GENETIC ANALYSIS OF YIELD AND QUALITY CHARACTERS IN ADVANCED BREEDING LINES OF RICE (*Oryza sativa* L.)

M.Sc. (Ag.) Thesis

By

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DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE
FACULTY OF AGRICULTURE
INDIRA GANDHI KRISHI VISHWAVIDYALAYA
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Thesis

Submitted to the

Indira Gandhi Krishi Vishwavidyalaya, Raipur

By

Bharti Singh

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FOR THE DEGREE OF

Master of Science

in

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CERTIFICATE – I

This is to certify that the thesis entitled **"Genetic analysis of yield and quality characters in advanced breeding lines 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 **Bharti Singh** under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of instructions.

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

Chairman

Date: 10|08|2021

THESIS APPROVED BY THE STUDENT'S ADVISORY COMMITTEE

Chairman	Dr. Deepak Gauraha	____________
Member	Dr. Abhinav Sao	____________
Member	Dr. V. B. Kuruwanshi	____________
Member	Dr. Ravi R. Saxena	____________
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COLLEGE OF AGRICULTURE RAIPUR (CHHATTISGARH)

CERTIFICATE

This is to certify that the thesis Viva-voce in respect of **Miss Bharti Singh** student of **M.Sc. (Ag.) Department of Genetics and Plant Breeding** has been conducted under the Chairmanship of Head of the Department/ Dean (in case of out campus) along with Advisory Committee on 30.09.2021 The necessary corrections have also been made as per comments/suggestions made by the Advisory Committee and Head of the Department/Dean.

Date: 30/09/2021

Signature of Major Advisor

Name: Dr. Deepak Gauraha

Certificate- II

This is to certify that the thesis entitled, **"Genetic analysis of yield and quality characters in advanced breeding lines of Rice (*Oryza sativa* L.)"** submitted by **Bharti Singh** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G), in partial fulfilment of the requirements for the degree of **Master of Science (Ag.)** 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/Dean.

Signature of Head of the Department

Date: 30.9.21

Major Advisor ____________________

Faculty Dean ____________________

Approved/ Not approved

Director of Instructions ____________________

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Bharti

Bharti Singh

Date: 10/08/2021

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%	Percent
°C	Degree Celsius
Mm	Millimeter
Cm	Centimeter
d.f.	Degree of freedom
et al.,	and others
G	Gram
i.e.	that is
viz.	For example
M	Meter
*	Significance at 5%
**	Significance at 1%

LIST OF ABBREVIATION

ABBREVIATION	DESCRIPTION
Approx.	Approximately
S.No.	Serial number
CV	Coefficient of variation
GA	Genetic Advance
GCV	Genotypic Coefficient of Variation
PCV	Phenotypic Coefficient of Variation
No.	Number
SD	Standard deviation
$h^2_{(bs)}$	Heritability in broad sense
ANOVA	Analysis of variance
HI	Harvest index
GC	Gel consistency
ASV	Alkali spreading value
HRR%	Head rice recovery %
L/B ratio	Length breadth ratio
GA% mean	Genetic advance as percent of mean

LIST OF APPENDICES

THESIS ABSTRACT

a) Title of the thesis	:	"Genetic analysis of yield and quality characters in advanced breeding lines of Rice (*Oryza sativa* L.)"
b) Full name of the student	:	Bharti Singh
c) Major subject	:	Genetics and Plant Breeding
d) Name and address of the major advisor :		Dr. Deepak Gauraha (Scientist) Department of Genetics and Plant Breeding, College of Agriculture, IGKV Raipur.
e) Degree to be awarded	:	Master of Science in Agriculture

Signature of the Student

Signature of Major Advisor

Date: 10/08/2021

Signature of Head of the Department

10.8.21

ABSTRACT

In this study, fifty advanced breeding lines and five checks of rice were taken for evaluation to determine the genetic diversity exhibited by the experimental material for the purpose of selecting diverse parents, estimating yield and quality trait's genetic parameters among lines, and the degree of correlation of yield with its attributing traits, and between head rice recovery % and quality traits including direct and indirect effects. The experiment was performed in a RBD with 2 replications during *kharif* 2020 at Research cum Instructional farm, Department of Genetics and Plant Breeding, CoA, IGKV, Raipur (C.G.) and the laboratory work was performed at Quality laboratory, Department of Genetics and Plant breeding, RRL, IGKV, Raipur (C.G.).

The variance studies showed extremely significant variations among the 55 advanced breeding lines, suggesting significant genetic variation in the material. Study of genetic parameters revealed that biological yield/plant, number of filled grains/panicle, harvest index %, number of unfilled grains/panicle, gel consistency, grain yield/plant (g), alkali spreading value, amylose % and head rice recovery % showed high phenotypic and genotypic coefficients of variation. This indicates that considering these traits for direct selection will result in genetic improvement.

The yield and quality traits which showed high values for genetic advance as % of mean along with high heritability were number of filled grain/ panicle, biological yield (g), number of unfilled grain/ panicle, 100 seed weight (g), grain yield/plant (g), paddy L/B ratio, gel consistency, brown rice L/B ratio, amylose %, cooked rice L/B ratio, kernel breadth after cooking (mm), alkali spreading value and head rice recovery %. Revealing a prevalence of additive gene action, thus providing scope for further improvement through selection.

Out of 50 advanced breeding lines 22 lines (excluding checks) gave acceptable value of head rice recovery %. Highest HRR % recorded in R1853-82-1-80-1 followed by R1762-197-1-131-1, R2302-383-2-269-1, R2307-99-1-75-1, R2298-353-3-238-1 have high head rice recovery %. Highest milling % was exhibited by R 2288-54-1-15-1 followed by R2298-354-2-240-1 and R2298-352-235-1. Out of fifty five lines two lines had long grain, forty five lines had medium long grain and eight lines had short size grains. Highest elongation ratio was obtained in line R2302-404-2-315-1 followed by R2298-354-1-239-1-1 and R2298-354-1-239-1. Gel consistency estimates varied from hard GC to soft GC. As per ASV estimates only one line showed low ASV, thirteen lines had low-intermediate ASV, fifteen lines had intermediate ASV and twenty six lines had high ASV. Fifteen lines had low amylose content, thirteen lines had intermediate amylose content and twenty seven lines had high amylose content.

Genotypic coefficient of correlation values were higher than phenotypic coefficient of correlation among most of the character combinations explaining that the cause for such observed relationship among various traits is due to genetic cause. Correlations studies showed that significant positive correlation of grain yield/ plant was obtained with days to 50 % flowering, biological yield per plant, panicle length, number of effective tillers/plant, plant height, number of filled grains/panicle and harvest index %, revealing importance of these traits for grain yield improvement. Whereas, highest significant positive correlation of head rice recovery % was obtained with milling%, brown rice L/B ratio, hulling %, gel consistency, kernel L/B ratio, elongation ratio and cooked rice L/B ratio. This indicated that simultaneous selections of these traits will be significant in higher yield as well as improving grain quality.

Yield traits which showed significant positive correlation and positive direct effect on grain yield/plant were number of biological yield/plant, number of filled grains/panicle, and harvest index %. Quality traits which exhibited significant positive correlation and positive direct effect on head rice recovery % were hulling %, elongation ratio and brown rice L/B ratio. Direct selection of genotypes based on these characters will be rewarding for improvement of both grain yield and grain quality.

On the basis of Cluster analysis based on the dissimilarity coefficient between lines using unweighted pair group of arithmetic means (UPGMA), fifty five lines were amalgamated into six major clusters covering 49.09% of total lines in cluster II (n= 27), 36.36% in cluster I (n=20). Whereas, rest 14.55% of the lines was unequally distributed in cluster III (n=4), IV (n=2), V (n=1) and VI (n=1). Range of intra cluster distance was from 0.00 (cluster V and VI) to 28.84 (cluster III). Maximum inter cluster distance was present between cluster II and VI (156.25). The breeding lines R2298-353-3-238-1, R1853-82-1-80-1, R2301-382-2-267-1, R2120-37-2-2-1 and C8-1-1 with highest mean values for different yield and quality traits might be employed directly for adaptation or as parents in a future hybridization procedure.

शोध ग्रन्थ सारांश

(अ) शोध ग्रन्थ का शीर्षक	:	"धान की उन्नत प्रजनन लाइनों में उपज और गुणवत्ता के लक्षणों का आनुवंशिक विश्लेषण (*ओराइजा सटाइवा* एल.)|"
(ब) छात्र का पूरा नाम	:	भारती सिंह
(स) मुख्य विषय	:	आनुवंशिकी एवं पादप प्रजनन विभाग
(द) मुख्य सलाहकार का नाम और पता	:	डॉ. दीपक गौरहा, वैज्ञानिक (आनुवंशिकी एवं पादप प्रजनन विभाग), कृषि महाविद्यालय, रायपुर
(इ) उपाधि से सम्मानित किया जाता है	:	कृषि विज्ञान में स्नातकोत्तर

Bharti

छात्र का हस्ताक्षर

मुख्य सलाहकार का हस्ताक्षर

10.8.21

दिनाँक 10/08/2021

विभागाध्यक्ष के हस्ताक्षर

सारांश

वर्तमान शोध शीर्षक " धान की उन्नत प्रजनन लाइनों में उपज और गुणवत्ता के लक्षणों का आनुवंशिक विश्लेषण (*ओराइजा सटाइवा* एल.)" आनुवंशिक एवं पादप प्रजनन विभाग, इंदिरा गाँधी कृषि विश्वविद्यालय, रायपुर (छत्तीसगढ़) विभाग द्वारा आनुवंशिक विविधता का आकलन,लाइनों के बीच उपज और गुणवत्ता विशेषता के आनुवंशिक मापदंडों का आकलन, उपज और हेड राइस रिकवरी % की उपज और गुणवत्ता के जिम्मेदार लक्षणों के साथ सहसंबंध की डिग्री और प्रत्यक्ष और अप्रत्यक्ष प्रभावों का आकलन करने के लिए ख़रीफ़ 2020 में आयोजित किया गया | जिसमे धान के पचास उन्नत प्रजनक लाइनें

और पांच चेक लिए गए। प्रयोग दो प्रतिकृति के साथ यादृच्छिक पुर्ण खण्ड में किया गया था एवं गुणवत्ता की जाँच गुणवत्ता प्रयोगशाला, आनुवांशिक एवं पादप प्रजनन विभाग, आरआरएल, इंदिरा गाँधी कृषि विश्वविद्यालय, रायपुर विभाग में किया गया।

विचरण का विश्लेषण समस्त 55 उन्नत प्रजनन लाइनों के बीच अत्यंत महत्वपूर्ण भिन्नताओं को प्रदर्शित करता है, जो लाइनों में महत्वपूर्ण आनुवांशिक भिन्नता का सुझाव देती हैं। आनुवांशिक मापदंडों के अध्ययन से पता चला है कि भरे हुए दाने /बाली, जैविक उपज/ पौधा, बिना भरे दाने / बाली, फसल सूचकांक%, जेल स्थिरता, अनाज की उपज / पौधा, क्षार प्रसार मूल्य, एमाइलोज% और हेड राइस रिकवरी % ने भिन्नता के उच्च फेनोटाइपिक और जीनोटाइपिक गुणांक दिखाए। यह इंगित करता है कि इन लक्षणों के प्रत्यक्ष चयन से आनुवंशिक सुधार होगा |

उपज और गुणवत्ता के लक्षणों के लिए उच्च आनुवांशिकता के साथ-साथ औसत उच्च जेनेटिक अड्वान्स % वाले लक्षण भरे हुए दाने /बाली, बिना भरे दाने / बाली, जैविक उपज/ पौधा, 100 बीज वजन , अनाज की उपज / पौधा, धान एल/बी अनुपात, जेल स्थिरता, ब्राउन चाँवल एल/बी अनुपात, एमाइलोज%, पके हुए चाँवल एल/बी अनुपात, पकाने के बाद कर्नेल चौड़ाई, क्षार प्रसार मूल्य और हेड राइस रिकवरी % में पाए गए । ये लक्षण ऐडिटिव जीन ऐक्शन को प्रदर्शित करती है तथा उपरोक्त घटकों का चयन चाँवल की उपज वृद्धि तथा गुणात्मक सुधार में मज़बूत आधार प्रदान करेगा |

50 उन्नत प्रजनन लाइनों में से 22 लाइनों ने एच. आर. आर. % (हेड राइस रिकवरी %) का स्वीकार्य मूल्य दिया | R1853-82-1-80-1, R1762-197-1-131-1, R2302-383-2-269-1, R2307-99-1-75-1, R2298-353-3-238-1 में उच्च हेड राइस रिकवरी % प्राप्त हुई । उच्चतम मिलिंग % R 2288-54-1-15-1 के बाद R2298-354-2-240-1 और R2298-352-235-1 द्वारा प्रदर्शित किया गया। पचपन लाइनों में से दो लाइनों में लंबे दाने, पैंतालीस लाइनों में मध्यम लंबे दाने और आठ लाइनों में छोटे आकार के दाने पाए गए । उच्चतम ईलाँगेशन अनुपात R2302-404-2-315-1 के पश्चात R2298-354-1-239-1 एवं R2298-354-1-239-1 में प्राप्त किया गया। जेल स्थिरता का अनुमान हार्ड जीसी से सॉफ्ट जीसी तक भिन्न था । ऐल्कलाई स्प्रेडिंग वैल्यू के अनुमानों के अनुसार केवल एक लाइन ने कम ऐल्कलाई स्प्रेडिंग वैल्यू, तेरह लाइनों में कम-मध्यवर्ती ऐल्कलाई स्प्रेडिंग वैल्यू, पंद्रह लाइनों में इंटरमीडिएट ऐल्कलाई स्प्रेडिंग वैल्यू एवं छब्बीस लाइनों में उच्च ऐल्कलाई स्प्रेडिंग वैल्यू प्राप्त हुआ | पंद्रह लाइनों में कम एमाइलोज %, तेरह लाइनों में मध्यवर्ती एमाइलोज % और सत्ताईस लाइनों में उच्च एमाइलोज % प्राप्त हुआ |

सहसंबंध मूल्यों के जीनोटाइपिक गुणांक अधिकांश लक्षणों के लिए फेनोटाइपिक गुणांक से अधिक थे, जो यह दर्शाता है कि विभिन्न लक्षणों के बीच इस तरह के देखे गए संबंध का कारण अनुवांशिक कारण है। सहसंबंध अध्ययनों से पता चला है कि अनाज की उपज/पौधे ने 50% फूल, प्रभावी टिलर/पौधे,

बाली की लंबाई, पौधे की ऊंचाई, जैविक उपज, भरे हुए दाने / बाली और फसल सूचकांक % के साथ महत्वपूर्ण सकारात्मक सहसंबंध प्रदर्शित किया, यह इन लक्षणों के अनाज की उपज में सुधार के महत्व को दर्शाता है । जबकि, हैड राइस रिकवरी % ने मिलिंग %, ब्राउन राइस एल/बी अनुपात, हलिंग%, जेल स्थिरता, कर्नेल एल/बी अनुपात, लम्बाई अनुपात और पके हुए चाँवल एल/बी अनुपात के साथ उच्चतम महत्वपूर्ण सकारात्मक सहसंबंध दिखाया। इससे संकेत मिलता है कि इन लक्षणों का एक साथ चयन उच्च उपज के साथ-साथ अनाज की गुणवत्ता में सुधार के लिए महत्वपूर्ण होगा। भरे हुए दाने /बाली, जैविक उपज/पौधे और फसल सूचकांक% ने उपज/पौधे के साथ महत्वपूर्ण सकारात्मक सहसंबंध और अनाज उपज/पौधे पर सकारात्मक प्रत्यक्ष प्रभाव प्रदर्शित किया । इसी प्रकार हलिंग %, ईलाँगेशन अनुपात और ब्राउन चाँवल एल /बी अनुपात ने हेड राइस रिकवरी % के साथ महत्वपूर्ण सहसंबंध प्रदर्शित किया और हेड राइस रिकवरी % पर सकारात्मक प्रत्यक्ष प्रभाव दर्शाया । इन लक्षणों पर आधारित जीनोटाइप का प्रत्यक्ष चयन अनाज की उपज और अनाज की गुणवत्ता दोनों में सुधार के लिए फायदेमंद होगा |

क्लस्टर विश्लेषण के आधार पर, पचपन लाइनों को छह प्रमुख समूहों में समायोजित किया गया जिसमें क्लस्टर II (एन = 27) कुल लाइनों के 49.09% को सम्मिलित करता है, क्लस्टर I में 36.36 % (एन = 20), जबकि, शेष 14.55% लाइनें क्लस्टर III (n=4), IV (n=2), V (n=1) और VI (n=1) में असमान रूप से वितरित की गई। इंट्रा क्लस्टर दूरी की सीमा 0.00 (क्लस्टर V और VI) से 28.84 (क्लस्टर III) तक थी। क्लस्टर II और VI (156.25) के बीच अधिकतम इंटर क्लस्टर दूरी मौजूद थी। प्रजनन लाइनें R2298-353-3-238-1, R1853-82-1-80-1, R2301-382-2-267-1, R2120-37-2-2-1 एवं C8-1-1 को उच्चतम उपज के साथ और गुणवत्ता लक्षणों के लिए सीधे अनुकूलन या भविष्य के संकरण प्रक्रिया में जनक के रूप में नियोजित किया जा सकता है|

CHAPTER – I

INTRODUCTION

Rice (*Oryza sativa* L.) (2n=24) is a major cereal crop that belongs to the Poaceae family and the Oryzoidea subfamily. It is known as the "Global Grain" because it is a staple food in over 100 countries. It is the world's longest domesticated grain (10,000 years) and the primary source of nutrition for 2.5 billion people. Rice is globally grown in 162.056 million ha area with 755.47 million tons rice production (Anonymous, 2019). Rice cultivation is the greatest single use of land for food production, accounting for 9% of all arable land on the planet. It is the primary food in 17 Asian and Pacific nations, 9 North and South American countries, and 8 African countries. Out of about 141 million ha of net cultivated area in India, rice occupies the maximum *i.e.*, about 43.78 million ha.

Rice has replaced wheat, corn, cassava, and potato as the most essential source of calories and protein for 20% of the world's poorest people, contributing more calories to the diet than wheat, maize, cassava, or potato. Rice is mostly a starchy food with amylose and amylopectin fractions (78-79 percent starch). It also provides significant protein and vitamin content. Rice is high in vitamin B (thiamin and nicotinamide), as well as iron (Fe), phosphorus (P), and magnesium (Mg). In comparison to other cereals, milled rice has a low protein content (6-7%). However, it contains a lot of defective amino acids like Lysine.

Rice is the keystone of India's national food security. It holds around 22 percent of cropped land and produces around 177 million tonnes per year, second after China. It accounts for 21.50 percent of global rice production and 40 to 43 percent of the country's overall food grain production. China is the world's leading producer of rice. China produced 211 million tonnes of rice, paddy in 2019, accounting for 27.92 percent of global rice, paddy demand. China, India, Indonesia, Bangladesh, and Vietnam are the top five nations respectively, accounting for 71.53 percent of the total. In India rice is grown on 43.78 million hectares, yielding 177.64 million tonnes and yielding 4.057 tonnes per hectare (Anonymous, 2019). The total paddy production in 2020 is expected to reach a new high of 184.5 million tonnes (Anonymous, 2021). West Bengal, Punjab, and Uttar Pradesh are the top three states in rice production, with total rice production of 14.97 million tonnes, 13.38 million tonnes, and 13.27 million tonnes respectively and contributing 13.26 %, 11.85 %, and 11.75 % to the total rice percent share of the country. Rice is also an export crop that contributes to the economy. India is the leading exporter of the Basmati Rice to the global market. In the financial year 2018-19, India exported around 4.4 million metric tons of Basmati rice worth USD 4.7 billion (Anonymous, 2020). In 2018-19, India exported 7.5 million metric tons of Non-Basmati rice worth USD 3 billion. (Annonymous, 2020). Rice exports are expected to reach a new high of 16.2 million tonnes in 2021 (calendar year) (Anonymous, 2021).

The state of Chhattisgarh is known as the "Rice Bowl of India" because it covers the most land with rice during the *kharif* season and contributes a large portion of the country's rice production. It covers a total area of 13.51 million hectares, with 5.90 million hectares under cultivation. In the final year 2017 the total rice production in the state was recorded to be 8.05 million metric tonnes, decrease was recorded in the final year 2018 with a total rice production of 4.93 million metric tonnes and in the final year 2019 the total rice production of the state is recorded to be 6.53 million metric tonnes (Statista Research Department, 2020). Due to growing population, per capita gross land supply is expected to decline from 0.32 ha in 2001 to 0.23 ha in 2025 and 0.19 ha in 2050, compared to the global average of 2.19 ha. The amount of land used for non-agricultural purposes has steadily increased over time. The net sown area has remained remarkably stable at 141 million ha over the last four decades (1970-71 to 2008-09).

By 2050, the world's population is anticipated to reach 9.1 billion, necessitating a 70 percent increase in food production (Godfray *et al*., 2010; Hodges *et al*., 2011; Parfitt *et al*., 2010). Rice yields have been stable or have gradually declined since the green revolution's initial success. To feed the increasing population, new projects are being developed in all rice-growing areas in order to increase yield per hectare. There is a decline in genetic base and increase in genetic vulnerability of rice due to large scale replacement of traditional varieties with modern and high yielding varieties. There is a direful need to broaden the genetic base of rice by introgressing genes from diverse sources. Thus, there is a need to collect, exploit and evaluate the untapped germplasm.

As a result of its value as a staple food for India's people, increasing its production has become important (Subbaiah *et al*., 2011). For genetic advancement, understanding the nature and magnitude of genetic variance regulating the inheritance of quantitative characteristics including yield and its components is critical. Improving grain quality without decreasing yield is desperately required in the current context to benefit both rice producers and consumers. Grain quality traits are very crucial in rice breeding as it is predominantly consumed as a whole grain. The milling percentage, hulling percentage, grain dimensions, cooking quality constitute the quality traits (Babu *et al*., 2012).

When selection is made based on yield contributing characteristics, heritability and genetic advance are essential selection parameters. Heritability estimates combined with genetic improvement are typically more effective in predicting selection benefit than heritability estimates alone (Paul *et al*., 2006). Yield is a dynamic quantitative characteristic that is influenced by several gene interactions with the environment and is the product of a number of factors known as yield components. Choosing parents solely on the basis of yield may be misleading. As a result, understanding the relationship between yield and its contributing characters is needed for plant breeders to develop an economically viable variety. In selecting the best kind of parents for a hybridization programme, the plant breeder's most effective method is genetic diversity. Agglomerative (bottom-up) hierarchical clustering cluster analysis (UPGMA) and Mahalanobis' D^2 analysis, which serve as the most promising method for classification, are a form of multivariate analysis that aids plant breeders in selecting suitable parents in tress situations in order to achieve superior segregants in breeding programmes. Path coefficient analysis offers information on the direct and indirect effect of each contributing trait on yield, as well as allowing breeders to rate genetic attributes according to their contribution.

In light of the above, the current research will be undertaken in order to obtain detailed data on genetic variations in relation to various yield and quality characters, correlation coefficients, and direct and indirect results. Keeping the aforesaid views into consideration, the present investigation was perfomed on following objectives:-

1. To estimate genetic variability parameters for yield and quality traits in advanced breeding lines of rice.

2. To study correlation and path analysis of yield and quality traits.

3. To study genetic divergence in the advanced breeding lines of rice for yield and quality traits and clusters analysis.

CHAPTER-II

REVIEW OF LITERATURE

Rice is a globally important staple food grain. There is a lot of scope to increase this crop's productivity *via* varietal enhancement and hybrid development.

The literature relevant to this study has been reviewed and organised under the following headings:

2.1. Genetic variability, heritability and genetic advance

2.2. Correlation coefficient analysis and path coefficient analysis

2.3. Genetic divergence and Cluster analysis

2.1 Genetic variability, heritability and genetic advance

The analysis of genetic variability is the most important factor to consider when trying to improve a crop's genetics. For a plant breeder to prepare successful breeding programmes, he or she must first assess variability for any trait. Heritability is a measure of how often characters are passed on from parents to offspring, and it plays an important role in plant breeding selection. Genetic advance tells us of the expected benefits of superior individual's selection. The important selection parameters are heritability and genetic advance that can be used to predict the amount of gain under selection. Several researchers presented the following findings on genetic diversity, heritability, and genetic advance in rice yield and yield-related traits:

Mall *et al.* (2005) conducted a study to evaluate 35 rice genotypes to estimate heritability, genetic variability and genetic advance for yield and yield component. Plant height, tillers obtained/plant, panicles produced/plant, and number of spikelets/panicle all showed high genetic advance and heritability. Variation of a wide range was obtained for mean values of days to panicle initiation, plant height, days to 50% flowering, number of panicles/plant, number of tillers/panicle, panicle length and number of spikelets/plant.

Singh *et al.* (2006) evaluated 30 rice genotypes for study of genetic variability and interrelationship among them for seven traits. Grain yield acquired highest genotypic and phenotypic coefficient of variations. As per recorded data a high heritability estimate along with high genetic advance was for plant height.

Akter *et al.* (2007) evaluated deep water rice 30 advanced breeding lines in order to estimate variability and genetic association for grain yield and its attributing traits. Filled grains/panicle followed by plant height showed highest genetic variability. High GCV and heritability in broad sense along with high genetic advance in % of mean was obtained for panicles/plant, grain yield and number of filled grains/ panicle.

Singh *et al.* (2008) made an experiment for the study of heritability, genetic advance and character association among 28 rice genotypes. The maximum genotypic and phenotypic coefficients of variability were recorded in number of grains/panicle, followed by grain yield/plant, number of tillers/plant, plant height and test weight. Number of tillers plant^{-1} and number of grains $\mathrm{panicle}^{-1}$ acquired high heritability estimates coupled with high genetic advance in percentage of mean.

Veerabadhiran *et al.* (2009) undertook an investigation in 15 rice hybrids for studying extent of variability and genetic parameters. It was observed that alkali spreading value and gel consistency recorded high (>20%) GCV and PCV. Kernel breadth, ratio of kernel length/breadth, breadth of kernel after cooking, kernel ratio of length/breadth after cooking, gelatinization temperature, gel consistency, grain yield, and amylose content all had high genetic advance and heritability.

Sreeparvathy *et al.* (2010) estimated genetic variability, genetic advance and heritability for various morphological and quality characters in 50 genotypes. High range of phenotypic variation was recorded for days to 50 per cent flowering, grain yield plant^{-1}, number of panicles plant^{-1}, plant height, panicle length, 1000-seed weight and number of grains $\mathrm{panicle}^{-1}$. It was also recorded that coefficient of variation (PCV and GCV) was lowest for days to 50 per cent flowering and highest for grain yield/plant. Number of grains/panicle, number of panicles/plant, and grain yield/plant all had high heritability and genetic gain. For trait days to 50% flowering, high heritability was observed with low genetic gain.

Seyoum *et al.* (2012) performed an experiment on 14 rice genotypes at three rainfed upland locations of southwest Ethiopia. High values of GCV and PCV were noted for the traits, plant height, grains/panicle, days to 50% flowering, 1000 grain weight, spikelets/panicle, and grain yield. High heritability was recorded for days to 50% flowering, plant height, 1000 grain weight, panicle length and spikelet/panicle. High to medium heritability along with genetic advance were recorded for panicles/plant, days to 50% flowering, grains/panicle, plant height, spikelets/panicle and 1000 grain weight.

Gangashetty *et al.* (2013) conducted a study on 42 genotypes to estimate the amount to which genetic variability possessed in the local non-basmati aromatic rice genotypes. The high estimates of GCV and PCV was recorded for number of tillers/plant, plant height, productive tillers produced/plant, grain length, panicle and grain yield/plant. The moderate estimates of PCV and GCV was noted for panicle length, grain breadth and L/B ratio. High heritability along with high genetic advance was recorded for all the traits excluding days to 50% flowering.

Lingaiah *et al.* (2014) conducted experiment on 33 rice genotypes for quantitative characters. Moderate to high estimates of GCV and PCV were recorded for number of test weight, grains panicle^{-1}, and yield. High heritability coupled with high GA as % of mean was observed for test weight, number of grains per panicle and yield.

Allam *et al.* (2015) studied on 25 rice genotypes for yield and quality characters. High estimates of GCV was recorded for the traits yield plant^{-1}, alkali spread value, and effective panicles. The characters effective panicles plant^{-1}, plant height, panicle length spikelets panicle^{-1}, days to 50% flowering, filled grains panicle^{-1}, yield plant^{-1} , test weight, kernal length, kernal L/B ratio, brown rice length, brown rice L/B ratio, kernal length after cooking, elongation ratio and alkali spread value showed high heritability along with high genetic advance as percent of mean.

Devi *et al.* (2016) conducted experiment on 27 rice genotypes for yield and kernal quality characters. The high estimates of GCV and PCV were recorded for the characters yield per plant and filled seeds per panicle while low GCV and PCV values were recorded for hulling percent, milling percent, kernel elongation ratio, days to 50 percent flowering, panicle length, kernel width and kernel length. High heritability in broadsense along with high genetic advance as % of mean was recorded for the characters, plant height, effective tillers, flag leaf length, filled seeds panicle^{-1}, test weight, yield plant^{-1}, head rice recovery and L/B ratio.

Srujana *et al.* (2017) studied on 29 rice genotypes for 13 quantitative traits. The characters grain yield/plant, harvest index, spikelets/panicle, tillers/plant, flag leaf length and panicles/plant showed high to moderate estimates of PCV and GCV. High heritability was recorded for spikelets/panicle, days to maturity, biological yield, grain yield/plant, tillers/plant and panicles/plant. The characters, Spikelets per panicle, seed yield/pland, tillers/plant, panicles/plant and biological yield/plant showed high heritability along with moderate to low estimates of genetic advance.

Sandeep *et al.* (2018) conducted experiment on 200 rice genotypes for 11 quantitative characters. High estimates of GCV and PCV were observed for number of grains per panicle, single plant yield, number of tillers plant^{-1}, spikelet fertility and pollen viability. High heritability along with high genetic advance as percent of mean is recorded for plant height, spikelet fertility, single plant yield, number of tillers plant^{-1}, number of grains per panicle, pollen viability, panicle length, number of productive tillers plant^{-1} and 1000 grain weight.

Behera *et al.* (2018) undertook 49 elite slender grain rice genotypes for 13 traits including grain yield. He found that both grain yield per plant and fertile grain per panicle had high GCV and PCV values. For days to 50% flowering, plant height, panicle length, flag leaf area, fertile grains/panicle, fertility percentage, 100 seed weight, and grain yield per plant, high heritability estimations were associated to moderate to high genetic gain over mean.

Singh *et al.* (2019) studied on 30 rice genotypes for 11 yield and its quality contributing traits. High GCV was observed for seeds per panicle, seed yield per plant and vigour index. High heritability for broad sense was observed for days to 50 % flowering, seedling dry weight, days to maturity, plant height, vigour index and seed yield per plant. High estimates of genetic advance was recorded for seed yield per plant, seeds per panicle, vigour index, plant height, days to 50 % flowering and seedling dry weight. High heritability coupled with high genetic advance was recorded for days to 50 % flowering, seedling dry weight, plant height, vigour index and seed yield per plant.

Rathi *et al.* (2019) studied heritability, coefficients of variability, genetic advance and trait association for eleven traits in rice $F_{2:3}$ segregating populations of biparental crosses For all of the characteristics investigated, phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV), showing that the environment had a significant impact. For filled grains and unfilled grains per panicle, moderate heritability was observed together with significant genetic advance, indicating that heritability is most likely due to additive gene impact and that selection for the characteristics will be successful.

Jan and Kashyap (2020) carried out an experiment on 35 rice genotypes for 15 cooking and quality characters. High estimates of GCV and PCV was estimated for gel consistency while low for hulling percentage. Broad sense heritability was recorded highest for head rice recovery and amylose content while lowest for kernel widening ratio. High genetic advance was observed for elongation percentage while low for kernel widening ratio. High genetic advance as per cent of mean was observed for gel consistency and amylose content while low for hulling percentage.

Ganpati *et al.* (2020) performed experiment for yield attributing traits in rice and found that Plant height, number of primary branches per panicle and number of grains per panicle showed high heritability, whereas plant height, panicle length, number of filled grains per panicle , and 1000 seed weight had high genetic advance.

2.2 Correlation coefficient and Path coefficient analysis

The development of high-yielding varieties entails a detailed understanding of existing genetic diversity, as well as the degree and direction of genetic association among yield-related characters. Knowledge of the direct and indirect effects of grain yield on other characteristics will aid in the efficient selection of suitable rice cultivars. Wright's (1921) statistical device, path coefficient analysis, aids in the partitioning of correlation coefficients into direct and indirect effects of independent variables on dependent variables. Grain yield is a complex character that is determined by a number of variables, so selecting based on a simple correlation without considering the component characters is ineffective. As a result, path analysis is crucial in any plant breeding programme. Correlation combined with path analysis will provide a greater understanding of the cause and effect relationship between various pairs of characters. Path coefficient analysis was first demonstrated in plant selection by Dewey and Lu (1959), and it has since been applied to almost every crop. In rice, several scientists studied correlation and path analysis :

Khatun *et al.* (2003) worked out simple correlation based on mean values from 16 aromatic rice varieties of 13 quality traits. It was found that kernel length had significant positive correlation with L/B ratio, gel consistency and kernel length after cooking. Also significant positive correlation was observed between head rice recovery % and milled rice, gel consistency and kernel breadth. Gel consistency showed highly significant positive correlation with Alkali spreading value but highly significant negative correlation with amylose content, water uptake ratio and elongation ratio.

Surek and Beser (2003) investigated association among some yield components on eighty breeding lines. Number of filled grains per panicle, harvest index, biological yield and productive tillers per square meter were found to be positively correlated with grain yield. Harvest index and biological yield showed highest positive significant direct effect on grain yield.

Gazafrodi *et al.* (2006) studied path analysis and correlation among 16 agronomic traits in 49 rice enteries grain yield showed a positive and significant correlation with number of productive tillers, total tillers, and grain per panicle, as per phenotypic and genotypic correlation analysis. The number of productive tillers showed the highest direct effect on grain yield, as per path analysis of the traits. Furthermore, the number of grains per panicle and the weight of 100 grains had a significant direct effect on yield.

Panwar and Ali (2007) studied association in 47 genotypes of rice among components of yield, their direct and indirect influence on grain yield. It was recorded that grain yield/plant had positive significant association with harvest index, grain yield/panicle, biological yield/plant and filled grains/panicle. Path coefficient analysis showed that grain yield/panicle possessed the highest direct effect on grain yield/plant.

Shivani *et al.* (2007) analysed maintainers and restorer lines of rice for various grain quality and physico-chemical traits. In this study hulling % exhibited significant positive correlation with head rice recovery% and milling %. Amylose content exhibited positive but non-significant correlation with volume expansion ratio, gel consistency and alkali spreading value.

Reddy *et al.* (2008) in 20 genotypes of rice performed correlation and component analysis for 12 characters. The characters panicle weight, number of spikelets panicle^{-1}, biological yield, and harvest index were found to have a positive and significant correlation with grain yield plant^{-1}.The number of tillers and the number of panicles plant^{-1}have a highly significant and positive correlation.

Chandra *et al.* (2009) studied correlation and path analysis in 49 diverse rice genotypes and found that grain yield per plant had significantly positive correlation with number of productive tillers per plant, panicle length, 1000 grain weight and number of grains per panicle. Through path analysis it was revealed that high positive direct effect on grain yield per plant was exhibited by number of grains per panicle, 1000 grain weight, days 50 % flowering and number of productive tillers per plant.

Patil and Sahu (2009) conducted an experiment to study character interrelationship using correlation and path analysis in 100 genotypes of rice. Days to 50% flowering, number of effective tillers plant^{-1}, and number of filled grains panicle^{-1}all had a positive significant correlation with grain yield plant^{-1}, as per the correlation coefficient.

Saravanan and Sabesan (2009) investigated forty six genotypes for estimating association among yield components and their direct and indirect influence on grain yield. Grain breadth, productive tillers per plant and total number of tillers per plant had significant positive association with grain yield. Highest direct positive effect on grain yield was exhibited by grain L/B ratio, grain breadth and total number of tillers/plant.

Nandan *et al.* (2010) conducted experiment on 33 rice genotypes for 20 grain yield and its quality traits. Number of grains per panicle, Days to 50% flowering, plant height, spikelet fertility and number of spikelets per panicle showed strong positive correlation on grain yield. Path analysis showed direct effect on grain yield/plant with kernel length after cooking, number of grains/panicle, days to 50% flowering, plant height, hulling percentage, kernel breath after cooking and harvest index.

Mathure *et al.* (2011) evaluated 88 aromatic cultivars for estimation of kernel quality and grain morphology. Significant positive correlation was seen between kernel length and productive tillers per plant, and negative between kernel length and filled grains per panicle. Kernel L/B ratio exhibited positive correlation with productive tillers per plant, and negative correlation with filled grains per panicle.

Rajamadhan *et al.* (2011) studied association between quantity traits on yield of rice. Positive significant association was obtained by 100 grain weight, grain breadth, number of productive tillers and number grains per panicle. Panicle length found to be positively associated with 100 grain weight, grain yield and number of grains per panicle.

Basavaraja *et al.* (2011) studied on 100 local cultivars of rice for yield and its components. The traits number of tillers plant^{-1}, panicle length, test weight, number of spikelets panicle^{-1}, spikelet fertility percentage, number of productive tillers plant^{-1} and amylose percent showed significant correlation on grain yield. Path analysis showed direct positive effect on grain yield with plant height, days to 50% flowering, panicle length, number of productive tillers/plant, panicle number, spikelet fertility percent and amylose percentage.

Babu *et al*. (2011) conducted research on twenty-one common rice hybrids to investigate correlation and path analysis. Grain yield per plant has a significant positive relationship with the number of productive tillers per plant. Number of productive tillers per plant and panicle length had a favourable direct influence on yield, according to path coefficient analysis. The number of productive tillers per plant had both a positive association and a significant direct influence among these characters.

Padmaja *et al*. (2011) studied correlation and path analysis studies for eleven characters on one hundred and fifty rice genotypes including five check varieties and it was found that yield/plant had the highest positive correlation with 100 seed weight and productive tillers/plant , followed by spikelet fertility, total tillers/plant , grains/ panicle , and panicle length.

Bhadru *et al.* (2011) evaluated 93 rice genotypes for studying correlation and path coefficient analysis for yield and yield contributing traits. Significant positive correlation on grain yield/plant was exhibited by productivity per day, plant height, days to 50% flowering, number of filled grains/plant and panicle weight.

Bagheri *et al.* (2011) studied relationship between grain yield and yield components in 26 rice genotypes grain yield was seen to be significantly positively correlated with total number of spikelets per panicle, panicle length, number of filled grains per panicle and number of panicles per plant.it was observed that panicle length had highest significant positive direct effect on grain yield.

Thomas *et al*. (2012) evaluated 6 different rice varieties for estimation of proximate composition, physiochemical properties and cooking qualities. Elongation of cooked rice exhibited positive correlation with both amylose content and L/B ratio. These results shows strong dependence of cooking and physiological properties on their amylose content.

Sharma *et al.* (2012) studied 40 rice genotypes for grain yield and its contributing characters. The characters, grains per panicle, fertility percentage, 1000 grain weight and grain breadth showed significant and positive correlation both at genotypic and phenotypic levels. Path analysis showed high positive direct effect on yield plant^{-1} with grains $\mathrm{panicle}^{-1}$, tillers plant^{-1}, grain breadth, 1000 grain weight and panicle length at genotypic level.

Mulugeta *et al.* (2012) conducted a field experiment on 14 rice genotypes for estimating genetic variability, heritability and correlation coefficients of grain yield and yield attributing traits. It was found that number of grains per panicle had maximum positive direct effect and also highly positive genotypic correlation with grain yield/plant.

Reddy *et al.* (2013) conducted experiment on 33 rice genotypes for yield and its attributing traits. Biological yield per hill, number of spikelets per panicle, flag leaf width, flag leaf length and plant height showed strong positive association on grain yield. Path analysis showed positive direct effect on grain yield/plant with biological yield/hill, harvest index, number of tillers/hill, flag leaf width and panicle length.

Veni *et al.* (2013) studied variability and association for yield and quality parameters. Days to 50% flowering, head rice recovery%, productive tillers per plant, volume expansion ratio and panicle length manifested positive significant association with grain yield. Panicle length, productive tillers, L/B ratio and kernel breadth exhibited positive direct effect on grain yield per plant.

Sanghera *et al.* (2013) carried out a study for the assessment of genetic variability on 14 red rice genotypes for grain yield and attributing traits. At both genotypic and phenotypic levels grain yield showed significant positive correlation with panicle density/m^2, number of tillers/plant and number of grain per panicle. Path analysis results revealed that plant height and days to 50% flowering had positive significant direct effect on grain yield.

Naseem *et al.* (2014) studied on 20 rice genotypes for yield and its contributing characters. Character association showed high positive genotypic correlation on grain yield plant^{-1} with number of productive tillers, 1000 grain weight, number of spikelets per panicle and number of grains panicle^{-1}. Path analysis showed positive direct effect on grain yield plant^{-1} with number of spikelets panicle^{-1}, number of productive tillers plant^{-1}, number of grains panicle^{-1} and days to maturity.

Ratna *et al*. (2015) examined 6 advanced Basmati rice lines and one commercial check, BRRI Dhan 29, for correlation and path coefficients among fourteen morphological characteristics. It was observed that at both the genotypic and phenotypic levels, there was a significant positive correlation between the number of filled spikelets/panicle and yield, while there was a significant negative correlation between plant height and yield. The number of filled spikelets/panicle had the greatest positive direct effect on grain yield, whereas plant height and the number of unfilled spikelets/panicle had the greatest negative direct effect on grain yield, as per path coefficient analysis.

Devi *et al.* (2015) evaluated 92 rice genotypes for estimating genetic variability, heritability and correlation coefficients for fourteen physiochemical and cooking quality traits. Kernel length after cooking exhibited positive correlation with elongation ratio and L/B ratio; alkali spreading value with water uptake, hulling% with milling% and Head rice recovery%.

Das and Sarma (2015) studied on 30 genotypes of rice for 21 morphological and yield related traits under boro season. Biological yield, harvest index, days to first flowering, panicle length, grains per panicle and 1000 grain weight showed significant positive correlation with grain yield plant^{-1} at both genotypic and phenotypic levels. Biological yield and harvest index showed high positive direct effect on grain yield plant^{-1}.

Bhati *et al*. (2015) conducted an experiment for studying genetic variability, correlation analysis on 30 rice elite genotypes. Grain yield per hill was positively correlated with harvest index, biological yield per hill, test weight, and plant height at both the genotypic and phenotypic levels, as per correlation studies. The harvest index, number of spikelets per panicle, biological yield per hill, plant height and number of tillers per hill, all showed a strong positive direct influence on grain yield at both the genotypic and phenotypic levels, according to path coefficients.

Kawochar and Begum (2016) studied variability and correlation for 12 grain traits (before cooking) and 8 traits (after cooking) on 6 lines. Rough rice L/B ratio exhibited significant positive correlation with brown rice L/B ratio, milled rice L/B ratio and cooked L/B ratio.

Dhurai *et al.* (2016) conducted experiment on 32 rice genotypes for yield and its contributing characters. Days to maturity, harvest index, and number of grains $\mathrm{panicle}^{-1}$ showed significant positive correlation on grain yield plant^{-1}. Path analysis showed high positive direct effects on grain yield with kernal elongation ratio, kernal length, harvest index and days to maturity.

Devi *et al.* (2017) estimated 27 genotypes of rice for yield and quality characters. Plant height, filled seeds per panicle, flag leaf width, flag leaf length, effective tillers and panicle length showed highest significant positive correlation on grain yield plant^{-1} while the characters milling percent and hulling percent was significantly and positively correlated on head rice recovery. Path coefficient analysis showed positive direct effect on grain yield plant^{-1} with test weight, effective tillers and filled grains $\mathrm{panicle}^{-1}$ while head rice recovery showed direct effect on kernal length, milling percent and kernel elongation ratio.

Prasad *et al.* (2017) studied 48 different rice hybrids for correlation and path analysis. Number of productive tillers per plant, 1000 grain weight and numbers of filled grains per panicle showed positive coreelation and positive direct effect on grain yield per plant. Aside from these parameters, spikelet fertility (%) and 1000 grain weight had direct positive effects on grain yield per plant.

Kumar *et al.* (2018) studied on 13 rice genotypes to estimate correlation and path analysis. The characters biological yield per plant, flag leaf area, harvest index and spikelets per panicle showed highest positive and significant correlation on grain yield

$plant^{-1}$. Path analysis showed direct positive effect on grain yield $plant^{-1}$ with spikelets $panicle^{-1}$, spikelets fertility and biological yield $plant^{-1}$.

Singh *et al.* (2019) studied on 101 rice genotypes for seven qualitative characters. The characters like Number of panicles and test weight showed significant positive association on grain yield. Path coefficient analysis showed positive direct effect on grain yield with plant height, ear bearing tillers, panicle length, number of filled grains per panicle and test weight.

Devi *et al.* (2019) studied variability, correlation and path analysis for yield and quality traits upon 36 rice genotypes. It was obtained that at the genotypic level, grain yield per plant had a positive and significant relationship with panicle length, panicle weight, and effective tillers, whereas head rice recovery had a positive and significant relationship with milling percent and hulling percent.

Kumar *et al.* (2020) conducted experiment on 30 rice genotypes for 22 yield and quality characters. The characters like flag leaf length, number of grains $panicle^{-1}$, 100 grain weight, 100 kernel weight, kernel length after cooking and kernal elongation ratio showed high significant and positive association on grain yield. Path analysis showed high positive direct effect on grain yield with 100 grain weight, 100 kernel weight after cooking, hulling percentage, number of grains $panicle^{-1}$ and flag leaf length while path analysis showed negative direct effect on grain yield with 100 grain weight and grain weight $panicle^{-1}$.

2.3 Genetic divergence and cluster analysis

With 22 wild and two cultivated rice species recognised so far, the genus Oryza has a lot of genetic diversity. Despite 6000 years of human selection and vigorous breeding activities in the last 100 years, the crop's genetic base is very narrow. New rice varieties, which ushered in the "Green Revolution," not only increased rice production dramatically across the world, but also provided a narrow genetic base for the crop. Rice production in farm fields has reached a yield plateau, according to several sources, and the crop's small genetic base is leading to yield instability caused by biotic and abiotic stresses.

Study of genetic divergence is an important tool for selecting the best parents for maximum heterosis. Genetic divergence study can be done by using Mahalanobis statistics (D^2) through which one can estimate the genetic distance and accordingly clusters are formed. The parents selected from two different most diverse clusters gives the best hybrids on crossing. The D^2 statistic and cluster analysis has been widely in use to measure genetic divergence in rice by many researchers.

Patil *et al.* (2005) evaluated 100 genotypes of rice germplasm for study of genetic diversity among the genotypes using Mahalanobis statistics (D^2). These genotypes were grouped into 8 different clusters on basis of genetic distance. Days to 50% flowering, panicle length, flag leaf weight, flag leaf length and plant height were the main contributors to overall genetic diversity among the characters tested.

Biswas *et al.* (2006) estimated genetic divergence of 58 cold tolerant irrigated rice genotypes using Mahalanobis statistics (D^2). On basis of genetic distance, genotypes were constellated into 5 clusters. Maximum number of genotypes along with the highest intra-cluster value were included in cluster V. Between cluster II and V maximum inter-cluster distance was found.

Chandra *et al.* (2007) studied 57 upland rice genotypes for the magnitude and nature of genetic divergence among them for 14 traits on basis of Mahalanobis statistics (D^2). All 57 genotypes were grouped into 5 different clusters following Tocher's method. Cluster I consisted maximum number of 50 genotypes. The most divergent clusters were cluster III and IV.

Joshi *et al.* (2008) conducted an experiment for the assessment of the genetic diversity among 19 rice varieties cultivated in Punjab. All cultivars were grouped into 4 different clusters showing sufficient amount of variation among the genotypes. Considerable contribution was obtained from days to 50% flowering and plant height accounting for 61% of total divergence.

Pandey *et al.* (2009) conducted an experiment to assess genetic diversity in 40 genotypes of rice for agro-economically important characters. The genotypes were grouped into seven clusters on basis of Mahalanobis D2 statistics. Characters like biological yield, plant height, and test weight contributed 86.16 % of total divergence.

Banumathy *et al.* (2010) conducted a study of 53 rice genotypes to study the diversity pattern among the genotypes for 8 yield and yield attributing traits using D^2 analysis. The genotypes were grouped into 11 clusters based on the analysis. Cluster

XI and Cluster I consisted maximum number of genotypes 16 and 15 respectively.Maximum inter cluster D2 value was observed between cluster I and X followed by cluster I and IV. Grain yield, days to 50% flowering, total grains per panicle and plant height together contributed 86.62% towards total divergence.

Parikh *et al.* (2011) conducted experiment on 71 rice accessions from Chhattisgarh and Madhya Pradesh. The genotypes were grouped into 8 different clusters. Maximum number of 17 genotypes were grouped into cluster III and cluster I and II consists of 12 genotypes each. The highest inter cluster distance was recorded between cluster VI and cluster VIII & cluster II and cluster VII which showed wide diversity. The highest intra cluster distance was recorded for the cluster VII and lowest was recorded for cluster V.

Ovung *et al.* (2012) conducted experiment on 70 genotypes of rice for 13 quantitative traits. The genotypes were grouped 9 different clusters. Maximum number of 12 genotypes were grouped into cluster I and III. Maximum genetic divergence was obseved for the genotypes present in cluster VII followed by cluster V and cluster I. The maximum inter-cluster distance was observed between cluster VI and cluster VII followed by cluster III and cluster IX. The characters, spikelets per panicle, biological yield and plant height contributed maximum towards genetic divergence.

Rashid *et al*. (2013) studied 20 rice diverse lines for study of correlation and cluster analysis of some yield and related traits. All 20 cultivars were grouped into 6 clusters out of which highest diversity was present between cluster I and cluster VI. Least genetic diversity was seen between cluster III and cluster IV.

Manohara and Singh (2013) studied 24 rice genotypes for genetic diversity on the basis of yield and its component traits. On the basis of D^2 analysis genotypes in 6 clusters genotypes were grouped. Cluster I possesed maximum of 13 genotypes in following was Cluster III with 6 genotypes. Among the different traits taken into account days to 50% flowering, 1000 grain weight, grain breadth and plant height made maximum contribution towards the total divergence.

Gangapur *et al.* (2014) studied on 208 rice genotypes for nine yield and its contributing characters. The genotypes were grouped into 14 clusters. Maximum number of 98 genotypes were grouped into cluster I followed by 32 genotypes in cluster

V. The maximum inter cluster distance was observed between cluster X and cluster XI whereas maximum intra cluster distance was observed in cluster IX and X. Maximum genetic diversity was shown for the traits, spikelets fertility, 100 grain weight and number of filled grains per panicle.

Priyanka (2015) studied on 60 indigenous aromatic genotypes of rice for 17 yield and quality traits. The genotypes were grouped into 8 different clusters. Maximum number of 13 genotypes were grouped into cluster V and cluster VIII while minimum number of one genotype was grouped into cluster II. Maximum inter cluster distance was observed between cluster I and cluster VIII and cluster II and cluster VIII. Maximum intra cluster distance was observed in cluster VII and V. The characters Days to 50% flowering, Kernel length after cooking and amylose content contributed maximum towards genetic divergence.

Chandramohan *et al.* (2016) carried out an experiment on 44 rice genotypes for yield characters. The genotypes were grouped into 11 different clusters. Inter cluster distance was observed between cluster IV and V & cluster V and IX whereas the genotypes present in these clusters can be utilized for further breeding programme. The characters 1000 grain weight and days to 50% flowering contributed maximum towards genetic divergence.

Supriya *et al.* (2017) studied on 48 genotypes of rice for 11 characters and the genotypes were grouped into seven different clusters. Maximum inter cluster distance was observed between cluster IV and VII while minimum for cluster II and IV. The characters 1000 grain weight, days to 50% flowering and days to maturity contributed maximum towards total divergence.

Srinivas (2018) evaluated 37 elite germplasm lines for yield and quality characters. The genotypes were grouped into 18 different clusters. Maximum inter cluster distance was observed between cluster XVI and cluster XVII. Maximum intra cluster distance was observed for cluster XVIII. The characters, days to 50% flowering, milling percentage, number of grains per panicle, head rice recovery and 1000 seed weight contributed 89.79 percent towards genetic divergence.

Kujur *et al.* (2019) studied on 47 rice genotypes to estimate genetic diversity for quantitative characters. The genotypes were grouped into five different clusters. Cluster

I consists of 15 genotypes, cluster II consists of 5 genotypes, cluster III consists of 11 genotypes, cluster IV consists of 9 genotypes and cluster V consists of 7 genotypes. The maximum inter-cluster distance was observed between cluster II and V. Maximum intra-cluster distance was observed for cluster IV.

Devi *et al.* (2020) conducted an experiment upon seventy one rice genotypes for assessing genetic diversity and variability. All genotypes were amalgamed into 11 clusters. Maximum inter cluster distance was noted between cluster VIII and cluster V followed by cluster VII and cluster I.

CHAPTER – III

MATERIALS AND METHODS

The present investigation entitled "**Genetic analysis of yield and quality characters in advanced breeding lines of Rice (*Oryza sativa* L.)**" was conducted during the *kharif* 2020. This chapter details the methods and materials used during the investigation.

3.1 Site of experiment

The present experiment was carried out at Research cum Instructional farm Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.) and the laboratory work was performed at Quality laboratory, Department of Genetics and Plant breeding, RRL, IGKV, Raipur(C.G.).

3.2 Climatic and weather conditions

Raipur is situated between 22° 33' N to 21°14'N Latitude and 82° 6' to 81° 38'E Longitude. Raipur is 305m above sea level. Climate of Raipur is classified as tropical. There is lesser rainfall in winter than in summer. This location is classified as Aw by Köppen and Geiger. Raipur's average annual temperature is 26.5 °C. Precipitation here is about 1401 mm per year. In February precipitation is the lowest, with an average of 11 mm. In july most of the precipitation falls, with an average of 398 mm. The given fig.3.1 shows the meteorological conditions during complete growing period of the crop:

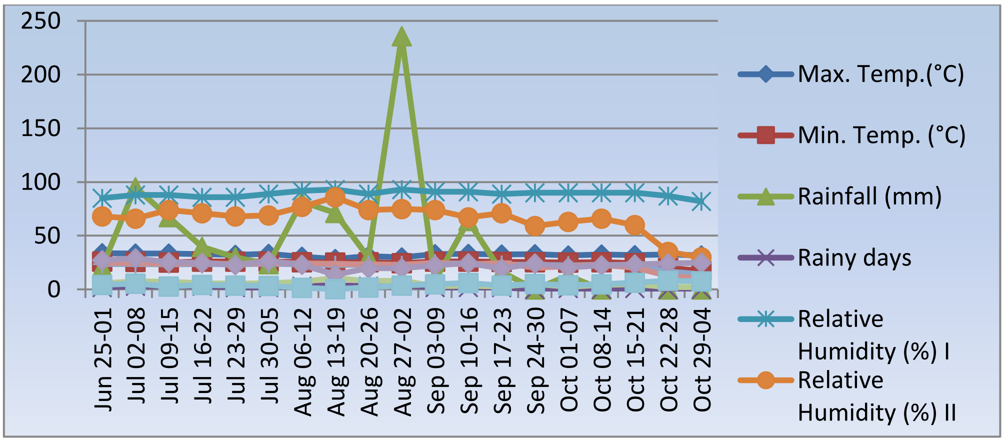

Fig.3.1 Graph showing meteorological conditions during the experiment

3.3 Experimental Materials

The required material for the experiment comprises of total 50 advanced breeding lines of rice along with 5 checks namely IR 64, IGKV R1, IGKV R 2, Karma Mahsuri and IGKV R 1244. During *kharif* 2020, the experiment was set up in a Randomized Block Design of two replications. The list of advanced breeding lines along with their designation is given below:

Table 3.3.1 List of experimental material

Entry No.	Designation	Entry No.	Designation
ABL01	R-1921-176-1-116-1	ABL30	R-2298-353-3-238-1
ABL02	R-1921-173-1-112-1	ABL31	R-2302-386-1-275-1
ABL03	R-BSP-18-3	ABL32	R-2120-37-2-2-1
ABL04	R-BSP-18-2	ABL33	R-2298-354-1-239-1-1
ABL05	R-2340-248-1-286-1	ABL34	R-2302-404-2-315-1
ABL06	R-2302-82-1-43-1	ABL35	R-2298-353-3-238-1
ABL07	R-2340-244-2-278-1	ABL36	R-2298-352-2-235-1
ABL08	R-2307-139-1-120-1	ABL37	R-2288-54-1-15-1
ABL09	R-2302-82-2-44-1	ABL38	R-2302-383-2-269-1
ABL10	R-2302-77-1-33-1	ABL39	R-2307-93-1-63-1
ABL11	R-2294-58-1-17-1	ABL40	R-2298-353-1-236-1
ABL12	R-2465-RP5509-DRR-SPS-154-1	ABL41	R-1774-1-2-2-1
ABL13	R-2298-233-1-73-1	ABL42	R-2311-143-1-123-1
ABL14	R-2307-108-2-86-1	ABL43	R-2307-99-1-75-1
ABL15	R-2307-117-1-95-1	ABL44	R-2298-352-235-1
ABL16	R-2341-265-1-305-1	ABL45	R-2326-187-2-180-1
ABL17	R -2020-295-1-85-1	ABL46	R-2301-382-2-267-1
ABL18	Bhatamasuri Selection 1	ABL47	R-2471-RP5391-DRR-SPS-95-1
ABL19	R-2341-330-2-171-1	ABL48	R-2462-RP5530-DRR-SPS-47-1
ABL20	R-2341-329-2-169-1	ABL49	R-2483-RP5525-B-DRR-SPS-285-1
ABL21	C3-1-5	ABL50	R-2221-272-1-163-1
ABL22	R-2404-638-1-371-1	CHECK1	IR 64
ABL23	R-2307-74-1-50-1	CHECK2	IGKV R1
ABL24	R-2307-74-2-51-1	CHECK3	IGKV R 2
ABL25	C8-1-1	CHECK4	Karma Mahsuri
ABL26	R-2298-354-2-240-1	CHECK5	IGKV R 1244
ABL27	R-1762-197-1-131-1		
ABL28	R-2298-354-1-239-1		
ABL29	R-1853-82-1-80-1		

3.4 Observations recorded

The observations during the investigation were recorded on the basis of five random plants selected at optimum stage of plant growth from each line in both the replications for the evaluation of yield and quality traits except for days to 50% flowering observations were taken on plot basis. The mean values from analyzed plants were considered for statistical analysis.

Table 3.4.1 List of observations recorded for yield and quality characters

Quantitative traits	**Quality traits**	
1. Days to 50% flowering	1. Hulling (%)	12. Kernel L/B ratio
2. Plant height (cm)	2. Milling (%)	13. Kernel length after cooking (mm)
3.Panicle length (cm)	3. Head rice recovery (%)	14. Kernel breadth after cooking (mm)
4. Number of effective tillers per plant	4. Paddy length (mm)	15. Cooked rice L/B ratio
5. Number of filled grains per panicle	5. Paddy breadth (mm)	16. Elongation ratio
6. Number of unfilled grains per panicle	6. Paddy L/B ratio	17. Gel consistency
7. Spikelet fertility (%)	7. Brown rice length (mm)	18. Alkali spreading value
8. 100 seed weight (g)	8. Brown rice breadth (mm)	19. Amylose percentage
9. Grain yield per plant (g)	9. Brown rice L/B ratio	
10. Biological yield per plant (g)	10. Kernel length (mm)	
11. Harvest index (%)	11. Kernel breadth (mm)	

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3.4.1 Yield characters

3.4.1.1 Days to 50% flowering

The cumulative number of days from the date of sowing to the full exersion of panicle in 50% of the total plants in the net plot.

3.4.1.2 Plant height (cm)

At the time of harvest, each plant's height was estimated in centimetres from ground level to the tip of the mother panicle.

3.4.1.3 Panicle length (cm)

It was measured in centimetres from the base of the panicle (neck node) to the tip of the last spikelet prior to harvesting at the time of plant maturity.

3.4.1.4 Effective tillers per plant

At maturity, each plant's tillers bearing a fully formed panicle were counted.

3.4.1.5 Number of filled grains per panicle

Following harvest, the total amount of filled grains per panicle was manually counted and recorded taking five random panicles.

3.4.1.6 Number of unfilled grains per panicle

The total number of unfilled grains was counted manually in five random panicles in the same manner as filled grains were counted.

3.4.1.7 Spikelet fertility %

The per cent of filled spikelets out of total spikelets was calculated and mean obtained.

$$\text{Spikelet fertility percentage} = \frac{No.\ of\ filled\ grains\ per\ panicle}{Total\ No.of\ grains\ per\ panicle} \times 100$$

3.4.1.8 100 seed weight (g)

One hundred sound filled grains were dried up to 12 % moisture level and weighed in grams.

3.4.1.9 Grain yield per plant (g)

Individual plant was threshed by hand, cleaned, dried to a moisture content of 12 percent, and weighed in grams.

3.4.1.10 Biological yield per plant (g)

After drying, the biological yield, including grain and straw, of five randomly chosen plants was weighed and averaged in grams.

3.4.1.11 Harvest index (%)

After calculating both the economic (grain yield) and biological yields in grams, the harvest index is measured as follows:

$$\textit{Harvest Index (\%)} = \frac{Economic\ yield\ (g)}{Biological\ yield\ (g)} \times 100$$

3.4.2 Quality characters

3.4.2.1 Hulling percentage

100 grams of rough rice is passed through a paddy sheller after optimum drying to a moisture level of 12-14 percent, and hulled rice weight was recorded and the percentage of hulling was calculated using the given formula and computed in percent:

$$\textit{Hulling percentage} = \frac{Total\ weight\ of\ hulled\ rice\ (g)}{Total\ weight\ of\ paddy\ (g)} \times 100$$

3.4.2.2 Milling percentage

Brown rice was put into Satake grain testing miller for polishing and weight of milled rice was recorded. Milling percentage was calculated by using given formula:

$$\textit{Milling percentage} = \frac{weight\ of\ milled\ rice\ (g)}{weight\ of\ paddy\ (g)} \times 100$$

3.4.2.3 Head rice recovery percentage (HRR %)

It is the proportion of milled rice with length greater or equal to $3/4^{th}$ of the average length of the whole kernel in total weight of paddy taken.

$$\text{Head rice recovery (\%)} = \frac{weight\ of\ \frac{3th}{4} or\ larger\ kernel + complete\ kernel\ (g)}{weight\ of\ paddy\ (g)} \times 100$$

3.4.2.4 Paddy length (mm)

Ten grains were selected at random without extracting the hull, and the average length in millimetres was recorded.

3.4.2.5 Paddy breadth (mm)

Ten grains were chosen at random without extracting the hull, and the average width in millimetres was recorded.

3.4.2.6 Paddy L/B ratio

Paddy L/B ratio was measured by using given formula:

$$\text{Paddy L/B ratio} = \frac{Paddy\ length\ (mm)}{Paddy\ width\ (mm)} \times 100$$

3.4.2.7 Brown rice length (mm)

Following hulling, ten grains were selected at random and the standard length in millimetres was measured.

3.4.2.8 Brown rice breadth (mm)

Following hulling, ten grains were selected at random and the standard breadth in millimetres was measured.

3.4.2.9 Brown rice L/B ratio

Brown rice L/B ratio was calculated by using given formula:

$$\textit{Brown rice L/B ratio} = \frac{Brown\ rice\ length\ (mm)}{Brown\ rice\ width\ (mm)} \times 100$$

3.4.2.10 Kernel length (mm)

Following milling, ten whole kernels were chosen at random and the average length was determined.

3.4.2.11 Kernel breadth (mm)

Following milling, ten whole kernels were chosen at random and the average breadth was determined.

3.4.2.12 Kernel L/B ratio

Kernel L/B ratio was computed by using given formula:

$$\textit{Kernel L/B ratio} = \frac{Kernel\ length\ (mm)}{Kernel\ width\ (mm)} \times 100$$

3.4.2.13 Length of kernel after cooking (mm)

Length of cooked kernel was measured in mm by taking ten kernels at random and arranging them end to end on graph paper.

3.4.2.14 Kernel breadth after cooking (mm)

After cooking, ten whole kernels were chosen at random and the average width was measured.

3.4.2.15 Cooked rice L/B ratio

Cooked rice L/B ratio was calculated by using given formula:

$$\textit{Cooked rice L/B ratio} = \frac{Cooked\ rice\ length\ (mm)}{Cooked\ rice\ width\ (mm)} \times 100$$

3.4.2.16 Elongation ratio

Elongation ratio was computed by using given formula:

$$\textit{Elongation Ratio} = \frac{Length\ of\ kernel\ after\ cooking\ (mm)}{Length\ of\ kernel\ before\ cooking\ (mm)} \times 100$$

3.4.2.17 Gel consistency

The gel consistency test was carried out using the Cagampang *et al*. (1973) technique. In test tubes, different samples of rice flour (0.1 g) were placed. The samples were prepared with a mixture of ethanol (0.2 mL; 95%) and thymol blue (0.025%), as well as 2 mL of 0.2 N KOH. The samples were heated for 10 minutes in a boiling water bath, the vortex and then let it cooled for 20 minutes in an ice water bath. After 30 minutes, the length of cold gel in test tubes held horizontally on graph paper was used to determine gel consistency.

Table 3.4.2: Classification of Gel Consistency

S. No.	Range	Consistency
1.	20-40 mm	Hard gel consistency
2.	41-60 mm	Medium gel consistency
3.	61-100 mm	Soft gel consistency

3.4.2.18 Alkali spreading value

Six milled rice kernels were uniformly distributed in petridishes containing 1.7 percent KOH solution and baked at 300°C for 23 hours, with the spreading scale recorded according to tables 3.4.3 and 3.4.4

Table 3.4.3: Alkali spreading value/score

1	Kernel is not affected
2	Kernel is swollen
3	Kernel is swollen, collar complete and narrow
4	Kernel is swollen, collar complete and wide
5	Kernel get splitted or dis-integrated, collar complete and wide
6	Kernel is dispersed, merging with collar
7	Kernel is completely dispersed and intermingled

Table 3.4.4: ASV and GT score

Classification	Alkali spreading value (ASV)
1-2	Low
3	Low, medium
4-5	Medium
6-7	High

3.4.2.19 Amylose percentage

Procedure

- 1 mg of well powdered milled rice was taken and 1 ml of rectified spirit was added in a volumetric flask.
- Then 9 ml of 1.0 N Sodium hydroxide added.
- Shaken well and boiled over water bath for 15 minutes and solution was made upto 100 ml in a volumetric flask.
- 1 ml, 2 ml, 3ml, 4 ml and 5 ml of the standard amylose into volumetric flasks in three replicate pipette out,
- For 1 ml of standard amylose solution, 0.2 ml of acetic acid and 2 ml iodine + KI added,
- For 2 ml of standard amylose solution, 0.4 ml of acetic acid and 2 ml of Iodine + KI added,
- For 3 ml of standard amylose solution 0.6 ml of acetic acid and 2 ml Iodine + KI added.
- For 4 ml of standard amylose solution 0.8 ml of acetic acid and 2 ml Iodine + KI added,
- For 5 ml of standard amylose solution 1.0 ml of acetic acid and 2 ml Iodine + KI added,
- After addition of Iodine + KI solution the solution was made up to 100 ml and cover the flasks with a black cloth,
- After 20 minutes readings were taken in spectrophotometer at 620 nm.

Procedure for analysis of amylose content in rice:

(1) Prepare standard rice samples:
   - It was made sure that all samples to be used have been stored in the same room for at least 2 days to ensure equal moisture content.
   - In choosing standard samples a range of rice included representing the low, intermediate and high amylose content.
   - 20 lots of each sample ground to a fine powder in a Wig-L-Bug amalgamator or similar device for 40 seconds a UD cyclone mill with 1 mm sieve may also be used for grinding.

(2) 100 mg rice flour is taken in a long test tube (2*19.5 cm) and 1 ml of rectified spirit and 9 ml pf 1.0 N Sodium hydroxide was added.

(3) Test tube was shaken thoroughly and heated on water bath for 15 minutes. The sample was poured after digestion in a volumetric flask (100 ml) rinsed twice with hot distilled water and later made up the sample to 100 ml.

(4) 5 ml solution was drawn in three replications into three 100 ml volumetric flasks.

(5) For each 5 ml solution 1 ml of acetic acid and 2 ml of I_2-KI reagent was added and it was madeup to 100 ml in a volumetric flask

(6) All flasks were covered with black cloths as I_2-KI loose colour when exposed to light.

(7) The spectrophotometer was adjusted for 620 nm and the readings were taken.

(8) Amylose content was assigned as per the presence of its presence as given below:

Waxy	1-2 %
Very low	2-9 %
Low	9-20 %
Intermediate	20-25 %
High	25-33 %

3.5 Statistical Analysis

The following statistical analysis was performed on the mean values for the above characters using normal statistical procedures:

1. Analysis of variance (ANOVA)

2. Genotypic and phenotypic coefficients of variation (GCV and PCV)

3. Heritability (h^2) and genetic advance (GA)

5. Estimation of correlation coefficients.

6. Direct and indirect effects of characters using path coefficient analysis

7. Genetic divergence and Cluster analysis

3.5.1 Analysis of Variance

As per standard statistical procedure, analysis of variance was calculated for each of the characters separately using a randomised block design (Panse and Sukhatme, 1978).The significance was tested by referring to the values of ‘F’ table (Fisher and Yates, 1967).

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

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

μ = general mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

e_{ij} = random error associated with ith genotype and jth replication

Analysis of variance

Source	Degree of freedom	Mean sum of squares	F-ratio
Replication	(r-1)	RMSS	RMSS/EMSS
Treatment	(t-1)	TrMSS	TrMSS/EMSS
Error	(r-1) (t-1)	EMSS	
Total	(rt-1)		

Where,

r = number of replications and,

t = number of treatments

RMSS = mean sum of squares due to replication

TrMSS = mean sum of square due to treatment and

EMSS = Mean sum of squares due to error.

Using following formula GV and PV was calculated (Burton, 1952):

$$\text{Genotypic variance } (\sigma^2 g) = \frac{TrMSS - EMSS}{r}$$

$$\text{Phenotypic variance, } (\sigma^2 p) = (\sigma^2 g) + (\sigma^2 e)$$

$(\sigma^2 e)$ = error variance

3.5.2 Genotypic and phenotypic coefficient of variance

The genotypic and phenotypic coefficient of variation were calculated according to the formula given by Falconer (1981).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{Genotypic\ standard\ deviation}{Mean} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{Phenotypic\ standard\ deviation}{Mean} \times 100$$

Categories of range of variation as given by Sivasubramanian and Madhavamenon (1973).

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

3.5.3 Heritability and genetic advance

Heritability

Broad sense heritability refers to the proportion of genotypic variation in a population's overall measured variance. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

$$h_{bs}^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h_{bs}^2 = heritability in broad sense

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance ($\sigma^2 g$) + ($\sigma^2 e$)

$\sigma^2 e$ = environmental variance

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

Low	:	0-30%
Medium	:	30-60%
High	:	above 60%

Genetic advance

The predicted benefit or gain in the next generation as a result of selecting superior individuals under a certain level of selection pressure is referred to as genetic advance. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K.\ h^2\ (b).\ \sigma_p$$

Where,

GA = expected genetic advance

K = Selection differential, the value of which is 2.06 at 5% selection intensity

σ_p = phenotypic standard deviation

h^2 (b) = heritability in broad sense

Genetic advance as a percent for mean was calculated to visualise the relative usefulness of genetic advance among the characters.

$$Genetic\ advance\ as\ percent\ of\ mean = \frac{GA}{Grand\ mean} \times 100$$

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

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

3.5.4 Correlation coefficient

Miller *et al* (1958) formula was used to measure correlation coefficients for all quantitative character combinations at the phenotypic, genotypic, and environmental levels.

$$r_{xixj} = \frac{CovX_iX_j}{\sqrt{(VarX_{i)}}.\sqrt{(VarX_j)}}$$

Where,

rX_iX_j	=	coefficient of correlation between X_{ith} and X_{jth} traits
$CovX_iX_j$	=	covariance between X_{ith} and X_{jth} traits
$VarX_i$	=	variancr of X_{ith} trait

$VarX_j$ = variance of X_{jth} trait

By substituting corresponding variance and covariance in the above formula, genotypic, phenotypic, and environmental correlations were calculated. The covariance between two traits was estimated using the same method as the corresponding variance component.

3.5.5 Path coefficient analysis

Path coefficient analysis was used to measure the direct and indirect contribution of different characters to yield, as proposed by Wright (1921) and expanded by Dewey and Lu (1959). For calculating direct and indirect results, the following series of simultaneous equations was created and solved.

$$\begin{bmatrix} r_1Y = P_1Y + r_{12}P_2Y + r_{13}P_3Y + \cdots \ldots\ldots\ldots\ldots\ldots + r_{1k}P_KY \\ r_2Y = r_{21}P_1Y + P_2Y + r_{23}P_3Y + \cdots \ldots\ldots\ldots\ldots\ldots + r_{2k}P_KY \\ : \\ : \\ : \\ r_kY = r_{k1}P_1Y + r_{k2}P_2Y + r_{k3}P_3Y + \cdots \ldots\ldots\ldots\ldots\ldots + P_KY \end{bmatrix}$$

Where,

r_1Y to r_kY = Coefficient of correlation between casual factors 1 to 'k' and independent character Y

P_1Y to P_KY = Direct effects of characters 1 to 'k' on character Y

r_{12} to $r_{k-1,1}$ = Coefficient of correlation among casual factors

The above equations were written in a matrix form as under

$$\underset{A}{\begin{bmatrix} r_1Y \\ r_2Y \\ \vdots \\ r_kY \end{bmatrix}} = \underset{C}{\begin{bmatrix} 1 & r_{12} & r_{13} & \cdots & r_{1k} \\ r_{21} & 1 & r_{23} & \cdots & r_{2k} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ r_{k1} & r_{k2} & r_{k3} & \cdots & 1 \end{bmatrix}} \quad \underset{B}{\begin{matrix} p_1Y \\ p_2Y \\ \vdots \\ p_kK \end{matrix}}$$

Then, B=$[C]^{-1}$.A

$$[C]^{-1} = \begin{bmatrix} C_{11} & C_{12} & C_{13} & \cdots & C_{1k} \\ C_{21} & C_{22} & C_{23} & \cdots & C_{2k} \\ \vdots & \vdots & \vdots & \vdots & \vdots \\ C_{k1} & C_{k2} & C_{k3} & \cdots & C_{kk} \end{bmatrix}$$

Then the direct effects were calculated as follows:-

$$P_1Y = \sum_{i=1}^{k} C_{1k} r_k Y$$

$$P_2Y = \sum_{i=1}^{k} C_{2k} r_k Y$$

$$P_1Y = \sum_{i=1}^{k} C_{ki} r_k Y$$

Residual effect was obtained as per the formula given below:

$$R = \sqrt{1 - \sum d_i r_{ij}}$$

Where,

d_i = Direct effect of the i^{th} character

r_{ij}= correlation coefficients of the i^{th} and j^{th}character

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973)

>1.00	=	Very high
0.3-0.99	=	High
0.2-0.29	=	Moderate
0.1-0.19	=	Low
0.0-0.09	=	Negligible

3.6.6 Genetic divergence and cluster analysis

The D^2 statistic, suggested by Mahalanobis in 1936, is one of the most powerful strategies for determining genetic divergence.

The error variance and covariance values were subjected to multivariate analysis after analysis of variance and covariance. The initial correlated variables (X's) were first converted into uncorrelated variables (Y's linear functions of X's) until D^2 values were calculated.

The inverse matrix of the error dispersion matrix was computed using the pivotal condensation procedure (Rao, 1952). The sum of squares of differences in Y's is the generalised distance function (D^2) between two genotypes. i.e.

$$D^1{}_{1.2} = \sum_{i=1}^{P} (Y_{ii} - Y_{2i})^2$$

The values between variables on the basis of P characters is:

$$D^2{}_P = \sum_{i=1}^{P} \sum_{j=1}^{P} \left(W_{ij} d_i d_j\right)$$

Where,

$D^2{}_P$ is the D^2 value on the basis of P characters between the variables.

W_{ij} is inverse matrix of the pooled common dispersion obtained from error matrix.

"d" is the difference in the mean value for the characters of respective genotypes as indicated by i and j .

In brief, the steps involved for the estimation of D^2 value are as follows (Rao, 1952):

1. Pivotal condensation of error variance and covariance to obtain inverse matrix.
2. Uncorrelated variables are obtained by transforming original correlated data.
3. Calculation of mean values of the transformed characters.

4. Calculation of D^2 values: For each combination deviation between the means was computed and the D^2 were computed and arranged in the form of matrix.

i) Determination of group constellations: The reason cluster concept is not well defined, there are no basic guidelines for creating clusters. The single basis seems to be that genotypes part of the same cluster must have a lower D^2 value on an average than genotypes part of two distinct clusters. The D^2 values of all of the combinations in the matrix form were ordered in ascending order of magnitude, and clustering was performed using Tocher's rule (Rao, 1952). The most closely related genotypes were selected first, followed by the third genotype with the smallest average D^2 values within the first two genotypes. Similarly, the fourth genotype was selected because it had the lowest average D^2 value of the first three genotypes, and the difference in D^2 value within a cluster due to the inclusion of additional genotype was calculated, and so on. New genotypes were added until the rise in average D^2 value became abruptly high, then this genotype was excluded from the previous population. For the purpose of creating new clusters, the genotypes of the first cluster were omitted, and the others were treated similarly.

ii) Intra and inter cluster distances: The intra cluster D^2 value was calculated as the sum of n (n-1)/2. The intra cluster D^2 value for a single genotype is always zero. The inter cluster D^2 value was calculated by adding all possible D^2 values between genotypes in two clusters and then dividing by n_1 x n_2, where n_1 and n_2 represents the number of genotypes in the I and II clusters, respectively. The intra and inter cluster distances were determined by calculating the square root of the D^2 value between genotypes in one cluster and genotypes in two clusters, respectively.

iii) Cluster mean value: The sum of the mean values of genotypes used in a cluster, divided by the number of genotypes in the same cluster, is the cluster mean of a particular character.

Cluster analysis is a set of technique of data reduction that are used to group related or similar observations in a dataset, in a way that in same group observations are as similar as possible, and in the same way, in different groups observations differ to each other as much as possible. In comparison with other data reduction techniques like principal components analysis (PCA) and factor analysis (FA), which are mean to group as per similarities across variables (columns) of a dataset, cluster analysis aims to group observations as per similarities across rows.

Sokal and Michener are credited with inventing the UPGMA clustering method. UPGMA is a clustering approach that employs the (unweighted) arithmetic averages of dissimilarity measurements to avoid characterising dissimilarity between genotypes by extreme values (minimum and maximum).

CHAPTER-IV

RESULTS AND DISCUSSION

The present investigation was performed upon fifty advanced breeding lines of rice and five checks. Experimental material was planted in RBD (randomized block design) with two replications at Research cum Instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, IGKV, Raipur (C.G.) and the laboratory work was performed at Quality laboratory, Department of Genetics and Plant breeding, RRL, IGKV, Raipur (C.G.). The genetic parameters of variability were explored in order to get a clear picture of genotype variability. Eleven yield characters and nineteen quality characters were taken in account for the various analysis. From each replication randomly five plants were selected for taking observation whereas days to 50% flowering observed on plot basis.

The degree of association of yield and head rice recovery % with yield contributing characters and other quality characters respectively was determined using correlation analysis. Simple correlation, on the other hand, does not give enough information on how each trait contributes to yield. As a result, path coefficient analysis is performed for studying the direct and indirect impacts of various independent characters on the dependent character. For yield characters, dependent variable taken was to be grain yield/plant and for quality characters, head rice recovery % was taken as dependent variable taking yield contributing characters and other quality characters as independent variables in respective cases. Cluster analysis was performed to study the genetic diversity for selection of diverse lines for hybridization in future. The UPGMA agglomerative clustering analysis based on dissimilarity coefficients was performed.

The results of experiment conducted are discussed under following heads:

4.1 Analysis of variance

4.2 Estimation of parameters of genotypic variation

4.3 Correlation analysis

4.4 Path coefficient analysis

4.5 Cluster analysis

4.1 Analysis of variance

The observed variations between lines for a given trait are referred to as analysis of variance and it was used to determine the degree of variation of observed characters among advanced breeding lines of rice and the results are presented in tables 4.1 and 4.2 for yield and quality characters respectively. For all of the characters, the study of variance showed extremely significant variations among the 55 advanced breeding lines, suggesting significant genetic variation in the material. For all yield and quality characters tested, an F-test revealed that the values of mean sum of squares were significant (at 1% level of significance).

High genetic variability for different yield traits in rice was also reported by Khan *et al*., (2009), Devi *et al*., (2017) and Srujana *et al*., (2017).

Table 4.1: Analysis of variance for yield characters in advanced breeding lines of rice

S. No.	Sources of variance	Mean sum of squares		
		Replication (df=1)	Advanced breeding lines (df=54)	Error (df=54)
1.	Days to 50% flowering	4.81	27.624**	1.402
2.	Plant height (cm)	25.34	91.529**	7.004
3.	Number of effective tillers per plant	0.22	2.307**	0.765
4.	Panicle length (cm)	0.02	3.721**	0.94
5.	Number of filled grains per panicle	281.6	2,566.94**	166.026
6.	Number of unfilled grains per panicle	281.6	910.541**	161.878
7.	Spikelet fertility %	64.298	103.072**	23.277
8.	100 seed weight (g)	0.011	0.356**	0.003
9.	Biological yield per plant (g)	26.118	194.946**	39.71
10.	Harvest index %	101.953	225.902**	67.088
11.	Grain yield per plant (g)	2.658	44.324**	6.835

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

Table 4.2: Analysis of variance for quality characters in advanced breeding lines of rice

S. No.	Sources of variance	Mean sum of squares		
		Replication (df=1)	Advanced breeding lines (df=54)	Error (df=54)
1.	Hulling %	10.172	18.202**	3.517
2.	Milling %	7.384	34.616**	1.926
3.	Paddy length (mm)	0.052	0.969**	0.08
4.	Paddy breadth (mm)	0.052	0.124**	0.016
5.	Paddy L/B ratio	0.105	0.365**	0.048
6.	Brown rice length (mm)	0.029	0.603**	0.007
7.	Brown rice breadth (mm)	0.006	0.083**	0.002
8.	Brown rice L/B ratio	0.02	0.24**	0.006
9.	Kernel length (mm)	0.001	0.41**	0.025
10.	Kernel breadth (mm)	0.009	0.07**	0.003
11.	Kernel L/B ratio	0.029	0.179**	0.01
12.	Kernel length after cooking (mm)	0.015	0.809**	0.15
13.	Kernel breadth after cooking (mm)	0.013	0.191**	0.006
14.	Cooked rice L/B ratio	0.002	0.21**	0.022
15.	Elongation ratio	0.003	0.016**	0.005
16.	Gel consistency	73.636	395.037**	43.673
17.	Alkali spreading value	0.909	5.364**	0.465
18.	Amylose %	0.611	148.221**	18.686
19.	Head rice recovery %	11.913	200.538**	3.143

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

4.2 Estimation of parameters of genotypic variation

The parameters of genetic variability, such as mean, range, genotypic and phenotypic coefficients of variance (percent), heritability in the broad sense (percent), genetic advance, and genetic advance as a % of mean, were analyzed and tabulated in table 4.3 (a) and 4.3 (b) for yield and quality characters respectively.

4.2.1. Genetic parameters for yield and yield contributing characters

4.2.1.1 Days to 50% flowering

The range of variation for days to 50% flowering was from 86.5 (R 2302-77-1-33-1) to 103 (R1762-197-1-131-1) days with a general mean value of 91.79 days. The values of GCV, PCV, h^2, GA as % of mean were 3.95%, 4.15%, 90.34% and 7.72% respectively.

4.2.1.2 Plant height (cm)

Plant height varied for the lines from 93.49 cm (R 1921-176-1-116-1) to 126.33 cm (R2326-187-2-180-1) with an average plant height of 108.10 cm. The values for PCV, GCV, h^2, GA as % of mean were 6.49%, 6.01%, 85.78% and 11.47% respectively.

4.2.1.3 Number of effective tillers per plant

The highest value of number of effective tillers/plant obtained was 10.30 (R2298-353-3-238-1) and least value for the same was 4.90 (R 2302-77-1-33-1) tillers/plant. There was an average obtained for this character was 7.18 tillers/plant. The values for PCV, GCV, h^2, GA as % of mean were 17.27%, 12.24%, 50.21% and 17.86% respectively.

4.2.1.4 Panicle length (cm)

The highest value for panicle length was 27.38 cm (R2311-143-1-123-1) and least was 21.43 cm (R2298-233-1-73-1) with a general mean value of 24.67 cm. The values obtained for PCV, GCV, h^2, GA as % of mean were 6.19%, 4.78%, 59.66% and 7.60% respectively.

4.2.1.5 Number of filled grains per panicle

The value for number of grains/panicle was as high as 256 (Bhatamasuri Selection 1) grains per panicle and as low as 90 (R 2307-139-1-120-1) grains per panicle with a general mean value of 141.51 grains per panicle. The values obtained for PCV, GCV, h^2, GA as % of mean were 26.12%, 24.48%, 87.85% and 47.27% respectively.

4.2.1.6 Number of unfilled grains per panicle

The value for trait number of unfilled grains/panicle was as high as 126 grains and as low as 14 grains per panicle (Karma Mahsuri) with a general mean of 39.33 grains per panicle (R 2307-108-2-86-1). Values obtained for PCV, GCV, h^2, GA as % of mean were 58.88%, 49.20%, 69.81% and 84.68% respectively.

4.2.1.7 Spikelet fertility %

The highest value obtained for spikelet fertility % was 89.62% (R2307-99-1-75-1) and least value obtained was 54.58% (R2298-353-3-238-1) with an average value of 78.79%. The PCV, GCV, h^2, GA as % of mean values obtained were 10.09%, 8.02%, 63.15% and 13.12% respectively.

4.2.1.8 100 seed weight (g)

The highest value obtained for 100 seed weight (g) was 3.37g (R2302-404-2-315-1) and least was 1.47g (R2326-187-2-180-1) with a general mean value of 2.35g. The values obtained for PCV, GCV, h^2, GA as % of mean were 18.01%, 17.87%, 98.41% and 36.52% respectively.

4.2.1.9 Biological Yield per plant (g)

The highest value for biological yield per plant obtained was 67.56g (R2298-354-1-239-1) and least value was 27.55g (R 2465-RP5509-DRR-SPS-154-1) with an average value of 42.91g. The values obtained for PCV, GCV, h^2, GA as % of mean were 25.25%, 20.53%, 66.15% and 34.40% respectively.

4.2.1.10 Harvest index %

The highest value obtained for harvest index% was 82.41% (R2302-404-2-315-1) and least value obtained was 25.74% (R2298-352-235-1) with a general mean value of 46.51%. The values obtained for PCV, GCV, h^2, GA as % of mean were 26.02%, 19.16%, 54.21% and 29.06% respectively.

4.2.1.11 Grain yield/plant (g)

The highest value obtained for grain yield/plant was 31.58g (R2302-404-2-315-1) and least value obtained was 11.13g (R 2020-295-1-85-1) with a general mean value of 19.33g. The values obtained for PCV, GCV, h^2, GA as % of mean were 26.17%, 22.40%, 73.28% and 39.50% respectively.

4.2.2 Genetic parameters for grain quality parameters

4.2.2.1 Hulling %

The highest value obtained for hulling % was 82.23% in R 2294-58-1-17-1 and lowest value obtained was 71.29 % (R 1921-176-1-116-1) with a general mean value of 77.03 %. This character had a low value for PCV and GCV 4.278 % and 3.52 % respectively. High h^2 value of 67.61% was obtained and a low value for G.A as % of mean (5.96%).

4.2.2.2 Milling %

The highest value obtained for milling % was 78.56% in R 2288-54-1-15-1 and least value obtained was 57.45% in R2341-329-2-169-1 with a general mean value of 68.41%. The PCV and GCV values obtained were low (6.25% and 5.91% respectively). A high heritability% of 89.46% and a moderate GA as % of mean of 11.51% value was obtained.

4.2.2.3 Paddy length (mm)

The highest value obtained for paddy length (mm) was 10.35 mm in R2120-37-2-2-1) and least value obtained was 7.4 mm in R1774-1-2-2-1 with a general mean value of 8.82 mm. The PCV and GCV values obtained were low (8.21% and 7.56% respectively). A high h^2 value of 84.82% was obtained with a moderate value of GA as % of mean (14.35%).

4.2.2.4 Paddy breadth (mm)

The highest value obtained for paddy breadth (mm) was 3.15 mm (R2302-383-2-269-1) and least value obtained was 2.10 mm (R2120-37-2-2-1) with a general mean value of 2.51 mm. The PCV and GCV values obtained were relatively low (10.52% and 9.25% respectively). A relatively high h^2 value of 77.28% was obtained with a moderate value of GA as % of mean (16.75%).

4.2.2.5 Paddy L/B ratio

The highest value obtained for paddy L/B ratio was 4.94 (R2120-37-2-2-1) and least value obtained was 2.50 (R2471-RP5391-DRR-SPS-95-1) with a general mean value of 3.56. The PCV and GCV values obtained were moderate (12.77% and 11.19% respectively). A relatively high h^2 value of 76.84% was obtained with a high value of GA as % of mean (20.21%).

4.2.2.6 Brown rice length (mm)

The highest value obtained for brown rice length (mm) was 7.9 mm (R2298-352-235-1) and least value obtained was 5.6 mm (R2298-352-235-1) with an average value of 6.7 mm. The PCV, GCV, h^2, GA as % of mean values obtained were 8.26% (low), 8.16% (low), 97.57 (high) and 16.59% (high) respectively.

4.2.2.7 Brown rice breadth (mm)

The highest value obtained for brown rice breadth (mm) was 2.55mm (R2341-329-2-1, R2341-330-2-171-1) and least value obtained was 1.80 mm (R1762-197-1-131-1, R2120-37-2-2-1, R2307-93-1-63-1 and R2311-143-1-123-1) with an average value of 2.14 mm. The PCV, GCV, h^2, GA as % of mean values obtained were 9.64% (low), 9.42% (low), 95.47% (high) and 18.96% (moderate) respectively.

4.2.2.8 Brown rice L/B ratio

The highest value obtained for brown rice L/B ratio was 3.92(R2120-37-2-2-1) and least value obtained was 2.43(R2341-329-2-169-1) with an average value of 3.17. The PCV, GCV, h^2, GA as % of mean values obtained were 11.06% (moderate), 10.77% (moderate), 94.97% (high) and 21.63% (moderate) respectively.

4.2.2.9 Kernel length (mm)

The highest value obtained for kernel length (mm) was 7.15 mm (R2307-74-2-51-1) and least value obtained was 4.95 mm (R2471-RP5391-DRR-SPS-95-1) with an average value of 6.02 mm. The PCV, GCV, h^2, GA as % of mean values obtained were 7.74% (low), 7.29% (low), 88.59% (high) and 14.13% (moderate) respectively.

4.2.2.10 Kernel breadth (mm)

The highest value obtained for kernel breadth (mm) was 2.5 mm (R2341-330-2-171-1) and least value obtained was 1.73 mm (R1762-197-1-131-1, R2298-354-1-239-1, R2298-353-1-236-1 and R2311-143-1-123-1) with an average value of 2.06 mm. The PCV, GCV, h^2, GA as % of mean values obtained were 9.24% (low), 8.90% (low), 92.78% (high) and 17.67% (moderate) respectively.

4.2.2.11 Kernel L/B ratio

The highest value obtained for kernel L/B ratio was 3.57% and least value obtained was 2.28 (R2120-37-2-2-1) with an average value of 2.99 (R2341-330-2-171-1). The PCV, GCV, h^2, GA as % of mean values obtained were 10.29% (moderate), 9.73% (low), 89.39% (high) and 18.94% (moderate) respectively.

4.2.2.12 Kernel length after cooking (mm)

The highest value obtained for kernel length after cooking (mm) was 10.35 mm (R2302-404-2-315-1) and least value obtained was 7.15 mm (R2471-RP5391-DRR-SPS-95-1) with an average value of 8.44 mm. The PCV, GCV, h^2, GA as % of mean values obtained were 8.21% (low), 6.81% (low), 68.76% (high) and 11.62% (moderate) respectively.

4.2.2.13 Kernel breadth after cooking (mm)

The highest value obtained for kernel breadth after cooking (mm) was 3.55 mm (R2301-382-2-267-1, R2302-404-2-315-1) and least value obtained was 2.15 mm (R2298-353-3-238-1) with an average value of 78.79%. The PCV, GCV, h^2, GA as % of mean values obtained were 10.44% (moderate), 10.09% (moderate), 93.49% (high) and 20.11% (moderate) respectively.

4.2.2.14 Cooked rice L/B ratio

The highest value obtained for cooked rice L/B ratio was 3.79 (R2298-353-3-238-1) and least value obtained was 2.13(R2471-RP5391-DRR-SPS-95-1) with an average value of 2.84. The PCV, GCV, h^2, GA as % of mean values obtained were 12% (moderate), 10.83% (moderate), 81.41% (high) and 20.13% (moderate) respectively.

4.2.2.15 Elongation ratio

The highest value obtained for elongation ratio was 1.60 (R2302-404-2-315-1) and least value obtained was 1.27 (IR 64 and R 2340-248-1-286-1) with an average value of 1.40. The PCV, GCV, h^2, GA as % of mean values obtained were 7.43% (low), 5.32% (low), 51.21% (medium) and 7.84% (low) respectively.

4.2.2.16 Gel consistency

The highest value obtained for gel consistency was 97.5 mm (R2298-353-3-238-1) and least value obtained was 31 mm (R 2340-248-1-286-1) with an average value of 49 mm. The PCV, GCV, h^2, GA as % of mean values obtained were 30.23% (high), 27.05 (high), 80.09 % (high) and 49.87 % (high) respectively.

4.2.2.17 Alkali spreading value

The highest value obtained for alkali spreading value was 7 and least value obtained was 2 with an average value of 4.86. The PCV, GCV, h^2, GA as % of mean values obtained were 35.17% (high), 32.24% (high), 84.06 % (high) and 60.90 (high) respectively.

4.2.2.18 Amylose %

The highest value obtained for amylose% was 44.80 % (IGKV R1) and least value obtained was 12.65 % (R2221-272-1-163-1) with an average value of 26.51%. The PCV, GCV, h^2, GA as % of mean values obtained were 34.46% (high), 30.36% (high), 77.61% (high) and 55.09% (high) respectively.

4.2.2.19 Head rice recovery %

The highest value obtained for head rice recovery % was 62.52% (R1762-197-1-131-1) and least value obtained was 22.12% (R2341-330-2-171-1) with an average value of 44.74%. The PCV, GCV, h^2, GA as % of mean values obtained were 22.56% (high), 22.20% (high), 96.91% (high) and 45.03% (high) respectively.

Acceptable range for head rice recovery % is >50%, intermediate alkali spreading value, amylose content between 20-25% and soft gel consistency. The mean for each quality trait of particular advanced breeding lines is presented in table 4.2.1 (b). The values of lines for quality characters falling under acceptable range of respective quality characters are in bold. Table 4.2.1.7 represents the frequency table and percent value of main quality characters. Out of 50 advanced breeding lines 41 lines gave more than 65 percent milling%. Highest milling % was exhibited by R 2288-54-1-15-1 (78.56%) followed by R2298-354-2-240-1 (75.77%) and R2298-352-235-1 (75.47%). Twenty two breeding lines showed more than 50% HRR including checks. R1853-82-1-80-1 (60.53), R1762-197-1-131-1 (62.52), R2302-383-2-269-1 (55.11), R2307-99-1-75-1 (54.33), R2298-353-3-238-1 (54.27) have high head rice recovery %. As per estimates of kernel length out of fifty five lines two lines R2307-74-1-50-1 and R2307-74-2-51-1 had long grain, forty five lines had medium grain and eight lines had short size grains. With the help of kernel L/B ratio estimates of grain shape was deduced as per which twenty six lines had long slender grain shape, twenty nine lines had medium slender grain shape and there was no line with bold or round grain shape. Highest elongation ratio was obtained in line R2302-404-2-315-1 (1.60) followed by R2298-354-1-239-1-1 (1.59) and R2298-354-1-239-1 (1.58). As per estimates of gel consistency twenty lines showed hard gel consistency, twenty three lines showed medium gel consistency and twelve lines showed soft gel consistency. Alkali spreading value estimates showed that only one line showed low alkali spreading value, thirteen lines had low-intermediate alkali spreading value, fifteen lines had intermediate alkali spreading value and twenty six lines had high alkali spreading. Fifteen lines had low amylose content, thirteen lines had intermediate amylose content and twenty seven lines had high amylose content.

Table 4.3 (a): Genetic parameter of variation for yield and yield contributing characters in advanced breeding lines of rice

S. No	Characters	Mean	Range		CD at 5 %	CV%	Coefficient of variance		h^2%	GA	GA% mean
			Max.	Min.			PCV	GCV			
1.	Days to 50% flowering	91.79	103.00	86.50	2.37	1.29	4.15	3.95	90.34	7.09	7.72
2.	Plant height (cm)	108.10	126.33	93.49	5.30	2.45	6.49	6.01	85.78	12.40	11.47
3.	Number of effective tillers per plant	7.18	10.30	4.90	1.75	12.18	17.27	12.24	50.21	1.28	17.86
4.	Panicle length (cm)	24.67	27.38	21.43	1.94	3.92	6.19	4.78	59.66	1.88	7.60
5.	Number of filled grains per panicle	141.51	256.00	90.00	25.83	9.11	26.12	24.48	87.85	66.90	47.27
6.	Number of unfilled grains per panicle	39.33	126.50	14.00	25.39	32.27	58.88	49.20	69.81	33.30	84.68
7.	Spikelet fertility %	78.79	89.62	54.58	9.68	6.13	10.09	8.02	63.15	10.34	13.12
8.	100 seed weight (g)	2.35	2.89	1.47	0.01	2.10	18.01	17.87	98.41	0.86	36.52
9.	Biological yield per plant (g)	42.91	67.56	27.55	19.44	22.60	25.25	20.53	66.15	14.76	34.40
10.	Harvest index %	46.51	82.41	25.74	20.63	21.80	26.02	19.16	54.21	13.52	29.06
11.	Grain yield per plant (g)	19.33	31.58	11.13	5.24	13.52	26.17	22.40	73.28	7.64	39.50

Table 4.3 (b): Genetic parameter of variation for quality characters in advanced breeding lines of rice

S. No	Characters	Mean	Range		CD	CV%	Coefficient of variance		h^2%	GA	GA% mean
			Max.	Min.			PCV	GCV			
1.	Hulling %	77.03	82.23	71.29	1.59	4.85	4.28	3.52	67.61	4.59	5.96
2.	Milling %	68.41	78.56	57.45	2.09	6.50	6.25	5.91	89.46	7.88	11.51
3.	Paddy length (mm)	8.82	10.35	7.40	2.92	8.71	8.21	7.57	84.82	1.27	14.35
4.	Paddy breadth (mm)	2.51	3.15	2.10	1.50	4.26	10.52	9.25	77.28	0.42	16.75
5.	Paddy L/B ratio	3.56	4.94	2.50	5.67	16.78	12.77	11.19	76.84	0.72	20.21
6.	Brown rice length (mm)	6.70	7.90	5.60	2.37	7.19	8.26	8.16	97.57	1.11	16.59
7.	Brown rice breadth (mm)	2.14	2.55	1.80	2.85	8.92	9.64	9.42	95.47	0.41	18.96
8.	Brown rice L/B ratio	3.17	3.92	2.43	3.38	9.82	11.06	10.77	94.97	0.69	21.63
9.	Kernel length (mm)	6.02	7.15	4.95	3.13	9.18	7.74	7.29	88.59	0.85	14.13
10.	Kernel breadth (mm)	2.06	2.50	1.73	2.40	7.32	9.24	8.90	92.78	0.36	17.67
11.	Kernel L/B ratio	2.99	3.57	2.28	3.03	8.05	10.29	9.73	89.39	0.57	18.94
12.	Kernel length after cooking (mm)	8.44	10.35	7.15	2.96	8.58	8.21	6.81	68.76	0.98	11.62
13.	Kernel breadth after cooking (mm)	3.01	3.55	2.15	2.78	7.22	10.44	10.09	93.49	0.61	20.11
14.	Cooked rice L/B ratio	2.84	3.79	2.13	2.31	6.58	12.00	10.83	81.41	0.57	20.13
15.	Elongation ratio	1.40	1.60	1.27	2.11	5.82	7.43	5.32	51.21	0.11	7.84
16.	Gel consistency	49.00	97.5	31.00	6.12	17.07	30.23	27.05	80.09	24.44	49.87
17.	Alkali spreading value	4.86	6.50	2.00	6.34	17.60	35.17	32.24	84.06	2.96	60.89
18.	Amylose %	26.51	44.80	12.65	3.24	9.83	34.46	30.36	77.61	14.61	55.09
19.	Head rice recovery %	44.74	62.52	22.12	4.17	12.94	22.56	22.20	96.91	20.15	45.03

4.2.3 Genotypic coefficient of variation and phenotypic coefficient of variation

Results of genetic variability revealed that all the characters under study showed greater phenotypic coefficient of variation than genotypic coefficient of variation which indicates that environment having masking effect on the expression of genetic variability. The range of variation obtained for all the studied characters indicated enough scope to study considerable range of variation. Trait number of unfilled grains/panicle (58.88; 49.20) had highest PCV and GCV value followed by grain yield^{-1} (26.17; 22.40) and number of filled grains/panicle (26.123; 24.49) lowest value of PCV and GCV was observed for days to 50% flowering (4.15; 3.95) followed by panicle length (6.19; 4.78) and plant height (6.49; 6.01). For quality characters also range of PCV and GCV was from low to high. Highest PCV and GCV value observed for trait alkali spreading value (35.17; 32.24) followed by amylose% (34.46; 30.36) and gel consistency (30.23; 27.05). Lowest PCV and GCV values obtained for trait hulling% (4.28; 3.52) which were followed by milling% (6.25; 5.91) and elongation ratio (7.43; 5.32). The yield and quality characters which showed low PCV and GCV were plant height(cm), days to 50 % flowering, panicle length(cm), spikelet fertility%, hulling%, milling%, paddy length(mm), brown rice length(mm), kernel length(mm), paddy breadth(mm), brown rice breadth(mm), kernel breadth(mm) and kernel length after cooking(mm). Characters which showed moderate value of GCV and PCV were number of effective tillers/plant, 100 seed weight (g), paddy L/B ratio, brown rice L/B ratio, kernel L/B ratio, kernel breadth after cooking (mm) and cooked rice L/B ratio. Characters showed high value of GCV and PCV were number of filled grains/panicle, biological yield per plant (g), number of unfilled grains/panicle, harvest index %, grain yield/plant (g), gel consistency, amylose %, alkali spreading value and head rice recovery %. The classification of characters as per the value of GCV and PCV obtained is done in three categories as low (0-10%), moderate (10-20%) and high (>20%) and presented in table 4.4

These results are in line with the findings of Rathi *et al.*, (2019), Longjam and Singh (2019) and Chakrabarty *et al.*, (2020).

Table 4.4: GCV and PCV range obtained for different yield and quality characters

Low (0-10%)	Moderate (10-20%)	High (>20%)
Yield characters:		
Plant height(cm), days to 50 % flowering, spikelet fertility %, panicle length(cm)	100 seed weight (g), number of effective tillers/plant,	Number of filled grains/panicle, biological yield per plant(g), number of unfilled grains/panicle, harvest index %, grain yield/plant (g)
Quality characters:		
Hulling %, paddy length(mm), milling %, brown rice length(mm), kernel length(mm), kernel length after cooking(mm), paddy breadth(mm), brown rice breadth(mm) and kernel breadth(mm)	Paddy L/B ratio, brown rice L/B ratio, kernel L/B ratio, kernel breadth after cooking (mm) and cooked rice L/B ratio	Head rice recovery %, amylose %, Gel consistency, alkali spreading value

4.2.4 Heritability%

Estimates of heritability for yield and quality characters ranged from medium to high heritability. The yield characters for which highest and lowest heritability obtained were 100 seed weight (98.41%) and number of effective tillers/plant (50.21%) respectively. Yield characters for which high heritability obtained were 100 seed weight (g) (98.41%), days to 50% flowering (90.34%), plant height (cm) (85.78%), number of filled grains/panicle (87.85%), grain yield/plant (g) (73.28%), number of unfilled grains/panicle (69.81%), biological yield per plant (g) (66.15%) and spikelet fertility% (63.15%). Medium estimates of heritability obtained for yield characters were panicle length (cm) (59.66%), harvest index (54.21%) and number of effective tillers/plant (50.21%). The highest and lowest value of heritability obtained for quality characters were brown rice length (mm) (97.57%) and elongation ratio (51.21%) respectively. Only for the quality trait elongation ratio medium heritability estimates were obtained and all other quality characters showed high estimates of heritability which were brown rice length (mm) (97.57%), head rice recovery% (96.91%), brown rice L/B ratio (94.97%), brown rice breadth (mm) (95.47%), kernel breadth after cooking (mm) (93.49%), kernel breadth (mm) (92.78%), milling% (89.46%), kernel L/B ratio (89.39%), paddy length (mm) (84.82%), paddy breadth (mm) (77.28%), kernel length (mm) (88.59%), cooked rice L/B ratio (81.41%), gel consistency (80.09%), alkali spreading value (84.06%), amylose% (77.61%), paddy L/B ratio (76.84%), kernel length after cooking (mm) (68.76%) and hulling% (67.61%).

Similar results were obtained by Saha *et al.*, (2019) and Parimala and Devi (2019).

Estimates of heritability observed by different yield and quality characters presented in table 4.5:

Table 4.5: Estimates of heritability (h^2) for different yield and quality characters

Medium (30-60%)	**High (>60%)**
Effective tillers/plant panicle length (cm), harvest index% and elongation ratio.	Days to 50% flowering, number of filled grains/panicle, plant height (cm), number of unfilled grains/panicle, 100 seed weight (g), spikelet fertility%, hulling%, biological yield per plant (g), milling%, paddy length (mm), brown rice length (mm), kernel length (mm), kernel length after cooking (mm), paddy breadth (mm), paddy L/B ratio, brown rice breadth (mm), brown rice L/B ratio, kernel breadth (mm), kernel L/B ratio, kernel breadth after cooking (mm), cooked rice L/B ratio, gel consistency, amylose%, alkali spreading value and head rice recovery %.

4.2.5 Genetic advance as % of mean

The advance breeding lines showed genetic advance as % of mean from low to high value. While noting for genetic advance as percent of mean, the yield characters observed with highest value was number of unfilled grains/panicle (84.68%) and least value was obtained for trait panicle length (7.6%). High estimates of genetic advance as % of mean obtained from characters were number of filled grain/panicle (47.27%), biological yield per plant (34.40%), number of unfilled grains/panicle (84.68%), grain yield/plant (39.50%), 100 seed weight (36.52%) and harvest index (29.06%). Moderate value of genetic advance as % of mean were obtained from characters plant height (11.47%), number of effective tillers/plant (17.86%) and spikelet fertility% (13.12%). Low estimates of genetic advance as % of mean was noted for trait panicle length (7.60%) and days to 50% flowering (7.72%). In the same manner observations for quality characters were taken which showed that trait with highest value of genetic advance as % of mean was alkali spreading value (60.89%) and lowest value was for hulling% (5.96%). Quality characters for which high estimates of genetic advance as % of mean obtained were paddy L/B ratio (20.21%), brown rice L/B ratio (21.63%), kernel breadth after cooking (20.11%), cooked rice L/B ratio (20.13%), amylose % (55.09%), gel consistency (49.87%), alkali spreading value (60.89%) and head rice recovery % (45.08%). Similar results were obtained by Rathi *et al.*, (2019), Ganpati *et al.*, (2020) and Behera *et al.*, (2018).

The table 4.6 presents the varying level of genetic advance as % of mean obtained in different characters i.e. low (<10%), moderate (10-20%) and high (>20%):

Table 4.6: Level of genetic advance as % of mean observed in different yield and quality characters

Low (<10%)	Moderate (10-20%)	High (>20%)
Panicle length (cm), days to flowering, hulling% and elongation ratio	Effective tillers/plant, plant height (cm), spikelet fertility%, milling%, paddy length (mm), kernel length (mm), kernel length after cooking (mm), brown rice length (mm), paddy breadth (mm), brown rice breadth (mm), kernel breadth (mm) and kernel L/B ratio.	Number filled grain/panicle, 100 seed weight (g), number of unfilled grain/panicle, biological yield per plant (g), grain yield/plant (g), harvest index%, paddy L/B ratio, cooked rice L/B ratio, brown rice L/B ratio, kernel breadth after cooking, amylose%, alkali spreading value, head rice recovery % and gel consistency.

4.2.6 Heritability and genetic advance as % of mean

The heritability (h^2) is a rough estimate of a character's expression. Heritability is defined by Falconer and Mackay (1996) as the measure of the relationship between breeding values and phenotypic values. Estimating heritability helps breeders manage the resources needed to successfully select for desirable characteristics and achieve maximum genetic gain with minimal effort and resources. The degree of gain achieved in a character under a certain selection pressure is referred to as genetic advance. The best conditions for selection are high genetic advance combined with high heritability estimates (Larik *et al.,* 2000). It also shows the existence of additive genes in the trait, implying that crop improvement can be achieved by selecting such characters. Individual assessment of the parameters is less trustworthy and useful than heritability estimates with genetic advance. Therefore, estimates of heritability with genetic advance are used for selecting characters for improvement.

The yield characters in which high heritability and high genetic advance as % of mean was obtained were number of filled grain/panicle, 100 seed weight (g), number of unfilled grain/panicle, biological yield per plant (g) and grain yield/plant (g). In quality characters the characters in which high heritability with high genetic advance obtained were paddy L/B ratio, brown rice L/B ratio, cooked rice L/B ratio, kernel breadth after cooking (mm), gel consistency, amylose %, alkali spreading value and head rice recovery %. Presence of high heritability and high genetic advance as % of mean shows presence of paramount of additive gene action in these characters thus selection (mass selection and progeny selection) will be successful for improvement of such characters. Similar results were observed in recent studies by Singh *et al.,* (2021) and Kumar *et al.,* (2020).

However, for yield characters plant height (mm) and spikelet fertility% and for the quality characters milling%, paddy length (mm), paddy breadth (mm), brown rice length (mm), brown rice breadth (mm), kernel length (mm), kernel breadth (mm), kernel L/B ratio and kernel length after cooking (mm) high heritability with moderate genetic advance as % of mean was obtained. Presence of high heritability and moderate genetic advance suggests presence of paramount of non-additive gene action thus heterosis breeding will be successful for improving these characters. Same outputs were obtained by previous studies by Singh *et al.,* (2021) and Kumar *et al.,* (2020).

Table 4.7: Estimates of heritability along with genetic advance for different yield and quality characters

S. No.	Category	Characters
1.	High heritability with high genetic advance as % of mean	Number of filled grain/panicle 100 seed weight (g), number of unfilled grain/panicle, biological yield per plant (g), brown rice L/B ratio, grain yield/plant (g), paddy L/B ratio, kernel breadth after cooking (mm), cooked rice L/B ratio, gel consistency, amylose%, head rice recovery % and alkali spreading value
2.	High heritability with moderate genetic advance as % of mean	Plant height (mm), spikelet fertility%, milling%, paddy length (mm), brown rice length (mm), kernel length (mm), paddy breadth (mm), brown rice breadth (mm), kernel breadth (mm), kernel length after cooking (mm) and kernel L/B ratio
3.	High heritability with low genetic advance as % of mean.	Days to 50 % flowering and hulling %
4.	Moderate heritability with high genetic advance as % of mean	Harvest index %
5.	Moderate heritability with moderate genetic advance as % of mean	Effective tiller/plant
6.	Moderate heritability with low genetic advance as % of mean	Elongation ratio, panicle length (cm)

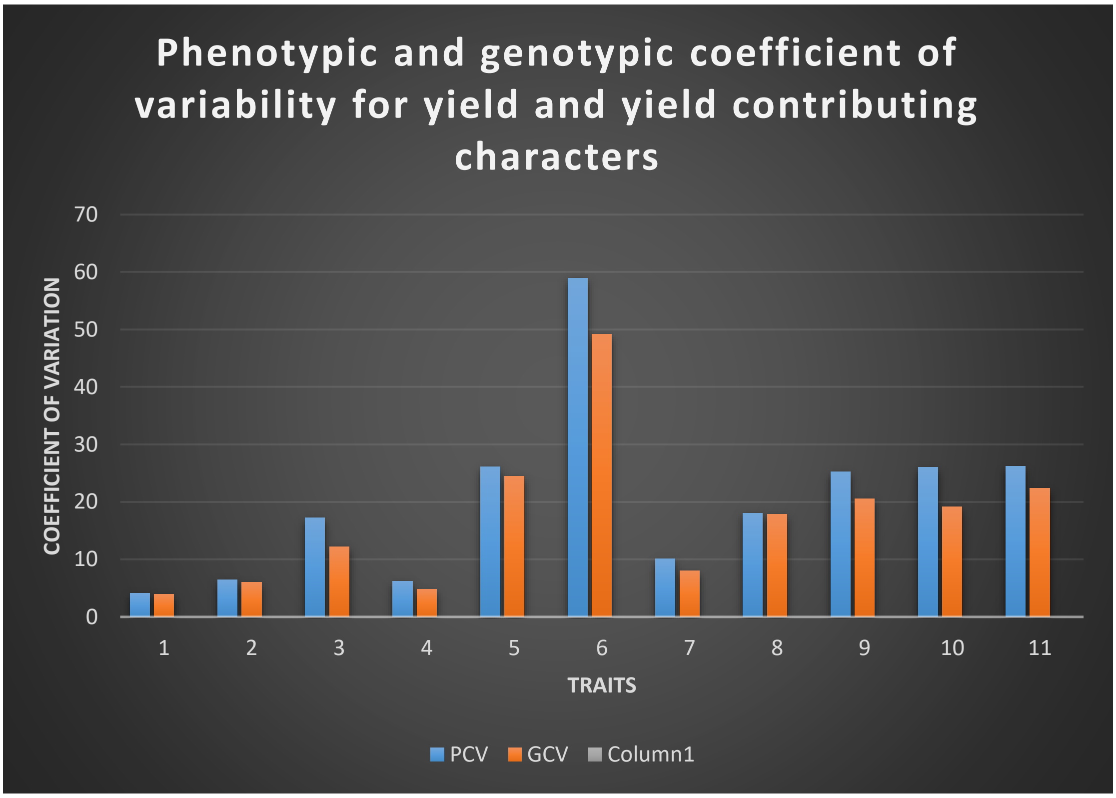

Fig. 4.1 Bar diagram showing phenotypic and genotypic coefficient of variability for yield and yield contributing characters

1. Days to 50% flowering
2. Plant height (cm)
3. Number of effective tillers
4. Panicle length (cm)
5. Number of filled grains per panicle
6. Number of unfilled grains per panicle
7. Spikelet fertility %
8. 100 seed weight (g)
9. Biological yield per plant (g)
10. Harvest index %
11. Grain yield per plant

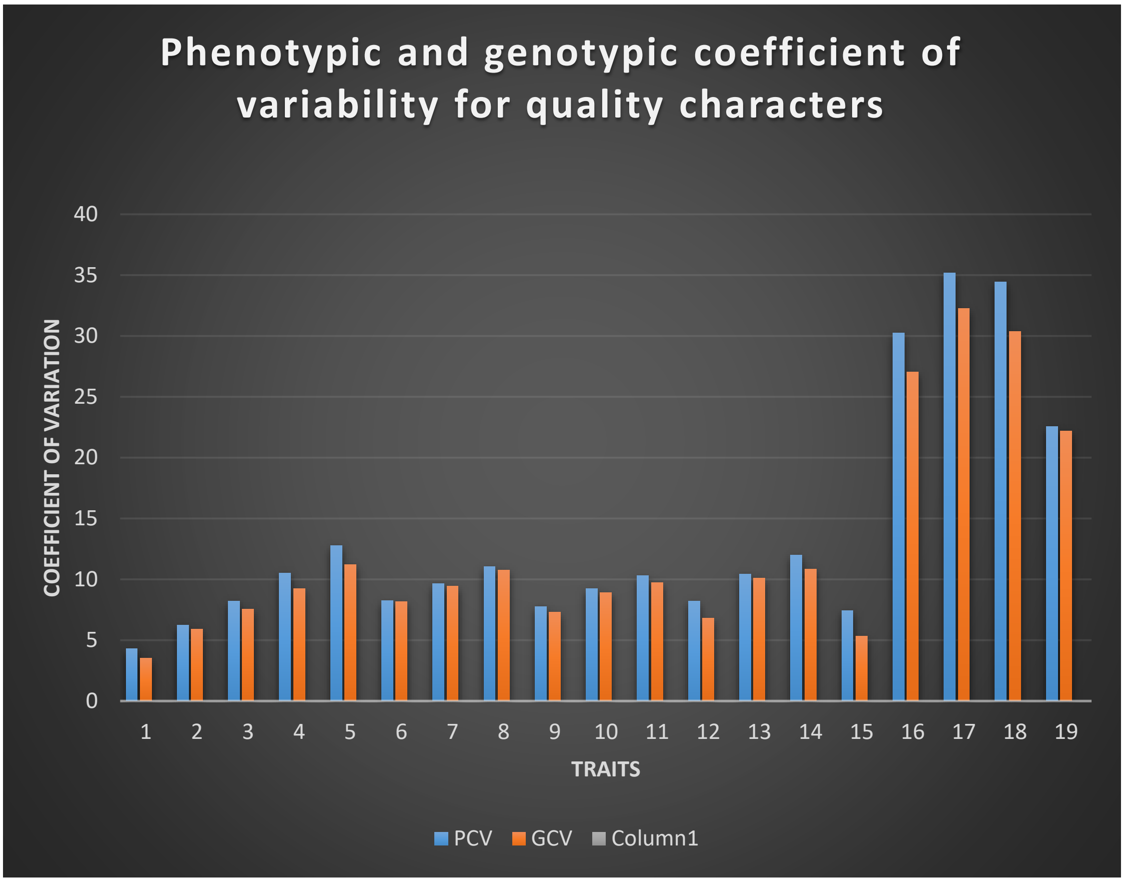

Fig. 4.2 Bar diagram showing phenotypic and genotypic coefficient of variability for quality characters

1. Hulling %
2. Milling %
3. Paddy length (mm)
4. Paddy breadth (mm)
5. Paddy L/B ratio
6. Brown rice length (mm)
7. Brown rice breadth (mm)
8. Brown rice L/B ratio
9. Kernel length (mm)
10. Kernel breadth (mm)
11. Kernel L/B ratio
12. Kernel length after cooking (mm)
13. Kernel breadth after cooking (mm)
14. Cooked rice L/B ratio
15. Elongation ratio
16. Gel consistency
17. Alkali spreading value
18. Amylose %
19. Head rice recovery %

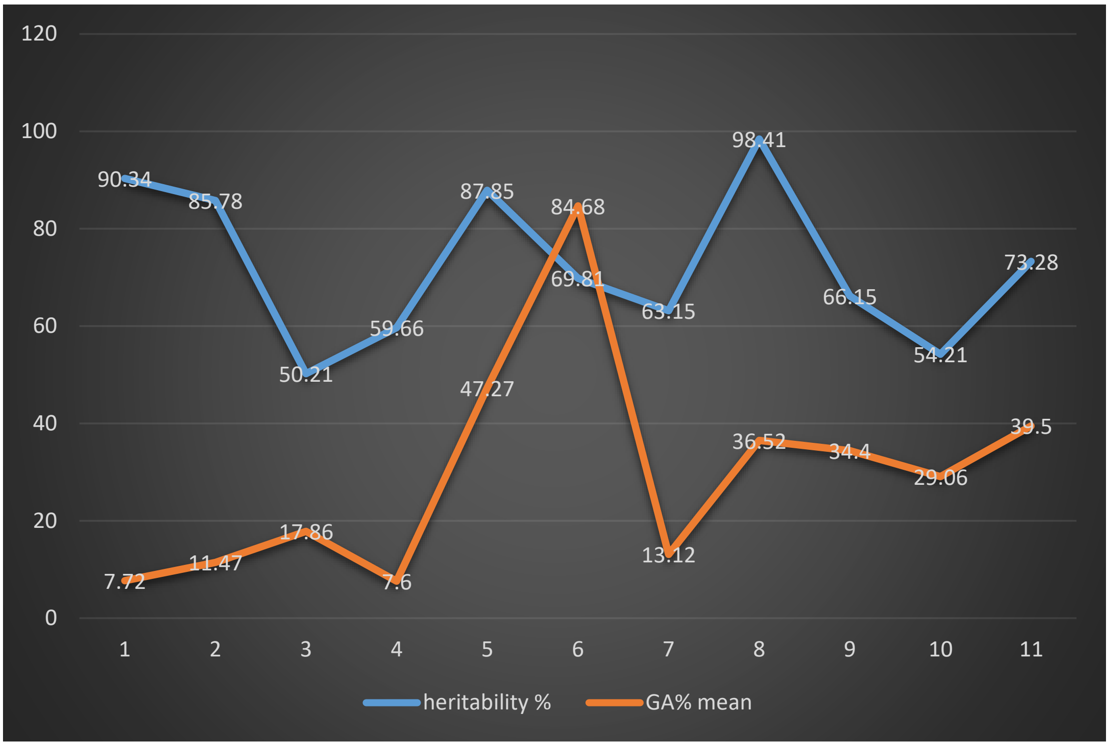

Fig.4.3 Frequency curve showing heritability estimates and genetic advance for yield and yield contributing characters

1. Days to 50% flowering
2. Plant height (cm)
3. Number of effective tillers
4. Panicle length (cm)
5. Number of filled grains per panicle
6. Number of unfilled grains per panicle
7. Spikelet fertility %
8. 100 seed weight (g)
9. Biological yield per plant (g)
10. Harvest index %
11. Grain yield per plant

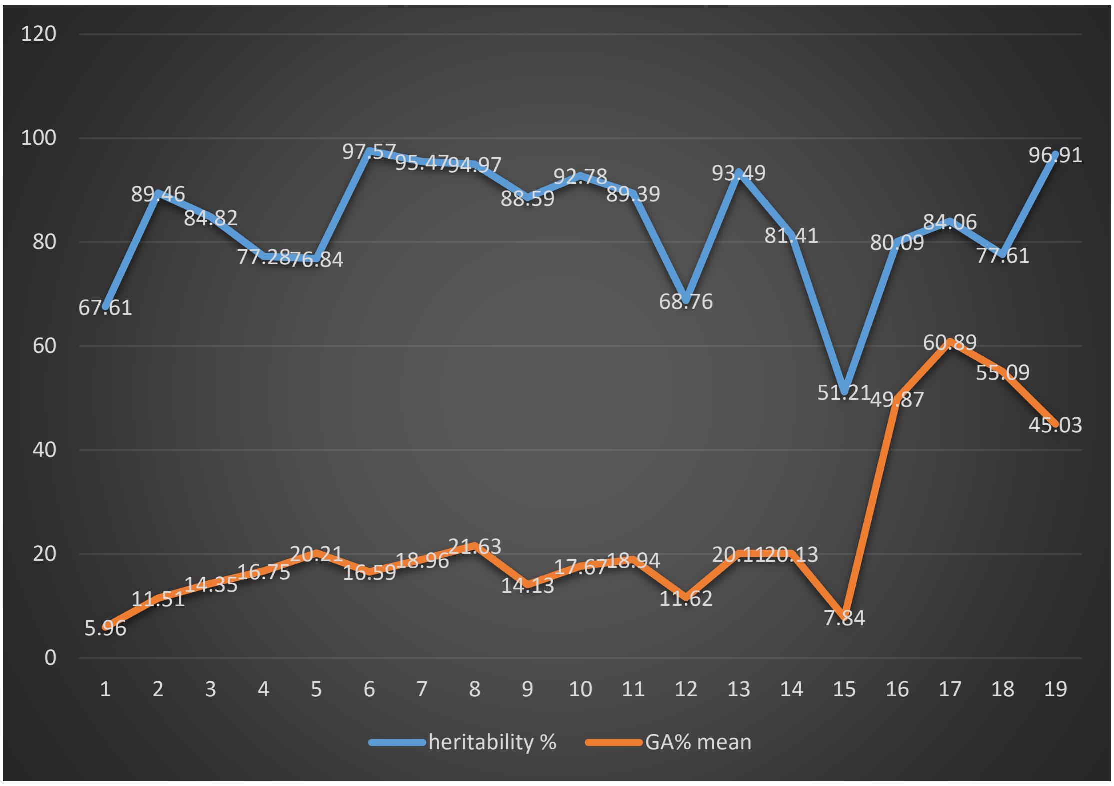

Fig.4.4 Frequency curve showing heritability estimates and genetic advance for quality characters

1. Hulling %	2. Milling %	3. Paddy length (mm)	4. Paddy breadth (mm)	5. Paddy L/B ratio
6. Brown rice length (mm)	7. Brown rice breadth (mm)	8. Brown rice L/B ratio	9. Kernel length (mm)	10. Kernel breadth (mm)
11. Kernel L/B ratio	12. Kernel length after cooking (mm)	13. Kernel breadth after cooking (mm)	14. Cooked rice L/B ratio	15. Elongation ratio
16. Gel consistency	17. Alkali spreading value	18. Amylose %	19. Head rice recovery %	

Table 4.8: Frequency distribution and percentage value of some quality characters

S. No.	Characters	Category	Number	Frequency %
1.	Kernel length	Extra-long	0	0
		Long	2	3.64
		Medium	45	81.82
		Short	8	14.54
2.	Grain shape	Long slender	26	47.27
		Medium slender	29	52.73
		Bold	0	0
		Round	0	0
3.	Gel consistency	Hard gel	20	36.36
		Medium gel	23	41.82
		Soft gel	12	21.82
4.	Alkali spreading value	Low	1	1.82
		Low, Intermediate	13	23.64
		Intermediate	15	27.27
		High	26	47.27
5.	Amylose content	Waxy	0	0
		Very low	0	0
		Low	15	27.27
		Intermediate	13	23.64
		High	27	49.09

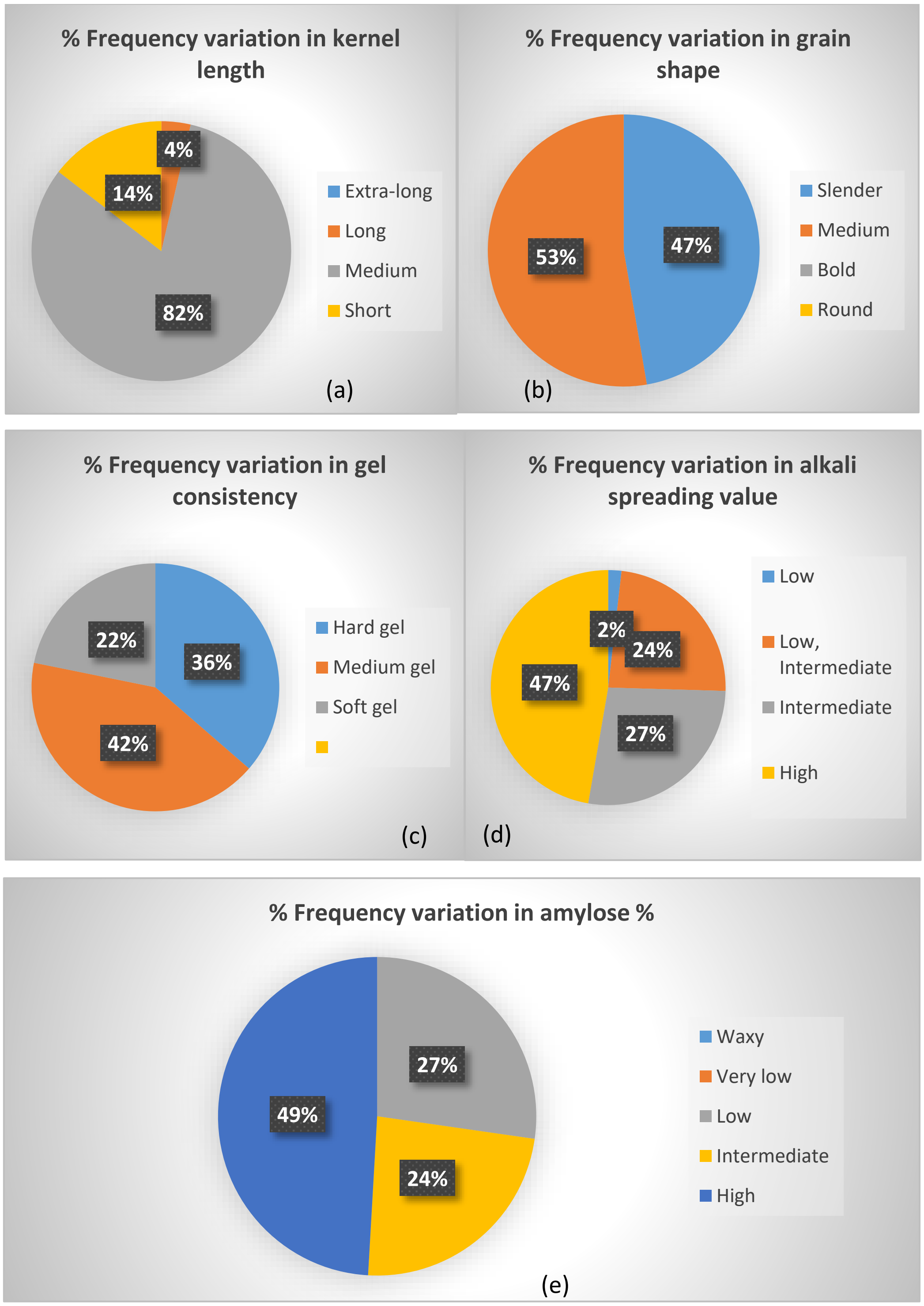

Fig. 4.5 Frequency variation in (a) Kernel length, (b) Grain shape, (c) Gel consistency, (d) Alkali spreading value and (e) Amylose % respectively

4.3 Correlation analysis

Improvement of a desired characteristic can be done in a realistic breeding project by using indirect selection via other characters. This necessitates a thorough understanding of the relationships between the various characters and the target attribute, as well as between the many characters themselves.

In present study, the relationship between all eleven yield and nineteen quality characters was investigated at both the phenotypic and genotypic levels taking yield and head rice recovery % as the dependent character for yield characters and quality characters respectively in the analysis. In general, genotypic coefficient of correlation values were higher than phenotypic coefficient of correlation among all character combinations explaining that the cause for such observed relationship among various characters is due to genetic cause. Out of 55 [n(n-1)/2] coefficients of correlation computed for yield characters 31 ‘r’ values were found to be significant irrespective of their direction of association. In the same way, for quality characters out of 171 ‘r’ values 119 were found to be significant irrespective of direction of association.

4.3.1 Yield characters

4.3.1.1 Grain yield/plant (g)

Studies on genotypic and phenotypic coefficient of correlations revealed that grain yield/plant had a significant and positive correlation with days to 50% flowering (0.561), effective tillers/plant (0.513), panicle length (0.293), plant height (0.257), number of filled grains/panicle (0.627), biological yield (0.590) and harvest index% (0.532).

Similar findings are obtained by Devi *et al.,* (2017) for plant height, panicle length, number of filled grains/panicle and number of effective tillers/plant; by Babu *et al.,* (2011) for days to 50% flowering and Bhati *et al.,* (2015) for biological yield, harvest index% and plant height and Panwar and Ali (2007) for harvest index, biological yield and number of filled grains/panicle.

4.3.1.2 Days to 50% flowering

For days to 50% flowering high significant and positive correlation was recorded with plant height (0.305), number of effective tillers/plant (0.453), number of unfilled grain/panicle (0.245), number of filled grains/panicle (0.263), and biological yield (0.511).

Similar results were concluded by Babu *et al.,* (2011) for plant height and Seyoum *et al.*, (2012) for number of filled grains/panicle.

4.3.1.3 Plant height (cm)

Highly significant and positive correlation was recorded between plant height and panicle length (0.275), 100 seed weight (0.339) and biological yield (0.418).

These results are similar as obtained by Chandra *et al.*, (2009) and Ratna *et al.,* (2015) for panicle length Yogameenakshi *et al.*, (2004) and Devi *et al.,* (2019) for 1000 grain weight.

4.3.1.4 Number of effective tillers per plant

Highest positive significant correlation of number of effective tillers were observed with biological yield (0.741) followed by filled grains/panicle (0.404).

These results were in line with findings of Padmaja *et al.*, (2011) for 1000 grain weight Devi *et al.* (2019) and Veni *et al.*, (2013) for number of filled grains/panicle.

4.3.1.5 Panicle length (cm)

Highly significant and positive correlation of panicle length with filled grains/panicle (0.305) was recorded. Moderate significant positive correlation was recorded between panicle length and spikelet fertility% (0.196) and biological yield (0.230).

These findings were in line with and Prasad *et al.,* (2017) and Devi *et al.,* (2019) for number of filled grains/panicle and test weight.

4.3.1.6 Number of filled grains per panicle

Number of filled grains/panicle had a highly positive significant correlation with number of unfilled grains/panicle (0.303), biological yield (0.434) and harvest index% (0.225).

Similar results were obtained by Ratna *et al.,* (2015) for grain yield.

4.3.1.7 Number of unfilled grains per panicle

Significant positive correlation of number of unfilled grains/panicle was recorded with biological yield (0.220) and negative and significant correlation with spikelet fertility % (-0.910).

4.3.1.8 Spikelet fertility %

Highly negative and significant correlation was exhibited by number of unfilled grains per panicle (-0.910) on spikelet fertility %.

4.3.1.9 Biological Yield per plant (g)

Biological yield didn't showed any positive correlation with any characters studied.

4.3.1.10 Harvest index %

Harvest index% showed highly significant and positive correlation with grain yield/plant (0.532).

Similar findings are done by Babu *et al.*, (2011).

4.3.2 Quality characters

4.3.2.1 Head rice recovery %

Head rice recovery % showed highest significant and positive correlation with milling% (0.726) followed by hulling% (0.610), gel consistency (0.404), elongation ratio (0.400), kernel L/B ratio (0.373), cooked rice L/B ratio (0.276) and brown rice L/B ratio (0.273). This character showed moderately significant and positive correlation with alkali spreading value (0.234).

These results are in line with the findings done by Devi *et al.* (2017) for milling%, hulling% and kernel breadth after cooking and Devi *et al.* (2019) for kernel breadth and Khatun *et al.* (2003) for gel consistency.

4.3.2.2 Hulling %

Highly significant and positive correlation was obtained between hulling% and milling% (0.715), elongation ratio (0.412), alkali spreading value (0.335) and gel consistency (0.256).

These results were similar to one found by Shivani *et al.* (2007) for grain yield and milling%.

4.3.2.3 Milling %

Highly positive significant correlation was seen between milling% and elongation ratio (0.489), cooked rice L/B ratio (0.342) and gel consistency (0.339) and moderately positive significant correlation with alkali spreading value (0.214).

Similar results were obtained by Devi *et al.* (2015) for kernel breadth after cooking.

4.3.2.4 Paddy length (mm)

Highly positive significant correlation was recorded between paddy length and kernel length (0.872), brown rice length (0.790), kernel length after cooking (0.751), kernel L/B ratio (0.635), paddy L/B ratio (0.598), brown rice L/B ratio (0.550). Paddy length has moderately positive correlation with kernel breadth after cooking (0.218) and cooked rice L/B ratio (0.209).

4.3.2.5 Paddy breadth (mm)

Highly positive significant correlation of paddy breadth was recorded with kernel breadth after cooking (0.636), brown rice breadth (0.613), kernel breadth (0.505), alkali spreading value (0.326), elongation ratio (0.257) and kernel length after cooking (0.245).

4.3.2.6 Paddy L/B ratio

Highly positive significant correlation of paddy L/B ratio was obtained with brown rice L/B ratio (0.826), kernel L/B ratio (0.775), brown rice length (0.617), kernel length (0.574), cooked rice L/B ratio (0.474), kernel length after cooking (0.299) and was found moderately significant positive correlation with gel consistency (0.198).

These results are similar to the findings of Kawochar and Begum (2016) for brown rice L/B ratio, kernel L/B ratio and cooked rice L/B ratio.

4.3.2.7 Brown rice length (mm)

Brown rice length was found to be highly significant and positively correlated with kernel length (0.858), kernel length after cooking (0.710), brown rice L/B ratio

(0.581), kernel L/B ratio (0.460) and was found moderate significant positive correlation with amylose% (0.201) and cooked rice L/B ratio (0.196).

4.3.2.8 Brown rice breadth (mm)

Highest positive significant correlation of brown rice width was recorded with kernel breadth (0.941) followed with kernel breadth after cooking (0.554), amylose% (0.454), kernel length after cooking (0.334) and was found moderate significant positive correlation with kernel length (0.194)

4.3.2.9 Brown rice L/B ratio

Brown rice L/B ratio showed highly significant positive correlation with kernel L/B ratio (0.920), kernel length (0.481), cooked rice L/B ratio (0.371) and gel consistency (0.367). A moderate significant positive correlation was recorded between brown rice L/B ratio and kernel breadth after cooking (0.241).

4.3.2.10 Kernel length (mm)

Highly significant positive correlation of kernel length was obtained with kernel length after cooking (0.725) and kernel L/B ratio (0.538). Moderate significant positive correlation was recorded with amylose% (0.231), kernel breadth after cooking (0.194) and “cooked rice L/B ratio (0.217).

Similar results were observed by Devi *et al.* (2015) for kernel breadth after cooking and cooked rice L/B ratio, Nandan *et al.,* (2010) and Mathure *et al.,* (2011) for kernel L/B ratio.

4.3.2.11 Kernel breadth (mm)

Highly significant positive correlation of kernel breadth was obtained with amylose% (0.502), kernel breadth after cooking (0.492) and kernel length after cooking (0.308).

Similar results were recorded by Devi *et al.,* (2015) for kernel breadth after cooking and kernel L/B ratio Devi *et al.,* (2017) for kernel L/B ratio and Devi *et al.,*(2019) for kernel breadth after cooking and kernel length after cooking.

4.3.2.12 Kernel L/B ratio

Highly significant positive correlation of kernel L/B ratio was recorded with gel consistency (0.448), cooked rice L/B ratio (0.397) and kernel length after cooking (0.252).

Similar results were recorded by Devi *et al.,* (2015) for kernel length after cooking and Devi *et al.,* (2019) for elongation. Khatun *et al.,* (2003) for gel consistency.

4.3.2.13 Kernel length after cooking (mm)

Highly positive significant correlation of kernel length after cooking was obtained with elongation ratio (0.385), kernel breadth after cooking (0.346), alkali spreading value (0.292) and cooked rice L/B ratio (0.259).

These findings are in line with the results obtained by Devi *et al.,* (2015) for elongation ratio and Devi *et al.,* (2019) for elongation ratio and alkali spreading value.

4.3.2.14 Kernel breadth after cooking (mm)

Kernel breadth after cooking didn't showed any positive correlation with any character under studied.

4.3.2.15 Cooked rice L/B ratio

Highly significant positive and moderately significant positive correlation of cooked rice L/B ratio was obtained with gel consistency (0.466) and alkali spreading value (0.189) respectively.

4.3.2.16 Elongation ratio

Highly positive significant correlation of elongation ratio was recorded with alkali spreading value (0.412). Moderate significant positive correlation of elongation ratio was obtained with amylose% (0.200).

Similar results were obtained by Thomas *et al*., (2010) for amylose%.

4.3.2.17 Gel consistency

Highly significant positive correlation and highly significant negative correlation of gel consistency was noted with alkali spreading value (0.371) and amylose% (-0.858) respectively.

These results are in line with the findings of Khatun *et al.*, (2003) for amylose%.

4.3.2.18 Alkali spreading value

Alkali spreading value didn’t showed any positive correlation with any characters under studied.

4.3.2.19 Amylose %

Amylose % didn’t showed any positive correlation with any characters under studied.

Table 4.9: Genotypic and phenotypic correlation coefficients of yield and yield contributing characters

		1	2	3	4	5	6	7	8	9	10	11
1	**G**		0.305**	0.453**	0.139	0.263**	0.245*	-0.167	-0.075	0.511**	0.147	0.561**
	P		0.267**	0.312**	0.081	0.256**	0.225*	-0.103	-0.066	0.403**	0.093	0.470**
2	**G**			-0.032	0.275**	0.132	-0.086	0.085	0.339**	0.418**	-0.136	0.257**
	P			0.070	0.303**	0.114	-0.091	0.097	0.323**	0.373**	-0.115	0.250**
3	**G**				0.121	0.404**	0.057	0.072	-0.405**	0.741**	-0.121	0.513**
	P				0.157	0.189*	0.100	-0.060	-0.259**	0.534**	0.064	0.577**
4	**G**					0.305**	0.036	0.196*	-0.251**	0.230*	0.082	0.293**
	P					0.182	0.078	0.071	-0.182	0.328**	-0.084	0.253**
5	**G**						0.303**	0.182	-0.596**	0.434**	0.225*	0.627**
	P						0.272*	0.206*	-0.559**	0.282**	0.197*	0.496**
6	**G**							-0.910**	-0.304**	0.210*	0.078	-0.123
	P							-0.887**	-0.215*	0.176	0.0053	-0.111
7	**G**								-0.082	-0.018	0.105	0.131
	P								-0.065	-0.016	0.047	0.066
8	**G**									-0.167	0.132	-0.069
	P									-0.120	0.104	-0.033
9	**G**										-0.355**	0.590**
	P										-0.487**	0.440**
10	**G**											0.532**
	P											0.540**
11	**G**											
	P											

1. Days to 50% flowering	2. Plant height (cm)	3. Number of effective tillers	4. Panicle length (cm)	5. Number of filled grains per panicle	6. Number of unfilled grains per panicle
7. Spikelet fertility %	8. 100 seed weight (g)	9. Biological yield per plant (g)	10. Harvest index %	11. Grain yield per plant	

Table No. 4.10 Genotypic and phenotypic correlation coefficients of quality characters

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	G	1	0.715**	-0.046	-0.011	0.013	-0.220*	-0.275**	0.020	-0.180	-0.383**	0.172	0.100	0.005	0.091	0.412**	0.256**	0.335**	-0.386**	0.610**
	P		0.610**	-0.022	0.048	-0.043	-0.156	-0.236*	0.052	-0.208*	-0.283**	0.072	0.022	0.003	0.034	0.269**	0.197*	0.201*	-0.327**	0.520**
2	G		1	-0.164	-0.032	-0.081	-0.178	-0.308**	0.04	-0.246**	-0.322**	0.055	0.059	-0.280**	0.342**	0.489**	0.339**	0.214*	-0.419**	0.726**
	P			-0.143	0.002	-0.087	-0.154	-0.281**	0.055	-0.243*	-0.309*	0.052	0.035	-0.254**	0.286**	0.339**	0.306**	0.169	-0.357**	0.684**
3	G			1	0.086	0.598**	0.790**	0.046	0.550**	0.872**	0.001	0.635**	0.751**	0.218*	0.209*	-0.209*	0.003	0.070	0.009	0.013
	P				0.081	0.560**	0.728**	0.069	0.473**	0.790**	0.003	0.577**	0.596**	0.207*	0.180	-0.141	0.038	0.107	-0.017	0.011
4	G				1	-0.742**	-0.107	0.613**	-0.574**	-0.012	0.505**	-0.458**	0.245**	0.636**	-0.429**	0.257**	-0.249**	0.326**	-0.033	-0.115
	P					-0.760**	-0.103	0.543**	-0.515**	-0.039	0.437**	-0.406**	0.174	0.530**	-0.333**	0.184	-0.211*	0.258**	-0.039	-0.108
5	G					1	0.617**	-0.455**	0.826**	0.574**	-0.400**	0.775**	0.299**	-0.355**	0.474**	-0.335**	0.198*	-0.203*	0.046	0.103
	P						0.545**	-0.383**	0.709**	0.526**	-0.343**	0.684**	0.211*	-0.286**	0.356**	-0.262**	0.192*	-0.128	0.037	0.098
6	G						1	0.165	0.581**	0.858**	0.157	0.460**	0.710**	0.186	0.196*	-0.199*	-0.137	-0.047	0.201*	-0.166
	P							0.165	0.573**	0.788**	0.141	0.429**	0.584**	0.177	0.177	-0.125	-0.116	-0.037	0.184	-0.155
7	G							1	-0.695**	0.189*	0.941**	-0.688**	0.334**	0.554**	-0.326**	0.160	-0.570**	0.053	0.454**	-0.532**
	P								-0.700**	0.199*	0.891**	-0.621**	0.269**	0.518**	-0.283**	0.098	-0.511**	0.070	0.402**	-0.508**
8	G								1	0.481**	-0.658**	0.920**	0.241*	-0.282**	0.371**	-0.302**	0.367**	-0.058	-0.222*	0.273**
	P									0.408**	-0.625**	0.829**	0.191*	-0.266**	0.325**	-0.189*	0.336**	-0.076	-0.200*	0.264**
9	G									1	0.206*	0.538**	0.725**	0.194*	0.217*	-0.349**	-0.108	-0.038	0.231*	-0.200*
	P										0.187	0.556**	0.580**	0.177	0.195*	-0.331**	-0.105	-0.006	0.207*	-0.185
10	G										1	-0.705**	0.308**	0.492**	-0.281**	0.117	-0.558**	0.019	0.502**	-0.624**
	P											-0.697**	0.239*	0.452**	-0.245**	0.081	-0.484	0.009	0.401**	-0.595**
11	G											1	0.252**	-0.283**	0.397**	-0.361**	0.448**	0.014	-0.310**	0.373**
	P												0.220*	-0.252**	0.349**	-0.302**	0.369**	0.045	-0.220*	0.351**

12	G												1	0.346**	0.259**	0.385**	-0.142	0.292**	0.030	0.075
	P													0.287**	0.391**	0.543**	-0.136	0.263**	0.082	0.066
13	G													1	-0.806**	0.132NS	-0.494**	0.038	0.147	-0.221*
	P														-0.754**	0.124	-0.425**	0.056	0.136	-0.204*
14	G														1	0.126	0.466**	0.189*	-0.184	0.276**
	P															0.263**	0.344**	0.160	-0.111	0.238*
15	G															1	-0.068	0.412**	-0.200*	0.400**
	P																-0.093	0.292**	-0.086	0.284**
16	G																1	0.371**	-0.858**	0.404**
	P																	0.289**	-0.773**	0.376**
17	G																	1	-0.512**	0.234*
	P																		-0.350**	0.214*
18	G																		1	-0.522**
	P																			-0.455**
19	G																			1
	P																			

1. Hulling %
2. Milling %
3. Paddy length (mm)
4. Paddy breadth (mm)
5. Paddy L/B ratio
6. Brown rice length (mm)
7. Brown rice breadth (mm)
8. Brown rice L/B ratio
9. Kernel length (mm)
10. Kernel breadth (mm)
11. Kernel L/B ratio
12. Kernel length after cooking (mm)
13. Kernel breadth after cooking (mm)
14. Cooked rice L/B ratio
15. Elongation ratio
16. Gel consistency
17. Alkali spreading value
18. Amylose %
19. Head rice recovery %

4.4 Path coefficient analysis

By dividing the correlations, path coefficient analysis allows separation of the direct and indirect effects through other characteristics, whereas correlation only gives the relationship between two variables (Wright, 1921). As a result, this goal was pursued in the current inquiry. The genotypic and phenotypic correlations were evaluated based on the data recorded on the advanced breeding lines in the current study to evaluate direct and indirect effects of yield and quality characters.

Grain yield is a polygenic trait that is impacted by a variety of other qualities, therefore selecting for it directly might be deceptive. Because correlation studies alone are insufficient to provide a full picture of association analysis, it is necessary to analyses the true contribution of individual character to grain output per plant. At the correlation level, path coefficient analysis gives a clearer and more accurate image of a complicated scenario. Grain yield/plant was used as an effect dependent variable on ten independent factors that were used as causes in this study which were plant height, days to 50% flowering, panicle length, number of filled grains/panicle, effective tillers, number of unfilled grains/panicle, 100 seed weight, spikelet fertility%, harvest index% and biological yield per plant (g). Similarly, head rice recovery % was taken as effect dependent variable on eighteen independent factors which were hulling%, paddy length, milling%, brown rice length, kernel length, kernel length after cooking, paddy breadth, paddy L/B ratio, brown rice breadth, brown rice L/B ratio, kernel breadth, kernel L/B ratio, kernel breadth after cooking, cooked rice L/B ratio, elongation ratio, alkali spreading value, amylose% and gel consistency. The direct and indirect effects of yield and quality characters are presented in table 4.11 and 4.12 respectively.

4.4.1 Path coefficient analysis for yield contributing characters

Considering direct effects of yield contributing characters on grain yield, biological yield per plant showed highest positive direct effect (1.087) on grain yield followed by harvest index (0.891), number of filled grains/panicle (0.147), days to 50% flowering (0.017) and panicle length (0.0003). Number of unfilled grains/panicle showed highest negative direct effect (-0.254) on grain yield followed by number of effective tillers (-0.248), spikelet fertility % (-0.154), 100 seed weight (-0.072) and plant height (-0.069).

This result is in line with findings of Sanghera *et al.,* (2013) and Bhadru *et al.,* (2011) for days to 50% flowering, Mulugeta *et al.,* (2012) for panicle length, Bagheri *et al.,* (2011) for number of filled grains/panicle. Surek and Beser (2003) for harvest index% and biological yield.

4.4.2 Direct and indirect effects of yield contributing characters on grain yield

4.4.2.1 Days to 50% flowering

This trait showed positive direct (0.017) effect on grain yield. However, positive indirect effect of days to 50% flowering on grain yield was via biological yield (0.555), harvest index % (0.131), number of filled grains/panicle (0.038), spikelet fertility% (0.025), 100 seed weight (0.005) and panicle length (0.00005). Negative effect of this trait on grain yield per plant was mainly via number of effective tillers (-0.112), number of unfilled grains/panicle (-0.079) and plant height (-0.021).

4.4.2.2 Plant height

Plant height had negative direct (-0.069) effect on grain yield. However, this trait showed positive indirect effect on grain yield via biological yield (0.454), number of filled grains/panicle (0.019), number of effective tillers (0.008), days to 50% flowering (0.005) and panicle length (0.00009). This trait showed negative indirect effect on grain yield via 100 seed weight (-0.024), spikelet fertility% (-0.013) and number of unfilled grains/panicle (-0.001).

4.4.2.3 Number of effective tillers per plant

Number of effective tillers per plant had negative direct effect (-0.248) on grain yield but it had positive indirect effect on grain yield mainly due to biological yield (0.805), number of filled grains/panicle (0.059) and 100 seed weight (0.029). Number of effective tiller had negative indirect effect on grain yield mainly through harvest index% (-0.107), number of unfilled grains/panicle (-0.024) and spikelet fertility% (-0.011).

4.4.2.4 Panicle length

Panicle length had positive direct effect (0.0003) on grain yield. Positive indirect effect of panicle length on grain yield was mainly through biological yield (0.249), harvest index% (0.073) and number of filled grains/panicle (0.044). However this trait had negative indirect effect on grain yield mainly through spikelet fertility% (-0.030), plant height (-0.019) and number of unfilled grains/panicle (-0.016).

4.4.2.5 Number of filled grains per panicle

Number of filled grains/panicle had third highest positive direct effect (0.147) on grain yield. This trait showed indirect positive effect on grain yield mainly through biological yield (0.472), harvest index% (0.200) and 100 seed weight (0.0432). However, this trait had indirect negative effect on yield mainly through number of unfilled grains/panicle (-0.102), number of effective tillers (-0.100) and spikelet fertility% (-0.028).

4.4.2.6 Number of unfilled grains per panicle

Number of unfilled grains per panicle showed negative direct effect (-0.254) on grain yield however, this trait had indirect positive effect on grain yield mainly through biological yield (0.239), spikelet fertility% (0.125) and harvest index% (0.078). This trait had indirect negative effect on grain yield mainly via number of effective tillers (-0.024) and plant height (-0.0004).

4.4.2.7 Spikelet fertility %

Spikelet fertility% showed negative direct effect on grain yield (-0.154) however this trait had indirect positive effect on grain yield mainly through number of unfilled grains/panicle (0.205), harvest index% (0.093) and number of filled grains/panicle (0.026). Spikelet fertility% showed negative indirect effect on grain yield mainly through biological yield (-0.019), number of effective tillers (-0.017) and plant height (-0.005).

4.4.2.8 100 seed weight (g)

100 seed weight showed negative direct effect (-0.072) on grain yield however it showed indirect positive effect on grain yield mainly through harvest index% (0.117), number of effective tillers (0.100) and number of unfilled grains/panicle (0.066). 100 seed weight had indirect negative effect on grain yield mainly through biological yield (-0.181), number of filled grains/panicle (-0.087) and plant height (-0.023).

4.4.2.9 Biological yield per plant (g)

Biological yield showed positive direct effect on grain yield (1.087). This trait showed positive indirect effect on grain yield mainly through number of filled grains/panicle (0.0639), 100 seed weight (0.012) and days to 50% flowering (0.009). However this trait had negative indirect effect on grain yield mainly via harvest index% (-0.316), number of effective tillers (-0.183) and number of unfilled grains/panicle (-0.055).

4.4.2.10 Harvest index %

Harvest index% had positive direct effect (0.891) on grain yield. This trait showed indirect positive effects on grain yield mainly through number of filled grains/panicle (0.033), number of effective tillers (0.029) and plant height (0.009). However this trait had negative indirect effect on grain yield mainly through biological yield (-0.386), number of unfilled grains/panicle (-0.022) and spikelet fertility% (-0.016).

4.4.3 Path coefficient analysis for quality characters

Considering direct effects of quality characters on head rice recovery %, brown rice L/B ratio showed highest positive direct effect (2.646) followed by cooked kernel length (1.648), brown rice breadth (1.408), hulling% (0.809), paddy breadth (0.710), kernel breadth (0.378), elongation ratio (0.159) and kernel length (0.148). Kernel breadth after cooking showed highest negative direct effect (-3.522) on head rice recovery %, followed by cooked rice L/B ratio (-2.598), brown rice length (-1.496), amylose% (-0.924), gel consistency (-0.543), alkali spreading value (-0.450), kernel L/B ratio (-0.262), paddy length (-0.133), paddy L/B ratio (-0.055) and milling % (-0.025).

Similar results obtained by Nandan and Singh (2010) for hulling%, Rajamadhan *et al.,* (2011) for kernel length and Saravanan and Sabesan (2009) for kernel L/B ratio.

4.4.4 Direct and indirect effects of quality characters on head rice recovery %

4.4.4.1 Hulling %

Hulling% (0.809) showed positive direct effect on head rice recovery %. This trait showed indirect positive effect on head rice recovery % mainly through amylose%

(0.356), brown rice length (0.329) and kernel length after cooking (0.164). However, hulling% had indirect negative effect on head rice recovery % mainly brown rice breadth (-0.387), cooked rice L/B ratio (-0.236) and alkali spreading value (-0.150).

4.4.4.2 Milling %

Milling% had negative direct effect (-0.025) on head rice recovery % however it had indirect positive effect on head rice recovery % mainly through kernel breadth after cooking (0.984), hulling% (0.578) and amylose% (0.387). Milling% had negative indirect effect on head rice recovery % mainly through cooked rice L/B ratio (-0.888), brown rice breadth (-0.433) and gel consistency (-0.184).

4.4.4.3 Paddy length (mm)

Paddy length showed negative direct effect (-0.133) on head rice recovery % however, this trait had positive indirect effect on head rice recovery % mainly through brown rice L/B ratio (1.456), kernel length after cooking (1.237) and kernel length (0.129). Paddy length had negative indirect effect on head rice recovery % mainly through brown rice length (-1.182), kernel breadth after cooking (-0.769) and cooked rice L/B ratio (-0.544).

4.4.4.4 Paddy breadth (mm)

Paddy breadth showed positive direct effect (0.710) on head rice recovery %. This trait indirect positive effect on head rice recovery % mainly through cooked rice L/B ratio (1.115), brown rice breadth (0.863) and brown rice length (0.160). However, it showed indirect negative effect on head rice recovery % mainly through kernel breadth after cooking (-2.241), brown rice L/B ratio (-1.518) and alkali spreading value (-0.146).

4.4.4.5 Paddy L/B ratio

Paddy L/B ratio had negative direct effect (-0.055) on head rice recovery % however, this trait showed positive indirect effect on head rice recovery % mainly through brown rice L/B ratio (2.187), kernel breadth after cooking (1.251) and kernel length after cooking (0.492). Paddy L/B ratio had negative indirect effect on head rice recovery % mainly through cooked rice L/B ratio (-1.231), brown rice length (-0.923) and paddy breadth (-0.527).

4.4.4.6 Brown rice length (mm)

Brown rice length showed third highest negative direct effect (-1.496) on head rice recovery % however, this trait had positive indirect effect on head rice recovery % mainly through brown rice L/B ratio (1.538), kernel length after cooking (1.169) and brown rice breadth (0.232). This trait showed negative indirect effect on head rice recovery % mainly through kernel breadth after cooking (-0.654), cooked rice L/B ratio (-0.51) and amylose% (-0.185).

4.4.4.7 Brown rice breadth (mm)

Brown rice breadth showed positive direct effect (1.408) on head rice recovery %. This trait showed indirect positive effect on head rice recovery % mainly via cooked rice L/B (0.848), kernel rice length after cooking (0.550) and paddy breadth (0.435). However, brown rice breadth had negative indirect effect on head rice recovery mainly through kernel breadth after cooking (-1.950), brown rice L/B ratio (-1.839) and amylose% (-0.419).

4.4.4.8 Brown rice L/B ratio

Brown L/B ratio showed highest positive direct effect (2.646) on head rice recovery %. This trait showed positive indirect effect on head rice recovery % mainly through kernel breadth after cooking (0.991), kernel length after cooking (0.397) and amylose% (0.205). However, it showed negative indirect effect on head rice recovery % mainly through brown rice breadth (-0.979), cooked rice L/B ratio (-0.964) and brown rice length (-0.870).

4.4.4.9 Kernel length (mm)

Kernel length (0.148) had positive direct effect on head rice recovery %. This trait showed positive indirect effect on head rice recovery % mainly through brown rice L/B ratio (1.273), kernel length after cooking (1.194) and gel consistency (0.588). However, kernel length had negative indirect effect on head rice recovery % mainly through brown rice length (-1.283), kernel breadth after cooking (-0.681), and cooked rice L/B ratio (-0.564).

4.4.4.10 Kernel breadth (mm)

Kernel breadth showed positive direct effect (0.378) on head rice recovery %. Kernel breadth had positive indirect effect on head rice recovery % mainly through brown rice breadth (1.325), cooked rice L/B ratio (0.729) and kernel length after cooking (0.507). However, it showed negative indirect effect on head rice recovery % mainly through brown rice L/B ratio (-1.742), kernel breadth after cooking (-1.732) and amylose% (-0.464).

4.4.4.11 Kernel L/B ratio

Negative direct effect (-0.262) of Kernel L/B ratio was obtained on head rice recovery % however, it showed positive indirect effect on head rice recovery % mainly through brown rice L/B ratio (2.434), kernel breadth after cooking (0.996) and kernel length after cooking (0.415). This trait showed negative indirect effect on head rice recovery % mainly through cooked rice L/B ratio (-1.030), brown rice breadth (-0.969) and brown rice length (-0.688).

4.4.4.12 Kernel length after cooking (mm)

Positive direct effect (1.648) on head rice recovery % was obtained by kernel length after cooking. Indirect positive effect of this trait on head rice recovery % were mainly through brown rice L/B ratio (0.637), brown rice breadth (0.470) and paddy breadth (0.174). However, this trait showed negative indirect effect on head rice recovery % mainly through kernel breadth after cooking (-1.218), brown rice length (-1.062) and alkali spreading value (-0.131).

4.4.4.13 Kernel breadth after cooking (mm)

Negative direct effect was shown by kernel breadth after cooking (-3.522) on head rice recovery %. However, it showed positive indirect effect on head rice recovery % mainly through cooked rice L/B ratio (2.095), brown rice breadth (0.779) and kernel length after cooking (0.57). This trait showed indirect negative effect on head rice recovery % mainly through brown rice L/B ratio (-0.744), brown rice length (-0.277) and amylose% (-0.136).

4.4.4.14 Cooked rice L/B ratio

Negative direct effect (-2.598) was shown by cooked rice L/B ratio on head rice recovery % however, it showed positive indirect effect on head rice recovery % mainly through kernel breadth after cooking (2.839), brown rice L/B ratio (0.981) and kernel length after cooking (0.427). This trait showed negative indirect effect on head rice recovery % mainly through brown rice breadth (-0.459), paddy breadth (-0.305) and brown rice length (-0.293).

4.4.4.15 Elongation ratio

Positive direct effect (0.159) of elongation ratio was obtained on HRR%. This trait showed indirect positive effect on HRR% mainly through hulling% (0.333), brown rice length (0.298) and brown rice breadth (0.225). However, this trait showed negative indirect effect on HRR% mainly through brown rice L/B ratio (-0.798), kernel breadth after cooking (-0.464) and cooked rice L/B ratio (-0.328).

4.4.4.16 Gel consistency

Negative direct effect (-0.543) of gel consistency was obtained on head rice recovery % however this trait showed positive indirect effect on head rice recovery % mainly through kernel breadth after cooking (1.738), brown rice L/B ratio (0.971) and amylose% (0.793). This trait showed negative indirect effect on head rice recovery % mainly through cooked rice L/B ratio (-1.21), brown rice breadth (-0.803) and kernel length after cooking (-0.234).

4.4.4.17 Alkali spreading value

Negative direct effect was obtained of alkali spreading value on head rice recovery %, however this trait showed positive indirect effect on head rice recovery % mainly through kernel length after cooking (0.481), amylose% (0.473) and hulling% (0.270). This trait showed negative indirect effect on head rice recovery % mainly through cooked rice L/B ratio (-0.491), gel consistency (-0.201) and brown rice L/B ratio (-0.153).

4.4.4.18 Amylose %

Negative direct effect of amylose % (-0.924) was obtained on head rice recovery %, however it showed positive indirect effect on head rice recovery % mainly through brown rice breadth (0.639), cooked rice L/B ratio (0.478) and gel consistency (0.466). This trait showed negative indirect effect on head rice recovery % mainly through brown rice L/B ratio (-0.587), kernel breadth after cooking (-0.518) and hulling% (-0.312).

Table No. 4.11 Direct and indirect effects of different yield contributing characters on grain yield

Character	Days to 50% flowering	Plant height (cm)	Number of effective tillers per plant	Panicle length (cm)	5 Number of filled grains per panicle	Number of unfilled grains per panicle	Spikelet fertility %	100 seed weight (g)	Biological yield (g)	Harvest index %	r_{xy}
Days to 50% flowering	**0.017**	-0.021	-0.112	0.00005	0.038	-0.079	0.025	0.005	0.555	0.131	0.560
Plant height (cm)	0.005	**-0.069**	0.008	0.00009	0.019	-0.001	-0.013	-0.024	0.454	-0.121	0.257
Number of effective tillers per plant	0.007	0.002	**-0.248**	0.00004	0.059	-0.024	-0.011	0.029	0.805	-0.107	0.512
Panicle length (cm)	0.002	-0.019	-0.030	**0.0003**	0.044	-0.016	-0.030	0.018	0.249	0.073	0.292
Number of filled grains per panicle	0.004	-0.009	-0.100	0.0001	**0.147**	-0.102	-0.028	0.0432	0.472	0.200	0.627
Number of unfilled grains per panicle	0.005	-0.0004	-0.024	0.00002	0.059	**-0.254**	0.125	0.019	0.239	0.078	-0.123
Spikelet fertility %	-0.002	-0.005	-0.017	0.00006	0.026	0.205	**-0.154**	0.005	-0.019	0.093	0.131
100 seed weight (g)	-0.001	-0.023	0.100	-0.00008	-0.087	0.066	0.012	**-0.072**	-0.181	0.117	-0.068
Biological yield (g)	0.0089	-0.028	-0.183	0.00008	0.06393	-0.055	0.0027	0.012	**1.087**	-0.316	0.589
Harvest index %	0.002	0.0094	0.029	0.00003	0.033	-0.022	-0.016	-0.009	-0.386	**0.891**	0.532

Residual = 0.005. The main diagonal (bold) is direct effect.

Table 4.12: Direct and indirect effects on head rice recovery (%) of other quality characters

Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	r_{xy}
1	**0.809**	-0.018	0.006	-0.007	-0.0007	0.329	-0.387	0.053	-0.026	-0.144	-0.045	0.164	-0.019	-0.236	0.065	-0.139	-0.150	0.356	0.609
2	0.578	**-0.025**	-0.021	-0.022	0.004	0.266	-0.433	0.129	-0.036	-0.121	-0.014	0.097	0.984	-0.888	0.078	-0.184	-0.096	0.387	0.725
3	-0.037	0.004	**-0.133**	0.061	-0.033	-1.182	0.065	1.456	0.129	0.0004	-0.166	1.237	-0.769	-0.544	-0.033	-0.001	-0.031	-0.008	0.012
4	-0.008	0.0008	-0.0114	**0.710**	0.041	0.160	0.863	-1.518	-0.001	0.191	0.120	0.403	-2.241	1.115	0.041	0.135	-0.146	0.030	-0.114
5	0.010	0.002	-0.079	-0.527	**-0.055**	-0.923	-0.641	2.187	0.085	-0.151	-0.203	0.492	1.251	-1.231	-0.053	-0.107	0.091	-0.042	0.102
6	-0.178	0.004	-0.105	-0.076	-0.034	**-1.496**	0.232	1.538	0.127	0.059	-0.120	1.169	-0.654	-0.510	-0.031	0.074	0.021	-0.185	-0.165
7	-0.222	0.007	-0.006	0.435	0.025	-0.246	**1.408**	-1.839	0.028	0.355	0.180	0.550	-1.950	0.848	0.0255	0.310	-0.023	-0.419	-0.531
8	0.016	-0.001	-0.073	-0.407	-0.046	-0.870	-0.979	**2.646**	0.071	-0.249	-0.241	0.397	0.991	-0.964	-0.048	-0.199	0.026	0.205	0.273
9	-0.145	0.006	-0.116	-0.008	-0.031	-1.283	0.266	1.273	**0.148**	0.077	-0.141	1.194	-0.681	-0.564	-0.055	0.588	0.017	-0.213	-0.200
10	-0.309	0.008	-0.0001	0.359	0.022	-0.235	1.325	-1.742	0.030	**0.378**	0.185	0.507	-1.732	0.729	0.018	0.303	-0.008	-0.464	-0.623
11	0.139	-0.001	-0.084	-0.325	-0.043	-0.688	-0.969	2.434	0.079	-0.266	**-0.262**	0.415	0.996	-1.030	-0.057	-0.243	-0.006	0.286	0.372
12	0.080	-0.001	-0.100	0.174	-0.016	-1.062	0.470	0.637	0.107	0.116	-0.066	**1.648**	-1.218	-0.061	0.0614	0.077	-0.131	-0.027	0.074
13	0.004	0.007	-0.029	0.452	0.019	-0.277	0.779	-0.744	0.028	0.186	0.074	0.570	**-3.522**	2.095	0.021	0.268	-0.016	-0.136	-0.220

14	0.073	-0.008	-0.027	-0.305	-0.026	-0.293	-0.459	0.981	0.0322	-0.106	-0.104	0.427	2.839	**-2.598**	0.020	-0.253	-0.085	0.17	0.275
15	0.333	-0.012	0.027	0.182	0.018	0.298	0.225	-0.798	-0.051	0.044	0.094	0.634	-0.464	-0.328	**0.159**	0.037	-0.185	0.184	0.400
16	0.207	-0.008	-0.0004	-0.176	-0.011	0.205	-0.803	0.971	-0.016	-0.211	-0.117	-0.234	1.738	-1.210	-0.010	**-0.543**	-0.167	0.793	0.403
17	0.270	-0.005	-0.009	0.231	0.011	0.070	0.074	-0.153	-0.005	0.007	-0.003	0.481	-0.132	-0.491	0.065	-0.201	**-0.450**	0.473	0.233
18	-0.312	0.010	-0.001	-0.023	-0.002	-0.300	0.639	-0.587	0.034	0.190	0.081	0.049	-0.518	0.478	-0.031	0.466	0.230	**-0.924**	-0.522

Residual = 0.34995. The main diagonal (bold) is direct effects.

1 = Hulling %	5 = Paddy L/B ratio	12 = Cooked kernel length (mm)
2 = Milling %	6 = Brown rice length (mm)	13 = Cooked kernel breadth (mm)
3 = Paddy length (mm)	7 = Brown rice breadth (mm)	14 = Cooked rice L/B ratio
4 = Paddy breadth (mm)	8 = Brown rice L/B ratio	15 = Elongation ratio
5 = Paddy L/B ratio	9 = Kernel length (mm)	16 = Gel consistency
6 = Brown rice length (mm)	10 = Kernel breadth (mm)	17 = Alkali spreading value
7 = Brown rice breadth (mm)	11 = Kernel L/B ratio	18 = Amylose %

4.5 Cluster analysis

Cluster analysis was performed based on the dissimilarity coefficient between lines using unweighted pair group method of arithmetic means (UPGMA). The UPGMA agglomerative clustering analysis amalgamated fifty five advanced breeding lines into six major clusters while covering 49.09% of total lines in cluster II (n= 27), 36.36% in cluster I (n=20). Whereas, rest 14.55% of the lines was unequally distributed in cluster III (n=4), IV (n=2), V (n=1) and VI (n=1). This shows the existence of substantial genetic diversity among the studied advanced breeding values. Name of advanced breeding lines and the cluster in which they are grouped are presented in table No. 4.13

Table 4.13: Cluster pattern of 55 advanced breeding lines

Cluster number	No. of advanced breeding lines	Advanced breeding lines
I	20	R-1921-176-1-116-1, R-2340-248-1-286-1, R-2302-82-1-43-1, R-2340-244-2-278-1, R-2294-58-1-17-1, R-2298-354-1-239-1, R-2298-353-3-238-1, R-2302-386-1-275-1, R-2120-37-2-2-1, R-2298-352-2-235-1, R-2288-54-1-15-1, R-2302-383-2-269-1, R-2298-353-1-236-1, R-2311-143-1-123-1, R-2298-352-235-1, R-2326-187-2-180-1, R-2462-RP5530-DRR-SPS-47-1, R-2483-RP5525-B-DRR-SPS-285-1, R-2221-272-1-163-1, IGKV R 1244.
II	27	R-1921-173-1-112-1, R-BSP-18-3, R-BSP-18-2, R 2307-139-1-120-1, R-2302-82-2-44-1, R-2302-77-1-33-1, R-2465-RP5509-DRR-SPS-154-1, R-2298-233-1-73-1, R-2307-108-2-86-1, R-2307-117-1-95-1, R-2341-265-1-305-1, R-2020-295-1-85-1, R-2341-330-2-171-1, R-2341-329-2-169-1, C3-1-5, R-2404-638-1-371-1, R-2307-74-1-50-1, R-2307-74-2-51-1, C-8-1-1, R-2298-354-1-239-1, R-2302-404-2-315-1, R-2307-93-1-63-1, R-2307-99-1-75-1, R-2471-RP5391-DRR-SPS-95-1, IR 64 , IGKV R1 , IGKV R 2.
III	4	Bhatamasuri Selection 1, R-2298-354-2-240-1, R-1762-197-1-131-1, R-1774-1-2-2-1
IV	2	R-1853-82-1-80-1, R-2301-382-2-267-1
V	1	R-2298-353-3-238-1
VI	1	Karma Mahsuri

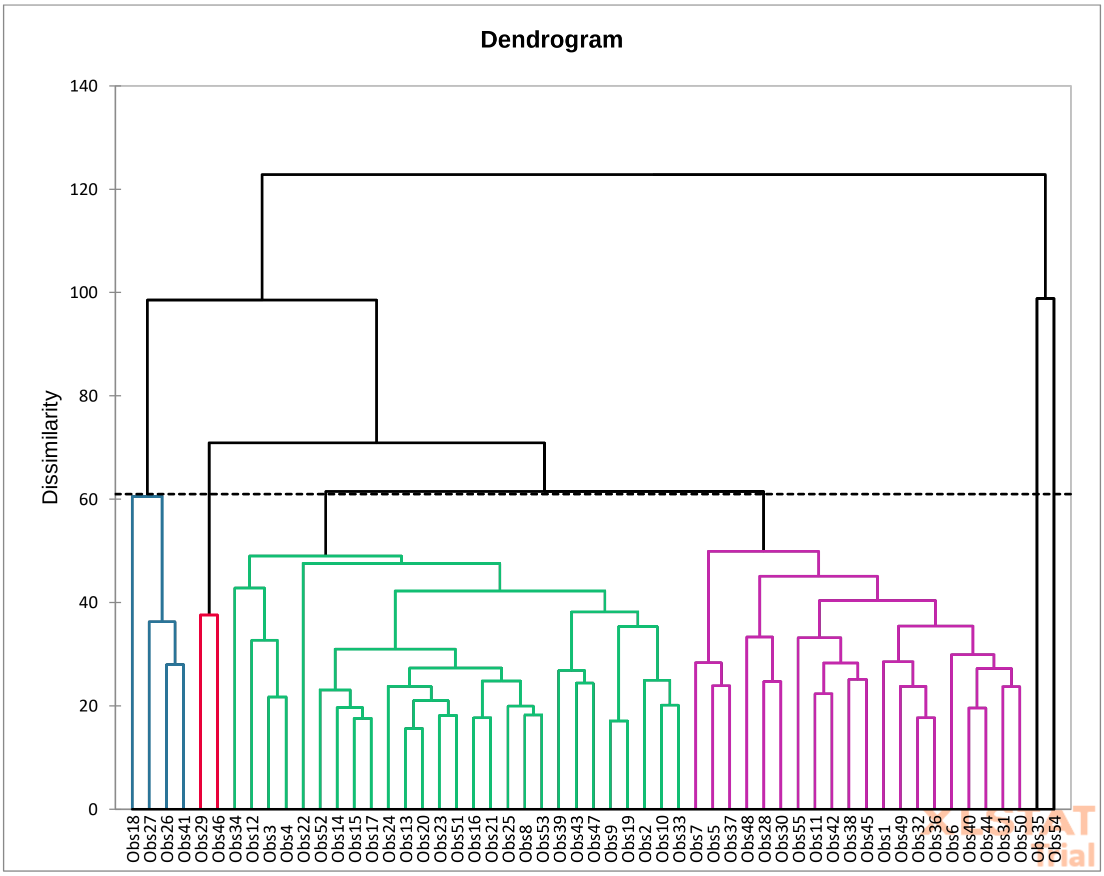

Fig. 4.6 UPGAM Dendrogram showed clusters of 55 advanced breeding lines of rice.

Inter and intra cluster distances among the six clusters were computed and presented in table 4.14 The intra cluster distance ranged from 0.00 (cluster V and VI) to 28.84 (cluster III). Maximum inter cluster distance was present between cluster II and VI (156.25) followed by between cluster III and V (125.01), cluster I and VI (119.64), cluster II and III (111.14). Minimum inter cluster distance was present between cluster I and II (48.57). Parents should be selected from the two clusters which have wider inter cluster distance for higher variability and heterotic effect.

Table 4.14 Average intra (diagonal) and inter-cluster mean values for thirty characters and fifty five advanced breeding lines

Cluster No.	1	2	3	4	5	6
1	**28.552**	48.569	65.062	53.564	96.830	119.637
2		**27.708**	111.141	69.221	109.284	156.246
3			**28.844**	89.936	125.028	94.368
4				**18.804**	69.217	102.849
5					**0**	98.848
6						**0**

Cluster means

Mean cluster values showed a wide range of variations for all the characters undertaken in the investigation (Table 4.15). Cluster I exhibited highest mean values only for trait brown rice L/B ratio (3.28) while, cluster II for trait brown rice length (6.83), kernel breadth (2.11) and amylose % (31.15%). Cluster III exhibited highest mean values for characters number of effective tillers (7.95), spikelet fertility % (84.36) and elongation ratio (1.43). Cluster IV exhibited maximum number of highest means which were for characters days to 50% flowering (97.00), plant height (119.68), 100 seed weight (2.68), biological yield (53.89), hulling% (79.59), milling% (71.59), paddy length (9.13), paddy breadth (2.80), brown rice breadth (2.30), kernel length (6.25), kernel length after cooking (8.93), kernel breadth after cooking (3.45) and elongation ratio (1.43). Highest mean values for paddy L/B ratio (3.85), kernel L/B ratio (3.20), cooked rice L/B ratio (3.79), gel consistency (97.50) and alkali spreading value (6.50) were exhibited by cluster V. Cluster VI exhibited highest mean values for traits panicle length (25.34), number of filled grains/panicle (228.50), number of unfilled grains/panicle (126.50), grain yield/plant (26.15), harvest index% (67.10), alkali spreading value (6.50) and % (59.80)

These results are similar to the findings of Devi *et al.* (2020) and Rashid *et al*. (2013). The findings suggest that genotypes with high cluster mean values for a specific attribute might be employed in a hybridization program for character improvement. A comprehensive examination of the data revealed that none of the clusters included genotypes with all of the desirable characters that could be selected and used directly. To judiciously incorporate all of the targeted characters, hybridization between selected genotypes from divergent clusters is required.

Table 4.15 Mean performance of breeding lines in individual clusters for characters

Clusters/characters	I	II	III	IV	V	VI
Days to 50% flowering	91.78	90.98	94.13	97.00	91.50	94.50
Plant height (cm)	108.90	106.67	109.48	**119.68**	102.14	108.02
Number of effective tillers	7.27	6.96	**7.95**	7.08	7.70	7.60
Panicle length (cm)	25.33	24.14	24.56	25.27	24.87	**25.34**
Number of filled grains/panicle	157.40	114.30	222.00	147.50	137.50	**228.50**
Number of unfilled grains/panicle	36.90	31.57	40.13	82.25	116.00	126.50
Spikelet fertility%	81.34	78.47	**84.36**	64.20	54.58	64.94
100 seed weight (gm)	2.23	2.54	1.70	**2.68**	2.01	1.68
Biological yield	46.79	38.14	49.53	**53.89**	48.62	39.43
Grain yield/plant	21.27	17.07	21.88	21.17	20.66	**26.15**
Harvest index %	47.73	46.70	44.89	40.15	46.34	**67.10**
Hulling%	77.87	75.72	79.58	**79.59**	78.21	79.21
Milling%	70.32	66.10	71.58	**71.80**	71.19	70.50

Paddy length (mm)	8.96	8.87	7.79	**9.13**	8.65	8.35
Paddy breadth (mm)	2.53	2.51	2.34	2.80	2.25	2.60
Paddy L/B ratio	3.58	3.58	3.40	3.26	3.85	3.26
Brown rice length (mm)	6.73	**6.83**	5.99	6.50	6.15	6.05
Brown rice breadth (mm)	2.07	2.19	1.94	2.30	2.00	2.00
Brown rice L/B ratio	3.28	3.15	3.11	2.87	3.08	3.03
Kernel length (mm)	5.95	6.15	5.38	**6.25**	6.15	5.85
Kernel breadth (mm)	1.96	2.11	1.88	2.10	1.93	1.95
Kernel L/B ratio	3.05	2.94	2.89	2.99	3.20	3.00
Kernel length after cooking (mm)	8.41	8.56	7.70	**8.93**	8.15	8.15
Kernel breadth after cooking (mm)	2.97	3.08	2.79	3.45	2.15	2.55
Cooked rice L/B ratio	2.85	2.79	2.81	2.59	3.79	3.20
Elongation ratio	1.42	1.39	**1.43**	**1.43**	1.33	1.39
Gel consistency	54.13	42.24	56.38	43.25	97.50	72.50
Alkali spreading value	4.98	4.65	4.50	5.50	6.50	6.50
Amylose %	22.23	31.15	23.45	24.00	14.50	15.15
Head rice recovery %	49.52	38.56	51.25	55.94	52.41	**59.80**

Note: Data in bold digits represents the highest mean value obtained for particular character. Characters in which highest values are not favourable are not in bold.

CHAPTER-V

SUMMARY AND CONCLUSIONS

Rice (*Oryza sativa* L.) is the staple food of over 70% of Indians and a source of income for around 120-150M rural families. The research work entitled "Genetic analysis of yield and quality characters in advanced breeding lines of Rice (*Oryza sativa* L.)" was conducted with fifty rice advanced breeding lines and five checks namely IR 64, IGKV R1, IGKV R 2, Karma Mahsuri and IGKV R1244 in RBD with two replications during *kharif* 2020 at Research cum Instructional farm, Department of Genetics and Plant Breeding, CoA, IGKV, Raipur (C.G.). The research's goals were to investigate the genetic variation and diversity present in the experimental material for the purpose of selecting diverse parents for yield and quality traits, and the degree to which yield, yield-attributing traits and quality characters are correlated. For all traits, in each replication five plants were randomly chosen for taking observations.

For all of the traits, the study of variance showed extremely significant variations among the 55 advanced breeding lines, suggesting significant genetic variation in the material. In yield traits highest variation exhibited by number of filled grains and lowest variation in 100 seed weight (g) and in quality traits highest variation exhibited by gel consistency and lowest variation by kernel breadth (mm).

For both yield and quality traits the value for PCV and GCV ranged from low to high. Number of unfilled grains/panicle (49.20), alkali spreading value (32.24), amylose% (30.36), gel consistency (27.05), number of filled grains/panicle (24.48), grain yield/plant (g) (22.40), head rice recovery% (22.20), biological yield (g) (20.53) and harvest index% (19.16) showed high values of GCV and PCV. Low estimates were exhibited by traits plant height(cm) (6.01), days to 50 % flowering (3.95), panicle length(cm) (4.78), spikelet fertility% (8.02), hulling% (3.52), milling% (5.91), paddy length(mm) (6.25), kernel length(mm) (9.18), brown rice breadth(mm) (7.74), kernel breadth(mm) (9.24), brown rice length(mm) (8.16), paddy breadth(mm) (9.25) and kernel length after cooking(mm) (6.81). Moderate estimates were obtained in traitsbkernel L/B ratio (9.73), paddy L/B ratio (11.19), number of effective tillers/plant (12.24), brown rice L/B ratio (11.06), 100 seed weight (g) (17.87), cooked rice L/B ratio (10.83) and kernel breadth after cooking (mm) (10.09).

The yield and quality traits which showed high values for genetic advance as % of mean along with high heritability were number of filled grain/panicle, biological yield per plant (g), number of unfilled grain/panicle, 100 seed weight (g), grain yield/plant (g), paddy L/B ratio, amylose %, kernel breadth after cooking (mm), brown rice L/B ratio, gel consistency, cooked rice L/B ratio, alkali spreading value and head rice recovery %. This implied that additive gene activity influenced the inheritance of these features. Following a simple selection method, these characteristics can be improved. For yield traits plant height (mm) and spikelet fertility% and for the quality traits paddy length (mm), milling%, paddy breadth (mm), brown rice length (mm), kernel length (mm), kernel length after cooking (mm), brown rice breadth (mm), kernel breadth (mm) and kernel L/B ratio high heritability along with moderate genetic advance as % of mean was obtained, in addition to the influence of the environment to some extent, suggested the presence of non-additive gene effects.

Out of 50 advanced breeding lines twenty two lines (excluding checks) showed >50% head rice recovery %. R1853-82-1-80-1 (60.53), R1762-197-1-131-1 (62.52), R2302-383-2-269-1 (55.11), R2307-99-1-75-1 (54.33), R2298-353-3-238-1 (54.27) have high head rice recovery %. Highest milling % was exhibited by R 2288-54-1-15-1 (78.56%) followed by R2298-354-2-240-1 (75.77%) and R2298-352-235-1 (75.47%). As per estimates of kernel length out of fifty five lines two lines (R2307-74-1-50-1 and R2307-74-2-51-1 had long grain, forty five lines had medium long grain and eight lines had eight lines had short size grains. With the help of kernel L/B ratio estimates of grain shape was deduced as per which twenty six lines had long slender grain shape, twenty nine lines had medium slender grain shape and there was no line with bold or round grain shape. Highest elongation ratio was obtained in line R2302-404-2-315-1 (1.60) followed by R2298-354-1-239-1-1 (1.59) and R2298-354-1-239-1 (1.58). As per estimates of gel consistency twenty lines exhibited hard gel consistency, twenty three lines exhibited medium gel consistency and twelve lines exhibited soft gel consistency. Alkali spreading value estimates showed that only one line showed low alkali spreading value, thirteen lines had low-intermediate alkali spreading value, fifteen lines had intermediate alkali spreading value and twenty-six lines had high alkali spreading value. Fifteen lines had low amylose content, thirteen lines had intermediate amylose content and twenty seven lines had high amylose content. Lines with good head rice recovery %, medium to long grain, slender shaped grain, higher elongation ratio, soft gel consistency, intermediate alkali spreading value and intermediate amylose % should be selected for improving grain quality.

Genotypic coefficient of correlation values were greater than phenotypic coefficient of correlation among most of the character combinations explaining that the cause for such observed relationship among various traits is due to genetic cause. Correlations studies showed that there was a positive significant correlation of grain yield/plant with panicle length, plant height, effective tillers/plant, harvest index%, days to 50% flowering, number of filled grains/panicle and biological yield. Thus, directing selection towards higher values of these yield attributing traits with optimum plant height and days to 50% flowering will result in higher grain yield. Highest significant and positive correlation of head rice recovery% was obtained with milling% and with hulling%, elongation ratio, kernel L/B ratio, gel consistency, cooked rice L/B ratio and brown rice L/B ratio. Indicating that selection of lines with higher milling%, hulling%, elongation ratio and L/B ratios would result in higher head rice recovery%. Thus, this is evident that simultaneous selection of all these yield and quality traits will be significant for both increasing production and improving grain quality.

Significant positive correlation of days to 50% flowering was observed with plant height (0.305), number of effective tillers/plant (0.453), number of filled grains/panicle (0.263), number of unfilled grain/panicle (0.245) and biological yield per plant (0.511). Highest positive significant correlation of number of effective tillers with biological yield per plant (0.741) followed by number of filled grains/panicle (0.404) was recorded. Highly significant and positive correlation of panicle length seen with filled grains/panicle (0.305). Number of filled grains/panicle showed a highly significant positive correlation with biological yield (0.434), number of unfilled grains/panicle (0.303) and harvest index% (0.225). On the other hand, within quality traits, highly significant and positive correlation of hulling% with milling% (0.715), elongation ratio (0.412), gel consistency (0.256) and alkali spreading value (0.335). Highly positive significant correlation was seen of milling% with elongation ratio (0.489), gel consistency (0.339) and cooked rice L/B ratio (0.342) and moderately significant positive correlation with alkali spreading value (0.214). Highly positive significant correlation of kernel length after cooking was obtained with elongation ratio (0.385), kernel breadth after cooking (0.346), alkali spreading value (0.292) and cooked rice L/B ratio (0.259). Highly significant positive correlation of gel consistency was noted with alkali spreading value (0.371). Highly positive significant correlation of elongation ratio was recorded with alkali spreading value (0.412).

Analysis of the results of path analysis showed that harvest index, biological yield, days to 50% flowering, number of filled grains/panicle and panicle length influenced grain yield/plant directly. Similarly, for quality traits cooked rice length, brown rice L/B ratio, hulling%, brown rice breadth, paddy breadth, kernel breadth, elongation ratio and kernel length were influencing head rice recovery %.

Yield traits which showed significant positive correlation and positive direct effect on grain yield/plant were number of filled grains/panicle, biological yield/plant (g) and harvest index %. Quality traits which exhibited significant correlation and positive direct effect on head rice recovery % were hulling %, elongation ratio and brown rice L/B ratio. Direct selection of genotypes based on these characters will be rewarding for improvement of both grain yield and grain quality.

Yield and quality traits which exhibited significant positive correlation but negative direct effect on grain yield/plant and head rice recovery % respectively were number of effective tillers/plant, number of unfilled grains per panicle, brown rice length, kernel L/B ratio, cooked rice L/B ratio, gel consistency and alkali spreading value. Direct selection based on these characters will not be effective but indirect selection through these characters may be effective in improving grain yield and grain quality.

Choosing parents with a higher number of effective tillers/plant, optimum plant height, higher number of filled grains/panicle, panicle length, biological yield, harvest index percent, and among quality traits with higher values of milling percent, hulling percent, and gel consistency should be emphasized, according to a thoughtful examination of correlation and path analysis.

Formation of a number of clusters with a varied range of inter-cluster distances, divergence analysis using the cluster analysis revealed the presence of considerable variation. Cluster analysis using unweighted pair group of arithmetic means (UPGMA) on the basis of their dissimilarities through quantitative and quality traits grouped 55 advanced breeding lines into 6 clusters. Maximum lines i.e. 49.09% of total lines grouped in cluster II (n= 27), 36.36% in cluster I (n=20). Whereas, rest 14.55% of the lines was unequally distributed in cluster III (n=4), IV (n=2), V (n=1) and VI (n=1). This shows existence of substantial genetic diversity among the studied advanced breeding values.

The intra-cluster distance varied between 0.00 (cluster V and VI) to 28.84 (cluster III). Cluster II and VI (156.25) had the greatest inter-cluster distance, followed by cluster III and V (125.01), cluster I and VI (119.64), and cluster II and III (111.14) indicating that crossings involving varieties from these clusters would result in recombination that would be broader and more desirable. Minimum inter cluster distance was present between cluster I and II (48.57). The 27 genotypes in Cluster II with maximum intra cluster distance were the most heterogenous and hence suitable for within group hybridization.

Cluster VI exhibited highest mean values for characters number of filled grains/panicle (228.50), harvest index% (67.10), grain yield/plant (26.15), and head rice recovery% (59.80), cluster V for paddy L/B ratio (3.85), kernel L/B ratio (3.20), cooked rice L/B ratio (3.79), cluster IV for plant height (119.68), 100 seed weight (2.68), biological yield (53.89), hulling% (79.59), milling% (71.80), paddy length (9.13), kernel length (6.25), elongation ratio (1.43), cluster I exhibited highest mean values only for trait brown rice L/B ratio (3.28) while, cluster II for trait brown rice length (6.83), kernel breadth(2.11) and amylose%(31.15).

Conclusion:

- High amount of variation among advance breeding lines for yield attributing and quality traits were observed.
- Higher GCV and PCV values were obtained from number of filled grains/panicle, harvest index%, number of unfilled grains/panicle, biological yield (g), grain yield/plant (g), gel consistency, alkali spreading value, head rice recovery % and amylose%. The genotypic variance was smaller than phenotypic variance, this indicates that environment have masking effect on the expression of genetic variability.
- Traits with high values for genetic advance as % of mean along with high heritability were number of filled grain/panicle, biological yield per plant (g), number of unfilled grain/panicle, 100 seed weight (g), grain yield/plant (g),

paddy L/B ratio, brown rice L/B ratio, amylose %, kernel breadth after cooking (mm), gel consistency, cooked rice L/B ratio, alkali spreading value and head rice recovery %. This shows that additive gene activity influenced the inheritance of these traits. Improvement in these traits can be made following a simple selection method.

- Direct selection of genotypes based on yield characters number of filled grains/panicle, harvest index% and biological yield/plant (g) and quality traits hulling%, elongation ratio and brown rice L/B ratio will be rewarding for improving grain yield and grain quality respectively.
- R1853-82-1-80-1 (60.53), R1762-197-1-131-1 (62.52), R2302-383-2-269-1 (55.11), R2307-99-1-75-1 (54.33), R2298-353-3-238-1 (54.27) have high head rice recovery %.
- The breeding lines R2298-353-3-238-1, R1853-82-1-80-1, R2301-382-2-267-1, R2120-37-2-2-1, C8-1-1 with highest mean values for different yield and quality traits might be employed directly for adaptation or as parents in a future hybridization procedure.
- Cluster IV exhibited maximum number of highest mean values which are for plant height (119.68), 100 seed weight (2.68), biological yield (53.89), hulling% (79.59), milling% (71.80), paddy length (9.13), kernel length (6.25) and elongation ratio (1.43).
- R1853-82-1-80-1 and R2301-382-2-267 from cluster IV may be taken under hybrid breeding for getting higher values of both grain yield and improved grain quality.

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APPENDIX-A: Mean values of fifty five advanced breeding lines for yield and yield attributing traits

ABL	1	2	3	4	5	6	7	8	9	10	11
R-1921-176-1-116-1	93.50	93.49	6.30	23.80	143.00	52.00	73.18	2.38	36.64	53.13	19.43
R-1921-173-1-112-1	92.50	96.68	7.40	24.16	115.00	36.00	76.04	2.40	32.57	58.45	18.97
R-BSP-18-3	87.50	106.56	5.80	26.31	141.50	37.50	79.05	2.30	30.31	58.31	17.40
R-BSP-18-2	86.50	106.56	6.80	25.11	134.50	44.00	75.31	2.50	31.91	63.84	20.53
R-2340-248-1-286-1	92.50	103.54	7.80	24.74	190.00	30.00	86.35	1.96	42.82	57.69	24.67
R-2302-82-1-43-1	89.50	107.19	5.70	23.90	150.00	35.50	80.81	2.27	38.67	40.33	15.59
R-2340-244-2-278-1	93.50	103.91	5.50	23.26	166.50	21.50	88.45	2.01	33.74	55.58	18.79
R-2307-139-1-120-1	91.00	102.62	6.40	23.46	90.00	25.50	77.91	2.52	29.97	44.83	13.40
R-2302-82-2-44-1	89.50	106.19	6.70	23.63	126.00	32.50	79.46	2.16	35.36	38.45	13.44
R-2302-77-1-33-1	86.50	102.61	4.90	23.95	127.00	22.50	84.94	2.15	29.66	47.79	14.20
R-2294-58-1-17-1	87.00	110.24	6.25	26.61	137.00	25.50	84.44	2.40	41.88	42.51	16.44
R-2465-RP5509-DRR-SPS-154-1	87.50	99.61	7.95	23.50	112.00	38.00	74.42	2.54	27.55	68.35	19.00
R-2298-233-1-73-1	87.00	107.84	6.70	21.43	110.00	26.00	81.02	2.53	35.21	45.46	15.74
R-2307-108-2-86-1	89.00	108.58	6.70	23.13	99.50	45.00	68.87	2.88	30.67	51.38	14.78
R-2307-117-1-95-1	90.50	106.83	5.70	23.46	111.50	49.00	68.86	2.92	38.38	39.07	14.94
R-2341-265-1-305-1	94.50	107.68	7.70	23.06	105.00	24.00	81.48	2.53	46.98	32.61	15.28
R-2020-295-1-85-1	89.50	101.19	6.30	24.31	103.50	43.50	70.51	2.20	29.96	37.76	11.13
Bhatamasuri Selection 1	86.50	107.36	7.90	22.02	256.00	40.00	86.50	1.92	45.44	42.26	18.93
R-2341-330-2-171-1	88.50	107.06	7.30	24.19	118.00	29.00	80.24	2.78	43.77	40.56	17.47
R-2341-329-2-169-1	89.50	109.43	7.10	23.49	117.50	25.50	82.19	2.60	36.84	41.96	15.38
C-3-1-5	94.00	107.23	9.30	25.67	102.00	32.50	75.92	2.02	47.30	36.86	17.45
R-2404-638-1-371-1	94.50	103.26	7.30	23.20	98.50	44.00	69.10	2.72	65.74	25.74	16.87
R-2307-74-1-50-1	92.50	108.72	7.10	25.64	107.00	28.50	79.82	3.02	33.98	48.76	16.42
R-2307-74-2-51-1	93.50	109.97	6.90	24.92	116.00	17.00	87.23	2.79	37.75	51.36	19.31
C-8-1-1	86.50	103.29	5.90	24.68	103.00	28.50	78.54	2.11	34.15	36.11	12.32
R-2298-354-2-240-1	93.50	106.68	8.40	25.41	214.00	27.50	88.50	2.00	47.10	55.13	25.86
R-1762-197-1-131-1	103.00	110.84	8.60	24.61	213.50	56.00	77.74	1.40	58.05	43.98	25.45
R-2298-354-1-239-1	93.00	104.70	10.10	25.58	167.50	58.00	74.37	1.88	67.56	46.67	31.44
R-1853-82-1-80-1	100.50	113.91	7.30	24.98	160.00	83.00	65.83	2.44	49.39	49.76	24.57
R-2298-353-3-238-1	90.50	103.42	10.30	26.13	166.50	40.00	80.63	1.93	62.00	36.11	22.24
R-2302-386-1-275-1	89.50	106.79	7.40	23.77	151.00	22.00	87.43	2.82	54.17	49.63	26.37
R-2120-37-2-2-1	97.50	108.17	7.70	24.82	155.00	52.00	75.02	2.12	48.73	53.13	23.46
R-2298-354-1-239-1-1	92.50	100.75	8.60	24.91	133.50	28.50	82.43	1.89	38.03	55.15	21.00

R-2302-404-2-315-1	100.50	118.57	7.10	24.11	143.50	37.00	79.51	3.37	38.31	82.41	31.58
R-2298-353-3-238-1	91.50	102.14	7.70	24.87	137.50	116.00	54.58	2.01	48.62	46.34	20.66
R-2298-352-2-235-1	88.50	99.64	7.50	25.97	160.00	47.00	77.76	1.95	41.56	56.78	20.71
R-2288-54-1-15-1	97.50	105.12	7.20	23.36	182.00	34.50	84.27	2.10	41.56	59.20	23.44
R-2302-383-2-269-1	90.50	122.59	6.40	24.96	149.50	44.50	77.10	2.95	48.55	54.94	22.73
R-2307-93-1-63-1	93.50	115.47	7.30	26.58	132.50	21.00	86.23	2.57	50.16	42.41	21.14
R-2298-353-1-236-1	88.50	104.44	6.50	27.14	151.00	24.00	86.54	1.99	42.69	40.25	17.16
R-1774-1-2-2-1	93.50	113.04	6.90	26.21	204.50	37.00	84.71	1.47	47.53	38.19	17.28
R-2311-143-1-123-1	94.00	111.00	8.10	27.38	149.50	24.00	86.11	1.91	48.65	48.47	22.18
R-2307-99-1-75-1	93.50	115.86	6.35	26.27	119.50	14.00	89.62	2.88	52.54	33.99	17.54
R-2298-352-235-1	89.50	104.58	7.25	25.66	159.50	32.50	83.23	2.02	51.08	44.42	20.33
R-2326-187-2-180-1	94.50	126.33	7.95	26.00	142.50	36.00	80.04	2.13	51.19	35.25	17.31
R-2301-382-2-267-1	93.50	125.45	6.85	25.55	135.00	81.50	62.58	2.92	58.40	30.54	17.77
R-2471-RP5391-DRR-SPS-95-1	96.50	112.25	9.25	22.13	115.50	29.00	79.92	2.40	57.29	34.51	19.76
R-2462-RP5530-DRR-SPS-47-1	92.50	108.63	6.00	25.24	170.50	61.50	73.62	2.05	46.62	27.95	13.02
R-2483-RP5525-B-DRR-SPS-285-1	91.50	110.06	7.10	26.48	149.50	44.00	77.24	2.39	42.06	46.30	19.36
R-2221-272-1-163-1	88.50	119.78	6.70	24.98	146.50	25.50	85.10	2.39	39.40	50.46	19.52
IR 64	92.00	102.62	6.60	24.93	112.00	33.50	77.68	2.31	29.10	52.90	15.33
IGKV R1	91.00	104.60	6.00	23.10	96.00	39.00	71.04	2.91	31.45	47.28	14.87
IGKV R 2	86.50	108.15	6.90	22.49	96.00	22.00	81.35	2.51	34.97	44.66	15.61
Karma Mahsuri	94.50	108.02	7.60	25.34	228.50	126.50	64.94	1.68	39.43	67.10	26.15
IGKV R 1244	9350	124.39	7.70	26.73	161.00	28.00	85.19	3.05	56.27	55.87	31.14

1 Days to 50% flowering

2 Plant height (cm)

3 Number of effective tillers per plant

4 Panicle length (cm)

5 Number of filled grains per panicle

6 Number of unfilled grains per panicle

7 Spikelet fertility %

8 100 seed weight (gm)

9 Biological yield per plant

10 Harvest index %

11 Grain yield/plant

APPENDIX-B: Mean values of fifty five advanced breeding lines for quality traits

Entry No.	ABL	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1.	**R-1921-176-1-116-1**	71.29	66.07	9.55	2.45	3.91	7.30	2.10	3.48	6.55	1.95	3.36	8.60	2.95	2.92	1.31	58.50	2.50	**21.95**	49.45
2.	**R-1921-173-1-112-1**	74.47	68.29	9.25	2.25	4.12	6.90	2.10	3.29	6.55	2.00	3.28	8.45	2.85	2.96	1.29	56.50	2.50	**21.75**	49.78
3.	**R-BSP-18-3**	78.77	69.89	8.60	2.15	4.00	7.05	2.05	3.44	6.00	1.95	3.08	7.70	2.85	2.71	1.28	37.00	4.50	33.50	46.23
4.	**R-BSP-18-2**	74.53	60.94	8.95	2.30	3.89	6.80	2.15	3.17	6.15	2.05	3.00	8.40	2.85	2.95	1.37	38.50	4.50	28.55	32.28
5.	**R-2340-248-1-286-1**	72.76	66.68	8.00	2.25	3.56	6.15	2.10	2.93	5.50	2.05	2.68	7.95	2.95	2.69	1.45	31.00	2.50	35.25	47.59
6.	**R-2302-82-1-43-1**	79.22	69.50	8.80	2.35	3.75	6.90	2.10	3.29	6.30	2.05	3.07	8.15	3.00	2.72	1.29	51.50	2.50	25.25	32.00
7.	**R-2340-244-2-278-1**	76.26	69.26	7.60	2.60	2.92	5.80	2.15	2.70	5.30	2.05	2.59	7.55	3.03	2.50	1.42	37.50	3.00	34.20	46.33
8.	**R-2307-139-1-120-1**	74.99	63.84	9.30	2.45	3.81	6.95	2.10	3.32	6.35	2.00	3.18	8.50	2.85	2.98	1.34	33.50	6.50	36.05	36.30
9.	**R-2302-82-2-44-1**	72.53	60.74	8.80	2.35	3.75	6.95	2.00	3.49	6.25	1.93	3.25	8.35	3.05	2.74	1.34	60.00	2.50	**21.65**	26.32
10.	**R-2302-77-1-33-1**	77.66	68.19	8.75	2.20	3.98	6.95	2.05	3.39	6.25	1.98	3.16	7.95	2.90	2.74	1.27	54.00	4.50	**24.75**	46.35
11.	**R-2294-58-1-17-1**	82.23	71.07	9.25	2.50	3.70	7.10	2.20	3.23	6.45	2.10	3.07	8.80	3.05	2.89	1.36	32.50	4.50	32.45	**51.67**
12.	**R-2465-RP5509-DRR-SPS-154-1**	79.13	70.36	8.70	2.40	3.87	7.35	2.30	3.20	6.45	2.23	2.90	9.15	3.05	3.00	1.42	33.50	6.50	38.10	44.96
13.	**R-2298-233-1-73-1**	71.25	64.91	8.55	2.75	3.11	6.35	2.50	2.55	5.85	2.43	2.41	8.20	3.05	2.69	1.40	37.50	6.50	29.05	31.24
14.	**R-2307-108-2-86-1**	75.84	68.81	8.80	2.45	3.60	6.95	2.35	2.90	6.40	2.30	2.78	8.45	3.10	2.73	1.32	39.50	5.00	29.15	28.28
15.	**R-2307-117-1-95-1**	76.60	67.42	9.00	2.95	3.05	7.15	2.45	2.92	6.35	2.38	2.67	9.05	3.50	2.60	1.43	40.50	4.50	29.60	29.38
16.	**R-2341-265-1-305-1**	76.55	66.30	8.35	2.70	3.10	6.15	2.30	2.68	5.60	2.10	2.67	8.50	3.05	2.79	1.52	40.50	6.50	33.05	37.28
17.	**R-2020-295-1-85-1**	71.64	61.46	8.90	2.60	3.43	6.75	2.15	3.16	6.00	2.00	3.00	8.45	2.85	2.97	1.41	40.50	6.50	32.52	33.26
18.	**Bhatamasuri Selection 1**	75.50	67.58	7.50	2.40	3.35	6.10	2.25	2.71	5.25	2.20	2.39	7.20	3.10	2.32	1.37	38.00	2.50	33.05	40.58
19.	**R-2341-330-2-171-1**	77.06	64.17	7.75	2.80	2.77	6.20	2.55	2.44	5.70	2.50	2.28	7.90	3.50	2.26	1.39	53.00	6.50	**22.00**	22.12
20.	**R-2341-329-2-169-1**	73.80	57.45	8.35	2.85	2.94	6.20	2.55	2.43	5.75	2.48	2.32	8.45	3.40	2.49	1.47	36.50	6.50	35.46	24.05

21.	**C-3-1-5**	72.40	66.05	8.20	2.45	3.37	6.60	2.05	3.22	5.90	2.00	2.95	8.25	3.00	2.75	1.40	36.50	2.50	32.60	48.17
22.	**R-2404-638-1-371-1**	75.55	66.76	9.50	2.25	4.25	7.20	2.10	3.43	6.10	2.05	2.98	9.35	2.90	3.23	1.54	36.50	2.00	37.45	36.71
23.	**R-2307-74-1-50-1**	78.93	65.28	10.00	2.30	4.35	7.60	2.10	3.63	6.95	2.05	3.39	9.15	3.00	3.05	1.32	33.50	2.50	43.90	37.91
24.	**R-2307-74-2-51-1**	72.70	67.90	9.80	2.50	3.93	7.70	2.15	3.59	7.15	2.10	3.41	9.05	3.10	2.92	1.27	38.50	4.50	44.05	38.27
25.	**C-8-1-1**	78.11	69.29	8.05	2.30	3.50	6.15	2.25	2.74	5.65	2.10	2.69	7.60	2.95	2.58	1.35	36.50	2.50	38.60	43.05
26.	**R-2298-354-2-240-1**	81.99	75.47	8.65	2.50	3.46	6.30	1.90	3.32	5.95	1.83	3.26	8.55	2.35	3.64	1.44	67.50	5.50	18.85	**56.01**
27	**R-1762-197-1-131-1**	81.88	74.24	7.60	2.15	3.56	5.60	1.80	3.11	5.05	1.73	2.93	7.60	2.75	2.77	1.50	57.50	3.50	**23.80**	**62.52**
28.	**R-2298-354-1-239-1**	78.88	73.46	8.50	2.35	3.62	6.50	1.93	3.38	5.60	1.83	3.07	8.85	2.45	3.61	1.58	67.50	6.50	14.35	**53.70**
29.	**R-1853-82-1-80-1**	79.01	72.58	8.95	2.65	3.38	6.90	2.10	3.29	6.35	2.00	3.18	8.85	3.35	2.64	1.39	44.00	4.50	**23.85**	**60.53**
30.	**R-2298-353-3-238-1**	78.44	71.03	8.70	2.25	3.87	6.75	1.80	3.75	5.85	1.73	3.39	8.10	2.85	2.84	1.38	67.50	6.50	16.25	**54.27**
31.	**R-2302-386-1-275-1**	77.47	69.91	9.80	2.70	3.63	7.50	2.10	3.57	6.45	2.03	3.19	8.80	3.05	2.89	1.36	70.00	4.50	17.15	42.91
32.	**TRR 104**	78.97	68.21	10.35	2.10	4.94	7.05	1.80	3.92	6.15	1.73	3.57	8.15	2.85	2.86	1.33	77.50	5.50	17.25	**50.50**
33.	**R-2298-354-1-239-1-1**	78.82	73.97	8.55	2.30	3.72	6.30	2.00	3.15	5.75	1.95	2.95	9.15	3.05	3.00	1.59	57.50	6.50	**21.45**	**51.94**
34.	**R-2302-404-2-315-1**	77.24	70.59	9.90	3.05	3.25	7.10	2.40	2.96	6.45	2.35	2.74	10.35	3.55	2.92	1.60	42.50	6.50	18.70	**51.46**
35.	**R-2298-353-3-238-1**	78.21	71.19	8.65	2.25	3.85	6.15	2.00	3.08	6.15	1.93	3.20	8.15	2.15	3.79	1.33	97.50	6.50	14.50	**52.41**
36.	**R-2298-352-2-235-1**	78.89	71.00	8.20	2.20	3.74	6.40	2.00	3.20	5.65	1.85	3.05	8.20	2.45	3.35	1.45	75.00	6.50	15.75	**52.48**
37.	**R-2288-54-1-15-1**	79.40	78.56	8.30	2.70	3.07	6.40	2.10	3.05	5.25	2.03	2.59	8.00	2.35	3.41	1.52	42.50	4.50	**24.50**	**50.62**
38.	**R-2302-383-2-269-1**	80.29	70.60	9.35	3.15	2.97	6.80	2.50	2.72	6.15	2.05	3.00	8.80	3.45	2.55	1.43	37.50	6.50	26.75	**55.11**
39.	**DH-17-SXR-P72**	77.24	57.63	9.65	2.55	3.79	6.40	1.80	3.56	6.15	1.75	3.51	7.90	3.35	2.35	1.29	47.50	4.50	19.85	43.95
40.	**R-2298-353-1-236-1**	78.41	70.62	9.05	2.90	3.12	6.10	2.00	3.05	5.75	1.85	3.11	8.15	3.05	2.67	1.42	60.00	6.50	**22.60**	**51.44**
41.	**R-1774-1-2-2-1**	78.95	69.05	7.40	2.30	3.22	5.95	1.80	3.31	5.25	1.75	3.00	7.45	2.95	2.53	1.42	62.50	6.50	18.10	45.92
42.	**R-2311-143-1-123-1**	80.03	70.15	8.20	2.50	3.28	6.15	2.10	2.93	5.40	2.03	2.67	8.20	3.25	2.52	1.52	42.50	2.50	25.05	**52.52**
43.	**R-2307-99-1-75-1**	78.92	68.05	9.50	2.45	3.91	7.70	2.10	3.67	6.55	2.03	3.23	10.25	3.45	2.97	1.56	42.50	6.50	25.75	**54.33**
44.	**R-2298-352-235-1**	81.79	75.77	8.90	2.55	3.49	6.40	1.90	3.37	6.05	1.83	3.32	8.90	3.25	2.74	1.47	52.50	6.50	17.25	**52.40**
45.	**R-2326-187-2-180-1**	78.82	67.55	9.10	2.70	3.39	6.10	2.00	3.39	5.95	1.95	3.05	8.35	3.05	2.74	1.40	39.00	4.50	29.50	**51.19**
46.	**R-2301-382-2-267-1**	80.18	71.02	9.30	2.95	3.15	6.10	2.50	2.44	6.15	2.20	2.80	9.00	3.55	2.54	1.46	42.50	6.50	**24.15**	**51.35**

47.	**R-2471-RP5391-DRR-SPS-95-1**	79.10	72.22	7.50	3.00	2.50	5.95	2.00	2.98	4.95	1.90	2.61	7.15	3.35	2.13	1.44	52.50	4.50	**21.00**	**50.07**
48.	**R-2462-RP5530-DRR-SPS-47-1**	74.31	71.12	8.85	2.40	3.69	6.90	1.90	3.63	6.05	1.85	3.27	8.30	2.85	2.91	1.37	64.00	6.50	15.75	**53.36**
49.	**R-2483-RP5525-B-DRR-SPS-285-1**	79.08	67.87	9.50	2.55	3.73	7.90	2.30	3.43	6.05	2.05	2.95	9.40	3.25	2.89	1.55	60.50	6.50	16.80	**50.39**
50.	**R-2221-272-1-163-1**	72.56	67.41	9.05	2.70	3.36	6.70	2.10	3.19	6.05	2.03	2.99	8.00	2.95	2.71	1.32	64.50	4.50	12.65	41.06
51.	**IR 64**	76.15	64.16	9.10	2.50	3.64	7.05	2.05	3.45	6.30	2.00	3.15	8.00	2.85	2.81	1.27	39.00	2.50	33.90	**55.73**
52.	**IGKV R1**	74.38	65.52	8.90	2.70	3.31	6.85	2.45	2.80	6.20	**2.38**	2.61	8.60	3.10	2.77	1.39	34.00	2.50	44.80	**56.22**
53.	**IGKV R 2**	70.05	64.52	8.75	2.35	3.73	7.20	2.10	3.43	6.30	2.05	3.07	8.70	2.70	3.22	1.38	42.50	4.50	43.90	**60.60**
54.	**Karma Mahsuri**	79.21	70.50	8.35	2.60	3.26	6.05	2.00	3.03	5.85	1.95	3.00	8.15	2.55	3.20	1.39	72.50	6.50	15.15	**59.80**
55.	**IGKV R 1244**	78.38	70.60	10.20	2.60	3.92	7.65	2.30	3.33	6.55	2.20	2.98	8.85	3.35	2.64	1.35	51.00	6.50	**23.85**	**55.54**

1.Hulling % **2.** Milling % **3.**Paddy length (mm) **4.**Paddy breadth (mm) **5.**Paddy L/B ratio **6.**Brown rice length (mm) **7.**Brown rice breadth (mm) **8.**Brown rice L/B ratio **9.**Kernel length (mm) **10.**Kernel breadth (mm)

11. Kernel L/B ratio **12.**Kernel length after cooking (mm) **13.** Kernel breadth after cooking (mm) **14.** Cooked rice L/B ratio **15.**Elongation ratio **16.**Gel consistency **17.** Alkali spreading value **18.** Amylose % **19.**Head rice recovery %

APPENDIX-C: Weekly meteorological data during crop growth period of rice (*kharif* 2020)

Date	Max. Temp.(°C)	Min. Temp. (°C)	Rainfall (mm)	Rainy days	Relative Humidity (%) I	Relative humidity (%) II	Vapour Pressure (mm of Hg)I	Vapour Pressure (mm of Hg) II	Wind Velocity (Kmph)	Evaporation (mm)	Sun Shine (hours)
Jun 25-01	33.9	26	20.6	2	85	68	23.7	24.9	5.7	27.3	4.2
Jul 02-08	33.6	25.8	95	3	88	66	23.7	24.6	7.5	28.9	5.4
Jul 09-15	33.4	25	67.5	3	88	74	23.3	24	7.2	25.5	2.8
Jul 16-22	33	26.1	39.8	3	86	71	23.5	24.5	5.9	24.9	4.4
Jul 23-29	32.3	25.9	29.9	2	86	68	23.2	23.5	5.5	22.8	3.8
Jul 30-05	33.3	26	23.6	2	89	69	23.9	24.8	5.9	26.7	3.3
Aug 06-12	30.5	25.5	81.6	3	92	77	23.3	24.3	7.1	22.9	1.5
Aug 13-19	28.4	25.1	71.2	4	93	86	22.8	23.8	10.4	13.9	0.5
Aug 20-26	31	25.5	29.8	3	89	74	23	23.2	7.8	19.9	2
Aug 27-02	29.8	24.6	235.8	4	93	75	22.6	22.9	8.2	19.9	3.7
Sep 03-09	32.9	26	8	2	91	74	24.3	24.8	3	22.5	4.9
Sep 10-16	33.2	26	64	2	91	67	24.2	23.4	3.4	24.6	6
Sep 17-23	32.7	25.8	16.4	2	89	71	23.1	24.5	2.9	19.5	3.6
Sep 24-30	32.8	25.3	0	0	90	59	22.9	20.4	5.1	24.1	5.3
Oct 01-07	31.8	25	12.8	1	90	63	22.3	21.6	2.6	20.5	4
Oct 08-14	32.5	25.3	0	0	90	66	23	22.6	4.4	22.4	5
Oct 15-21	31.9	24.4	7	1	90	60	22.4	20.4	5	23.3	6.5
Oct 22-28	32.6	20.1	0	0	87	35	16.8	12.7	2.1	24.1	8
Oct 29-04	31.8	17.4	0	0	82	30	14	10.3	2.2	24.9	7.6

Vitae

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Membership of Professional Societies (If): No

Awards / Recognitions (If any): No

Publications (If any): No

Signature