU 1010 (-4.12 **), Ganga kali X Indira Barani Dhan 1 (-8.34 **), Ajam dhan X IR 64 (-4.99 **), NPT 6 X INDIRA Barani Dhan 1 (-3.85 *) and Bega hundi XMTU 1010 (-6.15 **).

Biological yield per plant (g)

For biological yield per plant positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Aerobic 1 (17.44 **), Ganga kali X IR 64 (27.51 **), Ajam dhan X Indira Barani Dhan 1 (12.65 **), Safed Lalak X Indira Aerobic 1 (4.24 *), NPT 19 X MTU 1010 (5.60 **), NPT 6 X MTU 1010 (6.68 **), Bega hundi X Indira Barani Dhan 1 (7.73 **). The negative and highly significant or significant SCA effects exhibited in crosses RJR:II X IR 64 (-12.33 **), Ganga kali X Indira Barani Dhan 1 (-13.07 **), Ganga kali X Indira Aerobic 1 (-4.93 *), Ajam dhan X Indira Aerobic 1 (-5.02 *), Ajam dhan X IR 64 (-6.51 **), Safed Lalak X Indira Barani Dhan 1 (-6.33 **) and Bega hundi X Indira Aerobic 1 (-6.20 **).

Harvest index (%)

For harvest index positive and highly significant or significant SCA effects was recorded in crosses RJR:II X IR 64 (31.74 **), Banspatri X MTU 1010 (9.82 **), Ganga kali X Indira Aerobic 1 (19.05 **), Ganga kali X MTU 1010 (11.38 **), Safed Lalak X IR 64 (12.16 **), NPT 6 X IR 64 (10.28 **), Bega hundi X Indira Barani Dhan 1 (13.43 **) and Bega hundi X Indira Aerobic 1 (7.13 *). The negative and highly significant or significant SCA effects exhibited in crosses RJR:II X Indira Barani Dhan 1 (-7.88 *), RJR:II X Indira Aerobic 1 (-18.27 **), Banspatri X IR 64 (-13.06 **), Ganga kali X IR 64 (-26.38 **), Safed Lalak X Indira Aerobic 1 (-18.09 **) and Bega hundi X MTU 1010 (-15.98 **).

Quality traits

The general combining ability effects of thirty two crosses for quality traits are presented in Table 4.16.

Hulling (%)

For hulling percent positive and highly significant GCA effect was found in parental line Safed Lalak (4.48**), Bega hundi (4.20**) and NPT 6 (4.05**) and in tester IR 64 (4.59**), indicated as the good parental combiner in crosses.

Milling (%)

For milling percent positive and highly significant GCA effect was found in parental line RJR:II (4.48**), NPT 6 (3.92**) and Bega hundi (2.28**) and in tester IR 64 (3.71**), indicated as the good parental combiner in crosses. Similar findings were reported by Rani *et al.* (2015).

Table 4.16: Estimates of general combining ability (GCA) effects of parental lines for quality traits

S. no	Parent	H%	M%	HRR%	PL	PB	P L/B	BRL	BRW	B L/B	KL	KB	K L/B
	Line												
1	RJR:II	-0.34	5.29 **	4.58 **	-0.92 **	-0.00	-0.32 **	-0.20 **	0.05 **	-0.15 **	-0.19 **	-0.05	0.13
2	Banspatri	-8.51 **	-6.44 **	-5.21 **	-0.17 **	-0.02	0.06 **	-0.04 **	-0.15 **	0.17 **	-0.10 **	0.04	-0.12
3	Ganga kali	-4.08 **	-3.79 **	-6.09 **	-0.00	-0.22 **	0.27 **	-0.55 **	0.07 **	-0.31 **	-0.19 **	0.05	-0.16
4	Ajam dhan	1.29	-2.65 **	-1.71	0.52 **	0.01	0.15 **	0.40 **	0.12 **	0.02	0.33 **	0.10	-0.01
5	Safed Lalak	4.48 **	0.83	5.80 **	0.05 *	-0.08 **	0.13 **	-0.18 **	-0.03 **	-0.01	-0.04	0.00	-0.03
6	NPT 19	-1.09	0.56	2.86 *	-0.02	0.16 **	-0.22 **	-0.17 **	0.01	-0.10 **	-0.36 **	0.12 *	0.05
7	NPT 6	4.05 **	3.92 **	-2.38	-0.40 **	-0.01	-0.17 **	-0.09 **	-0.04 **	-0.01	-0.05	0.06	-0.13
8	Bega hundi	4.20 **	2.28 **	2.15	0.94 **	0.16 **	0.12 **	0.84 **	-0.04 **	0.39 **	0.58 **	-0.06	0.27 *
	SE(±)	1.017	0.84	1.29	0.02	0.01	0.01	0.01	0.009	0.01	0.03	0.06	0.124
	Testers												
1	Indira Barani Dhan 1	-2.21 **	-1.60 *	-1.80	0.31 **	-0.03 **	0.14 **	-0.02 *	0.02 **	-0.04 **	0.00	-0.04	0.06
2	Indira Aerobic 1	-2.52 **	-2.82 **	-7.32 **	-0.02	-0.01	0.03 *	0.17 **	0.03 **	0.05 **	-0.05	0.12 **	-0.17
3	IR-64	4.59 **	3.71 **	6.42 **	-0.06 **	0.04 **	-0.08 **	-0.09 **	0.02 *	-0.07 **	-0.06 *	0.03	-0.09
4	MTU 1010	0.15	0.70	2.71 **	-0.24 **	0.00	-0.08 **	-0.06 **	-0.07 **	0.05 **	0.11 **	-0.11 *	0.20 *
	SE(±)	0.72	0.60	0.91	0.02	0.01	0.01	0.07	0.01	0.01	0.03	0.04	0.09

Conti.....

S. no	Parent	ER	EI	ASV	GC	AC
	Line					
1	RJR:II	-0.02 *	-0.00	0.13	4.26 **	7.45 **
2	Banspatri	-0.09 **	-0.07 *	-0.50 **	5.07 **	5.11 **
3	Ganga kali	-0.03 **	-0.01	-1.38 **	-10.97 **	1.09 **
4	Ajam dhan	0.11 **	0.09 **	1.63 **	4.10 **	-5.68 **
5	Safed Lalak	-0.00	0.01	1.50 **	-8.32 **	-0.12
6	NPT 19	0.07 **	0.10 **	-0.13	6.66 **	-1.05 **
7	NPT 6	-0.06 **	-0.10 **	-1.13 **	-5.84 **	-2.83 **
8	Bega hundi	0.03 **	-0.02	-0.13	5.03 **	-3.97 **
	SE(±)	0.010	0.028	0.123	0.698	0.349
	Testers					
1	Indira Barani Dhan 1	-0.03 **	-0.03	0.13	1.05 *	-1.05 **
2	Indira Aerobic 1	0.03 **	0.02	1.13 **	0.67	0.15
3	IR-64	-0.03 **	-0.02	-0.25 **	-3.16 **	0.00
4	MTU 1010	0.04 **	0.03	0.00	1.43 **	0.90 **
	SE(±)	0.01	0.02	0.08	0.49	0.25

H%=hulling , M%=milling , HRR%=head rice recovery, PL=panicle length, PB=panicle breadth, PL/B=panicle length breadth ratio, BRL=brown rice length, BRW=brown rice width, KL=kernel length, KB=kernel breadth, KL/B=kernel length breadth ratio, ER=Elongation ratio, EI=Elongation index, ASV=Alkali spreading value, GC=Gel consistency, AC=Amylose content

Head rice recovery (%)

For head rice recovery positive and highly significant GCA effect was found in parental line RJR:II (4.58**), Safed Lalak (5.80**) and NPT-19 (2.86**) and in tester IR 64 (6.42**) and MTU 1010 (2.71%), indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line Banspatri (-6.09**), and in tester Indira Aerobic-1 (-7.32**).

Paddy length (mm)

For paddy length positive and highly significant GCA effect was found in parental line Ajam dhan (0.52**) and in tester Indira Barani Dhan-1 (0.31**) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line RJR:II (-0.92**), Banspatri (-0.17**) and NPT 6 (-0.40**) and in tester IR 64 (-0.06%) and MTU 1010 (0.24**).

Paddy breadth (mm)

For paddy breadth positive and highly significant GCA effect was found in parental line NPT-19 (0.16**) and Bega hundi (0.16**) and in tester IR 64 (0.04**) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line Ganga kali (-0.22**), Safed Lalak (-0.08**) and in tester Indira Barani Dhan-1 (-0.03%).

Paddy L/B ratio (mm)

For paddy L/B ratio positive and highly significant GCA effect was found in parental line Banspatri (0.06**), Ganga Kali (0.27**), Ajam Dhan (0.15**), Safed Lalak (0.13**), Bega Hundi (0.22**) and in tester Indira Barani Dhan-1 (0.14**) and Indir Aerobic-1 (0.03*), indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line RJR:II (-0.32**), NPT-19 (-0.22**), NPT 6 (-0.17**) and in tester IR 64 (-0.08**) and MTU 1010 (0.08**).

Brown rice length (mm)

For brown rice length positive and highly significant GCA effect was found in parental line Ajam Dhan (0.40**), Bega hundi (0.84**) and in tester Indira Aerobic-1 (0.17*) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line RJR:II (-0.20**), Ganga kali (-0.55**) and in tester IR 64 (-0.09**) and MTU 1010 (-0.06**).

Brown rice width (mm)

For brown rice width positive and highly significant GCA effect was found in parental line RJR:II (0.05**), Ganga kali (0.07**) Ajam Dhan (0.12**) and in tester Indira Barani Dhan-1 (0.02**), Indira Aerobic-1 (0.03**) and IR 64 (0.02*) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line Banspatri (-0.15**), Safed Lalak (-0.03**) and in tester MTU 1010 (-0.07**).

Brown rice L/B ratio (mm)

For brown rice L/B ratio positive and highly significant GCA effect was found in parental line Banspatri (0.17**), BEGA HUNDI (0.39**) and in tester Indira Aerobic-1 (0.05**) and MTU 1010 (0.05**) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line RJR:II (-0.15**), Ganga kali (-0.31**), NPT-19 (-0.10**) and in tester Indira Barani Dhan-1 (-0.04**) and IR 64 (0.07**).

Kernel length (mm)

For kernel length positive and highly significant GCA effect was found in parental line Ajam Dhan (0.33**), Bega hundi (0.58**) and in tester MTU 1010

(0.11**) indicated as the good parental combiner in crosses. Similar findings were reported by Rani *et al.* (2015), and Saravanan *et al.* (2018).

Kernel breadth (mm)

For kernel breadth positive and highly significant GCA effect was found in parental line NPT-19 (0.12**) and in tester Indira Aerobic-1 (0.12**) indicated as the good parental combiner in crosses. Similar findings were reported by Saravanan *et al.* (2018).

Kernel L/B ratio (mm)

For kernel L/B ratio positive and highly significant GCA effect was found in parental line Bega hundi (0.27**) and in tester MTU 1010 (0.20*) indicated as the good parental combiner in crosses. Similar findings were reported by Rani *et al.* (2015) and Saravanan *et al.* (2018).

Elongation ratio

For elongation ratio positive and highly significant GCA effect was found in parental line Ajam Dhan (0.11**), NPT-19 (0.07**), Bega hundi (0.03*) and in tester Indira Aerobic-1 (0.03**) and MTU 1010 (0.04**) indicated as the good parental combiner in crosses.

Elongation index

For elongation index positive and highly significant GCA effect was found in parental line Ajam Dhan (0.09**) and NPT 19 (0.07**) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line NPT 6 (-0.10**)

Alkali spreading value

For alkali spreading value positive and highly significant GCA effect was found in parental line Ajam Dhan (1.63**), Safed Lalak (1.50**) and in tester Indira Aerobic-1 (1.13**) indicated as the good parental combiner in crosses. Similar findings were reported by Nayak *et al.* (2016). The negative and highly significant and significant GCA effect was found in parental line Ganga kali (-1.38**), NPT 6 (-1.13**) and in tester IR 64 (-0.25**).

Gel Consistency

For gel consistency positive and highly significant GCA effect was found in parental line RJR:II (4.26**), Banspatri (5.07**), Ajam Dhan (4.10**), NPT-19(6.66**), Bega hundi (5.03**) and in tester Indira Barani Dhan-1(1.05*) and MTU-1010 (1.43**) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line Ganga kali (-10.97**), Safed Lalak (-8.32**) NPT 6 (-5.84**) and in tester IR 64 (-3.16**).

Amylose content

For amylose content positive and highly significant GCA effect was found in parental line RJR:II (7.45**), Banspatri (5.11**), Ganga kali (1.09**) and in tester MTU-1010 (0.90**) indicated as the good parental combiner in crosses. The negative and highly significant and significant GCA effect was found in parental line Ajam dhan (-5.68**), NPT 19 (-1.05**) NPT 6 (-2.83**), Bega Hundi (-3.97**) and in tester Indira Barani Dhan 1 (-1.05**).

4.2.2.3 Specific combining ability (SCA) effect for quality traits

Specific combining ability (GCA) effects for quantitative and quality traits are presented in table 4.17.

Hulling (%)

For hulling percent positive and highly significant or significant SCA effects was recorded in crosses Banspatri X MTU 1010 (13.79**), Banspatri X IR 64 (9.93**), Ganga kali X IR 64 (4.60*), Safed Lalak X Indira Barani Dhan 1 (4.81**), RJR:II X Indira Barani Dhan 1 (4.69**), Safed Lalak X Indira Aerobic 1 (4.33*) and (NPT 6) X Indira Barani Dhan 1 (5.14*).

Milling (%)

For milling percent positive and highly significant or significant SCA effects was recorded in crosses Banspatri X IR 64 (11.93**), Ganga kali X Indira Aerobic 1 (17.63**), Safed Lalak X Indira Barani Dhan 1 (5.23*), NPT 6 X Indira Barani Dhan 1 (7.88**), NPT 6 X MTU 1010 (4.83**), RJR:II X Indira Barani Dhan 1 (5.00**) and Bega hundi X MTU 1010 (7.14**). Nayak *et al.* (2016)

Head rice recovery (%)

For head rice recovery percent positive and highly significant or significant SCA effects was recorded in crosses BANSPATRI X IR 64 (14.90**), Banspatri X MTU 1010 (7.95**), Ganga kali X Indira Aerobic 1 (8.41**), NPT 19 X Indira Aerobic 1 (7.20**), (NPT 6) X Indira Barani Dhan 1 (17.14**), RJR:II X Indira Barani Dhan 1 (6.16**), Ajam dhan X MTU 1010 (16.20**) and (NPT 6) X IR 64 (24.37**) The negative and highly significant or significant SCA effects exhibited in crosses Banspatri X Indira Barani Dhan 1 (-15.67**), NPT 19 X Indira Barani Dhan 1 (-13.44**), (NPT 6) X Indira Aerobic 1 (-10.33**), (NPT 6) X IR 64 (-24.37**).

Paddy length (mm)

For paddy length positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Barani Dhan 1 (0.98**), Safed Lalak X MTU 1010 (0.58**), NPT 19 X Indira Aerobic 1 (0.22**), Bega Hundi X Ir64 (0.21**).

Table 4.17: Estimates of specific combining ability (SCA) effects for quality traits

S. No.	Crosses	H%	M%	HRR%	PL	PB	P L/B	BRL	BRW	B L/B
1	RJR:II X Indir Barani Dhan 1	4.69 *	5.00 **	6.16 *	0.91 **	-0.28 **	0.72 **	0.90 **	-0.09 **	0.48 **
2	RJR:II X Indira Aerobic 1	-5.15 *	-4.13 *	-9.27 **	0.18 **	0.10 **	-0.11 **	-0.36 **	0.06 **	-0.22 **
3	RJR:II X IR-64	0.04	1.48	3.96	-0.22 **	-0.17 **	0.07	-0.03	0.08 **	-0.08 **
4	RJR:II X MTU 1010	0.42	-2.36	-0.85	-0.87 **	0.35 **	-0.67 **	-0.52 **	-0.04 *	-0.18 **
5	Banspatri X Indir Barani Dhan 1	-5.37 *	-0.84	-15.67 **	0.35 **	0.19 **	-0.21 **	0.04	0.12 **	-0.14 **
6	Banspatri X Indira Aerobic 1	-18.34 **	-17.22 **	-7.18 **	1.42 **	-0.61 **	1.53 **	2.07 **	-0.14 **	1.11 **
7	Banspatri X IR-64	9.93 **	11.93 **	14.90 **	-0.82 **	0.32 **	-0.72 **	-0.64 **	-0.13 **	-0.14 **
8	Banspatri XMTU 1010	13.79 **	6.13 **	7.95 **	-0.95 **	0.10 **	-0.60 **	-1.47 **	0.15 **	-0.83 **
9	Ganga kali X Indir Barani Dhan 1	-12.47 **	-9.15 **	1.23	-0.11 *	-0.01	0.00	0.05 *	0.05 *	-0.02
10	Ganga kali X Indira Aerobic	13.68 **	17.63 **	8.41 **	-1.73 **	-0.01	-0.72 **	-0.43 **	0.07 **	-0.26 **
11	Ganga kali X IR-64	4.60 *	-2.63	-3.41	1.30 **	-0.13 **	0.74 **	0.15 **	-0.10 **	0.17 **
12	Ganga kali XMTU 1010	-5.81 **	-5.85 **	-6.23 *	0.54 **	0.15 **	-0.02	0.23 **	-0.03	0.11 **
13	Ajam dhan X Indir Barani Dhan 1	0.57	-2.37	-0.70	-0.50 **	-0.11 **	-0.02	0.05 *	-0.15 **	0.19 **
14	Ajam dhan X Indira Aerobic	3.99	9.03 **	13.31 **	0.78 **	0.09 **	0.16 **	-0.06 **	-0.21 **	0.20 **
15	Ajam dhan X IR-64	-3.24	-2.30	3.58	-0.20 **	0.02	-0.09 *	-1.04 **	0.04 *	-0.44 **
16	Ajam dhan XMTU 1010	-1.32	-4.37 *	-16.20 **	-0.08	0.00	-0.05	1.05 **	0.31 **	0.05
17	Safed Lalak X Indir Barani Dhan 1	4.81 *	5.23 **	1.75	-0.43 **	0.05	-0.25 **	-0.52 **	0.16 **	-0.40 **
18	Safed Lalak X Indira Aerobic 1	4.33 *	2.79	5.13	-0.10 *	0.20 **	-0.34 **	-0.62 **	0.16 **	-0.48 **
19	Safed Lalak X IR-64	0.14	-4.99 **	-2.35	-0.00	0.16 **	-0.23 **	0.60 **	0.01	0.20 **
20	Safed Lalak XMTU 1010	-9.28 **	-3.03	-4.54	0.52 **	-0.41 **	0.82 **	0.54 **	-0.33 **	0.67 **
21	NPT 19 X Indir Barani Dhan 1	1.35	-4.51 *	-13.44 **	-0.06	-0.04	0.03	-0.33 **	-0.09 **	-0.03
22	NPT 19 X Indira Aerobic 1	-0.57	3.16	11.10 **	0.22 **	0.19 **	-0.14 **	-0.34 **	0.13 **	-0.29 **
23	NPT 19 X IR-64	0.66	3.84 *	7.20 **	-0.37 **	-0.10 **	-0.01	0.13 **	-0.05 **	0.12 **
24	NPT 19 XMTU 1010	-1.44	-2.49	-4.85	0.21 **	-0.04	0.12 **	0.54 **	0.01	0.20 **
25	NPT 6 X Indir Barani Dhan 1	5.14 *	7.88 **	17.14 **	-0.12 *	0.12 **	-0.18 **	-0.05 *	0.01	-0.03
26	NPT 6 X Indira Aerobic 1	0.38	-6.43 **	-10.33 **	-0.20 **	0.00	-0.10 **	0.13 **	-0.05 *	0.10 **
27	NPT 6 X IR-64	-8.00 **	-6.28 **	-24.37 **	-0.04	-0.02	0.01	0.18 **	-0.04	0.13 **
28	NPT 6 X MTU 1010	2.47	4.83 **	17.56 **	0.37 **	-0.11 **	0.27 **	-0.26 **	0.08 **	-0.20 **
29	Bega hundi X Indira Barani Dhan 1	1.29	-1.26	3.53	-0.04	0.08 **	-0.10 **	-0.14 **	-0.00	-0.05 *
30	Bega hundi X Indira Aerobic 1	1.68	-4.84 **	-11.19 **	-0.57 **	0.04	-0.27 **	-0.41 **	-0.03	-0.16 **
31	Bega hundi X IR-64	-4.13 *	-1.04	0.50	0.36 **	-0.08 **	0.23 **	0.65 **	0.19 **	0.03
32	Bega hundi XMTU 1010	1.16	7.14 **	7.16 **	0.25 **	-0.04	0.14 **	-0.10 **	-0.15 **	0.19 **
SE(±)		2.03	1.70	2.59	0.04	0.03	0.04	0.02	0.02	0.02

H%=hulling , M%=milling , HRR%=head rice recovery, PL=panicle length, PB=panicle breadth, PL/B=panicle length breadth ratio, BRL=brown rice length, BRW=brown rice width, KL=kernel length, KB=kernel breadth, KL/B=kernel length breadth ratio, ER=Elongation ratio, EI=Elongation index, ASV=Alkali spreading value, GC=Gel consistency, AC=Amylose content

Conti....

S. No.	Crosses	KL	KB	K L/B	ER	EI	ASV	GC	AC
1	RJR:II X Indir Barani Dhan 1	0.89 **	-0.02	0.22	-0.37 **	-0.30 **	3.25 **	5.35 **	0.72
2	RJR:II X Indira Aerobic 1	-0.27 **	0.39 **	-0.60 *	0.04	0.10	-0.75 **	5.73 **	-1.05
3	RJR:II X IR-64	-0.21 **	0.25 *	-0.48	-0.15 **	-0.07	-1.88 **	-7.24 **	-3.63 **
4	RJR:II X MTU 1010	-0.41 **	-0.62 **	0.86 **	0.48 **	0.27 **	-0.63 *	-3.83 **	3.96 **
5	Banspatri X Indir Barani Dhan 1	0.21 **	0.16	-0.10	-0.18 **	-0.14 *	-1.13 **	-10.32 **	2.67 **
6	Banspatri X Indira Aerobic 1	1.14 **	-0.28 *	0.82 **	-0.15 **	-0.12 *	-2.13 **	0.92	2.68 **
7	Banspatri X IR-64	-0.45 **	-0.01	-0.14	0.15 **	-0.00	-0.75 **	6.75 **	1.47 *
8	Banspatri XMTU 1010	-0.90 **	0.14	-0.58 *	0.18 **	0.27 **	4.00 **	2.65	-1.46 *
9	Ganga kali X Indir Barani Dhan 1	0.11	0.06	-0.04	-0.05 *	0.15**	-0.25	5.07 **	0.83
10	Ganga kali X Indira Aerobic	-0.27 **	0.06	-0.13	0.07 **	0.07	-0.25	-3.05 *	-0.21
11	Ganga kali X IR-64	0.34 **	-0.21	0.40	-0.06 **	-0.03	0.63 *	1.78	-0.83
12	Ganga kali XMTU 1010	-0.17 *	0.09	-0.22	0.04	0.02	-0.13	-3.81 **	0.21
13	Ajam dhan X Indir Barani Dhan 1	-0.03	0.03	-0.05	-0.02	-0.02	-0.25	1.51	-3.58 **
14	Ajam dhan X Indira Aerobic	0.09	-0.21	0.28	0.23 **	0.18 **	0.25	0.89	-0.92
15	Ajam dhan X IR-64	-0.98 **	-0.06	-0.30	0.25 **	0.18 **	0.13	3.53 *	2.86 **
16	Ajam dhan XMTU 1010	0.93 **	0.24	0.07	-0.46 **	-0.34 **	-0.13	3.13*	1.64 *
17	Safed Lalak X Indir Barani Dhan 1	-0.49 **	0.27 *	-0.51 *	0.03	0.05	-0.13	16.42 **	0.92
18	Safed Lalak X Indira Aerobic 1	-0.21 **	-0.05	-0.06	-0.05 *	-0.13 *	0.38	-13.60 **	2.97 **
19	Safed Lalak X IR-64	0.22 **	0.02	0.07	0.05 *	0.05	1.75 **	-20.37 **	0.10
20	Safed Lalak XMTU 1010	0.48 **	-0.24	0.49	-0.03	0.03	-2.00 **	17.54 **	-4.00 **
21	NPT 19 X Indir Barani Dhan 1	-0.67 **	-0.50 **	0.51 *	0.26 **	0.28 **	-0.50 *	1.95	-1.66 *
22	NPT 19 X Indira Aerobic 1	-0.49 **	0.26 *	-0.53 *	0.05 *	0.03	3.00 **	-2.67	3.80 **
23	NPT 19 X IR-64	0.54 **	-0.04	0.21	-0.07 **	-0.07	-1.13 **	1.16	1.53 *
24	NPT 19 XMTU 1010	0.62 **	0.28 *	-0.20	-0.24 **	-0.24 **	-1.38 **	-0.43	-3.68 **
25	NPT 6 X Indir Barani Dhan 1	0.17 *	0.05	-0.00	0.12 **	0.09	-0.50 *	-24.55 **	-1.17
26	NPT 6 X Indira Aerobic 1	0.27 **	-0.13	0.27	-0.20 **	-0.16 **	0.50 *	11.83 **	-1.49 *
27	NPT 6 X IR-64	-0.29 **	-0.01	-0.07	0.01	0.04	0.38	14.66 **	-0.87
28	NPT 6 X MTU 1010	-0.14	0.08	-0.19	0.06 **	0.04	-0.38	3.93**	3.53 **
29	Bega hundi X Indira Barani Dhan 1	-0.18 *	-0.05	-0.02	0.20 **	0.10	-0.50 *	4.57 **	1.27
30	Bega hundi X Indira Aerobic 1	-0.26 **	-0.05	-0.05	0.01	0.05	-1.00 **	-0.05	-0.43
31	Bega hundi X IR-64	0.84 **	0.06	0.31	-0.17 **	-0.11	0.88 **	6.78 **	-0.64
32	Bega hundi XMTU 1010	-0.40 **	0.03	-0.24	-0.04	-0.04	0.63 *	-11.31 **	-0.20
	SE(±)	0.08	0.12	0.25	0.02	0.06	0.25	1.40	0.70

H%=hulling , M%=milling , HRR%=head rice recovery, PL=panicle length, PB=panicle breadth, PL/B=panicle length breadth ratio, BRL=brown rice length, BRW=brown rice width, KL=kernel length, KB=kernel breadth, KL/B=kernel length breadth ratio, ER=Elongation ratio, EI=Elongation index, ASV=Alkali spreading value, GC=Gel consistency, AC=Amylose content

Table 4.18: Promising general combiner for yield and yield contributing traits and quality traits

S. No	Traits	Parental line/tester
1	DFF	Banspatri, Ajam dhan, NPT 6 , Indira Barani Dhan 1, Indira Aerobic 1
2	PH	NPT-1, Bega hundi
3	TT	RJR:II, Banspatri, Ganga kali, Ajam dhan, Bega hundi
4	ET	RJR:II, Banspatri, Ganga kali, Ajam dhan,
5	FLA	Ajam dhan ,NPT 19, NPT 6
6	PL	Ganga kali
7	FG	Banspatri, Ganga kali, Safed Lalak , Bega hundi
8	TG	Banspatri,Safed Lalak , Bega hundi
9	SF	Safed Lalak , Bega hundi, Indira Barani Dhan 1
10	TW	RJR:II, Safed Lalak , NPT 6 , IR-64
11	EY	Ganga kali, Ajam dhan, Bega hundi , Indira Barani Dhan 1
12	BY	RJR:II, Ganga kali, Ajam dhan, Indira Barani Dhan 1
13	HI	Banspatri, Bega hundi
14	H%	NPT 6, Bega hundi
15	M%	RJR:II, NPT 6 , Bega hundiIR-64
16	HRR%	Safed Lalak ,NPT 19, IR-64, MTU 1010
17	PL	Ajam dhan . Safed lalak, Bega hundi, Indira Barani Dhan 1
18	PB	NPT-19, Bega hundi, Indira Barani Dhan 1, IR-64
19	PL/B	Banspatri, Ganga ali, Ajam dhan, Safed lalak, Bega hundi, Indira Barani Dhan 1, Indira Aerobic-1
20	BRL	Ajam dhan, Bega hundi,Indira Aerobic -1
21	BRW	RJR:II,Ganga kali, Ajam dhan, Indira Barani Dhan 1, Indira Aerobic 1, IR-64
22	BL/B	Banspatri, Bega hundi, MTU-1010
23	KL	Ajam dhan, MTU-1010
24	KB	NPT-19, Indira Aerobic 1
25	KL/B	Bega hundi, MTU-1010
26	ER	Ajam dhan, NPT-19, Bega hundi, Indira Aerobic -1, MTU 1010
27	EI	Ajam dhan, NPT-19
28	ASV	Ajam dhan, Safed lalak
29	GC	RJR:II, Banspatri, Ajam dhan, NPT 19, Indira Barani Dhan 1, MTU1010
30	AC	RJR:II, Banspatri, Ganga kali, MTU1010

DFF-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, SF- Spikelet fertility, TW-Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant, H%=hulling , M%=milling , HRR%=head rice recovery, PL=panicle length, PB=panicle breadth, PL/B=panicle length breadth ratio, BRL=brown rice length, BRW=brown rice width, KL=kernel length, KB=kernel breadth, KL/B=kernel length breadth ratio, ER=Elongation ratio, EI= Elongation index, ASV=Alkali spreading value, GC= Gel consistency, AC=Amylose content

Table 4.19: Selected desirable crosses for specific combining ability

Traits	Crosses
DFE	Barani Dhan 1, RJR:II X Indira Barani Dhan 1, Banspatri X IR-64 , Safed Lalak X Indira Barani Dhan1, NPT 19 X Indira Barani Dhan 1, NPT 19 X MTU 1010, NPT 6 X IR-64 , Bega hundi X MTU 1010 , NPT 19 X Indira Barani Dhan 1, NPT 19 X IR-64 , NPT 19 X MTU 1010 , Bega hundi X MTU 1010
PH	RJR:II X Indira Barani Dhan 1, NPT 6 X Indira Aerobic 1
TTP	Banspatri X Indira Barani Dhan 1, Ganga Kali X IR-64 , Ajam Dhan X Indira Barani Dhan 1
ETP	Banspatri X Indira Barani Dhan 1, Banspatri X MTU 1010 , Ganga Kali X IR-64
FLA	RJR:II X Indira Aerobic 1 , Banspatri X MTU 1010, Ganga Kali X IR-64, Safed Lalak X Indira Barani Dhan 1
PL	Banspatri X Indira Aerobic 1 , Bega Hundi X Indira Barani Dhan 1
FGP	RJR:II X IR-64 , Banspatri X Indira Barani Dhan 1, Banspatri X MTU 1010 , Ganga Kali X Indira Aerobic 1 , Ajam Dhan X IR-64 , Ajam Dhan X MTU 1010 , Safed Lalak X IR-64 , Safed Lalak X MTU 1010 , NPT 6X Indira Barani Dhan 1, NPT 6 X MTU 1010, Bega hundi X Indira Barani Dhan 1 , Bega hundi X Indira Aerobic 1
TGP	RJR:II X IR-64 , Banspatri X Indira Barani Dhan 1, Banspatri X MTU 1010 , Ganga Kali X Indira Aerobic 1 , Ajam dhan X MTU 1010 , Safed Lalak X IR-64 , NPT 19 X MTU 1010 , NPT 6 X MTU 1010 , Bega hundi X Indira Barani Dhan 1, Bega Hundi X Indira Aerobic 1
SF	NPT 19 X Indira Barani Dhan 1 , NPT 6X Indira Barani Dhan 1
TW	RJR:II X Indira Aerobic 1, RJR:II X IR-64 , Banspatri X Indira Barani Dhan 1 , Ganga Kali X MTU 1010 , Ajam Dhan X Indira Barani Dhan 1 , Safed Lalak X IR-64 , Safed Lalak X MTU 1010, NPT 19 X Indira Barani Dhan 1 , NPT 19 X Indira Aerobic 1 , NPT 6X IR-64 , Bega hundi X MTU 1010
GYP	RJR:II X IR-64 , Banspatri X MTU 1010 , Ganga Kali X Indira Aerobic 1 , Ajam Dhan X Indira Barani Dhan 1 , Safed Lalak X IR-64, NPT 19 X MTU 1010 , NPT 6 X MTU 1010 , Bega hundi X Indira Barani Dhan 1 ,
BYP	RJR:II X Indira Aerobic 1 , Ganga Kali X IR-64 , Ajam Dhan X Indira Barani Dhan 1 , Safed Lalak X Indira Aerobic 1 , NPT 19 X MTU 1010 , Bega hundi X Indira Barani Dhan 1
HI	RJR:II X IR-64, Banspatri X MTU 1010 , Ganga Kali X Indira Aerobic 1 , Safed Lalak X IR-64 , NPT 6 X IR-64 , Bega hundi X Indira Barani Dhan 1

DFE-Days to 50% flowering, PH-Plant height, TTP-Total tiller per plant, ETP-Effective tiller per plant, FLA-Flag leaf area, PL-Panicle length, FGP-Filled grain per panicle, TGP- Total grain per panicle, SF- Spikelet fertility, TW- Test weight, BYP-Biological yield per plant, HI-Harvest index, GYP-Grain yield per plant

Conti...

Traits	Crosses
Hulling (%)	RJR:II X IR-64 (90.94%), Ganga kali X IR-64 (85.89%), Safed Lalak X Indira Barani Dhan 1 (85.01%), Safed Lalak X Indira Aerobic - 1(85.09%), NPT 6 X Indira Barani Dhan 1 (87.00%)
Milling (%)	RJR:IIIX IR-64 (65.04%), Ganga kali X Indira aerobic-1 (66.40%), Safed Lalak X Indira Barani Dhan 1 (64.92), (NPT 6) X Indira Barani Dhan 1 (69.37%), (NPT 6) X MTU 1010 (70.80%), Bega hundi XMTU 1010 (68.01%)
Head rice recovery (%)	RJR:IIIX IR-64 (59.83%), RJR:II XMTU 1010 (56.43%), Ganga kali X IA-1 (56.60), NPT 19 X Indira aerobic-1 (56.30%), NPT 6 X Indira Barani Dhan 1 (60.31%), Ajam dhan XMTU 1010 (67.84), NPT 6 X IR-64 (64.72)
Paddy length (mm)	X Indira Barani Dhan 1 (9.15), Safed Lalak XMTU 1010 (9.77), NPT 19 X IA-1 (9.00), Bega hundi X IR-64 (9.00)
Paddy breadth (mm)	BANSPATRI X Indira aerobic-1 (2.77), RJR:IIIX IR-64 (2.80), Ganga kali XMTU 1010 (2.80), Safed Lalak X IR-64 (2.80), NPT 19 X Indira aerobic-1 (2.82), NPT 6 X Indira Barani Dhan 1 (2.89), Bega hundi X Indira Barani Dhan 1 (2.77)
Paddy L/B ratio (mm)	BANSPATRI X Indira Barani Dhan 1 (3.59), Safed Lalak XMTU 1010 (3.49)
Brown rice length (mm)	BANSPATRI X Indira Barani Dhan 1 (6.89), Ganga kali X MTU 1010 (7.10), Safed Lalak X IR-64 (8.20), Safed Lalak XMTU 1010 (7.48), NPT 6 X Indira aerobic-1 (8.10), Bega hundi X IR-64 (7.69)
Brown rice width (mm)	BANSPATRI X Indira aerobic-1 (2.38), RJR:IIIXMTU 1010 (2.02), Bega hundi X IR-64 (2.18)
Brown rice L/W (mm)	BANSPATRI X Indira Barani Dhan 1 (2.98), RJR:IIIX Indira aerobic-1 (2.37), Ganga kali X IR-64 (2.76), Ganga kali XMTU 1010 (2.96), Ajam dhan X Indira Barani Dhan 1 (2.73), Safed Lalak X IR-64 (3.15), Safed Lalak X MTU 1010 (3.43), NPT 6 X IR-64 (2.28)
Kernel length (mm)	BANSPATRI X Indira Barani Dhan 1 (6.35), RJR:IIIX Indira Barani Dhan 1 (5.38), Ganga kali X IR-64(6.03), Safed Lalak X IR-64 (7.23), Safed Lalak XMTU 1010 (6.20), Bega hundi X IR-64 (6.52)
Kernel breadth (mm)	BANSPATRI X Indira aerobic-1 (2.37), Safed Lalak X Indira Barani Dhan 1 (2.20),
Kernel L/B ratio (mm)	RJR:IIIX Indira aerobic- (2.31), BANSPATRI X MTU 1010 (2.82), NPT 19 X Indira Barani Dhan 1 (3.03)
Elongation ratio	RJR:IIIX MTU 1010 (1.55), Ganga kali X Indira aerobic-1 (1.69), Safed Lalak X IR-64(1.38), NPT 19 X Indira aerobic-1 (1.28), NPT 19 X Indira aerobic-1 (1.58), NPT 6 X Indira Barani Dhan 1 (1.66), NPT 6 X MTU 1010 (1.86), Bega hundi X Indira Barani Dhan 1 (1.41)
Elongation index	RJR:IIIX MTU 1010 (0.98), Ajam dhan X Indira aerobic-1 (0.68), Ganga kali X Indira aerobic-1 (1.07)
Alkali spreading value	BANSPATRI X Indira Barani Dhan 1 (5.00), RJR:IIIX MTU 1010 (3.00), Safed Lalak X IR-64 (4.00)
Gel consistency (mm)	BANSPATRI X Indira Barani Dhan 1 (96), BANSPATRI X Indira aerobic-1 (86.15), RJR:IIIX IR-64 (57.50), Ajam dhan X IR-64 (60.60), Ajam dhan XMTU 1010 (95.00), NPT 6 X MTU 1010 (67.25)
Amylose content	RJR:IIIX Indira Barani Dhan 1 (20.98), RJR:IIIX Indira aerobic-1 (24.21), Ajam dhan XMTU 1010(22.81), NPT 6 X MTU 1010 (23)

Paddy breadth (mm)

For paddy breadth positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Aerobic 1 (0.10**), Banspatri X IR 64 (0.35**), Ganga kali XMTU 1010 (0.15**), Safed Lalak X IR 64 (0.16**), NPT 19 X Indira Aerobic 1 (0.19**), (NPT 6) X Indira Barani Dhan 1 (0.12**) and Bega Hundi X Indira Barani Dhan 1 (0.08**).

Paddy L/B ratio (mm)

For paddy L/B ratio positive and highly significant or significant SCA effects was recorded in crosses Ganga kali X IR 64 (0.74**), RJR:II X Indira Barani Dhan 1 (0.72**) and Safed Lalak XMTU 1010 (0.82**). The negative and highly significant or significant SCA effects exhibited in RJR:II X MTU 1010 (-0.67**), Ganga kali X Indira Aerobic 1 (-0.72**) and Safed Lalak X Indira Aerobic 1 (-0.32**).

Brown rice length (mm)

For brown rice length positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Barani Dhan 1 (0.90**), Ganga kali XMTU 1010 (0.23**), Safed Lalak X IR 64 (0.60**), Safed Lalak XMTU 1010 (0.54**), (NPT 6) X Indira Aerobic 1(0.13**) and Bega Hundi X IR 64 (0.65**). The negative and highly significant or significant SCA effects exhibited in RJR:II X MTU 1010 (-0.52**), Banspatri X IR 64 (-0.64**), and Safed Lalak X Indira Aerobic 1 (-0.62**).

Brown rice width (mm)

For brown rice width positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Aerobic 1(0.08**), Banspatri Xmtu 1010 (0.15**), Bega Hundi X IR 64 (0.19**). The negative and highly significant or significant SCA effects exhibited in Banspatri X Indira Aerobic 1 (-0.14**), Banspatri X IR 64 (-0.13**), Ajam dhan X Indira Aerobic 1 (-0.21**) and Ajam dhan XMTU 1010 (-0.31**).

Brown rice L/B ratio (mm)

For brown rice L/B ratio positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Barani Dhan 1 (1.10**), Banspatri X Indira Aerobic 1 (0.17**), Ganga kali X IR 64 (0.17**), Ganga kali XMTU 1010 (0.11**) and Ajam dhan X Indira Barani Dhan 1(0.19**). The negative and highly significant or significant SCA effects exhibited in RJR:II X Indira Aerobic 1 (-0.22**), Banspatri Xmtu 1010 (-0.83**) and Safed Lalak X Indira Aerobic 1 (-0.48**).

Kernel length (mm)

For kernel length positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Barani Dhan 1 (0.89**), Banspatri X Indira Barani Dhan 1 (0.21**), Ganga kali X IR 64(0.34**), Safed Lalak X IR 64 (0.22**), Safed Lalak XMTU 1010 (0.22**) and Bega Hundi X IR 64 (0.84**). Nayak *et al.* (2016)

Kernel breadth (mm)

For kernel breadth positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Aerobic 1 (0.39**) and Safed Lalak X Indira Barani Dhan 1 (0.27**). Nayak *et al.* (2016)

The negative and highly significant or significant SCA effects exhibited in RJR:II X MTU 1010 (-0.62**), Banspatri X Indira Aerobic 1 (-0.28*) and NPT 19 X Indira Barani Dhan 1 (-0.50**).

Kernel L/B ratio (mm)

For kernel L/B ratio positive and highly significant or significant SCA effects was recorded in crosses Banspatri X Indira Aerobic 1 (0.82**), RJR:II X MTU 1010 (0.86**), NPT 19 X Indira Barani Dhan 1(0.51**). The negative and highly

significant or significant SCA effects exhibited in RJR:II X Indira Aerobic 1 (-0.60**) and Safed Lalak X Indira Barani Dhan 1(-0.51**).

Elongation ratio

For elongation ratio positive and highly significant or significant SCA effects was recorded in crosses Banspatri X MTU 1010 (0.18**), Ganga kali X Indira Aerobic 1 (0.07**), Safed Lalak X IR 64 (0.25**), NPT 19 X Indira Aerobic 1 (0.05**), NPT 19 X Indira Barani Dhan 1(0.26**), (NPT 6) X Indira Barani Dhan 1 (0.12**), (NPT 6) X MTU 1010 (0.06**), Bega Hundi X Indira Barani Dhan 1 (0.20**). Nayak *et al.* (2016)

Elongation index

For elongation index positive and highly significant or significant SCA effects was recorded in crosses Banspatri X MTU 1010 (0.27**), Ajam dhan X Indira Aerobic 1 (0.18**), Ganga kali X Indira Aerobic 1(0.07**). The negative and highly significant or significant SCA effects exhibited in RJR:II X Indira Barani Dhan 1(-0.30**), Banspatri X Indira Barani Dhan 1 (-0.14**), Ajam dhan XMTU 1010 (-0.34**) and (NPT 6) X Indira Aerobic 1 (-0.16**).

Alkali spreading value

For alkali spreading value positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Barani Dhan 1 (3.25**), Banspatri X MTU 1010 (4.00), Safed Lalak X IR 64 (1.75**). Similar findings were reported by Nayak *et al.* (2016). The negative and highly significant or significant SCA effects exhibited in RJR:II X IR 64 (-1.88**), Banspatri X Indira Aerobic 1 (-2.13**), Banspatri X Indira Barani Dhan 1 (-1.13**) and NPT 19 X MTU 1010 (-1.38*).

Gel consistency

For gel consistency positive and highly significant or significant SCA effects was recorded in crosses RJR:II X Indira Barani Dhan 1 (5.35**), RJR:II X Indira

Aerobic 1 (5.73**), Banspatri X IR 64 (6.75**), Ajam dhan X IR 64 (3.53**), Ajam dhan X MTU 1010 (3.31**) and (NPT 6) X MTU 1010 (3.93**). The negative and highly significant or significant SCA effects exhibited in RJR:II X MTU 1010 (-7.34**), Safed Lalak X Indira Aerobic 1(-13.60**), Safed Lalak X IR 64 (-20.37**) and (NPT 6) X Indira Barani Dhan 1 (-24.55**)

Amylose content

For amylose content positive and highly significant or significant SCA effects was recorded in crosses Banspatri X Indira Barani Dhan 1 (3.96**), Banspatri X Indira Aerobic 1 (2.68**), Ajam dhan X MTU 1010 (2.86**) and (NPT 6) X MTU 1010 (3.53**). The negative and highly significant or significant SCA effects exhibited in RJR:II X MTU 1010 (-3.63**), Ajam dhan X Indira Barani Dhan 1 (-3.58**) and Safed Lalak X MTU 1010 (-4.00**).

4.4 Heterosis for yield and yield contributing traits and quality traits

Heterosis was computed by percent increase or decrease in F_1 value over better parent (heterobeltiosis) and over commercial check variety (Indira Barani Dhan-1 and MTU1010).

In this study, estimates of heterosis for eight yield and yield contributing traits viz. days to fifty percent flowering, plant height, tillers per plant, effective tillers per plant, fertile grains per panicle, total grains per panicle, spikelet fertility and grain yield per plant and six quality traits viz. hulling percent, milling percent, head rice recovery percent, alkali spreading value, gel consistency and amylase content in thirty two cross combination are shown in table 4.18 and 4.19, respectively.

4.4.1 Quantitative traits

Days to 50% flowering

Negative heterosis is desirable for this trait because this will make the hybrids to mature earlier as compare to parents.

The magnitude of heterosis over better parent varied from Ganga kali X IR 64(-0.48) to RJR:II X IR 64 (16.10). When compared to better parent significantly

earlier flowering observed in twenty three crosses, while five crosses were identified for late flowering. The superior crosses having heterobeltiosis were Banspatri X IR 64 (-9.80**), Ajam dhan X Indira Aerobic 1(-9.30**), Safed Lalak X Indira Aerobic 1(-9.22), Ajam dhan X Indira Barani Dhan 1(-7.91**) and (NPT 6) X Indira Aerobic 1(-6.25**).

The magnitude of standard heterosis over Indira barani dhan-1 varied from Bega Hundi X Indira Aerobic 1 (-0.48) to RJR:II X IR 64 (16.10). When compare to standard heterosis over Indira barani dhan-1 ten crosses observed as earlier flowering and ten crosses identified for late flowering. The superior crosses having earlier flowering than Indira Barani dhan-1 were Banspatri X IR 64 (-9.36**), Banspatri X Indira Barani Dhan 1 (-3.45**), Banspatri X Indira Aerobic 1 (-3.94**), Ajam dhan X Indira Aerobic 1 (-3.94 **) and Safed Lalak X Indira Aerobic 1 (-2.96 **).

The magnitude of standard heterosis over Indira Aerobic -1 varied from Ganga kali X IR 64 (-0.74) to RJR:II X IR 64 (13.88). When compare to standard heterosis over Indira aerobic-1 nineteen crosses observed as earlier flowering and six crosses identified for late flowering. The superior crosses having earlier flowering than MTU-1010 were Banspatri X IR 64 (-11.96**), Banspatri X Indira Barani Dhan 1 (-6.22**), Banspatri X Indira Aerobic 1 (-6.70**), Ajam dhan X Indira Aerobic 1 (-6.70 **) and Safed Lalak X Indira Aerobic 1 (-5.74**).

Plant height (cm)

Semi dwarf plant height is desirable for high yielding in rice varieties. The magnitude of heterosis over better parent varied from Ajam dhan X MTU 1010 (-0.90) to RJR:II X IR 64 (34.74). None of the crosses showed negative significant, but positive highly significant found in twenty one crosses. The crosses having superior heterobeltiosis were Ganga kali X IR 64 (9.73**), NPT 19 X Indira Barani

Table 4.20: Estimation of Heterobeltiosis and standard heterosis for yield and yield contributing traits

S. no	Cross	DF			PH			TT		
		BP	1	2	BP	1	2	BP	1	2
1	RJR:II X Indir Barani Dhan 1	-3.90 **	-2.96 **	-5.74 **	10.09 *	10.09 *	16.35 **	71.72 **	76.60 **	49.55 **
2	RJR:II X Indira Aerobic 1	-3.37 **	-0.99	-3.83 **	33.44 **	27.19 **	34.42 **	69.60 **	80.51 **	76.58 **
3	RJR:II X IR-64	16.10 **	17.24 **	13.88 **	34.78 **	28.69 **	36.01 **	85.26 **	80.85 **	53.15 **
4	RJR:II X MTU 1010	7.37 **	10.54 **	7.37 **	27.92 **	21.03 **	27.92 **	61.98 **	801.06 **	70.27 **
5	Bapatri X Indir Barani Dhan 1	-3.92 **	-3.45 **	-6.22 **	7.24	16.90 **	23.55 **	10.06	96.81 **	66.67 **
6	Bapatri X Indira Aerobic 1	-6.25 **	-3.94 **	-6.70 **	13.84 **	24.10 **	31.16 **	29.60 *	62.77 **	37.84 **
7	Bapatri X IR-64	-9.80 **	-9.36 **	-11.96 **	4.28	13.68 **	20.14 **	51.02 **	46.81 **	24.32
8	Bapatri XMTU 1010	4.78 **	7.88 **	4.78 **	2.86	12.13 **	18.51 **	55.37 **	93.62 **	63.96 **
9	Ganga kali X Indir Barani Dhan 1	6.19 **	9.85 **	6.70 **	19.96 **	22.86 **	29.85 **	67.68 **	69.15 **	43.24 **
10	Ganga kali X Indira Aerobic	-1.90 *	1.48	-1.44	10.18 *	12.84 **	19.26 **	15.2	50.00 **	27.03 *
11	Ganga kali X IR-64	-0.48	2.96 **	0.9	9.73 *	12.38 **	18.78 **	41.05 **	80.85 **	95.50 **
12	Ganga kali XMTU 1010	-0.95	2.46 **	-0.48	6.8	9.38 *	15.60 **	11.57	31.91 *	11.71
13	Ajam dhan X Indir Barani Dhan 1	-7.91 **	-2.46 **	-5.26 **	-1.67	11.75 *	18.11 **	48.08 **	82.77 **	80.18 **
14	Ajam dhan X Indira Aerobic	-9.30 **	-3.94 **	-6.70 **	-4.99	7.98	14.12 **	48.80 **	91.49 **	62.16 **
15	Ajam dhan X IR-64	-5.58 **	0	-2.87 **	2.02	15.94 **	22.54 **	70.53 **	70.21 **	44.14 **
16	Ajam dhan XMTU 1010	-4.65 **	0.99	-1.91 *	-0.9	12.63 **	19.04 **	30.58 *	62.77 **	37.84 **
17	Safed Lalak X Indir Barani Dhan 1	-6.45 **	0	-2.87 **	16.18 **	16.18 **	22.79 **	-13.7	25.53	6.31
18	Safed Lalak X Indira Aerobic 1	-9.22 **	-2.96 **	-5.74 **	16.02 **	11.01 *	17.32 **	2.74	55.32 **	31.53 *
19	Safed Lalak X IR-64	-0.46	6.40 **	3.35 **	20.03 **	14.85 **	21.38 **	6.85	56.38 **	32.43 *
20	Safed Lalak XMTU 1010	-3.69 **	2.96 **	0.89	11.71 *	6.89	12.97 **	-23.29	13.83	-3.6
21	NPT 19 X Indir Barani Dhan 1	-2.93 **	-1.97 *	-4.78 **	9.35 *	9.35 *	15.57 **	0.98	3.19	-12.61
22	NPT 19 X Indira Aerobic 1	4.33 **	6.90 **	3.83 **	14.31 **	8.95	15.15 **	-3.2	19.15	0.9
23	NPT 19 X IR-64	-1.95 *	-0.99	-3.83 **	12.91 **	7.81	13.94 **	27.45	26.6	7.21
24	NPT 19 XMTU 1010	-2.39 **	0.49	-2.39 **	16.31 **	10.05 *	16.31 **	-17.36	3.19	-12.61
25	NPT 6 X Indir Barani Dhan 1	-1.97 *	-1.97 *	-4.78 **	18.34 **	18.34 **	25.07 **	-21.6	-3.19	-18.02
26	NPT 6 X Indira Aerobic 1	-6.25 **	-3.94 **	-6.70 **	18.60 **	13.05 **	19.48 **	-0.8	27.66	8.11
27	NPT 6 X IR-64	-3.94 **	-3.94 **	-6.70 **	26.50 **	20.79 **	27.66 **	0.9	26.6	7.21
28	NPT 6 X MTU 1010	-1.91 *	0.99	-1.91 *	34.86 **	27.60 **	34.86 **	-2.4	21.28	2.7
29	Bega hundi X Indira Barani Dhan 1	-0.94	3.45 **	0.48	7.11	7.11	13.20 **	70.71 **	69.15 **	43.24 **
30	Bega hundi X Indira Aerobic 1	-3.77 **	0.49	-2.39 **	12.20 **	9.16 *	15.36 **	20	54.26 **	30.63 *
31	Bega hundi X IR-64	-2.83 **	1.48	-1.44	7.5	4.59	10.54 *	87.37 **	84.04 **	55.86 **
32	Bega hundi XMTU 1010	-4.25 **	0.89	-2.87 **	9.24 *	6.28	12.32 *	40.50 **	74.47 **	47.75 **
SE m		0.8092			3.8676			2.2077		

* & ** represent significant levels at 5% and 1% respectively.

DF= Days to 50% flowering, PH= Plant height, TT= Tillers per plant, BP=Better parent, 1= Indira Barani Dhan-1, 2= MTU-1010

Conti....

S. no	Cross	ET			FG			TG		
		BP	1	2	BP	1	2	BP	1	2
1	RJR:II X Indir Barani Dhan 1	76.60 **	71.72 **	40.50 **	4.68	4.68	-0.94	6.89	6.89	2.15
2	RJR:II X Indira Aerobic 1	61.98 **	84.14 **	75.21 **	-21.68 **	5.84	0.17	-22.51 **	9.14	4.30
3	RJR:II X IR-64	84.78 **	77.78 **	45.45 **	22.55 **	17.61 **	11.30 **	25.89 **	24.20 **	18.69 **
4	RJR:II X MTU 1010	70.27 **	97.98 **	61.98 **	-0.44	5.21	-0.44	6.72	11.66 *	6.72
5	Bapatri X Indir Barani Dhan 1	96.81 **	106.06 **	68.60 **	33.79 **	33.79 **	26.62 **	38.80 **	38.80 **	32.65 **
6	Bapatri X Indira Aerobic 1	26.45 *	63.64 **	33.88 *	-22.10 **	5.28	-0.37	-21.28 **	10.87 *	5.95
7	Bapatri X IR-64	46.81 **	49.49 **	22.31	20.34 **	15.48 **	9.29 *	22.38 **	19.83 **	14.52 **
8	Bapatri XMTU 1010	63.96 **	89.90 **	55.37 **	33.59 **	41.16 **	33.59 **	43.27 **	49.91 **	43.27 **
9	Ganga kali X Indir Barani Dhan 1	69.15 **	67.68 **	37.19 *	4.58	5.92	0.23	7.55	11.01 *	6.09
10	Ganga kali X Indira Aerobic	16.53	45.45 *	19.01	13.66 **	53.60 **	45.36 **	12.12 **	57.91 **	50.91 **
11	Ganga kali X IR-64	95.87 **	131.31 **	89.26 **	1.15	2.44	-3.05	5.9	9.31	4.47
12	Ganga kali XMTU 1010	11.71	36.36 *	11.57	-2.01	3.54	-2.01	2.38	7.13	2.38
13	Ajam dhan X Indir Barani Dhan 1	81.77 **	80.08 **	70.25 **	-15.04 **	-2.16	-7.41	-14.19 **	2.53	-2.02
14	Ajam dhan X Indira Aerobic	48.76 **	87.88 **	53.72 **	-28.89 **	-3.9	-9.05 *	-27.38 **	2.28	-2.25
15	Ajam dhan X IR-64	73.91 **	63.64 **	33.88 *	-5.6	8.71 *	2.88	-5.53	12.88 *	7.87
16	Ajam dhan XMTU 1010	37.84 **	59.60 **	30.58 *	13.87 **	31.14 **	24.10 **	11.76 **	33.54 **	27.62 **
17	Safed Lalak X Indir Barani Dhan 1	-16.31	27.27	4.13	31.78 **	33.23 **	26.08 **	28.77 **	34.61 **	28.65 **
18	Safed Lalak X Indira Aerobic 1	3.55	51.52 **	23.97	-15.86 **	13.71 **	7.61	-17.13 **	16.72 **	11.54 *
19	Safed Lalak X IR-64	4.26	57.58 **	28.93 *	36.41 **	37.90 **	30.51 **	36.59 **	42.78 **	36.45 **
20	Safed Lalak XMTU 1010	-24.11 *	13.13	-7.44	33.12 **	40.67 **	33.12 **	38.21 **	44.62 **	38.21 **
21	NPT 19 X Indir Barani Dhan 1	-2.02	4.04	-14.88	-33.76 **	-3.19	-8.38 *	-35.27 **	0	-4.43
22	NPT 19 X Indira Aerobic 1	-7.44	22.22	0.8	-36.55 **	-7.26	-12.24 **	-33.70 **	2.42	-2.12
23	NPT 19 X IR-64	20.2	31.31	7.44	-34.10 **	-3.68	-8.85 *	-32.22 **	4.71	0.07
24	NPT 19 XMTU 1010	-12.61	1.01	-17.36	-28.87 **	3.97	-1.61	-22.70 **	19.42 **	14.13 **
25	NPT 6 X Indir Barani Dhan 1	-20.18	-1.01	-19.01	-1.45	-1.45	-6.74	4.85	4.85	0.2
26	NPT 6 X Indira Aerobic 1	-0.83	25.25	2.48	-42.10 **	-21.75 **	-25.95 **	-34.58 **	-7.86	-11.94 *
27	NPT 6 X IR-64	4.39	26.26	3.31	-23.70 **	-26.78 **	-30.71 **	-7.03	-8.97	-13.00 **
28	NPT 6 X MTU 1010	0.8	23.23	0.83	3.18	9.03 *	3.18	16.34 **	21.74 **	16.34 **
29	Bega hundi X Indira Barani Dhan 1	69.15 **	70.71 **	39.67 **	25.08 **	55.30 **	46.97 **	31.75 **	64.59 **	57.29 **
30	Bega hundi X Indira Aerobic 1	19.83	51.52 **	23.97	8.34 **	46.40 **	38.55 **	7.15 *	50.92 **	44.23 **
31	Bega hundi X IR-64	88.04 **	79.80 **	47.11 **	-17.18 **	2.83	-2.68	-16.85 **	3.88	-0.73
32	Bega hundi XMTU 1010	47.75 **	71.72 **	40.50 **	-19.03 **	0.53	-4.86	-16.87 **	3.84	-0.76
SE m		1.8162			3.21			6.56		

* & ** represent significant levels at 5% and 1% respectively.

ET=Effective tillers per , FG= Filled grai per panicle, TG= Total grai per panicle, BP=Better parent, 1= Indira Barani Dhan-1, 2= MTU-1010

Conti...

S. No		SF			EY		
		BP	1	2	BP		
1	RJR:II X Indir Barani Dhan 1	-2.07	-2.07	-3.01	8.68	8.68	19.42
2	RJR:II X Indira Aerobic 1	1.04	-3.02	-3.95	19.54	9.81	20.67
3	RJR:II X IR-64	-3.56	-5.32 *	-6.22 **	37.94 **	26.72 **	39.26 **
4	RJR:II X MTU 1010	-6.71 **	-5.81 **	-6.71 **	-23.90 *	-30.09 **	-23.17 *
5	Bapatri X Indir Barani Dhan 1	-3.61	-3.61	-4.53 *	13.1	13.1	24.29 *
6	Bapatri X Indira Aerobic 1	-3.35	-5.06 *	-5.97 **	31.18 **	9.22	20.02
7	Bapatri X IR-64	-1.85	-3.59	-4.52 *	-1.69	-10.93	-2.12
8	Bapatri XMTU 1010	-6.70 **	-5.80 **	-6.70 **	27.38 *	15.92	27.38 *
9	Ganga kali X Indir Barani Dhan 1	-4.61	-4.61 *	-5.52 *	6.43	6.43	16.95
10	Ganga kali X Indira Aerobic	-0.89	-2.74	-3.67	36.06 **	71.57 **	88.54 **
11	Ganga kali X IR-64	-4.53	-6.26 **	-7.16 **	60.19 **	45.14 **	59.49 **
12	Ganga kali XMTU 1010	-4.28	-3.36	-4.28 *	25.21 *	13.94	25.21 *
13	Ajam dhan X Indir Barani Dhan 1	-4.63	-4.63 *	-5.54 *	81.51 **	81.51 **	99.46 **
14	Ajam dhan X Indira Aerobic	-2.59	-6.05 **	-6.95 **	50.00 **	29.42 **	42.22 **
15	Ajam dhan X IR-64	-1.89	-3.67	-4.59 *	13.51	2.84	13.01
16	Ajam dhan XMTU 1010	-2.75	-1.81	-2.75	19.29	8.55	19.29
17	Safed Lalak X Indir Barani Dhan 1	-1.02	-1.02	-1.97	-21.39 *	-9.99	-1.09
18	Safed Lalak X Indira Aerobic 1	0.72	-2.57	-3.51	-25.56 **	-14.76	-6.33
19	Safed Lalak X IR-64	-1.62	-3.4	-4.33 *	-0.76	13.65	24.88 *
20	Safed Lalak XMTU 1010	-3.67	-2.74	-3.67	-20.06 *	-8.45	0.6
21	NPT 19 X Indir Barani Dhan 1	-3.16	-3.16	-4.09	2.32	2.32	12.44
22	NPT 19 X Indira Aerobic 1	-5.65 *	-9.44 **	-10.31 **	-9.9	-13.79	-5.27
23	NPT 19 X IR-64	-6.27 *	-7.98 **	-8.86 **	-25.81 *	-29.02 **	-22.00 *
24	NPT 19 XMTU 1010	-13.77 **	-12.93 **	-13.77 **	-2.51	-6.72	2.5
25	NPT 6 X Indir Barani Dhan 1	-6.03 *	-6.03 **	-6.93 **	-19.80 *	-19.80 *	-11.87
26	NPT 6 X Indira Aerobic 1	-13.31 **	-14.73 **	-15.54 **	-10.57	-11.15	-2.36
27	NPT 6 X IR-64	-18.15 **	-19.49 **	-20.27 **	-12.04	-12.61	-3.97
28	NPT 6 X MTU 1010	-11.30 **	-10.44 **	-11.30 **	-11.42	-11.99	-3.29
29	Bega hundi X Indira Barani Dhan 1	-5.64 *	-5.64 *	-6.54 **	82.64 **	100.64 **	120.48 **
30	Bega hundi X Indira Aerobic 1	-2.4	-3.01	-3.94	49.88 **	24.87 *	37.22 **
31	Bega hundi X IR-64	-0.38	-1	-1.95	28.65 **	16.56	28.09 **
32	Bega hundi XMTU 1010	-4.1	-3.18	-4.10	-2.42	-11.20	-2.42
SE m		2.28			2.66		

* & ** represent significant levels at 5% and 1% respectively.

SF= Spikelet fertility, GY=Grain yield per plant, BP=Better parent, 1= Indira Barani Dhan-1, 2= MTU-1010

Table 4.21: Estimation of Heterobeltiosis and standard heterosis for quality traits

S. No	Cross	H%			M%			HRR%		
		BP	1	2	BP	1	2	BP	1	2
1	RJR:II X Indir Barani Dhan 1	-3.75	-3.75	-5.69	16.40 **	16.40 **	9.09 *	10.64	10.64	8.45
2	RJR:II X Indira Aerobic 1	-18.54 **	-15.40 **	-17.10 **	0.27	0.16	-6.12	-21.37 *	-28.71 **	-30.12 **
3	RJR:II X IR-64	0.39	-1.28	-3.27	12.94 **	19.20 **	11.71 **	25.77 **	21.95 **	19.54 **
4	RJR:II X MTU 1010	-7.83 *	-5.93	-7.83 *	1.65	8.46 *	1.65	3.84	5.94	3.84
5	Bapatri X Indir Barani Dhan 1	-24.67 **	-24.67 **	-26.19 **	-12.54 *	-11.17 **	-16.75 **	-51.56 **	-48.76 **	-49.78 **
6	Bapatri X Indira Aerobic 1	-42.15 **	-39.92 **	-41.13 **	-39.74 **	-38.79 **	-42.63 **	-46.27 **	-43.17 **	-44.29 **
7	Bapatri X IR-64	2.15	0.69	-1.34	11.03 *	17.18 **	9.82 **	17.36 *	24.12 **	21.67 **
8	Bapatri XMTU 1010	-1.98	0.03	-1.98	-3.12	3.37	-3.12	-1.59	4.09	2.03
9	Ganga kali X Indir Barani Dhan 1	-27.73 **	-27.73 **	-29.19 **	-20.06 **	-20.06 **	-25.08 **	-18.65 *	-18.65 **	-20.26 **
10	Ganga kali X Indira Aerobic	-1.86	1.92	-0.13	20.16 **	20.04 **	12.51 **	-6.83	-15.53 *	-17.20 *
11	Ganga kali X IR-64	1.35	-0.34	-2.35	-6.68	-1.51	-7.70 *	-9.17	-11.93	-13.67 *
12	Ganga kali XMTU 1010	-19.05 **	-17.38 **	-19.05 **	-16.85 **	-11.28 **	-16.85 **	-25.71 **	-24.21 **	-25.71 **
13	Ajam dhan X Indir Barani Dhan 1	-6.61	-6.61	-8.50 *	-7.62	-7.62 *	-13.42 **	-14.05	-14.05 *	-15.76 *
14	Ajam dhan X Indira Aerobic	-6.65 *	-3.05	-5.00	8.46	8.35 *	1.54	12.4	1.91	-0.11
15	Ajam dhan X IR-64	-1.55	-3.18	-5.14	-4.48	0.81	-5.52	12.86	9.43	7.27
16	Ajam dhan XMTU 1010	-7.97 *	-6.07	-7.97 *	-12.99 **	-7.16	-12.99 **	-35.99 **	-34.70 **	-35.99 **
17	Safed Lalak X Indir Barani Dhan 1	1.66	1.92	-0.14	0.85	9.75 *	2.86	-7.62	4.67	2.60
18	Safed Lalak X Indira Aerobic 1	-2.74	1.01	-1.03	-4.42	4.02	-2.51	-11.18	0.64	-1.35
19	Safed Lalak X IR-64	4.1	4.36	2.25	-6.24	2.04	-4.37	-0.79	12.41	10.18
20	Safed Lalak XMTU 1010	-13.33 **	-11.55 **	-13.33 **	-7.75	0.39	-5.91	-10.58	1.32	-0.69
21	NPT 19 X Indir Barani Dhan 1	-8.44 *	-8.44 *	-10.29 **	-5.95	-5.95	-11.86 **	-29.41 **	-29.41 **	-30.81 **
22	NPT 19 X Indira Aerobic 1	-14.32 **	-11.01 **	-12.81 **	4.27	4.17	-2.37	17.28 *	6.33	4.23
23	NPT 19 X IR-64	0.08	-1.43	-3.42	9.42	15.48 **	8.23 *	28.72 **	24.81 **	22.34 **
24	NPT 19 XMTU 1010	-10.78 **	-8.94 **	-10.78 **	-5.51	0.82	-5.51	-6.69	-4.80	-6.69
25	NPT 6 X Indir Barani Dhan 1	1.62	1.81	-0.25	1.14	18.76 **	11.31 **	-2.79	18.21 **	15.87 *
26	NPT 6 X Indira Aerobic 1	-7.58 *	-4.02	-5.95	-19.61 **	-5.61	-11.54 **	-53.76 **	-43.78 **	-44.89 **
27	NPT 6 X IR-64	-5.65	-5.47	-7.38 *	-10.70 *	4.86	-1.72	-54.23 **	-44.35 **	-45.45 **
28	NPT 6 X MTU 1010	-0.6	1.45	-0.60	0.13	17.57 **	10.19 **	4.82	27.46 **	24.94 **
29	Bega hundi X Indira Barani Dhan 1	-5.5	-2.44	-4.41	-8.36	1.84	-4.55	-12.04	1.15	-0.86
30	Bega hundi X Indira Aerobic 1	-5.98	-2.35	-4.32	-15.15 **	-5.70	-11.62 **	-45.09 **	-36.86 **	-38.11 **
31	Bega hundi X IR-64	-3.97	-0.86	-2.86	-0.57	10.50 **	3.57	-3.56	10.90	8.70
32	Bega hundi XMTU 1010	-3.02	0.11	-1.91	6.73	18.61 **	11.17 **	1.27	16.45 *	14.14 *

* & ** represent significant levels at 5% and 1% respectively.

H= Hulling, M=Milling, HRR= Head rice recovery BP=Better parent, 1= Indira Barani Dhan-1, 2= MTU-1010

Conti....

		ASV			GC			AC		
S. No	Cross	BP	1	2	BP	1	2	BP	1	2
1	RJR:II X Indir Barani Dhan 1	27.27 **	40.00 **	100.00 **	3.01	15.61 **	1.52	37.26 **	37.26 **	38.34 **
2	RJR:II X Indira Aerobic 1	-57.14 **	-40.00 **	-14.29	7.09	15.61 **	1.52	26.67 **	34.46 **	35.51 **
3	RJR:II X IR-64	-75.00 **	-70.00 **	-57.14 **	-16.80 **	-3.82	-15.53 **	20.56 **	21.26 **	22.21 **
4	RJR:II X MTU 1010	-45.45 **	-40.00 **	-14.29	-8.80 **	5.43 *	-7.41 **	63.59 **	62.32 **	63.59 **
5	Bapatri X Indir Barani Dhan 1	-60.00 **	-60.00 **	-42.86 **	-13.99 **	-1.56	-13.55 **	35.40 **	35.40 **	36.46 **
6	Bapatri X Indira Aerobic 1	-85.71 **	-80.00 **	-71.43 **	-3.03	10.98 **	-2.54	8.58	15.25 **	16.15 **
7	Bapatri X IR-64	-66.67 **	-60.00 **	-42.86 **	-1.01	13.29 **	-0.51	33.90 **	34.67 **	35.72 **
8	Bapatri XMTU 1010	75.00 **	40.00 **	100.00 **	-0.51	13.87 **	0.00	25.77 **	24.79 **	25.77 **
9	Ganga kali X Indir Barani Dhan 1	-60.00 **	-60.00 **	-42.86 **	-13.78 **	-2.31	-14.21 **	7.00	7.00	7.83
10	Ganga kali X Indira Aerobic	-71.43 **	-60.00 **	-42.86 **	-22.45 **	-12.14 **	-22.84 **	1.48	7.72	8.57
11	Ganga kali X IR-64	-58.33 **	-50.00 **	-28.57 **	-21.43 **	-10.98 **	-21.83 **	3.44	4.04	4.86
12	Ganga kali XMTU 1010	-60.00 **	-60.00 **	-42.86 **	-22.84 **	-12.14 **	-22.84 **	14.30 **	13.41 **	14.30 **
13	Ajam dhan X Indir Barani Dhan 1	8.1	10.00	42.86 **	-1.54	10.98 **	-2.54	-47.14 **	-47.14 **	-46.73 **
14	Ajam dhan X Indira Aerobic	-21.43 **	10.00	57.14 **	-2.56	9.83 **	-3.55	-32.60 **	-28.45 **	-27.89 **
15	Ajam dhan X IR-64	-16.67 **	10.00	42.86 **	-11.03 **	0.29	-11.93 **	-11.36 *	-10.85 *	-10.15 *
16	Ajam dhan XMTU 1010	25.00 **	10.00	42.86 **	-2.54	10.98 **	-2.54	-11.76 *	-12.45 **	-11.76 *
17	Safed Lalak X Indir Barani Dhan 1	0.30	10.00	42.86 **	-1.5	13.87 **	0.12	1.57	1.57	2.37
18	Safed Lalak X Indira Aerobic 1	-21.43 **	10.00	57.14 **	-31.90 **	-21.27 **	-30.86 **	10.47 *	17.26 **	18.18 **
19	Safed Lalak X IR-64	8.33	30.00 **	85.71 **	-42.50 **	-33.53 **	-41.62 **	2.09	2.69	3.49
20	Safed Lalak XMTU 1010	-14.29	-40.00 **	-14.29	0.50	15.61 **	1.52	-12.20 *	-12.88 **	-12.20 *
21	NPT 19 X Indir Barani Dhan 1	-40.00 **	-40.00 **	-14.29	4.21	14.45 **	0.51	-15.42 **	-15.42 **	-14.76 **
22	NPT 19 X Indira Aerobic 1	-7.14	30.00 **	85.71 **	-1.05	8.67 **	-4.57 *	10.01 *	16.78 **	17.69 **
23	NPT 19 X IR-64	-66.67 **	-60.00 **	-42.86 **	-1.05	8.67 **	-4.57 *	4.5	5.11	5.93
24	NPT 19 XMTU 1010	-55.56 **	-60.00 **	-42.86 **	-1.52	12.14 **	-1.52	-15.18 **	-15.84 **	-15.18 **
25	NPT 6 X Indir Barani Dhan 1	-60.00 **	-60.00 **	-42.86 **	-39.39 **	-30.64 **	-39.09 **	-21.69 **	-21.69 **	-21.08 **
26	NPT 6 X Indira Aerobic 1	-57.14 **	-40.00 **	-14.29	-3.03	10.98 **	-2.54	-22.22 **	-17.43 **	-16.79 **
27	NPT 6 X IR-64	-58.33 **	-50.00 **	-28.57 **	-4.04	9.83 **	-3.55	-15.65 **	-15.16 **	-14.49 **
28	NPT 6 X MTU 1010	-50.00 **	-60.00 **	-42.86 **	-16.16 **	-4.05	-15.74 **	11.35 *	10.48 *	11.35 *
29	Bega hundi X Indira Barani Dhan 1	-40.00 **	-40.00 **	-14.29	15.61 **	15.61 **	1.52	-15.38 **	-15.38 **	-14.71 **
30	Bega hundi X Indira Aerobic 1	-64.29 **	-50.00 **	-28.57 **	7.34 **	9.83 **	-3.55	-22.56 **	-17.80 **	-17.15 **
31	Bega hundi X IR-64	-33.33 **	-20.00 **	14.29	3.16	13.29 **	-0.51	-19.98 **	-19.52 **	-18.89 **
32	Bega hundi XMTU 1010	-20.00 **	-20.00 **	14.29	-14.21 **	-2.31	-14.21 **	-12.40 **	-13.08 **	-12.40 **

* & ** represent significant levels at 5% and 1% respectively.

ASV= Alkali spreading value, GC= Gel coistenvy, AC=Amylose content, BP=Better parent, 1= Indira Barani Dhan-1, 2= MTU-1010

dhan 1(9.35**), Ganga kali X Indira Aerobic 1 (10.18**) and Bega Hundi X mtu 1010(9.24**). Similar positive significant heterosis reported by Thorat *et al.* (2017)

The magnitude of standard heterosis over Indira barani dhan-1 varied from Bega Hundi X IR 64 (4.59) to RJR:II X IR 64 (28.69). None of the crosses showed negative significant but twenty five crosses observed positive and highly significant. The superior crosses having positive significant plant height than Indira Barani dhan-1 were RJR:II X Indira Barani Dhan 1(10.09**), Ganga kali XMTU 1010 (9.38**) and Bega Hundi X Indira Aerobic 1 (9.16**).

The magnitude of standard heterosis over MTU-1010 varied from Bega Hundi X IR 64 (10.54**) to RJR:II X IR 64 (36.01**). None of the crosses showed negative significant and all crosses showed positive highly significant for this traits. The superior crosses having positive significant plant height than MTU-1010 were Bega Hundi X IR 64 (10.54**) and Bega Hundi Xmtu 1010 (10.54**).

Tillers per plant (No.)

More number of tillers per plant is associated with high grain yield per plant. The magnitude of heterosis over better parent varied from (NPT 6) X Indira Aerobic 1 (0.80) to Bega Hundi X Indira Barani Dhan 1 (87.37). None of the crosses showed negative significant, but positive highly significant found in sixteen crosses. The superior crosses having heterobeltiosis were RJR:II X Indira Aerobic 1 (69.60**), RJR:II X IR 64 (85.26**), Ajam dhan X IR 64 (70.53**), Bega Hundi X Indira Barani Dhan 1 (70.71**) and Bega Hundi X Indira Barani Dhan 1 (87.37**).

The magnitude of standard heterosis over Indira barani dhan-1 varied from NPT 19 XMTU 1010 (3.19) to Banspatri X Indira Aerobic 1 (96.81). None of the crosses showed negative significant but twenty two crosses observed positive and highly significant for this trait. The superior crosses having positive significant than Indira Barani dhan-1 were RJR:II X Indira Aerobic 1 (80.51**), RJR:II X IR 64 (80.85**), Banspatri X Indira Barani Dhan 1 (96.81**), Ganga kali X Indira Barani Dhan 1 (93.62**), Ajam dhan X Indira Aerobic 1 (91.49**) and Banspatri X Indira Aerobic 1 (96.81**).

The magnitude of standard heterosis over MTU-1010 varied from NPT 19 X Indira Aerobic 1 (0.90) to Ajam dhan X Indira Barani Dhan 1 (80.18**). None of the crosses showed negative significant but twenty crosses showed positive highly significant for this traits. The superior crosses having positive significant than MTU-1010 were RJR:II X Indira Aerobic 1 (76.58**), RJR:II X MTU 1010 (70.21**), Banspatri X Indira Barani Dhan 1 (63.96**), Ajam dhan X Indira Aerobic 1 (62.16**) and Ajam dhan X Indira Barani Dhan 1 (80.18**).

Effective tillers per plant (No.)

More number of panicle bearing tillers per plant is believed to associated with high grain yield per plant. The magnitude of heterosis over better parent varied from (NPT 6) X MTU1010 (0.80) to Banspatri X Indira Aerobic 1 (96.81). None of the crosses showed negative significant, but positive highly significant found in eight crosses. The superior crosses having heterobeltiosis were RJR:II X Indira Barani Dhan 1 (76.60**), RJR:II X IR 64 (84.78**), Ajam dhan X IR 64 (70.53**), Banspatri X Indira Barani Dhan 1 (70.27**), Ganga kali X IR 64 (95.87**) and Banspatri X Indira Aerobic 1 (96.81). Similar positive significant heterosis reported by Thorat *et al.* (2017)

The magnitude of standard heterosis over Indira barani dhan-1 varied from (NPT 6) X Indira Barani Dhan 1 (-1.10) TO RJR:II X MTU 1010 (97.98**). None of the crosses showed negative significant but twenty two crosses observed positive and highly significant for this trait. The superior crosses having positive significant than Indira Barani dhan-1 were RJR:II X Indira Aerobic 1 (84.14**), Banspatri X MTU 1010 (89.90**), Banspatri X Indira Barani Dhan 1 (86.06**), Ganga kali X IR 64 (81.31**), Ajam dhan X Indira Barani Dhan 1 (87.88) and RJR:II X MTU 1010 (97.98**).

The magnitude of standard heterosis over MTU-1010 varied from NPT 19 X Indira Aerobic 1 (0.80) to Ganga kali X IR 64 (89.26**). None of the crosses showed negative significant but seventeen crosses showed positive highly significant for this traits. The superior crosses having positive significant than MTU-1010 were RJR:II X

Indira Aerobic 1 (75.21**), RJR:II X MTU 1010 (61.981**), Banspatri X Indira Barani Dhan 1(68.60**), Banspatri X MTU 1010 (55.37**) and Ganga kali X IR 64 (89.26**).

Filled grains per panicle (No.)

The number of filled grains panicle direct contribute to grain yield per plant, hence positive heterotic effect would be highly desirable. The magnitude of heterosis over better parent varied from RJR:II X MTU 1010 (-0.44) to Safed Lalak X IR 64 (36.49). The negative significant observed in eleven crosses, but positive highly significant found in ten crosses. The superior crosses having heterobeltiosis were Banspatri XMTU 1010 (33.59**), Banspatri X Indira Aerobic 1 (33.79**), Safed Lalak X Indira Barani Dhan 1 (31.78**), Safed Lalak XMTU 1010 (33.12**) and Safed Lalak X IR 64 (36.49). Similar positive significant heterosis reported by Thorat *et al.* (2017)

The magnitude of standard heterosis over Indira barani dhan-1 varied from (NPT 6) X Indira Barani Dhan 1 (-1.45) to Bega Hundi X Indira Barani Dhan 1 (55.20). None of the crosses showed negative significant but sixteen crosses observed positive and highly significant for this trait. The superior crosses having positive significant than Indira Barani dhan-1 were Banspatri X MTU 1010 (41.16**), Safed Lalak X IR 64 (37.90**), Safed Lalak XMTU 1010 (40.67**), Bega Hundi X Indira Aerobic 1 (46.40**) and Bega Hundi X Indira Barani Dhan 1 (55.20).

The magnitude of standard heterosis over MTU-1010 varied from RJR:II X Indira Aerobic 1 (0.17) to Bega Hundi X Indira Barani Dhan 1 (46.97). The negative significant found in four crosses but eleven crosses showed positive highly significant for this traits. The superior crosses having positive significant than MTU-1010 were Banspatri X MTU 1010 (33.59**), Ganga kali X Indira Aerobic 1 (45.36**), Safed Lalak X IR 64 (30.51**), Bega Hundi X Indira Aerobic 1 (38.55**), and Bega Hundi X Indira Barani Dhan 1 (46.97**). Similar positive significant heterosis reported by Tiwari *et al.* (2011) for better parent and standard heterosis.

Spikelet fertility (%)

Spikelet fertility percent is very important in hybrid breeding programme, hence positive heterotic effect would be highly desirable. The magnitude of heterosis over better parent varied from Bega Hundi X IR 64 (-0.38) to (NPT 6) X IR 64 (18.15). The negative significant observed in nine crosses, but positive highly significant found in four crosses. The superior crosses having heterobeltiosis were Ajam dhan X Indira Aerobic 1 (13.77**), (NPT 6) X MTU 1010 (11.30**), and (NPT 6) X IR 64 (18.15). Similar findings were reported by Thorat *et al.* (2017).

The magnitude of standard heterosis over Indira barani dhan-1 varied from RJR:II X Indira Aerobic 1 (-1.00) to (NPT 6) X IR 64 (19.49). The negative significant found in fourteen crosses but two crosses showed positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were (NPT 6) X Indira Aerobic 1 (14.73**) and (NPT 6) X IR 64 (19.49**).

The magnitude of standard heterosis over MTU-1010 varied from (NPT 6) X Indira Barani Dhan 1 (-1.45) to (NPT 6) X IR 64 (15.54). The negative significant found in seventeen crosses but two crosses observed positive and highly significant for this trait. The superior crosses having positive significant than (NPT 6) X Indira Aerobic 1 (15.54**) and (NPT 6) X IR 64 (20.27**).

Grain yield per plant (g)

The grain yield is a very important and complex trait, hence positive heterotic effect would be highly desirable. The magnitude of heterosis over better parent varied from Safed Lalak X IR 64 (-0.76) to Bega Hundi X Indira Barani Dhan 1 (89.64). The negative significant observed in two crosses, but positive highly significant found in eleven crosses. The superior crosses having heterobeltiosis were Ganga kali X IR 64 (60.98**), Ajam dhan X Indira Barani Dhan 1 (81.51**), Bega Hundi X Indira Barani Dhan 1 (82.64**), Ajam dhan X Indira Aerobic 1 (50.00**) and Bega Hundi X Indira Barani Dhan 1 (89.64**).

The magnitude of standard heterosis over Indira barani dhan-1 varied from Safed Lalak X Indira Barani Dhan 1 (-9.99) to Bega Hundi X Indira Barani Dhan 1 (50.64). The negative significant found in two crosses but seven crosses showed

positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were Ganga kali X Indira Aerobic 1 (71.57**), Ganga kali X IR 64 (45.14**), Ajam dhan X Indira Barani Dhan 1 (81.51**) and Bega Hundi X Indira Barani Dhan 1 (50.64**).

The magnitude of standard heterosis over MTU-1010 varied from (NPT 6) X IR 64 (-2.36) to Ajam dhan X Indira Barani Dhan 1 (88.54). The negative significant found in one crosses but twelve crosses observed positive and highly significant for this trait. The superior crosses having positive significant than MTU-1010 were Ganga kali X Indira Barani Dhan 1 (88.54), Ganga kali X Indira Aerobic 1 (59.49**), Bega Hundi X Indira Barani Dhan 1 (90.48**), Ajam dhan X Indira Barani Dhan 1 (99.46**) and Ajam dhan X Indira Barani Dhan 1 (88.54). Similar findings were reported by Latha *et al.* (2013), Ambati *et al.* (2016), Kumar and Adilakshami (2016) and Reddy *et al.* (2018) for both better parent and standard heterosis.

4.4.2 Quality traits

For heterosis analysis six quality traits viz. hulling percent, milling percent, head rice recovery percent, alkali spreading value, gel consistency and amylase content in thirty two cross combination are shown in table 4.19.

Hulling (%)

The hulling percent positive heterotic effect would be highly desirable in rice varieties. The magnitude of heterosis over better parent varied from NPT 19 X IR 64 (0.08) to Banspatri X Indira Aerobic 1 (42.15). The negative significant observed in thirteen crosses, but none of the positive significant found in crosses.

The magnitude of standard heterosis over Indira barani dhan-1 varied from Banspatri X Indira Aerobic 1 (0.03) to Banspatri X Indira Aerobic 1 (39.92). The negative significant found in fourteen crosses but none of the crosses showed positive highly significant for this traits.

The magnitude of standard heterosis over MTU-1010 varied from Safed Lalak X Indira Barani Dhan 1 (-0.14) to Banspatri X Indira Aerobic 1 (41.13). The negative significant found in fourteen crosses but none of the crosses observed positive and highly significant for this trait.

Milling (%)

In milling percent positive heterotic effect would be highly desirable in rice varieties. The magnitude of heterosis over better parent varied from Bega Hundi X IR 64 (-0.57) to Ganga kali X Indira Aerobic 1 (20.16). The negative significant observed in four crosses, but positive highly significant found in nine crosses. The superior crosses having heterobeltiosis were RJR:II X Indira Barani Dhan 1 (16.40**), RJR:II X IR 64 (12.94**), Banspatri X IR 64 (11.03*) and Ganga kali X Indira Aerobic 1 (20.16**). Similar findings were reported by Kumar and Adilakshami (2016).

The magnitude of standard heterosis over Indira barani dhan-1 varied from RJR:II X Indira Aerobic 1 (0.16) to Ajam dhan X MTU 1010 (20.04). The negative significant found in five crosses but ten crosses showed positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were RJR:II X Indira Barani Dhan 1 (16.40**), RJR:II X IR 64 (12.94**), Banspatri X IR 64 (19.20**) and Ganga kali X Indira Aerobic 1 (20.04**), NPT 19 X IR 64 (15.48**), (NPT 6) X Indira Barani Dhan 1 (18.76**), (NPT 6) X MTU 1010 (17.57**) and Bega Hundi X MTU 1010 (18.61**)

The magnitude of standard heterosis over MTU-1010 varied from Banspatri X MTU 1010 (-3.84) to (NPT 6) X MTU 1010 (28.72*8). The negative significant found in seven crosses but six crosses observed positive and highly significant for this trait. The superior crosses having positive significant than MTU-1010 were RJR:II X IR 64 (11.71**), Ganga kali X Indira Aerobic 1 (12.51**), NPT 19 X IR 64 (8.23*), (NPT 6) X Indira Barani Dhan 1 (11.31**) and Bega Hundi X MTU 1010 (11.17**)

Head rice recovery (%)

In head rice recovery percent positive heterotic effect would be highly desirable in rice varieties. The magnitude of heterosis over better parent varied from Safed Lalak X IR 64 (-0.79) to (NPT 6) X MTU 1010 (28.72). The negative significant observed in ten crosses, but positive highly significant found in four crosses. The superior crosses having heterobeltiosis were RJR:II X IR 64 (25.77**),

Banspatri X IR 64 (17.36*8), NPT 19 X Indira Aerobic 1 (17.26**) and NPT 19 X IR 64 (28.72**).

The magnitude of standard heterosis over Indira barani dhan-1 varied from Safed Lalak X Indira Aerobic 1 (0.64) to Bega Hundi X Indira Barani Dhan 1 (27.46). The negative significant found in eight crosses and three crosses showed positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were RJR:II X IR 64 (21.95**), NPT 19 X IR 64 (24.81**) and Bega Hundi X Indira Barani Dhan 1 (27.46**).

The magnitude of standard heterosis over MTU-1010 varied from Ajam dhan X Indira Aerobic 1 (0.11) to (NPT 6) X IR 64 (24.94*8). The negative significant found in twelve crosses and four crosses observed positive and highly significant for this trait. The superior crosses having positive significant than MTU-1010 were RJR:II X IR 64 (19.51**), NPT 19 X IR 64 (22.34**) and Bega Hundi X Indira Barani Dhan 1 (24.94**).

Alkali spreading value

The magnitude of heterosis over better parent varied from Safed Lalak X Indira Barani Dhan 1 (0.30) to Banspatri X MTU 1010 (75.00). The negative significant observed in sixteen crosses, but positive highly significant found in three crosses. The superior crosses having heterobeltiosis were RJR:II X Indira Barani Dhan 1 (27.27**), Ajam dhan X MTU 1010 (25.00**) and to Banspatri X MTU 1010 (75.00**).

The magnitude of standard heterosis over Indira barani dhan-1 varied from Ajam dhan X Indira Aerobic 1 (10.00) to RJR:II X Indira Barani Dhan 1(40.00). The negative significant found in fifteen crosses and four crosses showed positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were RJR:II X Indira Barani Dhan 1 (40.00**) and Banspatri X MTU 1010 (40.00**).

The magnitude of standard heterosis over MTU-1010 varied from RJR:II X Indira Aerobic 1 (-14.98) to Banspatri X MTU 1010 (100). The negative significant found in ten crosses and thirteen crosses observed positive and highly significant for

this trait. The superior crosses having positive significant than MTU-1010 were Safed Lalak X IR 64 (85.71**), Safed Lalak X Indira Aerobic 1 (57.14**), Ajam dhan X Indira Aerobic 1 (57.14**), NPT 19 X Indira Aerobic 1 (85.51**) and Banspatri X MTU 1010 (100**).

Gel consistency (mm)

The magnitude of heterosis over better parent varied from Safed Lalak X MTU 1010 (0.50) to Bega Hundi X Indira Aerobic 1 (15.61). The negative significant observed in thirteen crosses and positive highly significant found in two crosses. The superior crosses having heterobeltiosis were Bega Hundi X Indira Aerobic 1 (7.34**) and Bega Hundi X Indira Aerobic 1 (15.61**).

The magnitude of standard heterosis over Indira barani dhan-1 varied from Ajam dhan X IR 64 (0.29) to RJR:II X Indira Barani Dhan 1 (15.61). The negative significant found in thirteen crosses and two crosses showed positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were Bega Hundi X Indira Barani Dhan 1 (15.61*8), Safed Lalak X MTU 1010 (15.61*8), Banspatri X MTU 1010 (13.87*8), Banspatri X IR 64 (13.29**) and RJR:II X Indira Barani Dhan 1 (15.61**).

The magnitude of standard heterosis over MTU-1010 varied from Ajam dhan X MTU 1010 (0.12) to RJR:II X Indira Aerobic 1 (1.52). The negative significant found in fifteen crosses but none of the cross observed positive and highly significant for this trait.

Amylose content

The magnitude of heterosis over better parent varied from Safed Lalak X Indira Barani Dhan 1 (1.51) to RJR:II X MTU 1010 (63.59). The negative significant observed in ten crosses, but positive highly significant found in eleven crosses. The superior crosses having heterobeltiosis were RJR:II X Indira Barani Dhan 1 (37.26**), Banspatri X Indira Barani Dhan 1 (35.40**), Banspatri X IR 64 (33.90**), Banspatri X MTU 1010 (22.77**) and RJR:II X MTU 1010 (63.59**)

The magnitude of standard heterosis over Indira barani dhan-1 varied from Safed Lalak X Indira Barani Dhan 1 (1.57) to RJR:II X MTU 1010 (62.32). The

negative significant found in thirteen crosses but twelve crosses showed positive highly significant for this traits. The superior crosses having positive significant than Indira Barani dhan-1 were RJR:II X Indira Barani Dhan 1 (37.26*8), Banspatri X Indira Aerobic 1 (35.40**), Banspatri X MTU 1010 (34.67**), BANSPATRI X MTU 1010 (24.79*8) and RJR:II X MTU 1010 (62.32**).

The magnitude of standard heterosis over MTU-1010 varied from Safed Lalak X IR 64 (3.49) to RJR:II X MTU 1010 (63.59). The negative significant found in twelve crosses but ten crosses observed positive and highly significant for this trait. The superior crosses having positive significant than MTU-1010 were RJR:II X Indira Barani Dhan 1 (38.34*8), Banspatri X Indira Barani Dhan 1 (36.46**), Banspatri X IR 64 (35.72**), RJR:II X Indira Aerobic 1 (35.51*8) and RJR:II X MTU 1010 (63.59**).

4.5 Stability analysis for seed yield and its components.

Stability analysis in thirty seven rice genotypes on three environments was done by the Eberhart and Russell model (1966). Stability analysis was done in thirteen yield and yield contributing traits viz. days to 50 per cent flowering, plant height, total number of tillers per plant, number of effective tillers per plant, flag leaf area, panicle length, number of filled grains per panicle, total number of grains per panicle, spikelet fertility percent, 100 grain weight, grain yield per plant, biological yield per plant and harvest index.

4.5.1 Pooled analysis of variance

The result of pooled analysis of variance for stability as analyzed by Eberhart and Russell model (1966) is presented in table 4.22. The thirty seven genotypes showed significant differences for most of the traits except panicle length and 100 grain weight. It revealed that the selected genotypes are rice in variation for various characters and may not be uniform performance in different environments. Similar findings were reported by Ramezani and Torabi (2011).

Environments showed highly significant and significant difference for all the characters except plant height, flag leaf area, panicle length and 100 grain weight. E + (G X E) interaction was highly significant for all the characters except total tillers per plant, effective tillers per plant, flag leaf area, panicle length and 100 grain weight. Similar findings were reported by Biswas *et al.* (2011) Lal and Singh (2012) Tariku *et al.* (2013) and Ajmera *et al.* (2017). Environment (linear) was highly significant for all the traits except flag leaf area, 100 grain weight and biological yield. G X E (linear) and pooled deviation showed highly significant and significant difference for six traits viz. filled grains per panicle, total grains per panicle, spikelet fertility, grain yield per plant, biological yield per plant and harvest index. Highly significant for the traits, indicated that performance of genotypes is entirely unpredictable in nature and importance of non-linear component in determining interaction of genotypes with environment.

4.5.2 Stability parameters

According to Eberhart and Russel model (1966), a stable genotype is one which shows (i) high mean yield (ii) regression coefficient ($b_i=1$) equal to unity and (iii) a mean square deviation from regression (s^2d_i) near to zero. In interpreting the results of the present investigation, s^2d_i was considered as the measure of stability as suggested by Breeze (1969), then the type of stability (measure of response or sensitivity to environment changes) was decided on the regression coefficient (b_i) and mean values (Finlay and Wilkinson, 1963). If b_i is equal to unity, a genotype is considered to possess average stability and widely adaptable to different environments, if b_i is more than unity, it is considered to possess less than average stability and is adaptable to favorable environments, if b_i is less than unity, it is considered to possess more than the average stability and is adaptable to poor environments.

4. 5.2.1 Mean and stability parameters

The stability parameters mean (μ), regression coefficient (b_i) and deviation from regression (s^2_{di}) are presented in Appendix-D and selected stable genotypes are presented in table 4.24.

Days to 50% flowering

Days to 50% flowering ranged from 70.83 (Nagina 22) to 97.50 (Swarna) with population mean of 81.06 days.

Stability parameters indicated that the genotypes had early flowering were Barhasal (78.17days) and Indira Aerobic (75.50 days) with below average stability ($b_i > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had early flowering were Banspatri (75.00 days) and NPT 26 (79.33 days), with above average stability ($b_i < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment.

Stability parameters indicated that the early flowering genotypes were Ajawain (76.83 days) and Khurabal (78.17 days), with near to unit regression and non-significant deviation from regression line, thus found to be stable over the environment and indicating predictable performance.

Table 4.22: Analysis of variance of Eberhart and Russel model (1966)

Source of variation	df	DF	PH	TT	ET	FLA	PL	FG	TG
Varieties	36	73.79**	263.72**	20.16**	18.54**	50.43**	8.17	3057.19**	3271.70**
Environment	2	994.87**	15.14	55.71*	53.45*	5.92	1.74	668.80**	113.33**
Env. + (Varieties X Env.)	74	48.53**	10.89**	3.99	4.12	1.03	2.36	258.20**	163.14**
Environment (linear)	1	2542.72**	30.27*	111.42**	106.90**	11.84	3.48	2911.96**	226.66**
Varieties X Env. (linear)	36	16.39	9.73	2.49	3.06	2.68	3.25	339.67**	69.86**
Pooled Deviation	37	12.39	11.49	2.54	2.37	0.91	1.45	107.22**	252.18**
Pooled Error	108	1.05	8.21	1.71	1.38	1.70	0.93	61.55	45.15

Cont...

Source of variation	df	SF	TW	EY	BY	HI
Varieties	36	284.70**	0.19	22.04*	124.44**	152.81**
Environment	2	263.87**	0.11	257.60**	15.48	1427.78**
Env. + (Varieties X Env.)	74	45.01**	0.04	36.47**	58.03**	129.00**
Environment (linear)	1	527.74**	0.21	39.52**	30.95	2855.55**
Varieties X Env. (linear)	36	49.65**	0.06	55.36**	62.82**	84.44**
Pooled Deviation	37	27.46**	0.01	26.65*	54.11**	98.66**
Pooled Error	108	7.68	0.01	10.53	8.23	19.56

* & ** represent significant levels at 5% and 1% respectively.

Table 4.24: Selected genotypes on the basis of Eberhat and Russell stability model (1966)

S. No	Traits	b=1	b>1	b<1
1	Days to 50% flowering	Ajawain (76.83), Khurabal (78.17),	Barhasal (78.17), Indira Aerobic (75.50)	RJR:II(75), NPT 26 (79.33),
2	Plant height (cm)	Indira Barani Dhan 1 (86.01)	Ganga kali (88.49cm), Kolhin khosa (83.05), Jeera Baba (84.74),	Digamber dhan (82.54cm), NPT 8 (75.62cm), N-22 (79.65) Indira Aerobic 1 (80.86)
3	Tillers per plant (No.)	-	NPT 26 (13.48), Dadbako (14.04), Khurabal (13.59), Nagina 22 (18.74), Indira Barani Dhan 1(17.48) Indira Aerobic 1(18.50)	Tewan dhan (15.38), Jeera Baba (17.30), Swarna (17.78),
4	Effective tillers per plant (No.)	--	Dadbako (13.52), N-22 (18.13), Swarna (16.86), Samleshwari (18.22), Indira Aerobic 1 (18.20)	Tewan dhan (14.87), Jeera Baba (16.00),
5	Flag leaf area (cm ²)	-	Bansapatri (30.50), E-1986 (30.23), Dadhmaini dhan (28.73), Gangtai (30.24) Bhatamokdo (33.99), IR-64 (28.73),	Digamber dhan (31.25),
6	Panicle length (cm)	--	RJR:II(33.62), Baikoni (32.49), Indira Barani Dhan 1 (31.04), Indira Aerobic 1 (32.06),	E-1986 (31.83), Dadbako (31.05),
7	Filled grains per panicle (No.)	-	Ajam dhan (149.51),, Safed Lalak (163.54), Jeera Baba (159.18), Bega hundi(174.84), Baikoni (166.54), Gangtai (172.15), NPT 6 (191.85)	Dadhmaini dhan (154.84), Digamber dhan (198.76), NPT 19 (163.43),
8	Total grains per panicle (No.)	-	Bega hundi (195.30), Swarna (224.27),	Jeera Baba (178.03), NPT 19 (176.62),
9	Spikelet fertility (%)	-	Ganga kali (90.86), Tewan dhan (91.65), Samleshwari (89.23),	Bansapatri (93.31), Ajawain (92.61), Dadhmaini dhan (92.00), Indira Barani Dhan 1 (89.81)
10	100 grain weight (g)	-	NPT 6 (2.41) Banko (2.86), MTU 1010 (2.44),	Safed Lalak (2.43), Khurabal (2.66), Indira Aerobic 1 (2.34)
11	Grain yield per plant (g)	Barhasal (22.47),	Safed Lalak (25.85), Kolhin khosa (24.99), Dadhmaini dhan (23.76), Dadbako (24.41), N-22 (24.40),	Bhatamokdo (24.87),
12	Biological yied per plant (g)	-	Digamber dhan (54.08), Jeera Baba (56.70), Swarna (59.50), MTU 1010 (64.12), Samleshwari (57.90)	Dadbako (54.57),
13	Harvest index (%)	-	Dadhmaini dhan (69.30), Dadbako (64.21), Indira Barani Dhan 1 (65.61), Samleshwari (63.02), Indira Aerobic 1 (69.08)	NPT 26 (65.15), NPT 8 (63.67),

Plant height (cm)

The plant height ranged from 75.34 cm (NPT 6) to 75.34 cm (Khurabal) with population mean of 89.29cm.

Stability parameters indicated that the genotypes had dwarf stature were Ganga kali (88.49cm), Kolhin khosa (83.05cm) and Jeera Baba (84.74cm), with below average stability ($b_i > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes were dwarf stature were Digamber dhan (82.54cm), NPT 8 (75.62cm), N-22 (79.65cm) and Indira Aerobic 1 (80.86cm), with above average stability ($b_i < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment.

Stability parameters indicated that the dwarf stature genotypes were Indira Barani Dhan 1 (86.01cm), with near to unit regression and non-significant deviation from regression line, thus found to be stable over the environment and indicating predictable performance. Similar results were finding by Lal and Singh (2012).

Total tillers per plant

The total tillers per plant ranged from 9.56 (90 Number) to 18.78 (Samleshwari) with population mean of 13.38.

Stability parameters indicated that the genotypes had high tillers per plant were NPT 26 (13.48), Dadbako (14.04), Khurabal (13.59), N-22 (18.74), Indira Barani Dhan 1(17.48) and Indira Aerobic 1(18.50) with below average stability ($b_i > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high tillers per plant were Tewan dhan (15.38), Jeera Baba (17.30) and Swarna (17.78), with above average stability ($b_i < 1$) and non-significant

deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype found as stable for this trait.

Effective tillers per plant

The effective tillers per plant ranged from 9.18 (90 Number) to 18.22 (Samleshwari) with population mean of 12.76.

Stability parameters indicated that the genotypes had high effective tillers per plant were Dadbako (13.52), N-22 (18.13), Swarna (16.86), Samleshwari (18.22) and Indira Aerobic 1 (18.20) with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high effective tillers per plant were Tewan dhan (14.87) and Jeera Baba (16.00), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment.

Flag leaf area (m²)

The flag leaf area ranged from 19.08 (NPT 26) to 38.20 cm² (BANKO) with population mean of 38.20 m².

Stability parameters indicated that the genotypes had high flag leaf area were RJR:II (30.50 cm²), Chingar Bnko (30.23 cm²), Dadhmaini dhan (28.73 cm²), Gangtai (30.24 cm²) Bhatamokdo (33.99 cm²) and IR 64 (28.73 cm²), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotype had high flag leaf area was Digamber dhan (31.25), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment.

Panicle length

The panicle length ranged from 27.15 (Tewan dhan) to 34.73cm (Bhatamokdo) with population mean of 30.46 cm.

Stability parameters indicated that the genotypes had high panicle length were Banspatri (33.62cm), BAIKONI(32.49cm), Indira Barani Dhan 1 (31.04cm) and Indira Aerobic 1 (32.06cm), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high panicle length were Chingar Bnko (31.83cm) and Dadbako (31.05cm), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment.

Filled grains per panicle

The filled grains per panicle ranged from 55.31 (P:357 III) to 212.17 (Bhatamokdo) with population mean of 140.99.

Stability parameters indicated that the genotypes had high filled grains per panicle were Ajam dhan (149.51), Safed Lalak (163.54), Jeera Baba (159.18), Bega Hundi (174.84), Baikoni (166.54), Gangtai (172.15) and NPT 6 (191.85) with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high filled grains per panicle were Dadhmaini dhan (154.84), Digamber dhan (198.76), NPT 19 (163.43), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment.

Total grains per panicle

The total grains per panicle ranged from 106.38 (Nagina 22) to 231.29 (Bhatamokdo) with population mean of 163.61.

Stability parameters indicated that the genotypes had high total grains per panicle were Bega Hundi (195.30) and Swarna (224.27), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high total grains per panicle were Jeera Baba (178.03) and NPT 19 (176.62), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment for this trait.

Spikelet fertility (%)

The spikelet fertility ranged from 40.40% (P:357 III) to 94.54% (NPT-8) with population mean of 85.59%.

Stability parameters indicated that the genotypes had high spikelet fertility were Ganga kali (90.86), Tewan dhan (91.65%) and Samleshwari (89.23%), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high total grains per panicle were RJR:II (93.31%), Ajawain (92.61%), Dadhmaini dhan (92.00%) with Indira Barani Dhan 1 (89.81%), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment for this trait.

100 grain weight (g)

The 100 grain weight ranged from 1.52 g (Digamber dhan) to 2.86 (Banko) with population mean of 2.21 g.

Stability parameters indicated that the genotypes had high 100 grain weight were NPT 6 (2.41g) Banko (2.86g), MTU 1010 (2.44g), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high 100 grain weight were Safed Lalak (2.43g), Khurabal (2.66g) and Indira Aerobic 1 (2.34g), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment for this trait.

Grain yield per plant (g)

The grain yield per plant ranged from 11.51g (P:357 III) to 25.85g (Safed Lalak) with population mean of 27.49 g.

Stability parameters indicated that the genotypes had high grain yield per plant were Safed Lalak (25.85g), Kolhin khosa (24.99g), Dadhmaini dhan (23.76g), Dadbako (24.41g), N-22 (24.40g), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high grain yield per plant was Bhatamokdo (24.87g), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment.

Stability parameters indicated that genotype had high grain yield per plant was Barhasal (22.47), it showed near to unit regression and non-significant deviation from regression line, thus found to be stable over the environment and indicating predictable performance. Similar results were finding by Rasyad et al. (2012), Subudhi et al. (2012) Lal and Singh (2012) Tariku et al. (2013) and Ajmera et al. (2017).

Biological yield per plant (g)

The biological yield per plant ranged from 38.02g (P:357 III) to 64.12g (MTU 1010) with population mean of 52.00g.

Stability parameters indicated that the genotypes had high biological yield per plant were Digamber dhan (54.08g), Jeera Baba (56.70g), Swarna (59.50g), MTU 1010 (64.12g), Samleshwari (57.90g), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotype had high biological yield per plant was Dadbako (54.57g), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment for this trait.

Harvest index (%)

The harvest index ranged from 41.71% (P:357 III) to 71.96 % (Nagina 22) with population mean of 62.92%.

Stability parameters indicated that the genotypes had high harvest index were Dadhmaini dhan (69.30g), Dadbako (64.21g), Indira Barani Dhan 1 (65.61g), Samleshwari (63.02g), Indira Aerobic 1 (69.08g), with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found to be suitable for favorable environment through its performance was predictable.

Genotypes had high harvest index were NPT 26 (65.15) and NPT 8 (63.67), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment. None of the genotype was found to be stable over the environment for this trait.

4.6 Expression of small heat shock proteins

For present study at flowering stage of ten rice genotypes (RJR:II, Ganga dhan, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, NPT 6, Bega Hundi, Baikoni, Bhatamokdo) and two checks (Nagina 22, IR 64) were selected for the expression of small HSPs using semi quantitative RT-PCR. Nagina 22 (heat tolerant) and IR 64 (heat susceptible) were used as a tolerant and susceptible check. Expression analysis of sHSPs by semi quantitative RT-PCR was undertaken at flowering stage to assess the different expression in heat stress conditions in genotypes.

4.6 .1 Expression analysis using semi quantitative RT-PCR

Among the seventeen sHSP genes, six genes (sHSPs 18.8, sHSPs 16.9A, sHSPs 18.6, sHSPs 16.0, sHSPs 24.0 and sHSPs 17.9) were expressed under stress conditions. Semi quantitative RT-PCR analysis showed differential expression of these six genes in rice genotypes under stress with respect to the checks genotypes (Fig 4.1). The results are discussed below in detail. The genes showed distinct variation in level of expression among genotypes at flowering stage of rice.

Expression of sHSPs gene

sHsp 18.8-CV

In this study, Semi quantitative RT-PCR of sHsp 18.8-CV gene expressed in all genotypes. All genotypes showed enhanced transcript level when compare to tolerant (Nagin 22) and susceptible check (IR 64) under heat stress condition. Guan *et al.* (2004) studied Oshsp16.9A gene induced strongly after a 2-h heat shock treatment in rice (*Oryza sativa* Tainung No.67).

sHsps 16.9A-CI

sHsps 16.9A-CI showed up regulation in nine genotypes RJR:II, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, NPT 6, Bega Hundi, E-1894, Bhatamokdo and down regulation in Ganga dhan, when compare to tolerant check. When compare to susceptible check increase transcript level was found in two genotype viz. NPT 6, Bega Hundi and down regulation was found in eight genotypes RJR:II, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, Ganga dhan, Baikoni, Bhatamokdo. Jung *et al.* (2014) also analyzed that expression of the Oshsp16.9 gene at heat (45°C) through RT-PCR analysis and Chen *et al.* (2014) reported up-regulated in Nipponbare during anthesis stages in heat stress. Guo *et al.* (2016) reported that Os16.9A play important roles not only for heat shock response, but also for normal development in rice.

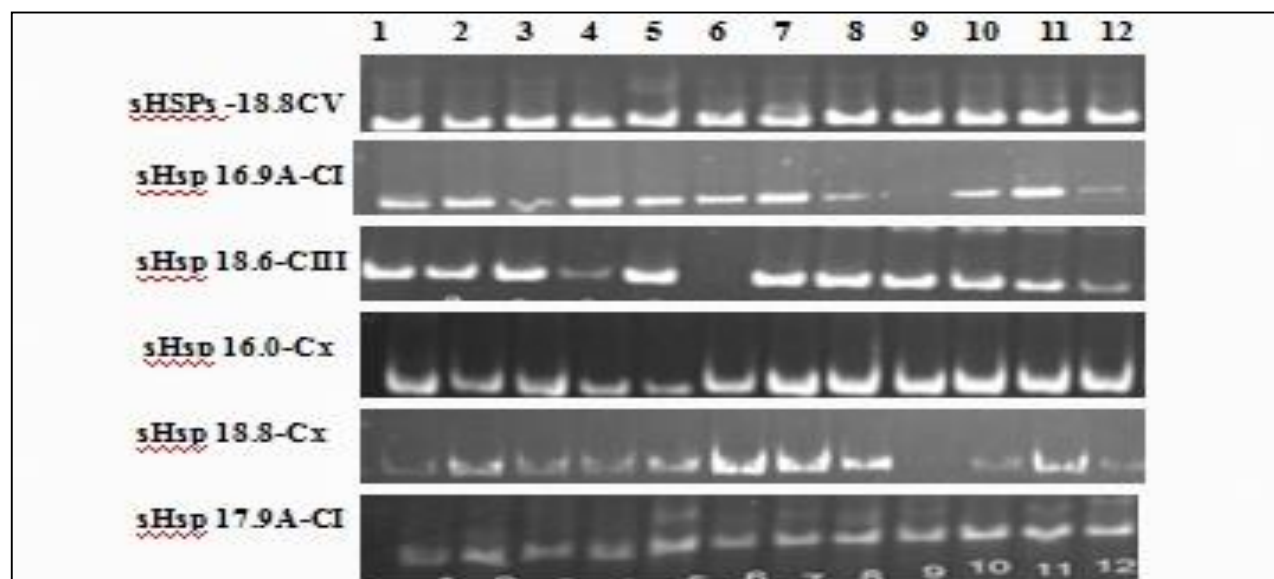
sHsps 18.6A-CIII

sHsps 18.6A-CIII was observed up regulation in two genotypes Kolhin khosa, NPT 26 and down regulation in eight genotypes RJR:II, Ganga dhan, Ajam dhan, Digamber dhan, NPT 6, Bega Hundi, Baikoni, Bhatamokdo, when compared to tolerant check. When compared to susceptible check two genotypes NPT 6, Bega Hundi showed up regulation and eight genotypes RJR:II, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, Ganga dhan, Baikoni, Bhatamokdo showed down regulation. Sarkar *et al* (2009) also reported up regulation of sHsps 18.6A-CIII at 10 minute at

Table 4.14: Gel score of genotypes under heat stress condition

S. No	HSPs	1	2	3	4	5	6	7	8	9	10	11	12
1	Hsp 18.8-CV	0.92	0.97	1.00	0.99	0.99	0.99	0.99	0.99	0.94	0.93	0.65	0.76
2	Hsp 16.9A-CI	0.42	0.67	0.35	0.48	0.42	0.35	0.47	0.27	0.04	0.36	0.53	0.12
3	Hsp 18.6-CIII	0.16	0.39	0.36	0.57	0.36	0.92	0.43	0.34	0.06	0.4	0.46	0.29
4	Hsp 16.0-Px	0.67	0.6	0.63	0.49	0.45	0.54	0.6	0.53	0.61	0.51	0.57	0.55
5	Hsp 18.8CX	0.09	0.34	0.21	0.16	0.25	0.48	0.41	0.37	0.12	0.12	0.32	0.11
6	Hsp 17.9A-CI	0.49	0.22	0.43	0.42	0.38	0.02	0.04	0.45	0.04	0.35	0.36	0.21

1. RJR:II, 2. Ganga dhan, 3. Ajam dhan, 4. Kolhin khosa, 5. Digamber dhan 6. NPT-26, 7. NPT 6, 8. Dan Banko, 9. Baikoni, 10. Bhata mokdo, 11. Nagina 22, 12. IR 64



1. RJR:II, 2. Ganga dhan, 3. Ajam dhan, 4. Kolhin khosa, 5. Digamber dhan
 6. NPT-26, 7. NPT 6, 8. Dan Banko, 9. Baikoni, 10. Bhata mokdo, 11. Nagina 22,
 12. IR 64

Fig 4.1: Expression of rice genotypes in different band pattern on heat stress conditio

42°C in and down regulation further exposure for 1 hr at 42°C rice. Wang *et al.* (2015) categorized OsHSP18.6 could be induced by diverse stresses, such as salt, cold and drought, especially under heat. This gene was found expressed in leaf, stem, root, internode and spikelet.

sHsps 16.0-Px

sHsps 16.0-Px gene was observed up regulation in five genotypes RJR:II, Ganga dhan, Ajam dhan, NPT 6, Baikoni, and down regulation in five genotypes Kolhin khosa, Digamber dhan, NPT 26, Bega Hundi, Bhatamokdo, when compared to tolerant check. When compared to susceptible check up regulation in five genotypes RJR:II, Ganga dhan, Ajam dhan, NPT 6, Baikoni, and down regulation in five genotypes Kolhin khosa, Digamber dhan, NPT 26, Bega Hundi, Bhatamokdo. Sarkar *et al* (2009) also reported up regulation of sHsps 16.0-Px-CI in rice. Chandel *et al.* (2013) reported that gene encoding OsHsp 16.0-Px showed strong induction upon heat stress.

sHsps 18.8CX

sHsps 18.8CX gene was observed up regulation in four genotypes Ganga dhan, NPT 26, NPT 6, Bega Hundi, and down regulation in six genotypes RJR:II, Ajam dhan, Kolhin khosa, Digamber dhan, Baikoni, Bhatamokdo, when compared to tolerant check. When compared to susceptible check up regulation in nine genotypes Ganga dhan, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, NPT 6, Bega Hundi, Baikoni, Bhatamokdo, and down regulation in one genotype RJR:II.

sHSP 17.9A-CI

sHSP 17.9A-CI was observed up regulation in five genotypes RJR:II, Ajam dhan, Kolhin khosa, Digamber dhan, , Bega Hundi, and down regulation in five genotypes Ganga dhan, NPT 26, NPT 6 Baikoni, Bhatamokdo, when compared to tolerant check. When compared to susceptible check up regulation in eight genotypes RJR:II, Ganga dhan, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, , Bega Hundi, Bhatamokdo and

down regulation in two genotypes NPT 6 and E-1894. Sarkar *et al* (2009) also reported up regulation of sHsps 17.9A-CI and also Chen *et al.* (2014) studied up-regulated in Nipponbare during seedling and anthesis stages in heat stress.

CHAPTER - V

SUMMARY AND CONCLUSIONS

Rice is the most important cereal food crop of India. India is the second largest producer of rice after China. In India major share of rice is cultivated during *Kharif* season and small area is grown in *rabi* or *summer* season with assured irrigation. Since 1970s, the rice cultivation pattern has gradually changed from double-season to single-season planting; because the flowering phase of *rabi* or *summer* season rice occurs at the period with the high temperature stress that negatively affect the grain yield. Rice is a temperature responsive crop, during the early growth stages of rice, the occurrence of low temperature stress inhibits seedling establishment and ultimately leads to non uniform crop maturation. One of the major challenges in future agriculture is to sustain food grain production under changing climate and limited natural resources. The sowing time of summer rice is November to February and harvesting time is March to June. The nurseries raised during December usually faces prolonged low temperature. In germination phase, the low temperature delayed and lower percentage of germination and suppresses the normal growth of seedlings. At flowering stage summer rice faces high temperature, this leads to lower spikelet fertility resulted in lesser filled grains, low grain weight per panicle, low grain yield and lower harvest index. Therefore, farmers are not interested in summer rice cultivation. Thus there is need to develop high yielding early medium duration varieties which can tolerate temperature stress with high head rice recovery. Therefore, the present investigation was undertaken to select the heat tolerance, medium duration, high yield and good quality genotypes.

The present investigation entitled “**Combining ability for yield, cold, heat and grain quality improvement in rice (*Oryza sativa* L.)**” was carried on eighty seven rice genotypes. Eighty seven rice genotypes were studied for variability analysis and association analysis on *Summer-2017* for grain yield and yield contributing traits

viz., days to 50 per cent flowering, plant height, tillers per plant, effective tillers per plant, flag leaf area, panicle length, filled grains per panicle, total number of grains per panicle, spikelet fertility, 100 grain weight, grain yield per plant, biological yield per plant and harvest index. The analysis of variance showed a wide range of variation and significant differences for all the traits under study, indicating the presence of sufficient amount of variability. Further the presence of variability in the base material ensures better chances of selection for desirable plant types.

In the present study estimates of phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) for all the traits, but the difference was relatively small for all traits, it indicating that these characters were less influenced by the environment. In this study, the highest PCV and GCV was recorded for filled grains per panicle, grain yield per plant, total grains per panicle, biological yield per plant, total tillers per plant, effective tillers per plant and flag leaf area, indicating the presence of considerable genetic variability and less influence of environment on the expression on this traits. High heritability coupled with high genetic advance as percent of mean was found in days to fifty percent flowering, flag leaf area, total grains per panicle, filled grain per panicle, 100 grain weight, spikelet fertility per panicle, grain yield per plant, biological yield per plant, effective tillers per plant, plant height, total tillers per plant and harvest index, it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effective for crop improvement.

Grain yield per plant exhibited positive and highly significant correlation with biological yield per plant, filled grain per panicle, total tiller per plant, effective tillers per plant, total grains per panicle, spikelet fertility per panicle and harvest index. This indicated that simultaneous selection of all these characters was important for yield improvement. So, they may used as a selection criteria to improve the grain yield in rice.

On the basis of grain yield per plant, spikelet fertility percent and pollen fertility percent, thirty seven rice genotypes were selected for cold, heat and quality traits. Selected thirty seven genotypes were evaluated in *Summer*-2018 for cold, heat and quality study. For cold screening rice genotypes were examined at germination stage at two different temperatures (13°C and 28°C). These experiment following the protocol established by da Cruz and Milach (2004). On the basis of germination index (%), percent of seeds with coleoptiles length greater than 5mm (PERCOL5 %), percent of reduction in coleoptile length (REDCOL%), coleoptile regrowth (COLREG mm) and radicle regrowth (REDREG mm), eight genotypes were selected viz. RJR:II, BANSPATRI, Ganga dhan, Tewan dhan, Digamber dhan, Barhasaal, Indira Barani Dhan-1 and Inbira Aerobic-1 as a cold tolerance genotype.

Selected thirty seven genotypes were also evaluated for heat screening at flowering condition for different heat parameters viz. canopy temperature (°C), membrane stability index (%), pollen fertility (%) and spikelet fertility (%). On the basis of these heat parameters thirteen genotypes Dadbko, NPT 6 Gangtai, RJR:II, Ganga kali, NPT 19, NPT 6, Dan Banko, Kolhin khosa, Banspatri, Ganga dhan, Safed Lalak and Ajam dhan were selected.

On the basis of both cold and heat screening parameters the three genotypes viz RJR:II, Banspatri and Ganga Kali identified as tolerance for both heat and cold.

After study of cold and heat effect on thirty seven selected genotypes, eight lines selected for combining ability analysis. Out of eight lines, three lines (RJR:II, Banspatri and Ganga kali) showed tolerant in both cold and heat stress and five lines (Ajam dhan, Safed lalak, NPT-19, NPT 6 and Dan banko) only showed tolerant in heat stress condition. Selected four testers (Indira Barani Dhan-1, Indira Aerobic 1, IR 64 and MTU 1010) were early maturity released variety. Thirty two crosses were derived by crossing eight lines with each of four testers and they were evaluated along with parents in randomized block design with two replications.

For grain yield per plant three lines (Ganga kali, Ajam dhan, Dan banko) and one tester (Indira Barani Dhan 1) showed positive and significant gca effects. For head

rice recovery two lines (Ajam dhan , Safed Lalak) and two testers (IR 64, MTU 1010) showed positive and significant gca effects. Therefore, a multiple crossing programme involving these parents will give superior genotype .Among the thirty two crosses eight crosses viz. Dan Banko X Indira Barani Dhan 1, Ajam dhan X Indira Barani Dhan 1, Ganga kali X Indira Aerobic 1, RJR:II X IR 64, Banspatri X MTU 1010, Safed Lalak X IR 64, NPT 19 X MTU 1010, NPT 6 X MTU 1010 showed positive and significant sca effects. Therefore, these hybrids are recommended for heterosis breeding. The four crosses viz. RJR:II X Indira Barani Dhan 1, Banspatri X IR 64, Banspatri X MTU 1010, NPT 6 X Indira Barani Dhan 1 showed positive and significant sca effects for hulling, milling and head rice recovery. The one cross Banspatri X MTU 1010 recorded positive and significant sca effects for grain yield per plant, hulling, milling and head rice recovery.

In this study, estimates of heterosis for eight yield and yield contributing traits viz. days to fifty percent flowering, plant height, tillers per plant, effective tillers per plant, fertile grains per panicle, total grains per panicle, spikelet fertility and grain yield per plant and six quality traits viz. hulling percent, milling percent, head rice recovery percent, alkali spreading value, gel consistency and amylose content in thirty two cross combination.

For grain yield per plant superior crosses having heterobeltiosis were Ganga kali X IR 64, Ajam dhan X Indira Barani Dhan 1, Dan Banko X Indira Barani Dhan 1, Ajam dhan X Indira Aerobic 1 and Dan Banko X Indira Barani Dhan 1. The superior crosses having positive significant than Indira Barani dhan-1 were Ganga kali X Indira Aerobic 1, Ganga kali X IR 64, Ajam dhan X Indira Barani Dhan 1 and Dan Banko X Indira Barani Dhan 1. The superior crosses having positive significant than MTU 1010 were Ganga kali X Indira Barani Dhan 1, Ganga kali X Indira Aerobic 1, Dan Banko X Indira Barani Dhan 1, Ajam dhan X Indira Barani Dhan 1 and Ajam dhan X Indira Barani Dhan 1.

Stability analysis in thirty seven rice genotypes on three environments was done by the Eberhart and Russell model (1966). Stability analysis was done in thirteen

yield and yield contributing traits viz. days to 50 per cent flowering, plant height, total number of tillers per plant, number of effective tillers per plant, flag leaf area, panicle length, number of filled grains per panicle, total number of grains per panicle, spikelet fertility percent, 100 grain weight, grain yield per plant, biological yield per plant and harvest index. The thirty seven genotypes showed significant differences for most of the traits except panicle length and test weight. It revealed that the selected genotypes are rich in variation for various characters and may not be uniform performance in different environments.

Stability parameters indicated for early flowering Ajawain and Khurabal,, for plant height dwarf stature genotype Indira Barani Dhan 1 and for grain yield per plant Barhasal, found to be stable over the environment and indicating predictable performance. The genotypes had high grain yield per plant were Safed Lalak, Kolhin khosa, Dadhmaini dhan, Dadbako, Nagina 22, with below average stability ($bi > 1$) and non-significant deviation from regression line, therefore, this genotype was found highly sensitive to environment and suitable for favorable environment through its performance was predictable. Genotypes had high grain yield per plant was Bhatamokdo (24.87g), with above average stability ($bi < 1$) and non-significant deviation from regression line, therefore, its performance was predictable and it could perform better under poor environment.

For expression analysis at flowering stage of ten rice genotypes (RJR:II, Ganga dhan, Ajam dhan, Kolhin khosa, Digamber dhan, NPT 26, NPT 6, Dan Banko, Baikoni and Bhatamokdo) and two checks (Nagina 22, IR 64) were selected for the expression of small HSPs using semi quantitative RT- PCR. Nagina 22 (heat tolerant) and IR 64 (heat susceptible) were used as a tolerant and susceptible check. Expression analysis of sHSPs by semi quantitative RT-PCR was undertaken at flowering stage to assess the different expression in heat stress conditions in genotypes. Among the seventeen sHSP genes, six genes (sHSPs 18.8, sHSPs 16.9A, sHSPs 18.6, sHSPs 16.0, sHSPs 24.0 and sHSPs 17.9) were expressed under stress conditions. The three genotypes RJR:II, Ganga dhan, and Ajam dhan in most of the genes showed

upregulation, when compare to tolerant and susceptible checks. So, these genotypes indicated as the tolerant genotypes in heat stress condition.

CONCLUSIONS

Major conclusion with have been drawn from the present investigation are listed below:

- Among the eighty seven genotypes, the analysis of variance showed a wide range of variation and significant differences for all the traits under study, indicating the presence of sufficient amount of variability.
- High heritability coupled with high genetic advance as percent of mean was found in days to 50% flowering, flag leaf area, total grains per panicle, filled grain per panicle, 100 grain weight, spikelet fertility, grain yield per plant, biological yield per plant, effective tillers per plant, plant height, total tillers per plant and harvest index, it indicates that these traits are under the influence of additive gene action with least environment influence and simply phenotypic selection would be effective for crop improvement.
- Grain yield per plant exhibited positive and highly significant correlation with biological yield per plant, filled grain per panicle, total tiller per plant, effective tiller per plant, total grain per panicle, spikelet fertility and harvest index. This indicated that simultaneous selection of all these characters was important for yield improvement. So, they may used as a selection criteria to improve the grain yield in rice.
- On the basis of cold tolerance test genotypes were selected viz. RJR:II, Banspatri, Ganga dhan, Tewan dhan, Digamber dhan, Barhasaal, Indira Barani Dhan-1 and Indira Aerobic-1.
- On the basis of heat screening thirteen genotypes Dadbko, NPT 6, Gangtai, RJR:II, Ganga kali, NPT 19, NPT 9, Dan Banko, Kolhin khosa, Banspatri, Ganga dhan, Safed Lalak and Ajam dhan were selected.

- On the basis of both cold and heat test parameters the three genotypes viz RJR:II, Banspatri and Ganga Kali identified as tolerance for both heat and cold stress.
- For grain yield per plant three lines (Ganga kali, Ajam dhan, Dan Banko) and one tester (Indira Barani Dhan 1) and for head rice recovery two lines (Ajam dhan , Safed Lalak) and two testers (IR 64 and MTU 1010) identified as superior genotypes for general combining ability. A multiple crossing programme involving these parents will give superior genotype .
- For grain yield per plant among the 32 crosses eight crosses viz. Dan Banko X Indira Barani Dhan 1, Ajam dhan X Indira Barani Dhan 1, Ganga kali X Indira Aerobic 1, RJR:II X IR 64, Banspatri X MTU 1010, Safed Lalak X IR 64, NPT 19 X MTU 1010, NPT 6 X MTU 1010 and four crosses viz. RJR:II X Indira Barani Dhan 1, Banspatri X IR 64, Banspatri X MTU 1010, NPT 6 X Indira Barani Dhan 1 for hulling, milling and head rice recovery, identified as superior crosses. The cross Banspatri X MTU 1010 identified as superior cross for grain yield per plant, hulling, milling and head rice recovery. Therefore, these hybrids are recommended for heterosis breeding.
- For grain yield per plant superior crosses having heterobeltiosis were Ganga kali X IR 64, Ajam dhan X Indira Barani Dhan 1, Dan Banko X Indira Barani Dhan 1, Ajam dhan X Indira Aerobic 1 and Dan Banko X Indira Barani Dhan 1. The superior crosses over Indira Barani dhan 1 were Ganga kali X Indira Aerobic 1, Ganga kali X IR 64, Ajam dhan X Indira Barani Dhan 1 and Dan Banko X Indira Barani Dhan 1. The superior crosses over MTU 1010 were Ganga kali X Indira Barani Dhan 1, Ganga kali X Indira Aerobic 1, Dan Banko X Indira Barani Dhan 1, Ajam dhan X Indira Barani Dhan 1 and Ajam dhan X Indira Barani Dhan 1.
- Stability parameters indicated for early flowering Ajawain and Khurabal, for plant height dwarf stature genotype Indira Barani Dhan 1 and for grain yield per plant Barhasal found to be stable over the environment and indicating predictable performance.

- For expression analysis at flowering stage the three genotypes RJR:II, Ganga dhan, and Ajam dhan in most of the genes showed upregulation, when compared to tolerant and susceptible checks. So, these genotypes indicated as the tolerant in heat stress condition.

SUGGESTIONS FOR FUTURE RESEARCH WORK

- The selected genotypes on the basis of cold and heat screening should be validated by the linked genetic marker.
- Identified desirable general combiner and specific combiner genotypes for yield and quality traits, should be utilized in breeding programme.
- Performance of identified stable genotypes over location should be further evaluated in field.

REFERENCES

- Abebe, T., Alamerew, S., & Tulu, L. 2017. Genetic variability, heritability and genetic advance for yield and its related traits in rainfed lowland rice (*Oryza sativa* L.) genotypes at Fogera and Pawe, Ethiopia. Adv. Crop Sci. Tech., 5, (272): 56-61.
- Abeyesiriwardena, D.S.de.Z., Buss, G.R., Reese Jr., P.F. 1991. Analysis of multi environmental yield trails for testing adaptability of crop genotypes, Tropical Agriculturist. 147: 85–97.
- Abuali, A.I., Abdelmulla, A.A., Khalafalla, M.M., Idris A.E. and Osman. A.M. 2012. Combining ability and heterosis for yield and yield components in maize (*Zea mays* L.). Aust. J. Basic Appl. Sci. 6(10): 36-41.
- Acharya, S., Shrestha, A., Acharya, N., Poudel, A. and Acharya, S. 2018. Genetic Variability, Heritability And Correlation Analysis In Quantitative Traits Of Irrigated Rice (*Oryza Sativa* L.).Biosciences Biotechnology Research Asia. 15(3):729-735.
- Acharya, S., Shrestha , A., Acharya, N., Poudel, A. and Acharya, S. 2018. Genetic Variability, Heritability And Correlation Analysis In Quantitative Traits Of Irrigated Rice (*Oryza Sativa* L.). Biosciences Biotechnology Research Asia. 15(3): 729-735.

- Adhikari, B.N., Pokhrel, B.B., & Shrestha, J. 2018. Evaluation and development of finger millet (*Eleusine coracana* L.) genotypes for cultivation in high hills of Nepal. *Fmg. & Mngmt.*, 3(1), 37-46.
- Aditya, J.P and Anuradha, B. 2013. Genetic variability, correlation and path analysis for quantitative characters in rain-fed upland rice of Uttarakhand hills. *Journal of Rice Research*. 6(2): 24-34.
- Aditya, J.P. and Bhartiya, A. 2013. Genetic variability, correlation and path analysis for quantitative characters in rainfed upland rice of Uttarakhand hills. *Journal of Rice Research*, 6(2), 24-34.
- Agarie, S., Hanaoka N., Kubota F., Agata W. and Kaufman P.B. 1995. Measurement of cell membrane stability evaluated by electrolyte leakage as a drought and heat tolerance test in rice (*Oryza sativa* L.). *J. Fac. Agr., Kyushu Univ.* 40: 233-24.
- Ajmera, S., Kumar, S.S. and V. Ravindrababu, V. 2017. Studies on Stability Analysis for Grain Yield and its Attributes in Rice (*Oryza sativa* L.). *Int. J. Pure App. Biosci.* 5 (4): 892-908
- Alam, M. S., Islam, M. M., Hassan, L., Begum, S. N. and Gupta, R. 2014. Study of correlation, magnitude of genetic diversity and selection indices in popular rice (*Oryza sativa* L.) Landraces of Bangladesh, *International Journal of Innovation and Applied Studies*. 8(3): 1329-1338.

- Ali, Q., Ali, A., Awan, M. F., Tariq, M., Ali, S., Samiullah, T. R., Azam S., Din S., Ahmad M., Sharif, N. M. 2014. Combining ability analysis for various physiological, grain yield and quality traits of *Zea mays* L. Life Science Journal, 11:8 540-551.
- Allard, R. W. 1960. Principles of Plant Breeding. John Wiley AndSons. Inc. New York. 485.
- Allard, R.W. 1960. Principles of Plant Breeding, John Wiley and Sons Inc, New York, USA.
- Allard, R.W. 1960. Principles of Plant Breeding, John Wiley and Sons Inc, New York, USA.
- Anis, G., Sabagh, A.E.L., Ghareb, A and Rewainy, A.E.L. 2016. Evaluation of promising lines in rice (*Oryza sativa* L.) to agronomic and genetic performance under Egyptian conditions. International Journal of Agronomy and Agricultural Research. 8(3): 52-57.
- Anonymous, 2017. Food and Agriculture Orgnization of the United Nations.
- Anonymous, 2018. Directorate of Economics and Statistics. New Delhi. 14-15.
- Anonymous, 2019. Krishi Darshika, IGKV, Raipur. 7-8.
- Anyaocha, C., Felix, A., Uyokei, U., Bosede, P., Vernon, G., Semon, M., Ejiro, O and Mamadou, F. 2018. Genetic diversity of selected upland rice genotypes (*Oryza sativa* L.) for grain yield and related traits. International Journal of Plant & Soil Science. 22(5): 1-9.

- Arulmozhi, R. and Muthuswamy, A. 2013. Correlation studies on grain yield and its component traits in rice (*Oryza sativa* L.) International Journal of Scientific Research. 2(11): 2277-8179.
- Arunachalam, V. 1974. The fallacy behind the use of a modified line x tester design. Indian J. Gen. Plant Breeding. 34: 280-287.
- Arunachalam, V. 1981. Genetic distances in plant breeding. Indian Journal Genetics and Plant Breeding. 41: 226- 236.
- Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G. and Shankar, A.S. 2012. Correlation and path analysis studies in popular rice hybrids of India. International Journal of Science and Research Publication. 2(3): 1-5.
- Bagheri, Babauan Jelodar. Heterosis and combining ability analysis for yield and related yield traits in hybrids rice. Intl. J. Biology. 2010; 2(2):222-231.
- Baker J T, Allen Jr L H, Boote K J. 1992. Temperature effects on rice at elevated CO₂ concentration. J Exp Bot, 43: 959–964.
- Basavaraja, T., Gangaprasad, S., Dhusyantha Kumar, B.M and Shilaja Hittlamani. 2011. Correlation and path analysis of yield and yield attributes in local rice cultivars (*Oryza sativa* L.). Electronic journal of plant breeding. 2(4): 523-526.
- Behera, B. Sahu, S. Ra Kar, R. K. and Pandey, R. K. 2018. Studies on genetic variability for some metric traits in slender grain rice genotypes. Journal of Applied and Natural Science 10(1): 375 – 378.
- Bertin, P., Kinet, J.M and Bouharmont, J. 1996. Evaluation of chilling sensitivity in different
- Betran, J. M., Ribaut, D. B. and Gonzales, L. 2003. Genetic diversity, SCA and Heterosis in Tropical Maize under stress. Crop Science. 43: 797- 806.

- Bhadru, D., Reddy, D.L., Ramesha, M.S. 2011. Correlation and path coefficient analysis of yield and yield contributing traits in rice hybrids and their parental lines. *Electronic Journal of Plant Breeding*. 2(1): 112-116.
- Bhinda, M. S., Karnwal, M.K. and Choudhary M. K. 2017. Estimates of genetic variability, heritability and genetic advance for yield contributing and quality traits in advance breeding lines of rice (*Oryza Sativa* L.). *Int. J. Adv. Biotechnol. Res.* 7 (2): 229-233.
- Bhujel, J., Sharma, S., Shrestha, J. and Bhattarai, A. 2018. Correlation and path coefficient analysis in normal irrigated rice (*Oryza sativa* L.). *Fmg. & Mngmt.* 3 (1) : 19-22.
- Bisne, R. and Motiramani, N. K .2005. Study on gene action and combining ability in rice. *Oryza* 42(2): 153-155.
- Biswas, P.L., Barman, H.N., Ghosal, S., Tohiduzzaan, S. and Hazrat Ali, M. 2011. Stability study for growth duration and grain yield of exotic hybrid rice genotypes in Bangladesh. *Bangladesh Journal of Agriculture Resoure.* 36 (1): 97-102.
- Bitew , J. M., Mekbib, F. and Assefa, A. 2018. Correlation Coefficient and Path Analysis among Yield and Yield Related Traits in Upland Rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) Genotypes in Northwestern Ethiopia. *International Journal of Plant Breeding and Crop Science*. 5(3): 429-436.
- Bitew, J.M. 2016. Estimation of genetic parameters, heritability and genetic advance for yield related traits in upland rice (*Oryza sativa* L. and *Oryza glaberrima* Steud) genotypes in North Western Ethiopia. *World scientific news*. 47(2): 340-350.

- Bosetti, F. Montebelli, C. Dionísia, A. Novembre, C. Chamma, H.P. and Pinheir, J. B. 2012. Genetic variation of germination cold tolerance in Japanese rice germplasm. *Breeding Science* 62: 209–215.
- Breeze, E.L. 1969. The measurement and significance of genotype – environment interactions in grasses. *Heredity*. 24:181-200.
- Burton, G .W .and Devane, E. H. 1952. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. *Agronomy Journal*, 45: 478-481.
- C. Issac Sunil, 2006. LINE x TESTER analysis for earliness yield and its components in rice (*oryza sativa* L.) For the cauvery delta zone Indian J. Agric. Res., 40 (4) : 255 - 261
- Ceccareli, S., Grando, S., Maatougui, M., Michael, M., Slash, M., Haghparast, R., Rahmanian, M., Taheri, A., Al-Yassin, A., Benbelkacem, A., Labdi, M., Mimoun, H. and Nachi,t M. 2010. Plant breeding and climate changes. *J Agric Sci*, 148: 627–637.
- Chakraborty, R. and Chakraborty. 2010. Genetic variability and correlation of some morphometric traits with grain yield in boldgrained rice (*Oryza sativa* L.) gene pool of Barak valley. *American-Eurasian Journal of Sustainable Agriculture*. 4(1): 26-29.
- Chakravorty, A., Ghosh, P.D. and Sahu, P.K. 2013. Multivariate analysis of landraces of rice of West Bengal. *American Journal of Experimental Agriculture*, 3(1): 110-123.

- Chandel, G., Dubey, M. and Meena R. 2013. Differential expression of heat shock protein and heat stress transcription factor gene in rice expose to different levels of heat stress. J. Plant Biochem. Biotechnol. DOI 10.1007/s13562-012-0156-8.
- Chandramohan, Y., Srinivas, B., Thippaswamy, S and Padmaja, D. 2016. Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.). Indian Journal of Agricultural Research. 50(6):609-613.
- Chang, P. L., Jinn, T., Huang, W. and Chen, y. 2007. Induction of a cDNA clone from rice encoding a class II small heat shock protein by heat stress, mechanical injury, and salicylic acid. Plant Science. 172: 64–75.
- Chaudhari, b. A. Patel S. R. Patel P. B. Mistry P. M. Makwana, R. R. And Patil S. S. 2017. Genetic analysis for quantitative traits using line x Tester mating design in rice (*oryza sativa* l.). AGRES – An International e-Journal. 6 (1): 16-27.
- Cheabu, S., Ngam, P. M., Arikait, S., Vanavichit, A. and Malumpong, C. 2018. Effects of Heat Stress at Vegetative and Reproductive Stages on Spikelet Fertility. Rice Science. 25(4):218-226.
- Chen, Z., Zhou, T., Wu, X., Hong, Y., Fan ,Z. and L,i H. 2014. Influence of cytoplasmic heat shock protein 70 on viral infection of *Nicotiana benthamiana*. Mol Plant Pathol. 9:809–817.
- Chowdhary, B.; Nath, A. and Dasgupta, D. 2016. Characterization and variability analysis of rice genotypes with reference to cooking quality parameters. J. of Agri. and Vet . Science, **9**(4): 8-12.
- Cruz, R.P and Milach, S.C.K. 2004. Cold tolerance at the germination stage of rice: Methods

- Dacruz, R. P., and S. C. K. Milach. 2000. Breeding for cold tolerance in irrigated rice. *Ciencia Rural*, 30: 909–917.
- Das, S. 2015. Genetic studies of yield variation in mid duration irrigated rice. *Journal of Agriculture and Veterinary Science*. 8(4):41-43.
- Devi, B. and Lal, G. M. 2015. Combining ability analysis for yield & yield components in rice (*Oryza sativa* L.). *Electronic Journal of Plant Breeding*. 6(2):360-365.
- Devi, K.R., Parimala, K., Venkanna, V., Lingaiah, N., Hari, Y and Chandra, B.S. 2016. Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). *International Journal of Pure and Applied Bioscience*. 4(2): 250-255.
- Devi, R. K., Venkanna, V., Satish Chandra, B. and Hari, Y. 2018. Gene Action and Combining Ability for Yield and Quality Traits in Rice (*Oryza sativa* L.) using Diallel Analysis. *International Journal of Current Microbiology and Applied Sciences*. 7(1): 2834-2843.
- Dhurai, S.Y., Reddy, D.M and Ravi, S. 2016. Correlation and path analysis for yield and quality characters in rice (*Oryza sativa* L.). *Rice Genomics and Genetics*. 7(4): 1-6.
- Dien, C. and Yamakawa, D. 2016. Phenotypic Variation and Selection for Cold-Tolerant Rice (*Oryza sativa* L.) at Germination and Seedling Stages. *Agriculture*. 9(8): 162.
- Duvick D.N. 1999. Heterosis: Feeding people and protecting natural resources. *Genetics and Exploitation of Heterosis in Crops*, Coors J.G., Pandey S., editors. , Madison, WI: American Society of Agronomy and Crop Science Society of America. pp. 19–29.

- Dwivedi, D. K., and Pandey, M. P. 2012. Gene Action and Heterosis for Yield and Associated Traits in Indica and Tropical Japonica Crosses of Rice (*Oryza sativa* L.) Involving Wide Compatibility Gene(s). *International Journal of Plant Breeding and Genetics* 6: 140-150.
- Eberhart, S. A and Russell, W. A. 1966. Stability parameters for comparing varieties. *Crop Science*.6: 36-40.
- Ekka R E, Sarawgi A K and Kanwar R R. 2015. Genetic variability and inter - relationship analysis for various yield attributing and quality traits in traditional germplasm of rice (*Oryza sativa* L.). *Plant Archives*. 15(2): 637-645.
- Fahmi, A., Eissa, R. A., Nagaty, H. H., El-Malky, M. and ElSherif, A. 2015. Genetic Components and Correlation Coefficient for Earliness and Grain Yield in Rice. *Vegetos- An International Journal of Plant Research*. 30:4-15.
- Falconer, D.S.1989. *Introduction to Quantitative Genetics*. 3rd. New York, NY, USA: Longman.
- FAO. Food and Agricultural organization. Online Interactive Database on Agriculture, 2016. FAOSTAT. www.fao.org..
- Finlay, K.W. and Wilkinson, G.N. 1963. The analysis of adaptation in plant-breeding programme. *Aust J Agric Res*. 14: 742-754.
- Fisher, R. A. and Yates, F. 1963. *Statistical Tables for Biological, Agriculture and Medical Research*, 6th ed. Hafner, New York. (4th ed., 1953; 5th ed., 1957.).
- Fukrei, P.K., Kumar, A., Tyagi, W. and Pattanayak A. 2011. Genetic Variability in Yield and its Components in Upland Rice Grown in Acid Soils of North East India. *Journal of Rice Research*. 4(1) :4-7.

- Gande, N. K., Soman, R., Kundur, P. J., Rajeswari, A., Bekele, B. D. and Shashidhar, H. E. 2013. Evaluation of recombinant inbred lines of rice (*Oryza sativa* L.) for grain zinc content, yield related traits and identification of transgressant lines grown under aerobic conditions. *Asian J. Exp. Biol. Sci.* , 4(4): 567-574.
- Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences*, 9:4 463-493.
- Guan, Y.S., Serraj R., Liu S.H., Xu J.L., Ali J., Wang W.S., Venus E., Zhu L.H., Li Z.K. 8 2010. Simultaneously improving yield under drought stress and non-stress conditions: A case study of rice (*Oryza sativa* L.). *J Exp Bot* 61: 4145–4156.
- Guan, J. C., Jinn, T. L., Yeh, C. H., Feng, S. P., Chen, Y. M. , Lin, C. Y. 2004. Characterization of the genomic structures and selective expression profiles of nine class I small heat shock protein genes clustered on two chromosomes in rice (*Oryza sativa* L.) *Plant Mol Biol*. 56:795–809.
- Guo, M., Lu, J. P., Zhai, Y. F., Chai, W. G., Gong, Z. H. and Lu, M. H. 2016. Genome-wide analysis, expression profile of heat shock factor gene family (CaHsfs) and characterisation of CaHsfA2 in pepper (*Capsicum annuum* L.) *BMC Plant Biology*. 15:151.
- Hakata, M., Wada, H., Kubo, C. M., Tanaka, R., Sato, H. and Morita, S. 2017. Development of a new heat tolerance assay system for rice spikelet sterility. *Plant Methods*. 10: 13-34.
- Hallauer A. R. and Miranda J. B. 1988. *Quantitative Genetics in Maize breeding*. 2nd d. Iowa state univ. press, Ames, IA.

- Harsha, Deo, I., Kumar, S and Talha, M. 2017. Assessment of Genetic Variability and Inter-Character Association Studies in Rice Genotypes (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences. 6(9): 2041-2046.
- Hossain, S. Salim, Md., Azam M. G. and Noman, S. 2018. Variability, correlation and path analysis in drought tolerant rice (*Oryza sativa* L.) Journal of Bioscience and Agriculture Research. 18(02): 1521-1530.
- ISTA. 1985. International Rules for Seed Testing. Seed Science and Technology, Supplement Rules. 27: 30–35.
- Jagadish, S.V.K., Craufurd, P.Q. and Wheeler, T.R. 2007. High temperature stress and spikelet fertility in rice (*Oryza sativa* L.) Journal of Experimental Botany. 58:1627–1635.
- Jan, N., Lal, E. P., Kashyap, S. C., Gaur, A., Parray, G. A. and Ramteke, P. W., 2017. Genetic Variability, Character Association and Path Analysis Studies for Grain Yield and Contributing Traits in Rice (*Oryza Sativa* L.) under Temperate Conditions of Kashmir. Vegetos, 30: 2.
- Jennings, P.R., Coffman, W.R. and Kauffman. H.E. 1979. Grain quality. Rice Improvement, Intl. Rice Res. Inst, Los Banos, Laguna, Philippines. pp. 101-120.
- Jung, K. H., Gho, H. J., Nguyen, M. X., Kim, S.R. 2013. An G: Genome-wide expression analysis of HSP70 family genes in rice and identification of a cytosolic HSP70 gene highly induced under heat stress. Funct Integr Genomics. 13 (3): 391-402.
- Jung, Y. J., Nou, S. and Kang, K. K. 2014. Overexpression of Oshsp16.9 Gene Encoding Small Heat Shock Protein Enhances Tolerance to Abiotic Stresses in Rice. Plant Breeding and Biotechnology. 2:370-379.

- Jung, Y. J., Nou, S. and Kang, K. K. 2014. Overexpression of Oshsp16.9 Gene Encoding Small Heat Shock Protein Enhances Tolerance to Abiotic Stresses in Rice. *Plant Breeding and Biotechnology*. 2(4):370-379.
- Kalyan, B., Radha Krishna, K.V. and Subba Rao, L.V. 2017. Studies on Variability, Heritability and Genetic Advance for Quantitative Characters in Rice (*Oryza sativa* L.) Germplasm, *Int. J. Pure App. Biosci*. 5(5): 1619-1624.
- Karim M.J., Jesmin, F., Ali, M.H., Islam, M.N and Mahmud, E. 2016. Variability, heritability and genetic advances for quantitative characters in T. aman rice. *International Journal of Biological Papers*. 1(2): 1-5.
- Karl Pearson, 1932, Tables for statisticians and biometricians, Stat .J. Biometrics.
- Kempthorne, O. 1957. An introduction to genetic statistics. Wiley and Sons, Oxford, England.
- Ketan, R. and Sarkar, G. 2014. Studies on variability, heritability, genetic advance and path analysis in some indigenous Aman rice (*Oryza sativa* L.). *Journal of Crop and Weed*. 10(2): 308-315.
- Khalique, M.A., O.I. Joarder and A.M. Euus, 1977. Heterosis and combining ability in a diallel cross of rice (*Oryza sativa* L.). *Bangladesh J. Agric. Sci*. 4: 137-145.
- Kiani, G. 2012. Character association and path coefficient analysis of yield components in rice varieties. *Research on Crops*. 13(2): 552-555.
- Kishore, C., Kumar, A., Pal, A.K., Kumar, V., Prasad B.D and Kumar, A. 2018. Character association and path analysis for yield components in traditional rice (*Oryza sativa* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences*. 7(3): 283- 291.

- Kishore, N.S., Srinivas, T., Nagabhushanam, U., Pallavi, M and Sameera, S. 2015. Genetic variability, correlation and path analysis for yield components in promising rice (*Oryza sativa* L.) genotypes. SAARC Journal of Agriculture. 13(1): 99-108.
- Koli N. R., Prakash C., Punia S. S. and Kumhar B. L. 2013. Line x tester analysis for grain yield and its contributing traits in aromatic rice (*oryza sativa* l.). Int. J. Int sci. Inn. Tech. Sec. A, 2(2), 1-4.
- Kolom, R., Changkija, S., and Sharma, M.B., 2014: Combining ability analysis for yield and yield components in some important upland rice germplasms of Nagaland. Indian J. Hill Farming, 27 (1): 118-125.
- Konate A. K., Zongo A., Kam, H., Sanni, A. and Audebert, A. 2016. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits. Afr. J. Agric. Res. 11(35): 3340-3346.
- Konate, A.K., Adama, Z., Honore, K., Ambaliou, S and Alain, A. 2016. Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro morphological traits. African Journal of Agricultural Research. 11(35): 3340-3346.
- Kr, U. D., Madan, P., Shah, D. And Sini, T. 2016. Identifying Veritable Sources of Heat Tolerance In Rice (*Oryza Sativa* L.). International Journal of Agriculture Sciences. 8 (53): 2743-2746.
- Kr, U. Madan,P. Divya, S. and Sini, T. 2015. Identifying veritable sources of heat tolerance in rice (*oryza sativa* L.). International Journal of Agriculture Sciences. 53: 2743-2746.

- Kumar, I. and Khush, G.S. 1986. Genetics of amylose content in rice (*Oryza sativa* L.). J Genet 65(1-2):1-11
- Kumar, A. Rangare, N. R. And Vidyakar, V. 2013. study of genetic variability of indian and exotic rice germplasm in allahabad agroclimate. The Bioscan 8(4): 1445-1451.
- Kumar, A. S. and Adilakshmi, D. 2016. Heterosis for yield, yield components and quality traits in rice hybrids (*Oryza sativa* L.). Plant Archives. 16 (1): 237-242.
- Kumar, M., Singh, R. P., Verma, R. and Singh, O. N. 2016. Analysis of combining ability in short duration rice genotypes (*Oryza sativa* L.) . The Pharma Innovation Journal 2018; 7(8): 362-366.
- Kumar, N. Kumar, N. Shukla, A. Shankhdhar S.C. and Shankhdhar, D. 2015. Impact of Terminal Heat Stress on Pollen Viability and Yield Attributes of Rice (*Oryza sativa* L.) Cereal Research Communications 43(4): 616-626.
- Kumar, N., Kumar, N., Shukla, A., Shankhdhar, S.C. and Shankhdhar, D. 2015. Impact of Terminal Heat Stress on Pollen Viability and Yield Attributes of Rice (*Oryza sativa* L.). Cereal Research Communications 43(4): 616-626.
- Kumar, N.V.M and Uma, M.S. 2016. Genetic variability for nitrogen use efficiency and yield related traits in rice under low nitrogen and available soil nitrogen conditions. International Journal of Applied and Pure Science and Agriculture. 2(7): 83-90.
- Kumar, R., Suresh, B.G., Lavanya, G.R., Rai, S.K., Sandhya and Devi, L.B. 2014. Genetic Variability and character association among biometrical traits in F3

generation of some rice crosses. International Journal of Food, Agriculture and Veterinary Sciences. 4 (1): 155-159.

Kumar, V. 2015. Variability and correlation studies for grain physicochemical characteristics of rice (*Oryza Sativa* L.). The Bioscane. 10(2): 917-922.

Lal, M and Pal singh, D. 2012. Genotype X Environment interaction in rice. (*Oryza sativa*. L). Annals of Biology. 28(1): 53-55..

Latha, S., Sharma, D. and Sanghera, G. S. 2013. Combining ability and heterosis for grain yield and its component trait in rice (*Oryza sativa* L.). Not. Sci. Biol., 5(1): 90-97.

Lee, D., Ahsan, N., Kim, Y. and Lee, K. W. 2013. Expression of Heat Shock Protein and Antioxidant Genes in Rice Leaf Under Heat Stress. Journal of the Korean Society of Grassland and Forage Science. 33(3) : 159-166.

Lee, I., Blom, U.M., Wang, P.I., Shim, J.E. and Marcotte, E.M. 2011. Prioritizing candidate disease genes by network-based boosting of genome-wide association data. Genome Research. 21:1109–1121.

Li, H., Cai1, J., Jiang, D., Liu, F., Dai T., Cao, W. 2013. Carbohydrates accumulation and remobilization in wheat plants as influenced by combined waterlogging and shading stress during grain filling. J. of Agron. and Crop Sci. 199: 38–48.

Lingaiah, N., Venkanna, V., Cheralu, C. and Satish Chandra, B. 2014. Correlation and path analysis for yield and yield attributes. In mid early group genotypes of rice (*Oryza sativa* L.). International Journal of Innovative Science, Engineering and Technology, 1(9): 79-82.

- Lone, J. A. Khan, M. N., Bhat, A. M., Shikari, Asif B. , Wani, Shabir H. ., Sofi, Najeeb R ., Khan, M. Imran and Lone. Rayees A. 2018. Cold Tolerance at Germination and Seedling Stages of Rice: Methods of Evaluation and Characterization of Thirty Rice Genotypes under Stress Conditions. *Int.J.Curr.Microbiol.App.Sci.* 7(01): 1103-1109.
- Lush, J. L. 1940. Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. *Proc. Ame. Soc. Anim. Prod.* 33: 293-301.
- Ma, C., Haslbeck, M., Babujee, L., Jahn, O., Reumann, S. 2006. Identification and characterization of a stress-inducible and a constitutive small heat-shock protein targeted to the matrix of plant peroxisomes. *Plant Physiol.* 141:47–60.
- Maclean, J.L., Dawe, D.C., Hardy, B and Hettel, G.P. (ed.). 2002. Rice Almanac, Los Banos (Philippines): International Rice Research Institute, Bouaké (Côte d'Ivoire): West Africa Rice Development Association, Cali (Colombia): International Center for Tropical Agriculture, Rome (Italy): Food and Agriculture Organization.
- Mahantashivayogayya, K., Basavaraj S., Lakkundi, M.S., Amaregouda, R. Ibrahim, M., Reddy, M., Guruprasad G.S. and Pramesh, D. 2016. Response of Rice Genotypes for Heat Stress during Summer Season in the Northern Parts of Karnataka. *Journal of Rice Research.* 9 (1):24-29.
- Makumbi, D., Betran, F.J., Banziger, M., Ribaut, J .2011. Combining ability, heterosis and genetic diversity in tropical maize (*Zea mays* L.) under stress and non-stress conditions. *Euphytica.* 180 (2): 143-162.
- Makumbi, D., Betrán, J. F., Bänziger, M., Ribaut, J. M. 2011. Combining ability, heterosis and genetic diversity in tropical maize (*Zea mays* L.) under stress and non-stress conditions. *Euphytica*, 180:2 143-162.

- Makumbi, D., Javier, F., Betran, M.B., Jean-Marcel, Ribaut .2012. Combining ability, heterosis and genetic diversity in tropical maize (*Zea mays* L.) under stress and non-stress conditions. *Euphytica*. 180: 143-162
- Manonmani, S. and Khan, A.K.F. 2003. Studies on combining ability and heterosis in rice. *Madras Agric. J.*, 90(4-6):228-231..
- Marinkovic, R., Skoric, D., Dozet, B., Jovanovic, D. 2000. Line x tester analysis of the combining ability in sunflower (*H. annuus* L.). Paper presented at the Proceedings of 15th International Sunflower Conference, 12-15 June, Toulouse, France.
- Markam, N. K., Verma, R. K. and Tiwari, A. 2015. Screening of rice genotypes against high temperature stress. *The Ecoscan*. 8: 209-214.
- Markam, N. K.. Verma, R. K. and Tiwari, A. 2015. Screening of rice genotypes against high temperature stress. *The Ecoscan*, 3: 209-214
- Maruyama, A., Weerakoon, W. M. W., Wakiyama, Y., & Ohba, K. (2013). Effects of increasing temperatures on spikelet fertility in different rice cultivars based on temperature gradient chamber experiments. *Journal of Agronomy and Crop Science*, 199, 416–423.
- Masuduzzaman, A.S.M., Ahmad, H.U., Haque M. and Ahmed, M.M.E. 2016. Evaluation of Rice Lines Tolerant to Heat during Flowering Stage. *Rice Research*. 4 (3): 170.
- Maya, O.I.M. 1988. Identificacion de metodologias para la evaluacion de tolerancia a temperaturas bajas en arroz (*Oryza sativa* L.) Palmira: Universidade Nacional de Colombia / Facultad de Ciencias Agropecuarias. 123.

- Menaka J. and Ibrahim, S. M. 2016 .Combining ability for yield and different quality traits in rice (*Oryza sativa* L.) Journal of Applied and Natural Science. 8 (4): 2298-2304
- Miedema, P., 1982. The effects of low temperature on *Zea mays*. Advances in Agronomy, 35: 93-128.
- Mohammadi, A.A., G. Saeidi and A. Arzani, 2010. Genetic analysis of some agronomic traits in flax (*Linum usitatissimum* L.). Aust. J. Crop Sci., 4: 343-352.
- Montazeri, Z., Jelodar, N. B. and Bagheri, N. 2014. Genetic dissection of some important agronomic traits in rice using line x tester method. International Journal of Advanced Biological and Biomedical Research, 2(1): 181-191.
- Moosavi, M., Gholamali, R., Zarrini, H.N. and Gilani, A. 2015. Correlation between morphological and physiological traits and path analysis of grain yield in rice genotypes under Khuzestan conditions. Biological Forum – An International Journal, 7(1): 43-47.
- Motamedi, M., Choukan, R., Hervan, E. M., Bihamta, M. R., Kajouri, F. D. 2014. Investigation of genetic control for yield and related traits in maize (*Zea mays* L.) lines derived from temperate and sub-tropical germplasm. International Journal of Biosciences, 5:12 123-129.
- Murthy, P.S.N and Govindaswamy, S. 1967. Inheritance of grain size and its correlation with the hulling and cooking qualities. Oryza, 4(1): 12-21.
- Mustafa, M. A. and Elsheikh, M. 2007. Variability, correlation and path coefficient analysis for yield and its components in rice. African Crop Science Journal. 15:143-189.

- Nagarajan, S., Jagadish, S.V.K., Prasad, A.S.H., Thomar, A.K., Anand, A., Pal, M., Agarwal, P.K. 2010. Local climate affects growth, yield and grain quality of aromatic and non-aromatic rice in northwestern India. *Agriculture Ecosystem and Environment*. ;138:274–281.
- Nagesh, V., Ravindrababu, V., Usharani, G. and Reddy, D. T. 2012. Grain iron and zinc association studies in rice (*Oryza sativa* L.) F₁ progenies. *Archives of Applied Science Research*, 4(1): 696-702.
- Nanculao, G. D., Carcamo, M. P. Oscar, de los Santos, A. and Velasquez, V. B. 2013. Cold tolerance evaluation in Chilean rice genotypes at the germination stage. *Chilean J. of Agric. Res.*, 73 (1): 3-8.
- Naseer, S., Kashif, M., Ahmad, H. M., Iqbal, M. S. and Ali, Q. 2015. Estimation of genetic association among yield contributing traits in aromatic and non-aromatic rice (*Oryza sativa* L) cultivars. *Life Science Journal*. 12(4):68-73.
- Nayak, A.R., Chaudhury, D., Reddy, J.N. 2004. Studies on variability and character association in scented rice on various environments. *Indian J Agric Res*. 38:250- 255.
- Nayak, P. G., Sreedhar, M., Surender. R. and Vanisree, S. 2016. Heterosis and gene action studies involving aromatic lines for grain quality traits in rice. *International journal of life sciences*. 4 (4): 517-528.
- Nirmaladevi, G., Padmavathi, G., Kota, S. and Babu, V. R. 2015. Genetic variability, heritability and correlation coefficients of grain quality characters in rice (*Oryza sativa* L.). *SABRAO J. of Breeding and Genetics*, 47(4): 424-433.
- Nishanth, G.K., Kumar, B.M.D., Prasad, S.G., Gowda, T.H., Nataraju, S.P and Shashidhar, H.E. 2017. Screening and genetic variability studies in submergence tolerance rice germplasm lines under flood prone low lands of

hill zone of Karnataka, India. International Journal of Current Microbiology and Applied Sciences. 6(7): 1254-1260.

Panse, V .G .and Sukhatme, P. V. 1967. Statistical methods for agricultural workers. ICAR New Delhi. 2nd Edn. Pp: 381.

Panwar, L. L .2005 Line x tester analysis of combining ability in rice (*Oryza sativa* L.). Indian Journal of Genetics and Plant Breeding 65(1): 51-52.

Patel, J.R., Saiyad, M.R., Prajapati, K.N., Patel, R.A and Bhavani, R.T.2014. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). Electronic journal of plant breeding. 5(3): 531- 537.

Patel, J. R.; Saiyad, M. R.; Prajapat i, K. N.; Patel, R. A. and Bhavani, R. T. 2014. Genetic variability and character association studies in rainfed upland rice (*Oryza sativa* L.). El. J. of Plant Breeding, 5(3): 531-537.

Patra, M. and Das S.R. 2018. Genetic variability, correlation and path analysis in hybrid rice. International Journal of Agriculture Sciences. 10 (14):6691-6693.

Pradhan , S. and Rani, K. R. Screening techniques to measure cold tolerance in rice.2017. Journal of Pharmacognosy and Phytochemistry. 6(6): 781-785.

Pradhan, S., Rani, K. J. and Raju, ch D. 2017. Cold tolerance in rice at seedling and reproductive stage. Journal of Pharmacognosy and Phytochemistry. 6(6): 984-988.

Pradhan, S. K., Nayak, D. K., Guru, M., Pandit, E., Sujata, D., Barik, S. R, Mohanty, S. P. and Anandan, A. 2006. Screening and classification of genotypes for seedling-stage chilling stress tolerance in rice and validation of the trait using SSR markers. Plant Genet. Resour., 14 (3):173-182.

- Pragnya K, K. Radha Krishna V L V, Subba Rao and Suneetha K. Estimation of Genetic Variability Parameters in Soft Rice (*Oryza sativa* L.) Genotypes. Int.J.Curr.Microbiol.App.Sci. 2018; 7(06): 2029-2042.
- Prasad, K. R., Krishna, K.V. R., Bhawe, M.H.V. and Rao, L.V. S. 2017. Genetic variability, Heritability and Genetic advance in Boro Rice (*Oryza sativa* L.) germplasm. Int. J. Curr. Microbiol. App. Sci., 6(4) : 1261-1266.
- Prasad, P. V. V., Boote, K. J., Allen, L. H., Sheehy, J. E., Thomas, J. M. G. 2006. Species, ecotype and cultivar differences in spikelet fertility and harvest index of rice in response to high temperature stress. Field Crops Res., 95:398-411.
- Pratap, N., Singh, P.K., Shekhar, R., Soni, S.K and Mall, A.K. 2012. Genetic variability, character association and diversity analyses for economic traits in rice (*Oryza sativa* L.). South Asian Association for Regional Cooperation Journal of Agriculture. 10(2): 83-94.
- Premchandra, G.S., Saneoka, H. and Ogata, S. 1990. Cell membrane stability, an indicator of drought tolerance as affected by applied nitrogen in soybean. J. Agri. Sci. 115:63-66.
- Priyanka, K., Jaiswal, H.K. Waza S. A. and Sravan, T. 2015. Response of rice seedlings to cold tolerance under boro conditions. SABRAO J. 47(2): 185-190.
- Rab, A. and Saltveit M . E . 1996. Differential chilling sensitivity in cucumber (*Cucumis sativus*) seedlings. Plant Physiol. 96:375-382.
- Rahaman, Md. Asadur .2016. Study of nature and magnitude of gene action in hybrid rice (*Oryza sativa* L.) through experiment of line x tester mating design. International Journal of Applied Research, 2(2): 405-410.

- Rahman, M., Patwari, A.K. and Miah, A.J. 1981. Combining ability in rice. Indian J. Agric. Sci., 51: 543-546.
- Rahman, M.A., Hossain, M.S., Chowdhury, I.F., Matin, M.A and Mehraj, H. 2014. Variability study of advanced fine rice with correlation, path coefficient analysis of yield and yield contributing characters. Int. J. Appl. Sci. Biotechnol. 2(3): 364-370.
- Rahul, S. Bhadru, N., D. Sreedhar, M. and Vanisri, S. 2017. Screening of Cold Tolerant Rice Genotypes for Seedling Traits under Low Temperature Regimes. Int.J.Curr.Microbiol.App.Sci. 6(12): 4074-4081 .
- Rajpoot, P., Singh, P.K., Verma, O.P and Neeta T. 2017. Studies on genetic variability and heritability for quantitative characters in rice (*Oryza sativa* L.) under sodic soil. Journal of Pharmacognosy and Phytochemistry. 6(4): 1162-1165.
- Rajeswari, S. Robin, R. Chandirakala, N. Premalatha and S. Muthuramu 2010. Genetic analysis and character association of quality in rice. *Oryza*. 47 (2): 86-90.
- Ramezni, A. and Torabi, M. 2011. Stability analysis of grain yield and its components of rice (*Oryza sativa* L.) genotypes. Electronic Journal of Plant Breeding. 2(4):484-487.
- Ranganathan, T.B., Menon, P.M. and Sreerangaswamy, S.R. 1973. Combining ability of earliness and yield in dwarf varieties of rice. Madras Agric. J. 60: 1134-1138.
- Rani, P. J., Satyanarayana, P.V., Chamundeswari, N., Ahamed, M. L., Rani, Y. A., and Rao, V. S. 2015. Studies of combining ability for physical quality traits in

- rice (*Oryza Sativa* L.). International Journal of Tropical Agriculture. 33(4): 2877-2881.
- Rao, A.V., Krishna, T.S. and Prasad, A.S.R. 1980. Combining ability analysis in rice. Indian J. Agric. Sci., 50: 193-197.
- Ratre, S., Koshta, N. and Verma, R. K. 2014. Identification and genetic divergence of heat tolerant rice genotypes. Trends in Biosciences. 7:3838-3843.** Ramya, R., Sanjeeva, Rao., D., Ravindra Babu, V and Bharathi, M. 2017. Correlation and Path Coefficient Analysis for Yield, Yield Attributing and Nutritional Traits in Rice (*Oryza sativa* L.). International Journal of Current Microbiology and Applied Sciences. 6(11): 183-188.
- Rang, Z.W., Jagadish, S.V.K., Zhou, Q.M., Craufurd, P.Q., Heuer, S. 2011. Effect of high temperature and water stress on pollen germination and spikelet fertility in rice. Environmental and Experimental Botany. 70:58–65.
- Rangare, N.R., Krupakar, A., Ravichandra, K., Shukla, A.K. and Mishra, A.K. 2012. Estimation of characters association and direct and indirect effects of yield contributing traits on grain yield in exotic and Indian rice germ-plasm. International Journal of Agriculture Sciences. 2(1): 54-61.
- Rani, J. and Satyanarayana, P.V. 2015. Identification of Best Heterotic Cross Combinations for Physical Quality Traits in Rice (*Oryza sativa* L.). Trends in Biosciences. 8 (12): 3050-3054.
- Rasyad, A., Manurung, G.M.E. and Van Sanford, D.A. 2012. Genotype x environment interaction and stability of yield components among rice genotypes in Riau Province Indonesia, Journal of Breeding and Genetics. 44(1) : 102-111.
- Rather, A. G., Zargar, M. A. and Sheikh, F. A. 2001. Genetic divergence in rice (*Oryza sativa* L.) under temperate conditions. Indian. J. Agric. Sci., 71(5): 344-345.

- Ratre, S. Koshta, N. And Verma, R. K. 2014. Identification and Genetic Divergence of Heat Tolerant Rice Genotypes. Trends in Biosciences 7(23): 3838-3843.
- Ravindra, Babu, V., Shreya, K., Kuldeep, S.D., Usharani, G. and Siva Shankar, A. 2012. Correlation and path analysis studies in popular rice hybrids of India. International journal of Scientific and Research Publications. 2(3): 1-5.
- Reinoso, A. D. S., Varon, G. G. and Diaz, H. R. 2014. Biochemical and physiological characterization of three rice cultivars under different daytime temperature conditions. Chilean journal of agricultural research. 74 (4): 373-379.
- Roy, S., Banerjee, A., Senapati, B.K. and Sarkar, G. 2010. Comparative analysis of agro-morphology, grain quality and aroma traits of traditional and basmati type genotypes of rice, (*Oryza sativa* L.). Plant Breeding, 131(4): 486–492
- Reddy, M. C. S., Raju, C. S., Sravani, D., Reddy, T. and Reddy, G. 2018 Heterosis for yield and kernel size in aromatic rice. Annals of Biological Research, 3(6): 2662-2666.
- Roy, A. and Ponwar, D. V. S. 1993. Genetic divergence in rice. *Oryza*. 30: 197-201.
- Rukmanidevi, K., Parimala,, K., Venkanna, V., Lingaiah, N. Hari, Y. and Satishchandra, B. Estimation of variability for grain yield and quality traits in rice (*Oryza sativa* L.). Int. J. Pure App. Biosci., 2016; 4(2): 250- 255.
- Rukmanidevi, K., Parimala, K., Venkanna, V. and Cheralu, C. 2014. Genetic variability, heritability, correlation and path analysis for yield and quality traits in rice (*Oryza sativa* L.). The J. Res. PJTSAU, 42(4): 7- 14.

- Saadalla, M.M., J.S. Quick, and J.F. Shanahan. 1990. Heat tolerance in winter wheat: II. Membrane thermostability and field performance. *Crop Sci.* 30:1248–1251.
- Sahu, A., Verma, R. K., Sarawagi A. K., Verulkar, S. B., Guhey, A. and Saxena, R. R. 2014. Impact of low temperature tolerance at seedling stage on rice genotypes. *Journal of Rice Research.* 7(1-2):36-44.
- Saidaiyah, P., Kumar, S.S. and Ramesha, M.S. 2010. Combining ability studies for development of new hybrids in rice over environments. *J. Agric. Sci.*, 2: 1-5.
- Sairam, R.K. 1994. Effect of moisture stress on physiological activities of two contrasting wheat genotypes. *Indian. J. Exp. Biol.* 32:594-597.
- Saleem, M, Y., Mirza, J. I. and Haq, M. A., 2008, Heritability, genetic advance and Heterosis. *J. Agric. Res.*, 46: 15-27.
- Sales, E., Virue, J., Domingo, C. and Marqués, L. 2017 Genome wide association analysis of cold tolerance at germination in temperate japonica rice (*Oryza sativa* L.) varieties. *PLoS ONE* 12: e0183416.
- Salgotra, R. K., Gupta, B. B. and Praveen Singh. 2009. Combining ability studies for yield and yield components in Basmati rice. *Oryza* 46 (1) : 12-16.
- Sameera, S. K., Srinivas, T., Rajesh, A. P., Jayalakshmi V. and Nirmala, P. J. 2016. Variability and path co-efficient for yield and yield components in rice. *Bangladesh J. Agril. Res.* 41(2): 259-271.
- Sameera, S., Srinivas, T., Rajesh, A. P., Jayalaxmi, V. and Nirmala, P. J . 2015. Genetic variability studies for yield and yield components in rice (*Oryza Sativa* L.) *El. J. of Pl. Breeding*, 6(1): 269-273.
- Sandhya, Babu. SG and Kumar, R. 2014. Genetic Variability, Interrelationship and Path Analysis for Yield Improvement of Rice Genotypes. *The Bioscan.* 9(3):1161-1164.

- Saravanan, K., Sabesan, T. and Kumar, S. T. 2008. Heterosis for yield and yield components in rice (*Oryza sativa* L.). Adv. Plant Sci., 21(1): 119-121.
- Sarawagi, A.K., Ojha, G.C., Koshta, N. and Pachauri, A. 2015. Genetic divergence and association study for grain yield in rice (*Oryza sativa* L.) germplasm accessions. The Ecoscan, 9(1&2): 217-223.
- Sarawgi, A. K., Parikh, M., Sharma, B. and Sharma, D. 2014. Phenotypic divergence for agro-morphological traits among dwarf and medium duration rice germplasm and inter-relationship between their quantitative traits. The Bioscane, 9(4): 1677-1681.
- Sarkar, B.C., Haque, M. M., Bashir, M. A., Roy, B and Rahman, M.S. 2013. Physiological responses of rice seedlings towards screening out cold tolerant rice cultivars in Northwest Bangladesh. Asian Journal of Experimental Biological Sciences. 4(4): 623-628.
- Sarkar, N. K., Kim, Y. K. and Grover, A. 2009. Rice sHsp genes: genomic organization and expression profiling under stress and development. BMC Genomics. 10:393.
- Sarker, U., Biswas, P.S., Prasad, B. and Mian, M.A.K. 2002. Heterosis and genetic analysis in rice hybrid. Pak. J. Bio. Sci., 5 (1):1-5.
- Satheesh Kumar, Saravanan, K. and Sabesan, T. 2016. Selection of superior genotypes in rice (*Oryza sativa* L.) through combining ability analysis. Int. J. of Agril Sci., 12(1):15-21.
- Seema, and Roy, A. K. 2007. Effect of low temperature on germination percentage, germination relative index and vigour of various genotypes of boro rice (*Oryza sativa* L.). Int. J. Agric. Sci., 3: 170-73.
- Selvaraj, I. C., Nagarajan, P., Thiagarajan, K., Bharathi, M. and Rabindran, R. S. 2011. Genetic parameters of variability, correlation and pathcoefficient studies for grain yield and other yield Attributes among rice blast disease

resistant genotypes of rice (*Oryza sativa* L.). African Journal of Biotechnology 10(17): 3322-3334.

Seyoum, M., Alamerew, S. and Bantte, K. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice. Journal of Plant Sciences, 7(1): 13-22.

Shabir, G., Shahzad, A.N. and Muhammad, A. 2013. Estimation of phenotypic variability and mutual association of yield and its component in rice germplasm using multivariate analysis. Journal of Agric. Res., 51(4): 361-375.

Shaikh, S.A., Umate, S.M., Syed, A.J and Deosarkar, D.B. 2017. Study on genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) genotypes. International Journal of Pure and Applied Bioscience. 5(4): 511-515.

Sharma, S., Singh, S., Kuldeep, R and Beniwal, D.C. 2014. Genetic variability and heritability estimates of rice new plant types lines for various quantitative traits. Agriculture for Sustainable Development. 2(2): 137-140.

Sheehy, J.E., Mitchell, P. L., Beerling, D.J., Tsukaguchi, T. and Woodward, F. I. 1998. Temperature of rice spikelets: thermal damage and the concept of athermal burden. Agronomie 18, 449–460.

Shiva Prasad, G., Subba Rao, L. V. 2013 .Sujatha, M. and Chaitanya, U. Heterosis and combining ability analysis for few cold tolerant rice Germplasm lines at their seedling stage International Journal of Development Research. 3(8): 010-012.

Siddique, M., Port, M., Tripp, J., Weber, C., Zielinski, D., Calligaris, R., Winkelhaus, S., Scharf, K.D. 2003. Tomato heat stress protein Hsp16.1-CIII represents a

member of a new class of nucleocytoplasmic small heat stress proteins in plants. *Cell Stress Chaperones*. 8:381–394.

Singh, N. and Verma O.P. 2018. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) under salt stressed soil. *Journal of Pharmacognosy and Phytochemistry*. 7(3):3114-31

Singh, P. Singh, A. P. Singh, N. A., Singh, S., Singh, H., Mishra, S. and SV Singh. 2018. Selection of most desirable genotypes for varietal development in rice (*Oryza sativa* L.) *International Journal of Chemical Studies*. 6(4): 3186-3188.

Singh, R.K., Chaudhary, B.D. 1977. Biometrical methods in quantitative genetic analysis, Kalyani Publishers, New Delhi. pp. 57-58.

Singh, S.P. 1985. Sources of cold tolerance in grain sorghum. *Canadian Journal of Plant Sciences*. 65: 251-257.

Sivasubramanian, J. and Madhavamenon, P. 1973. Genotypic and phenotypic variability in rice. *Madras Agric. J.* 12: 15-16.

Sivasubramanian, S and Madhavamenon, P. 1973. Combining ability in rice. *Madras Agricultural Journal*. 60: 419-421.

Sivnath and Singh, S. P. 2013. Study of genetic variability in rice (*Oryza sativa* L.). *Sci. Dev. In Agric. and Tech.*, **8**: 52-54.

Sravan, T., Rangare, N. R., Suresh, B. G. and Kumar, S. R. 2012. Genetic Variability and Character Association in rainfed upland rice (*Oryza sativa* L.). *Journal of Rice Research*, 5(1&2): 24-29.

Sreedhar, S. 2017. Studies On Variability, Heritability, Genetic Advance And Divergence For Yield And Yield Components In Various Maturity And

Grain Type Groups Of Rice (*Oryza Sativa* L.) Genotypes. Bull. Env. Pharmacol. Life Sci. 6 (1)467-474.

Sreedhar, S., Dayakar Reddy, T and Ramesha, M.S.2011. Genotype x Environment interaction and stability for yield and its components in hybrid rice cultivars (*Oryza sativa* L.). International Journal of Plant Breeding and Genetics. 5 (3): 194-208.

Sreelakshmi, Ch. and babu P. Ramesh. 2018. Identification of parents and hybrids for yield and its components using line x tester analysis in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding, 9 (1) : 220 – 225.

Srujana, G., Suresh B.G, Lavanya, G.R., Ram B. J. and Sumanth V. 2017. Studies on Genetic Variability, Heritability and Genetic advance for yield and quality components in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry. 6(4): 564-566.

Subbaiah, P.V., Sekhar, M.R., Reddy, K.H.P. and Reddy, N.P.E. 2011. Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). International journal of applied biology and pharmaceutical technology, 2(3): 603-609.

Subedi, S., Sharma, S., Umer, S. and ,Jabeen, S. 2018. Heritability, correlation, genotypic and phenotypic coefficient of variance, and path coefficient analysis of pipeline spring rice genotypes in western hills of Nepal. International Journal of Agronomy and Agricultural Research. 13(2): 128-135.

Subudhi, H.N., Bose, L. K., Singh, O. N and Rao, G. J. N. 2012. Genotype x Environment interaction for grain yield and its component traits in irrigated rice. Madras Agriculture Journal. 99 (4-6): 178-180.

- Sultan, M.S. Abdel-Moneam, M.A., Hammoud S.A and Hefena, A. G. 2016. Estimates of combining ability for some agro-morphological traits on some rice genotypes. J. Plant Production, Mansoura Univ.6 (10) :1705 -1720.
- Sumanth V., Suresh, B.G., Ram, B.J., & Srujana, G. 2007. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). Journal of Pharmacognosy and Phytochemistry, 6, 1437-1439.
- Tariku, S., Lakew, T., Bitew, M and Asfaw, M. 2013. Genotype by environment interaction and grain yield stability analysis of rice (*Oryza sativa* L.) genotypes evaluated in north western Ethiopia. Net Journal of Agricultural Science. 1(1): 10-16.
- Tenorio, F. A., Ye, C., Redoña, E., Sierra, S., Laza, M., & Argayoso, M. A. 2013. Screening rice genetic resources for heat tolerance. SABRAO Journal of Breeding and Genetics, 45, 341–351.
- Thorat, B. S. Kunkerkar R.L. and Bagkar T. A. 2017. Studies on heterosis for yield and its contributing traits in hybrid rice (*Oryza sativa* L.). International Journal of Chemical Studies. 5(5): 07-12.
- Thorat, B. S., Kunkerkar, R. L., Thaware, B. L., Burondkar, M. M. and Bhave, S.G. Combining Ability Analysis for Yield and Yield Contributing Traits in Hybrid Rice (*Oryza sativa* L.). Journal of Rice Research.10 (1): 21-26.
- Tiwari, D. K., Pandey, P., Giri, S. P. and Dwivedi, J. L. 2011. Heterosis studies for yield and its components in rice hybrids using CMS system. Asian J. Plant Sci., 10(1): 29-42.
- Umadevi, M.; Sarawathi, R.; Shanthi, P.; Suresh, R.; Sanjeeva Rao, D. and Rajendran, R. 2016. Assessment of genetic variability in traditional rice

varieties based on agro-morphological traits and iron zinc content for crop improvement. International J. of Sci. and N., 7(2): 244- 250.

Vanisree, S., Swapna, K., Damodar, Raju Ch., Surender Raju, Ch and Sreedhar, M. 2013. Genetic variability and selection criteria in rice. Journal of Biological and Scientific Opinion. 1(4):342-346.

Veni, B. K.; Lakshmi, B. V. and Ramana, J. V. 2013. Variability and association studies for yield components and quality parameters in rice genotypes. J. of Rice Research. 6(2): 314-318.

Vijaykumar. 2015. Variability and correlation studied for grain physicochemical characteristics of rice (*Oryza sativa* L.). The Bioscan, 10(2): 917-922.

Wahid A., Gelani S., Ashraf M., and Foolad M.R., 2007. Heat tolerance in plants: an overview. Environ. Exp. Bot. 61: 199-223.

Wang, W. and Vinocur, B., Shoseyov O, Altman A.2015. Role of plant heat-shock proteins and molecular chaperones in the abiotic stress response. Trends Plant Sci. 9(5):244–252.

Wattoo, J.I., A.S. Khan, Z. Ali, M. Babar, M. Naeem, M. Aman ullah and N. Hussain, 2010. Study of correlation among yield related traits and path coefficient analysis in rice (*Oryza sativa* L.). Afr. J. Biotechnol., 9: 7853-7856.

Xiang, C-Y., Cai, N. -J., Li, J. and Yang, J. 2016. Cloning and characterization of a small heat shock protein (SHSP) gene in rice plant. Chinese Journal of Rice Science. 30(6): 587-592.

Yadav, R.K. 2000. Studies on genetic variability for some quantitative characters in rice (*Oryza sativa* L.). Advances in Agriculture Research.13:205-207.

- Yamakawa, H., Hakata, M. 2010. Atlas of rice grain filling-related metabolism under high temperature: joint analysis of metabolome and transcriptome demonstrated inhibition of starch accumulation and induction of amino acid accumulation. *Plant Cell Physiol.* 51:795–809.
- Yan,C.,Ding,Y.,Wang,Q.,Liu,Z.,Li,G.,Muhammad,I.,etal.(2010).The impact of relative humidity, genotypes and fertilizer application rates on panicle, leaf temperature, fertility and seed setting of rice. *J. Agric.Sci.* 148, 329–339.
- Yan, C., Fukai, S., Reinke, R., Godwin, I., Snell, P and Basnayake, J. 2008. Screening of rice genetic resources for cold tolerance at different growth stages. *In: Proceedings of the 14th Australian Society of Agronomy Conference, Adelaide, South Australia*, 21-25.
- Ye, C., Fukai, S., Godwin, I., Reinke, R., Snell, P., Schiller, J. and Basnayake, J. 2009. Cold tolerance in rice varieties at different growth stages. *Crop & Pasture Science*, 60: 328–338.
- Yogameenakshi, P., Nadarajan, N. and Anbumalarmathi, J. 2004. Correlation and path analysis on yield and drought tolerant attributes in rice (*Oryza sativa* L.) under drought stress. *Oryza*. 41(3&4): 68-70.
- Yoshida, S.1981. Climatic environment and its influence. Los Banos: IRRI, 2: 65-110.
- Zhang, H., Li H. W., Yuan L. M., Wang Z. Q., Yang J. C., Zhang J. H. 2012. Post-anthesis alternate wetting and moderate soil drying enhances activities of key enzymes in sucrose-to-starch conversion in inferior spikelets of rice. *J. Exp. Bot.* 63 215–227.

- Zhang, G.L., L.Y. Chen, S.T. Zhang, H. Zheng, and G.H. Liu. 2009. Effects of high temperature stress on microscopic and ultrastructural characteristics of mesophyll cells in flag leaves of rice. *Rice Science*.
- Zhou, L., Zeng, Y. and Hu, G.. 2012. Characterization and identification of cold tolerant near-isogenic lines in rice. *Breeding Science*. 62: 196–201.
- Zhou, L., Zeng, Y. and Hu G. 2012. Characterization and identification of cold tolerant near-isogenic lines in rice. *Breeding Science*, 62:196–201.

APPENDIX – A

Table: Meteorological data of *Summer-2017*

SM W	Date	Max. Temp. (°C)	Min. Temp. (°C)	Rainf all (mm)	Rainy days	RH I (%)	RH II (%)	Wind Velocity (Kmph)	EP (mm)	SSR (hours)
52	24 - 31 Dec 2016	28.2	9.9	0	0	86	26	1.1	22.5	7.4
1	2017 Jan 01-07	28.6	12.2	0	0	78	32	1.5	19.9	6.4
2	08-14	27.2	11.9	5.6	1	85	35	2.6	21.1	6.5
3	15-21	28.9	11.8	0	0	85	27	1.2	21.5	8
4	22-28	29.9	14.3	0	0	83	29	1.9	25.3	7.7
5	29-04	30.4	12	0	0	69	26	1.6	27	9.4
6	Feb 05-11	32.2	14.1	0	0	81	26	1.8	30	9.3
7	12-18	31	15.8	0	0	80	31	2.6	30.9	6.8
8	19-25	34.1	15.5	0	0	68	17	2.6	41.7	10.1
9	26-04	34.3	15.8	0	0	73	15	2.2	40.4	9.7
10	Mar 05-11	33	19.2	5.5	1	69	36	3.3	36.5	6.7
11	12-18	32.9	17	0	0	58	18	3.3	43.5	8.9
12	19-25	36.5	19.7	0	0	63	15	2.9	50	9.2
13	26-01	35.9	23	0	0	58	13	2.7	58.5	8.9
14	Apr 02-08	41.4	26.6	0	0	45	17	5.1	66.7	8.3
15	09-15	40.7	22	0	0	36	9	3.2	69.6	9.4
16	16-22	42.6	26.7	0	0	41	10	4.6	72.3	9.5
17	23-29	42.3	24.9	0	0	37	8	5.4	87.4	10.3
18	30-06	42	27.6	0.4	0	39	14	4.6	74.7	9.2
19	May 07-13	41.4	27.6	0.8	0	49	22	5.5	70	8.7
20	14-20	44.5	30.1	0	0	37	13	5.2	83.2	9.7
21	21-27	44.4	28.9	0	0	34	14	4.6	88.2	9.9
22	2017 May 28-03	41.3	27.1	6.6	1	59	27	7.7	72.9	7.9

APPENDIX – B

Table: Meteorological data of *Summer-2018*

Date	Max. Temp (°C)	Min. Temp. (°C)	Rainfall (mm)	Rain days	RH I (%)	RH II (%)	Wind Velocity (Kmph)	EP (mm)	SSR (hours)
2017 Dec									
24-31	28.3	9.5	0	0	85	26	1.8	22.5	8.7
Jan 01-07	27.4	10	0	0	82	26	8.2	20.2	7.8
08-14	28.2	10.1	0	0	80	23	7.9	22.2	8.9
15-21	29.5	9.9	0	0	85	22	8.2	23.9	9.3
22-28	28.6	10.2	0	0	83	25	8.2	23.9	8.5
29-04	30.8	11	0	0	80	17	8.2	30.6	9.8
Feb 05-11	31.3	16.2	0	0	78	34	11.2	24.5	6.3
12-18	28.4	14.5	16.4	3	89	41	11.6	23.8	7.9
19-25	33.5	15.7	0	0	78	22	10.9	31.7	9.5
26-04	35.5	17.2	0	0	76	22	12	36.5	9.4
Mar 05-11	34.7	19.6	0	0	65	22	11.9	39.3	7.4
12-18	34.3	20.3	1.2	0	73	33	13.8	37.2	6.3
19-25	37.5	20.1	0	0	54	16	11	45.7	8.8
26-01	39.2	19.8	0	0	58	15	10.8	50.4	9.1
Apr 02-08	38.3	21.8	21.6	3	68	23	14.6	51.2	7.7
09-15	37	23.4	17.8	1	68	28	16.1	49.3	7.5
16-22	40.3	24.2	2	0	64	19	16.4	54.3	10.4
23-29	41	24.8	0	0	47	19	13.4	63.5	9.6
30-06	41.2	26.2	2.8	1	60	24	17.2	72.4	9.9
May 07-13	42.9	28.2	5.8	0	49	20	16	70.7	9.3
14-20	40.6	26	6.8	1	68	37	20.8	57.9	8.2
21-27	41.7	28.9	0	0	64	36	21.3	10.4	8.4
2018 May				1					
28-03	40.6	28	3		71	39	22.1	63.7	6.6

APPENDIX – C

Table: Cold tolerance screening

S. No.	Genotype/ Variety	GI (%)	PERCOL5 (%)	REDCOL (%)	COLREG (mm)	REDREG (mm)
1	RJR:II	92.50	91.00	47.66	8.70	10.65
2	Ajawain	84.50	80.00	51.88	5.55	8.40
3	Baikoni	93.50	81.00	55.05	5.95	6.30
4	Banspatri	92.00	78.00	47.71	10.45	7.80
5	Chingar Bnko	90.00	79.00	50.32	5.35	4.20
6	Ganga kali	85.00	85.00	55.49	2.80	5.20
7	Ganga dhan	85.00	68.00	44.46	9.75	8.95
8	Ajam dhan	73.00	62.00	53.14	2.50	3.35
9	Safed Lalak	87.50	79.00	65.11	5.05	6.75
10	Tewan dhan	96.00	75.00	35.52	10.85	8.60
11	Kolhin khosa	70.50	72.00	62.05	4.45	6.80
12	Dadhmaini dhan	66.00	62.00	63.61	5.25	4.35
13	Digamber dhan	93.00	81.00	36.90	8.75	8.50
14	Jeera Baba	62.00	68.00	57.96	3.30	4.75
15	NPT 19	89.50	83.00	54.15	7.65	8.15
16	NPT 26	80.50	82.00	63.32	7.55	4.70
17	NPT 6	84.50	83.00	57.67	5.60	4.95
18	Barhasal	76.00	72.00	48.04	9.05	9.15
19	Dan Banko	86.50	77.00	59.81	5.55	4.95
20	Baikoni	76.20	71.00	43.00	4.33	5.32
21	Gangtai	80.00	78.00	51.76	5.99	6.98
22	90 Number	79.00	76.00	65.83	6.53	4.32
23	Dadbako	73.00	67.00	55.90	4.32	6.20
24	Tendhumori dhan	84.50	78.00	64.99	4.98	3.28
25	Bhatamokdo	71.00	69.00	52.98	6.43	4.32
26	NPT 6	70.00	66.50	55.90	5.32	4.90
27	NPT 8	82.50	54.50	46.00	4.32	5.50
28	Banko	70.00	69.00	46.80	4.20	6.32
29	Khurabal	76.00	63.13	54.90	5.32	4.21
30	P:357 III	74.00	53.70	64.90	7.30	5.20
31	Nagina 22	78.80	72.90	47.90	5.66	7.33
32	Swarna	76.50	68.50	55.20	6.30	4.30
33	Indira Barani Dhan 1	83.50	71.00	49.04	10.00	8.10
34	MTU 1010	74.00	69.00	58.78	7.55	7.90
35	Samleshwari					
36	IR 64	64.00	63.00	53.92	4.00	5.00
37	Indira Aerobic 1	81.00	79.00	39.91	9.20	8.20

GI=Germination index, PERCOL5= Percentage of seeds with coleoptile superior to 5 mm, REDCOL= Percentage of reduction in coleoptile length, COLREG= Coleoptile regrowth, REDREG= Redicle regrowth

APPENDIX – D

Table: Heat tolerance screening

S. No.	Genotype/Variety	Canopy temperature (°C)	MSI (%)			Pollen fertility (%)	Spikelet fertility (%)
			Control	Stress	Reduction		
1	RJR:II	30.77	72.22	66.67	5.56	99.08	89.12
2	Ajawain	30.87	86.36	71.43	14.94	98.93	88.82
3	Baikoni	31.75	86.96	52.38	34.58	98.93	86.2
4	Banspatri	31.5	91.3	83.3	8	95.57	90.44
5	Chingar Bnko	32.9	86.36	75	11.36	98.76	86.9
6	Ganga kali	32.13	87.54	81.59	6.01	99.53	87.76
7	Ganga dhan	30.67	80	70.59	9.41	99.15	88.32
8	Ajam dhan	29.93	91.67	81.57	10.08	99.17	88.05
9	Safed Lalak	30.52	84.62	75	9.62	98.83	87.47
10	Tewan dhan	31.6	86.36	66.67	19.7	99.34	86.62
11	Kolhin khosa	30.32	80	72.22	7.78	98.92	89.11
12	Dadhmaini dhan	29.2	93.33	72.73	20.61	99.24	92
13	Digamber dhan	30.55	83.33	65	18.33	99.07	91.52
14	Jeera Baba	30.77	84	66.67	17.33	98.73	89.35
15	NPT 19	30.35	86.36	80	6.36	97.43	92.53
16	NPT 26	31.2	86.36	72.73	13.64	99.35	88.55
17	NPT 6	31.83	78.26	75	3.26	99.87	92.14
18	Barhasal	29.93	81.82	70.59	11.23	99.01	88.74
19	Dan Banko	31.03	84.21	76.67	7.54	99.03	90.07
20	Baikoni	31.55	87.5	66.67	20.83	99.04	90.52
21	Gangtai	29.17	78.26	72.73	5.53	98.19	93.41
22	90 Number	31.27	82.14	64.29	17.86	99.31	93.69
23	Dadbako	30.5	75.76	75	0.76	95.5	90.14
24	Tendhumori dhan	30.68	85	66.67	18.33	99.05	94.64
25	Bhatamokdo	31.77	92.31	78.57	13.74	99.76	91.57
26	NPT 6	30.13	88.24	81.25	6.99	99.06	88.14
27	NPT 8	30.13	89.47	71.43	18.05	99.34	89.68
28	Banko	31.93	78.26	61.54	16.72	99.34	87.17
29	Khurabal	31.63	94.74	71.43	23.31	94.89	84.32
30	P:357 III	31.53	79.31	75	4.31	98.77	40.4
31	Nagina 22	31	86.36	72.73	13.64	99.16	92.43
32	Swarna	29.1	96.43	57.14	39.29	94.95	69.44
33	Indira Barani Dhan 1	31.5	86.67	68.75	17.92	96.77	89.81
34	MTU 1010	30.75	82.61	66.67	15.94	96.34	82.19
35	Samleshwari	31.4	81.48	71.43	10.05	98.2	85.29
36	IR 64	30.87	78.26	64.29	13.98	93.72	73.38
37	Indira Aerobic 1	31.3	83.33	76.92	6.41	98.84	75.65
	Maximum	32.9	96.43	81.25	39.29	99.87	94.64
	Minimum	29.1	72.22	52.38	0.76	93.72	40.4

APPENDIX – E

Table: Stability parameters of Eberhart and Russell model (1956) for thirty seven genotypes on Summer-2018

S. No	Genotype	DTF			PH			TT		
		μ	bi	S ² di	Mean	bi	S ² di	μ	bi	S ² di
1	RJR:II	84.50	1.39	0.46	75.49	-3.14	-8.21	11.97	1.74	-0.52
2	Ajawain	76.83	1.04	0.36	96.13	-2.23	-4.34	14.24	0.73	7.43**
3	Baikoni	75.50	0.99	6.22**	92.84	-0.97	0.41	10.24	-0.68	-1.49
4	Banspatri	75.00	0.95	1.51	93.95	1.42	24.37*	11.65	0.19	-1.55
5	Chingar Bnko	78.50	0.99	25.95**	96.51	0.80	-8.20	12.80	0.39	-0.19
6	Ganga kali	78.67	1.04	6.70**	88.41	1.55	3.60	10.93	0.04	-1.59
7	Ganga dhan	78.50	1.23	3.36**	85.32	0.77	-7.91	12.02	0.98	-0.48
8	Ajam dhan	80.83	2.39	59.99**	84.37	2.39	19.74	11.47	1.16	-1.66
9	Safed Lalak	84.50	1.49	104.11**	96.50	-1.91	2.48	11.45	0.07	0.29
10	Tewan dhan	75.50	0.86	2.15**	93.23	0.14	-1.74	15.38	0.36	2.71
11	Kolhin khosa	79.33	0.62	10.63**	83.05	2.72	-8.19	12.74	0.14	-1.08
12	Dadhmaini dhan	85.00	0.14	-0.45	98.09	1.43	2.82	11.96	0.89	-1.58
13	Digamber dhan	80.83	1.08	72.84**	82.54	0.84	-6.15	12.84	0.77	5.80*
14	Jeera Baba	78.33	0.45	13.59**	84.74	2.55	-2.39	17.30	0.78	0.18
15	NPT 19	79.33	0.60	2.57**	81.55	3.34	2.69	12.03	1.29	18.16**
16	NPT 26	78.00	0.10	0.28	101.27	-4.45	-6.51	13.43	1.93	-0.73
17	NPT 6	79.83	0.49	5.13**	75.34	0.70	0.19	12.73	0.86	1.74
18	Barhasal	78.17	1.67	2.40	77.70	1.04	14.92	11.18	0.05	-1.55
19	Dan Banko	76.17	0.88	6.67**	80.88	2.48	-5.63	12.56	1.19	-1.69
20	Baikoni	86.50	1.48	1.28	95.67	-3.07	2.38	11.59	1.41	-1.68
21	Gangtai	88.83	0.95	10.25**	95.04	1.08	1.67	11.85	0.81	-1.31
22	90 Number	81.00	0.48	3.42**	92.75	3.01	11.12	9.56	0.08	-1.60
23	Dadbako	82.83	0.40	-0.52	97.87	1.30	-0.62	14.04	1.44	-1.18
24	Tendhumori dhan	86.50	0.52	26.29**	85.03	1.27	-7.52	12.83	0.50	2.34
25	Bhatamokdo	87.33	0.67	1.11	95.66	2.28	-6.49	10.40	0.49	-1.71
26	NPT 6	88.00	1.57	3.89**	93.77	-1.65	-5.11	11.08	0.34	1.10
27	NPT 8	80.00	0.92	8.37**	75.62	-0.67	-3.10	12.49	0.21	2.27
28	Banko	81.17	1.46	2.01**	107.97	-1.73	12.92	12.99	0.12	1.05
29	Khurabal	78.17	0.99	0.54	111.83	3.78	-3.33	13.59	2.60	-1.01
30	P:357 III	84.67	1.11	-0.52	106.32	17.77	117.72**	11.63	1.68	0.05
31	Nagina 22	70.83	0.75	1.68**	79.65	-0.10	-6.88	18.68	2.38	-1.68
32	Swarna	97.50	2.18	11.02**	87.96	-0.34	-7.21	18.63	0.80	1.42
33	Indira Barani Dhan									
33	1	79.33	0.84	23.81**	86.01	1.01	19.76	17.48	1.88	2.40
34	MTU 1010	81.33	1.01	7.32**	81.20	2.42	-8.00	16.32	3.90	1.76
35	Samleshwari	84.50	1.10	1.84**	83.41	2.29	-7.62	18.74	1.32	-0.81
36	IR 64	82.00	0.93	12.96**	79.37	-1.54	7.49	15.75	2.30	7.28
37	Indira Aerobic 1	75.50	1.23	-0.19	80.86	0.40	-7.85	18.50	1.89	-0.40
Population mean		83.79			89.29			13.38		

DTF= Days to 50% flowering, PH= Plant height, TT= Tillers per plant, μ = Population mean, bi= Reression coefficient, S²di= Deviation from the regression line

Conti..

S. No	Genotype	ET			FLA			PL		
		μ	bi	S ² di	μ	bi	S ² di	μ	bi	S ² di
1	RJR:II	11.04	1.64	1.19	30.50	-5.32	-1.00	28.25	6.52	-0.56
2	Ajawain	13.95	1.18	5.97*	23.24	0.84	-1.41	29.74	-4.27	-0.92
3	Baikoni	9.82	-0.64	-1.11	26.36	1.11	-1.44	30.51	-2.34	-0.23
4	Banspatri	11.36	-0.70	-1.38	23.30	0.40	-1.68	33.62	-3.31	0.38
5	Chingar Bnko	11.33	0.44	-0.76	30.23	5.38	-0.60	31.83	-0.55	-0.47
6	Ganga kali	10.25	0.06	-1.32	26.87	6.74	-1.23	30.95	-1.21	8.26**
7	Ganga dhan	10.84	0.23	-1.34	29.01	-0.44	-1.70	29.77	9.60	-0.63
8	Ajam dhan	10.83	0.95	-1.32	24.10	3.63	-0.93	30.52	-5.04	-0.92
9	Safed Lalak	11.03	0.14	0.38	27.53	5.19	1.65	30.15	2.24	-0.90
10	Tewan dhan	14.87	0.45	2.40	24.01	-2.78	-1.44	27.15	9.44	2.03
11	Kolhin khosa	12.05	-0.02	-1.01	23.10	-2.54	-1.38	29.66	6.26	1.48
12	Dadhmaini									
12	dhan	11.53	0.93	-1.28	28.73	-4.83	-1.06	27.96	9.50	1.44
13	Digamber dhan	12.23	0.98	5.84*	31.25	-0.92	-0.33	30.11	3.22	-0.87
14	Jeera Baba	16.03	0.68	-0.80	25.51	4.13	2.13	29.48	3.66	2.03
15	NPT 19	11.57	1.59	14.64**	22.78	3.09	-0.93	28.49	5.73	1.89
16	NPT 26	12.71	2.16	-1.14	19.08	5.91	-0.70	30.68	-1.05	-0.51
17	NPT 6	12.37	0.49	5.72	27.94	2.14	-1.68	30.23	3.72	1.84
18	Barhasal	10.47	0.05	-1.34	24.90	-0.99	0.91	28.56	1.44	0.51
19	Dan Banko	12.25	1.40	-1.35	31.18	-0.23	-1.51	31.79	1.42	4.99**
20	Baikoni	11.08	1.20	-1.33	29.39	0.19	-1.54	32.49	-7.91	0.99
21	Gangtai	11.33	1.03	-0.97	30.24	2.73	-1.09	30.00	-4.97	-0.27
22	90 Number	9.18	0.03	-1.36	27.66	-1.28	1.00	29.21	6.42	0.12
23	Dadbako	13.52	1.46	-1.07	28.54	-0.98	-0.62	31.05	0.06	-0.91
24	Tendhumori									
24	dhan	12.31	0.40	3.41*	26.70	0.71	-0.24	28.58	7.62	1.26
25	Bhatamokdo	10.18	0.49	-1.38	33.99	-3.25	1.12	34.73	12.67	4.74**
26	NPT 6	10.74	0.21	0.19	30.13	4.35	-1.20	31.31	-5.64	-0.87
27	NPT 8	12.09	0.08	1.21	24.57	0.77	-1.03	31.43	-8.92	-0.92
28	Banko	12.54	-0.09	0.46	38.20	4.18	1.20	30.95	6.05	-0.84
29	Khurabal	12.99	2.50	-1.22	38.00	1.07	-1.70	31.43	-0.19	0.11
30	P:357 III	11.34	1.66	0.42	30.59	2.08	-1.63	31.62	-5.29	0.92
31	Nagina 22	18.13	2.24	-1.15	24.43	1.18	-1.70	28.24	13.01	-0.32
32	Swarna	16.86	2.04	0.56	23.20	0.58	-1.68	28.27	5.87	0.22
33	Indira Barani									
33	Dhan 1	16.78	1.37	3.77*	27.67	1.53	-0.52	31.04	5.91	-0.93
34	MTU 1010	15.48	4.34	4.79	21.86	0.48	-1.60	32.63	0.03	-0.92
35	Samleshwari	18.22	1.25	0.68	29.91	-2.60	-1.64	30.63	-0.59	-0.90
36	IR 64	14.75	2.71	9.12**	28.76	3.45	-1.05	31.89	-2.08	-0.31
37	Indira Aerobic									
37	1	18.20	2.05	-1.36	26.47	1.30	-0.89	32.06	-4.64	-0.61
Mean		12.76			27.57			30.46		

ET= Effective tillers per plant, FLA= Flag leaf area, PL=Panicle length, μ = Population mean, bi= Reression coefficient, S²di= Deviation from the regression line

Conti...

S. No	Genotype	FG			TG			SF		
		μ	bi	S ² di	μ	bi	S ² di	μ	bi	S ² di
1	RJR:II	136.14	0.68	51.91	153.10	0.88	33.48	93.31	0.34	-7.68
2	Ajawain	114.13	0.98	140.58**	128.44	0.76	-20.92	92.61	0.51	-6.84
3	Baikoni	97.65	1.07	13.13	112.72	-1.28	-11.89	90.56	1.17	-2.02
4	Banspatri	112.91	1.69	-30.05	124.80	1.59	106.10**	90.45	0.82	-7.29
5	Chingar Bnko	118.99	5.50	54.71	134.93	6.78	1107.19**	86.90	2.79	15.79
6	Ganga kali	103.65	-1.43	47.91	120.66	0.85	206.03**	90.86	0.41	5.31
7	Ganga dhan	110.03	-1.79	-15.76	125.10	-2.60	556.48**	88.32	1.28	4.09
8	Ajam dhan	149.51	3.95	-22.23	169.17	0.42	426.22**	88.05	2.28	25.98
9	Safed Lalak	163.54	5.63	-22.63	186.79	-4.50	1960.68**	87.47	1.44	101.89**
10	Tewan dhan	116.66	1.03	38.80	136.02	2.55	105.37**	91.65	1.43	-6.92
11	Kolhin khosa	123.92	-0.27	36.23	139.59	0.74	158.95**	89.11	1.96	54.87
12	Dadhmaini dhan	154.84	-0.47	-14.60	168.46	-0.45	78.54*	92.00	0.91	-0.28
13	Digamber dhan	198.76	-0.06	16.19	216.11	1.12	139.36**	92.92	0.41	1.52
14	Jeera Baba	159.18	2.06	-26.02	178.03	0.38	-12.92	90.26	1.75	9.04
15	NPT 19	163.43	0.74	21.87	176.62	0.62	-16.33	92.53	0.42	8.88
16	NPT 26	140.48	0.39	-30.75	160.82	8.26	296.72**	92.61	0.75	16.59
17	NPT 6	130.51	-0.12	-7.44	141.79	1.33	68.88**	92.14	1.23	-7.52
18	Barhasal	109.93	-1.31	32.90	125.46	2.05	205.04**	88.74	0.66	-7.14
19	Dan Banko	174.87	2.53	96.96	195.30	-2.04	50.94	90.07	2.76	-7.23
20	Baikoni	166.56	2.77	11.22	184.32	0.33	172.52**	91.82	1.37	-5.57
21	Gangtai	172.15	1.16	237.15**	184.20	-2.31	-10.82	93.41	1.50	14.43
22	90 Number	139.57	0.78	-7.51	148.98	0.58	-11.30	94.00	0.63	-0.84
23	Dadbako	141.78	-0.51	-6.00	157.39	0.04	30.68	90.14	0.49	9.11
24	Tendhumori dhan	197.28	0.10	160.51**	209.02	-1.37	103.37**	88.91	1.20	-7.60
25	Bhatamokdo	212.17	4.81	152.86**	231.29	5.35	840.36**	94.02	0.62	1.04
26	NPT 6	191.58	2.25	36.76	217.54	-6.17	477.70**	89.80	0.09	-6.63
27	NPT 8	147.13	2.01	130.60**	165.58	4.07	-18.39	94.52	0.68	0.19
28	Banko	121.68	0.74	123.04**	139.83	-0.35	-0.99	92.17	0.04	-7.23
29	Khurabal	130.88	2.01	52.64	155.30	-1.54	-22.40	93.38	0.21	-3.20
30	P:357 III	55.31	0.73	788.38**	136.74	0.81	82.13**	40.40	1.29	414.01
31	Nagina 22	100.07	-2.84	30.17	106.38	1.09	421.22**	92.43	2.54	0.20
32	Swarna Indira Barani	144.75	4.82	-31.20	224.27	1.52	-16.29	69.44	8.10	25.70
33	Dhan 1	150.97	-1.68	14.63	171.38	-0.90	257.68**	89.81	0.94	6.09
34	MTU 1010	150.21	-2.30	149.39**	201.79	-2.86	46.07	85.50	2.86	58.43
35	Samleshwari	148.92	1.05	342.04**	177.66	4.95	75.15**	89.25	0.14	-5.28
36	IR 64	138.52	-0.85	-8.72	193.43	5.29	515.18**	73.38	1.82	1.47
37	Indira Aerobic 1	127.93	1.13	270.81**	154.48	10.96	120.48**	75.65	5.43	46.56
Mean		7.42			11.39			88.07		

FG=Filled grain per panicle, TG= Total grains per panicle, SF= Spikelet fertility, μ = Population mean, bi= Reression coefficient, S²di= Deviation from the regression line

Conti...

S. No	Genotype	100 GW			GYP			BYP		
		Mean	bi	S ² di	Mean	bi	S ² di	Mean	bi	S ² di
1	RJR:II	2.24	1.01	0.00	21.25	1.82	5.85	48.97	7.03	97.15
2	Ajawain	2.23	-3.46	0.00	22.10	-0.83	-0.98	47.96	0.76	22.62
3	Baikoni	2.46	0.01	-0.01	19.58	3.66	-4.90	39.60	1.50	18.78
4	Banspatri	2.42	-0.82	0.01	20.32	-1.81	1.82	48.37	14.69	4.93
5	Chingar Bnko	2.20	-2.03	0.00	18.91	0.25	-4.28	47.40	23.61	19.96
6	Ganga kali	1.97	1.58	0.00	21.04	-1.44	-1.47	47.50	7.63	10.55
7	Ganga dhan	2.09	-0.77	0.01	19.00	1.25	-4.26	42.08	2.66	57.89**
8	Ajam dhan	2.08	-1.16	-0.01	21.31	-0.27	-4.86	59.54	19.12	363.73**
9	Safed Lalak	2.43	2.62	0.03	25.85	2.69	-4.23	49.76	-10.67	164.74**
10	Tewan dhan	2.15	-2.99	-0.01	20.87	6.60	-5.06	52.68	-6.65	82.81
11	Kolhin khosa	2.21	-0.67	0.00	24.99	3.23	-4.83	47.73	-6.02	28.06
12	Dadhmaini dhan	2.23	6.41	-0.01	23.76	-2.77	0.32	48.56	-7.83	7.21
13	Digamber dhan	1.52	-2.11	0.00	19.25	3.59	-1.63	54.08	-22.02	34.48
14	Jeera Baba	2.12	0.50	-0.01	19.33	4.57	-1.34	56.70	-8.97	-2.54
15	NPT 19	1.96	-0.67	0.00	21.87	-1.50	-2.20	64.07	-4.64	169.87**
16	NPT 26	2.04	-0.01	0.00	23.08	1.08	-3.78	52.63	3.02	-8.22
17	NPT 6	2.41	-2.98	0.01	22.55	-2.87	-0.87	57.18	-3.03	18.87
18	Barhasal	2.27	3.34	0.00	22.47	0.95	2.16	40.47	2.46	7.88
19	Dan Banko	2.09	1.59	-0.01	23.55	0.97	13.84*	52.50	4.01	33.27
20	Baikoni	1.97	8.89	0.16	19.84	1.58	-4.62	53.62	-2.80	24.20
21	Gangtai	2.60	-0.22	0.04	20.27	3.47	-1.01	53.70	8.50	118.34**
22	90 Number	2.18	2.18	0.01	21.36	0.60	-4.09	44.05	-0.33	11.24
23	Dadbako	2.00	9.56	0.00	24.41	1.41	-0.43	54.57	-0.36	38.24
24	Tendhumori dhan	1.80	7.43	0.01	22.88	0.73	-2.68	61.90	2.69	-0.80
25	Bhatamokdo	2.26	-0.18	0.00	24.87	0.14	0.78	54.09	-0.01	9.19
26	NPT 6	2.18	0.76	0.00	20.30	-0.23	-2.73	59.13	1.68	-5.13
27	NPT 8	2.12	-0.22	-0.01	23.99	5.59	-1.72	54.12	-7.79	13.10
28	Banko	2.86	2.58	0.02	17.25	-1.63	91.64**	53.17	0.76	18.27
29	Khurabal	2.66	-0.14	0.02	16.46	0.89	18.39**	58.82	11.87	24.40
30	P:357 III	2.59	0.59	0.00	11.51	-3.15	-4.31	38.02	3.57	0.72
31	Nagina 22	2.32	-2.93	0.02	24.20	2.50	-0.79	49.27	0.50	-1.31
32	Swarna	1.97	0.75	0.00	22.54	1.90	-4.35	59.50	13.22	24.39
33	Indira Barani Dhan									
33	1	2.12	-0.09	-0.01	22.68	0.65	0.23	51.55	-9.18	-3.20
34	MTU 1010	2.44	1.10	0.00	19.57	-0.09	-3.24	64.12	1.80	244.77**
35	Samleshwari	2.06	4.61	0.01	20.52	0.44	-5.05	57.92	3.10	19.22
36	IR 64	2.20	2.87	0.01	20.30	1.62	-5.02	49.48	-3.79	37.75
37	Indira Aerobic 1	2.34	0.06	-0.01	21.84	1.43	0.88	49.23	-3.07	-7.96
Mean		2.2096			1.85			52.00		

100 GW= 100 grain weight, GYP= Grain yield per plant, BYP= Biological yield per plant, μ = Population mean, bi= Reression coefficient, S²di= Deviation from the regression line

Conti..

S. No	Genotype	HI		
		Mean	bi	S ² di
1	RJR:II	65.14	1.49	9.57
2	Ajawain	65.35	0.11	133.92**
3	Baikoni	66.56	0.26	71.54**
4	Banspatri	64.65	1.18	-12.36
5	Chingar Bnko	58.92	1.03	-12.22
6	Ganga kali	48.37	1.27	31.79
7	Ganga dhan	58.04	1.05	163.87**
8	Ajam dhan	53.94	0.15	291.45
9	Safed Lalak	64.01	0.71	223.24**
10	Tewan dhan	57.04	1.38	-17.68
11	Kolhin khosa	64.24	0.05	138.20**
12	Dadhmaini dhan	69.35	1.81	-4.44
13	Digamber dhan	46.45	0.46	-19.01
14	Jeera Baba	60.07	1.24	37.75
15	NPT 19	47.50	-1.03	-19.03
16	NPT 26	65.15	0.19	1.13
17	NPT 6	56.95	-2.06	53.62*
18	Barhasal	66.32	1.70	111.05**
19	Dan Banko	68.89	0.31	355.26**
20	Baikoni	57.82	1.38	383.69**
21	Gangtai	66.46	2.95	110.74**
22	90 Number	57.62	1.61	56.39*
23	Dadbako	64.21	1.87	-2.75
24	Tendhumori dhan	54.10	2.26	-15.88
25	Bhatamokdo	71.26	1.14	135.02**
26	NPT 6	58.34	1.29	49.17
27	NPT 8	63.67	0.19	-18.57
28	Banko	69.40	1.70	41.25
29	Khurabal	62.65	1.15	-2.00
30	P:357 III	41.71	-0.53	168.77**
31	Nagina 22	71.96	0.47	9.67
32	Swarna	56.75	2.16	-18.31
33	Indira Barani Dhan 1	65.78	1.77	-17.17
34	MTU 1010	60.65	0.41	505.9**1
35	Samleshwari	63.02	3.08	-17.91
36	IR 64	59.32	0.35	35.74*
37	Indira Aerobic 1	69.08	2.46	-14.66
Mean		61.10		

HI=Harvest index, μ = Population mean, bi= Reression coefficient, S²di= Deviation from the

regression line

RESUME

Name : Laxmi Singh
 Date of birth : 10/11/1988
 Present Address : C/O Shri Kailash Sathpathi
 House No.- 547, Sai Nagar, Jora, Raipur (C.G.)
 Phone : 9691848086
 E. mail : laxmisingh8811@gmail.com
 Permanent address : C/O Shri JitendrNath Singh
 Vill + Post- Lokhandi
 Distt.- Jashpur (C.G.) -496338

Academic Qualification:

Degree	Year	University/ Institute
B. Sc. (Ag)	2011	RMDCARS, Ajirma, Ambikapur
M. Sc. (Ag)	2013	COA, IGKV, Raipur
Ph. D. (Ag)	2019	COA,IGKV,Raipur

Professional Experience (If any): RAWE 2011
 Membership of Professional Society (If any): No
 Award/ Recognitions (If any): No
 Publications (If Any) - 3


 Signature