

**“STUDIES ON GENETIC DIVERGENCE IN YIELD AND
EARLY SEEDLING VIGOUR FOR EARLY DURATION
GENOTYPES UNDER DIRECT SEEDED CONDITION
OF RICE (*Oryza sativa* L.)”**

M. Sc. (Ag.) Thesis

by

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

2020

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OF RICE (*Oryza sativa* L.)”**

**Thesis
Submitted to the**

**Indira Gandhi Krishi Vishwavidyalaya, Raipur
By**

Rakesh Koshle

**IN PARTIAL FULFILMENT OF THE
REQUIREMENTS**

FOR THE DEGREE OF

Master of Science

**in
Agriculture
(Genetics and Plant Breeding)**

Roll No. 120118136

ID No. 20131417501

SEPTEMBER, 2020

CERTIFICATE I

This is to certify that the thesis entitled “**Studies on genetic divergence in yield and early seedling vigour for early duration genotypes under direct seeded condition of rice (*Oryza sativa* L.)**” submitted in partial fulfillment of the requirements for the degree of “**Master of Science in Agriculture**” of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Rakesh Koshle** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degressed or diploma or certificate course. All the assistance and help received during the course of the investigations have been duly acknowledged.



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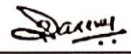


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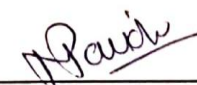
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Date: 16-10-2020




16.10.2020

Signature of Major Advisor

Name: Dr. A. K. Sarawgi

CERTIFICATE II

This is to certify that the thesis entitled “**Studies on genetic divergence in yield and early seedling vigour for early duration genotypes under direct seeded condition of rice (*Oryza sativa* L.)**” submitted by **Rakesh Koshle** to the **Indira Gandhi Krishi Vishwavidyalaya, Raipur**, in partial fulfilment of the requirements for the degree of **Master of Agriculture** in the **Department of Genetics and Plant Breeding** has been approved by the external evaluator and Student's Advisory Committee after oral examination, under the chairmanship of head of the Department.


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ACKNOWLEDGEMENT

First and foremost, I would like to award gratitude to the almighty my parent being a ray of hope and shielding me up with strength and keeping all my Fiasco at bay while Crafting this thesis. Without my parent and their support, my thesis could have been jeopardized and enlightenment could have not be possible.

I take immense pleasure to express my sincere and deep sense of gratitude to my major advisor Dr. A.K. Sarawgi Professor and Head, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.), for his sustained enthusiasm, creative suggestions, extra efforts, broad and profound knowledge, his patient instruction, motivation and exemplary guidance throughout the course of my master research has given me great inspiration and help at every step during my thesis and pleasure to conduct this thesis under his supervision.

I would like to express my sincere gratitude to my co-major advisor Dr. Bhawana Sharma, Scientist, Genetics and Plant Breeding, College of Agriculture Chhuikhadan, Rajnandgaon (C.G.) for the continuous support of my M.Sc. study and related research, for her patience, motivation, and immense knowledge. Her guidance helped me in all the time of research and writing of this thesis.

I emphatically and gratefully acknowledge extend my loyal and venerable thanks to members of my Advisory Committee, Dr. Mangla Parikh, Department of Genetics and Plant Breeding, Smt. Archana S. Prashad, assistance professor Department of Plant Molecular Biology and Biotechnology, Dr. R.R. Saxena, Professor (ADR), Department of Agriculture Statistics and Social Science, College of Agriculture, IGKV, Raipur and Dr. Sunil Kumar Verma, Scientist, Department of Plant Molecular Biology and Biotechnology. They were always ready to provide valuable guidance, regular encouragement and timely advice whenever required for enriching with productive scientific discussion, during the most trying times in the tenure of this research work.

I would like to specially thank to Dr. Mangla parikh and Dr. Ritu R. Saxena, Principle Scientist, Department of Genetics and Plant Breeding, COA, IGKV Raipur, for her kind help and valuable suggestions during the course of investigation.

I wish to record my grateful thanks to Dr. S. K. Patil, Hon'ble Vice Chancellor, Dr. Prabhakar Singh, Registrar, Dr. R.K. Bajpai, Director Research Services, Dr. M. P. Thakur, Director of Instructions and Dr. S.S. Rao, Dean, College of Agriculture, IGKV, Raipur for providing necessary facilities technical and administrative supports for the conductance of this research work,

I am immensely thankful to Dr. R. N. Sharma, Dr. H. C. Nanda, Dr. P. K. Joshi, Dr. N. K. Rastogi, Dr. Rajeev Shrivastava, Dr. Sandeep Bhandarkar, Dr. S. K. Nair, Dr. P. L. Johnson, Dr. Abhinav Sao, Dr. Ravindra K. Verma, Dr. Alice Turkey, Dr. Sunil K. Nag, Dr. Mayuri Sahu, Dr. Prabha R. Choudhari, and Ms. Krishna Tandekar for their co-operation and support during my work period for their encouragement and constant help throughout course of my studies. I extend my thanks to other non-teaching staff specially Dr. Parmeshwar Sahu, Mr. Atul Pachauri department of Genetics and Plant breeding for their timely co-operation.

I would like to express my sincere gratitude to Dr. Madhav Pandey (Librarian, Nehru library, IGKV, Raipur) and all other members of the Nehru library for giving me their kind help during the study. My sincere thanks are extended to non-teaching staffs, Lime Dai and Ganga didi, Bedi bhaiya, Sanju bhaiya, Gendlal bhaiya, Badku bhaiya and Manish bhaiya of the Department of Genetics and Plant Breeding.

I sincerely acknowledge my seniors Mr. Rohit, Dr. Suman Rawte, Ms. Prakriti Meshram, Mrs. Hamsa Poorna Prakash, Dr. Hemant Sahu, Dr. Ajay Tiwari, Avinash Dubey, Ashutosh Mishra, Kanushree Nandedkar, Sujit Roy, Smriti, Pooman Lakshida, Luchika Rana, for their support and encouragement in my studies and research work. It is with immense pleasure I express my thankfulness to my batchmates Harish Pandey and Hemkumar your support and suggestions always courage to me. I would like to thank you Chandrapal Chaukse, Hemendra, Parmindar, Sourabh Gupta, Vageesh, Priyanka, Geetanjali, Suraj ware, Manish, Dilharan, Aanchal, Khuleshwari, Karobi Biswas, Pooja Bhagat, Amita Ekka, Abhishek Mishra, Rupali Badhautiya, Jhanendra, Anil Koshle, Ritesh, Aniket and beloved juniors Shwati, Pushpalata, Chandra, Love, Rajendra and many others who helped me in several ways.

Last but not least, I would like to convey my cordial thanks to all the teachers and well-wishers from my schooling days onwards who have directly and indirectly helped me to reach up to this level in my life.

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Dated:



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LIST OF NOTATIONS

%	percentage
⁰ C	degree Celsius
⁰ F	degree Fahrenheit
cm	centimeter
m	meter
mm	millimeter
kg	kilogram
g	gram
ha	hectares
<i>et al.</i>	and others
<i>i.e.</i>	that is
>	greater than
<	less than
ml	milliliter
μl	microlitre
M	molar
hr	hours
min	minute
sec	second
rpm	revolution per minute
V	volts
d.f	degree of freedom

LIST OF ABBREVIATIONS

ANOVA	Analysis of Variance
DNA	Deoxyribo Nucleic Acid
dNTPs	deoxynucleotide triphosphates
DUS	Distinct Uniform Stable
EC	Exotic Collection
EDTA	Ethylene Diamine Tetra Acetic Acid
GCV	Genotypic Coefficient of Variation
IC	Indegenous Collection
NBPGR	National Bureau of Plant Genetic Resources
NMR	Nuclear Magnetic Resonance
PCR	Polymerase Chain Reaction
PCV	Phenotypic Coefficient of Variation
SSR	Simple Sequence Repeat
TBA	Tris Boric Acid
NL10D	Number of leaves in 10 days
SL10D	Seedling length in 10 days,
SDW10D	Seedling dry weight in 10 days,
NL20D	Number of leaf in 20 days,
SL20D	Seedling length in 20 days,
SDW20D	Seedling dry weight in 20 days,
NL30D	Number of leaves in 30 days,

SL30D	Seedling length in 30 days,
SDW30D	Seedling dry weight in 30 days,
GP	Germination percent,
D50%F	Days to 50% Flowering,
PL	Panicle length,
PH	Plant height,
FLL	Flag leaf length,
FLL	Flag leaf width,
PPMS	Panicle per meter square,
1000 GW	1000 grain weight,
FS	Filled spikelet,
UFS	Unfilled spikelet,
SFP	Spikelet fertility percent,
PB	Paddy Breadth,
P L/B R	Paddy L/B ratio and
GY	Grain yield per meter square.

THESIS ABSTRACT

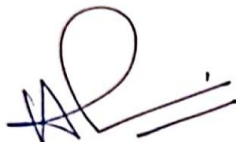
Title of thesis: "Studies on genetic divergence in yield and early seedling vigour for early duration genotypes under direct seeded condition of rice (*Oryza sativa* L.)"

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Major subject: GENETICS AND PLANT BREEDING


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College of Agriculture, IGKV, Raipur (CG)

Degree to be awarded: M.Sc. (Agriculture, Genetics and Plant Breeding)

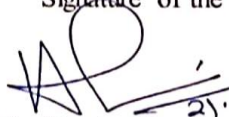


Signature of Major Advisor:

Date: 21.09.2020



Signature of the student



Signature of the Head of the department

21.9.2020

ABSTRACT

"Rice is the most important cereal of the world providing 21% of global human per capita energy and 15% of per capita protein. *Oryza sativa* is the major food crop for people in Asia and nearly 90% of the world's rice is produced and consumed in this region." Chhattisgarh state is renowned by the name "Rice Bowl of India" because rice is cultivated in maximal land area. The research study was carried out by using

eighty rice germplasm “at Research cum Instructional farm of IGKV, Raipur during *Kharij*” 2019 under direct seeded condition in Randomized Complete Block Design (RCBD), with two replications. Based on grain yield, genotypes namely, R1004-2552-1-1 recorded high grain yield followed by Indira aerobic-1, Asam chidi, Surekha, IR 08 L 152, Pokali and Aditya. The traits showed significant variation. Highest values of PCV and GCV was recorded for number of unfilled spikelet, vigor indexII, seedling dry weight on 30 DAS, seedling dry weight on 20 DAS, number of filled spikelet, grain yield per meter square. Highest heritability were found for seedling length on 20 days, seedling dry weight on 20 days, seedling length on 30 days, seedling dry weight on 30 days, germination%, vigor indexI, vigor indexII, days to 50% flowering, “panicle length, plant height, panicle per meter square, 1000 grain weight,” filled spikelet, unfilled spikelet, spikelet fertility %, “paddy length, paddy breadth, paddy L/B ratio and grain yield. The magnitude of genetic advance as percent of mean was recorded high for” maximum traits except some trait showed moderate genetic advance that was seedling length on 10 days, germination%, “days to 50% flowering, panicle length and flag leaf” width, and also these traits showed low genetic advance *viz* number of leaves on 10 days, number of leaves on 20 days and number of leaves on 30 days after sowing.

“Grain yield per meter square showed positive and significant genotypic correlation with days to 50% flowering, panicle length and number of filled spikelet, likewise days to 50% flowering and number of filled spikelet showed positive phenotypic correlation coefficient for grain yield per meter square. The very high direct and positive effect on yield per meter square” were observed for vigor indexII followed by seedling length on 30 DAS, germination per cent, seedling dry weight on 10 DAS, number of filled spikelet, panicle per meter square, flag leaf width, seedling length on 10 DAS, paddy L/B ratio, paddy width, panicle length, flag leaf length, seedling dry weight on 20 DAS. The highest negative direct effect showed by seedling dry weight on 30 DAS, followed by spikelet fertility per cent, number of unfilled

spikelet, number of leaves on 10 DAS, paddy length, “days to 50% flowering, plant height, number of leaf” on 30 DAS.

The “PC with higher Eigen values and variables which had high factor loading were considered as best representative of system attributes.”“The PC1 showed 24.51% while, PC2, PC3, PC4, PC5 and PC6 exhibited” 9.68%, 9.32%, 7.51%, 6.79% and 6.24% “variability respectively among the accessions for the traits under study.” Highest 10 principle component scores in each PC revealed that Pokali is the best genotype for early seedling vigor, yield and its contribution characters followed by R1182-31-2-151, Bangoli-3, CG zinc rice-2, Aditya, Gulta 2614, Aganni, Asha, Lal mati and Gurmetta 2697.

Spark method of clustering grouped the accessions into seven clusters. “The pattern of constellation proved the existence of significant amount of variability. Cluster IV and VII constituted of 15 accessions, forming the largest cluster. In this cluster have much variability. Cluster VI having a largest number of traits, Birsa gova, Gulta 2614 and Pokali falls under cluster VI.

The marker trait associations based on mixed linear model indicated that 18 markers were found to be associated with 23 traits. For grain yield RM 26 (C#6), RM 13 (C#5), RM 225 (C#5), RM 263 (C#2), RM218 (C#3), RM 6091 (C#11), RM 87 (C#5), RM 341 (C#2) and RM 3428 (C#11) exhibited tight association.

For number of leaves on 30 DAS were such marker showed tightly linked with RM 26, RM 19 and RM 22. Seedling length on 30 DAS was tightly linked with RM 252, RM 13, RM 21, and RM 225. Seedling dry weight on 30 DAS was tightly linked with RM 252, for germination per cent RM 341 and RM 1339 marker were showed tightly linked. All these traits are related to early seedling vigor.

The research provided imperative information for further extraction of these elite genes within rice germplasm and using them for rice breeding. The results have

revealed that structures association in one of the sufficient options to recognize major effect quantitative trait loci for early seedling vigor and yield traits in rice.

शोध ग्रन्थ सारांश

शोध ग्रन्थ का शीर्षक	"उपज और प्रारंभिक नवोद्-भिद ओज के लिए अरुणा अवधि के जीनीप्रारूप में धान (<i>ओरियाजा सैटिवा</i> एल.) की सीधी बुआई गई स्थिति के तहत अरुणा अवधि के जीनोटाइप के लिए में आनुवांशिक विविधता का अध्ययन"
छात्र का पूरा नाम: प्रमुख विषय:	राकेश कोशले अनुवांशिकी एवं पादप प्रजनन
प्रमुख सलाहकार का नाम और पता:	डॉ. ए. के. सरावगी विभाग के प्रोफेसर और प्रमुख अनुवांशिकी एवं पादप प्रजनन विभाग, कृषि महाविद्यालय, IGKV, रायपुर (छग)
प्रदान किया जाने वाला डिग्री:	एम. एस. सी. कृषि, (अनुवांशिकी एवं पादप प्रजनन)



प्रमुख सलाहकार का हस्ताक्षर



छात्र का हस्ताक्षर

दिनांक: 21.09.2020



विभागाध्यक्ष का हस्ताक्षर

सारांश

धान विश्व का सबसे महत्वपूर्ण फसल है, जो वैश्विक स्तर पर प्रति व्यक्ति ऊर्जा का 21% और प्रोटीन का 15% प्रदान करता है। *ओरियाजा सैटिवा* एशिया में लोगों के लिए प्रमुख खाद्य फसल है, और दुनिया के लगभग 90% चावल का उत्पादन और खपत इसी क्षेत्र में होता है। छत्तीसगढ़ राज्य "चावल का कटोरा" के नाम से प्रसिद्ध है, क्योंकि चावल की खेती अधिकतम भूमि क्षेत्र में की जाती है। दो पुनरावृत्ति के साथ यादृच्छिक पूर्ण खण्ड अभिकल्पना (आरसीबीडी) में सीधी बोई गई स्थिति के तहत इं. गां. कृ. वि. रायपुर के अनुसंधान सह

इंस्ट्रक्शनल फार्म में अस्सी धान जननद्रव्य का उपयोग करके शोध अध्ययन किया गया। अनाज की पैदावार के आधार पर जनन्द्रव्य R1004-2552-1-1, इंदिरा एरोबिक -1 , असम चुडी, सुरेखा, आईआर 08, एल 152, पोकाली और आदित्य द्वारा सर्वोच्च उपज दर्ज की गई। सभी 26 प्रारंभिक नवोद्-भिद ओज तथा उपज और इसके घटक लक्षणों में महत्वपूर्ण भिन्नता पाई गई। जीसीवी के साथ पीसीवी खाली स्पाइकलेट की संख्या , ओज सूचकांक२, 30 दिन पर नवोद्-भिद के सूखे वजन, 20 दिन पर नवोद्-भिद सूखे का वजन, भरे हुए स्पाइकलेट की संख्या प्रति वर्ग मीटर में अनाज की उपज के लिए दर्ज किया गया। नवोद्-भिद लंबाई 20 दिन में , नवोद्-भिद शुष्क वजन 20 दिन में, नवोद्-भिद की लंबाई 30 दिन में, नवोद्-भिद शुष्क वजन 30 दिन में, अंकुरण %, ओज सूचकांक१, ओज सूचकांक२, 50% फुल आने के दिन , बाली की लम्बाई, पौध की ऊँचाई , पेनिकल प्रति मीटर वर्ग में , 1000 दानों का वजन , भरे हुए स्पाइकलेट की संख्या, खाली स्पाइकलेट , स्पाइकलेट फर्टिलिटी%, धान की लंबाई , धान की चौड़ाई , धान लम्बाई/चौड़ाई का अनुपात और अनाज की उपज प्रति वर्ग मीटर में सबसे अधिक वन्शागातित्व पाई गई ।

सकारात्मक और महत्वपूर्ण जिनीप्ररूप सहसंबंध 50% फुल आने के दिन, बाली की लंबाई और भरे हुए स्पाइकलेट की संख्या में पाया गया , इसी तरह से 50% फुल आने के दिन और भरे हुए स्पाइकलेट की संख्या ने प्रति वर्ग मीटर में धान की उपज के लिए के लिए सकारात्मक लक्षणप्ररूपी सहसंबंध पाया। ओज सूचकांक२, नवोद्-भिद की लंबाई 30 दिन में , अंकुरण प्रतिशत , 10 दिन पर नवोद्-भिद के सूखे वजन , भरे हुए स्पाइकलेट की संख्या , पैनिकल प्रति वर्ग मीटर और ध्वज पत्ती की चौड़ाई 10 दिन पर नवोद्-भिद की लंबाई , धान लम्बाई/चौड़ाई अनुपात, धान की चौड़ाई, बाली की लंबाई, ध्वज पत्ती की लंबाई तथा 20 दिन नवोद्-भिद पर सूखा वजन के लिए पाया गया। उच्चतम नकारात्मक प्रत्यक्ष प्रभाव 20 दिन नवोद्-भिद पर सूखा वजन के लिए प्रति मीटर वर्ग पर पैदावार पर बहुत ही सीधा और सकारात्मक प्रभाव, इसके बाद स्पाइकलेट फर्टिलिटी प्रतिशत, खाली स्पाइकलेट की संख्या, १० दिन पर पत्ती की संख्या, धान की लंबाई, ५०% फुल आने के दिन, पौधे की ऊँचाई तथा पत्ती की संख्या ३० दिन द्वारा पाया गया।

उच्च ईगन मूल्यों और विविधताओं के साथ पीसी जिसमें उच्च कारक लोडिंग रखते हैं उन्हें विशेषताओं का सबसे अच्छा प्रतिनिधि माना जाता है। अध्ययनो में पाया गया की पीसी १ में २४.५१% परिवर्तनशीलता दिखाया गया, जबकी पीसी २, पीसी ३, पीसी ४, पीसी ५ और पीसी ६ में प्रदर्शन ९.६८%, ९.३२%, ७.५१%, ६.७८% और ६.२४% क्रमशः पाया गया। प्रत्येक पीसी में उच्चतम 10 पीसी स्कोर से पता चला कि पोकाली प्रारंभिक नवोद्-भिद ओज और पैदावार एवं इसके योगदान गुण के लिए सबसे अच्छा जीनीप्रारूप है, इसके बाद आर1182-31-2-151 , बैंगोली -3 , सीजी जिक चावल -2 , आदित्य, गुटला 2614 , अगत्री, आशा, लाल माटी और गुरमेट्टा 2697अच्छे जीनप्रारूप हैं।

क्लस्टरिंग की स्पार्क विधि द्वारा जिनीप्रारूप को सात समूहों में वर्गीकृत किया गया। समूह के पैटर्न ने विभिन्नताओं की महत्वपूर्ण मात्रा के अस्तित्व को साबित किया। सबसे बड़ा समूह IV और VII ने 15 परिग्रहण का गठन किया। समूह VI में सबसे अधिक संख्या में गुण हैं, बिरसा गोवा, गुटला 2614 और पोकाली, समूह VI के अंतर्गत आता है।

मिश्रित रैखिक मॉडल के आधार पर 18 मार्करों को 23 लक्षणों के साथ घनिष्ठता पाया गया था। धान की उपज के लिए आरएम 26, आरएम 13, आरएम 225, आरएम 263, आरएम 218, आरएम 6091, आरएम 87, आरएम 341 और आरएम 3428 ने घनिष्ठ संबंध का प्रदर्शन किया।

30 डीएस पर पत्ती की संख्या के लिए आरएम 26, आरएम 19 और आरएम 225 मार्कर के साथ से जुड़ा पाया गया, वहीं 30 दिन पर नवोद्-भिद की लंबाई को आरएम 252 आरएम 13, आरएम 21 और आरएम 225 के साथ मजबूती से जोड़ा गया था। सूखा नवोद्-भिद की वजन ३० दिन में RM 252 के साथ घनिष्ठता से जुड़ा पाया गया। अंकुरण प्रतिशत आरएम 341 और आरएम 1339 मार्कर के साथ कसकर जोड़ा गया। ये सभी जल्द नवोद्-भिद ओज लक्षण हैं।

अनुसंधान ने धान के जनन्द्रव के भीतर उत्कृष्ट जीनों का पता लगाने और धान के प्रजनन में उपयोग करने के लिए आवश्यक जानकारी प्रदान की। परिणाम से पता चला है कि

संरचनाओं में उनके पास पर्याप्त विकल्प हैं, जो शुरुआती नवोद्-भिद ओज और उपज के लिए प्रमुख प्रभाव क्यूटीएल को पहचानते हैं।

CHAPTER-I

INTRODUCTION

Rice is the dominant cereal in the world that provides 21 per cent of global human energy per capita and 15 per cent of protein per capita. Rice (*Oryza* genus) has only two domesticated species i.e. *Oryza sativa* and *Oryza glaberrima*, *Oryza sativa* is known as Asian rice and *Oryza glaberrima* is the African rice. Hence, *Oryza sativa* is Asia's main food crop, producing and consuming almost 90 per cent of the world's rice in this region. Rice is also the staple food in Asia for nearly 2.4 billion people including China, Japan and parts of India, Thailand, Sri Lanka, Bangladesh and many more (Warussawithana 2017).

India had around 44 million hectares of land area for rice cultivation by the end of fiscal year 2017. Over the time frame surveyed this region had been fairly stable throughout. Rice was the most developed food grain in the South Asian nation during fiscal year 2017. Total rice production is forecast at a record 117.47 million tonnes during 2019 (Anonymous 2019). It is 9.67 million tonnes higher than the average production of 107.80 million tonnes for the five years. (Anonymous 2019).

Chhattisgarh is popularly known as the “Rice bowl of India”. Chhattisgarh has an ample area under various varieties of rice i.e. Mahamaya, IGKVR1, HMT, Kalimooch, MTU-1010, Sawrna, IR-36, IR-64 etc. These varieties are grown by the farmers in different agro-climatic zones of Chhattisgarh state. Total area for growing rice in Chhattisgarh is 3711.48 lakh hectares in which produces with 73 lakh tonnes of rice production, and the productivity is 1967 kg per hectare production productivity (Ministry of agriculture Chhattisgarh).

Rice is widely grown under irrigated and rainfed conditions, with improved varieties and landraces that adapt specifically to these situations. In India, under rainfed conditions, more than 50 per cent of rice areas are grown as direct seeded rice (DSR). Under the rainfed situation direct seeded rice has become standard practice due to

erratic rainfall patterns. Due to the shortage of labor and the lack of timely irrigation water, the farmers in the irrigated ecosystems often adapt to dry direct seeding. However, DSR has major disadvantages such as the non-uniform emergence and uneven seedling population, as well as high growth of weeds (Chauhan and Abugho, 2013). In such situation, Early Seedling Vigour (ESV) comes in rescue. Early seedling vigor (ESV) determines the rapid, uniform emergence and development of seedlings under a wide range of field conditions and has been considered as one of the key characteristics of successful crop establishment (Zhang *et al.*, 2005), under DSR. Strong seedling strength is desirable feature in direct seeded rice to enhance crop establishment and the ability to compete against weeds. Nonetheless, modern irrigated rice varietal architecture currently available with semi-dwarf stature and reduced seedling vigor is not ideal for dry direct seed conditions. Irrigated rice varieties, compared to rainfed varieties, are high yielding but relatively low in early seedling vigour. It is important to identify and transfer the genes that promote vigorous growth in young rice seedlings into high yielding cultivars. This will rely on identifying the top donors for early seedling intensity and the characteristics that best predict field success (Redona and Mackill, 1996).

Correlation and path analysis determine the magnitude of the association between yield and its components and also show the relative importance of their direct and indirect effects, thus providing an obvious understanding of their association with a yield of grain (Babu *et al.* 2012). Correlation is a powerful method for researching character association, and is thus very useful in determining selection strategy to improve a character without losing benefit in the other traits (Patil, 2014).

Genetic variability is the main component of rice and other crops breeding programs. Combined with heritability estimation, the genetic coefficient of variation will provide the best image of the amount of advance to be anticipated from selection. The amount of genetic gain under selection depends primarily on how much genetic diversity there is present in the materials studied. Most crop development projects are essentially aimed at achieving a significant increase in crop yield. Yet yield is a

dynamic character governed by the interaction of various characters. Therefore, knowledge about the relationship of yield attributes and their direct and indirect impact on grain yield is of utmost importance. Therefore path analysis in any plant breeding system is of great importance. Early vigor is a dynamic character and end product of several variables, called vigor parameters, is multiplicative. A detailed understanding of the vigor indicating criteria, interrelationship between them and vigor is also important to make successful selection for early vigor(Jayasudha, 2010).

Genetic diversity is an important tool for a program of crop improvement, as it determines the genetic variation among the genotypes and helps to develop superior recombinants (Manonmani and Fazlullah Khan 2003). Genetic divergence between the genotypes plays a major role in choosing parents with broader differences for specific traits (Patil, 2014).

To know the genetic relationship among the wide collection of cultivated genotypes by using DNA markers efficiently is essential for better understanding of early seedling vigor trait. Simple sequence repeats (SSR) are most widely used among the various DNA markers, as they are hyper-variable, co-dominant, durable and multi-allelic in nature, chromosome-specific and highly facilitated linkage map development and use in plant breeding. SSR markers are commonly used in the rice to determine genetic variation and genetic structure(Anandan, 2016).

Keeping the above mentioned views into consideration, the current investigation has been formulated with the following objectives:

1. To estimate variability parameters for early seedling vigor and yield under direct seeded condition.
2. To estimate the correlation among early seedling vigour, yield and its contributing traits.
3. To estimate the genetic diversity for early seedling vigor and yield.
4. To study the association of SSR markers with early seedling vigor and yield.

CHAPTER-II

REVIEW OF LITERATURE

The existence of genetic variability in the base population is the key factor that is required for the improvement of a crop species. The estimates of different genetic parameters help to understand the nature and magnitude of genetic variability and diversity and also tells about the association between various characters with their direct or indirect effects on yield and grain quality so that selection is performed accordingly. Thus, knowledge of these parameters related to the above aspects is important to design a breeding program for further upgrading the base population.

Modern rice varieties phenotype has been converted into adaptable to transplanted rice with a thirst for water and selection pressure for semi-dwarf structure resulting in reduced early vigor. Falling the availability of fresh water and rising labor costs are driving the search for an appropriate alternative management system to enhance the productivity of grain yields for the escalating world population. Because of these problems, a lot of attention has been focusing on dry direct-seeded rice, because of it has low input demand. In cases of direct seeding, a rice variety with a good early seedling vigor attribute is desirable.

Therefore the rice literature relevant for this investigation has been reviewed and summarized below:

2.1 Genetic variability

2.2 Correlation and path coefficient analysis

2.3 Genetic diversity

2.4” Marker trait association

2.1 Genetic variability

A systematic assessment of genetic diversity and a thorough analysis of the crop's genetic structure is the critical groundwork for the implementation of crop development programmes. The variation found in any population may be attributed to genetic factors, as well as an association between them. A brief review has been summarized below:

Chaudhary and Motiramani (2003) tested 54 accessions of aromatic rice. The highest phenotypic coefficient of variation (PCV) was observed for spikelets fertility percent followed by 100 seed weight, biological yield, grain yield per plant, fertile spikelets per panicle and effective tillers per plant.” The genotypic coefficient of variations (GCV) was followed the same trend as the phenotypic variation coefficient (PCV) for the above-mentioned traits.

Sankar *et al.* (2006) studied on variability, correlation and path-coefficients were made on single plant yield and its components in 34 rice genotypes. High heritability and genetic advance were obtained for the traits days to 50 per cent flowering, plant height, productive tillers per plant, panicle length, grains per panicle, 100 seed weight and single plant yield. Spikelet fertility exhibited high heritability with moderate genetic advance.

Mustafa and Elsheik (2007) revealed presence of wide range of variability for most characters and high heritability with high genetic advance by plant height, days to 50% flowering and 1000 grain weight.

Padmaja *et al.* (2008) investigated genetic variability, genotypic and phenotypic coefficients of variation, heritability and genetic advance. The analysis of variance revealed that there were highly significant differences for all the characters except leaf width and 100- seed weight among the genotypes. The estimates of 32 genotypic and phenotypic coefficients of variation (GCV and PCV) were high for all

the characters except days to 50% flowering and panicle length. Heritability and genetic advance were high for all the characters except days to 50% flowering and panicle length.

Bisne *et al.* (2009) observed that the low, moderate and high genotypic and phenotypic coefficient of variation was expressed by the harvest index, the total number of spikelets filled per panicle, the weight of 100 grains and the percentage of spikelet fertility.

Akinwale *et al.* (2011) estimated phenotypic and genotypic coefficients of variation, broad sense heritability, genetic gain and correlations in rice. Genotypic coefficients of variation were lower than the corresponding phenotypic coefficients in all the traits studied. High to medium broad sense heritability estimates were observed on days to heading, days to maturity, plant height, grain yield and number of grains per panicle and panicle length. High to genetic advance were recorded for the number of grains per panicle, grain yield and the number of panicles per plant.

Seyoum *et al.* (2013) performed a field experiment using 14 rice genotypes to estimate the variability, heritability and coefficient of variation for grain yield and contributing characters. For days to 50 per cent flowering, days to maturity, plant height, panicle length and 1000 grain weight” were found to be highly significant variability.

Kumar *et al.* (2013) studied the genetic variability in 73 international rice genotypes including one local check. The results revealed that high variability found with fertile tillers per plant, number of spikelets per panicle and grain yield per plant. It showed high genetic base among the genotypes.

Kumar *et al.* (2013) recorded a very strong positive correlation between grain yield per plant and harvest index at the genotypic, phenotypic and environmental levels, whereas the number of effective tillers per plant and the biological yield per plant showed a very strong positive association at the phenotypic and genotypic

levels. The harvest-index followed by the number of effective tillers per plant, the biological yield per plant, the kernel length, the L/B ratio, the percentage of fertility and the weight of 1000 grains emerged as the most important grain yield associates in scented rice.

Abebe *et al.* (2017) evaluated 36 rice genotype at two sites, namely Fogera and Pawe. The combined variance analysis showed statistically significant variations ($p < 0.05$) for all the evaluated characters suggesting the presence of sufficient genetic variation among the 36 genotypes. For days to maturity, plant height, panicle length, flag leaf length, number of filled grains per panicle, number of total spikelet per panicle, grain yield and harvest index, genotype \times environment interactions were important. Higher PCV and GCV values were shown by plant height, a number of unfilled grain per panicle, yield of biomass and yield of grain, indicating the possibility of improving the trait by selection. High heritability was associated with culm length followed by plant height, yield of biomass and length of the panicle.

Limhani *et al.* (2017) examined the magnitude of the genetic variability in 72 upland rice genotypes. The characters, number of unfilled grains per panicle, harvest index, grain yield per plot and number of effective tillers per plot displayed high estimates of the genotypic and phenotypic coefficient of variation and also high heritability coupled with high genetic advancement. Coupled with a high genetic advance, phenotypic variation coefficient and also high heritability coupled with high genetic progress.

Anusha *et al.* (2018) assessed 36 genotypes of aerobic rice for early vigor under conditions of dry direct sowing. A significant variation for germination percentage, seedling vigor index and coefficient of germination percentage was observed among the genotypes. Eight genotypes, JGL-11727, JGL-20171, MTU-7029, MTU-1010, NLR-40024, NLR-33671, NLR-3042 and NLR-4002 were found to be extremely vigorous and were selected for dry direct seeding.

Iqbal *et al.* (2018) assessed 18 advanced green super rice lines (GSRs) for genetic variability, heritability and genetic advancement. Significant differences for all the characters were found between the GSR lines. The phenotypic coefficient of variation (PCV) was found to be slightly higher than the Genotypic Variation Coefficient (GCV) indicating negligible environmental influence on yield and components. Similarly, for all traits except for the panicle length, a high heritability coupled with genetic advancement was found which indicates that selection can be used to improve these traits.

Meena *et al.* (2018) collected 38 rice genotypes for yield and its contributing character analysis. PCV was found higher than GCV hence more environmental fluctuations. Yield and its contributing characters were found highest for genotype RP 5125-17-6-3-2-1. Days to 50 percent flowering followed by days to maturity showed the highest heritability. Path analysis showed that “days to 50 percent flowering directly contributed to the yield per plant. Correlation analysis showed a positive association of that days to 50 percent flowering, a number of effective tillers, panicle length, filled grain per panicle with the grain yield.”

Nandedkar *et al.* (2019) estimates of the phenotypic variation coefficient were found to be higher than those of the genotypic variation coefficient suggesting the environmental impact. The PCV and GCV values for leaf, blade length, leaf width period maturity, plant height, panicle length, 100 seed weight, paddy length, paddy breadth, paddy L/B ratio suggesting a less environmental impact on these traits were found to be in good agreement.

2.2 Correlation and path coefficient analysis:

The correlation coefficient is used to determine the mutual association between two variables in plant breeding and to determine component characters for the basis of selection. Path coefficient analysis measures the direct and indirect contributions of independent variables on dependent variable.

Satyavathi *et al.* (2001) studied 15 rice varieties for their “expression of “yield and grain quality characters except L/B ratio and panicle length. Positive and significant correlation for the grain yield was manifested in number of effective tillers per plant, number of grains per panicle, L/B ratio and 100 rice grain weight by correlation studies and they can be used in selection procedure. Number of productive tillers per plant, number of grains per panicle, L:B ratio and 100 rice grain weight were found to be the main contributors to grain yield by the” results of path coefficient.

Surek and Beser (2003) evaluated 80 rice breeding lines for yield and its related traits. A significant correlation was found among grain yield and harvest index, biological yield and number of effective tillers per square meter. A positive direct effect was seen by the biological yield and harvest index. Selection must be done on these mention components. For direct and indirect influence of yield components in 80 breeding lines, based on the result, “number of productive tillers per square meter, biological yield, harvest index, and the number of filled grains per panicle had significant correlation with grain yield. Path coefficient analysis results revealed that biological yield and harvest index had the highest positive direct effects on grain yield. The selection based on the biological yield, harvest index, number of productive tillers per square meter and number of filled grains per panicle will be effective in improvement of grain yield under temperate conditions. Both high biological yield and high harvest index should be taken into account together in this selection due to their negative correlations and indirect effects via each other.”

Chandra *et al.* (2009) studied character association in rice genotypes revealed the “number of effective tillers per plant, the weight of 1000 grains, the length of the panicle and the number of grains per panicle and the yield of grains per plant. The results of the path analysis showed the number of grains per panicle, days to 50 percent flowering, 1000-grain weight and number of effective tillers per plant had high positive direct effects on grain yield.

Sabesan *et al.* (2009) evaluated 54 diverse rice varieties for genetic variability and correlation analysis. The effect of environmental fluctuation on genotypes could be seen. Kernel length, kernel breadth, plant height, 100-grain weight and effective tillers showed high heritability and genetic advance hence direct selection could be useful. Positive significant association was found with grain yield and effective tillers and with grain yield per plant.

Chakraborty *et al.* (2010) carried out a path analysis in twenty nine boro rice genotypes to estimate the direct and indirect effects of yield components. High positive indirect effect on yield per plant was shown by plant height and panicles per plant via harvest index. Results concluded that five component characters, namely harvest index, effective grains per plant, panicle length, panicles/plant and plant height influenced the yield of boro rice.

Yadav *et al.* (2010) experimented of genetic variation and genotypic and phenotypic association in rice was done in this experiment for yield and its associated components. The correlation coefficient and path association were analyzed. Significant differences were found in the case of genetic variability. Moderate genetic advance along with high heritability was found on seed yield/plant, harvest index, biological yield etc. There was a positive and significant correlation between grain yield and the number of panicles per plant, harvest index, number of spikelets per panicle. Major contributors to yield were found to be the biological yield, harvest index, number of tillers per hill and panicle length analyzed by path coefficient analysis.

Babu *et al.* (2012) carried out an investigation to study the correlation and path analysis in twenty one popular hybrids of rice. The results revealed that significant positive association of grain yield per plant with number of productive tillers. Path coefficient analysis revealed that the positive direct effect on yield was exhibited by panicle length and number of productive tillers per plant. Number of productive tillers

per plant possessed both positive association and high direct effect. Hence, this trait could be used in selection for yield.

Chaitanya *et al.* (2013) examined the relationships among seed vigor and yield components in 48 rice genotypes “under dry direct sowing conditions. Results showed that plant height and number of ear bearing tillers have positive and significant correlation with grain yield, while the dry matter at 14 days after sowing and germination percentage had a negative and significant association with grain yield. Path analysis showed that plant height, number of ear bearing tillers, test weight, shoot length at seven days after sowing has a positive direct effect on grain yield and in addition it also has positive association with grain yield.”

Gangashetty *et al.* (2013) studied 42 diverse genotypes of rice for the study of different yield and yield related traits. ANOVA showed a presence of significant variation. Number of productive tillers per plant, number of tillers per plant, test weight, grain breadth and panicle length showed positive and significant association with grain yield. Days to 50 per cent flowering and plant height showed a negative significant association with yield. These traits may help for the selection process. The direct effect was found high for a number of productive tillers per plant and number of tillers per plant on yield.

Khare *et al.* (2014) analyzed the rice germplasm, in which moderate GCV and PCV and genetic advance along high heritability were obtained for the traits like “test weight, plant height, total grains per plant in terms of percent of the mean. Total grains per spikelet, filled grains, panicle length, plant height, days to 50 per cent flowering were found to be absolutely related with grain yield per plant. Filled grains, days to 50 per cent flowering” showed the maximum direct effect on yield. Seven clusters were formed with 14 (highest accessions) in cluster III adhered to 11 in cluster I and the lowest 5 in cluster II.

Lakshmi *et al.* (2014) evaluated 70 genotypes of rice and found that kernel length, days to maturity, plant height and a number of productive tillers per plant showed positive and significant association with yield.

Allam *et al.* (2015) studied the correlation and path analysis in 23 genotypes of basmati rice for grain yield, its component traits and grain quality traits. High significant positive genotypic and phenotypic correlation for grain yield was observed in days to maturity, effective panicles, spikelets per panicle. Effective panicles per plant imparted the highest positive direct effects on yield followed by test weight, spikelets per panicle, kernel length and spikelet fertility when assessed for path coefficient analysis.

Bhati *et al.* (2015) studied 30 elite lines of rice for the study of genetic parameters like path, correlation and genetic variability. Significant differences were found for the characters studied. Value for PCV and GCV was observed high for grain yield and harvest index, hence selection would be suitable. Heritability along with genetic advance was found high for spikelet per panicle and plant height. A positive association was found between plant height, test weight, biological yield and harvest index and grain yield direct influence on yield was found by a number of spikelets per panicle, biological yield and harvest index.

Sarwar *et al.* (2015) conducted experiment with 42 Aman rice germplasm lines. A positive association was found between yield and total and effective tillers per plants at a genotypic and phenotypic level whereas only genotypic in days to maturity with yield. Hence selection could be done on these traits basis but a significant and negative association was found between yield and unfilled grains per plant. Direct influence on yield could be seen by days to maturity, days to 50% flowering, plant height, total and effective tillers per plant. Hence above mentioned traits could be found valid for selection criteria phenotypic and genotypic manner.

Dhurai *et al.* (2016) during kharif 2009, a field experiment was conducted using thirty-two rice genotypes to estimate the correlation coefficients and path analysis for grain yield and contributing rice characteristics. Based on the results of character association studies, significant and positive association of grain yield per plant with harvest index, days to maturity, and number of grains per panicle was manifested.

Thippeswamy *et al.* (2016) Experimented 55 rice germplasm to find a diverse parent for crop improvement. The ANOVA analyzed the important quantity of variability among the genotypes for nine characters calculated. A number of grains per panicle and test weight showed the supremacy of additive gene effect as high 17 heritability along with high genetic advance was observed. The correlation was shown by total and effective tiller per plant, days to flowering with yield. Cluster diagram formed V clusters in which maximum genotypes were present in cluster I by 42 and lowest by cluster III by 2. The maximum genetic distance was observed between cluster V and cluster III.

Devi *et al.* (2017) experimented with 27 rice varieties for the study of path, correlation and variability analysis for yield and its traits. Yield per plant and filled seed per panicle showed a higher value of PCV and GCV as 42.04 and 33.9 respectively. Hence direct selection could be effective. Elongation ratio, head rice recovery, yield per plant and test weight showed high heritability and genetic advance in terms of percent of the mean, hence indicating the presence of additive gene action. A significant positive association was found between yield and flag leaf, width, effective tillers, plant height, and filled grains per panicle. The direct effect was shown by filled grains per panicle equals to 1.41 and effective tillers equal to 1.57 on yield/plant.

Gunasekaran *et al.* (2017) evaluated on nine rice genotypes for 11 morphological and quality traits. The environmental influence was found as PCV was slightly greater than GCV. High genetic advance along with heritability and GCV was

recorded for grain yield per plant governed by dominant and epistatic gene action. A positive correlation was obtained between yield and 1000 grains weight and effective tillers. Hence these characters could be kept on mind during the selection of diverse parents.

Priya *et al.* (2017) studied Character association found “that traits like Productive tillers per plant, grains per panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to % 50 flowering and kernel length were found to possess significant positive association with grain yield per plant at the phenotypic level. Further, path analysis studies revealed that kernel breadth, L/B ratio, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant showed a true relationship with grain yield per plant by establishing a significant positive association and high positive direct effect.”

Oladosu *et al.* (2018) Evaluated at two different locations for five seasons in 15 different genotypes. The evaluation was done for vegetative and yield component traits. Other than panicle length and 100 seed weight all other traits showed significant differences among 15 genotypes when analyzed with the help of ANOVA. A positive correlation was found between yield and panicle per hill filled grain per panicle. While moderate with 20 elongation ratio of flag leaf and days to maturity. The direct major effect was found by Filled grains per panicle (0.491) followed by grain weight per hill (0.449) and the maximum indirect effect was found by panicle per hill with yield.

Rasel *et al.* (2018) evaluated 28 local rice landraces for eleven morphological characters useful for salt tolerance. Non-addition gene action was prominent as PCV was found greater than GCV hence selection for these characters was found useful. Plants that showed high survivability were found to have high PCV and GCV and had high variability and those with low PCV and GCV showed low variability and found to have a low survival rate. Correlation useful for salt tolerance in plants were found to have negative correlation which was found to be useful for screening purpose of the following experiment as shoot length, root length, root dry weight, root dry weight.

Root length, shoot dry weight and root dry weight showed a positive direct effect on the salt tolerance level of experimental material found path analysis.

Singh *et al.* (2018) experimented on 27 genotypes plus 3 checks with 14 quantitative characters. Tiller per plant, panicle bearing tiller per plant, days to maturity showed a significant and positive correlation with grain yield. Besides seed yield per plant, all colors showed a high association with each other.

Saha *et al.* (2019) Studied 40 landraces for better accession for yield by analyzing 13 yield-related traits. The influence of the environment was found high as there was more value of PCV compared to that of GCV difference was found in unfilled rains instead of filled grains and also because of the flag leaf area. Number of filled grains per panicle and number of grains per panicle showed high heritability with a high genetic advance which suggests direct selection on a phenotypic basis would right for these characters. Number of effective tillers per hill, days to maturity, number of total tillers per hill, 50% flowering, flag leaf area, number of filled grains per panicle and number of grains per panicle showed a significant and positive correlation with yield. Days to 50 % flowering, effective tillers per hill showed a positive direct effect on yield by path coefficient analysis.

2.3 Genetic diversity

The spectrum of variations in the segregating population is based on the genetic diversity of combining parents. The knowledge of the environment and the extent of genetic divergence is essential for plant breeders in selecting the correct type of parents for a breeding programme.

Akram *et al.* (2001) evaluated 57 diverse genotypes of rice for seed and seedling vigor traits *viz.*, germination rate, root length, shoot length and dry weight of seedlings, and 100 seed weight. Significant differences were found for all the traits. The genotypes IR50, IR25924-92-1-2, IR31779-19-3-3-2-3, TNAU (AD) 103 and PUSA 510 proved superior in respect of most of the traits studied. These genotypes

could be used as donor parents, for improving seed and seedling vigor while breeding rice varieties for direct seeding. Significant differences among the cultivars for different vigor traits indicated the involvement of genetic control in the manifestation of seed and seedling vigor in rice.

Anandan *et al.* (2011) used the Principal Component Analysis (PCA) to assess the diversity of 44 rice genotypes from different geographic regions. The PCA revealed that axes 1 and 2 represented 82.88 percent, and 11.14 per cent, respectively, of the variance. The highest contributing variable in PC1 was grain number per panicle and in PC2 plant height. Both PCs revealed that morphometric diversity was pedigree-based and independent of geographic origin.

Parikh *et al.* (2011) studies 71 accessions to rice and revealed a pattern of genotype diversity. Accessions of the germplasm are arranged into eight clusters. The genotypes in these clusters, i.e. Tulsi Mala (cluster II), Kali Kamod (cluster VI), Bhata Dubraj Shankar Jeera and (cluster VII) and Lohandi and Til Kasturi (cluster VIII) may be used as potential donors for future yielding hybridization breeding programmes.

Medhabati *et al.* (2012) evaluated the genetic diversity of 32 indigenous rice germplasms and five wild rice. The 37 wild and cultivated germplasm were divided into 5 clusters based on 12 agro-morphological traits. Based on the total rank, grain yield/plant, grain length, spikelet/panicle, 100-grain weight, ear bearing tillers/plant, days to 50 per cent flowering, and flag leaf length were the traits which associated maximum to genetic divergence.

Kumar *et al.* (2012) assessed the diversity in a set of 72 rice genotypes of different villages for Chhattisgarh state, by using fifteen polymorphic SSR markers. SSR analysis produced 44 different alleles with an average of 2.93, with a range of 1 to 4 allele per locus. The results led to the conclusion that the amount of genetic diversity was present in the collected rice genotypes.

Gana *et al.* (2013) conducted the experiment and the results of the principal component analysis showed that the first 5 principal component axes explained 68.9% (first year) and 61.6% (second year) of the total variations in the rice population. The combined results showed that 65.4% of the variations were accounted for by the first 5 principal components axes. Number of grains per panicle loaded more on the component loading correlation plot using the combined results. It accounted for about 17.8% of the variation in the population. High levels of variability were expressed among the varieties and the characters studied which will allow further improvement in the varieties.

Islam *et al.* (2014) screened 43 high yield rice varieties and an anoxia/hypoxia resistant land breed for direct seeding. It was observed the percentage of parameters for seedling establishment, first leaf, plant height, leaf number, and seedling length. The varieties have been classified into six distinct groups. The screening showed that under lowland conditions BR6 is the best variety for direct seeding.

Mahendran *et al.* (2015) this investigation was conducted to determine the relationship and genetic diversity between 293 accessions of rice germplasm using the main component analysis for high-temperature tolerance. Component 1 had the contribution from the characteristics in this study, i.e. panicle exertion, days to 50 percent flowering and panicle length, which accounted for 23.35 percent of the total variability. Total number of tillers, number of productive tillers, biomass and yield has contributed 17.75% to the total variability in component 2. The remaining variability of 17.13%, 9.93% and 9.22% was consolidated in component 3, component 4 and component 5 by various traits like grain length, grain breadth, L/B ratio, 100-grain weight, number of grains per panicle and spikelet sterility. The cumulative variance of 77.38% of total variation among 15 characters was explained by the first five axes. Thus the results of the principal component analysis revealed, wide genetic variability exists in this rice germplasm accession.

Ayesha *et al.* (2015) genetic variability, using agro-morphological traits, between the *Oryza sativa* germplasm. Cluster analysis and principal component analysis estimated the results. Based on the hierarchical clustering framework the 116 accessions were divided into 7 clusters. The most important PCI accounted for 28.41 percent of the overall morphological variation, PC II contributed 13.38 percent, and PC III accounted for 11.69 percent.

Islam *et al.* (2016) observed that the first nine axes accounted for about 90 per cent of total PCA variations in 113 aromatic and fine grain rice landraces. Sohrabi *et al.* (2012) on the other hand. Chakravorty *et al.* (2013) observed a contribution of 76.7 per cent and 75.9 per cent of the first six and four components respectively to the total variation in rice. A two dimensional chart (Z1-Z2) of the 31 genotypes was constructed on the basis of main component axes I (PCA score 1) and II (PCA score II). The genotypes were distributed into 5 clusters according to the scattered diagram. Similar findings for the traditional Biroin rice germplasm also reported by Habib *et al.* (2005).

Gour *et al.* (2017) studies of 83 rice genotypes consisting of traditional landraces and JNKVV released varieties were evaluated for 33 quantitative and quality traits using main component analysis to determine variation patterns, individual relationships and characteristics. The main analysis of the components was used to examine the variation and to estimate the relative contribution of different traits to total variability. The PC1 showed 18.683%, while, PC2, PC3, PC4, and PC5 exhibited 15.404%, 13.401%, 9.433%, 8.037%, and 5.232% variability. The rotated component matrix revealed that PC3 accounts for yield and yield attributing traits. PC1 was also dominated by yield related traits. The PC2, PC4 and PC5 was dominated by quality traits. It can be observed that scoring germplasm R-304, Mahamaya, R-710, R-435, IR 64, Lakna, Shriram, Rani Kajar, Surajone and Safari-17 comes in a different principal component which has relation with yield and quality attributing trait both. Sugandha-2 comes in PC2, PC4 and PC5 which all related quality aspects. Thus the results of

principal component analysis used in the study have revealed the traits contributing to the variation were identified.

MAU *et al.* (2017) characterized 40 accessions of upland red and black rice in order to assess the rice germplasm's genetic diversity based on agro-morphological traits. A total of 26 quality characteristics and 16 quantitative features were analyzed. The rice accessions were divided into 4 clusters and 15 sub-clusters by cluster analysis retaining qualitative variables. The same quantitative trait analysis set the 40 rice accessions into 5 clusters and 8 sub-clusters.

Islam *et al.* (2018) studied the genetic diversity using 10 “microsatellite markers across twenty aromatic rice landraces along with four improved varieties of Bangladesh. The result revealed that a number of alleles per locus ranged from 2 to 8, with a mean value of 4.30 alleles across 10 loci. Total of 43 polymorphic alleles were found. The values of Polymorphic information content (PIC) ranged from 0.217 to 0.835 (average 0.495) which indicates high genetic diversity among the studied aromatic rice genotypes. It was concluded by the PIC value of RM5339 that it might be the finest marker for diversity estimation and characterize of these aromatic rice genotypes, followed by RM334, RM414 and RM28502 markers.”

Shivani *et al.* (2018) reported that the nature and magnitude of the genetic difference between the 26 genotypes of rice with eleven quantitative characteristics *viz.*, seedling vigor, days to 50 per cent flowering, plant height, panicle bearing tillers per plant, number of spikelets per panicle, number of grains per panicle, test weight, biological yield per plant, yield of grain per plant and harvest and The 26 genotypes were grouped into six clusters with cluster I comprising a utmost of 11 genotypes, based on Euclidean cluster analysis.

Gupta, *et al.* (2019) studies in 48 genotypes including 4 checks analyzed inter-cluster distance were larger than intra cluster thus, suggesting greater variability among different clusters observed similar results. The first cluster composited 46

genotypes which showed comparatively lesser genetic diversity with each other. Cluster II included one genotype and cluster III had one genotype.

Kumari *et al.* (2019) study that principle component analysis (PCA) showed that the first four principle components had >1.00 Eigen value and accounted 80.24% of total variation. The rotated component matrix revealed that each principle component is separately loaded with various submergence tolerant related traits. PC1 was constituted by Tolerance score (0.41). PC2 was maximum correlated with total shoot elongation (0.59) followed by relative shoot elongation (0.48), panicle length (0.43) and plant height (0.42) while, PC3 was maximum correlated with panicle length (0.52) followed by plant height (0.51). Therefore, the intensive selection is recommended to bring about rapid improvement of submergence tolerance by selecting lines from PC1, PC2 and PC3. All the 243 lines (including checks) were grouped into 16 clusters. Cluster VIII and X have higher mean value for the maximum no. of traits indicating mutant lines from this trait can be used for further improvement.

2.4 Marker-trait association

Studies of association analysis may be used for testing associations between molecular markers and quantitative trait loci (QTL).

Balwant *et al.* (2011) analyzed the genetic diversity of a group of 50 elite rice genotypes *via* morphological, quality and SSR markers and revealed that the morphological, physiochemical and microsatellite marker cluster analysis for similar cultivars provides greater confidence in the assessment of genetic diversity and relationships that could be used in subsequent breeding programmes.

Mengistu (2011) studied the morphological and molecular characterization of Ethiopia's 18 rice varieties and lines (*Oryza sativa* L.). Five primers of the ISSR (810, 824, 834, 873, and 878) used inter-simple sequence 11 repetitions (ISSR) as a molecular marker to evaluate genetic diversity within and between species. A total of

75 simple, reproducible bands have been amplified, of which 62 are polymorphic (82.67 percent). For the primer-873 the number of polymorphic loci for the primer-810 varied from 8 to 16.

Padmaja *et al.* (2011) based on 22 SSR markers, the genetic variation of 72 rice germplasm lines was analyzed. Seven markers exhibited polymorphism which produced 20 alleles.

Abe *et al.* (2012). studies in temperate regions, seedling vigour is one of the key determinants of a healthy stand establishment for direct seeded rice (*Oryza sativa* L.) Using 250 recombinant inbred lines (RILs) derived from a cross between two Japonica rice cultivars Kakehashi and Dunghan Shali, quantitative trait loci (QTL) for seedling vigor was defined. Seedling heights assessed for Kakehashi and Dunghan Shali were 20.3 and 29.4 cm at 14 days after sowing, respectively. The height for the RILs ranged from 14.1 to 31.7 cm. Four putative seedling height based QTLs have been identified. qPHS3-2, the major QTL on the long arm of chromosome 3, represented 26.2 per cent of the phenotypic variance.

Kumar *et al.* (2012) studied characterizing and assessing rice diversity using molecular (SSR) markers in a collection of 72 rice genotypes obtained from different villages in the Chhattisgarh state. Analysis of SSR with 15 polymorphic SSR primers generated 44 different alleles on 2, 5 percent agarose gel with an average of 2.93, ranging from 1 to 4 alleles per locus.

Mazid (2013) the genetic variation of the 41 rice genotypes was evaluated using 26 SSR and 20 ISSR markers. A total of 88 alleles and 310 polymorphic loci were observed for the 26 SSR markers and 20 ISSR markers, respectively..

“Utami *et al.* (2013) studied the genetic diversity of 96 rice accessions based on their specific DNA fingerprints using microsatellite markers. The 96 rice accessions that consisted of varieties with diverse maturing ages were genotyped using 30 SSR markers linked to the heading date (HD) genes that were spread out in 12

chromosomes of a rice genome. A total of 297 alleles were detected, indicating the level of marker informativeness.”

Dang *et al.* (2014) For rice seed vigor twenty-seven QTLs were found, of which 16 were novel QTLs. Fifteen elite parental combinations have been planned to enhance seed vigor in rice. Key message 27 QTLs for rice seed vigor have been identified, in which 16 were novel QTLs. Fifteen combinations of elite parents were designed to improve seed vigor in rice. Seed vigor is closely related to direct rice seeding (*Oryza sativa* L.). Estimated population structure based on 262 basic Sequence Repeat (SSR) markers. Seed vigor was measured by shoot length (SL), and shoot dry weight. The surveyed population has found significant phenotypic and genetic diversities.

Patel *et al.* (2014) studied the diversity using 14 Simple Sequence Repeat (SSR) and 21 Insertion Deletion (INDEL) markers for 19 genotypes of coloured and white rice. To these ends, polymorphic tests were obtained for 9 SSR and 12 INDEL markers.

Al-Turki and Basahi (2015) estimated genetic diversity among 27 landraces of Hassawi rice growing in the Al-Ahsa region of Saudi Arabia by using 14 primers of the ISSR marker. The analysis of ISSR polymorphism divided the examined rice landraces into two groups and results indicate that ISSR fingerprints are efficient in the identification and resolution of genetic diversity between the landraces of the Hassawi rice and will be an efficient method in the authentication of the rice germplasm in the gene bank of Saudi Arabia.

Sarawgi *et al.* (2015) studied association analysis (path and correlation) on 188 rice germplasm accessions (landraces) and result obtained from this experiment concluded that the characters like leaf length, leaf width, panicle length and effective tiller could be used as a direct selection criterion for higher grain yield as showed positive significant correlation with grain yield.

Vu *et al.* (2016) reported that the system of direct-seeding rice cultivation, seedling vigor is one of the most important features for the establishment of stable stands during early seedling stages, particularly when submerged due to temporary flash flooding. In a collection of 40 Vietnamese lowland rice varieties, we studied genetic diversity using 30 simple sequence repeat (SSR) markers which cover all rice chromosomes. A total of 111 alleles have been detected, averaging 3.7 alleles per locus. The number of polymorphic alleles per SSR marker detected ranged from 2 to 6. The fragment size of a given SSR locus ranged from 85 to 650 bp and the frequency of a major allele ranged from 32.5% to 76.9% at each locus. The value of the knowledge content for polymorphism ranged from 0.355 to 0.774, with an average of 0.594. Calculated genetic similarity between pairs of rice varieties ranged from 0.03 to 0.97, with an average of 0.27. His findings indicated the utility of the SSR marker method for testing genetic diversity in Vietnamese rice germplasms concerning their submerged seedling vigor.

Anandan *et al.* (2016) identified early seedling vigor (ESV) as the basic characteristic of direct seed rice. In this regard, under the directly seeded aerobic situation, 629 rice genotypes have been analyzed for their morphological and physiological responses in the field. The genotypes utilized for studying diversity patterns by employing trait linked markers have categorized early vigor and non-early vigor genotypes. The results of distance based approach and principal coordinate analysis were in accordance with model based structure analysis. Further, the study has identified significantly associated markers and markers with pleiotropic effects indicating that association mapping served as an effective tool. Genotypes identified from this study possessing favorable alleles can be utilized for improving early seedling vigor after functionally characterizing them.

Raghavendra *et al.* (2016) analyzed a set of 66 rice varieties using 8 ISSR primers to assess genetic diversity. A total of 70 bands were detected out of which 56 were polymorphic, 14 were monomorphic and shows 78 percent polymorphism. The maximum number of polymorphic bands 10 was obtained in primers 843 and 879. The

PIC value ranged between 0.15 (884) to 0.47 (807) with an average of 2.8 per locus. Out of eight ISSR primers unique specific allele was generated for the variety IR 50 with a specific molecular weight of 672 bp, which 14 can be used as molecular Id. Genetic similarity among genotypes varied from 0.5 to 1.0 with an average of 0.75.

Warusawithana *et al.* (2017) evaluated the genetic diversity of twenty traditional Rice 'Pachchaperumal' accessions, together with two control varieties Bg360 and 'Suwandal' Rice. Morphological analysis was performed using seven standard rice morphological seed descriptors, and 16 SSR primers were used for molecular analysis. The results revealed that, morphologically as well as molecularly, a significant degree of genetic diversity was found among the test accessions. Two distinct accessions, accession numbers 3752 and 5547, were identified as potential off types of 'Pachchaperumal'.

Zhang *et al.* (2017) study in the direct-seeded rice technology is widely used, seedling vigor is an imperative agricultural attribute. To investigate the genetic mechanisms underlying seedling vigor in rice, seeds of 132 recombinant inbred lines (RILs) consequent from 93-11 and PA64, harvested from Lingshui and Hangzhou were grown in the nutrient solution, and four seedling vigor indices including “seedling shoot length (SSL) and seedling dry weight (SDW)” were measured. Significant similarities between the indexes, as well as between 1000-seed weight (TSW) and SDW were observed. Among 57 QTLs for seedling vigor, 28 were detected from seeds harvested in both sites and 33 were first identified. There was no significant difference between the two parents from the seeds harvested in Lingshui for SSL and SRL of seedlings while a statistically significant difference was found in Hangzhou.

Rana *et al.* (2018) used SSR markers for the study of 10 rice genotypes. The 10 rice genotypes showed clear diversification for the primers RM510, RM351 and RM215. A total of 10 alleles were detected among the 10 rice genotypes. 3.33 were found as alleles per locus as an average. 40 % of the total was the common major

alleles at each locus. The average PIC value was 0.608 locus-1 ranged from 0.492 of RM 510 to 0.745 of RM 351. PIC value was highest for RM 351. Using the UPGMA method grouping was done into 4 clusters. 1, 3, 1 and 5 were genotypes present in clusters I, II, III and IV. Cluster I, II, III and IV contained 1, 3, 1 and 5 genotypes respectively. Results revealed RM 351 as the best screening material.

Gasim *et al.* (2019) experimented on 558 SSR markers that are used to evaluate 31 rice accessions obtained from Sudan and IRRI. 483 primers showed polymorphism and showed 1274 unique alleles. PIC value was found to an average of 0.39 ranged from 0.06 to 0.69. allele frequency per locus was found to be between 32% to 97% with an average of 64%. RM7643 showed the highest PIC value was highly informative as it recorded the highest PIC value (0.69). UPGMA divided accessions into four different clusters with a genetic dissimilarity.

Ishaq *et al.* (2019) evaluated 13 SSR markers 27 rice genotypes to check the duplicity of commercially released varieties names. PIC value was found to be 6.233 bands per primer and 81 distinct alleles were found. 0.94 was the highest allelic frequency for Primer RM400 from 20 alleles. The average PIC value was found to be 0.54 ranged from 0.31 and 0.93. UPGMA culture analysis grouped 27 genotypes into 13 distinct clusters, hence showed a wide variety of diversity. SSR primers showed polymorphism hence demolishing doubt of duplicity suspicion.

Nandedkar *et al.* (2019) characterized 48 genotypes with three checks in Complete Randomized Block Design. The results revealed the presence of highly significant variability for all the characters except effective tillers per plant which was non-significant. Total molecular analysis showed a polymorphic reaction of 29 markers with a total of 144 alleles amplified between 48 genotypes with a range of 1 to 7 alleles per locus with an average of 3.67 alleles per locus.

CHAPTER-III

MATERIAL AND METHODS

The present research work “**Studies on genetic divergence in yield and early seedling vigour for early duration genotypes under direct seeded condition of rice (*Oryza sativa* L.)**” was carried out during the *Kharif*, 2019-20. The techniques and materials used in this study are presented below.

3.1 Experimental site

The experiment was conducted at “Research cum Instructional Farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidalaya Raipur, Chhattisgarh, India.”

3.2 Climate and weather

Chhattisgarh is situated between 17°14'N and 24°45'N latitudes and 79°16' E and 84°15' E longitudes. Raipur (C.G.) is lies at 21°16'N latitude and 81°36' E longitude with an altitude of 289.60m, above the mean sea level. The maximum mean temperature was 32.30°C & minimum mean temperature was 23.99°C during the crop development stage. The overall total rainfall during crop growing period was 1199.2 mm. The highest rainfall received during August month was (316.4 mm). The data pertaining to weekly rainfall, lower and highest temperatures, RH, evaporation and shining sunshine hours of total crop growing time have been presented in Fig. 3.1.

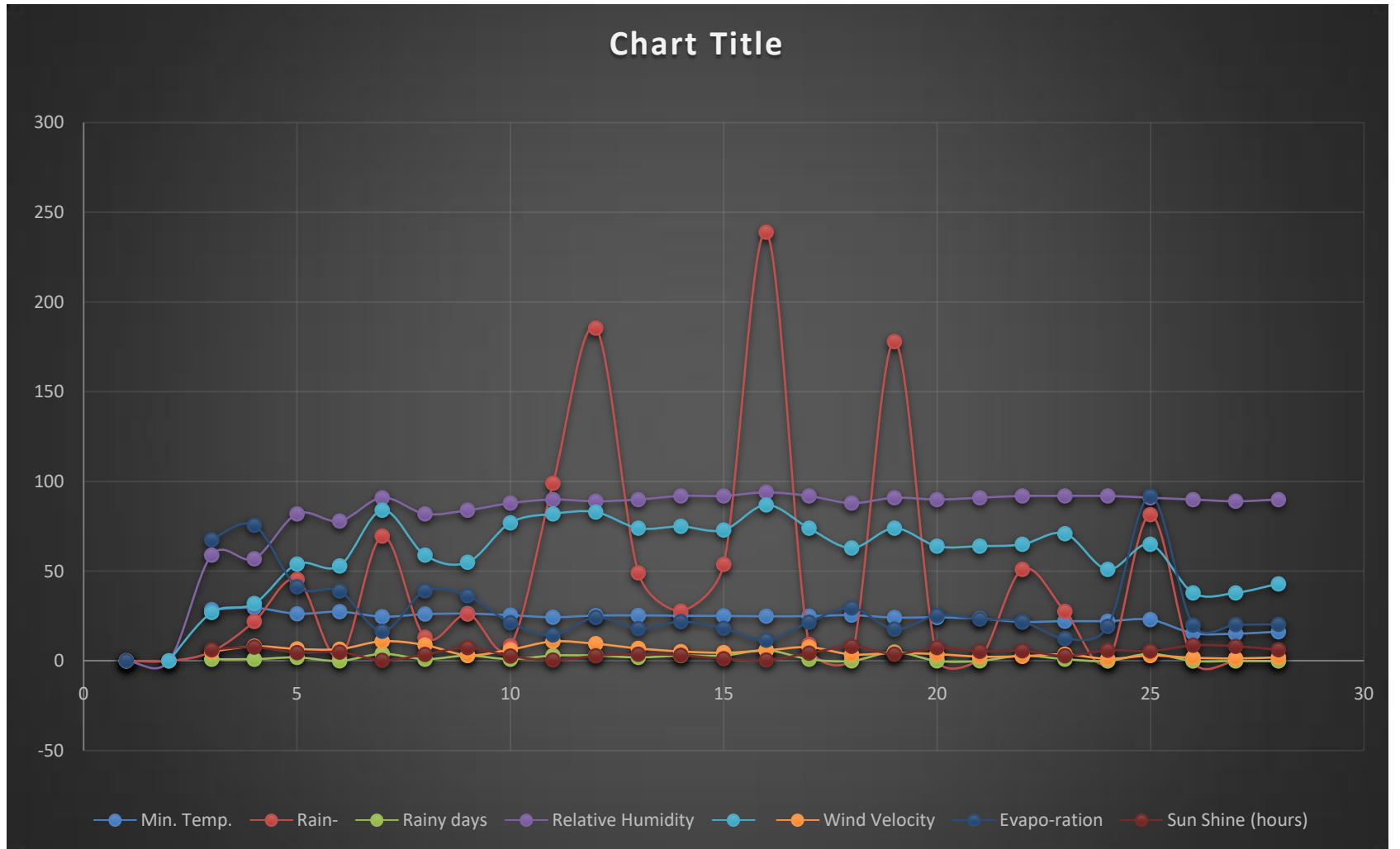


Fig. 3.1: Meteorological data for *kharif* season 2019

3.3 Experimental Materials

The experimental materials comprised of eighty genotypes of rice including two checks *viz.*, Shamleshwari and MTU-1010. The list of rice genotypes is presented in Table 3.1. The experimental materials received from IGKV, Raipur.

Table 3.1: List of eighty rice genotypes along with two checks used in the present study

S. N.	Name of genotypes	S. N.	Name of genotypes
1	Aditya	26	DU-95-0-137-1
2	Kalinga-3	27	Sawas-D-137-1
3	Bala	28	Birsa gova
4	Poorva	29	Danwas 2511
5	Lallu-14	30	Duma-bada-25-55
6	MR 1523	31	Fent 2679
7	IR-38	32	Gutla 2614
8	Surekha	33	Gurmetta 2697
9	Tripti	34	Danwar 2129
10	T-10	35	R1558-1419-2-1442-1
11	Aganni	36	R1519-769-2-1442-1
12	Jhitpiti	37	R1551-2169-1
13	R1558-2423-1-1445-1	38	R1448-578-2
14	Kaweri	39	R1013-2307-1-4
15	Shwnong-89366	40	IR-7866-BIO-BBB-SBI
16	Chom phool	41	R971-25-2-1
17	Asha	42	R1152-2-64-1
18	Bangoli-3	43	R1004-2552-1-1
19	Nipon bare	44	CR-306-37-13
20	Lal mati	45	CR-314-5-10

21	Usai buta-2408	46	Asam chidi
22	Banisar No-31	47	R1723-1411-1-3551
23	Karhani-No-9	48	ARC-15831
24	Balsi balu kanb-694	49	Danteshwari
25	Banso bnisa B-1021	50	Poornima
51	Salim paket	66	CR-Dhan-40
52	R1238-19361	67	R1882-306-4-243-1
53	R1182-31-2-151	68	R1986-296-2-867
54	R1122-167-2-1571	69	R1973-206-2-86-1
55	Vandana	70	CG zinc rice-1
56	R1546-1382-1-40-1	71	CG zinc rice-2
57	MTU-15	72	R1779-321-1-112-1
58	Mamhar	73	R1882-301-1-234-1
59	C101 LAC	74	R2221-391-1-248-1
60	Shyamla	75	R1882-310-4-257-1
61	IR-64	76	IR-36
62	Pokali	77	IR-64 (DRT)
63	Krishna hansa	78	Indira aerobic-1
64	IR 08 L 152	79	Samleshwari (Check)
65	RP-5125-2-4	80	MTU-1010 (Check)

3.4 Experimental Methods

The germplasm accessions of rice were sown in the field during *kharif* season 2019-20 at Research cum Instructional Farm of College of Agriculture, IGKV, Raipur. The trial were conducted in rainfed situation. The experimental design was Randomized Complete Block Design (RCBD). The experimental material was planted in two replication and each replication comprised of eighty genotypes. Each entry was sown in a plot size of 1.20 meter length and 1.0 meter width with spacing of 20 cm

between rows. The checks were randomized within replication. The standard agronomic practices were adopted for normal crop growth.

3.5 Observations recorded

In the present study, observations on different characters related to early seedling vigor and yield and its components were recorded to accomplish the objectives of the study. From each plot, five random plants were taken for recording data of different characters at optimum plant growth stage, average of the data from the sampled plants concerning different characters were used for various statistical analysis.

3.5.1 Germination percent:

Hundred seed taking for evaluating germination percent using petriplate in lab condition. Germination count was recorded on eighth day according to ISTA rules. The equation to calculate germination percentage is: $GP = \frac{\text{seeds germinated}}{\text{total seeds}} \times 100$.

3.5.2 Seedling length on 10, 20 and 30 days after sowing (cm):

Seedling length observed on 10 days after sowing (DAS) followed by 20 and 30 DAS. Observations recorded on randomly five plants for each treatment from the soil surface to tip portion of the leaves.

3.5.3 Number of leaves on 10, 20 and 30 DAS:

Five randomly selected plants were taken from each treatment and number of leaves from each plant was recorded.

3.5.4 Seedling dry weight (g) 10, 20 and 30 DAS:

Seedling was taken from the field after that dried in oven for 3 days in 60°C on oven, after all the moisture evaporated than recorded the seedling dry weight on weighing balance.

3.5.5 Vigor index I and vigor index II:

The formula for calculating vigor index is -

$$VI\ 1 = \text{Germination per cent} \times \text{Seedling length (cm)}$$

$$VI\ 2 = \text{Germination per cent} \times \text{Seedling dry weight (g)} \text{ (Zhang 2010)}$$

3.5.6 Days to 50 per cent flowering(days):

The number of days were recorded from date of sowing to date of 50 per cent flowering and assessed through visual observation of a group of plants.

3.5.7 Leaf length (cm):

Flag leaf length is measured in centimeter after 25 days of 50 percent flowering from the base to tip of the leaf. From five random plants, data was recorded and averaged.

3.5.8 Leaf width (cm):

Flag leaf width is measured in centimeter after 25 days of 50 per cent flowering at the widest portion of the leaf. The data was recorded from five random plants and averaged.

3.5.9 Panicles per meter square:

This observation was recorded after counting of the total number of panicles presenting inside the one meter of observation plot from each treatment.

3.5.10 Plant height (cm):

Plant height was measured in centimeter on the primary culm (or the tallest tiller) at maturity, from ground level to the tip of the panicle. From five random plants, data was recorded and averaged.

3.5.11 Panicle length (cm):

Panicle length was measured in centimeter at full maturity, from panicle base to tip of the panicle. Five plants were used for observations and data was averaged.

3.5.12 Number of filled grains per panicle:

After harvesting, the total number of filled grains per panicle was counted manually.

3.5.13 Number of unfilled grains per panicle:

The total number of unfilled grains was recorded in the same way by counting it manually in five random panicles as filled grains were counted and averaged.

3.5.14 Per cent spikelet fertility(%):

Spikelet fertility percentage was calculated as follows:

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

3.5.15 1000 seed weight (g):

Thousand well developed and whole grains of each accession were taken and dried up to 13 per cent moisture and weighted.

3.5.16 Grain yield per meter square(g):

Grain yield was taken from 1 meter square from each treatment of both replication in grams and was dried under the sunlight for 6-8 days after harvesting and then measure the grain weight.

3.5.17 Paddy length (mm):

Ten grains were aligned straight in a graph paper from tip to base in a successive manner and then measured in cm with the help of scale and averaged.

3.5.18 Paddy breadth (mm):

Ten grains were aligned straight in a graph paper by keeping grain attached to each other from the bulged region of each grain one forward of others and are then measured with the help of a scale and averaged.

3.5.19 Paddy L/B ratio

This was calculated as-

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



Fig 3.2:Preparation of field



Fig 3.3: Plant at seedling stage



Fig 3.4: Plant at flowering stage



Fig 3.5: Plant harvesting

Fig 3.6: Kalinga-3 (paddy breadth)



Fig 3.7: R1519-769-2-1442-1 (paddy length)



3.6 Statistical analysis:

The statistical analysis were carried out using the mean value of genotypes for each characters. The following statistical procedures were followed in present investigation.

3.6.1 Randomized Complete Block Design

The Randomized Complete Block Design (RCBD) may be defined as the design in which the experimental material is divided into blocks/groups of homogeneous experimental units (experimental units have the same characteristics) and each block/group contains a complete set of treatments which are assigned at random to the experimental units.

Actually RCBD is one restriction design, used to control a variable that influences the response variable. The main aim of the restriction is to control the variable causing the variability in response. Efforts of blocking is done to create the situation of homogeneity within the block. Blocking is a source of variability. RCBD is a mixed model in which a factor is fixed and the other is random. The main assumption of the design is that there is no contact between the treatment and block effect.

Model for RCBD

The following two-way linear model was used to represent the mean performance of eighty genotypes (treatments) in the plot of i th replication. (Cochran and Cox, 1962).

$$Y_{ij} = \mu + \eta_i + \epsilon_j + e_{ij}$$

Where,

Y_{ij} is any observation for which $X_1 = i$ and $X_2 = j$

X_1 is the primary factor

X_2 is the blocking factor

μ is the general location parameter (i.e., the mean)

η_i is the effect for being in treatment i (of factor X_1)

ϵ_j is the effect for being in block j (of factor X_2)

e_{ij} is random error

Table: 3.2 Skeleton of Analysis of Variance (ANOVA)

Source of variation	d.f.	S.S.	M.S.S.	
Replications	r-1	SSr	MSr	MSr/MSe
Treatments	g-1	SSg	MSg	MSg/MSe
Error	(r-1)(g-1)	SSe	MSe	
Total	rg-1	SSt		

where,

r = Number of replications

g = Number of genotypes/treatments

SSr = Sum of squares due to replications

SSg = sum of squares due to genotypes/treatments

SSe = Sum of squares due to error

For the testing significance of differences among treatment mean, F-calculated was compared with F tabulated values at 5 and 1% level of significance against (r-1)(g-1) error degree of freedom.

3.6.2 Assessment of variability

Mean, Range, standard deviation, CD, SEd and coefficient of variation for different characters were worked out for all test genotypes.

3.6.2.1 Mean

The mean is calculated by the following formula:

$$\bar{X} = \Sigma Xi/N$$

where,

ΣXi = Sum of all the observations

N = Total number of observations

3.6.2.2 Range

The range of a set of data is the difference between the largest and smallest values, which is expressed as follows:

$$\text{Range} = \text{highest value} - \text{lowest value.}$$

3.6.2.3 Standard deviation (SD)

Standard deviation is a measure of dispersment in statistics. It shows how much the data is spread out around the mean or average. SD is calculated by the formula:

$$SD = \sqrt{\Sigma d^2/N}$$

where,

Σd^2 = Sum of squares of deviation

N = Total number of observations

3.6.2.4 Standard error (SE)

Standard error is a statistical term that measures the accuracy with which a sample represents a population. It's formula is:

$$SE = SD/\sqrt{N}$$

where,

SD = Standard deviation

N = Total number of observations

3.6.2.5 Phenotypic and Genotypic coefficient of variation (PCV and GCV)

The phenotypic and genotypic coefficient of variation was computed as per Burton and De Vane (1953).

$$PCV \% = \frac{\sigma_P}{\bar{x}} \times 100$$

$$GCV \% = \frac{\sigma_G}{\bar{x}} \times 100$$

where,

σ_P = Phenotypic standard deviation.

σ_G = Genotypic standard deviation,

\bar{x} = Grand mean of character

3.6.2.6 Heritability (h^2) in broad sense

Broad Sense Heritability was calculated using the formula (Hanson *et al.* 1956).

$$h^2_{(bs)} \% = \frac{V_g}{V_p} \times 100$$

where,

$h^2_{(bs)} \%$ = Heritability percentage in broad sense

V_g = Genotypic variance

V_p = Phenotypic variance

Heritability Percentage was categorized as follows (Robinson *et al.* 1949).

0-30% was considered as low,

30-60% was considered as moderate

60% and above as high

3.6.2.7 Genetic advance (GA)

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

$$GA = K \times \sigma_p \times h^2$$

where,

h^2 = Heritability (Broad sense) in fraction

σ_p = Phenotypic standard deviation

K = Selection differential which is 2.06 at 5% intensity of Selection. (Lush, 1949)

Genetic advance as per cent of mean for each character was calculated as suggested by Jonson *et al.* (1955) as:

$$GA\% = \frac{GA}{\text{mean}} \times 100$$

3.7.1 Correlation analysis

Correlation is a statistical measure that indicates the extent to which two or more variables fluctuate together. It measures the mutual relationship between various characters with the help of the following formula suggested by Webber and Moorthy (1952).

$$r_{xy} = \text{COV}(XY) / (\text{Var X} \cdot \text{Var Y})^{1/2}$$

$$\text{Phenotypic correlation} = \text{PCOV}_{xy} / (\text{PV}_x \cdot \text{PV}_y)^{1/2}$$

$$\text{Genotypic correlation} = \text{GCOV}_{xy} / (\text{GV}_x \cdot \text{GC}_y)^{1/2}$$

where,

PCO V_{xy} = Phenotypic covariance between variable x and y

PV_x = Phenotypic variance of variable x

PV_y = Phenotypic variance of variable y

GCOV_{xy} = Genotypic covariance between x and y variable

GC_x = Genotypic variance of variable x

GV_y = Genotypic variance of variable y

Correlation coefficients were tested for their significance using “t” statistics at (n-2) degrees of freedom (Snedecor and Cochran, 1967)

$$t_{cal} = r \sqrt{\frac{n-2}{1-r^2}}$$

where,

n = number of genotypes

3.7.2 Path coefficient analysis

Path analysis is simply a standardized partial regression coefficient partitioning the correlation coefficients into the measures of direct and indirect effects of a set of independent variables on the dependent variable. It is also known as the causes and effect relationship. If a character y is determined by correlated characters x_1 , x_2 and x_3 a path diagram must be formulated. Thus we get a set of simultaneous equations as given below:

$$R(x_1, Y) = a + r(x_1, x_2) b + r(x_1, x_3) c.$$

$$R(x_2, Y) = a + r(x_2, x_1) b + r(x_2, x_3) c.$$

$$R(x_3, Y) = a + r(x_3, x_1) b + r(x_3, x_2) c$$

Considering the three factors i.e., x_1 , x_2 and x_3 , the simultaneous equations given above can be matrix notation as: $\begin{matrix} 1 & 2 & 3 \end{matrix}$

$$\begin{matrix} \begin{bmatrix} r(y_1, x) \\ r(y_2, x) \\ r(y_3, x) \end{bmatrix} \\ A \end{matrix} = \begin{matrix} \begin{bmatrix} r(y_1y_1) & r(y_2y_1) & r(y_3y_1) \\ r(y_1y_2) & r(y_2y_2) & r(y_3y_2) \\ r(y_1y_3) & r(y_2y_3) & r(y_3y_3) \end{bmatrix} \\ B \end{matrix} \begin{matrix} \begin{bmatrix} a \\ b \\ c \end{bmatrix} \\ C \end{matrix} \quad q$$

where,

r_{x_1y} = Correlation coefficient between character x_1 and y .

r_{x_2y} = Correlation coefficient between character x_2 and y .

r_{x_3y} = Correlation coefficient between character x_3 and y .

a = Direct effect of character x_1 and y .

b = Direct effect of character x_2 and y .

a = Direct effect of character x_1 and y .

b = Direct effect of character x_2 and y .

c = direct effect of character x_3 and y .

The solution for vector c may be obtained as follows:

$$A = B.C$$

$$\text{or } C = B^{-1} A$$

where, B^{-1} = inverse of matrix B .

After calculation the values of path coefficient i.e., “ C ” vector the residual effect can be estimated by the given formula:

$$R = 1 - \Sigma (rij)$$

Where, R = Residual effect.

rij = Correlation coefficient between i^{th} character and j^{th} dependent variable

Table 3.3 The result of path coefficient analysis is interpreted as per the following scale suggested by Lenka and Misra (1973).

Value of direct/indirect effect	Rate/Scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.99	High
> 1.00	Very High

3.8 Genetic Diversity Analysis

3.8.1 Principle Component Analysis (PCA)

“Principal Component Analysis (PCA) is a powerful tool in modern data analysis because it is a simple, non-parametric method for extracting relevant information from confusing data sets. With minimal effort, PCA provides a roadmap for how to reduce a complex data set to a lower dimension to reveal the sometimes hidden, simplified structures that often underlie it. It reduces the dimensionality of the data while retaining most of the variation in the data set. PCA accomplishes this reduction by identifying directions, called principal components (PCs), along which the variation in the data is maximal. By using a few components, each sample can be represented by relatively few numbers instead of by values for thousands of variables (Ringer, 2008). Thus, the primary benefit of PCA arises from quantifying the importance of each dimension for describing the variability of a data set in more interpretable and more visualized dimensions through linear combinations of variables that accounts for most of the variation present in the original set of variables. Therefore, principal component analysis is a variable reduction procedure.

Thus the principle component is concerned with explaining the variance-covariance structure through a few linear combinations of the original variables. Its general objectives are (1) Data reduction and (2) Interpretation.

Algebraically, principle components are particular linear combinations of the p random variables X_1, X_2, \dots, X_p . Geometrically, these linear combinations represent the selection of a new coordinate system obtained by rotating the original system with X_1, X_2, \dots, X_p as the coordinate axes. The new axes represent the directions with maximum variability and provide a simpler and more parsimonious description of the covariance structure.

Principle component depends solely on the covariance matrix Σ (or the correlation matrix ρ) of X_1, X_2, \dots, X_p . The Eigen value and Eigen vector pairs created from data matrix is utilized to identify the principle components.

Let the random vector $X' = [X_1, X_2, \dots, X_p]$ have the covariance matrix Σ with eigen values $\lambda_1 \geq \lambda_2 \geq \dots \geq \lambda_p \geq 0$.

Consider the linear combinations

$$\begin{aligned} Y_1 &= \ell_{11} X_1 + \ell_{21} X_2 + \ell_{31} X_3 + \dots + \ell_{p1} X_p \\ Y_2 &= \ell_{12} X_1 + \ell_{22} X_2 + \ell_{32} X_3 + \dots + \ell_{p2} X_p \\ \dots \\ Y_p &= \ell_{1p} X_1 + \ell_{2p} X_2 + \ell_{3p} X_3 + \dots + \ell_{pp} X_p \end{aligned}$$

Then ,

$$\begin{aligned} \text{var}(Y_i) &= \ell_i \sum_{i=1,2,\dots,p} \ell_i \\ \text{Cov}(Y_i, Y_k) &= \ell_i \sum_{k=1,2,\dots,p} \ell_k \end{aligned}$$

The principle components are those uncorrelated linear combinations Y_1, Y_2, \dots, Y_p . variances in (equation) are larger as possible.

The first principle component is the linear combination with the maximum i.e., it maximizes variance $(Y_1) = \ell_1 \sum \ell_1$. It is clear that $\text{Var}(Y_1) = \ell_1 \sum \ell$ can be increased by multiplying any by some constant. To eliminate this indeterminacy, it is convenient to restrict attention to coefficient vector of unit length.

3.8.1.1 Eigen Values and Eigen Vectors

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

$$\begin{aligned} \left(\begin{array}{l} \textit{proportion of} \\ \textit{total population} \\ \textit{variance due to} \\ \textit{pth principle} \\ \textit{component} \end{array} \right) &= \frac{\lambda_p}{\lambda_1 + \lambda_2 + \lambda_3 + \dots + \lambda_p} \quad (p = 1, 2, \dots, k) \\ &= \frac{\lambda_p}{\text{Trace}(s)} \end{aligned}$$

The Eigen vector (loadings) defines the correlation of each variable with the principle components. The correlation between the k^{th} original variable X^k and the i^{th} principle component Y is given by

$$r_{Y_i, X_k} = \frac{\ell_{ki} \sqrt{\lambda_i}}{\sqrt{\sigma_k}} \quad i, k = 1, 2, \dots, p$$

Here σ_k is the standard deviation of x_k and $(\lambda_1, \ell_1), (\lambda_2, \ell_2), \dots, (\lambda_p, \ell_p)$ are the Eigen value-Eigen vector pairs for Σ .

Once the principal components have been calculated it need to decide how many to keep. Different methods are used to decide which principal components to retain.

1. Choose sufficient principal components account for a particular percentage (e.g.75%) of the total variability in the data.
2. Choose only those principal components with Eigen values over 1 (if using the correlation matrix).
3. Use the Scree plot of the eigenvalues. This will indicate whether there an obvious cut off between large and small Eigen values.

3.8.2 Cluster analysis:

The analysis was performed by Spark is a general-purpose distributed data processing engine that is suitable for use in a wide range of circumstances. Cluster analysis is a multivariate method that aims to categorize a sample of subjects (or objects) on the basis of a set of measured variables into several diverse groups such that similar subjects are placed in the equal group. Cluster analysis has no mechanism for differentiating between relevant and irrelevant variables. Therefore, the choice of variables integrated with a cluster analysis must be underpinned by conceptual considerations. This is extremely important because the clusters twisted can be very dependent on the variables included. The analysis was performed by Spark is a general purpose distributed data processing engine, that is suitable for use in a wide range of circumstances.

3.9 Molecular analysis:-

3.9.1 Reagents and Solutions:-

The following reagents and solutions were used during the molecular analysis of the experimental material-

1. 1M Tris HCl (pH 8.0 at 25⁰ C)

31.52g of Tris HCl/Trizma base was dissolved in 100ml of distilled water. Adjust the pH to 8.0 using concentrated HCl. Adjusted the volume with distilled water to 200ml and sterilized by autoclave.

2. EDTA (0.5M, pH8)

186.12g of EDTA (disodium eteylene diamine tetra acetic acid) was dissolved in 700ml of distilled water. NaOH pellets were added for the proper dissolving of EDTA. The pH was set to 8.0 using NaOH/HCl. Makeup the final volume to 1000ml with distilled water and sterilize by autoclaving.

3. 4M NaCl

35.04g of NaCl is to be dissolved in 100ml of distilled water. Make up the final volume to 150ml and sterilize by autoclaving it.

4. DNA Extraction Buffer

Components	For 1000ml
100mM tris HCL	12.1g
1.4M NaCl	81.8g
20mM EDTA	7.45g
CTAB	30g

Volume makeup by autoclaved distilled water

Autoclave for 20 minutes

Maintain the pH 8.0 before autoclave

5. TE buffer pH(8.0)

1M Tris- HCl (pH 8.0)	1.0 ml
0.5 EDTA (8.0)	0.2 ml

Volume make up to 100 ml by autoclaved distilled water.

6. 70% Ethanol

70 ml of absolute Ethanol + 30 ml of distilled water

7. RNase (10mg/ml)

Dissolve 10mg of RNase powder in 1ml of distilled water.

8. dNTPs

Take 20 μ l of dNTPs (100mM) + 980 μ l water.

9. SSR primer dilution:-

- Add the TE buffer into the lyophilized tubes after centrifuge with given nmol values which is to be changed into pmols. Spin, vortex and centrifuge it. This is the stock dilution.
- Take 10 μ l each from forward and reverse primers into a fresh tube and then add 180 μ l TE buffer to make working primers dilution.

10. 10X TBE (Tris base + Boric Acid + EDTA)

Volume make up to 1000 ml by autoclaved distilled water

Volume makeup by autoclaved distilled water

11. 5% PAGE (Poly Acrylamide Gel Electrophoresis)

Components	For 1000ml
Acrylamide	47.5g
Bis-Acrylamide	2.5g
10X TBE	100ml

Note – Proper care should be taken while using chemicals like TEMED and Ethidium bromide as they are carcinogenic in nature.

Dissolve Acrylamide and Bis-Acrylamide one by one in 500ml distilled water and then add 100ml of 10X TBE. Make up the volume by adding autoclaved double distilled water and sterilized by passing the solution through 0.22 micron filter and store in amber colour bottle.

12. 10% APS (Ammonium Per Sulphate)

Ammonium Per Sulphate	1.0 g
Distilled water	10 ml

13. 1M KCl

18.64g of KCl to be dissolved in 200ml distilled water and make up the volume to 250ml.

14. 6X Loading Dye

0.25g of Bromophenol blue + 40ml glycerol + volume make up to 100ml.

15. Formamide Dye

49 ml Formamide + 0.05g BPB + 0.05g Xylene Cyanol + 1ml 0.5M EDTA (pH 8.0). Makeup the volume to 50 ml.

16. Ethidium bromide

10 μ l of ETBR + 200 ml distilled water.

17. 50bp ladder

Ladder + 400 μ l dye + 1100 μ l water.

3.9.2 Genomic DNA Isolation:-

CTAB method was used for isolation of DNA, protocol of which is given below-

1. Young tender leaves are taken and cut into small pieces in a 2ml Eppendorf tube.
2. After that 700 μ l of CTAB buffer is added in it and grinded in tissue lyzer using beads.
3. Let it settle down and then add 300 μ l of CTAB.
4. Add 700 μ l of CIA (24ml Chloroform: 1ml Isoamyl alcohol)
5. Vortex the samples.
6. Centrifuge the samples for 5min at 14000 rpm.
7. Collect the supernatant in a fresh 1.5 ml tube.
8. Add 700 μ l of CIA (24ml Chloroform: 1ml Isoamyl alcohol)
9. Collect the supernatant in a fresh 1.5 ml tube.
10. Add 70 μ l of 3M sodium acetate and 400 μ l of pre-chilled iso-propanol and keep it at 4 $^{\circ}$ C for 2 hrs or at -20 $^{\circ}$ C overnight.
11. Centrifuge the samples for 20 min at 14000rpm.
12. Discard the supernatant.

13. Wash the pellets with 50µl of 70% ethanol by centrifuging it at 14000 rpm for 3 min.

14. Air dry the pellets.

15. Add 100µl TE buffer and dissolve the pellets and store them for further use.

3.9.3 Quantification of DNA:-

Nanodrop spectrophotometer based quantification of DNA was done. For quantification, isolated DNA samples were quantified on Nanodrop spectroscopy (NANODROP, 2000c).

3.9.4 PCR amplification using SSR markers

Firstly, 1µl of diluted DNA sample of each genotype was added to the PCR plate at the bottom and after that, the separately prepared cocktail was added to each sample. Then the PCR was set up to the profile as described in Table 3.6

Table: 3.4 PCR mix for one reaction

Reagent	Stock concentration	Volume (µl)
DNA tamplate	50ng/µl	1.0µl
PCR buffer	10X	1.0µl
dNTPs	1mM	1.0µl
Primer (forward+reverse)	5pMole	1.0µl
Taq polymerase	1 unit/µl	0.5µl
Distilled water		5.5µl
Total		10 µl

Table: 3.5 temperature profile used for PCR amplification using SSR markers.

Stage	Step	Temperature	Duration	Cycle	Activity
1	1	95.0	5:00	1	Denaturation
2	1	95.0	0:30	↑	Denaturation
	2	58.0	0:30	35	Annealing
	3	72.0	1:0	↓	Extension

3	1	72.0	7:0	1	Final extension
4	2	4	∞		Storage

3.9.5 Visualization of amplified products in Polyacrylamide gel electrophoresis

Polyacrylamide gel provides good resolution thus 5% PAGE (vertical) was used for visualization and separation of the amplified PCR product. Before the preparation of gel and casting of gel in the electrophoresis unit, glass plate structures are prepared from properly cleaned glass plates (both outer and inner notched plates cleaned with warm water and detergent).

3.9.6 Assembling and pouring the gel

So firstly the glass structure was prepared in which gel has to be poured. To prepare the glass structure first the gasket was fixed to the three sides of the outer plate *i.e* the plate without notch then the spacer of about 1.5mm thickness was placed along the sides of the gasket fixed plates such that the gasket and spacers are in contact with each other. After that the second plate *i.e* the plate with a notch was placed over the first plate such that the spacers separate these two plates. Lastly, the clamps were attached to the three sides where the gasket was fixed leaving the notch portion of the structure prepared and checked by pouring distilled water in it for the presence of any leakages.

For casting gel, 65 ml of 5% polyacrylamide gel was taken and in that 70 μ l of TEMED and 700 μ l of 10% APS (ammonium persulfate) was added so that the process of polymerization gets initiated. The contents were continuously swirled so that the contents get mixed properly and to prevent the setting of gel before pouring it in structure. For pouring, the structure was kept on the bench top so that it makes 45⁰angle with the bench top and then the gel was poured into the structure from the notch side with proper care to avoid air bubbles in the gel. After that a comb of 1.5 mm thickness was inserted inside the gel and left for polymerization for about 20 minutes.

3.9.7 Polyacrylamide gel electrophoresis

After polymerization process when the gel gets set completely the gasket was removed and the assembly was kept in electrophoresis unit in a manner such that the

notch side of the structure faces inside and the plate without notch faces outward in the upper and bottom tank of the electrophoresis unit 1X TBE was poured and the comb was removed properly without disturbing the wells. 3µl of 50 bp ladder was loaded in the first well of the gel. Then 5 µl of PCR product added with loading dye (3µl) was loaded in the wells. The gel was then run at 130-180 volts till the dye reached the bottom of the gel.

3.9.8 Visualization of bands

After completion of electrophoresis, the structure was removed from the electrophoresis unit, the clamps were removed and spacers were pulled out gently from the corners. After that the notch plate was separated from the other plate with proper care without damaging the gel. Then by pouring some amount of water onto the gel and with the help of spatula the gel was flipped and taken out from the plate into the staining box. Now in staining box Ethidium bromide solution was poured which was prepared by adding 10µl Ethidium bromide to 200ml double distilled water to stain the gel. It was agitated continuously for at least 5 minutes so that the gel gets stained properly. Then the stained gel was washed with water to obtain a clear image. Now lastly the gel was scanned with Gel Doc and the bands were visualized in obtained images.

3.9.9 Detection of varietal polymerization using SSR marker:

Through 22 simple sequences repeat (SSR) marker detected the varietal polymorphism.

3.9.10 Scoring and Analysis of molecular data:

The banding pattern of population developed by each set of primer was scored separately. The size of amplified fragments was determined by comparing the migration distance of amplified fragments relative to the molecular weight of known size markers, 50bp DNA ladder. Specifically base pair position was scored as per the reported amplicon size.

3.9.11 Population structure analysis based on SSR markers:

A set of 22 SSR markers were chosen for population structure analysis. The model based program structure v2.3.4 (Earl and von Holdt, 2012) was used to infer the population structure of the 80 rice accessions using a burn in time of 100,000 and Monte Carlo Markov Chain replicates of 100,000. The number of groups (K) was set from one to ten, with 5 independent runs each. Evanno's method (Evanno *et al.* 2005) was used to estimate the most probable structure number of K. The rice lines were classified into various sub-groups with a membership probability threshold (Q) of 0.80 (Zhang *et al.* 2011b). The admixed group consisted of those lines with Q less than 0.80.

3.9.12 Association analysis using MLM:

The method of association analysis was tackle using the mixed linear model (MLM) method in TASSEL v2.3 (Zhang *et al.* 2010). The model MLM_Q+K, using kinship matrix & Q-matrix as the associated variable, was used to identify the marker-trait association. False discovery rate was applied to spot statistically significant loci. Marker trait association at $P < 0.01$ were considered as significant.

CHAPTER- IV

RESULTS AND DISCUSSION

The present investigation was carried out on 80 accessions of rice for early seedling vigor, yield and its attributing traits. To get a clear picture of variability in genotypes, the genetic parameters of variability were studied. Correlation analysis was performed to find out the degree of relationship between characters. However, a simple correlation does not provide adequate information about the contribution of each trait towards yield. Therefore, the technique of path coefficient analysis was utilized to have an idea of the direct and indirect contribution of a trait on yield which enables the breeder to rank genetic attributes according to their contribution. Despite these, principal component analysis (PCA) was used to quantify the importance of each dimension for describing the variability of a data set. In particular, the measurement of the variance along each principal component provides a means for comparing the relative importance of each dimension. Cluster analysis was performed for grouping of genotypes into various clusters and to select good lines for further improvement. Besides morphological characterization, molecular characterization was also performed to get more precise information on variability. The experimental results obtained from the present investigation have been described in the following heads:

- 4.1 Estimation of Genetic Variability
 - 4.1.1 Analysis of variance
 - 4.1.2 Mean performance and variability parameters of different characters
 - 4.1.3 Genotypic and phenotypic component of variation
 - 4.1.4 Heritability and genetic advance as percent of mean
- 4.2 Correlation analysis and Path coefficient analysis
 - 4.2.1 Correlation Coefficient Analysis
 - 4.2.2 Path coefficient analysis
- 4.3 Genetic diversity analysis
 - 4.3.1 Principle component analysis
 - 4.3.2 Cluster analysis
- 4.4 Association analysis using SSR marker
 - 4.4.1 SSR marker analysis

4.4.2 Polymorphism Information Content of SSR markers

4.4.3. STRUCTURE and TASSEL Analysis

4.4.3.1 Population structure analysis

4.4.3.2 Marker trait association

4.1 Estimation of genetic variance (ANOVA)

4.1.1 Analysis of variance

The analysis of variance of 26 early seedling vigor, yield and yield attributing traits of rice germplasm accessions are presented in Table 4.1a, 4.1b. The statistical procedure which separates or splits the total variation into different components is known as analysis of variance.

The mean sum of squares due to genotype/treatments were found to be highly significant for all the traits except number of leaves on 10 DAS and the Number of leaves on 20 DAS. This clearly indicates that variability exist in all the genotypes for all the traits. Sravan *et al.* 2012 reported significant variability among all the genotypes for all the characters. Our results confirm to the results of the above researchers indicating the presence of a considerable amount of variability among the genotypes.

4.1.2 Mean performance and variability parameters for different characters.

The mean and genetic variability parameters for 26 early seedling vigor and yield traits are presented in Table 4.2

4.1.2.1 Number of leaves on 10 days:

The range for number of leaves on 10 days varied from 2.0 (Bala, Lallu-14, Sawas-D-137-1, Danteshwari, Shamleshwari and MTU-1010) to 2.8 (Gutla 2614) with the overall mean of 2.30 with the CV was 8.15%.

4.1.2.2 Seedling length on 10 days (cm):

The range for seedling length on 10 days varied from 9.62 cm (CR-Dhan-40) to 15.45 (Gutla 2614) with the overall mean of 11.81 days, CV was 10.55%.

4.1.2.3 Seedling dry weight on 10 days (g)

The range for seedling dry on 10 days weight varied from 0.01 (R1448-578-2, Poornima, Salim paket, Krishma hansa, IR 08 L 152 and R2221-391-1-248-1) to 0.02 g (Gutla 2614) with the overall mean of 0.01 (gm). The coefficient of variation of seedling dry weight on 10 days was 19.72%.

4.1.2.4 Number of leaves on 20 days:

The range for number of leaves on 20 days varied from 3.6 (CR-306-37-13, CR-314-5-10, R1723-1411-1-3551, ARC-15831 and MTU-15) to 4.8 (Balsi balu kanb-694) with the overall mean of 4.15 days with the CV was 7.49%.

4.1.2.5 Seedling length in 20 days (cm):

The range of seedling length on 20 days varied from 14.96 (CR-306-37-13) to 29.79 cm (Gurmetta 2697) with the overall mean of 20.43 (cm) with CV the was 16.49%.

4.1.2.6 Seedling dry weight on 20 days (g):

The range for seedling dry weight on 20 days varied from 0.04 (Chom phool) to 0.12 (g) (Pokali) with the overall mean is 0.07 (g). The coefficient of variation was 27.48%.

4.1.2.7 Number of leaves on 30 days:

The range for number of leaves on 30 days varied from 4.0 (Asam chidi) to 5.7 (Aganni) with the overall mean of 4.64 days with the CV was 6.49%.

4.1.2.8 Seedling length on 30 days (cm):

The range for seedling length on 30 days varied from 28.4 (Aditya) to 67.62 cm (Pokali) with the overall mean of 41.18 cm and CV was 19.05%.

4.1.2.9 Seedling dry weight on 30 days (g):

The range for seedling dry weight on 30 days varied from 0.098 (IR-64) to 0.42 gm (Pokali) with the overall mean is 0.22 (gm). The coefficient of variation was 30.68%.

4.1.2.10 Germination %

The range for germination % varied from 69 (Lallu-14) to 98.5 (MTU-1010) with the overall mean of 81.71. The coefficient of variation was 10.37%.

4.1.2.11 Vigor index I

The range for vigor index I varied from 2101.38 (Bala) to 6322.47 (Pokali) with the overall mean of 3359.96. The coefficient of variation was 20.43%.

4.1.2.12 Vigor index II

The range for vigor indexII varied from 6.94 (IR-64) to 38.91 (Pokali) with the overall mean of 18.59. The coefficient of variation was 30.96%.

4.1.2.13 Days to 50% flowering:

The range for days to 50% flowering varied from 60.5 days (Kalinga-3) to 90.00 days (Danteshwari and Pokali) with the overall mean of 79.83 days with the CV was 8.99%.

4.1.2.14 Panicle Length (cm):

Highest panicle length was found 17.84 cm in (R1152-2-64-1) to 27.85 cm in Bongali-3 with a mean of 23.12 cm. The coefficient of variation was 9.60%.

4.1.2.15 Plant height (cm):

The range for plant height varied from 75.58 cm (Banisar No-31) to 160.84 cm (Pokali) with an overall mean of 102.96 cm. The coefficient of variation of plant height was 15.04%.

4.1.2.16 Flag leaf length (cm):

The range for flag leaf length varied from 17.11 cm (R1519-769-2-1442-1) to 50.08 cm (Gurmetta 2697) with the overall mean of 32.60 cm. The coefficient of variation was 19.21 %.

4.1.2.17 Flag leaf width (cm):

The range for flag leaf width varied from 11.0 cm (Jhitpiti and R1973-206-2-86-1) to 20.3 cm (Shamleshwari) with the overall mean of 14.83 cm. The coefficient of variation was 11.74 %.

4.1.2.18 Panicle per meter square:

It ranged from 125.5 (Vandana) to 291.0 (Lallu-14) with the overall mean of 209.98. The coefficient of variation was 17.60%.

4.1.2.19 1000-grain weight (g):

1000-grain weight ranged from 14.02g (Lal mati) to 32.23g (R1448-578-2) with an average weight of 24.67g. The coefficient of variation was 13.6%.

4.1.2.20 Number of filled spikelet:

Number of filled spikelet ranged from 47.5 (Kaweri) to 188.5 (IR 08 L 152) with an average of 106.55. The coefficient of variation was 26.99%.

4.1.2.21 Number of unfilled spikelet:

Number of unfilled spikelet ranged from 9 (Salim paket) to 69 (R1551-2169-1) with an average of 20.95. The coefficient of variation was 50.81%.

4.1.2.22 Spikelet fertility %:

Spikelet fertility % ranged from 60.77 (Asha) to 92.2 (R1551-2169-1) with an average of 83.37. The coefficient of variation was 7.98%.

4.1.2.23 Paddy length (mm):

The range for paddy length varied from 6.65 mm (Banisar No-31) to 11.25 mm (R1519-769-2-1442-1) with the overall mean of 8.75 mm. The coefficient of variation was 9.38%.

4.1.2.24 Paddy breadth (mm):

The range for paddy breadth varied from 1.85 mm (Lal mati) to 3.25 mm (MTU-15) with the overall mean of 2.54 mm. The coefficient of variation was 10.93%.

4.1.2.25 Paddy L/B ratio:

The range for paddy L/B ratio varied from 2.35 mm (R2221-391-1-248-1) to 5.49 (R1519-769-2-1442-1) with the overall mean of 3.50 mm. The coefficient of variation was 16.52%.

4.1.2.26 Grain yield (g):

The range for grain yield/m² (g) varied from 76.5 g (Banisar No-31 and Birsa gova) to 409 g (R1004-2552-1-1) with a mean value of 235.82 g. The coefficient of variation was 26.16%.

Based on grain yield, genotypes namely, R1004-2552-1-1 recorded high grain yield followed by Indira aerobic-1, Asam chidi, Surekha, IR 08 L 152, Pokali and Aditya.

The genetic variability in any breeding material is a pre-requisite as it does not only provide a basis for selection but also provides some valuable information regarding the selection of diverse parents for use in the improvement program. The coefficient of variation was evolved by Karl Pearson. It is very useful for the study of variation. It indicates that when the CV% is high the sample is less consistent or more variable. Coefficient of variation truly provides a relative measure of variability among different traits. In the present investigation, a wide range of variability was observed for most of the quantitative traits. High magnitude of coefficient of variation (more than 20%) for seedling dry weight on 20 days (27.44), seedling dry weight on 30 days (30.68), vigor indexI (20.43), vigor indexII (30.96), filled spikelet (26.99) and unfilled spikelet (50.81) and grain yield per meter square (26.16).

4.1.3 Phenotypic and Genotypic coefficient of variation:

Coefficient of variation was calculated at genotypic and phenotypic levels as analysis of variance permits estimation of phenotypic, genotypic and environmental coefficient of variation (Burton, 1952). The phenotypic coefficient of variation was higher than genotypic coefficient of variation. The PCV and GCV are classified as suggested by Siva Subramanian and Madhavamenon (1973) (low <10%; moderate 10-20% and high >20%). The estimates of phenotypic and genotypic coefficient of variation for different quantitative characters are present in Table 4.3.

The high GCV observed for seedling dry weight on 10 days (23.76), seedling dry weight on 20 days (29.53), seedling dry weight on 30 days (32.69),

seedling length on 30 days (20.23), vigor index I (21.92), vigor index II (33.04), Flag leaf length (21.76), filled spikelet (27.25), unfilled spikelet (51.17) and grain yield (27.03). Likewise, PCV was obtained high in seedling dry weight on 20 days (24.51), seedling dry weight on 30 days (28.68), vigor index II (28.87), filled spikelet (26.73), unfilled spikelet (50.45) and grain yield (25.25). However, moderate values of GCV observed for number of leaves on 10 days (10.86), seedling length on 10 days (12.66), number of leaves on 20 days (10.56), seedling length on 20 days (18.03), germination% (10.64), panicle length (10.02), plant height (16.13), flag leaf width (13.92), panicle per meter square (19.14), 1000 grain weight (13.83), paddy breadth (11.07) and paddy L/B ratio (16.57). Likewise, characters for PCV was recorded for seedling dry weight on 10 days (16.79), seedling length on 20 days (14.78), seedling length for 30 days (17.85), vigor index I (19), plant height (13.87), flag leaf length (16.28), panicle per meter square (15.91), 1000 grain weight (13.37), paddy breadth (10.82) and paddy L/B ratio (16.33). The values of PCV is higher than GCV, indicates the apparent variation is not only due to genotypes but also due to the influence of the environment. The high magnitude of genotypic coefficient of variation reveals the high genetic variability present in the material studied similar findings of high PCV coupled with GCV for traits namely, number of filled grains and thousand-grain weight was reported by Sravan *et al.*, 2012 and Vanisree *et al.* 2013. Satheesh kumar and Saravanan (2012) reported high estimates for these genetic parameters for all the yield traits.

4.1.4 Heritability and Genetic advance as a percentage of mean:

Heritability estimates provide information regarding the amount of transmissible genetic variation to total variation and determine genetic improvement and response to selection. Thus, heritability is the heritable portion of the phenotypic variance. It is a good index of the transformation of characters from parents to their offspring (Falconer, 1981). Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advances are more helpful in predicting the grain under selection than heritability estimates alone. Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain

under selection. The success of genetic advance under selection depends on genetic variability, heritability and selection intensity. In the present investigation, heritability in a broad sense and genetic advance were calculated for twenty six characters and related traits and is presented in Table 4.3

High estimates of high heritability (>60%) were found for seedling length on 20 days (67.21), seedling dry weight on 20 days (68.90), seedling length on 30 days (74.05), seedling dry weight on 30 days (77.00), germination % (81.76), vigor indexI (75.09), vigor indexII (76.34), days to 50% flowering (95.15), panicle length (83.44), plant height (74.01), panicle per meter square (69.07), 1000 grain weight (93.42), filled spikelet (96.21), unfilled spikelet (97.19), spikelet fertility % (97.29), paddy length (97.84), paddy breadth (95.53), paddy L/B ratio (97.10) and grain yield (87.25). However, moderate heritability for seedling length on 10 days (39.08), seedling dry weight on 10 days (49.88), number of leaf on 30 days (51.53), flag leaf length (55.95) and flag leaf width (42.21).

Genetic advance is a measure of genetic gain under selection. The success of genetic advance under selection depends on heritability of the character under consideration. This indicates that though the character is less influenced by environmental effects, the selection for improvement of such trait may not be useful because heritability is based on total genetic variance which includes fixable (additive) and non-fixable (dominance and epistatic) variance.

The magnitude of genetic advance as percent of mean was recorded high for maximum traits, except some trait. Moderate genetic advance showed by seedling length on 10 days (10.19), germination % (12.11), days to 50% flowering (17.85), panicle length (17.23) and flag leaf width (12.11), and also such trait showed low genetic advance *viz* number of leaf on 10 days (2.71), number of leaf on 20 days (0.10) and number of leaf on 30 days (7.69). All the traits possessing high values of genetic advance indicate that the characters are governed by additive genes and selection will be rewarding for the improvement of such trait. It clearly indicates that most likely the heritability is due to additive gene effects and selection may be effective. These findings are in agreement with the findings of

Choudhary *et al.* 2004; Satheesh kumar and Saravanan. 2012; Sravan *et al.* 2012
and Khare *et al.* 2015.

Table 4.1a:- Analysis of variance for early seedling vigor, yield and its components during (2019 at IGKV Raipur C.G.)

			Mean Sum of Square												
Traits			NL10D	SL10 (cm)	SDW 10 (gm)	NL20D	SL20 (cm)	SDW 20 (gm)	NL30D	SL30 (cm)	SDW 30 (gm)	GP (%)	VI 1	VI 2	D50PF
SN	SOV	DF	1	2	3	4	5	6	7	8	9	10	11	12	13
1	Replication	1	0.324*	6.687*	0	0.21	16.777	0	0.012	53.246	0.001	49.506	7,72,520.33*	0.003	6.006
2	Genotype	79	0.07	3.111**	0**	0.193	22.713**	0.001**	0.182**	123.524**	0.01**	137.633**	9,50,228.50**	66.743**	103.164**
3	Error	79	0.055	1.363	0	0.192	4.453	0	0.058	15.39	0.001	13.81	1,35,137.13	8.954	2.563

Table 4.1b:- Analysis of variance for early seedling vigor, yield and its components during (2019 at IGKV Raipur C.G.)

			PL (cm)	PH (cm)	FLL (cm)	FFW (mm)	PPMS	1000 GW	FS	UFS	SF (%)	Paddy Length (mm)	PB (mm)	P L/B R	GY
SN	SOV	DF	14	15	16	17	18	19	20	21	22	23	24	25	26
1	Replication	1	1.131	768.734**	121.139*	12.266*	709.806	0.198	18.225	0.025	0.003	0.009	0.001	0	970.225
2	Genotype	79	9.864**	480.119**	78.524**	6.071**	2,733.16**	22.552**	1,654.75**	226.66**	88.74**	1.324**	0.155**	0.664**	7,612.22**
3	Error	79	0.89	71.695	22.179	2.467	499.971	0.766	31.896	3.228	1.216	0.014	0.004	0.01	518.022

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

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, VI = Vigor index, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

Table 4.2: Mean data of 80 rice genotypes for 26 early seedling vigor, yield its attributing traits in *kharif* 2019

S N	Treatment/ Traits	NL1 OD	SL10 (cm)	SDW 10 (gm)	NL2 OD	SL20 (cm)	SDW 20 (gm)	NL3 OD	SL30 (cm)	SDW 30 (gm)	GP (%)	VI 1	VI 2	D50P F	PL (cm)	PH (cm)	FFL (cm)	FFW (mm)	PPMS	1000 GW	FS	UFS	SF (%)	Paddy length (mm)	PB (mm)	P L/B R	GY(g)
1	Aditya	2.20	10.38	0.01	3.70	16.03	0.07	4.70	28.40	0.11	77.0 0	2186.80	8.43	89.50	20.70	96.0 5	30.9 8	16.40	288.0 0	31.01	156.5 0	30.5 0	83.69	8.75	2.70	3.24	324.0 0
2	Kalinga-3	2.40	11.54	0.02	4.10	23.29	0.07	4.90	49.85	0.20	72.0 0	3582.46	13.95	60.50	22.97	105. 19	31.9 2	13.70	231.0 0	32.09	77.00	14.0 0	84.77	8.60	3.20	2.69	210.0 0
3	Bala	2.00	12.31	0.02	3.90	20.85	0.07	4.80	29.98	0.18	70.0 0	2101.38	12.74	69.50	19.49	86.5 6	25.4 5	13.70	228.0 0	22.42	112.5 0	14.5 0	88.61	7.00	2.85	2.46	210.5 0
4	Purva	2.10	10.39	0.02	4.00	18.14	0.09	4.40	35.96	0.20	81.5 0	2928.58	16.51	67.00	19.27	91.1 6	24.0 5	16.00	216.0 0	20.22	125.0 0	13.0 0	90.55	8.70	2.50	3.48	161.0 0
5	Lallu-14	2.00	11.27	0.01	4.20	20.42	0.06	5.10	53.52	0.38	69.0 0	3697.66	26.10	67.00	22.02	101. 34	48.3 2	12.20	291.0 0	16.76	127.5 0	30.5 0	80.69	7.95	2.25	3.54	265.0 0
6	MR 1523	2.30	10.70	0.02	4.60	19.17	0.06	4.60	42.04	0.30	74.5 0	3130.39	22.31	72.00	25.80	78.1 2	29.9 9	13.30	214.0 0	26.55	121.0 0	31.5 0	79.34	8.45	2.75	3.08	255.0 0
7	IR38	2.60	12.65	0.02	4.40	19.83	0.09	4.70	33.27	0.20	70.0 0	2327.44	14.08	73.50	22.69	93.1 5	32.3 4	12.80	266.0 0	23.60	105.0 0	17.0 0	86.11	8.65	2.65	3.27	268.0 0
8	Surekha	2.30	12.89	0.02	3.80	19.73	0.08	4.50	39.36	0.30	80.5 0	3158.36	24.28	71.00	22.63	91.4 7	28.9 6	14.20	197.0 0	25.71	95.50	15.0 0	86.49	8.70	2.40	3.63	335.0 0
9	Tripti	2.50	11.55	0.01	4.00	18.89	0.08	4.60	34.12	0.19	91.5 0	3120.48	17.43	78.50	22.74	88.3 8	19.2 3	11.60	251.0 0	25.47	117.0 0	10.5 0	91.80	8.50	2.70	3.15	246.0 0
10	T-10	2.30	11.56	0.02	3.90	19.68	0.06	4.40	39.18	0.18	71.5 0	2800.35	13.08	75.00	22.86	92.2 4	27.4 2	11.50	211.0 0	23.76	50.50	12.0 0	80.79	7.85	2.60	3.02	205.0 0
11	Aganni	2.30	13.76	0.01	4.50	26.14	0.07	5.70	47.71	0.15	81.5 0	3887.69	12.55	79.00	25.99	115. 55	36.5 9	11.60	242.0 0	25.32	77.00	13.0 0	85.58	8.55	2.85	3.00	230.5 0
12	Jhitpiti	2.10	13.79	0.02	4.70	24.10	0.06	4.70	52.81	0.17	83.0 0	4374.95	14.40	80.50	26.61	107. 20	32.1 5	11.00	259.0 0	25.16	61.50	17.0 0	78.37	9.05	2.85	3.18	232.0 0
13	R1558- 2423-1- 1445-1	2.20	10.98	0.01	4.20	18.63	0.06	4.40	31.84	0.15	85.5 0	2722.97	12.49	79.50	21.04	89.7 1	26.8 4	14.50	192.5 0	20.86	72.00	23.0 0	75.79	9.05	2.45	3.70	294.0 0
14	Kaweri	2.10	12.02	0.01	4.30	17.25	0.06	4.10	41.91	0.25	75.0 0	3145.40	19.14	77.50	19.09	93.3 5	31.1 0	12.85	215.0 0	24.37	47.50	14.0 0	77.19	8.35	2.60	3.21	244.0 0
15	Shwnog- 89366	2.30	11.63	0.02	4.10	19.67	0.08	4.30	41.84	0.32	72.0 0	3007.20	22.61	70.50	21.08	106. 94	35.9 8	14.90	206.0 0	23.99	94.50	14.5 0	86.70	9.25	2.45	3.78	205.0 0
16	Chom phool	2.30	11.80	0.02	4.10	15.60	0.04	4.50	43.73	0.21	80.0 0	3495.87	16.90	86.50	19.38	92.0 5	36.4 3	13.70	259.0 0	24.74	51.50	16.5 0	75.69	9.10	2.60	3.50	252.0 0
17	Asha	2.30	11.54	0.02	3.90	17.96	0.05	5.10	34.49	0.22	77.5 0	2681.30	16.65	81.00	20.92	88.1 9	27.1 0	13.00	247.0 0	24.01	83.00	53.5 0	60.77	9.55	2.35	4.07	195.0 0
18	Bangoli-3	2.70	12.07	0.02	4.30	23.95	0.06	4.80	49.85	0.19	80.5 0	4013.40	15.13	86.00	17.84	141. 59	31.6 2	12.40	270.5 0	24.23	58.00	21.5 0	62.32	10.05	2.30	4.37	248.0 0
19	Nipon bare	2.30	12.28	0.02	4.70	20.22	0.06	4.60	39.80	0.21	72.5 0	2887.37	14.98	77.00	20.06	112. 54	25.1 4	17.80	236.0 0	24.80	93.00	14.0 0	86.92	7.75	2.65	2.93	195.0 0
20	Lal mati	2.50	11.33	0.01	4.50	18.38	0.05	4.60	47.63	0.18	79.0 0	3764.43	14.05	71.00	22.45	104. 71	34.3 2	13.90	166.5 0	14.02	102.5 0	28.0 0	78.55	7.80	1.85	4.22	195.0 0
21	Usai buta- 2408	2.60	11.07	0.02	4.30	26.60	0.10	4.40	51.33	0.29	76.0 0	3891.28	21.94	86.00	23.38	115. 92	39.8 6	15.70	229.5 0	26.67	125.0 0	15.5 0	88.97	8.55	2.75	3.11	232.0 0
22	Banisar No- 31	2.40	12.42	0.02	4.30	17.20	0.05	4.10	41.66	0.14	80.0 0	3332.80	11.32	62.00	21.99	75.5 8	31.2 1	12.50	178.0 0	18.76	113.0 0	13.5 0	89.32	6.65	2.80	2.38	76.50
23	Karhani- No-9	2.50	11.70	0.02	4.70	23.09	0.06	4.50	53.45	0.33	73.5 0	3930.92	23.98	86.50	24.27	114. 59	39.3 7	13.30	211.0 0	27.17	153.5 0	16.5 0	90.30	8.70	2.75	3.17	236.0 0
24	Balsi balu kanb-694	2.50	13.85	0.02	4.80	23.77	0.08	4.50	45.99	0.37	86.0 0	3961.63	31.97	85.00	21.17	135. 86	44.3 4	17.00	212.0 0	26.05	92.50	15.0 0	86.06	8.55	2.95	2.90	192.0 0

25	Banso bnisa B-1021	2.30	13.46	0.02	4.10	23.84	0.10	4.50	48.48	0.26	87.0 0	4226.70	22.84	84.00	22.07	106. 51	42.3 7	15.90	179.5 0	29.41	93.50	11.0 0	89.50	8.80	2.85	3.09	220.0 0
26	DU-95-0-137-1	2.60	12.68	0.02	4.10	20.62	0.10	4.40	50.53	0.36	83.5 0	4218.70	29.70	83.00	21.04	113. 67	37.8 0	17.40	225.0 0	27.80	86.00	14.0 0	85.99	8.35	2.95	2.83	204.0 0
27	Sawas-D-137-1	2.00	12.26	0.02	4.30	20.11	0.08	4.30	45.39	0.31	71.0 0	3226.71	22.05	87.00	22.51	109. 62	39.9 0	16.10	197.0 0	26.64	124.0 0	17.5 0	87.64	8.35	2.85	2.93	245.0 0
28	Birsa gova	2.40	12.30	0.02	4.30	26.17	0.08	4.90	57.55	0.26	83.0 0	4781.60	21.42	65.50	21.10	117. 63	38.8 0	16.90	152.0 0	30.88	84.50	12.5 0	87.12	9.95	2.55	3.91	76.50
29	Danwas 2511	2.40	13.28	0.02	4.40	22.15	0.10	4.70	42.21	0.30	74.0 0	3125.25	22.29	83.00	22.82	117. 53	40.2 6	15.40	239.5 0	24.84	105.5 0	13.0 0	89.09	8.20	2.95	2.78	179.0 0
30	Dumabada-25-55	2.10	12.95	0.02	4.30	23.59	0.11	5.50	45.17	0.31	75.0 0	3387.75	23.07	82.00	20.53	121. 36	36.0 6	16.30	229.0 0	27.08	92.00	15.0 0	86.00	8.25	2.90	2.85	240.0 0
31	Fent 2679	2.20	13.83	0.02	4.10	28.62	0.11	4.70	51.05	0.37	80.0 0	4081.64	29.58	81.00	23.43	121. 70	31.2 4	14.00	224.0 0	29.85	92.50	14.5 0	86.48	9.70	2.80	3.46	213.0 0
32	Gutla 2614	2.80	15.45	0.03	4.40	28.61	0.10	4.70	59.08	0.24	80.0 0	4726.40	18.80	82.50	25.99	126. 70	35.5 7	16.40	265.5 0	31.38	134.5 0	17.0 0	88.82	9.55	2.85	3.35	138.0 0
33	Gurmetta 2697	2.60	14.27	0.02	4.50	29.79	0.10	4.40	55.23	0.29	75.0 0	4146.56	21.49	78.50	23.03	132. 35	50.0 8	15.00	248.0 0	25.54	109.5 0	34.0 0	76.31	8.75	2.70	3.24	91.00
34	Danwar2129	2.60	14.15	0.02	4.60	21.04	0.07	4.90	45.30	0.20	78.0 0	3532.60	15.57	82.50	21.38	105. 90	37.5 6	15.20	250.0 0	24.57	87.50	13.5 0	86.64	8.45	2.75	3.08	175.0 0
35	R1558-14-19-2-1442-1	2.20	12.04	0.02	4.30	18.58	0.08	4.50	39.22	0.23	88.0 0	3461.76	20.40	90.00	19.78	98.0 0	27.7 1	12.70	241.5 0	25.10	64.00	14.5 0	81.54	9.25	2.55	3.63	273.0 0
36	R1519-769-2-1442-1	2.10	11.08	0.01	4.20	20.00	0.05	4.50	38.22	0.12	73.0 0	2793.24	8.55	78.50	22.47	102. 80	17.1 1	17.20	174.0 0	21.54	121.5 0	24.0 0	83.52	11.25	2.05	5.49	194.0 0
37	R1551-2169-1	2.40	10.81	0.01	4.10	19.36	0.10	4.30	36.24	0.20	95.0 0	3454.02	19.33	84.50	22.22	97.9 8	27.5 3	16.30	249.0 0	23.16	106.0 0	9.00	92.20	8.45	2.50	3.38	237.0 0
38	R1448-578-2	2.20	11.24	0.01	4.20	20.18	0.10	5.30	41.02	0.25	77.5 0	3172.34	19.25	82.00	22.67	103. 29	31.4 7	16.00	210.5 0	32.23	101.5 0	17.5 0	85.29	10.25	2.55	4.02	258.5 0
39	R1013-230-7-07-1-4	2.40	10.56	0.01	3.80	18.23	0.05	4.70	44.28	0.25	79.5 0	3522.24	20.11	83.50	21.29	98.4 5	29.4 0	17.10	181.0 0	24.48	86.00	21.5 0	80.02	9.85	2.40	4.11	297.0 0
40	IR-78-66-BIO-BBB-SBI	2.50	11.39	0.01	4.00	17.69	0.05	4.50	35.50	0.22	72.0 0	2552.48	15.49	83.00	23.17	89.1 2	24.6 3	13.70	253.5 0	23.20	99.00	57.0 0	63.48	8.70	2.50	3.48	224.0 0
41	R971-25-52-1-1	2.50	10.79	0.01	4.10	21.73	0.06	4.50	41.45	0.26	92.0 0	3810.61	23.36	81.50	22.94	96.5 5	27.9 2	16.10	199.0 0	26.07	107.5 0	31.0 0	77.62	9.55	2.55	3.75	312.0 0
42	R1152-2-64-1	2.10	11.28	0.01	3.70	18.67	0.05	4.50	39.28	0.14	79.0 0	3110.84	11.18	87.00	27.85	93.7 7	33.7 1	15.80	240.5 0	23.43	110.0 0	13.5 0	89.06	9.50	2.40	3.96	279.0 0
43	R1004-2552-1-1	2.60	12.11	0.01	3.70	18.98	0.06	4.70	33.23	0.19	76.0 0	2524.95	14.29	85.00	23.39	96.3 6	28.8 4	17.50	206.5 0	26.88	111.0 0	19.5 0	85.06	9.20	2.45	3.76	409.0 0
44	CR-306-37-13	2.20	10.52	0.02	3.60	14.96	0.06	5.30	37.65	0.20	75.0 0	2817.30	14.95	64.00	24.30	88.9 9	37.9 3	17.10	186.5 0	23.37	87.50	20.5 0	81.01	8.10	2.55	3.18	314.0 0
45	CR-314-5-10	2.20	11.11	0.02	3.60	22.39	0.06	4.50	40.54	0.21	93.0 0	3760.42	19.46	69.00	22.01	103. 44	23.3 5	13.90	138.0 0	25.69	121.0 0	25.0 0	82.88	8.65	2.45	3.54	174.0 0
46	Asam chidi	2.30	10.14	0.02	3.80	15.49	0.05	4.00	39.10	0.18	85.0 0	3324.70	15.08	74.00	23.16	91.1 3	25.7 2	14.60	168.0 0	24.98	103.5 0	12.5 0	89.21	7.80	2.95	2.65	338.0 0
47	R1723-1411-1-3551	2.10	11.61	0.01	3.60	16.57	0.05	4.90	29.31	0.21	74.5 0	2188.59	15.95	88.50	21.39	97.0 4	40.0 1	15.30	247.5 0	23.49	108.0 0	23.5 0	82.13	9.45	2.35	4.03	312.0 0
48	ARC-15831	2.20	12.04	0.01	3.60	23.81	0.06	4.50	55.27	0.21	80.0 0	4444.28	16.40	73.00	23.16	121. 47	40.1 3	14.00	225.0 0	23.13	89.00	25.5 0	77.75	8.90	2.55	3.49	294.0 0
49	Danteshwar i	2.00	11.56	0.01	3.90	19.31	0.07	4.70	41.70	0.36	80.0 0	3336.00	29.12	90.00	22.19	98.6 2	27.3 5	16.10	177.5 0	28.48	106.0 0	16.0 0	86.89	9.35	2.45	3.82	274.0 0
50	Poornima	2.20	10.68	0.01	3.90	22.58	0.09	4.90	38.20	0.21	87.5 0	3353.84	17.98	87.50	22.29	96.9 5	26.2 0	16.00	167.0 0	22.89	130.5 0	40.5 0	76.29	9.40	2.30	4.09	236.5 0

51	Salim paket	2.10	10.72	0.01	3.80	20.98	0.06	4.30	44.62	0.30	81.0 0	3614.22	24.30	77.50	24.73	120. 89	38.5 7	14.50	201.0 0	22.64	167.0 0	69.0 0	70.74	8.05	2.65	3.04	281.0 0
52	R1238- 19361	2.30	12.10	0.02	3.70	17.25	0.07	4.90	39.11	0.24	75.5 0	2955.78	18.26	88.00	18.90	82.6 4	28.4 0	13.40	169.5 0	24.03	72.00	21.5 0	77.03	9.25	2.25	4.12	190.0 0
53	1182-31-2- 151	2.70	14.62	0.02	3.90	17.79	0.08	4.70	40.92	0.27	77.5 0	3165.55	20.99	79.50	23.12	104. 35	30.4 3	15.90	187.0 0	22.91	72.00	31.0 0	69.89	10.20	2.05	4.98	150.0 0
54	R1122-167- 2-1571	2.10	10.89	0.02	4.60	26.43	0.10	4.70	48.18	0.29	76.0 0	3686.16	22.27	80.00	23.33	135. 69	31.8 2	17.20	198.0 0	30.36	128.5 0	33.0 0	79.61	9.15	2.45	3.74	234.0 0
55	Vandana	2.50	12.90	0.02	4.00	20.17	0.08	4.50	36.53	0.23	79.0 0	2880.53	18.17	66.50	21.22	90.5 0	29.2 3	15.40	125.5 0	25.69	95.50	35.0 0	73.17	9.85	2.45	4.02	166.0 0
56	R1546- 1382-1-40- 1	2.30	11.20	0.02	4.00	19.77	0.09	4.60	38.53	0.22	92.0 0	3544.76	20.24	85.50	23.87	89.1 8	32.2 0	14.10	163.5 0	26.67	119.5 0	18.5 0	86.62	8.40	2.40	3.50	294.5 0
57	MTU-15	2.50	14.00	0.02	3.60	20.60	0.06	4.70	40.27	0.29	75.5 0	3043.94	21.93	79.00	23.67	133. 92	39.7 6	14.90	143.0 0	23.24	143.0 0	17.0 0	89.39	8.35	3.25	2.58	218.0 0
58	Mamhar	2.30	10.10	0.01	3.70	16.49	0.07	4.50	32.63	0.31	91.0 0	2971.70	28.05	82.00	21.24	91.8 9	32.3 7	14.80	154.5 0	25.84	68.00	16.0 0	80.97	9.60	2.35	4.09	256.0 0
59	C101 LAC 59	2.50	13.51	0.02	3.80	28.79	0.04	4.50	44.84	0.35	82.5 0	3698.80	28.83	77.00	24.82	91.7 5	33.3 2	14.10	171.5 0	23.09	91.00	30.0 0	75.23	8.05	2.80	2.88	270.5 0
60	Shyamla	2.10	10.41	0.01	3.90	16.65	0.06	4.20	30.01	0.10	71.5 0	2146.46	7.26	86.50	24.37	82.7 7	28.9 5	14.90	162.0 0	25.15	98.50	17.5 0	84.91	9.60	2.45	3.92	123.0 0
61	IR64	2.30	12.43	0.01	4.00	19.12	0.06	4.70	33.43	0.10	69.5 0	2329.85	6.95	89.00	25.65	99.7 0	30.2 0	15.60	153.0 0	20.69	122.0 0	19.0 0	86.50	9.15	2.05	4.47	186.0 0
62	Pokali	2.40	13.71	0.02	4.10	28.70	0.12	5.00	67.62	0.42	93.5 0	6321.81	38.91	90.00	26.04	160. 84	42.9 2	16.20	133.0 0	27.68	157.5 0	24.5 0	86.55	7.60	2.75	2.76	328.0 0
63	Krishna hansa	2.20	9.98	0.01	4.00	17.91	0.08	5.20	36.74	0.21	75.0 0	2755.50	15.61	88.50	26.89	105. 07	33.5 2	15.10	259.5 0	24.53	118.5 0	14.5 0	89.10	9.60	2.35	4.09	231.5 0
64	IR 08L 152	2.10	10.60	0.01	4.30	19.59	0.07	4.90	42.51	0.22	81.0 0	3447.42	17.85	76.00	26.12	109. 94	30.9 1	14.70	220.0 0	24.38	188.5 0	21.0 0	89.98	8.75	2.50	3.50	332.0 0
65	PR-1525-2- 4	2.40	11.27	0.01	4.30	21.71	0.08	5.10	48.92	0.26	80.5 0	3936.84	21.24	79.00	26.30	119. 89	43.6 9	16.60	214.0 0	25.49	117.5 0	17.0 0	87.37	8.25	2.65	3.11	297.0 0
66	CR dhan-40	2.40	9.62	0.01	4.40	19.21	0.06	4.50	44.28	0.22	96.0 0	4258.62	20.63	69.00	27.47	116. 55	42.3 5	17.00	230.0 0	20.86	174.0 0	31.0 0	84.88	7.05	2.30	3.07	291.5 0
67	R1882-306- 4-243-1	2.30	12.24	0.02	4.40	19.62	0.10	4.90	36.08	0.19	97.0 0	3502.52	18.73	81.00	26.03	97.2 1	24.9 2	15.20	218.0 0	22.82	87.00	10.5 0	89.23	8.55	2.10	4.08	264.0 0
68	R1986-296- 2-867	2.20	12.32	0.02	4.60	17.88	0.07	4.70	31.40	0.16	97.0 0	3041.64	15.80	87.50	26.08	98.2 9	30.2 0	14.60	232.0 0	22.97	118.0 0	19.5 0	85.82	8.95	2.20	4.08	279.0 0
69	R1973-206- 2-86-1	2.10	10.20	0.02	4.50	18.62	0.05	4.70	34.16	0.16	91.5 0	3118.05	14.10	80.00	25.08	87.8 3	23.4 5	11.00	209.0 0	21.78	85.50	23.0 0	78.75	9.45	2.15	4.40	228.0 0
70	CG zinc rice-2	2.30	12.43	0.02	4.00	19.48	0.05	4.60	32.32	0.15	76.5 0	2474.70	11.30	77.00	25.32	93.2 5	30.2 3	13.10	213.0 0	27.38	75.50	12.5 0	85.78	8.30	2.35	3.54	203.0 0
71	CG zinc rice-2	2.30	10.34	0.01	4.60	18.60	0.05	4.80	37.30	0.21	97.0 0	3617.34	20.70	89.00	23.99	82.8 2	38.0 5	13.70	227.0 0	14.79	128.0 0	22.0 0	85.36	7.90	2.05	3.86	164.0 0
72	R1779-321- 1-112-2	2.40	11.72	0.01	4.60	17.76	0.07	4.70	35.66	0.19	93.5 0	3333.25	17.26	84.00	23.30	92.0 6	36.2 2	14.70	190.0 0	25.05	108.5 0	27.5 0	79.79	7.75	2.30	3.37	223.0 0
73	R1882-301- 1-234-1	2.10	11.41	0.01	4.20	17.33	0.06	4.30	34.37	0.20	95.0 0	3268.06	19.17	79.00	25.65	99.4 7	30.1 9	13.90	215.0 0	22.11	117.5 0	13.0 0	90.00	8.15	2.40	3.40	229.0 0
74	R2221-391- 1-248-1	2.30	9.79	0.01	4.50	18.13	0.07	4.60	30.03	0.15	89.0 0	2664.15	13.33	79.50	23.96	95.7 9	28.2 5	14.90	160.5 0	25.76	139.5 0	40.5 0	77.50	7.40	3.15	2.35	179.0 0
75	R1882-310- 4-257-1	2.40	12.30	0.01	4.30	17.20	0.04	4.20	29.13	0.12	96.0 0	2796.89	11.90	87.50	25.94	103. 66	32.6 5	15.80	211.5 0	21.74	97.00	11.5 0	89.40	8.50	2.20	3.86	278.0 0
76	IR36	2.20	10.91	0.01	4.10	17.34	0.05	4.70	32.11	0.17	95.5 0	3066.07	16.15	79.50	27.10	90.5 8	30.6 2	14.10	172.0 0	21.99	125.0 0	13.5 0	90.26	9.45	2.55	3.71	205.5 0
77	IR64 (Drought)	2.40	12.06	0.01	4.30	19.92	0.05	4.70	40.71	0.24	97.0 0	3948.87	22.94	78.50	25.68	100. 22	31.5 5	13.60	187.5 0	28.59	123.5 0	14.0 0	89.80	9.95	2.50	3.98	265.0 0

78	Indira aerobic-1	2.20	10.38	0.01	4.40	19.89	0.05	4.60	33.73	0.15	81.00	2732.88	12.25	79.50	22.91	96.46	31.76	13.80	229.50	21.69	175.50	22.00	88.84	8.00	2.25	3.56	361.50
79	Samleshwari (C)	2.00	11.11	0.01	4.30	20.42	0.06	4.40	38.04	0.25	86.00	3263.96	21.28	88.00	22.96	104.21	34.60	20.30	244.50	23.33	131.00	19.00	87.34	8.15	2.45	3.33	224.00
80	MTU1010 (C)	2.00	10.54	0.01	4.00	19.53	0.05	4.50	40.57	0.19	98.50	3997.92	18.52	82.00	23.90	95.10	27.49	16.10	212.50	27.13	106.00	15.00	87.58	9.60	2.45	3.92	200.00

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

Table 4.3: Mean and genetic variability parameters for 26 early seedling vigor, yield and it's attributing traits during wet season *Kharif* 2019:

Characters	Range		Mean	S.D	Coefficient of variation (%)		CV%	h ² (bs) (%)	GA	GA as % of mean
	Maximum	Minmum			Phenotypic	Genotypic				
NL10D	2.80	2.00	2.31	0.19	10.87	3.78	8.16	12.11	0.06	2.71
SL10 (cm)	15.45	9.62	11.81	1.25	12.66	7.92	10.56	39.09	1.20	10.20
SDW10D (gm)	0.02	0.01	0.02	0.00	23.79	16.80	19.72	49.88	0.00	24.44
NL20D	4.80	3.60	4.15	0.31	10.57	0.74	7.49	0.49	0.00	0.11
SL20D (cm)	29.79	14.96	20.43	3.37	18.04	14.79	16.49	67.22	5.10	24.98
SDW20D(g)	0.12	0.04	0.07	0.02	29.54	24.52	27.49	68.90	0.03	41.92
NL30D	5.70	4.00	4.65	0.30	7.46	5.37	6.50	51.83	0.37	7.96
SL30D(cm)	67.62	28.40	41.19	7.85	20.24	17.85	19.06	77.84	13.36	32.45
SDW30D (gm)	0.42	0.10	0.23	0.07	32.69	28.69	30.68	77.01	0.12	51.86
GP(%)	98.50	66.50	81.58	8.47	10.64	9.62	10.38	81.76	14.66	17.93
V I	6322.47	2098.60	3351.03	684.80	21.93	19.00	20.44	75.10	1139.65	33.92
V I I	38.94	6.82	18.55	5.74	33.04	28.87	30.97	76.34	9.68	51.97
D50PF	90.00	60.50	79.83	7.18	9.11	8.88	9.00	95.15	14.25	17.85
PL (cm)	27.85	17.84	23.13	2.22	10.03	9.16	9.60	83.45	3.99	17.24
PH (cm)	160.84	75.58	102.96	15.49	16.13	13.88	15.05	74.02	25.33	24.60
FLL (cm)	50.08	17.11	32.60	6.27	21.77	16.28	19.22	55.95	8.18	25.09

FFW (mm)	20.30	11.00	14.83	1.74	13.93	9.05	11.74	42.21	1.80	12.11
PPMS	291.00	125.50	209.98	36.97	19.15	15.91	17.60	69.07	57.21	27.25
1000 GW	32.23	14.02	24.68	3.36	13.84	13.38	13.61	93.43	6.57	26.63
FS	188.50	47.50	106.55	28.76	27.26	26.73	27.00	96.22	57.56	54.02
UFS	69.00	9.00	20.95	10.65	51.18	50.45	50.82	97.19	21.47	102.46
SF (%)	92.20	60.77	83.38	6.66	8.04	7.93	7.99	97.30	13.44	16.12
PL (mm)	11.25	6.65	8.76	0.82	9.33	9.23	9.38	97.84	1.65	18.81
PB (mm)	3.25	1.85	2.54	0.28	11.07	10.82	10.94	95.54	0.55	21.79
P L/B R	5.49	2.35	3.50	0.58	16.58	16.34	16.52	97.10	1.16	33.16
GY	409.00	76.50	235.83	61.69	27.04	25.26	26.16	87.26	114.61	48.60

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

4.2.1 Correlation coefficient analysis:

Association analysis is an important approach in a breeding programme. It gives an idea about relationship among the various characters and determines the component characters, on which selection can be based on genetic improvement in the grain yield. Degree of association also affects the effectiveness of selection process. The degree of association between independent and dependent variables was suggested by Galton 1888, theory was developed by Pearson (1904) and their mathematical utilization at phenotypic, genotypic and environmental levels was described by Searle (1961).

The correlation coefficients analysis is the index of association between two variables. These have been dealt with in all possible combinations for important characters at genotypic and phenotypic level are presented in Table 4.4 and 4.5

4.2.1.1 Number of leaves on 10 DAS:

Number of leaves on 10 days is showing the highly positive correlation with seedling length on 10 days (0.82), seedling dry weight on 10 days (0.74), seedling length on 20 days (0.69), seedling dry weight on 20 days (0.34), seedling length on 30 days (0.53), vigor index I (0.50), plant height (0.41), flag leaf length (0.38) at phenotypic and genotypic level. It showed a highly significant negative correlation with filled spikelets (-0.024), spikelet fertility percent (-0.32) and grain yield per meter square (-0.45).

4.2.1.2 Seedling length on 10 DAS:

Seedling length on 10 days is showing the highly positive correlation with seedling dry weight on 10 days (0.66), number of leaf in 20 days (.060), seedling length on 20 days (0.68), seedling dry weight on 20 days (0.38), seedling length on 30 days (0.54), seedling dry weight on 30 days (0.36), vigor index I (0.30), vigor index II (0.28), plan height (0.41), flag leaf length (0.49), 1000 grain weight (0.32) and paddy breadth (0.43) at phenotypic and genotypic level. It showed highly significant negative correlation with germination percent, filled spikelet (-0.035), unfilled spikelet(-0.26), paddy L/B ratio (-0.15) and grain yield (-0.20).

4.2.1.3 Seedling dry weight on 10 DAS:

Seedling dry weight on 10 days is showing the highly positive correlation with number of leaves on 20 days (2.33), seedling length on 20 days (0.54), seedling dry weight on 20 days (0.45), seedling length on 30 days (0.57), seedling dry weight on 30 days (0.44), vigor index I (0.41), vigor index II (0.35), plant height (0.43), flag leaf length(0.39), 1000 grain weight (0.24) and paddy breadth (0.35) at phenotypic and genotypic level. It showed highly significant negative correlation with unfilled spikelet(-0.26), paddy L/B ratio (-0.28) and grain yield (-0.42).

4.2.1.4 Number of leaves on 20 DAS:

Number of leaves on 20 days is showing the highly positive correlation with seedling length on 20 days (2.14), seedling length on 30 days (2.61) and vigor index I (2.70) at phenotypic and genotypic level. It showed highly significant negative correlation with 1000 grain weight (0.47), unfilled spikelet (-1.08), paddy length (-2.10), paddy L/B ratio (-1.65) and grain yield (-2.76).

4.2.1.5 Seedling length on 20 DAS:

Seedling length on 20 days is showing the highly positive correlation with seedling dry weight on 20 days (0.52), seedling length on 30 days (0.82), seedling dry weight on 30 days (0.55), vigor index I (0.72), vigor index II (0.53), plant height(0.82), flag leaf length(0.48), 1000 grain weight (0.47), spikelet fertility percent (0.42) and paddy breadth (-0.26) at phenotypic and genotypic level. It showed positive significant correlation with number of leaf on 30 days (0.20). It also showed highly significant negative correlation with paddy L/B ratio(-0.26) and grain yield (-0.24).

4.2.1.6 Seedling dry weight on 20 DAS:

Seedling length on 20 days is showing the highly positive correlation with number of leaf in 30 days (0.29), seedling length on 30 days (0.40) and seedling dry weight in 30 days (0.55), vigor index I (0.36), vigor index II (0.53), plant height (0.55), flag leaf length (0.29), flag leaf width (0.44), 1000 grain weight (0.55), spikelet fertility percent (0.23), and paddy breadth (0.349) at phenotypic and genotypic level. It showed highly significant negative correlation with paddy L/B ratio (-0.26).

4.2.1.7 Number of leaf on 30 DAS:

Number of leaves on 30 days is showed positive correlation with plant height (0.18). It showed highly significant negative correlation with germination percent (-0.21).

4.2.1.8 Seedling length on 30 DAS:

Seedling length on 30 days is showing the highly positive correlation with seedling dry weight on 30 days (0.62), vigor index I (0.27), vigor index II (0.58), plant height(0.76), flag leaf length (0.71), 1000 grain weight(0.32) and paddy breadth (0.34) at phenotypic and genotypic level. It showed highly significant negative correlation with paddy L/B ratio (-0.24).

4.2.1.9 Seedling dry weight in 30 days:

Seedling length on 30 days is showing the highly positive correlation with vigor index I (0.54), vigor index II (0.94), plant height (0.50), flag leaf length (0.66), 1000 grain weight (0.31), and paddy breadth (0.34) at phenotypic and genotypic level. It showed highly significant negative correlation with paddy L/B ratio (-0.26).

4.2.1.10 Germination percent:

Germination percent had a highly significant positive correlation with vigor index I (0.33), days to 50 percent flowering (0.20) and panicle length (0.32). It was showed highly negative correlation with the panicle per meter square (-0.20).

4.2.1.11 Vigor indexI:

Vigor index I had showed highly significant positive correlation with vigor indexII (0.65), plant height (0.70), flag leaf length (0.58), 1000 grain weight (0.27) and paddy breadth (0.22). It had showed a significant positive correlation with panicle length (0.16).

4.2.1.12 Vigor indexII:

Vigor indexII had showed highly significant positive association with plant height (0.48), flag leaf length (0.59), flag leaf width (0.27), 1000 grain weight (0.30) and paddy breadth (0.27). It had showed highly significance negative correlation with panicle per meter square (-0.21) and paddy L/B ratio (-0.23).

4.2.1.13 Days to 50% flowering

The characters days to 50% flowering had a highly significant positive correlation with paddy length (0.27), paddy L/B ratio (0.23) and grain yield (0.22).

4.2.1.14 Panicle length (cm):

Panicle length recorded the highly significance positive correlation with filled spikelet (0.43) and spikelet fertility percent (0.39). It had showed significant positive correlation at genotypic level at grain yield per meter square (0.19).

4.2.1.15 Plant height (cm):

The character plant height recorded the highly significant positive correlation with flag leaf length (0.68), flag leaf width (0.23), 1000 grain weight (0.34), filled spikelet (0.22), and paddy breadth (0.34).

4.2.1.16 Flag leaf length:

Flag leaf length showed highly significant positive correlation with paddy breadth (0.32). It had showed highly significant negative correlation with paddy L/B ratio (-0.40).

4.2.1.17 Flag leaf width:

Flag leaf width showing highly significant positive correlation with spikelet fertility percent (0.21), 1000 grain weight (0.29) and filled spikelet (0.23). It had showed highly significant negative correlation with panicle per meter square (0.20).

4.2.1.18 Total number of tillers per meter square:

Total number of tillers per meter square is not showing any positive and negative correlation with any other trait.

4.2.1.19 1000-seed weight (g):

The character 1000-seed weight showed a highly significant positive correlation with paddy length (0.31) and paddy breadth (0.49).

4.2.1.20 Filled spikelets per panicle:

Filled spikelet per panicle is showing the highly positive correlation with unfilled spikelet (0.27), spikelet fertility percent (0.35) and grain yield (0.22) at phenotypic and genotypic level. It showed highly significant negative correlation with paddy length (0.26).

4.2.1.21 Unfilled spikelets per panicle:

Unfilled spikelets per panicle showed highly significant negative association with spikelet fertility percentage () at phenotypic, genotypic level.

4.2.1.22 Spikelet fertility percentage:

The character spikelet fertility percentage showed highly significant positive correlation with paddy breadth (0.21). Also had a highly significant negative correlation with paddy length (-0.22) and paddy L/B ratio (-0.027) at phenotypic and genotypic level.

4.2.1.23 Paddy length:

The paddy length expressed highly significant positive correlation with paddy L/B ratio (0.77). It was showed highly significant negative association with paddy breadth (-0.032).

4.2.1.24 Paddy width:

The paddy width showed highly significant negative correlation with paddy L/B ratio (-0.88).

4.2.1.25 Paddy L/B ratio

The paddy L/B ratio cannot show any correlation with other trait.

4.2.1.26 Grain yield per meter square:

The character grain yield per meter square showed highly significant positive correlation with days to 50 percent flowering (0.22), panicle length (0.19) and filled spikelet (0.22). It was showed highly significant negative correlation with number of leaf on 10 days (-0.45), seedling length on 10 days (-0.47), seedling dry weight on 10 days (-0.42), number of leaf on 20 days (-0.76) and seedling dry weight on 20 days (-0.15).

In the present investigation grain yield per plant was positively and significantly associated with days to 50 percent flowering filled spikelet and panicle length. The positive association of grain yield per plant with filled spikelet per panicle is in similar to the finding of Chauhan *et al.* (1993), Sarawgi *et al.* (1997), Prashanth *et al.* (1999), Singh *et al.* (2000), and Surek and Beser (2003). Vanishree *et al.*, 2013; Madhavilatha *et al.*, 2005. Based on correlation studies, it can be concluded that the selection criteria based on filled spikelet per panicle,

days to 50 percent flowering and panicle length can provide better results for improvement of yield and other traits.

It indicates strong correlation of these traits with grain yield per meter square, the selection of these traits will be useful in improving grain yield.

Table 4.4 Genotypic correlation coefficient for early seedling vigor, yield and contributing character:

Traits	NL10D	SL10D (cm)	SDW 10 (gm)	NL20D	SL20D (cm)	SDW 20D (gm)	NL30 D	SL30 (cm)	SDW 30D (gm)	GP (%)	VI 1	VI 2	D50PF	PL (cm)	PH (cm)	FFL (cm)	FFW (mm)	PPMS	1000 GW	FS	UFS	SF (%)	Panicle length (mm)	PB (mm)	P L/B R	
SL10 (cm)	0.822**																									
SDW 10D (gm)	0.746**	0.665**																								
NL20D	9.518**	0.603**	2.330**																							
SL20D (cm)	0.695**	0.682**	0.549**	2.149**																						
SDW 20D(gm)	0.346**	0.385**	0.453**	1.411**	0.527**																					
NL30D	-0.161*	0.123 ^{NS}	0.005 ^{NS}	0.091 ^{NS}	0.200*	0.292**																				
SL30D (cm)	0.536**	0.548**	0.579**	2.677**	0.826**	0.402**	0.178 ^s																			
SDW 30D (gm)	0.061 ^{NS}	0.361**	0.440**	1.169**	0.555**	0.551**	0.063 ^s	0.628**																		
GP (%)	-0.036 ^{NS}	-0.274**	-0.277**	1.192**	0.101 ^{NS}	0.060 ^s	0.212**	0.146 ^s	0.117 ^s																	
VI1	0.503**	0.394**	0.419**	2.703**	0.737**	0.361**	0.077 ^s	0.877**	0.541**	0.338**																
VI2	0.086 ^{NS}	0.285**	0.351**	1.221**	0.532**	0.536**	0.001 ^s	0.587**	0.946**	0.197*	0.658**															
D50PF	-0.002 ^{NS}	0.099 ^{NS}	-0.195*	0.416**	0.002 ^{NS}	0.133 ^s	0.050 ^s	0.114 ^s	0.040 ^s	0.208**	0.005 ^{NS}	0.121 ^{NS}														
PL (cm)	-0.143 ^{NS}	0.109 ^{NS}	-0.176*	1.708**	0.116 ^{NS}	0.828**	0.161*	0.015 ^s	0.169*	0.325**	0.168*	0.064 ^{NS}	0.083 ^{NS}													
PH (cm)	0.417**	0.578**	0.431**	2.807**	0.828**	0.550**	0.180*	0.763**	0.502**	-0.081 ^{NS}	0.702**	0.489**	0.171*	0.086 ^{NS}												
FFL (cm)	0.383**	0.496**	0.392**	2.679**	0.488**	0.295**	0.234**	0.710**	0.665**	-0.159*	0.586**	0.595**	0.052 ^{NS}	0.171*	0.682**											
FFW (mm)	-0.160*	-0.161*	0.059 ^{NS}	-0.468**	0.037 ^{NS}	0.421**	0.100 ^s	0.023 ^s	0.256**	-0.023 ^{NS}	0.036 ^{NS}	0.272**	0.275**	-0.033 ^{NS}	0.238**	0.111 ^{NS}										
PPMS	-0.065 ^{NS}	0.097 ^{NS}	0.112 ^{NS}	4.313**	0.048 ^{NS}	0.012 ^s	0.231**	0.017 ^s	0.120 ^s	-0.209**	0.109 ^{NS}	-0.218**	0.160*	-0.057 ^{NS}	0.047 ^{NS}	0.206**	-0.246**									
1000 GW	0.294**	0.327**	0.354**	-0.588**	0.470**	0.555**	0.211**	0.322**	0.316**	-0.085 ^{NS}	0.275**	0.301**	0.141 ^{NS}	-0.034 ^{NS}	0.343**	0.054 ^{NS}	0.299**	0.001 ^{NS}								
FS	-0.244**	-0.385**	0.139 ^{NS}	0.931**	0.086 ^{NS}	0.111 ^s	0.024 ^s	0.013 ^s	0.054 ^s	0.138 ^{NS}	0.089 ^{NS}	0.098 ^{NS}	0.038 ^{NS}	0.434**	0.222**	0.193*	0.362**	0.062 ^{NS}	0.077 ^{NS}							
UFS	0.055 ^{NS}	-0.267**	-0.268**	-1.087**	0.017 ^{NS}	0.132 ^s	0.021 ^s	0.004 ^s	0.086 ^s	-0.095 ^{NS}	0.043 ^{NS}	0.054 ^{NS}	-0.032 ^{NS}	0.013 ^{NS}	0.029 ^{NS}	0.019 ^{NS}	0.011 ^{NS}	0.056 ^{NS}	-0.161*	0.272**						
SF (%)	-0.329**	0.031 ^{NS}	0.147 ^{NS}	1.377**	0.019 ^{NS}	0.233**	0.062 ^s	0.037 ^s	0.027 ^s	0.185*	0.053 ^{NS}	0.032 ^{NS}	0.014 ^{NS}	0.318**	0.031 ^{NS}	0.092 ^{NS}	0.295**	0.031 ^{NS}	0.138 ^{NS}	0.356**	-0.746**					
PL (mm)	0.034 ^{NS}	0.055 ^{NS}	0.154 ^{NS}	-2.109**	0.036 ^{NS}	0.019 ^s	0.196*	0.020 ^s	0.042 ^s	-0.055 ^{NS}	0.049 ^{NS}	0.052 ^{NS}	0.272**	-0.085 ^{NS}	0.026 ^{NS}	-0.300**	0.154 ^{NS}	0.066 ^{NS}	0.316**	-0.266**	0.003 ^{NS}	-0.221**				
PB (mm)	0.325**	0.439**	0.498**	0.759**	0.421**	0.340**	0.019 ^s	0.345**	0.344**	-0.219**	0.223**	0.273**	-0.143 ^{NS}	-0.081 ^{NS}	0.324**	0.326**	0.012 ^{NS}	0.069 ^{NS}	0.519**	0.021 ^{NS}	0.148 ^{NS}	0.213**	-0.323**			
P L/B R	-0.143 ^{NS}	-0.224**	-0.383**	-1.656**	-0.266**	0.226**	0.131 ^s	0.248**	0.267**	0.093 ^{NS}	-0.194*	-0.231**	0.239**	0.002 ^{NS}	-0.188*	-0.409**	0.079 ^{NS}	0.124 ^{NS}	-0.194*	-0.166*	0.105 ^{NS}	-0.273**	0.778**	-0.833**		
GY	-0.453**	-0.472**	-0.425**	-2.763**	-0.249**	-0.159*	0.120 ^s	0.186*	0.035 ^s	0.130 ^{NS}	0.096 ^{NS}	0.079 ^{NS}	0.222**	0.194*	-0.046 ^{NS}	-0.032 ^{NS}	0.062 ^{NS}	0.121 ^{NS}	0.065 ^{NS}	0.221**	0.047 ^{NS}	0.042 ^{NS}	0.062 ^{NS}	0.086 ^{NS}	-0.012 ^{NS}	

Table 4.5 Phenotypic correlation coefficient for early seedling vigor, yield and contributing character:

Traits	NL10D	SL10D (cm)	SDW 10 (gm)	NL20D	SL20D (cm)	SDW 20D (gm)	NL30D	SL30 (cm)	SDW 30D (gm)	GP (%)	VI 1	VI 2	D50PF	PL (cm)	PH (cm)	FFL (cm)	FFW (mm)	PPMS	1000 GW	FS	UFS	SF (%)	Panicle length (mm)	PB (mm)	P L/B R	
NL10D																										
SL10 (cm)	0.382**																									
SDW 10D (gm)	0.329**	0.575**																								
NL20D	0.078 ^{NS}	0.171*	0.157*																							
SL20D (cm)	0.184*	0.485**	0.415**	0.220**																						
SDW 20D(gm)	0.161*	0.327**	0.426**	0.136 ^{NS}	0.538**																					
NL30D	0.012 ^{NS}	0.128 ^{NS}	0.016 ^{NS}	0.055 ^{NS}	0.1-90*	0.196*																				
SL30D (cm)	0.224**	0.392**	0.468**	0.167*	0.697**	0.425**	0.137 ^{NS}																			
SDW 30D (gm)	0.156*	0.300**	0.330**	0.025 ^{NS}	0.413**	0.423**	0.082 ^{NS}	0.562**																		
GP (%)	0.003 ^{NS}	0.144 ^{NS}	-0.163*	0.113 ^{NS}	0.050 ^{NS}	0.024 ^{NS}	0.081 ^{NS}	0.103 ^N	0.085 ^N																	
VII	0.203**	0.303**	0.364**	0.197*	0.629**	0.394**	0.095 ^{NS}	0.883**	0.479**	0.366**																
VI2	0.157*	0.254**	0.276**	0.000 ^{NS}	0.398**	0.416**	0.056 ^{NS}	0.525**	0.948**	0.221**	0.593**															
D50PF	0.023 ^{NS}	0.020 ^{NS}	-0.180*	0.048 ^{NS}	0.036 ^{NS}	0.071 ^{NS}	0.031 ^{NS}	0.123 ^N	0.019 ^N	0.164*	0.026 ^N	0.083 ^N														
PL (cm)	0.008 ^{NS}	0.002 ^{NS}	0.057 ^{NS}	0.084 ^{NS}	0.093 ^{NS}	0.078 ^{NS}	0.083 ^{NS}	0.055 ^N	0.119 ^N	0.281**	0.180*	0.031 ^N	0.065 ^N													
PH (cm)	0.235**	0.364**	0.334**	0.149 ^{NS}	0.607**	0.445**	0.208**	0.662**	0.458**	0.030 ^N	0.606**	0.451**	0.119 ^N	0.066 ^N												
FFL (cm)	0.157*	0.237**	0.175*	0.112 ^{NS}	0.328**	0.211**	0.134 ^{NS}	0.483**	0.379**	0.112 ^N	0.394**	0.332**	0.033 ^N	0.112 ^N	0.464**											
FFW (mm)	0.063 ^{NS}	0.001 ^{NS}	0.016 ^{NS}	0.071 ^{NS}	0.083 ^{NS}	0.246**	0.014 ^{NS}	0.075 ^N	0.141 ^N	0.056 ^N	0.107 ^N	0.169*	0.153 ^N	0.009 ^N	0.329**	0.188*										
PPMS	0.035 ^{NS}	0.046 ^{NS}	0.010 ^{NS}	0.104 ^{NS}	0.028 ^{NS}	0.066 ^{NS}	0.143 ^{NS}	0.062 ^N	0.038 ^N	-0.174*	0.041 ^N	0.116 ^N	0.129 ^N	0.058 ^N	0.075 ^N	0.124 ^N	0.128 ^N									
1000 GW	0.080 ^{NS}	0.188*	0.249**	0.018 ^{NS}	0.328**	0.404**	0.111 ^{NS}	0.262**	0.247**	0.072 ^N	0.220**	0.235**	0.135 ^N	0.026 ^N	0.286**	0.035 ^N	0.200*	0.012 ^N								
FS	0.085 ^{NS}	0.228**	0.123 ^{NS}	0.041 ^{NS}	0.068 ^{NS}	0.062 ^{NS}	0.007 ^{NS}	0.001 ^N	0.053 ^N	0.127 ^N	0.068 ^N	0.090 ^N	0.044 ^N	0.390**	0.179*	0.151 ^N	0.237**	0.059 ^N	0.072 ^N							
UFS	0.009 ^{NS}	-0.157*	0.209**	0.085 ^{NS}	0.013 ^{NS}	0.140 ^{NS}	0.026 ^{NS}	0.030 ^N	0.068 ^N	0.089 ^N	0.064 ^N	0.039 ^N	0.023 ^N	0.007 ^N	0.005 ^N	0.014 ^N	0.020 ^N	0.051 ^N	0.152 ^N	0.281**						

SF (%)	0.105 ^{NS}	0.006 ^{NS}	0.111 ^{NS}	0.082 ^{NS}	0.022 ^{NS}	0.214 ^{**}	0.041 ^{NS}	0.006 ^N _s	0.009 ^N _s	0.170 [*]	0.071 ^N _s	0.042 ^N _s	0.009 ^N _s	0.288 ^{**}	0.050 ^N _s	0.078 ^N _s	0.205 ^{**}	0.021 ^N _s	0.127 ^N _s	0.347 ^{**}	0.745 ^{**}				
PL (mm)	0.010 ^{NS}	0.026 ^{NS}	0.125 ^{NS}	0.130 ^{NS}	0.035 ^{NS}	0.019 ^{NS}	0.106 ^{NS}	0.015 ^N _s	0.050 ^N _s	0.049 ^N _s	0.040 ^N _s	0.057 ^N _s	0.264 ^{**}	0.067 ^N _s	0.015 ^N _s	0.245 ^{**}	0.087 ^N _s	0.052 ^N _s	0.313 ^{**}	0.258 ^{**}	0.003 ^N _s	0.216 ^{**}			
PB (mm)	0.115 ^{NS}	0.274 ^{**}	0.352 ^{**}	0.023 ^{NS}	0.343 ^{**}	0.290 ^{**}	0.016 ^{NS}	0.316 ^{**}	0.287 ^{**}	-0.187 [*]	0.208 ^{**}	0.225 ^{**}	0.150 ^N _s	0.060 ^N _s	0.281 ^{**}	0.220 ^{**}	0.009 ^N _s	0.069 ^N _s	0.495 ^{**}	0.017 ^N _s	0.147 ^N _s	0.207 ^{**}	0.308 ^{**}		
P L/B R	0.064 ^{NS}	-0.157 [*]	0.289 ^{**}	0.085 ^{NS}	0.216 ^{**}	-0.191 [*]	0.072 ^{NS}	0.227 ^{**}	0.241 ^{**}	0.075 ^N _s	-0.178 [*]	0.209 ^{**}	0.241 ^{**}	0.001 ^N _s	-0.172 [*]	0.302 ^{**}	0.057 ^N _s	0.109 ^N _s	-0.182 [*]	-0.159 [*]	0.104 ^N _s	0.267 ^{**}	0.768 ^{**}	0.832 ^{**}	
GY	0.097 ^{NS}	0.203 ^{**}	0.271 ^{**}	-0.167 [*]	0.151 ^{NS}	0.089 ^{NS}	0.103 ^{NS}	0.108 ^N _s	0.069 ^N _s	0.131 ^N _s	0.030 ^N _s	0.108 ^N _s	0.186 [*]	0.147 ^N _s	0.009 ^N _s	0.021 ^N _s	0.055 ^N _s	0.125 ^N _s	0.032 ^N _s	0.198 [*]	0.033 ^N _s	0.048 ^N _s	0.054 ^{NS}	0.079 ^N _s	0.012 ^N _s

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, VI = Vigor index, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

4.2.2 Path analysis:

The genetic architecture of economic yield must be resolved with the genetic contribution of all other characters influencing it directly or indirectly. Path coefficient analysis helps partition the correlation into the measures of direct and indirect effects. It measures the direct and indirect contribution of independent variables on the depended variable Table 4.6

4.2.2.1 Number of leaves on 10 DAS:

Number of leaves in 10 days showed very high negative direct effect of (-6.13) on grain yield per meter square and very high positive indirect effect was shown by traits like seedling length on 30 days, vigor indexII, seedling dry weight on 10 days, spikelet fertility percent, seedling length on 10 days, filled spikelet per panicle and flag leaf length. Number of leaves on 10 days showed high positive indirect effect like flag leaf length and paddy breadth, very high negative indirect effect of number of leaves on 10 days was shown by vigor indexI seedling dry weight on 30 days, number of leaves on 20 days and filled spikelet, and high negative indirect effect showing traits were plant height, flag leaf width, unfilled spikelet, paddy L/B ratio and panicle length. All leftover traits showed moderate, low or negligible indirect effect which was either positive or negative.

4.2.2.2 Seedling length on 10 DAS:

Seedling length on 10 days showed very high positive direct effect of (3.77) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 days, vigor indexII, seedling dry weight on 10 days, and unfilled spikelet per panicle. Seedling length on 10 days showed high positive indirect effect such trait like flag leaf length, panicle per meter square, paddy breadth and seedling dry weight on 20 days, very high negative indirect effect was shown by vigor indexI, seedling dry weight on 30 days, germination percent, number of leaves on 10 days and filled spikelet, and high negative indirect effect showing traits were plant height, paddy L/B ratio, flag leaf width, spikelet fertility percent and number of leaves on 20 days. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

4.2.2.3 Seedling dry weight on 10 DAS:

Seedling dry weight on 10 days showed very high positive direct effect of (7.76) on grain yield per meter square, very high positive indirect effect was shown by traits like seedling length on 30 days, vigor indexII, seedling length on 10 days and unfilled spikelet. Seedling dry weight on 10 days showed high positive indirect effect for a trait like paddy breadth, flag leaf length, seedling dry weight on 20 days, paddy length and days to 50 percent flowering, very high negative indirect was shown by vigor indexI seedling dry weight on 30 days, germination percent, number of leaves on 10 days, spikelet fertility percent, number of leaves on 20 days and paddy L/B ratio and high negative indirect effect showing traits were plant height, and panicle length. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

4.2.2.4 Number of leaves on 20 DAS:

Number of leaves on 20 days showed high negative direct effect of (-0.64) on grain yield per meter square, very high positive indirect effect was shown by traits like seedling length on 30 days, vigor indexII, germination percent, panicle per meter square, seedling dry weight on 10 days, unfilled spikelet filled spikelet paddy length flag leaf length, panicle length, seedling length on 10 days, paddy breadth and seedling dry weight on 20 days. Number of leaves on 20 days showed high positive indirect effect only for trait like seedling length on 20 days, very high negative indirect effect was shown by vigor indexI seedling dry weight on 30 days, number of leaf on 20 days, spikelet fertility percent, paddy L/B ratio, plant height and flag leaf width, and high negative indirect effect showing traits were days to 50 percent flowering. All leftover traits showed moderate, low, or negligible indirect effect either positive or negative.

4.2.2.5 Seedling length on 20 DAS:

Seedling length on 20 days showed moderate positive direct effect of (0.21) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length in 30 days, vigor indexII, seedling dry weight on 10 days, and seedling length on 10 days. Seedling length on 20 days showed high positive indirect effect for trait like flag leaf length, paddy breadth, seedling dry weight on 20 days, spikelet fertility percent and panicle length, very

high negative indirect effect was shown by vigor indexI, seedling dry weight on 30 days, number of leaves on 10 days germination percent, number of leaves on 20 days and plant height, and high negative indirect effect showing traits were paddy L/B ratio. All leftover traits showed moderate, low, or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.6 Seedling dry weight on 20 DAS:

Seedling dry weight on 20 days showed very high positive direct effect of (1.38) on grain yield per meter square, very high positive indirect effect was shown by traits like vigor indexII, seedling length in 30 days, seedling dry on 10 days and flag leaf width, seedling length on 10 days and unfilled spikelet. Seedling dry weight on 20 days showed high positive indirect effect for trait like filled spikelet, paddy breadth and flag leaf length, very high negative indirect effect was shown by seedling dry weight on 30 days, vigor indexI, spikelet fertility percent, number of leaves on 10 days and germination percent, and high negative indirect effect showing traits were number of leaves on 20 days, plant height, paddy L/B ratio, number of leaves on 30 days and panicle length.. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

4.2.2.7 Number of leaves on 30 DAS:

Number of leaves on 30 days showed very high negative direct effect of (-1.26) on grain yield per meter square, very high positive indirect effect was shown by traits like vigor indexII, seedling dry weight on 10 days and seedling length on 10 days. Number of leaves on 30 days showed high positive indirect effect for trait like number of leaves on 10 days, spikelet fertility per cent, seedling length on 10 days, panicle length, flag leaf length, seedling dry weight on 20 days and paddy L/B ratio, very high negative indirect effect on grain yield per meter square was shown by vigor indexI, seedling dry weight on 30 days and germination percent, and high negative indirect effect showing traits were paddy length and flag leaf width. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

4.2.2.8 Seedling length on 30 DAS:

Seedling length on 30 days showed very high positive direct effect of (102.85) on grain yield per meter square, very high positive indirect effect was

shown by traits like vigor indexII, seedling dry weight on 10 days and seedling length on 10 day. Seedling length on 30 days showed high positive indirect effect for trait like paddy breadth, spikelet fertility per cent and dry weight on 20 days, very high negative indirect effect on grain yield per meter square was shown by vigor index1, seedling dry weight on 30 days, germination per cent, number of leaves on 20 days and plant height, and high negative indirect effect showing traits was paddy L/B ratio. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect.

4.2.2.9 Seedling dry weight on 30 DAS:

Seedling dry weight on 30 days showed a very high negative direct effect of (-106.18) on grain yield per meter square, very high positive indirect effect was shown by traits like vigor indexII, seedling length on 30 days, seedling dry on 10 days, seedling length on 10 days, flag leaf length and flag leaf width. Seedling dry weight on 30 days showed high positive indirect effect for trait like seedling dry weight on 20 days, paddy breadth and spikelet fertility percent, very high negative indirect effect was shown by vigor index1 and germination per cent, high negative indirect effect showing traits were paddy L/B ratio, plant height, unfilled spikelet, number of leaves on 20 days, panicle per meter square, panicle length and number of leaves on 10 days. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

4.2.2.10 Germination per cent:

Germination per cent showed very high positive direct effect of (25.15) on grain yield per meter square, very high positive indirect effect was shown by traits like vigor indexII, seedling dry weight on 30 days and filled spikelet. Germination per cent showed high positive indirect effect for trait like panicle length and unfilled spikelet, very high negative indirect effect was shown by vigor indexI, seedling length on 30 days, spikelet fertility percent, seedling dry weight on 10 days, panicle per meter square and seedling length on 10 days, and high negative indirect effect showing traits were number of leaves on 20 days, days to 50 per cent flowering and paddy breadth. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.522.11 Vigor indexI:

Vigor indexI showed very high negative direct effect of (-111.82) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 day, vigor indexII, germination per cent, seedling dry weight on 10 days, seedling length on 30 days and flag leaf length. Vigor indexI showed high positive indirect effect for trait like filled spikelet, seedling dry weight on 20 days, panicle length, paddy breadth, and unfilled spikelet, very high negative indirect effect on grain yield per meter square was shown by seedling dry weight on 30 days, number of leaves on 10 days and number of leaves on 20 days and plant height, and high negative indirect effect showing traits were spikelet fertility percent, panicle per meter square and paddy L/B ratio. All leftover traits showed a moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.12 Vigor indexII:

Vigor indexII showed very high positive direct effect of (106.11) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 day, germination per cent, seedling dry weight on 10 days, flag leaf length, flag leaf width and seedling dry weight on 30 days. Vigor indexII showed high positive indirect effect for trait like filled spikelet, seedling dry weight on 20 days and paddy breadth, very high negative indirect effect on grain yield per meter square was shown by seedling dry weight on 30 days, vigor indexI and panicle per meter square, and high negative indirect effect showing traits were number of leaves on 20 days, paddy L/B ratio, plant height, number of leaf on 10 days, spikelet fertility per cent and unfilled spikelet. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.13 Days to 50% flowering

Days to 50% flowering showed very high negative direct effects of (-2.22) on grain yield per meter square, very high positive indirect effect on grain yield per meter square was shown trait like vigor indexII, germination per cent and flag leaf length. It was shown high positive indirect effect panicle per meter square, paddy L/B ratio and seedling length on 10 days, very high negative indirect effect on grain yield like seedling dry weight on 30 days, seedling length in 30 days and

seedling dry weight on 10 days, and high negative indirect effect on grain yield sowing were paddy length and vigor indexI. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.14 Panicle length (cm)

Panicle length had expressed very high positive direct effect of (2.66) on grain yield per meter square, very high positive indirect effect on grain yield per meter square was shown by trait like seedling dry weight on 30 days, germination per cent, filled spikelet per panicle, high positive indirect effect on grain yield such trait like number of leaves on 10 days and flag leaf length, very high negative indirect effect on grain yield like vigor indexI spikelet fertility per cent, vigor indexII, seedling dry weight on 30 days and number of leaves on 20 days. Panicle length showed high negative indirect effect for seedling length and panicle per meter square. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.15 Plant height (cm)

Plant height showed very high negative direct effect of (-1.58) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 days, vigor indexII, seedling dry weight on 10 days, seedling length on 10 days, filled spikelet per panicle and flag leaf length. Plant height showed high positive indirect effect for trait like flag leaf width, seedling dry weight on 20 days and paddy breadth, very high negative indirect effect on grain yield per meter square was shown by vigor indexI seedling dry weight on 30 days, number of leaves on 10 days, germination per cent, number of leaves on 20 days, and high negative indirect effect showing traits were paddy L/B ratio, spikelet fertility per cent and days to 50 per cent flowering. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.16 Flag leaf length:

Flag leaf length showed very high positive direct effect of (1.85) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 day, vigor indexII, seedling dry weight on 10 days, seedling length on 10 days, filled spikelet and panicle length per meter

square. Flag leaf length showed high positive indirect effect for trait like paddy length, paddy breadth, flag leaves width, panicle length and seedling dry weight, very high negative indirect effect on grain yield per meter square was shown by seedling dry weight on 30 days, vigor indexI, germination percent, number of leaves on 10 days, number of leaf on 10 days, spikelet fertility per cent, paddy L/B ratio and plant height. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.17 Flag leaf width:

Flag leaf width showed very high positive direct effect (4.01) on grain yield per meter square, very high positive indirect effect of flag leaf width on grain yield was shown by traits like vigor indexII, seedling length on 30 days and filled spikelet. Flag leaf width showed high positive indirect effect for traits like paddy length, paddy breadth, flag leaf width, panicle length and seedling dry weight, very high negative indirect effect on grain yield per meter square was shown by seedling dry weight in 30 days, vigor indexI germination per cent, number of leaves on 10 days, number of leaf on 20 days, spikelet fertility percent, paddy L/B ratio and plant height. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.18 Panicle per meter square:

Panicle per meter square expressed very high positive direct effect of (5.70) on grain yield per meter square, very high positive indirect effect on grain yield per meter square like seedling dry weight on 30 days, vigor indexI, seedling length on 30 days, it also showed high positive indirect effect on grain yield such trait was unfilled spikelet, spikelet fertility percent, number of leaves on 10 days, flag leaf length and seedling length on 10 days. It was shown very high negative indirect effect for vigor indexII, germination percent and number of leaves on 20 days, flag leaf width, seedling dry weight, filled spikelet per panicle and days to 50 percent flowering, high negative indirect effect for flag leaf width, seedling dry weight, filled spikelet, paddy L/B ratio and days to 50 percent flowering. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.19 1000-seed weight (g)

1000-seed weight showed moderate negative direct effect of (-0.30) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 days, vigor indexII, seedling dry weight on 10 days, unfilled spikelet, seedling length on 10 days, flag leaf width and paddy breadth, 1000 seed weight showed high positive indirect effect for trait like a seedling dry weight on 20 days and number of leaves on 20 days, very high negative indirect effect on grain yield per meter square was shown by seedling dry weight on 30 days, vigor indexI, spikelet fertility percent, germination percent and number of leaves on 10 days, and high negative indirect effect showing traits were paddy length, paddy L/B ratio, filled spikelet, plant height and days to 50 percent flowering. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.20 Filled spikelets per panicle:

Filled spikelets per panicle expressed very high positive direct effect of (7.71) on grain yield per meter square, very high positive indirect effect on grain yield per meter square was shown by traits like germination per cent, number of leaves on 10 days, flag leaf width, seedling length on 30 days and panicle length, and high positive indirect effect on grain yield for trait like paddy length and flag leaf length. It had shown very high negative indirect effect for vigor indexI, spikelet fertility percent, seedling dry weight on 30 days, unfilled spikelet, seedling length on 10 days and seedling dry weight on 10 days, and high negative indirect effect for number of leaves on 20 days, paddy L/B ratio, panicle per meter square and plant height. All leftover traits showed moderate, low or negligible indirect effect either positive or negative on grain yield. Leftover traits showed moderate, low or negligible indirect effect either positive or negative on grain yield.

4.2.2.21 Unfilled spikelets per panicle:

Unfilled spikelets per panicle showed very high negative direct effect of (-9.16) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like spikelet fertility per cent, vigor indexII. Unfilled spikelets per panicle showed high positive indirect effect for trait like number of leaves on 20 days, Paddy L/B ratio, very high negative indirect effect on grain yield per meter square was shown by seedling dry weight on 30 days, germination per cent, seedling dry weight on 10 days and seedling length on 10 days, and high negative indirect effect showing traits were seedling length on 30 days number of leaves on 10 days. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.22 Spikelet fertility per cent:

Spikelets fertility per cent showed very high negative direct effect of (-15.68) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like unfilled spikelet, germination per cent, vigor indexII, seedling dry weight on 30 days, number of leaves on 10 days, flag leaf width and seedling dry weight on 10 days, and high positive indirect effect on grain yield showed by panicle length, paddy length, paddy breadth and seedling dry weight on 20 days, very high negative indirect effect on grain yield per meter square was shown by vigor indexI and seedling length on 30 days, and high negative indirect effect showing traits were number of leaves on 20 days and Paddy L/B ratio. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

4.2.2.23 Paddy length:

Paddy length expressed very high negative direct effect of (-2.88) on grain yield per meter square, very high positive indirect effect on grain yield per meter square was shown by traits like vigor indexI seedling dry weight on 30 days, spikelet fertility per cent, paddy L/B ratio and number of leaves on 20 days, and high positive indirect effect on grain yield for trait like flag leaf width only. It had shown very high negative indirect effect for vigor indexII, seedling length on 30 days, filled spikelets, germination per cent and seedling dry weight on 10 days. and high negative indirect effect for paddy breadth, days to 50 per cent flowering, flag

leaf length and panicle per meter square. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.24 Paddy breadth:

Paddy breadth showed very high positive direct effect of (1.93) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling length on 30 days, vigor index II, seedling dry weight on 10 days, seedling length on 20 days and unfilled spikelet. Paddy breadth showed high positive indirect effect for trait like spikelet fertility per cent, flag leaf length, seedling dry weight and panicle per meter square, very high negative indirect effect on grain yield was shown by trait like seedling dry on 30 days, vigor index I, germination per cent, paddy L/B ratio and number of leaves on 10 days, high negative indirect effect on grain yield per meter square was shown by days to 50 per cent flowering. All leftover traits showed moderate, low or negligible indirect effect either positive or negative effect on grain yield.

4.2.2.25 Paddy L/B ratio:

Paddy L/B ratio showed very high positive direct effect of (3.08) on grain yield per meter square, very high positive indirect effect on grain yield was shown by traits like seedling dry weight on 30 days, vigor index I, spikelet fertility per cent, germination per cent and number of leaves on 20 days, and high positive indirect effect showed by number of leaf on 10 days, flag leaf length and plant height, very high negative indirect effect was shown by seedling length on 30 days, vigor index II, seedling dry weight on 10 days, paddy length paddy breadth and filled spikelet, and high negative indirect effect showing traits were flag leaf length, unfilled spikelet, seedling length on 10 days, panicle per meter square, days to 50 percent flowering and seedling dry weight 20 days. All leftover traits showed moderate, low or negligible indirect effect either positive or negative.

The path analysis discerns correlation into direct and indirect effects. The present investigation was undertaken to establish the relationship between component characters. The direct and indirect effect of different characters on grain yield per meter square is summarized below:

- i) Number of leaves on 10, 20 and 30 das showed a very high negative direct effect on grain yield.

- ii) Seedling length on 10 and 30 DAS showed very high positive direct effect on grain yield, and seedling length on 20 DAS were showed high positive direct effect on grain yield.
- iii) Seedling dry weight 10 and 20 DAS showed very high positive direct effect on grain yield and 30 DAS were very high direct negative effect showed on grain yield, also germination per cent showed very high positive direct effect on grain yield.
- iv) Vigor indexI and vigor indexII showed very high positive and very high negative direct effect on grain yield respectively.
- v) Days to 50 per cent flowering, plant height, unfilled spikelet, spikelet fertility percent and paddy length had showed very high negative direct effect on grain yield. Also 1000 grain weight was showed moderate negative direct effect on grain yield.
- vi) Panicle length, flag leaf length, flag leaf width, panicle per meter square, filled spikelet, paddy breadth and paddy L/B ratio were showed very high positive effect on grain yield.

The characters which is showed positive very high direct effect on grain yield per meter square should be considered in selection criteria for increasing grain yield per meter square. The residual effect (0.81) on grain yield per meter square was negligible, thereby suggestion that no other major yield component is leftover.

Table 4.6 Path coefficient analysis for ESV yield and its attributing characters:

S N		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	
	traits	NL10 D	SL1 0 (cm)	SD W 10 (gm)	NL20 D	SL2 0 (cm)	SD W 20 (gm)	NL30 D	SL30 (cm)	SDW 30 (gm)	GP (%)	VI 1	VI 2	D50P F	PL (cm)	PH (cm)	FF L (cm)	FF W (mm)	PPM S	100 0 GW	FS	UF S	SF (%)	Paddy length(m m)	PB (mm)	P L/ B R	C GY
1	NL10D	-6.13	3.10	5.78	-6.09	0.15	0.48	0.20	55.18	-6.53	0.91	56.23	9.13	0.00	0.38	0.66	0.71	-0.64	-0.37	0.09	1.88	0.50	5.15	-0.10	0.63	0.44	0.45
2	SL10(cm)	-5.04	3.77	5.16	-0.39	0.14	0.53	-0.16	56.34	38.35	6.89	44.09	30.20	-0.22	0.29	0.91	0.92	-0.64	0.55	0.10	2.97	2.44	0.49	-0.16	0.85	0.69	-0.47
3	SDW 10 (gm)	-4.57	2.51	7.76	-1.49	0.12	0.62	-0.01	59.58	46.71	6.96	46.85	37.25	0.43	0.47	0.68	0.73	-0.24	-0.64	0.11	1.07	2.45	2.31	0.44	0.96	1.18	-0.42
4	NL20D	-58.38	2.27	18.07	-0.64	0.46	1.94	-0.11	275.36	124.09	29.99	302.22	129.56	-0.92	4.55	4.43	4.96	-1.88	24.58	0.17	7.18	9.96	21.59	6.06	1.46	5.10	-2.7
5	SL20 (cm)	-4.26	2.57	4.26	-1.38	0.21	0.73	-0.25	84.95	58.88	2.54	82.39	56.45	-0.01	0.31	1.31	0.90	0.15	0.28	0.14	0.66	0.16	0.30	-0.10	0.81	0.82	0.24
6	SDW 20 (gm)	-2.13	1.45	3.52	-0.90	0.11	1.38	-0.37	41.36	58.45	1.52	40.41	56.85	-0.30	0.34	0.87	0.55	1.69	0.07	0.16	0.86	1.21	3.65	-0.06	0.66	0.69	0.15
7	NL30D	0.99	0.47	0.04	-0.06	0.04	0.40	-1.26	18.26	-6.68	5.32	-8.57	0.10	-0.11	0.43	0.28	0.43	-0.40	1.32	0.06	0.18	0.19	0.97	-0.56	-0.04	0.40	0.12
8	SL30 (cm)	-3.29	2.07	4.49	-1.71	0.18	0.55	-0.22	102.85	66.72	3.68	98.09	62.24	0.25	0.04	1.20	1.31	0.09	0.10	0.10	0.10	0.04	0.57	0.06	0.66	0.76	0.18
9	SDW 30 (gm)	-0.38	1.36	3.41	-0.75	0.12	0.76	-0.08	64.63	106.18	2.95	60.46	100.38	-0.09	0.45	0.79	1.23	1.03	-0.68	0.09	0.41	0.79	0.43	0.12	0.66	0.82	0.03
10	GP (%)	0.22	1.03	2.15	-0.76	0.02	0.08	0.27	15.03	12.44	25.15	37.83	20.92	-0.46	0.87	0.13	0.29	-0.09	-1.19	0.03	1.06	0.87	2.90	0.16	-0.42	0.29	0.13
11	VI 1	-3.08	1.49	3.25	-1.73	0.16	0.50	-0.10	90.22	57.41	8.51	111.82	69.84	-0.01	0.45	1.11	1.08	0.15	-0.62	0.08	0.69	0.39	0.84	0.14	0.43	0.60	0.09
12	VI 2	-0.53	1.07	2.72	-0.78	0.11	0.74	0.00	60.32	100.44	4.96	73.59	106.11	-0.27	0.17	0.77	1.10	1.09	-1.24	0.09	0.76	0.49	0.51	0.15	0.53	0.71	0.07
13	D50PF	0.01	0.37	1.51	-0.27	0.00	0.18	-0.06	11.69	-4.21	5.23	-0.54	12.86	-2.22	0.22	0.27	0.10	1.10	0.91	0.04	0.29	0.30	0.22	-0.78	-0.28	0.74	0.22
14	PL (cm)	0.88	0.41	1.36	-1.09	0.02	0.18	-0.20	1.50	17.89	8.18	18.78	-6.81	-0.18	2.66	0.14	0.32	-0.13	-0.33	0.01	3.35	0.12	4.99	0.25	-0.16	0.01	0.19
15	PH (cm)	-2.56	2.18	3.35	-1.80	0.18	0.76	-0.23	78.47	53.26	2.04	78.52	51.84	-0.38	0.23	1.58	1.26	0.95	0.27	0.10	1.71	0.26	0.49	-0.07	0.63	0.58	0.04
16	FFL (cm)	-2.35	1.87	3.04	-1.72	0.10	0.41	-0.29	73.06	70.60	4.00	65.56	63.17	-0.12	0.45	1.08	1.85	0.45	1.18	0.02	1.49	0.17	1.44	0.86	0.63	1.26	0.03
17	FFW (mm)	0.98	0.61	0.46	0.30	0.01	0.58	0.13	2.35	27.21	0.58	-4.06	28.88	-0.61	0.09	0.38	0.21	4.01	-1.40	0.09	2.80	0.10	4.63	-0.44	0.02	0.24	0.06

18	PPMS	0.40	0.37	0.87	-2.76	0.01	0.02	-0.29	1.74	12.74	5.25	12.17	23.11	-0.35	0.15	0.07	0.38	-0.99	5.70	0.00	0.48	0.19	0.13	0.38	0.12		
19	1000 GW	-1.81	1.23	2.74	0.38	0.10	0.76	-0.27	33.15	33.59	2.13	30.71	31.91	-0.31	0.09	0.54	0.10	1.20	0.01	0.30	0.59	1.48	-2.16	-0.91	1.00	0.60	
20	FS	1.50	1.45	1.08	-0.60	0.02	0.15	0.03	1.29	-5.69	3.47	-9.94	10.39	-0.08	1.16	0.35	0.36	1.45	-0.36	0.02	7.71	2.49	-5.59	0.77	0.04	0.51	
21	UFS	-0.34	1.01	2.08	0.70	0.00	0.18	-0.03	-0.41	-9.17	2.39	4.81	5.69	0.07	0.03	0.05	0.03	-0.04	-0.32	0.05	2.10	9.16	11.69	-0.01	-0.29	0.32	
22	SF (%)	2.02	0.12	1.14	-0.88	0.00	0.32	0.08	-3.76	2.89	4.65	-5.97	3.42	-0.03	0.85	0.05	0.17	1.18	-0.18	0.04	2.75	6.84	15.68	0.63	0.41	0.84	
23	PL (mm)	-0.21	0.21	1.19	1.35	0.01	0.03	-0.25	-2.09	4.47	1.37	5.52	-5.53	-0.60	0.23	0.04	0.55	0.62	-0.37	0.09	2.05	0.03	3.46	-2.88	-0.62	2.39	
24	PB (mm)	-1.99	1.66	3.86	-0.49	0.09	0.47	0.02	35.44	36.57	5.52	24.99	28.96	0.32	0.21	0.51	0.60	0.05	0.39	0.15	0.16	1.36	3.34	0.93	1.93	2.57	
25	P L/B R	0.88	0.85	2.97	1.06	0.06	0.31	-0.17	25.46	28.33	2.35	21.71	24.48	-0.53	0.01	0.30	0.76	0.32	-0.71	0.06	1.28	0.96	4.27	-2.24	-1.61	3.08	0.08

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, VI = Vigor index, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square. C GY = correlation with grain yeild per meter square.

Residual effect are **0.81**

4.3 Genetic diversity

4.3.1 Principal Component Analysis:

In the present investigation, PCA was performed for 26 early seedling vigor and yield contributing trait of rice presented in Table 4.7. As per the criteria set by Brejda *et al.* (2000), the PC with eigen values >1 and which explained at least 5% of the variation in the data were considered in the present study. The PC with higher eigen values and variables which had high factor loading were considered as best representative of system attributes. Out of 26, only six principal components (PCs) exhibited more than 1.62 eigen value and showed about 64.055% cumulative variability among the traits studied. So, these 6 PCs were given due importance for further explanation. The PC1 showed 24.51% while, PC2, PC3, PC4, PC5 and PC6 exhibited 9.68%, 9.32%, 7.51%, 6.79% and 6.24% variability respectively among the accessions for the traits under study (Table 4.7). The first PC accounts for as much of the variability in the data as possible, and each succeeding component accounts for as much of the remaining variability as possible.

Table 4.7 Principal component analysis for 26 early seedling vigor, yield and its attributing traits of 80 rice genotypes.

S.N.	Traits/PCs	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
1	NL10D	0.15	0.15	-0.15	-0.03	0.18	-0.08
2	SL10(cm)	0.25	0.16	-0.23	0.11	0.14	0.02
3	SDW 10 (gm)	0.26	0.02	-0.27	0.09	0.06	-0.14
4	NL20D	0.12	-0.10	-0.05	0.00	0.46	0.13
5	SL20 (cm)	0.32	0.10	0.02	-0.02	0.11	0.06
6	SDW 10 (gm)	0.26	0.05	0.06	0.22	-0.13	0.06
7	NL30D	0.06	0.12	0.08	0.03	0.02	0.46
8	SL30 (cm)	0.34	0.09	0.03	-0.13	0.11	0.00
9	SDW 30D	0.29	0.07	0.13	-0.14	-0.26	-0.12
10	GP (%)	-0.03	-0.11	0.30	0.08	0.28	-0.37

11	VI 1	0.30	0.04	0.17	-0.08	0.23	-0.19
12	VI 2	0.27	0.04	0.23	-0.11	-0.18	-0.25
13	D50PF	-0.01	0.12	0.29	0.21	0.03	0.20
14	PL (cm)	0.01	-0.22	0.27	0.02	0.33	0.10
15	PH (cm)	0.31	0.07	0.16	-0.03	0.06	0.14
16	FLL (cm)	0.25	-0.09	0.07	-0.20	0.05	0.19
17	FFW (mm)	0.07	-0.01	0.28	0.21	-0.23	-0.03
18	PPMS	0.01	-0.02	-0.11	-0.01	0.13	0.56
19	1000 GW	0.18	0.10	0.02	0.33	-0.29	0.08
20	FS	0.03	-0.32	0.35	-0.13	0.00	0.09
21	UFS	-0.05	0.17	0.14	-0.55	-0.12	0.06
22	SF (%)	0.06	-0.41	0.07	0.46	0.06	-0.03
23	Panicle Length (mm)	-0.06	0.48	0.14	0.28	-0.01	0.03
24	PB (mm)	0.22	-0.24	-0.25	0.05	-0.28	0.06
25	P L/B R	-0.19	0.44	0.23	0.12	0.19	-0.03
26	GY	-0.06	-0.13	0.30	-0.04	-0.24	0.22
	Eigenvalue	6.37283	2.51795	2.42214	1.95303	1.76495	1.62338
	% variance	24.511	9.6844	9.3159	7.5116	6.7883	6.2438
	Cumulative variance	24.511	34.1954	43.5113	51.0229	57.8112	64.055

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, VI = Vigor index, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

Scree plot explained the percentage of variation associated with each principal component obtained by drawing a graph between eigen values and principal component numbers. The PC1 showed 24.511% variability with eigen value 6.37 which then declined gradually. Elbow type line is obtained which after

6th PC tended to straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 (Fig 4.1).

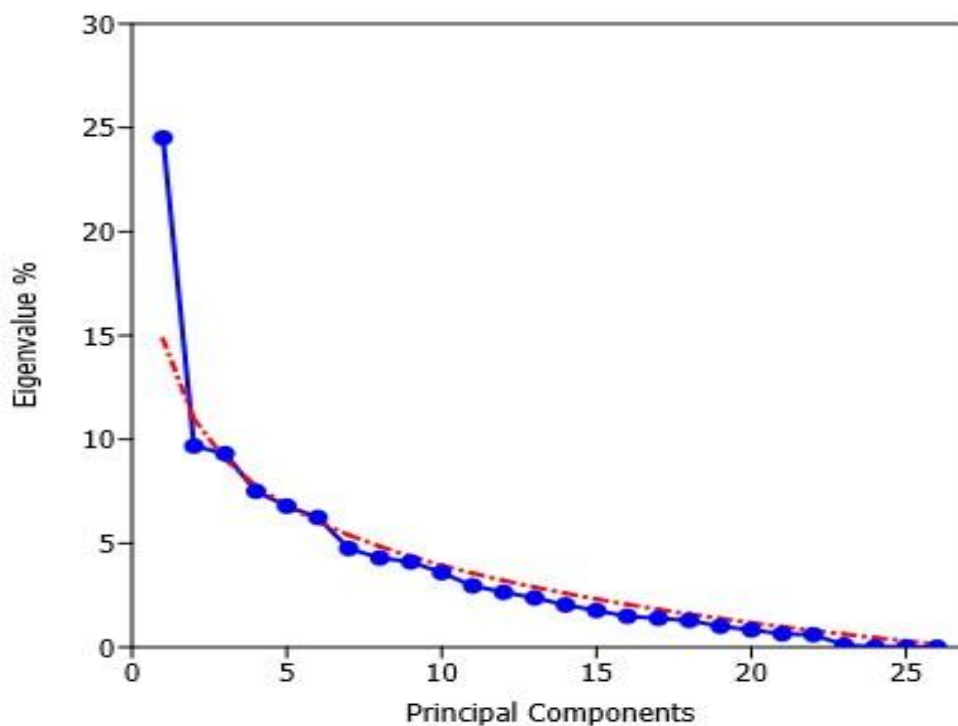


Fig. 4.1 Scree plot of 26 PCs showing eigen value

The result of the PCA explained the genetic diversity of the early seedling vigor, yield and its attributing traits of rice genotype. ‘Proper value’ measures the importance and contribution of each component to total variance, whereas each coefficient of proper factors indicates the degree of contribution of every original variable with which each principal component is associated. The higher the coefficients, regardless of the direction (positive or negative), the more effective they will be in discriminating between accessions (Sanni *et al.*, 2010). Within each PC, only highly loaded factors or traits (having absolute values within 10% of the highest factor loading) were retained for further explanation. Component matrix revealed that the PC1 which accounted for the highest variability (24.511%) was mostly related with traits such as Seedling length on 30 DAS (0.34), seedling

length on 20 DAS (0.32), plant height (0.31), vigor index I (0.30), seedling dry weight on 30 days, (0.29) and vigor index II (0.27) (Table 4.7). As a result, the first component differentiated those accessions that have high seedling length on 30 DAS. The second principal component accounted for 9.68% of the total variance. Variables highly and positively correlated were paddy length, paddy L/B ratio, spikelets fertility percent and filled spikelet respectively. The third principal component accounted for 9.32% of the variability and was highly loaded with the three most important grain yield per meter square, filled spikelets and germination per cent.

The PC4 was positively more related to spikelet fertility percent and 1000 grain weight, while PC5 was highly loaded with number of leaves on 20 DAS and panicle length. The PC6 which accounts for only 6.24 % variability was highly related with panicle per meter square and number of leaves on 30 DAS. Thus, the prominent characters coming together in different principal components and contributing towards explaining the variability have the tendency to remain together which may be kept into consideration during utilisation of these characters in breeding program. So, for early seedling vigor and yield a good breeding programme can be initiated by selecting the accessions from PC1, PC2 and PC3. These results are in agreement with the findings of earlier workers Table 4.8 (Annandan *et al.*, 2016).

Table 4.8 Principal component score of 80 rice genotype.

SN	Accessions	Score					
		PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
1	Aditya	-1.13	-0.64	0.34	0.65	-1.99	2.42
2	Kalinga-3	0.80	-0.45	-2.01	0.37	-0.73	0.62
3	Bala	-0.50	-1.57	-2.28	0.08	-1.39	0.53
4	Poorva	-0.62	-0.66	-0.76	0.56	-0.64	-1.10
5	Lallu-14	0.42	-0.26	0.16	-2.87	0.10	1.59
6	MR 1523	0.02	-0.65	-0.44	-1.09	-0.27	0.03
7	IR-38	-0.14	-0.33	-1.61	0.25	0.20	1.34
8	Surekha	-0.02	0.03	0.03	0.27	-1.09	-0.77
9	Tripti	-0.49	-0.87	-0.69	1.00	0.21	-0.24
10	T-10	-0.59	-0.25	-2.04	-0.19	-0.15	-0.24

11	Aganni	0.71	-0.18	-0.83	0.25	1.80	2.34
12	Jhitpiti	0.65	0.15	-1.16	-0.11	2.09	0.93
13	R1558-2423-1-1445-1	-1.26	0.35	-0.37	-0.24	-0.12	-0.37
14	Kaweri	-0.44	0.19	-1.41	-0.46	-0.72	-0.61
15	Shwnong-89366	0.28	0.36	-0.67	0.14	-0.65	-0.80
16	Chom phool	-0.44	0.80	-0.99	-0.25	-0.22	0.35
17	Asha	-1.05	2.24	-0.55	-2.00	-0.56	0.99
18	Bangoli-3	0.34	3.00	-0.67	-0.81	1.21	1.06
19	Nipon bare	0.10	-0.59	-1.20	0.57	-0.16	0.47
20	Lal mati	-0.65	0.39	-0.20	-1.96	2.19	-0.95
21	Usai buta-2408	1.37	-0.36	0.31	0.35	-0.04	0.34
22	Banisar No-31	-0.36	-2.10	-2.90	-0.87	1.10	-2.01
23	Karhani-No-9	1.36	-0.65	0.08	-0.10	0.66	0.19
24	Balsi balu kanb-694	2.03	-0.04	0.01	0.18	0.08	-0.48
25	Banso bnisa B-1021	1.46	-0.12	-0.19	1.19	-0.35	-0.88
26	DU-95-0-137-1	1.68	-0.04	-0.44	0.58	-0.89	-0.94
27	Sawas-D-137-1	0.75	-0.84	0.10	0.27	-1.27	0.21
28	Birsa gova	1.55	1.32	-0.37	0.99	0.52	-1.47
29	Danwas 2511	1.14	-0.64	-0.72	0.44	-0.27	0.84
30	Duma-bada-25-55	1.39	-0.03	-0.33	0.74	-1.21	1.57
31	Fent 2679	1.83	0.92	0.18	1.03	-0.57	-0.10
32	Gutla 2614	2.41	0.66	-0.54	1.39	1.65	0.61
33	Gurmetta 2697	2.03	0.95	-0.63	-1.27	1.13	0.57
34	Danwar 2129	0.77	0.03	-1.46	0.53	1.08	0.87
35	R1558-1419-2-1442-1	-0.24	0.67	-0.31	0.65	-0.04	-0.04
36	R1519-769-2-1442-1	-1.60	1.88	0.75	1.07	0.69	-0.26
37	R1551-2169-1	-0.25	-0.78	0.51	1.25	0.13	-0.55
38	R1448-578-2	0.08	1.02	0.91	1.51	-1.04	1.36
39	R1013-2307-1-4	-0.46	1.17	0.84	0.15	-1.00	-0.50
40	IR-7866-BIO-BBB-SBI	-0.96	1.18	-0.68	-2.34	-0.59	0.77
41	R971-25-2-1	-0.10	0.66	1.13	-0.40	-0.38	-0.81
42	R1152-2-64-1	-0.93	-0.35	0.82	0.97	0.35	0.91
43	R1004-2552-1-1	-0.71	0.22	0.67	0.88	-1.27	0.85
44	CR-306-37-13	-0.62	-0.64	-0.31	-0.53	-1.44	0.52
45	CR-314-5-10	-0.27	0.04	0.04	-0.32	-0.37	-2.30
46	Asam chidi	-0.66	-1.87	-0.58	0.17	-1.18	-1.55
47	R1723-1411-1-3551	-1.15	0.50	0.56	0.01	-1.29	1.70
48	ARC-15831	0.40	0.44	0.25	-1.21	-0.08	0.23
49	Danteshwari	-0.02	0.48	1.44	0.80	-1.73	-0.53
50	Poornima	-0.64	1.04	1.54	-0.55	-0.47	-0.17

51	Salim paket	0.08	-0.34	1.60	-3.74	-1.30	0.06
52	R1238-19361	-0.72	1.67	-0.62	0.11	-0.83	-0.55
53	R1182-31-2-151	0.02	3.01	-0.36	-0.16	0.60	-0.97
54	R1122-167-2-1571	1.15	0.71	0.99	0.00	-0.41	0.41
55	Vandana	-0.30	1.59	-0.65	-0.47	-0.71	-1.65
56	R1546-1382-1-40-1	-0.04	-0.44	0.71	0.57	-0.17	-0.96
57	MTU-15	1.08	-1.00	-0.62	-0.11	-1.20	-0.52
58	Mamhar	-0.63	0.91	0.76	0.37	-1.36	-1.83
59	C101 LAC	0.85	0.13	-0.27	-1.67	-0.54	-1.31
60	Shyamla	-1.54	0.13	-0.58	1.15	-0.25	-0.38
61	IR-64	-1.27	0.49	0.20	0.79	1.00	0.45
62	Pokali	3.55	-0.62	2.63	-0.76	-0.04	-1.09
63	Krishna hansa	-0.69	0.05	1.15	0.99	0.19	2.10
64	IR 08 L 152	-0.26	-1.34	1.63	-0.20	0.11	1.16
65	RP-5125-2-4	0.70	-0.72	0.56	-0.18	-0.26	1.88
66	CR-Dhan-40	0.19	-2.07	1.82	-1.85	1.21	-0.18
67	R1882-306-4-243-1	-0.26	-0.06	0.71	1.34	1.54	-0.33
68	R1986-296-2-867	-0.72	-0.27	0.91	0.72	1.72	0.35
69	R1973-206-2-86-1	-1.33	0.57	0.08	-0.12	1.75	-0.30
70	CG zinc rice-1	-0.84	-0.23	-1.14	0.66	0.47	0.32
71	CG zinc rice-2	-0.78	-0.66	0.98	-1.07	2.36	-0.32
72	R1779-321-1-112-1	-0.35	-0.39	0.31	-0.48	0.93	-0.26
73	R1882-301-1-234-1	-0.66	-1.31	0.45	0.24	0.87	-0.86
74	R2221-391-1-248-1	-0.61	-1.66	-0.30	-1.11	-0.58	-0.22
75	R1882-310-4-257-1	-1.06	-0.71	0.49	0.92	1.63	-0.43
76	IR-36	-1.02	-0.84	0.75	0.65	0.98	-0.76
77	IR-64 (DRT)	-0.06	0.03	1.20	0.82	0.94	-0.75
78	Indira aerobic-1	-1.00	-1.44	0.70	-0.48	0.46	1.06
79	Shamleshwari (Check)	-0.15	-0.92	1.38	0.34	-0.46	0.23
80	MTU-1010 (Check)	-0.62	-0.05	1.17	0.99	0.32	-0.93

Top 10 principal component scores (PC scores) for all the accessions were estimated in six principal components and presented in Table 4.9. These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal component. High PC score for a particular accession in a particular component denotes high values for the variables in that particular accession. Perusal of results revealed that the “Pokali” had highest PC score followed by Gutla 2614, Gurmetta 2697, Balsi ralu kanb-694,

Fent 2679, Du-95-0137-1, Birsa gova, Banso bnisa B-1021, Duma-bada-25-55 and Usai buta-2408 in PCI exhibited high seedling length on 30 DAS, seedling length on 20 DAS, plant height and vigor index. In PC2, R1182-31-2-151 had the highest score followed by Bangoli-3, Asha, R1519-769-2-1442-1, R1238-19361, Vandana, Brown gova Danwas-2511, IR-7866-BIO-BBB-SBI, R1013-2307-1-4 and Poornima exhibited paddy length, paddy L/B ratio, spikelets fertility percent filled spikelet. The highest PC3 score of Pokali followed by CR-Dhan-40, IR 08 L 152, Salim paket. Poornima, Danteshwari, Shamleshwari (Check), IR-64 (Drought), MTU-1010 (Check) and Krishna hansa exhibited grain yield, filled spikelets and germination per cent. In the highest PC4 were R1448-578-2 followed by Gulta 2614, R1882-306-4-243-1, R1551-2169-1, Banso bnisa B-1021, Shyamla, R1519-769-2-1442-1, Fent 2679, Tripti and MTU-1010 (Check) which had spikelet fertility per cent and 1000 grain weight. In PC5, CG zinc rice-2 had highest PC score followed by Lal mati, Jhitpiti, Aganni, R1973-206-2-86-1, R1986-296-2-867, Gulta 2614, R1882-310-4-257-1, R1882-306-4-243-1 and CR-Dhan-40 indicated that they have high value number of leaves on 20 DAS and panicle length. Aditya recored highest PC score followed by Aganni, Krishna hansa, RP-5125-2-4, R1723-1411-1-3551, Lallu-14, Duma-bada-25-55, R1448-578-2, IR-38 and IR 08 L 152 in PC6 for high panicle per meter square and number of leaves on 30 DAS. On the basis of top 10 PC scores in each principal component, accessions are selected and presented as a summarised form in Table 4.9.

Thus, it is cleared that the principal component analysis highlights the characters with maximum variability. So, intensive selection procedures can be designed to bring about rapid improvement of ESV, yield and there attributing traits. PCA also helps in ranking of genotypes based on PC scores in the corresponding component. From the above result, it is cleared that Pokali is the best accession for both early seedling vigor and yield attributing traits followed by R1182-31-2-151, Bangoli-3, CG zinc rice-2, Aditya, Gulta 2614, Aganni, Asha, Lal mati and Gurmetta 2697. These identified accessions may be used as a donor to improve the ESV and yield traits in varietal development programme for direct seeded rice under rainfed condition.

Table 4.9: List of selected accession in each principal component based on top 10 PC score:

PC 1 with score	PC 2 with score	PC 3 with score	PC 4 with score	PC 5 with score	PC 6 with score
Pokali (3.55)	R1182-31-2-151 (3.01)	Pokali (2.63)	R1448-578-2 (1.51)	CG zink rice-2 (2.36)	Aditya (2.42)
Gulta 2614 (2.41)	Bangoli-3 (3.00)	CR-Dhan-40 (1.82)	Gulta 2614 (1.39)	Lal mati (2.19)	Aganni(2.34)
Gurmetta 2697 (2.03)	Asha (2.24)	IR 08 L 152 (1.63)	R1882-306-4-243-1(1.34)	Jhitpiti (2.09)	Krishna hansa (2.10)
Balsi ralu kanb-694 (2.03)	R1519-769-2-1442-1 (1.88)	Salim paket(1.60)	R1551-2169-1 (1.25)	Aganni (1.80)	RP-5125-2-4 (1.88)
Fent 2679 (1.83)	R1238-19361 (1.67)	Poornima (1.54)	Banso bnisa B-1021 (1.19)	R1973-206-2-86-1 (1.75)	R1723-1411-1-3551 (1.70)
DU-95-0-137-1 (1.68)	Vandana (1.59)	Danteshwari (1.44)	Shyamla (1.15)	R1986-296-2-867 (1.72)	Lallu-14 (1.59)
Birsa gova (1.55)	Birsa gova (1.32)	Shamleshwari (Check) (1.38)	R1519-769-2-1442-1 (1.07)	Gulta 2614 (1.65)	Duma-bada-25-55 (1.57)
Banso bnisa B-1021 (1.46)	IR-7866-BIO-BBB-SBI (1.18)	IR-64 (Dft) (1.20)	Fent 2679 (1.03)	R1882-310-4-257-1 (1.63)	R1448-578-2 (1.36)
Duma-bada-25-55 (1.39)	R1013-2307-1-4 (1.17)	MTU-1010 (Check) (1.17)	Tripti (1.00)	R1882-306-4-243-1 (1.54)	IR-38 (1.34)
Usai buta-2408 (1.37)	Poornima (1.04)	Krishna hansa (1.15)	MTU-1010 (Check) (0.99)	CR-Dhan-40 (1.21)	IR 08 L 152 (1.16)

4.3.2 Cluster analysis

The eighty accessions of rice were grouped into seven clusters (Table 4.10). The accessions were not evenly distributed among the clusters. Cluster IV and cluster VII constituted 15 accessions, forming the largest cluster followed by cluster II (14 accessions), cluster V (13 accessions), cluster III (11 accessions), clusters I (9 accessions) and cluster VI (3 accessions). The pattern of group constellation proved the existence of a significant amount of variability.

The inter cluster and intra cluster distances among seven clusters were computed and have been given in Table 4.11. The intra cluster distance ranged from 17487 (cluster VII) to 1689533 (cluster VI). The inter cluster distance was maximum between cluster VI (9381068) and minimum inter cluster distance was observed between cluster VII (83499). To realize much variability and high heterotic effect, parents should be selected from two clusters having wider inter cluster distance.

The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4.12). Cluster VI exhibited highest mean value for number of leaves on 10 DAS (2.53), seedling length on 10 DAS (13.5), seedling dry weight on 10 DAS (0.02), seedling length on 20 DAS (4.87), seedling dry weight (0.1), number of leaves on 30 DAS (4.87), seedling length on 30 DAS (61.42), seedling dry weight on 10 DAS (0.3), vigor index I (5276.6), vigor index II (26.38), panicle length (24.38), flag leaf length (39.1), flag leaf width (16.5), 1000 grain weight (29.98), filled spikelet (125.5) and spikelet fertility percent (87.49), while cluster IV contained genotypes with the highest mean value for seedling dry weight of 10 DAS (0.02), number of leaves on 20 DAS (4.31), panicle per meter square (224.63), and cluster VII highest mean value for seedling dry weight on 10 DAS (0.02) and paddy length (9.04). Unfilled spikelet (17.82) showed lesser mean value than other six clusters. Cluster I had highest mean value for most important traits: days to 50 per cent flowering and grain yield per meter square and had a shorter plant height (92.67). Cluster II had highest mean value for the seedling dry weight for 10 DAS (0.02), and cluster III had germination per cent (86%).

The selection and choice of parents mainly depend upon the contribution of characters towards divergence. It is well known that crosses between divergent parents usually produce a greater heterotic effect than between closely related ones. Considering the importance of genetic distance and relative contribution of characters towards total divergence, the present study indicated that genotype selected from cluster VI (Birsa gova, Gulta 2614 and Pokali) number of leaves on 10 DAS, seedling length on 10 DAS, seedling dry weight on 10 DAS, seedling length on 20 DAS, seedling dry weight, number of leaves on 30 DAS, seedling length on 30 DAS, seedling dry weight on 10 DAS, vigor indexI, vigor indexII, panicle length, plant height, flag leaf length, flag leaf width, 1000 grain weight, filled spikelet and spikelet fertility per cent, and from cluster IV (Aganni, Jhitpiti, Bangoli-3, Usai buta-2408, Karhani-No-9, Balsi balu kanb-694, Banso bnisa B-1021, Salim paket, Fent 2679, Gurmetta 2697, ARC-15831, CR-Dhan-40, RP-5125-2-4, IR-64 (Drought) and MTU-1010 Check) for seedling dry weight of 10 DAS, number of leaves on 20 DAS, panicle per meter square. In cluster I (Aditya, Bala, IR-38, IR-7866-BIO-BBB-SBI, R1004-2552-1-1, R1723-1411-1-3551, CG zinc rice-2, IR-64, CG zinc rice-1 and Shyamla) had lowest mean value for plant height and highest mean value for days to 50 per cent flowering and grain yield per meter square could be used in crossing programmes to achieve desired segregants.

Table 4.10: Distribution of rice accessions among seven clusters:

Cluster No.	Number of accessions	Name of accession
I	9	Aditya, Bala, IR-38, IR-7866-BIO-BBB-SBI, R1004-2552-1-1, R1723-1411-1-3551, CG zinc rice-2, IR-64, CG zink rice-1 and Shyamla
II	14	Kalinga-3, Lallu-14, Chom phool, Lal mati, Danwar 2129, R1013-2307-1-4, R971-25-2-1, CR-314-5-10, Salim paket, R1122-167-2-1571, R1546-1382-1-40-1, C101 LAC, R1882-306-4-243-1 and CG zinc rice-2
III	11	Duma-bada-25-55, R1558-1419-2-1442-1, Banisar No-31, R1551-2169-1, Asam chidi, Danteshwari, Poornima , IR 08 L 152, R1779 321-1-112-1, Shamleshwari (Check) and R1882-301-1-234-1
IV	15	Aganni, Jhitpiti, Bangoli-3, Usai buta-2408, Karhani-No-9, Balsi balu kanb-694, Banso bnisa B-1021, Salim paket, Fent 2679, Gurmetta 2697, ARC-15831, CR-Dhan-40, RP-5125-2-4, IR-64 (DRT) and MTU-1010 (Check)
V	13	R1558-2423-1-1445-1, Poorva, T-10, Asha , Nipon bare, R1519-769-2-1442-1, CR-306-37-13, R1238-19361, Vandana , Krishna hansa, R2221-391-1-248-1, R1882-310-4-257-1 and Indira aerobic-1
VI	3	Birsa gova, Gulta 2614 and Pokali
VII	15	Mr 1523, Surekha , Tripti, Sawas-D-137-1, Danwas 2511, Kaweri, Shwnong-89366, R1448-578-2, R1152-2-64-1, R1182-31-2-151, MTU-15, Mamhar, R1986-296-2-867, IR-36 and R1973-206-2-86-1

Table 4.11: Estimates of intra (diagonal and bold) and inter cluster distances among seven clusters:

Cluster	I	II	III	IV	V	VI	VII
I	78987	1783560	1139972	3215884	287246	9381068	671699
II		33990	100031	260330	718368	3294246	298462
III			23983	576170	338216	4252936	83499
IV				74133	1705854	2015651	1006255
V					30770	6710371	116024
VI						1689533	5285234
VII							17487

Table 4.12: Cluster mean values of seven clusters for different early seedling vigor, yield and its attributing characters of rice:

Traits \Cluster	I	II	III	IV	V	VI	VII
NL10D	2.3	2.32	2.2	2.39	2.26	2.53	2.28
SL10(cm)	11.74	11.53	11.4	12.4	11.22	13.82	11.93
SDW 10 (gm)	0.01	0.02	0.01	0.02	0.01	0.02	0.02
NL20D	3.91	4.16	4.18	4.31	0.01	4.27	4.12
SL20 (cm)	18.35	21.09	19.2	23.65	18.47	27.83	18.97
SDW 20 (gm)	0.06	0.06	0.07	0.08	0.06	0.1	0.07
NL30D	4.64	4.68	4.57	4.66	4.67	4.87	4.59
SL30 (cm)	31.71	43.99	39.26	49.08	35.57	61.42	38.58
SDW 30D	0.16	0.25	0.23	0.26	0.18	0.3	0.25
GP (%)	73	83.43	86	83.87	79.38	85.5	81.53

VI 1	2314.74	3630.72	3360.32	4088	2801.3	5276.6	3106.93
VI 2	11.83	20.32	19.26	21.55	14.36	26.38	19.83
D50PF	82.39	77.96	81.55	80.73	77.81	79.33	79.73
PL (cm)	22.91	22.94	22.74	23.69	22.36	24.38	23.57
PH (cm)	92.67	101.8	98.66	117.21	95.37	135.06	99.29
FFL (cm)	30.18	33.44	30.34	38.04	28.42	39.1	31.83
FFW (mm)	14.78	14.61	15.28	14.71	15.04	16.5	14.36
PPMS	224.17	206.75	207.23	224.63	201.46	183.5	204.53
1000 GW	24.87	23.48	24.12	26.16	23.23	29.98	24.79
FS	109.78	105.82	114.59	103.93	102.35	125.5	101.87
UFS	23.44	25.93	18.32	18.3	23.46	18	17.8
SF (%)	82.92	80.97	86.23	83.81	81.11	87.49	84.51
PL (mm)	8.76	8.58	8.36	8.85	8.83	9.03	9.04
PB (mm)	2.48	2.46	2.55	2.68	2.45	3.34	2.55
P L/B R	3.57	3.53	3.31	3.33	3.68	2.72	3.62
GY (g)	251.06	242	243.91	229.73	228	180.83	238.87

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

4.4 Association analysis using SSR markers:

4.4.1 SSR marker analysis

Genetic associations among 80 accessions were analyzed, based on phenotypic variation of yield traits with the help of 22 SSR markers covering ten chromosomes. A total of 151 alleles were amplified and the number of alleles per locus generated by each marker ranged from 3 to 15 alleles with an average number of 6.86 alleles per locus. Maximum number of alleles (15) was amplified by marker RM 336 and RM 7075 (Table 4.13 and Fig 4.2).

4.4.2 Polymorphism Information Content of SSR markers:

The PIC value across markers ranged from 0.2059 to 0.84 with an average of 0.636733. Maximum PIC value was observed on chromosome 1 (RM 7075 = 0.84) followed by RM 252 of chromosome 5 (0.825469) (Table 4.12). (Fig: 4.2).

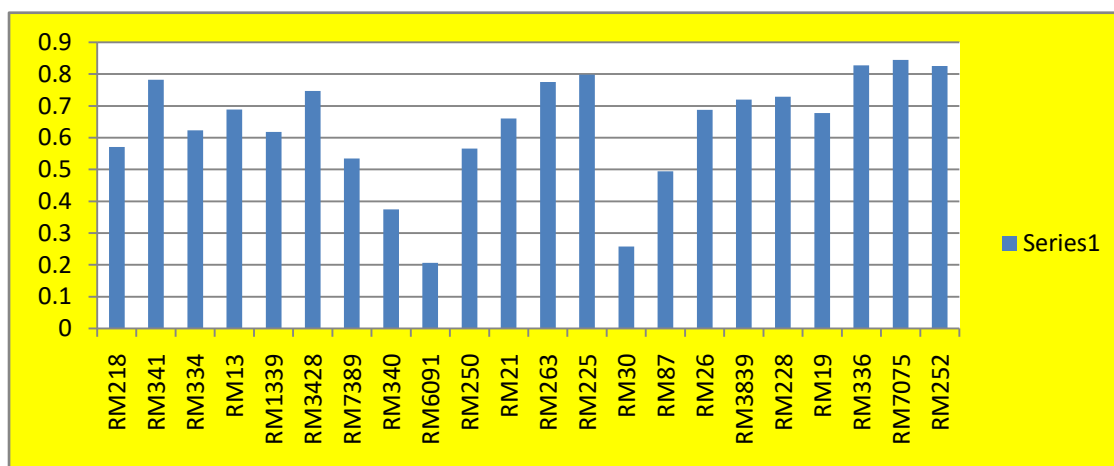


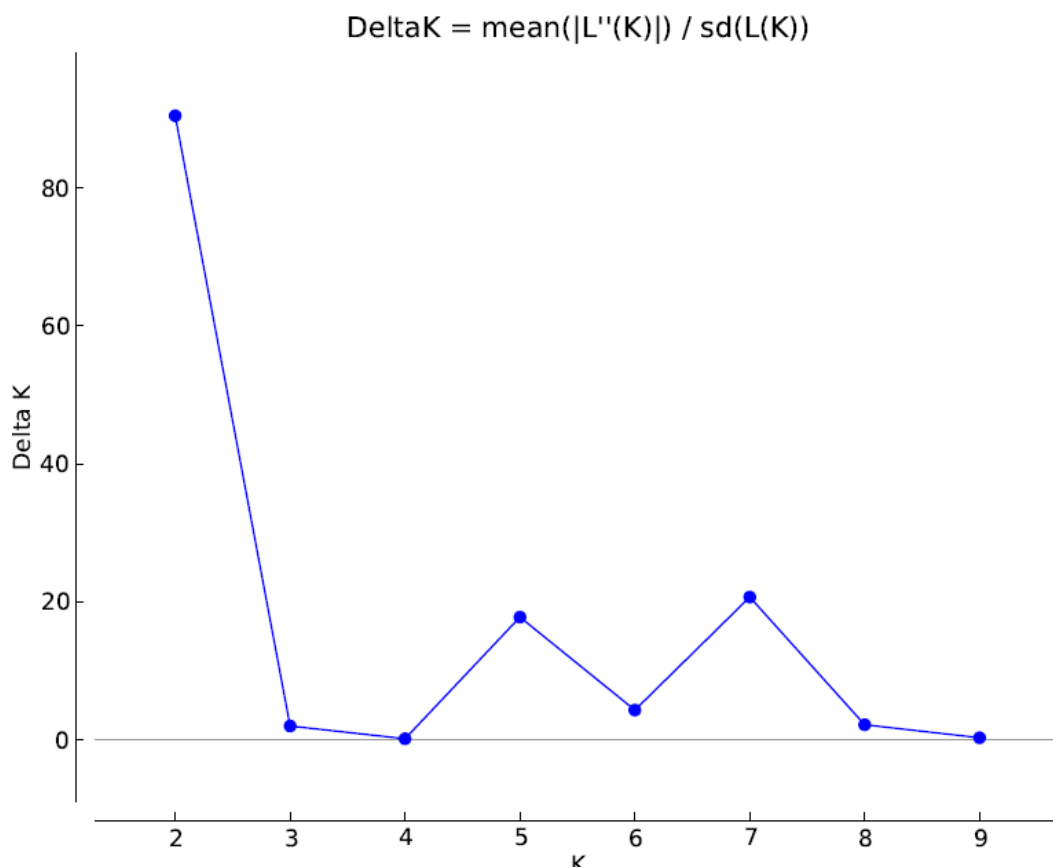
Fig 4.2: Graphical representation of PIC value of 22 polymorphic SSR markers

4.4.3 STRUCTURE and TASSEL analysis

4.4.3.1 Population Structure analysis:

The Bayesian model-based STRUCTURE v2.3.4 program was used to infer population structure of rice genotypes. The 80 lines were separated into two sub groups (Fig 4.5) based on the result of Structure Harvester, as delta K kinship was highest at K=2. With population inferred ancestry (Q) = 0.80, 35 lines were assigned to subgroup POP1, rest 39 lines were assigned to subgroup POP2 and six

genotypes/lines namely, Bala (3), R971-25-2-1 (41), R1152-2-64-1 (42), R1004-2552-1-1 (43), CR-306-37-13 (44) and R2221-391-1248-1 (74) were assigned to admixture (AD) which has less than <0.80 inferred ancestry (Fig 4.5). Courtois *et. al.* (2012) have effectively detected two subgroups in their study population and assigned rice varieties into two groups with 6 admixture lines. Our results are also in conformity with the findings of Borba (2010) signifying that using structure analysis, the accessions were sub divided into two panels. Likewise, the association of yield traits with SSR markers was undertaken with MLM model, with markers and sub inhabitants as fixed factors, and kinship matrix as random factor.



Optimum number of K=2

Figure 4.3: Evaluation of K and population structure. Changes in ΔK value with the number of subpopulations

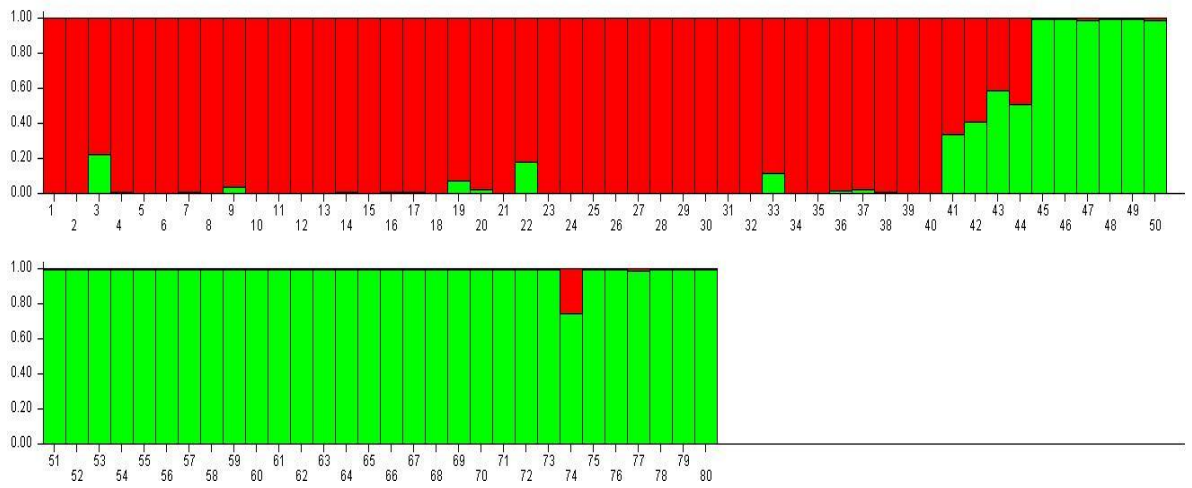


Figure 4.4: Bar plot viewing the population structure of 80 rice germplasm accessions based on SSR markers at K=2

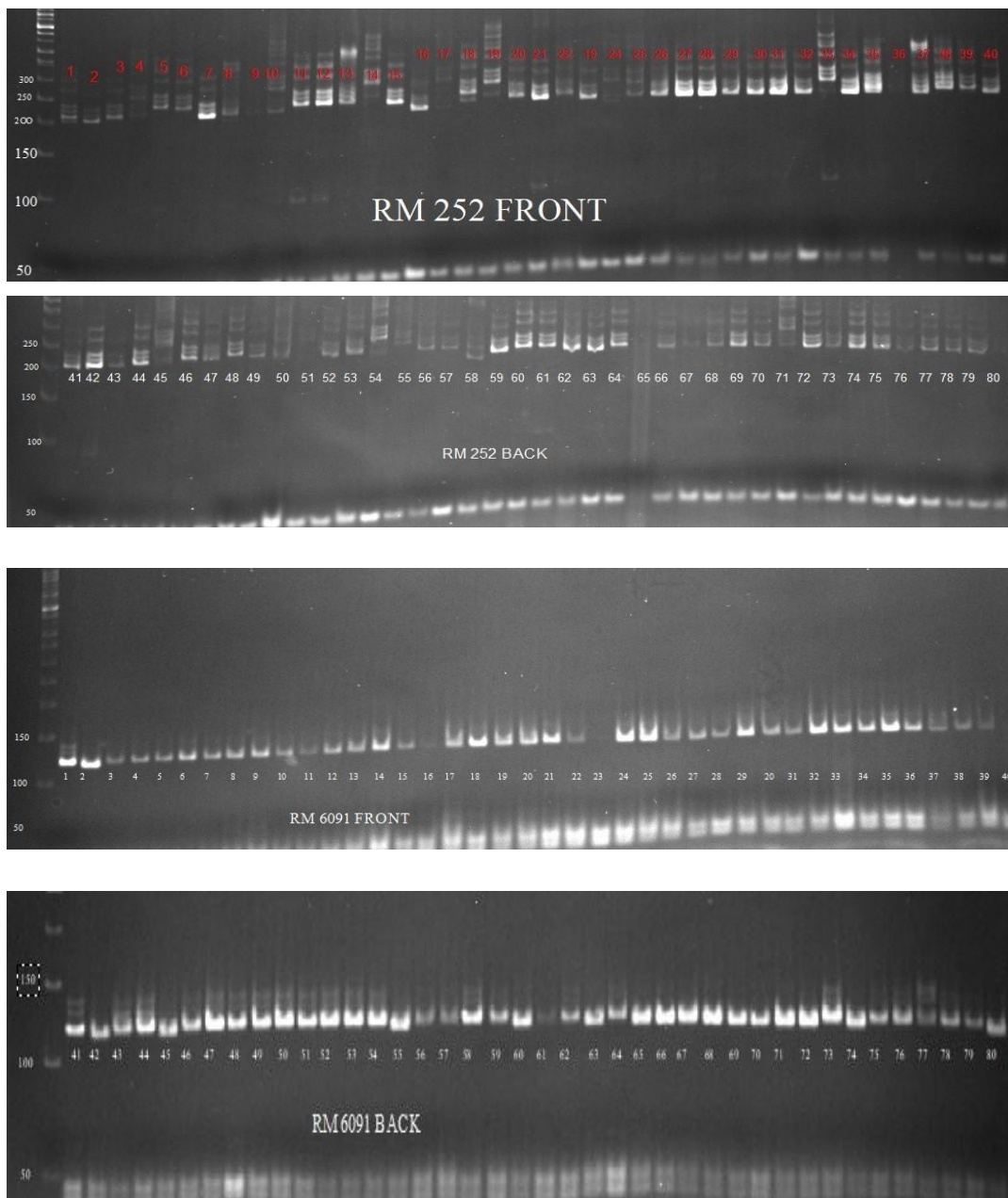
Table 4.13: List of 22 microsatellite markers with their chromosome locations, number of alleles, allele size and PIC value found among 80 rice accessions

SN	Name of markers	Forward sequence	Reverse sequence	C#	Amplicon Size (bp)	PIC value	Position (cM)	Alleles
1	RM218	TGGTCAAACCAAGGTCCTTC	GACATACATTCTACCCCGG	3	120-140	0.570313	67	3
2	RM252	TTCGCTGACGTGATAGGTTG	ATGACTTGATCCCGAGAACG	5	130-350	0.825469	99	11
3	RM334	GTTCAGTGTTCAGTGCCACC	GACTTTGATCTTTGGTGGACG	5	160-193	0.623438	141.8	5
4	RM341	CAAGAAACCTCAATCCGAGC	CTCCTCCCGATCCCAATC	2	140-185	0.7825	82.7	5
5	RM19	CAAAAACAGAGCAGATGAC	CTCAAGATGGACGCCAAGA	12	210-320	0.677188	20.9	11
6	RM263	CCCAGGCTAGCTCATGAACC	GCTACGTTTGAGCTACCACG	2	165-215	0.775625	127.5	7
7	RM3839	AATGGGACCAGAAAGCACAC	AAAAAGAGCATGGGGGCTAC	4	185-340	0.719376	117	8
8	RM340	GGTAAATGGACAATCCTATGGC	GACAAATATAAGGGCAGTGTGC	6	160-180	0.374844	133.5	3
9	RM21	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG	11	130-165	0.660313	85.7	6
10	RM250	GGTCAAACCAAGCTGATCA	GATGAAGGCCCTCCACGCAG	2	145-153	0.566094	170.1	3
11	RM30	GGTTAGGCATCGTCACGG	TCACCTCACCACACGACACG	6	95-158	0.2575	125.4	7
12	RM87	CCTCTCCGATACACCGTATG	GCGAAGGTACGAAAGGAAAG	5	125-190	0.494063	129.2	7
13	RM1339	ATCAAAGCATGTAAACCAGC	CGTAAGATCTCCCTACCACC	1	126-144	0.618125	147.5	5
14	RM228	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC	10	108-220	0.728437	87.6	8
15	RM225	TGCCCATATGGTCTGGATG	GAAAGTGGATCAGGAAGGC	6	105-140	0.798281	26.2	7
16	RM13	TCCAACATGGCAAGAGAGAG	GGTGGCATTTCGATTCCAG	5	123-155	0.68875	28.6	5
17	RM26	GAGTCGACGAGCGGCAGA	CTGCGAGCGACGGTAACA	5	90-425	0.6875	118.8	7
18	RM3428	ATTCATGCTTCCTTTCAGTG	GATTACTGGTTTGCCATTTG	11	145-165	0.746875	56.2	5
19	RM336	CTTACAGAGAAACGGCATCG	GCTGGTTTGTTCAGGTTTCG	7	125-205	0.827656	61	15
20	RM6091	GCTGTCCTGTCCTTGAATCC	TGGTAGGCTGGTGACATGC	11	115-125	0.205938	56.2	3
21	RM7075	TATGGACTGGAGCAAACCTC	GGCACAGCACCAATGTCTC	1	110-200	0.844844	74.2	15
22	RM7389	AGCGACGGATGCATGATC	TTGAGCCGGAGGTAGTCTTG	3	100-200	0.535	178.8	5

4.4.3.2 Marker-trait association:

Association analysis between SSR markers for 26 early seedling vigor, yield and its attributing traits was carried out using MLM model over the 80 rice germplasm lines.

The marker trait associations based on mixed linear model (MLM) are presented in Table 4.14. The results indicate that 18 markers were found to be associated with 23 traits.



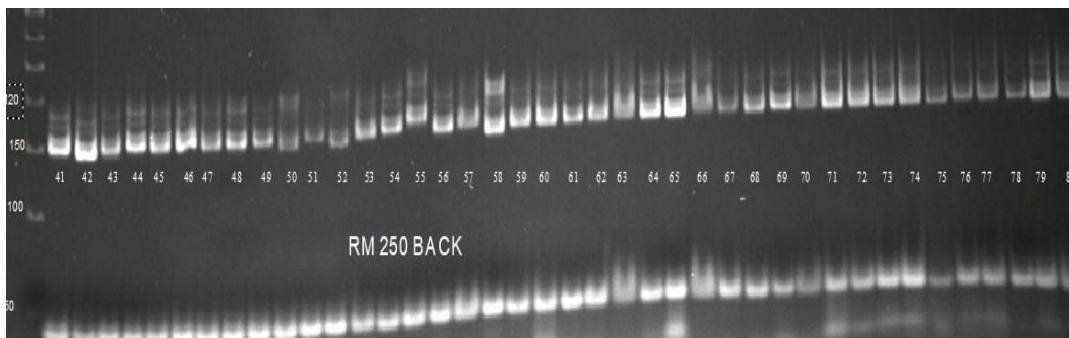
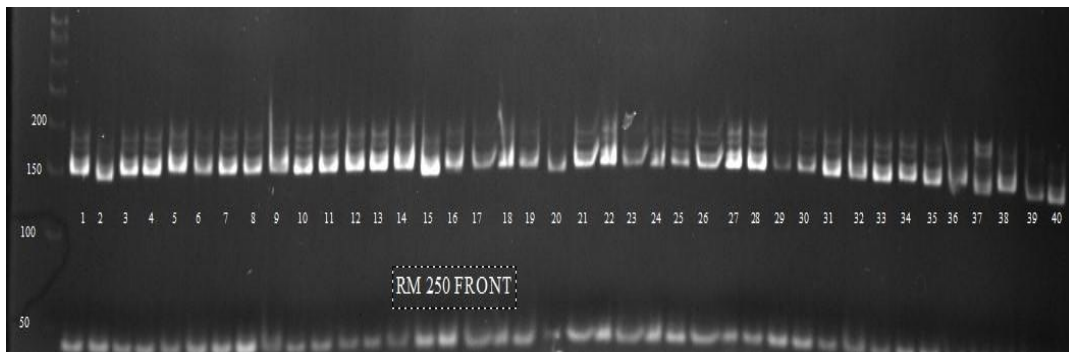
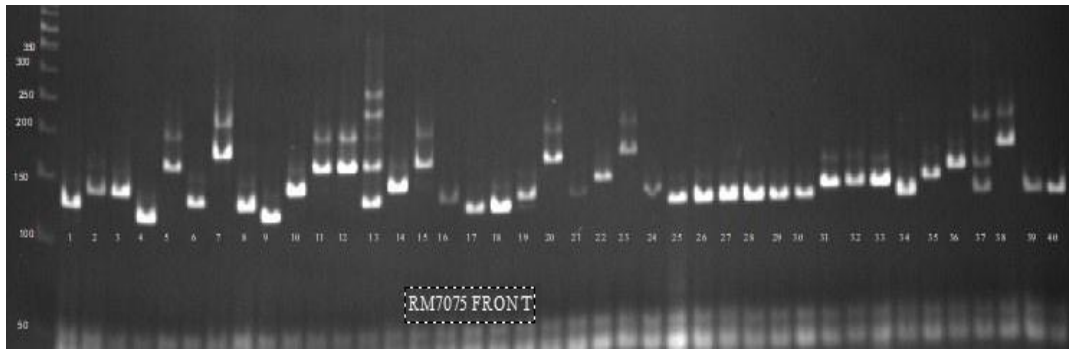


Fig4.5: PCR amplification of 80 rice germplasm accessions with SSR primer RM 252 (C#5), RM 6091 (C#3), RM 7075 (C#1), RM 250, RM (C#2).

For number of leaves in 10 days, RM 13 (C# 5) was found to have tight association.

RM3438 (C#11), RM13 (C#5), RM225 (C#6), RM263 (C#2) and RM252 (C#5) showed a tight association with the seedling length in 10 days. Seedling dry weight in 10 days had shown an association with RM 3428 (C#11) and RM 225 (C#6). Number of leaves in 20 days exhibited tight association with RM 252 (C#5), RM26 (C#5), RM3428 (C#11), RM250 (C#2), RM218 (C#3) and RM87 (C#5). RM 252 (C#5), RM19 (C#12), RM225 (C#6), RM 263 (C#2) and RM 13 (C#5) showed tight linked with seedling length in 20 days, and seedling dry weight in 30 days showed lightly linked with RM 7075 (C#10), RM 225 (C#6) and RM 263 (C#2).

For number of leaves in 30 days RM 26 (C#5), RM 19 (C#12) and RM 7075 (C#1) tightly linked. RM 252 (C#5), RM 13 (C#5), RM 21 (C#11) and RM 225 (C#6) showed lightly linked with seedling length in 30 days. For seedling dry weight in 30 days only RM 252 (C#5) showed lightly associated.

For germination per cent was lightly linked with RM 341 (C#2) and RM 1339 (C#1), also days to 50% flowering showed lightly linked with RM 341 (C#2), RM 340 (C#6), RM 7389 (C#3), RM 263 (C#2) and RM 336 (C#7).

For panicle length showed lightly linked with RM 252 (C#5), RM26 (C#5), M 336 (C#7), RM 19 (C#12) ADN RM 250, and flag leaf length showed lightly linked with RM 13 (C#5), RM225 (C#5), RM 218 (C#3), RM 6091 (C#11), RM 30 (C#6), RM 334 (C#5), RM 87 (C#5) and RM 263 (C#2), also flag leaf width showed lightly linked with RM 252 (C#5), RM225 (C#6), RM 218 (C#3) and RM 7075 (C#1). Likewise, plant height had lightly linked with RM 225 (C#6) and RM 252 (C#5).

For panicle per meter square RM 1339 (C#1) had showed lightly linked, and 1000 grain weight showed tightly linked with RM 336 (C#7), RM 334 (C#5), RM 3428 (C#11), RM 225 (C#6). RM 218 (C#3), for filled spikelet was tightly associated with RM 3839 (C#4), and for unfilled spikelet had showed lightly linked with RM 7075 (C#1), RM 228 (C#10) and RM 19 (C#12). However, RM 30 (C#6), RM 26 (C#5), RM 252 (C#5) and RM 7075 also possessed tight linkage with spikelet fertility per cent.

For paddy breadth RM 218 (C#3), RM 225 (C#6) RM 7075 (C#1) and RM 336 (C#7), and paddy L/B ratio also showed tightly associated with RM 340 (C#6).

Apart from this, for grain yield RM 26 (C#5), RM 13 (C#5), RM 225 (C#6), RM 263 (C#2), RM 218 (C#3), RM 6091 (C#11), RM 87 (C#5), RM 341 (C#2) and RM 3428 (C#11) exhibited tight association.

The marker trait associations based on mixed linear model (MLM) are obtainable in Table 4.13. The results indicated that 18 markers were found to be associated with 23 traits.

Agrama *et al.*, 2006 studies that to make advance in rice breeding it is essential to understand the relatedness and ancestry of introduced rice accessions and identify SSR markers associated with agronomical significant phenotypic traits, for example yield. Taking MLM model into reflection RM 26 (C#5), RM 13 (C#5), RM 225 (C#6), RM 263 (C#2), RM 218 (C#3), RM 6091 (C#11), RM 87 (C#5), RM 341 (C#2) and RM 3428 (C#11) showed tight linkage with grain yield.

The research provided imperative information for further mining these elite genes within rice landraces and using them for rice breeding. The result have revealed that structures association in one of the sufficient options to recognize major effect QTLs for early seedling vigor and yield traits in rice (Swamy *et al.*, 2017). These marker-trait associations could be further validated and used in marker assisted breeding for improving particular trait in any rice variety and can be further confirmed in new set of population. Genetic variability is the key determinant for any breeding program. The uneven reports on germplasm evaluation of landraces and genetics of early seedling vigor traits in rice confident us to take up this study. Conventional native landraces those grown-up under rainfed are competitive weeds. By beginning of modern high yielding with low early seedling vigor semi dwarf varieties, weed competitive landraces are nearly extinct and disappearing in farmer's field (Annandan *et. al.* 2016).

Breeding for improved seedling vigour has been earlier attempted by several workers, but improvement has been slow due to the lack of suitable donors, limited knowledge on the genetics of seedling vigour, the involvement of several

compound mechanisms, and complex genetic backgrounds and methods used for measurement (Jiang *et. al.* 2004). Seedling vigour is a major breeding target in rice and other crops (Redona and Mackill 1996; Trachsel *et. al.* 2010) under direct-seeded scheme, because it is intimately linked with crop growth and yield. Seshu and Krishnasamy (1987) reported the likelihood of incorporate ESV traits in the genetic background of high-yielding varieties through the conservative breeding and marker-assisted selection (MAS) approach.

Table 4.14: Significant marker-trait associations based on MLM model (P>0.05) during Kharif 2019

Trait	Locus	Chr	p_Marker	Rsq_Marker	Trait	Locus	Chr	p_Marker	Rsq_Marker
NL10D	RM 13	5	0.0266	0.1856		RM 13	5	0.0013	0.2747
	RM 3428	11	0.007	0.2164		RM 225	5	0.0047	0.2226
	RM 13	5	0.0072	0.216		RM 218	3	0.0074	0.1208
SL10D	RM 225	6	0.0101	0.1894	FLL	RM 6091	11	0.0091	0.1159
	RM 263	2	0.0185	0.1736		RM 30	6	0.0264	0.1937
	RM 252	5	0.0193	0.3327		RM 334	5	0.0323	0.1307
SDW10D	RM 3428	11	0.0121	0.2019		RM 87	5	0.0338	0.1492
	RM 225	6	0.0138	0.1809		RM 263	2	0.0434	0.1604
	RM 252	5	2.31E-04	0.4441		RM 252	5	0.0014	0.4272
	RM 26	5	2.83E-04	0.2923	FLW	RM 225	6	0.0188	0.1829
RM 250	2	0.0016	0.1716	RM 218		3	0.0228	0.0933	
NL20D	RM 3428	11	0.0034	0.2358		RM 7075	1	0.0393	0.4223
	RM 218	3	0.0154	0.0975	PPMS	RM 1339	1	0.058	0.0925
	RM 87	5	0.016	0.1602		RM 336	7	0.0076	0.3253
	RM 252	5	0.0018	0.4071		RM 334	5	0.0129	0.1516
SL20D	RM 19	12	0.0079	0.4364	1000GW	RM 3428	11	0.0148	0.2059
	RM 225	6	0.0102	0.1947		RM 225	6	0.0245	0.1734
	RM 263	2	0.0136	0.187		RM 218	3	0.0278	0.0876
	RM 13	5	0.0294	0.1834	FS	RM 3839	4	0.0485	0.1866
SDW20D	RM 7075	1	0.0162	0.4281		RM 7389	3	0.0134	0.2272
	RM 225	6	0.0252	0.165	UFS	RM 228	10	0.0288	0.2856
	RM 263	2	0.0339	0.1568		RM 19	12	0.0361	0.3998
	RM 26	5	0.0037	0.249		RM 30	6	0.002	0.2645
NL30D	RM 19	12	0.0202	0.4289	SFP	RM 26	5	0.0204	0.2014
	RM 7075	1	0.042	0.426		RM 252	5	0.0328	0.337
	RM 252	5	0.0122	0.3335		RM 7075	1	0.0356	0.431
SL30D	RM 13	5	0.0142	0.1934		RM 218	3	0.0124	0.0952
	RM 21	11	0.016	0.1553	PB	RM 225	6	0.0137	0.1699
	RM 225	6	0.0292	0.1573		RM 7075	1	0.023	0.3911
SDW30D	RM 252	5	0.0179	0.3509		RM 336	7	0.0496	0.2383

GP	RM 341	2	0.0066	0.146	P L/B R	RM 340	6	0.0331	0.104
	RM 1339	1	0.0398	0.1059		RM 26	6	8.53E-04	0.2761
	RM 341	2	0.0018	0.1991		RM 13	5	0.0015	0.2624
	RM 340	6	0.0141	0.1274		RM 225	6	0.0053	0.2128
D50%F	RM 7389	3	0.0256	0.2071	GY/M2	RM 263	2	0.0071	0.2055
	RM 263	2	0.0259	0.1715		RM 218	3	0.0244	0.0899
	RM 336	7	0.0392	0.2736		RM 6091	11	0.0249	0.0895
	RM 252	5	3.87E-04	0.3734		RM 87	5	0.0284	0.1494
PL	RM 26	5	0.0017	0.2143	PH	RM 341	2	0.0291	0.1294
	RM 336	7	0.0113	0.2562		RM 3428	11	0.0436	0.1726
	RM 19	12	0.0315	0.3327		RM 225	6	0.0097	0.2028
	RM 250	2	0.0408	0.0825		RM 252	5	0.0183	0.3548

NL10D = Number of leaves in 10 days, SL10D = Seedling length in 10 days, SDW10D = Seedling dry weight in 10 days, NL20D = Number of leaf in 20 days, SL20D = Seedling length in 20 days, Seedling dry weight in 20 days, NL30D = Number of leaves in 30 days, SL30D = Seedling length in 30 days, SDW30D = Seedling dry weight in 30 days, GP = Germination percent, D50%F = Days to 50% Flowering, PL = Panicle length, PH = Plant height, FLL = Flag leaf length, FLL = Flag leaf width, PPMS = Panicle per meter square, 1000 GW, 1000 grain weight, FS = Filled spikelet, UFS = Unfilled spikelet, SFP = Spikelet fertility percent, PB= Paddy Breadth, P L/B R = Paddy L/B ratio and GY = Grain yield per meter square.

CHAPTER- V

SUMMARY AND CONCLUSION

5.1 Summary

The present study “**Studies on genetic divergence in yield and early seedling vigour for early duration genotypes under direct seeded condition of rice (*Oryza sativa* L.)**” was carried out by using eighty rice accessions including two checks *Viz.* Shamleshwari and MTU-1010. “The experiment was conducted at Research cum Instructional farm of IGKV, Raipur during *Kharif* 2019 in randomized complete block design (RCBD) with two replications.”

The mean sum of squares due to genotypes are found to be highly significant for all the characters except number of leaves on 10 DAS and number of leaves on 20 DAS only.

PCV was higher in magnitude than the GCV for all the characters. High PCV coupled with GCV was noted for number of unfilled grains (50.45), vigor index₂ (28.87) and seedling dry weight on 30 DAS (28.68).

Based on grain yield per meter square, genotypes namely, R1004-2552-1-1 (409) recorded high grain yield per meter square followed by Indira aerobic-1 (361), Asam chidi, Surekha (338), IR 08 L 152 (335), Pokali (332) and Aditya (328).

High heritability was found paddy length (97.84), paddy width (95.53), spikelet fertility percent (97.29), number of unfilled grain per panicle (97.19) and paddy L/B ratio (97.11). The genetic advance as percent of mean was found highest for the traits was number of unfilled grain (102), number of filled grain per panicle (54), vigor index_{II} (51), seedling dry weight on 30 DAS (51) and grain yield per meter square (48).

Grain yield showed positive and significant genotypic correlation with days to 50 percent flowering (0.22), panicle length (0.19) and number of filled spikelet (0.22), and significant phenotypic correlation showed with days to 50 percent flowering (0.18) and number of filled spikelet (0.19).

Path coefficient analysis was used to partition of observed correlation coefficients between grain yield meter square as dependent variable and its component traits into direct and indirect effects. The direct very high positive effect on yield per meter square was observed for" vigor index II (106.11) followed by seedling length on 30 DAS (102.85), germination percent (25.25), seedling dry weight on 10 DAS (7.76), number of filled spikelet (7.71), panicle per meter square (5.70), flag leaf width (4.01), seedling length on 10 DAS (3.77), paddy L/B ratio (3.08), paddy width (1.93), panicle length (2.66), flag leaf length (1.85), seedling dry weight on 20 DAS (1.38), The highest negative direct effect showed by vigor indexI (-111.82) followed by seedling dry weight on 30 DAS (-106.18), spikelet fertility percent (-15.68), number of unfilled spikelet (-9.16), number of leaf on 10 DAS (-6.13), paddy length (-2.88), days to 50 percent flowering (-2.22), plant height (-1.58), number of leaf on 30 DAS (-1.26). The improvement in grain yield will be efficient if the selection is based on vigor indexII (106.11), seedling length on 30 DAS (102.85) and germination per cent (25.15).

The PCs with higher Eigen values and variables which had high factor loading were considered as best representative of system attributes. Out of 26, only six principal components (PCs) exhibited more than 1.62 Eigen value, 6.24 % variance and showed about 64.055% cumulative variability among the traits studied. So, these 6 PCs were given due importance for further explanation. The PC1 showed 24.511% while, PC2, PC3, PC4, PC5 and PC6 exhibited 9.68%, 9.32%, 7.51%, 6.79% and 6.24% variability respectively among the accessions for the traits under study. The first PC was mostly related with seedling length on 30 days (0.34), seedling length on 20 days (0.32), plant height (0.31), vigor index I (0.30), seedling dry weight on 30 days (0.29 and vigor index II (.027).

PCA also help in ranking of genotypes on the basis of PC scores in corresponding component. From the above result, it is cleared that Pokali is the best accession for both early seedling vigor and yield attributing traits followed by R1182-31-2-151, Bangoli-3, CG zinc rice-2, Aditya, Gutla 2614, Aganni, Asha, Lal mati and Gurmetta 2697. These identified accessions may be used as donor to

improve the yield and early seedling vigor in varietal development programme for rainfed conditions.

Cluster analysis revealed that first cluster composited 9 genotypes, Cluster II included 14 genotypes and cluster III had 11 genotypes. Cluster IV had 15 genotype which was highest genotype, 13 genotype were found in cluster V, and cluster VI were found 3 genotype which was lowest cluster group, cluster VII included 15 genotype which was highest cluster group. Highest intra-cluster distance (1689533) was found in cluster VI, were highest inter cluster found in cluster VI followed by cluster VII.

The 80 lines were divided into two sub groups based on the result of Structure Harvester, as delta K kinship was highest at K=2. With population inferred ancestry (Q) = 0.80, 35 lines were assigned to subgroup POP1, rest 30 lines were assigned to subgroup POP2 and six genotypes/lines namely, Bala (3), R971-25-2-1 (41), R1152-2-64-1 (42), R1004-2552-1-1 (43), CR-306-37-13 (44) and R2221-391-1248-1 (74) were assigned to admixture (AD) which has less than <0.80 inferred ancestry.

The marker trait associations based on mixed linear model indicated that 18 markers were found to be associated with 23 traits. For grain yield RM 26 (C#6), RM 13 (C#5), RM 225 (C#5), RM 263 (C#2), RM218 (C#3), RM 6091 (C#11), RM 87 (C#5), RM 341 (C#2) and RM 3428 (C#11) exhibited tight association.

For number of leaf on 10 days RM 13 (C#5), were tightly linked in seedling length on 10 DAS RM 3428 (C#11), RM 13 (C#5), RM 225 (C#6), RM 263 (C#2) and RM 252 (C#5). Number of leaf on 20 DAS tightly linked with RM 252 (C#5), RM 26 (C#5), RM 250 (C#2), RM 3438 (C#11), RM 218 (C#3) and RM 87 (C#5). RM 252(C#5), RM 26 (C#12), RM 250 (C#2), RM 3438 (C#11) and RM 218 (C#3), were RM 87 (C#5) tightly linked with seedling length on 20 DAS. Seedling dry weight on 20 DAS showed lightly linked with RM 252 (C#5), RM 7075 (C#1), RM 225 (C#6) and RM 263 (C#2), for number of leaf on 30 DAS were such marker showed tightly linked with RM 26 (C#5), RM 19 (C#12) and RM 225 (C#6), seedling length on 30 DAS were tightly linked with RM 252 (C#5), RM 13 (C#5), RM 21 (C#11), and RM 225 (C#6). Seedling dry weight on 30 DAS was

tightly linked with RM 252 (C#5), for germination percent RM 341 (C#2) and RM 1339 (C#1) marker were showed tightly linked. All those traits are early seedling vigor traits.

5.2 Conclusions

- The analysis of variance showed significant variation for all traits except number of leaves on 10 DAS and number of leaves on 20 DAS. Highest value of PCV coupled with GCV was recorded for number of unfilled grain, vigor indexII and number of leaf on 30 DAS.
- High heritability was found in paddy length (97.84%), paddy width (95.53%), spikelet fertility percent (97.29%), number of unfilled grain per panicle (97.19%) and paddy L/B ratio (97.11%).
- The genetic advance as percent of mean was found highest for the traits was number of unfilled grain (102), number of filled grain per panicle (54), vigor indexII (51), seedling dry weight on 30 DAS (51) and grain yield per meter square (48).
- R1004-2552-1-1 recorded high grain yield per meter square followed by Indira aerobic 1, Asham chidi, Surekha, IR 08 L 151, Pokali and Aditya.
- The correlation analysis revealed positive and significant genotypic association of grain yield per meter square with days to 50 per cent flowering, panicle length and number of filled spikelet, likewise days to 50 per cent flowering and number of filled spikelet showed positive and significant phenotypic association of grain yield per meter square.
- Magnitude of the direct effects on grain yield revealed the order of yield components as vigor indexII followed by seedling length on 30 DAS, germination percent, seedling dry weight on 10 DAS, number of filled spikelet panicle per meter square, flag leaf width, seedling length on 10 DAS, paddy L/B ratio, paddy width, panicle length, flag leaf length, seedling dry weight on 20 DAS.

- Principal component analysis highlights the characters *viz.* Seedling length on 30 DAS, Seedling length on 20 DAS, plant height and vigor index I, seedling dry weight on 30 days and vigour index II in first PCs with maximum variability. Thus, intensive selection procedure can be designed to bring about rapid improvement of yield and early seedling vigor traits.
- Top 10 PC scores in each principal component revealed that Pokali is the best accession for both early seedling vigor, yield and its attributing traits followed by R1182-31-2-151, Bangoli-3, CG zinc rice-2, Aditya, Gutla 2614, Aganni, Asha, Lal mati and Gurmetta 2697.
- Spark method of clustering grouped the accessions into seven clusters. The pattern of constellation proved the existence of significant amount of variability. Cluster IV and VII constituted of 15 accessions, forming the largest cluster. To realize much variability and high heterotic effect, cluster VI having a largest number of traits, Birsa gova, Gutla 2614 and Pokali comes under cluster VI.
- A total of 151 alleles were detected across the 80 accessions using 22 SSR markers. The number of alleles per locus ranged from 3 to 15 with an average of 6.86.
- For grain yield RM 26 (C#6), RM 13 (C#5), RM 225 (C#5), RM 263 (C#2), RM218 (C#3), RM 6091 (C#11), RM 87 (C#5), RM 341 (C#2) and RM 3428 (C#11) exhibited tight association.
- In mixed linear model some marker tightly associated with number of leaves on 10 days RM 13 (C#5), were tightly linked in seedling length on 10 DAS RM 3428 (C#11), RM 13 (C#5), RM 225 (C#6), RM 263 (C#2) and RM 252 (C#5). Number of leaves on 20 DAS tightly linked with RM 252 (C#5), RM 26 (C#5), RM 250 (C#2), RM 3438 (C#11), RM 218 (C#3) and RM 87 (C#5). RM 252 (C#5), RM 26 (C#12), RM 250 (C#2), RM 3438 (C#11) and RM 218 (C#3), were RM 87 (C#5) tightly linked with seedling length on 20

DAS. Seedling dry weight on 20 DAS showed lightly linked with RM 252 (C#5), RM 7075 (C#1), RM 225 (C#6) and RM 263 (C#2), for number of leaves on 30 DAS were such marker showed tightly linked with RM 26 (C#5), RM 19 (C#12) and RM 225 (C#6), seedling length on 30 DAS were tightly linked with RM 252 (C#5), RM 13 (C#5), RM 21 (C#11), and RM 225 (C#6). Seedling dry weight on 30 DAS was tightly linked with RM 252 (C#5), for germination percent RM 341 (C#2) and RM 1339 (C#1) marker were showed tightly linked.

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APPENDIX - A

Table: List of early seedling vigor (ESV) traits associated with polymorphic microsatellite markers of rice.

Serial number	Name of markers	Forward sequence	Reverse sequence	#C	Amplification size
1	RM218	TGGTCAAACCAAGGTCCTTC	GACATACATTCTACCCCCGG	3	148
2	RM252	TTCGCTGACGTGATAGGTTG	ATGACTTGATCCCGAGAACG	5	216
3	RM334	GTTCAAGTGTTCAGTGCCACC	GACTTTGATCTTTGGTGGACG	5	182
4	RM341	CAAGAAACCTCAATCCGAGC	CTCCTCCCGATCCCAATC	2	172
5	RM19	CAAAAACAGAGCAGATGAC	CTCAAGATGGACGCCAAGA	12	226
6	RM263	CCCAGGCTAGCTCATGAACC	GCTACGTTTGAGCTACCACG	2	199
7	RM3839	AATGGGACCAGAAAGCACAC	AAAAAGAGCATGGGGGCTAC	4	218
8	RM340	GGTAAATGGACAATCCTATGGC	GACAAATATAAGGGCAGTGTGC	6	163
9	RM21	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG	11	157
10	RM250	GGTTCAAACCAAGCTGATCA	GATGAAGGCCTTCCACGCAG	2	153
11	RM30	GGTTAGGCATCGTCACGG	TCACCTACCACACGACACG	6	105
12	RM87	CCTCTCCGATACACCGTATG	GCGAAGGTACGAAAGGAAAG	5	151
13	RM1339	ATCAAAGCATGTAAACCAGC	CGTAAGATCTCCCTACCACC	1	144
14	RM228	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC	10	154
15	RM225	TGCCCATATGGTCTGGATG	GAAAAGTGGATCAGGAAGGC	6	140
16	RM13	TCCAACATGGCAAGAGAGAG	GGTGGCATTCCGATTCCAG	5	141
17	RM26	GAGTCGACGAGCGGCAGA	CTGCGAGCGACGGTAACA	5	112
18	RM3428	ATTCATGCTTCCTTTCAGTG	GATTACTGGTTTGCCATTTG	11	156
19	RM336	CTTACAGAGAAACGGCATCG	GCTGGTTTGTTCAGGTTTCG	7	154
20	RM6091	GCTGTCTGTCTTGAATCC	TGGTAGGCTGGTGACATGC	11	126
21	RM7075	TATGGACTGGAGCAAACCTC	GGCACAGCACCAATGTCTC	1	155
22	RM7389	AGCGACGGATGCATGATC	TTGAGCCGGAGGTAGTCTTG	3	111

APPENDIX - B

Table: Weekly Meteorological Data during Crop Growth Period of *Kharif* - 2019

Date	Max. Temp. (°C)	Min. Temp. (°C)	Rain-fall (mm)	Rainy days	Relative Humidity (%)		Wind Velocity (Kmph)	Evapo-ration (mm)	Sun Shine (hours)
					I	II			
Jun 04-10	42.7	28.6	5.2	1	59	27	5.2	67.6	6.2
11-17	43.5	29.7	22	1	57	32	8.2	75.7	7.8
18-24	37.4	26.3	45.4	2	82	54	6.7	41.3	4.6
25-01	36.8	27.5	2	0	78	53	6.6	39	5
Jul 02-08	29.5	24.7	69.6	4	91	84	11	16.6	0.4
09-15	33.5	26.1	13.2	1	82	59	8.9	39.1	3.6
16-22	35.5	26.4	26.1	3	84	55	3.2	36.3	7.5
23-29	32.3	25.5	8.4	1	88	77	6.3	21.3	2.7
30-05	28	24.4	99	3	90	82	10.9	14.5	0.5
Aug 06-12	30.2	25.3	185.6	3	89	83	9.6	24.3	2.9
13-19	30.8	25.4	49.2	2	90	74	7	18.1	3.8
20-26	31.7	25.2	27.8	3	92	75	5.3	21.9	3.2
27-02	30.9	25.1	53.8	3	92	73	4.6	18.2	1.3

Sep 03-09	29.5	24.9	239	6	94	87	5.9	11.6	0.5
10-16	30.7	25	9.2	1	92	74	7.7	21.6	4.3
17-23	33	25.5	2.4	0	88	63	3.6	29.6	8.2
24-30	30.2	24.2	178.1	5	91	74	4.5	17.7	3.8
Oct 01-07	32	24.3	1.8	0	90	64	3.8	25.3	7.5
08-14	31.3	23.6	1.2	0	91	64	2.4	23.4	5.4
15-21	30.9	21.8	51	3	92	65	2.6	21.9	5.7
22-28	28.1	22.2	27.6	1	92	71	3.7	12.5	2.8
29-04	31.4	22.2	0	0	92	51	1.2	19.2	6
Nov 05-11	30.6	23	81.6	4	91	65	3	92	5.5
12-18	29.6	15.5	0	0	90	38	1.8	20	8.7
19-25	30.2	15.2	0	0	89	38	1.4	20.2	8.2
26-02	29.7	16.3	0	0	90	43	2	20.4	6.3

RESUME

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