

**QUANTITATIVE & QUALITATIVE CHARACTERIZATION  
AND QUALITY ASSESSMENT OF RICE  
(*Oryza sativa* L.) GENOTYPES**

**M. Sc. (Ag.) Thesis**

**by**

**Love Vyas**

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

**2021**

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AND QUALITY ASSESSMENT OF RICE  
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**Thesis**

**Submitted to the**

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

**by**

**Love Vyas**

**IN PARTIAL FULFILMENT OF THE REQUIREMENTS  
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**In**

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**(Genetics and Plant Breeding)**

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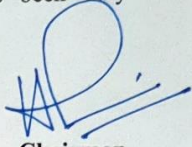
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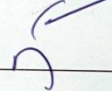

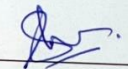
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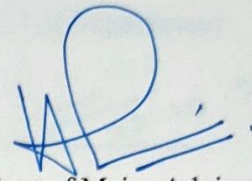
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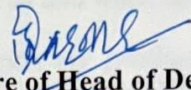
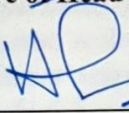


Signature of Major Advisor

Name: Dr. Arbind Sarawgi

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Date:	22/10/2021	Signature of Head of Department
Major Advisor		  22.10.2021
Faculty Dean		_____
Approved/ Not Approved		
Director of Instructions		_____

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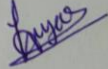
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Date 17/09/2021  
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## LIST OF SYMBOLS/ NOTATIONS

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%	Percent
° C	degree Celsius
Cm	Centimeter
d.f.	Degree of freedom
<i>et al.</i>	and others
g	Gram
<i>i.e.</i>	that is
mm	Millimeter
No.	Number
<i>viz.,</i>	Namely

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## **LIST OF ABBREVIATIONS**

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ANOVA	Analysis of Variance
CV	Coefficient of Variation
Df	Degree of freedom
Fig.	Figure

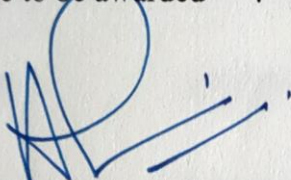
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## THESIS ABSTRACT

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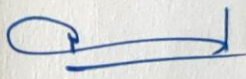
- a) Title of Thesis : Quantitative & qualitative characterization and quality assessment of rice (*Oryza sativa* L.) genotypes.
- b) Full name of the Student : Love Vyas
- c) Major Subject : Genetics & Plant Breeding
- d) Name and Address of Major Advisor : Dr. Arbind Sarawgi (Professor)  
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c) Degree to be awarded : M.Sc. (Ag.)

  
Signature of the Major Advisor

  
Signature of the Student

Date 17/09/2021

  
Signature of the Head of the Department

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### ABSTRACT

For providing fundamental information for plant breeding programme, the agro-morphological as well as quality characterization of rice act as the basic criteria. The current field experiment, titled Quantitative and qualitative characterization and quality assessment of rice (*Oryza sativa* L.) genotypes, was performed at the IGKV research farm during the *kharif* 2020-21. The material for the experiment included 52 rice germplasm accessions for quantitative as well as qualitative characterization while 21 selected accessions for quality characterization along with 6 checks *viz.*, Indira Aerobic, Samleshwari, IGKVR1244 (Maheshwari), IGKVR1

(Rajeshwari), Chhattisgarh Devbhog, IR 64. The investigation was conducted using a Randomised block design (RBD) with the goal of characterising rice germplasm accessions for Quantitative, qualitative and Quality characterization. Except for qualitative traits like the presence, shape, and colour of the ligule, the presence of leaf auricles, and leaf collar, all characters showed a lot of variation in terms of agromorphological characterization.

The analysis of variance revealed a large range of variation among genotypes for all of the traits studied. It suggested that each character had enough variation.

Analysis of genetic parameters revealed that among 10 yield and its contributing traits highest magnitude of PCV as well as GCV was noted for hundred seed weight while for Alkali spreading value among 16 quality traits. The highest heritability as well as genetic advance as a percent of mean was recorded for hundred seed weight for yield and its contributing traits while for milling percent for quality traits.

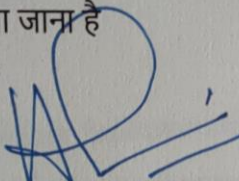

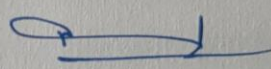
Association analysis for quantitative traits reflected that traits like hundred seed weight, biological yield and harvest index showed a positive as well as significant correlation with Grain yield plant<sup>-1</sup> while among quality traits Head Rice Recovery showed positive and significant correlation with Milling %, Gel Consistency, Amylose Content and Kernel L/B ratio.

Mahalanobis D<sup>2</sup> analysis for genetic divergence showed 52 accessions into 8 clusters for grain yield and its contributing traits and 21 accessions into 5 clusters for quality traits. Parents should be selected from cluster VII and V among grain yield and its contributing traits and from V and II among quality traits to realize much variability and high heterotic effect as they had highest inter cluster distance

Germplasm accessions which are outstanding among both yield and its contributing characters as well as among quality traits are IC0301123, ICO577803, ICO463073, IC0463875, IC0449608 and Acc 2971. Thus, selecting these accessions would be highly beneficial for increasing yield as well as quality in future rice breeding programmes.

## शोध सारांश

- क) शोध का शीर्षक : चावल (ओराइजा सटाइवा एल.) के जननद्रव्य का मात्रात्मक, गुणात्मक लक्षण वर्णन और गुणवत्ता मूल्यांकन
- ख) छात्र का पूरा नाम : लव व्यास
- ग) प्रमुख विषय : आनुवंशिकी एवं पादप प्रजनन विभाग
- घ) प्रमुख सलाहकार का नाम एवं पता : डॉ अरबिंद सरावगी (प्राध्यापक)  
आनुवंशिकी एवं पादप प्रजनन विभाग, कृषि महाविद्यालय  
ई. गा. कृ. वि., रायपुर (छ. ग.)
- ड) उपाधि से सम्मानित किया जाना है : एम. एस. सी. (कृषि),

किया जाना है	
	
प्रमुख सलाहकार का हस्ताक्षर	छात्र का हस्ताक्षर
दिनांक 17/09/2021	
	विभागाध्यक्ष का हस्ताक्षर

### सारांश

पादप प्रजनन कार्यक्रम के लिए मूलभूत जानकारी प्रदान करने हेतु चावल की फसल का कृषि-रूपात्मक और गुणवत्ता लक्षण वर्णन बुनियादी है। वर्तमान प्रक्षेत्र प्रयोग जिसका शीर्षक "चावल

(ओराइजा सटाइवा एल.) के जननद्रव्य का मात्रात्मक और गुणात्मक लक्षण वर्णन और गुणवत्ता मूल्यांकन है जो कि ई. गा. कृ. वि. के अनुसंधान फार्म में खरीफ 2020-21 के दौरान किया गया। प्रयोगात्मक सामग्री में मात्रात्मक और गुणात्मक लक्षण वर्णन के लिए चावल के 52 जननद्रव्य परिग्रहण शामिल हैं जबकि गुणवत्ता वर्णन के लिए 21 चयनित परिग्रहण सहित 6 तुलनात्मक किस्मों जैसे कि इंदिरा एरोबिक, समलेश्वरी, आई. जी. के. वि. R1244 (माहेश्वरी), आई जी के वि R1 (राजेश्वरी), छत्तीसगढ़ देवभोग, आईआर 64 का प्रयोग किया गया था। जननद्रव्य को मात्रात्मक, गुणात्मक और गुणवत्ता लक्षण वर्णन के लिए चिह्नित करने के उद्देश्य से रैंडमाइज्ड ब्लॉक डिजाइन (आर.बी.डी) का उपयोग किया गया। गुणात्मक लक्षणों लिगयूल का रंग, उपस्थिति और आकार, लीफ ऑरिकल्स की उपस्थिति और लीफ कॉलर की उपस्थिति को छोड़कर, सभी लक्षणों ने कृषि रूपात्मक लक्षण वर्णन के संदर्भ में काफी विविधता दिखाई।

विचरण के विश्लेषण से अध्ययन के तहत सभी पात्रों के लिए, जीनोटाइप के बीच व्यापक भिन्नता का पता चला, इसने प्रत्येक लक्षणों के लिए पर्याप्त परिवर्तनशीलता का संकेत दिया।

आनुवंशिक मापदंडों के विश्लेषण से पता चला है कि 10 उपज और उसके योगदान लक्षणों में से 100 बीज वजन और 16 गुणवत्ता लक्षणों के बीच क्षार प्रसार के लिए मूल्य के लिए उच्चतम पीसीवी और जीसीवी के परिमाण को देखा गया था। उपज और उसके योगदान लक्षणों में से 100 बीज वजन और 16 गुणवत्ता लक्षणों के बीच मिलिंग % के लिए उच्चतम औसत के प्रतिशत के रूप में आनुवंशिक प्रगति के साथ आनुवंशिकता दर्ज की गई थी।

मात्रात्मक लक्षणों के लिए एसोसिएशन विश्लेषण दर्शाता है कि लक्षण जैसे 100 बीज वजन, जैविक उपज और फसल सूचकांक ने प्रति पौधे अनाज की उपज के साथ सकारात्मक और महत्वपूर्ण सहसंबंध दिखाया जबकि गुणवत्ता लक्षणों के बीच प्रमुख साबुत चावल प्रतिशत ने मिलिंग%, जेल कन्सिस्टेन्सी, एमाइलोज मात्रा और कर्नेल एल/बी अनुपात के साथ सकारात्मक और महत्वपूर्ण सहसंबंध दिखाया।

महलोनोबिस डी <sup>2</sup> आनुवंशिक विचलन के लिए विश्लेषण ने अनाज की उपज और इसके योगदान लक्षणों के लिए 52 परिग्रहणों को 8 समूहों में और गुणवत्ता लक्षणों के लिए 21 परिग्रहणों को 5 समूहों में शामिल किया गया। बहुत अधिक परिवर्तनशीलता और उच्च विषमता प्रभाव का एहसास करने के लिए अनाज की उपज और इसके योगदान करने वाले लक्षण के लिए पैरेंट को सबसे अधिक इंटर क्लस्टर दूरी होने के कारण क्लस्टर VII और V से तथा गुणवत्ता के लक्षणों के लिए पैरेंट को क्लस्टर V और II से चयनित किया जाना चाहिए।

जर्मप्लाज्म अभिगम जो उपज और इसके योगदान करने वाले चरित्रों के साथ-साथ गुणवत्ता लक्षणों के बीच उत्कृष्ट हैं, वे हैं IC0301123, IC0577803, IC0463073, IC0463875, IC0449608 और Acc 2971। इस प्रकार, इन परिग्रहणों का चयन भविष्य में चावल प्रजनन कार्यक्रम में उपज और गुणवत्ता बढ़ाने के लिए अत्यधिक फायदेमंद होगा।

## CHAPTER I

### INTRODUCTION

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Rice is regarded as the world's most important staple crop. Rice is projected to be the main source of food for half of the world's population, and Asia is regarded the rice motherland. *Oryza* is a genus of rice with two cultivated species and around 20 wild species. *Oryza sativa* ( $2n = 24 AA$ ) is cultivated worldwide, while *Oryza glaberrima* ( $2n = 24 AA$ ) is sown on a small scale in West Africa. AA, BB, CC, BBCC, CCDD, EE, FF, GG, and HHJJ genomes are represented in wild species ( $2n=24$  or  $48$ ). (Vaughan, 1989).

The *sativa* rice species are divided into three sub-species: Indica, Japonica, and Javanica. Rice was first farmed in tropical Asia, with the earliest evidence reaching back to 5000 BC, although it later spread to temperate areas (Watanabe, 1997; Choi and Jung, 2018).

In many parts of the world, it is one of the most significant components of the human diet. Furthermore, it is a nutrient-dense cereal crop, delivering 20% of the calories and 15% of the proteins consumed by the global population. Although it is Asia's primary source of carbohydrates and protein, it also contains minerals and fibre.

The world's population, which is currently approximately 6 billion people, is expected to reach 8 billion by 2030, necessitating a 40% increase in rice yield to fulfil the rising demand (Khush and Brar, 2002; Bhavsar *et al.*, 2017). Rice is a crucial component of food security, as well as the staple food for the majority of people living in rural and urban areas of tropical and subtropical Asian countries (Cottyn, 2002; Cottyn *et al.*, 2009).

The rice crop possesses the world's largest germplasm collection. Rice has evolved into an enormously broad basis for genetic variation as a result of the dispersal process during domestication, as seen by the number of land races that exist today (Shivapriya and Hittalmani, 2006). In addition to their importance as a genetic resource for rice genetic improvement, this accessible collection of diverse cultivated varieties, landraces, and related wild species has made significant contributions to rice breeding and has played an important role in local food security

and agricultural sustainability.

Rice is grown in a variety of agro-climatic zones in India, where a vast number of local cultivars and landraces with unique traits and high adaptability are grown. Due to its lower productivity, India has the world's largest rice-growing land but ranks second in production (producing about 285 million tonnes of food grains per year, with rice accounting for roughly 115 million tonnes). In recent years, a large number of high-yielding cultivars have been produced and notified, with many of them currently in the seed production chain.

In terms of paddy cultivation, Chhattisgarh is a major player. The state contributes 5.26 percent of India's total rice production. The rice germplasm section of IGKV houses a collection of more than 23,250 genotypes, making it India's largest and the world's second largest after IRRI in the Philippines. With more than 80% of the kharif cultivable area under paddy, Chhattisgarh is a paddy-dominated mono-cropped state.

Green revolution has had a significant impact on improving food grain output in our country, and its contribution in achieving food grain self-sufficiency is undeniable. High yielding varieties, however, which are the backbone of the green revolution, have indirectly accelerated the extinction of rice landraces and wild types. Currently, high yielding rice types account for more than 90% of all rice cultivation. The condition is rapidly weakening indigenous rice cultivars. Another significant aspect is the region's shifting climate. The maturation and reproductive cycle of plants are negatively affected by climatic conditions.

According to Oteng and Sant'Anna (1999), the rice crop has seen constant increases in demand over the last three decades, and its growing relevance is seen in many countries' strategic food security planning plans. Rice production self-sufficiency, on the other hand, is dwindling as demand rises. Rice varieties must be produced from existing germplasm collected and conserved by national, regional, and international genetic resource centres.

One of the primary criteria for the success of any breeding programme and the attainment of the basic goals for plant development, such as improving yield potential, adaptability, quality, and resistance to biotic and abiotic stress, is the

presence of genetic diversity in the breeding material.

One of the most important requirements for the conservation and long-term use of rice genetic resources is the characterization and evaluation of existing rice germplasm. Rice germplasm that has been characterised boosts its utility in breeding programmes. This guarantees that the greatest amount of variability is recorded when developing breeding techniques to boost output. Information on diversity and population structure is expected to assist plant breeders in selection of parents to be used in hybridization programmes, provide a more rational basis for expanding the gene pool and for identifying plant materials that harbour more valuable alleles for genetic improvement (Semon *et al.*, 2005). As a result, rice diversity provides the cornerstone for variety improvement programmes, and a greater understanding of it can aid in the resolution of biotic and abiotic production difficulties as well as the development of cultivars that are resistant to these constraints. Almost all important crop species have morphological and physiological descriptors that can be used to determine a variety's uniqueness (Moukoumbi, *et al.*, 2011). As a result, rice cultivar characterisation and identification are critical for varietal improvement, release, and seed production programmes.

With the introduction of high yielding varieties and new technology, the age-old practise of growing traditional varieties and landraces, which may have enormous potential for various critical characters, is under threat. Because the existing UPOV models of plant variety protection did not meet Indian needs, the Indian government enacted the “Protection of Plant Varieties and Farmers Act” (PPV&FRA) in 2001 to provide protection to plant varieties based on distinctiveness, uniformity, and stability (DUS) tests in addition to novelty. This is a one-of-a-kind and model act that provides equal protection to all plant varieties. Identification of a variety, confirmation of the variety, distinctness of the variety from all others in common knowledge, purity of the variety, and characterization of the variety, which enumerates its entire descriptors are all steps in the variety identification process. The concepts of distinctness, regularity, and stability are thus crucial in describing a variation as a one-of-a-kind creation.

Information on character associations, as well as the direct and indirect effects that each character has on yield, will be useful in the selection process. Correlation

and path analysis reveal the magnitude of the relationship between grain yield and its components, as well as the relative importance of their direct and indirect effects, providing a clear picture of their relationship with grain yield. Finally, this type of study could aid the breeder in developing grain yield-improving selection strategies. Finally, this type of study could aid the breeder in developing grain yield-improving selection strategies. In light of the foregoing scenario, the current study is being conducted with the goal of determining the character connections in rice hybrids for yield improvement.

Therefore present field experiment entitled **Quantitative & qualitative characterization and Quality assessment of Rice (*Oryza sativa* L.) genotypes** has been carried out during *kharif* 2020-21 at research farm of IGKV, Raipur with following objectives:-

- Characterisation of germplasm accession as per DUS guidelines
- To study the physical and quality parameter of selected rice accession.
- To carry out path analysis and estimation of correlation of yield & yield contributing traits.
- Analysis of genetic divergence.

## CHAPTER II

### REVIEW OF LITERATURE

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The available literature on rice of present experiment has been reviewed below the following heads:

2.1 Agro-morphological characterisation

2.2 Quality parameter

2.3 Path coefficient Analysis

2.4 Correlation Analysis

2.5 Genetic Divergence Analysis

#### **2.1 Agro-morphological characterisation**

The morphological characterization of plant is the fundamental standard in order to produce basic knowledge of rice crop. The literary texts available on those aspects are reviewed in the following paragraphs:

Rosta (1975) used leaf blade length and width, leaf colour, colour of ligule and auricle colour for grouping rice varieties. Chauhan and Nanda (1984) observed kernel colour as well as milled grains appearance to be major identifying characters of varieties of rice. Vanangamudi *et al.* (1988) classified 85 rice varieties based on the grain length, shape & hundred grain weight.

Ahmad and Das (1994) studied 85 indigenous glutinous varieties of rice and characterised them on the basis of pigment distribution in 11 plant parts.

Bisne and Sarawgi (2008) carried out to characterization of 32 aromatic rice accessions of badshah bhog. Evaluation of germplasm accessions was done for 22 morphological, 6 agronomical and 8 quality traits. The specific genotypes which were identified for quality and agronomical characteristics are B: 1340, B: 2039, B: 2495, B: 2816, B: 16930 B: 2354, B: 163, B: 2094. These may be used in

hybridization programme to achieve desired segregants for good grain quality with higher yield.

Mathure *et al.* (2011) characterised 69 genotypes for agronomic traits. He found 36 exquisite genotypes out of them that possessed 1 or more superior traits like dwarf stature, early flowering, higher number of productive tillers/plant, long panicles, higher number of filled grains/panicle and strong aroma.

Nascimento *et al.* (2011) carried out qualitative and quantitative characterization of 146 accessions of upland rice (*Oryza sativa* L.), and observed polymorphism among 12 of 14 qualitative characters evaluated.

Sinha *et al.* (2013) conducted agro-morphological characterization over 20 landraces of rice cultivars for 20 qualitative & 13 quantitative morphological characters and observed that except coleoptiles colour, presence of leaf collar, shape of ligule and presence of secondary branching in panicle, majority of characters were polymorphic.

Subba Rao *et al.* (2013) characterised 65 rice landraces by using 43 agro-morphological traits with the help of DUS test. 65 varieties were studied, out of which based on 22 essential & 24 additional traits, 32 were found to be distinctive.

Sajid *et al.* (2015) studied the indigenous rice germplasm and characterised them on the basis of morphological characteristics. On 32 different agro-morphological traits (15 qualitative and 17 quantitative) the data were recorded. There was sufficient amount of genetic variation among rice germplasm for most of the qualitative and quantitative characters except the traits anther color and ligule shape.

Umarani *et al.* (2017) based on 14 DUS characters characterised 70 landraces of rice. Out of 14 traits, stem anthocyanin colouration of node was found to be dimorphic while 3 traits viz., spikelet colour of stigma, stem length and panicle exertion were trimorphic. Characters like basal leaf sheath colour, time of heading, flag leaf attitude (late observation), panicle length, decorticated grain length and shape were came out as tetramorphic and five states of expression were observed for

lemma anthocyanin colouration of apex and amylose content showed while on six groups were made on the basis of decorticated grain colour.

Manjunatha *et al.* (2018) characterized Sixty landraces of rice (*Oryza sativa* L.), for both qualitative and quantitative characters and found out that out of 24 descriptors studied, five characteristics were found monomorphic, thirteen were dimorphic, four were of trimorphic, one character (Basal leaf sheath colour) is tetramorphic and stem length (excluding panicle) showed five states of expression.

Ramalingam *et al.* (2019) evaluated and characterised thirty seven landraces for 30 morphological traits. Out of 30 descriptors studied, three characters were found monomorphic, while rest of the characters showed variations among the accessions.

## **2.2 Quality parameter**

Different scientists have reported their investigations on quality parameters in rice, some of which are given as below:

Mohammad *et al.* (2002) found out that characters like L/B ratio, effective tillers and 1000 grain weight can be involved in a selection programme based on the values of heritability as well as genetic advance.

Sarkar *et al.* (2007) evaluated 41 rice genotypes for 10 different quality parameters of grains to assess the genetic variability. It was found that the phenotypic as well as genotypic coefficient of variations was maximum for cooked kernel L/B ratio and 1000 grain wt.

Parikh *et al.* (2012) evaluated 36 genotypes of rice and from these Rajim-12 and Rajabhog were found superior genotype for kernel length, grain yield, L:B ratio, and kernel length after cooking and Bikoni were found superior for elongation ratio, and head rice recovery.

Allam *et al.* (2015) led an examination for quality attributes in 23 genotypes of basmati rice and found out that kernel length, kernel L/B ratio, KLAC, elongation

ratio are important traits which should be used as selection criteria to develop high yielding and better quality varieties in basmati rice.

Kumar *et al.* (2016) evaluated 64 germplasm of aromatic rice over 35 agro morphological & quality characters. The results reflected that high amount of variation was exhibited by grain: length and decorticated grain: length while showed small amount of variation was exhibited by grain: width and de-corticated grain: width among the genotypes.

Ritika *et al.* (2016) carried out a study over Indian basmati rice varieties and non-basmati cultivars of rice for physicochemical, pasting, cooking and textural properties and observed that the grains L/B ratio of basmati varieties was significantly greater than that of non-basmati cultivars.

Shivani *et al.* (2007) studied several rice accessions and concluded that traits like Hulling % is significantly associated with milling % and head rice recovery as well thus selection for hulling % could increase milling % and head rice recovery.

Oko *et al.* (2012) observed significant correlation (positive or negative) with some of the cooking quality traits (elongation during cooking and optimum cooking time) during their study carried out on 20 rice cultivars.

Shejul *et al.* (2013) obtained high heritability coupled with high to moderate genetic advance for the trait gel consistency in their study over 22 genotypes of rice along with two checks which indicated scope for selection of this trait.

Nirmaladevi *et al.* (2015) studied 92 genotypes of rice and obtained high estimates of GCV and PCV for gel consistency and alkali spreading value.

Tamu *et al.* (2017) studied 87 rice varieties and found out that varieties differed significantly for Grain length; Gel consistency, elongation ratio, alkaline spread value, gelatinization temperature and aroma.

Charupa *et al.* (2021) used large broken rice (LBR) and small broken rice (SBR) of 4 commercially important varieties and analysed them for properties like alkali spreading value, gel consistency and amylose content.

## 2.4 Correlation Analysis

Correlation is used to relate the linear association among two or more variables. In general, correlation likely to be used when there is no identified response variable. It is used to determine the strength and direction of a linear relationship between two or more variables.

Ramalingam *et al.* (1993) carried out correlation analysis and observed positive association of panicle traits viz; total filled grains, primary length & secondary length with yield.

Rajamani *et al.* (2004) found out positive association of panicle length, total number of spikelets/panicle, plant height, days to 50 percent flowering, hundred grain weight with grain yield/plant as well as among themselves.

*Marchezan et al.* (2005) studied 88 rice genotypes for the variables viz. plant height, seed yield, spikelet sterility, number of seeds per panicle, thousand seed weight and head grains for evaluating the relationship among components of yield. Correlation studies revealed that seed yield in rice plants was most affected by grain weight.

Gnanasekaran *et al.* (2008) reported positive correlation between grain yield and L/B ratio.

Ratna *et al.* (2015) carried out correlation analysis in 6 basmati lines as well as 1 commercial check for 14 morphological traits. The analysis revealed that yield had a significant positive correlation with number of filled spikelets/panicle while a significant negative correlation with plant height.

Chandrashekhar Haradari & Shailaja Hittalmani, (2017) studied some rice genotypes and conducted correlation analysis among 12 yield component characters which revealed that selection of the characters viz., productive tillers/plant, filled spikelets/panicle, spikelet fertility and harvest index could be very effective in selecting high yielding rice genotypes as they exerted high direct effects and exhibited significant positive correlation with grain yield/plant.

Tewachew (2018) studied and conducted correlation studies over 23 rice genotypes and observed that days to maturity and kernel length exhibits highly significant positive genotypic correlation with grain yield. He concluded that the strong positive correlation between grain yield and other traits helps in identifying traits that could be used for indirect selection for the improvement of grain yield.

Mervat *et al.* (2019) conducted correlation analysis which revealed high significant and positive correlations between grain yield and each of number of panicles per plant, panicle length, number of filled grains per panicle and thousand-grain weight.

Rathan *et al.* (2019) studied 17 quantitative traits among 24 genotypes of rice and carried out correlation analysis. The results indicated the usefulness of the characters viz., days to maturity, plant height, effective tillers per plant and spikelet fertility percent in selection for increasing the grain yield as they had positive direct effect as well as significant positive correlation with grain yield per plant.

Hasan-Ud-Daula and Sarker Umakanta (2020) studied 7 advanced rice breeding lines. They found out significant and desirable correlations for number of filled grains per panicle, number of secondary branches per panicle, spikelet sterility (%) and days to flowering both at the level of genotype as well as phenotype.

Singh *et al.* (2020) conducted an experiment over 112 rice genotypes for 16 different yield and yield-contributing traits. The correlation analysis revealed very strong correlation of grain yield/plot with biomass yield/plot.

## **2.4 Path coefficient**

The Path analysis is more systematized dividing the correlation coefficients into the measures of direct and indirect effect of set of independent variables on dependent variables. Many workers have reported their results on path coefficient analysis in rice, some of which are presented as below:

Jun (1985) observed that traits viz; grain weight and L/B ratio showed direct effect on grain length.

Reuben and Katuli (1988) reported that tillers per plant and thousand grain weight showed direct positive effect while panicle length showed negative direct effect on grain yield.

Sarawagi *et al.* (1997) carried out path coefficient analysis in rice accessions. Analysis reflected that for increasing grain yield direct selection would be beneficial for the traits number of fertile spikelets panicle<sup>-1</sup> as well as harvest index.

Satish *et al.* (2003) reported significant positive correlation of number of productive tillers per hill and number of grains per panicle with yield from the correlation study over 13 quantitative and physiological traits.

Chakraborty *et al.* (2010) carried out path analysis in 29 genotypes of boro rice. From the results, he concluded that 5 component characters, namely Harvest index, effective grains/plant, panicle length, panicles per plant and plant height influenced the yield of boro rice.

Gohari *et al.* (2010) carried out path analysis among 11 rice cultivars which revealed that there is a significant and positive relationship between grain yield and Harvest Index., biological yield, number of panicles/m<sup>2</sup>, and number of panicles/plant.

Zaved *et al.* (2010) carried out path coefficient studies over 30 genotypes of rice which revealed that the selection of biological yield components, number of productive tillers per plant and flag leaf area would be beneficial in order to bring improvement in grain yield.

Fiyaz *et al.* (2011) conducted path analysis studies over rice genotypes which revealed that Harvest Index had high direct effects on grain yield. Thus these traits which contribute to the grain yield could be exploited for further breeding programme.

Babu *et al.* (2012) reported that panicle length and number of productive tillers/plant exhibited positive direct effect on yield through the path coefficient studies carried out over 21 popular rice hybrids. Among these characters, selection

for number of productive tillers/plant could bring improvement in yield as well as yield components as it exerted both positive association and high direct effects.

Solomon *et al.* (2016) evaluated 10 rice genotypes. Path analysis revealed that the harvest index exhibited highest and positive direct effect on grain. Hence, those traits have to be taken in to consideration in rice breeding program for further improvement of rice production and productivity.

Francis *et al.* (2018) carried out path analysis over 32 rice varieties for direct as well as indirect effects on yield which showed significant high direct effects for number of panicles /plant, number of grains/ panicle, 1000 grain weight, days to 50 % flowering and time to maturity.

Muthuswamy and Arulmozhi (2019) studied 74 rice genotypes and carried out path coefficient studies for yield and quality traits. They found out that grains/panicle, productive tillers/plant and amylose content had significant and positive direct effects on yield at genotypic level, thus, selection for these characters helps in selection of superior cross combinations for improvement of yield.

## **2.5 Genetic Divergence Analysis**

Genetic divergence studies were carried out by Pradhan and Roy (1990) which showed highest contribution of thousand grain weight to total divergence and by Vivekanandan and Subramanian (1993) which revealed grain yield contributed maximum towards divergence.

Rather *et al.* (2001) carried out D<sup>2</sup> analysis and grouped 56 genotypes of rice into eight clusters and observed that 100 grain weight and L/B ratio of grain to be main contributors of diversity.

Sanker *et al.* (2005) divided 34 genotypes into seven clusters and found out that days to 50% flowering, grains per panicle and single plant yield contributed maximum towards genetic divergence.

Thayumanavan *et al.* (2009) evaluated 26 genotypes for genetic diversity. The genotypes were grouped into 13 clusters. From the analysis, he found out that days

to first flower, number of grains per panicle, kernel length, kernel breadth, 1000 grain weight and grain yield per plant were likely to produce heterotic combinations and high variability in segregating generations.

Banumathy *et al.* (2010) studied 53 rice genotypes to assess the diversity pattern for 8 yield and yield attributing characters using D<sup>2</sup> analysis. He found out grain yield, days to 50% flowering, total grains per panicle and plant height together contribute 86.62% towards total divergence. Therefore, these characters may be given importance during hybridization programme.

Palaniraja and Anbuselvam (2010) studied 51 rice genotypes for different yield and yield component traits and analysed them for genetic divergence. All the 51 genotypes were grouped under 15 different clusters based on genetic distance. He concluded that, maximum contribution towards genetic diversity was due to the characters like plant height, panicle length and grain yield per plant.

Chakma *et al.* (2012) studied 39 rice genotypes to assess genetic diversity. The genotypes were grouped into 6 clusters based on mahalanobis's D<sup>2</sup>. Number of unfilled grains/panicle, 1000 grain weight and grain yield showed maximum contribution towards genetic divergence. The genotypes from these clusters with desirable characters may be used as potential donor for future hybridization program to develop high yielders.

Nikhil and Rangare (2012) studied 40 rice genotypes for genetic divergence using Mahalanobis D<sup>2</sup> statistic which grouped these genotypes into seven clusters based on 13 agro-morphological characters and concluded that Biological yield per hill, days to maturity and spikelets per panicle highly contributed to the formation of clusters.

Vennila *et al.* (2012) conducted an experiment with 41 rice genotypes which were evaluated for 9 yield and yield attributing characters using Mahalanobis D<sup>2</sup> statistics which revealed that characters like number of grains per panicle, plant height, grain length and grain breadth contributed maximum towards genetic

diversity. Hence these characters could be given due importance for selection of genotypes in crop improvement programme.

Majumder *et al.* (2015) studied 30 aromatic rice genotypes, based on 23 characters the genotypes were grouped into 5 clusters. From the analysis he found out that Panicle length, days to initial flower opening, spikelet sterility, pollen fertility and harvest index had maximum contribution towards genetic divergence.

Islam *et al.* (2018) studied 36 aromatic rice landraces for the agromorphological traits to assess the genetic variation. He found out that, maximum contribution towards genetic divergence was due to yield, grain breadth, days to maturity, culm diameter and ligule length.

Pragnya *et al.* (2018) evaluated 75 genotypes of rice to study the genetic diversity present in the experimental material for selection of the diverse parents. From the investigation he concluded that the characters per cent filled grains per panicle, plant height, seed yield per plant contributed maximum to the genetic divergence.

Singh *et al.* (2020) studied 22 rice genotypes which were characterized based on 16 quantitative traits and analysed them for genetic divergence using mahalanobis  $D^2$  statistic which distributed the 22 genotypes into six clusters the maximum inter-cluster distance was observed between the clusters III and V indicating the importance of the genotypes present in these clusters for exploiting heterosis for the desirable traits of these cluster.

**Material and methods**

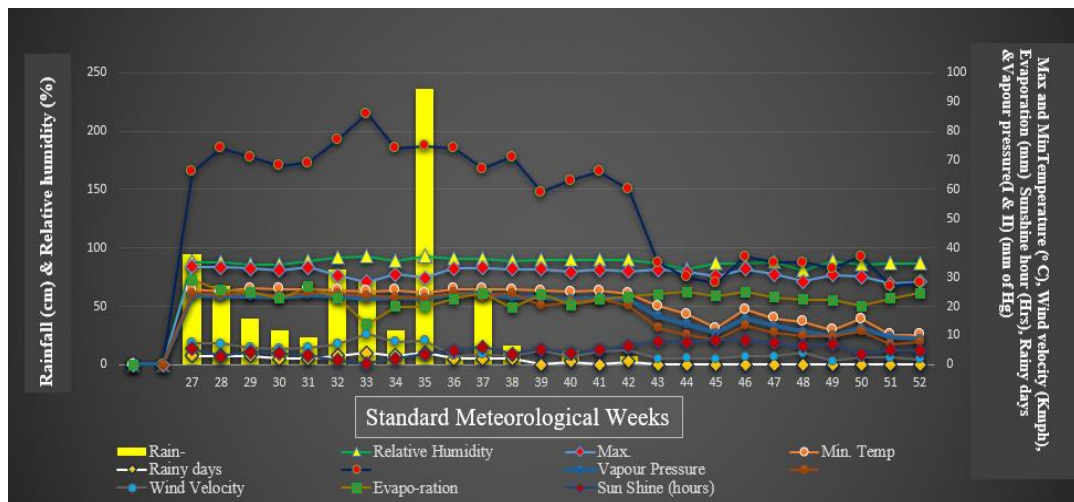
The current study took place during *kharif* 2020. The methodology and procedures employed throughout the investigation, as well as the materials used, are described below.

**3.1 Experimental site**

The investigation was performed at Research cum instructional farm, Dept. of Genetics & Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India.

**3.2 Climate and weather**

Chhattisgarh is located between the latitudes of 17° 14' N and 24° 45' N, and the longitudes of 79° 16' E and 84° 15' E. Raipur, the state capital of Chhattisgarh, is located at 21° 16' N latitude and 81° 36' E longitude, at an elevation of 289.70 metres above sea level. At the time of crop growth, the total rainfall received was 1124mm. Data on weekly rainfall, minimum and maximum temperatures, bright sunlight hours, evaporation & relative humidity for the full crop growing season are displayed in Fig. 3.1



**Fig 3.1 Graph representing meteorological data during crop season**

The meteorological data showed a favourable season for growth of crop, however the crop was harmed by the uneven distribution of rains.

### 3.3 EXPERIMENTAL MATERIALS

The experimental material included 52 rice accessions along with six check varieties. viz., Indira aerobic, Samleshwari, IGKVR1244 (Maheshwari), IGKVR1 (Rajeshwari), Chhattisgarh Devbhog, and IR 64. Table 3.1 lists rice accessions along with their accession numbers.

**Table 3.1 Germplasm accessions used as experiment material during Kharif 2020.**

S.no	Accessions	S.no	Accessions	S.no	Accessions	S.no	Accessions
1	IC0577803	16	IC0256817	31	IC0565360	46	Acc 3367
2	IC0578975	17	IC0377173	32	IC0375799	47	Indira Aerobic
3	IC0578996	18	IC0377238	33	IC0463875	48	Samleshwari
4	IC0578999	19	IC0326451	34	IC0577148	49	IGKVR1244 (Maheshwari)
5	IC0577396	20	IC0384190	35	IC0449608	50	IGKVR1 (Rajeshwari)
6	IC0459649	21	EC0491242	36	IC0449908	51	Chhattisgarh Devbhog
7	IC0463073	22	EC0491282	37	Acc 2955	52	IR 64
8	IC0463190	23	EC0491353	38	Acc 2971		
9	IC0299989	24	EC0491389	39	Acc 2980		
10	IC0300191	25	EC0497077	40	Acc 2986		
11	EC0497166	26	EC0497100	41	Acc 2991		
12	IC0300822	27	IC0382568	42	Acc 2992		
13	IC0301119	28	IC0565343	43	Acc 3236		
14	IC0301123	29	IC0565344	44	Acc 3251		
15	IC0301206	30	IC0565346	45	Acc 3349		

### 3.4 EXPERIMENTAL METHODS

During the *kharif* of 2020, genotypes of rice were evaluated at the Research cum Instructional farm, Department of Genetics & Plant Breeding, College of Agriculture, IGKV, Raipur. Irrigated transplanted conditions were used for the field trials. Raised bed nursery was employed for sowing the plant material on June 17, 2020. In a Randomised block design (RBD), the experimental material was planted in to 2 replications. Transplanting was carried out on July 28, 2020 in 2 rows per plot with a 20 cm row to row spacing while spacing between plants was 15cm. Fertilizer was applied at a rate of 80N: 50P: 30K kg/ha. Half of the nitrogen dose, as well as the full doses of phosphate and potassium, were applied prior to transplanting. The remaining nitrogen was administered in 2 stages, the 1<sup>st</sup>, at the start of tillering and the 2<sup>nd</sup> at the time of panicle initiation.



**Fig 3.2 Field Preparation**



**Fig 3.3 Vegetative Stage**

### **3.5 Observation Recorded**

The observation on various agro- morphological & quantitative traits were noted as per stage and categories given in table 3.2 (DRR DUS Descriptor).

#### **3.5.1 Morphological traits**

##### **3.5.1.1 Coleoptile colour**

The Coleoptile colour was documented at 1<sup>st</sup> leaf stage by observing individual plants visually. The genotypes were grouped into classes namely colourless, light purple, purple according to coleoptile colour.

##### **3.5.1.2 Basal leaf: sheath colour**

The colour of the leaf sheath was observed at the time of late vegetative stage.

### **3.5.1.3 Leaf intensity of green colour**

By examining a set of plants during the booting stage, the intensity of green colour of leaves was assessed visually and classified into 3 major categories namely light, medium, and dark green colour.

### **3.5.1.4 Leaf: anthocyanin colouration**

At the time of early booting stage, absence or presence of leaf anthocyanin colouration was recorded through assessing of a group of plants visually.

### **3.5.1.5 Leaf: distribution of anthocyanin colouration**

The presence or absence of anthocyanin colouration of leaf sheath was observed at the booting stage.

### **3.5.1.6 Leaf sheath: Anthocyanin colouration**

Absence or presence of anthocyanin colouration of leaf sheath was observed at time of booting stage.

### **3.5.1.7 Leaf sheath: intensity of anthocyanin colouration**

At booting stage, intensity of leaf sheath's anthocyanin colouration was recorded visually for a group of plant. Based on anthocyanin colouration, classification was done under the classes namely very weak, weak, medium & strong,

### **3.5.1.8 Leaf: Pubescence of blade surface**

At the time of booting, pubescence of leaf blade was observed by visually inspecting individual plants. It has the following categories: absent, weak, medium, strong, and very strong.

### **3.5.1.9 Leaf: auricles**

Auricles are pair of small appendages on either side of the base of the blade present in most of the leaves. Their presence or absence was noted during booting stage.

### **3.5.1.10 Leaf: anthocyanin colouration of auricles**

At the booting stage, the anthocyanin coloration of auricles, i.e. colourless, light purple, and purple colour in auricles, was documented by assessing the individual plants visually.

### **3.5.1.11 Leaf: collar**

Leaf collar is the juncture between leaves blade & leaf sheath and its presence or absence was observed at booting stage by visually assessing the individual plant.

#### **3.5.1.12 Leaf: anthocyanin colouration of collar**

The presence or absence of anthocyanin colouration at collar was documented at booting stage through evaluating the individual plants visually.

#### **3.5.1.13 Leaf ligule**

Ligule is a thin outgrowth at the junction of leaf sheath and blade, and its presence or absence was recorded at the time of booting stage.

#### **3.5.1.14 Leaf: shape of ligule**

Shape of ligule was assessed at booting stage under the classes: truncate, acute and split ligule.

#### **3.5.1.15 Leaf: colour of ligule**

Individual plants or portions of plants were visually assessed for ligule colour under the categories of green, light purple, or purple at the booting stage.

#### **3.5.1.16 Leaf: length of blade (cm)**

Measurement of length of leaf blade (in centimetres) was carried out at the time of booting and categorised under short, medium and long leaves.

#### **3.5.1.17 Leaf: width of blade (cm)**

Measurement of width of leaf blade (in centimetres) was carried out at the time of booting and classified under narrow, medium and broad leaves.

#### **3.5.1.18 Culm: attitude**

At the time of booting stage culm attitude was recorded by visual evaluation and grouped into erect, semi erect, open or spreading type of culm attitude by observing plants individually.

#### **3.5.1.19 Time of heading/ flowering**

During the vegetative growth stage, duration of emergence of primary panicle in 50 percent of plants was noted in days based on which plants were divided into the classes namely very early, early, medium, late and very late.

#### **3.5.1.20 Spikelet density of pubescence of lemma**

The density of lemma's pubescence was observed during the starting of anthesis to dough stage by evaluation of the plants individually and then they were grouped into the classes namely absent, weak, medium, strong and very strong density of pubescence.

#### **3.5.1.21 Spikelet: colour of stigma**

The genotypes were documented for their stigma colour into white, light green, yellow, light purple, purple by visual evaluation.

#### **3.5.1.22 Stem: thickness**

Thickness of stem was measured in centimetre and recorded at milk development stage, based on stem thickness plants were grouped into the classes thin, medium and thick stem.

#### **3.5.1.23 Stem: anthocyanin colouration of node**

During milking stage, the presence or absence of anthocyanin colouration of node was documented.

#### **3.5.1.24 Stem: intensity of anthocyanin colouration of node**

By assessing the plants visually, intensity of anthocyanin colouration of node was observed at the time of milking stage & plants were classified under the categories weak, medium and strong intensity of anthocyanin colouration of node.

#### **3.5.1.25 Stem: anthocyanin colouration of internodes**

During milk development stage, the presence or absence of anthocyanin colouration of internode was observed.

#### **3.5.1.26 Flag leaf: attitude of blade**

At the time of ripening stage, flag leaf's attitude was documented by observing visually and categorised into erect, semi erect, horizontal and deflexed categories in accordance with the qualities of majority of plants of the accessions.

#### **3.5.1.27 Panicle curvature of main axis**

The accessions were documented into straight, semi-straight, deflexed, dropping by observing the panicle of plant visually at ripening stage.

#### **3.5.1.28 Panicle: awns**

Individual accessions of a group of plants were visually analysed at the ripening stage and were classified based on the absence or presence of awns.

#### **3.5.1.29 Panicle: colour of awns**

The individual plants were evaluated visually for colour of awns at ripening stage and were grouped into categories yellowish white, yellowish brown, brown, reddish brown, light red, red, light purple, purple and black based on the colour of awn.

#### **3.5.1.30 Panicle: length of longest awn**

At the time of ripening, the length of the longest awn of plants was measured in cm and based on those plants were subjected to categorization into classes namely very short, short, medium and long awn length.

#### **3.5.1.31 Panicle: distribution of awns**

By the observation of individual plants visually for the distribution of awns, the plants were grouped into classes viz. presence of awns at tip only, upper half only & whole length.

#### **3.5.1.32 Panicle: presence of secondary branching**

During ripening stage, group of plants were observed visually and were recorded for the presence or absence of secondary branching.

#### **3.5.1.33 Panicle: secondary branching**

The panicles with secondary branching were visually inspected and divided into three classes: weak, strong, and clustered secondary branching.

#### **3.5.1.34 Panicle: attitude of branches**

During the ripening stage, the attitude of panicle's branches was observed and the plants were classified into the groups namely weak, strong and clustered.

#### **3.5.1.35 Panicle: exertion**

A group of plants was visually observed at the ripening stage and plants were subjected to categorization under the classes partly exerted, mostly exerted and well exerted.

#### **3.5.1.36 Time of maturity**

The duration of time between sowing and maturity was measured, and genotypes were divided into very early, early, medium, late, and very late durations based on the findings.

#### **3.5.1.37 Leaf: Senescence**

The leaf senescence was evaluated visually over a group of plants at the stage when caryopsis became hard and plants were categorised as early, medium and late senescence.

#### **3.5.1.38 Panicle: Length of main axis**

At the time of milk development stage to ripening, the length of the panicle of three randomly chosen plants was measured and recorded data was averaged.

### **3.5.1.39 Grain: Weight of 100 fully developed grains (g)**

100 fully developed, whole grains (dried up to 13 percent moisture content) from every selected plant were picked in a random manner and weighed and data was recorded in grams.

### **3.5.1.40 Grain yield per plant (g)**

The grain (filled) yield of the 3 selected plants after drying under the sun for 5 to 8 days after harvesting was recorded and then averaged.

### **3.5.1.41 Harvest index (%)**

After harvesting, harvest index which is ratio of grain yield and the biological yield was calculated and its values were presented in terms of percentage.

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

## **3.4.2 Quality traits**

Following physico-chemical quality traits were observed and recorded.

### **3.4.2.1 Paddy length (mm)**

Without removing hull, 10 grains were picked in random manner and an average length was noted in millimetres.

### **3.4.2.2 Paddy width (mm)**

10 grains were picked in random manner without removing hull and an average width was noted in millimetres.

### **3.4.2.3 Paddy L/B ratio:**

This was calculated as-

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

### **3.4.2.4 Brown Rice length (mm)**

10 grains were picked after hulling at random and the standard length was measured in mm.

### **3.4.2.5 Brown rice width (mm)**

10 grains were chosen after hulling at random and the standard length was measured in mm.

### **3.4.2.6 Brown rice L/B ratio**

This was calculated as –

$$\text{Brown rice L/B ratio} = \frac{\text{Brown rice length}}{\text{Brown rice width}} \times 100$$

#### **3.4.2.7 Kernel length (mm)**

After milling, ten whole kernels were chosen at random and the average length was measured.

#### **3.4.2.8 Kernel breadth (mm)**

Width was measured in the same way by taking 10 whole milled kernels.

#### **3.3.2.9 Kernel L/B ratio**

This was determined by using the formula given below

$$\text{Kernel L/B ratio} = \frac{\text{Kernel length}}{\text{Kernel width}} \times 100$$

#### **3.4.2.10 Hulling percentage**

Physical contaminants such as rice stalks, leaves, mud lumps, and other foreign substances were removed from the sample before it was weighed at 100g. With the use of a stake sheller, shelling of the clean sample was done followed by hulling of the samples and then weight of the dehulled grains was noted.

This was determined using the following formula: -

$$\text{Hulling \%} = \frac{\text{Weight of the dehusked kernel (g)}}{\text{Weight of paddy (g)}} \times 100$$

#### **3.4.2.11 Milling percentage**

Hulling was then followed by milling, with the weight of milled grains being recorded. The following formula was used to calculate the milling percentage: -

$$\text{Milling \%} = \frac{\text{Wt. of polished kernel}}{\text{Weight of paddy (g)}} \times 100$$

#### **3.4.2.12 Head rice recovery (%)**

It is the proportion of paddy rice that retains 75% of its length after milling. Full (¾ kernel) and broken rice was sorted from the milled sample and their weight was recorded.

The following is the formula for calculating the percentage of head rice recovery: -

$$\text{Head rice recovery \%} = \frac{\text{Wt. of whole polished kernel (g)}}{\text{Wt. of paddy (g)}} \times 100$$

**Table 3.2 Description of morphological traits.**

<b>S.no</b>	<b>Traits</b>	<b>Classes</b>	<b>Scores</b>
<b>1.</b>	<b>Coleoptile: Colour</b>	Colourless Light Purple Purple	1 2 3
<b>2.</b>	<b>Basal leaf: Sheath colour</b>	Green Light purple Purple lines Uniform purple	1 2 3 4
<b>3.</b>	<b>Leaf: intensity of green colour</b>	Light Medium Dark	3 5 7
<b>4.</b>	<b>Leaf: anthocyanin colouration</b>	Absent Present	1 9
<b>5.</b>	<b>Leaf: distribution of anthocyanin colouration</b>	On tips only On margins only In blotches only Uniform	1 2 3 4
<b>6.</b>	<b>Leaf sheath: anthocyanin colouration</b>	Absent Present	1 9
<b>7.</b>	<b>Leaf sheath: intensity of anthocyanin colouration</b>	Very weak Weak Medium Strong Very strong	1 3 5 7 9
<b>8.</b>	<b>Leaf: pubescence of blade surface</b>	Absent Weak Medium Strong Very strong	1 3 5 7 9
<b>9.</b>	<b>Leaf: auricles</b>	Absent Present	1 9
<b>10.</b>	<b>Leaf: anthocyanin colouration of auricles</b>	Colourless Light purple Purple	1 2 3
<b>11.</b>	<b>Leaf: collar</b>	Absent Present	1 9
<b>12.</b>	<b>Leaf: anthocyanin colouration of collar</b>	Absent Present	1 9
<b>13.</b>	<b>Leaf: ligule</b>	Absent Present	1 9
<b>14.</b>	<b>Leaf: shape of ligule</b>	Truncate Acute Split	1 2 3
<b>15.</b>	<b>Leaf: colour of ligule</b>	White Light purple	1 2

		Purple	3
16.	Leaf: length of blade	Short (45 cm)	3
		Medium (30-45 cm)	5
		Long (more than 45 cm)	7
17.	Leaf: width of blade	Narrow (2 cm)	3
		Medium (1-2 cm)	5
		Broad (>2 cm)	7
18.	Culm: attitude	Erect	1
		Semi-erect	3
		Open	5
		Spreading	7
19.	Time of heading/ flowering	Very early (<71 days)	1
		Early (71-90 days)	3
		Medium (91-110 days)	5
		Late (111-130 days)	7
		Very late (more than 131 days)	9
20	Spikelet: density of pubescence of lemma	Absent	1
		Weak	3
		Medium	5
		Strong	7
		Very strong	9
21	Spikelet: colour of stigma	White	1
		Light green	2
		Yellow	3
		Light purple	4
		Purple	5
22	Stem: thickness	Thin (0.55 cm)	3
		Medium (0.40-0.55 cm)	5
		Thick (more than 0.55 cm)	7
23	Stem: anthocyanin coloration of nodes	Absent	1
		Present	9
24	Stem: intensity of anthocyanin colouration of nodes	Weak	3
		Medium	5
		Strong	7
25	Stem: anthocyanin colouration of inter nodes	Absent	1
		Present	9
26	Flag leaf: attitude of blade	Erect	1
		Semi-erect	3
		Horizontal	5
		Deflexed	7
27	Panicle: curvature of main axis	Straight	1
		Semi-straight	3
		Deflexed	5
		Drooping	7
28	Panicle: awns	Absent	1
		Present	9

<b>29</b>	<b>Panicle: colour of awns</b>	Yellowish White	1
		Yellowish Brown	2
		Brown	3
		Reddish brown	4
		Light red	5
		Red	6
		Light purple	7
		Purple	8
		Black	9
<b>30</b>	<b>Panicle: length of longest awn</b>	Very short	1
		Short	3
		Medium	5
		Long	7
		Very long	9
<b>31</b>	<b>Panicle: distribution of awns</b>	Tip only	1
		Upper half	3
		Whole length	5
<b>32</b>	<b>Panicle: Presence of secondary branching</b>	Absent	1
		Present	9
<b>33</b>	<b>Panicle: secondary branching</b>	Weak	1
		Strong	2
		Clustered	3
<b>34</b>	<b>Panicle: attitude of branches</b>	Erect	1
		Erect to semi-Erect	3
		Semi-erect	5
		Semi-erect to spreading	7
		Spreading	9
<b>35</b>	<b>Panicle: exertion</b>	Partly exerted	3
		Mostly exerted	5
		Well exerted	7
<b>36</b>	<b>Time of maturity (days)</b>	Very early (less than 100)	1
		Early (101-120)	3
		Medium (121-140)	5
		Late (141-160)	7
		Very late (more than 160)	9
<b>37</b>	<b>Leaf: senescence</b>	Early	3
		Medium	5
		Late	7
<b>38</b>	<b>Grain: Weight of 100 fully developed grains</b>	Very low (less than 15g)	1
		Low (15-20 g)	3
		Medium. (21-25 g)	5
		High (26-30)	7
		Very high (>30 g)	9
<b>39</b>	<b>Paddy: Length</b>	Very short (less than 6mm)	1
		Short (6.1-8.5 mm)	3
		Medium (8.6-10.5 mm)	5
		Long (10.6-12.5 mm)	7
		Very long (>12.5 mm)	9

<b>40</b>	<b>Paddy: Width</b>	Very narrow (less than 2mm)	1
		Narrow (2.1-2.5 mm)	3
		Medium (2.6-3.0 mm)	5
		Broad (3.1-3.5 mm)	7
		Very broad (more than 3.5 mm)	9
<b>41</b>	<b>Brown rice: Length</b>	Short	1
		Medium	3
		Long	5
		Long* (Long for Basmati type)	7
		Extra long	9
<b>42</b>	<b>Brown rice: Width</b>	Narrow (2.0 mm)	3
		Medium (2.0-2.5 mm)	5
		Broad (more than 2.5 mm)	7
<b>43</b>	<b>Endosperm: Presence of amylose</b>	Absent	1
		Present	9
<b>44</b>	<b>Endosperm: Content of amylose</b>	Very low (less than 10%)	1
		Low (10-19%) amylose	3
		Medium (20-25%)	5
		High (26-30%)	7
		Very high (more than 30%)	9
<b>45</b>	<b>Gelatinization temperature through alkali spreading value</b>	Low	1
		Medium	3
		High medium	5
		High	7

### 3.4.2.13 Endosperm: amylose content

The simplified procedure for the determination of amylose content was given by Juliano (1970).

Procedure for determination of the amylose content: -

- In a 100 ml volumetric flask, 0.10 g fine powdered rice grain was weighed.
- After that, 4 mL methanol was added and the mixture was left for 2.30 hours.
- Methanol was then extracted.
- After that, 9 ml of 1N NaOH and 1ml of 9.5 percent ethanol were added, and it was heated for 10 minutes in a pre-heated water bath.
- After cooling, distilled water was used to make a volume of 100 ml.
- 5 mL of the above-made solution was placed into a volumetric flask, along with 1 mL of acetic acid and 2 mL of potassium iodide (KI).
- Again, distilled water was used to make a 100ml volume, which was held for 20 minutes.

- Finally, using a spectrophotometer, a reading of sample at 620 nm was taken.

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

R = Reading at 620 nm spectrophotometer

**Table: 3.3 Scale for Amylose test**

State	Content of amylose	Score/ Scale
Very low	3-9%	1
Low	10-19%	3
Medium	20-25%	5
High	26-30%	7
Very high	> 30%	9

#### 3.4.2.14 Cooking Procedure

- 5g of milled rice sample was mixed with 15ml water in a test tube, soaked for 10 minutes, and then placed in a hot water bath for 20 minutes.
- The test tubes were then removed and cooled.
- Cooked rice was then transferred to a filter paper-lined petri plate.
- 10 cooked whole grains were then chosen & placed on graph paper that had filter paper mounted on it.
- Following these processes, the following characters were recorded: -

#### 3.4.2.15 Cooked rice length (mm): -

A total of ten cooked whole grains were chosen at random and their lengths were measured in millimeters.

#### 3.4.2.16 Cooked rice width (mm)

10 Cooked whole grains were chosen and their width was documented in millimeter.

#### 3.4.2.17 Elongation ratio (ER)

It is the ratio of L/B (after cooking) and L/B (before cooking)

$$\text{Elongation ratio} = \frac{\text{Ratio of L/B (after cooking)}}{\text{Ratio of L/B (before cooking)}}$$

#### 3.4.2.18 Gel Consistency

**Method of determining gel consistency:**

- In a culture tube, place 100 mg of flour quadruplicates
- Add 0.2 mL of ethanol having 0.25 percent thymol blue to the mixture.
- Add 2.0 mL of 0.2N potassium hydroxide to the mixture.

- Using a cyclone mixer, mix the solution.
- After placing one glass tube marble on each test tube, place the test tube in a water bath at 90-100°C for 8 minutes.
- Cool the culture tubes for 5 minutes after removing them from the water bath.
- Using a cyclone mixer, mix the solution. Place the culture tubes in a low temperature bath at 0-2 °C for 20 minutes.
- The cultured tubes are withdrawn from the ice bath and set horizontally over ruled or graph paper for one hour.
- The gel consistency of the sample was determined by measuring the length of the blue-coloured gel from the bottom of the test tube up to the gel front.
- Classification was given according to DUS descriptive by Shobha *et al.* (2006).

**Table 3.4: Classification of gel consistency:**

<b>Range</b>	<b>Gel Consistency</b>
26 – 40 mm	Hard gel consistency
41 – 60 mm	Medium gel consistency
61 – 100 mm	Soft gel consistency

#### **3.4.2.19 Gelatinization temperature through alkali spreading value**

The gelatinization temperature was determined using the procedure outlined below.

- 6 milled rice kernels (without cracks) were randomly picked and placed in petri plates from each replication of each variety.
- 10 mL of 1.7 percent KOH was then added to each petri dish
- Petri dishes were uniformly covered and kept at a temperature of 27-30°C for 23 hours.
- Visual evaluations for endosperm disintegration were recorded as per the table 3.5.

**Table 3.5 Numerical scale for scoring alkali spreading values**

Score	Spreading Scale	Clearing Scale
1	Kernel not affected	Kernel chalky
2	Kernel Swollen	Kernel chalky collar powdery
3	Kernel swollen, collar complete and narrow	Kernel chalky collar cottony or cloudy
4	Kernel swollen, collar complete and wide	Center cottony, collar cloudy
5	Kernel split or segregated, collar complete and wide	Center cottony, collar clearing
6	Kernel dispersed merging with collar	Center cloudy collar clear
7	Kernel completely dispersed and intermingled	Center and collar clear

**Table 3.6 Classification of Alkali spreading value and Gelatinization temperature.**

Alkali spreading value	Classification	GT	Note
6-7	High	Low	1
4-5	Medium	Medium	3
3	Low medium	High medium	5
1-2	High	High	7

### 3.6 Statistical analysis

The following data was noted with respect to different quantitative and qualitative traits on the accessions of rice along with six checks were estimated by the statistical analysis:

#### 3.6.1 Analysis of variance

Using analysis of variance technique (Panse and Sukhatme, 1985) differences among 45 genotypes for various traits were tested for significance.

Where,

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

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

$m$  = general mean

$g_i$  = effect of  $i$ th genotype

$v_j$  = effect of  $j$ th replication

$e_{ij}$  = random error

**Table 3.7 The analysis of variance for each trait was carried out as follows:**

Source of variation	Degree of freedom	Total sum of square	Mean sum of square	'F' ratio
Replication	$(r-1) = 1$	RSS	MSR	MSR/MSE
Treatment	$(t-1) = 51$	TrSS	MST	MST/MSE
Error	$(r-1)(t-1) = 51$	ESS	MSE	-
Total	$(rt-1) = 103$	TSS	-	-

Where,

$r$  = number of replications

$t$  = number of treatments

RSS = Replication sum of squares

TrSS = Treatment sum of squares

ESS = Error sum of squares

TSS = Total sum of square

MSR = Replication Mean Sum of squares

MST = Treatment Mean Sum of Squares

MSE = Error Mean Sum of Squares

Using the 'F' tabulated values given by Fisher and Yates (1967) the significance test was conducted. The 'F' calculated value was then compared with 'F' tabulated value at 5 and 1% level of probability against error degree of freedom, *i.e.*  $(r-1)(t-1)$ .

### 3.6.2 Parameters of variation

#### 1) Mean

$$\bar{x} = \sum Xi / N$$

Where,

$\sum Xi$  = sum of all observations of  $i^{\text{th}}$  character

N = number of observations

## 2) Range

The range of distribution was reflected by the limit of the smallest and the largest value of observations.

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

## 3) Standard error (SE):

$$\text{Standard error} = \frac{s}{\sqrt{n}}$$

Where,

S = Standard deviation

$\sqrt{n}$  = Total number of observations

## 4) Coefficient of variation (CV %)

The coefficient of variation for different traits was calculated by formula suggested by Burton and De Vane (1953).

$$CV \% = \frac{SD}{N} \times 100$$

Where,

SD = Standard deviation

N = Mean of character

## 5) Phenotypic variance:

Phenotypic variance calculating given formula:

$$VP = VG + VE$$

Where,

VP = Phenotypic variance

VG = Genotypic variance

VE = Environmental variance

## 6) Genotypic variance:

Phenotypic variance calculating given formula:

$$VG = VP - VE$$

Where,

VG = Genotypic variance

VP = Phenotypic variance

VE = Environmental variance

**7) Phenotypic coefficient of variation (PCV %)**

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

Where,

PCV (%) = Phenotypic coefficient of variation

$\sigma^2 p$  = Phenotypic variance

$\bar{x}$  = Mean of the character

**8) Genotypic coefficient of variation (GCV %)**

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

Where,

GCV (%) = Genotypic coefficient of variation

$\sigma^2 g$  = Genotypic variance

$\bar{x}$  = Mean of the character

The GCV and PCV were classified as per the method suggested by Sivasubramanian and Madhavamenon (1973):

0-10% = Low

10-20% = Moderate

More than 20% = High

**9) Heritability (broad sense)**

Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage (Falconer, 1981).

$$h^2(bs)\% = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

The heritability was classified into 3 groups as suggested by Johnson *et al.* (1955):

0-40% = Low

40-60% = Moderate

More than 60% = High

### 10) Expected genetic advance (GA)

Genetic advance was worked out by adopting the following formula given by Johnson *et al.* (1955):

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

Where,

h = Heritability in broad sense

k = Selection differential, which is equal to 2.06 at 5% intensity of selection (Lush, 1949)

$\sqrt{\sigma^2 p}$  = Phenotypic standard deviation

### 11) Genetic advance as per cent of mean (GAM)

Genetic advance as per cent of mean for each character was estimated using the following formula suggested by Johnson *et al.* (1955).

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

Where,

GA = Genetic advance

X = General mean

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

0-10 % = Low

10-20 % = Moderate

More than 20 % = High

### 3.6.2 Correlation analysis

Correlation coefficients analysis measures the mutual relationship between various characters with the help of formula given below which was suggested by Miller *et al.* (1958).

$$R_{x_i x_j} = \frac{\text{Cov}X_i X_j}{\sqrt{\text{Var}X_i} \sqrt{\text{Var}X_j}}$$

Where,

$R_{x_i x_j}$  = Coefficient of correlation between  $X_i^{\text{th}}$  and  $X_j^{\text{th}}$  traits

$\text{Cov}X_i X_j$  = Covariance between  $X_i^{\text{th}}$  and  $X_j^{\text{th}}$  traits

$\text{Var}X_i$  = Variance of  $X_i^{\text{th}}$  trait

$\text{Var}X_j$  = Variance of  $X_j^{\text{th}}$  trait

Correlation coefficients were tested for their significance using t statistics at (n-2) degrees of freedom as given below.

$$t_c = \frac{|r| \sqrt{n-2}}{\sqrt{(1-r^2)}}$$

### Test of significance

By comparing the phenotypic and genotypic correlation coefficients with the tabulated values (Fisher and Yates, 1967) at (n-2) degrees of freedom at 5% and 1% level of significance, correlation coefficients was estimated, where, 'n' denotes the number of pairs of observations used in the calculation.

### 3.6.3. Path coefficient analysis

Path coefficient analysis divides the correlation coefficient into the measures of indirect and direct effects of independent variable on dependent variable. If a character y is determined by correlated character x1, x2 and x3, a path diagram must be drawn. Thus, we get a set of simultaneous equations as given below:

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

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

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

Considering the 3 factors i.e., X1, X2 and X3, the equation given above can be matrix notation as:

$$\begin{matrix} \begin{bmatrix} r_{x_1 y} \\ r_{x_2 y} \\ r_{x_3 y} \end{bmatrix} \\ A \end{matrix} = \begin{matrix} \begin{bmatrix} r_{x_1 x_1} & r_{x_1 x_2} & r_{x_1 x_3} \\ r_{x_2 x_1} & r_{x_2 x_2} & r_{x_2 x_3} \\ r_{x_3 x_1} & r_{x_3 x_2} & r_{x_3 x_3} \end{bmatrix} \\ B \end{matrix} \begin{matrix} \begin{bmatrix} a \\ b \\ c \end{bmatrix} \\ C \end{matrix}$$

Where,

$r_{x_1 y}$  = Correlation coefficient between character x1 and y.

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

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

$a$  = Direct effect of character  $x_1$  and  $y$

$b$  = Direct effect of character  $x_2$  and  $y$

$c$  = Direct effect of character  $x_3$  and  $y$

The solution for vector  $c$  could be obtained as follows:

$$A = B.C$$

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

Where,

$B^{-1}$  = inverse of matrix  $B$ .

After estimating the values of path coefficient i.e.,  $C$  vector the residual effect can be determined by following formula:

$$R = 1 - \sum (r_{ij})$$

Where,

$R$  = residual effect

$r_{ij}$  = correlation coefficient between  $i^{\text{th}}$  and  $j^{\text{th}}$  dependent variable

The findings of path coefficient analysis are interpreted based on the following scale

**Table 3.8 Interpretation of path coefficient analysis.**

Value of direct/ indirect effect	Rate/ scale
0.00 to 0.09	Negligible
0.10 to 0.19	Low
0.20 to 0.29	Moderate
0.30 to 0.39	High
>1.00	Very high

### 3.6.4 Genetic divergence Analysis

In 1936, P.C. Mahalonobis originally developed the  $D^2$  statistic. The application of this technique for the assessment of genetic divergence between the populations was suggested by Rao, (1952). It measures the forces of differentiation at intra as well as inter cluster levels .

$$D^2 = \sum \sum \lambda_{ij} \sigma_{ai} \sigma_{aj}$$

Where,

$D^2$  = square of generalized distance

$\lambda_{ij}$  = reciprocal of the common dispersal matrix

$$\sigma_{ai} = (\mu_{i1} - \mu_{i2})$$

$$\sigma_{aj} = (\mu_{j1} - \mu_{j2})$$

$\mu$  = general mean

The  $D^2$  values were calculated as the sum of squares of the differences between pairs of corresponding uncorrelated (gs) values of any two uncorrelated genotype of  $D^2$  value. All  $n(n-1)/2$   $D^2$  value were clustered using Toucher's method described by Rao (1952). By using the formula given by Singh and Choudhary (1997) the intra cluster distances were calculated:

$$\text{Square of the inter cluster distance} = \Sigma D^2 i / n$$

Where,

$\Sigma D^2 i$  = sum of distance between all possible combinations of the entries included in a cluster and  $n$  is number of all possible combinations.

The inter cluster distances were calculated by the formula described by Singh and Choudhary (1997):

$$\text{Square of the intra cluster distance} = \Sigma D^2 i / n_i n_j$$

Where,

$\Sigma D^2 i$  = sum of distances between all possible combinations ( $n_i n_j$ ) of the entries included in the clusters under study.

$n_i$  = number of entries in cluster  $i$

$n_j$  = number of entries in cluster  $j$ .

Clustering was based on the criteria that any two genotype belonging to the same cluster, at least on an average, show a small  $D^2$  value than those belonging to 2 different clusters.

## CHAPTER IV

# RESULT AND DISCUSSION

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The current study was conducted on 52 rice accessions with 6 agro-morphological checks and on 21 rice accessions with 6 quality characterization checks in order to identify accessions for using the right attribute-based donor for hybridization and conserving the unique rice. Genetic characteristics of variability were investigated to gain a clear picture of genotype variability. The purpose of association analysis was to determine the degree of relationship between traits. Simple correlation, on the other hand, does not provide sufficient information about each trait's contribution to yield. Thus, path analysis was used to get a sense of a trait's direct and indirect contribution to yield per plant, allowing the breeder to rank genetic traits based on their value.

The current investigation's experimental results have been presented under the following headings:

- 4.1 Agro morphological and quality characterization
- 4.2 Analysis of variance (ANOVA)
- 4.3 Genetic parameters for different characters
- 4.4 Association analysis
  - 4.4.1 Correlation analysis
  - 4.4.2 Path coefficient analysis
- 4.5 Genetic divergence analysis

### **4.1 Agro – morphological and quality characterization**

#### **4.1A Agro morphological characterization (Quantitative and qualitative characters)**

The results of the current investigation on 52 accessions, including 6 morphological character checks, at various stages of rice plant growth. For each trait, three plants were chosen at random from each entry. Appendix B contains the results of the agro-morphological characterization. Table 4.1 shows the frequency distribution & percentage value of agro-morphological characters.

##### **4.1.1 Coleoptile colour**

The analysis of accessions of rice showed that out of 52 accessions, 50 were green

while 2 were purple. (Fig 4.1).

#### **4.1.2 Basal leaf: sheath colour**

The results reflect that out of a total of 52 accessions, 26 showed green, 23 showed purple lines while 2 showed light purple and only 1 showed uniform purple. (Fig 4.2)

#### **4.1.3 Leaf: intensity of green colour**

The analysis of accessions of rice showed that out of 52 accessions, 30 accessions were having medium, 12 were having light while 10 were having dark intensity of green colour. (Fig 4.3)

#### **4.1.4 Leaf: anthocyanin coloration**

Out of 52 accessions studied, only 4 had anthocyanin colouration while 48 had no anthocyanin colouration in leaf . (Fig 4.4)

#### **4.1.5 Leaf: distribution of anthocyanin colouration**

The results reflect that out of 52 accessions, 4 accessions had anthocyanin distributed on margins only while remaining had no leaf anthocyanin. (Fig 4.5).

#### **4.1.6 Leaf sheath: anthocyanin colouration**

The analysis of accessions of rice showed that out of 52 accessions, 27 accessions had no anthocyanin while 25 had anthocyanin in their leaf sheath. (Fig 4.6).

#### **4.1.7 Leaf sheath: intensity of anthocyanin colouration**

The findings of accessions of rice reflected that out of 52 accessions, 13 accessions had very weak, 7 had weak, 4 had strong while 1 accession had very strong intensity of anthocyanin colouration. (Fig 4.7).

#### **4.1.8 Leaf: pubescence of blade surface**

The analysis reflects that out of 52 accessions, 25 accessions had weak, 18 had medium, 5 had strong pubescence while pubescence was absent in 4 accessions. (Fig 4.8).

#### **4.1.9 Leaf: auricles**

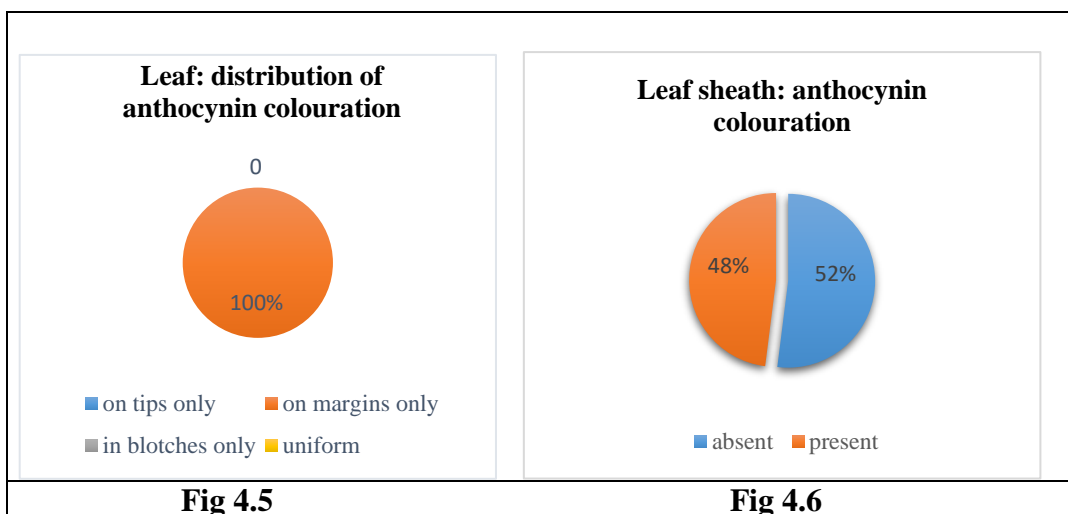
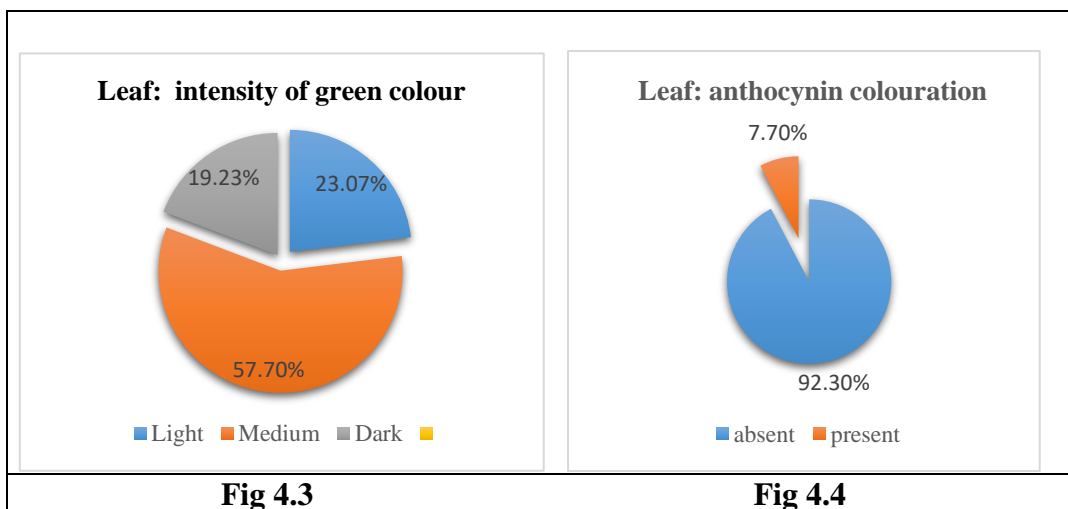
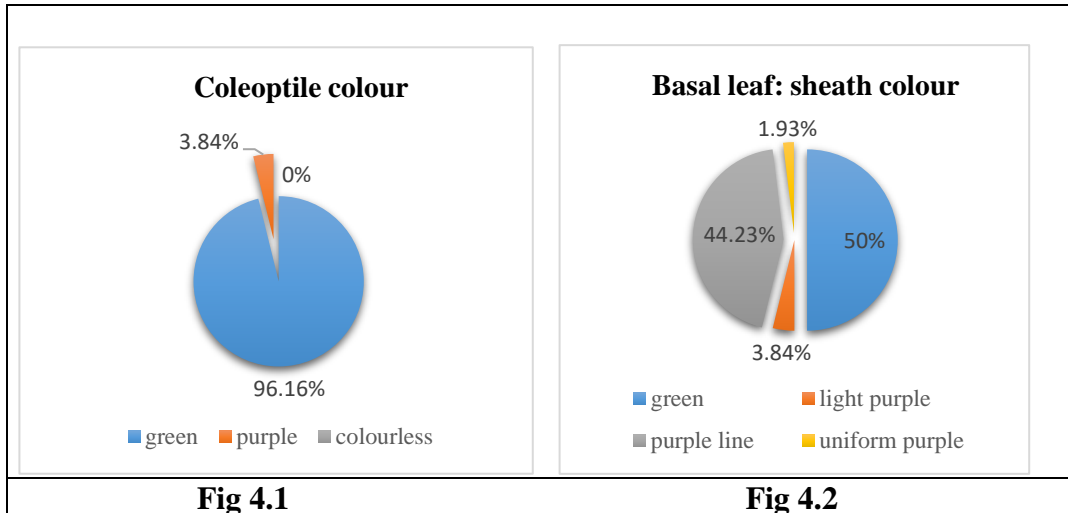
All 52 rice accessions studied had leaf auricles. (Fig. 4.9).

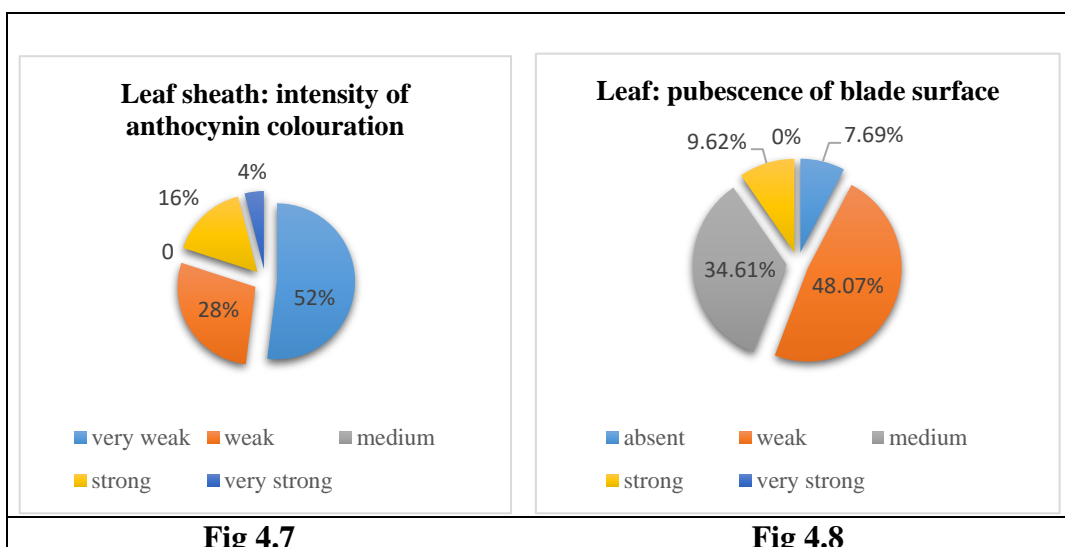
#### **4.1.10 Leaf: anthocyanin colouration of auricles**

It has been found that out of 52 accessions, 32 accessions had light purple, 7 had purple anthocyanin colouration of auricles while 13 accessions were colourless. (Fig 4.10).

#### 4.1.11 Leaf: collar

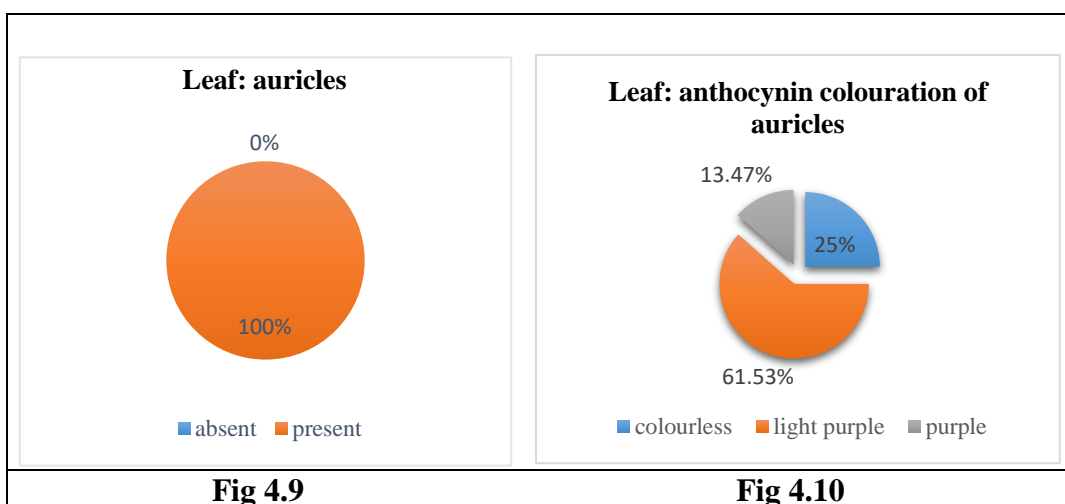
All the 52 accessions studied in present investigation had leaf collar (Fig 4.11).





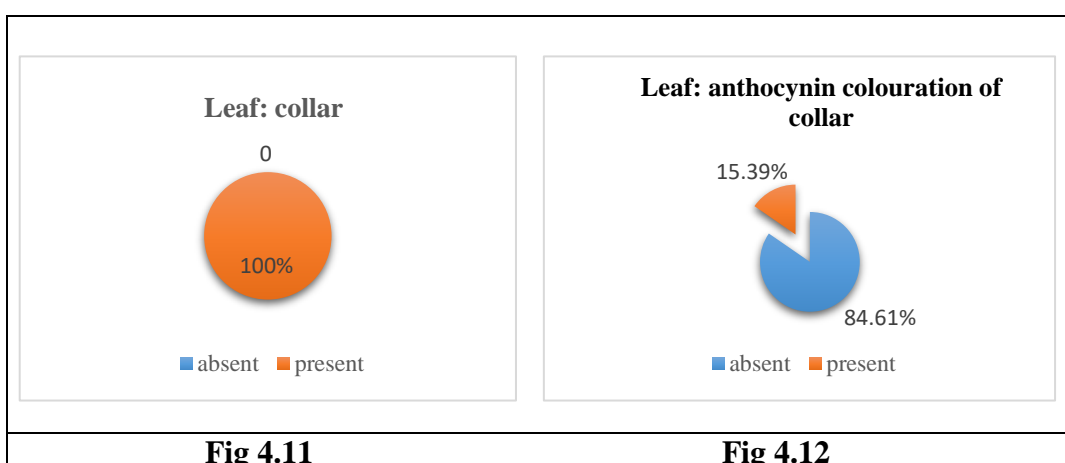
**Fig 4.7**

**Fig 4.8**



**Fig 4.9**

**Fig 4.10**



**Fig 4.11**

**Fig 4.12**

**4.1.12 Leaf: anthocyanin coloration of collar**

The analysis revealed that 44 of the 52 accessions did not have anthocyanin

colouration of the collar, whereas it was present in 8 of them. (Fig. 4.12).

#### **4.1.13 Leaf: ligule**

Results reflected that all 52 accessions had leaf ligule studied. (Fig. 4.13).

#### **4.1.14 Leaf: shape of ligule**

Results reflected that out of 52 rice accessions, all had split ligule. (Fig. 4.14).

#### **4.1.15 Leaf: colour of ligule**

The investigation of rice accessions revealed that 50 of the 52 accessions had white ligule, 1 had light purple ligule, and 1 had purple ligule. (Fig. 4.15).

#### **4.1.16 Leaf: length of blade**

The analysis of accessions of rice reflected that out of 52 accessions, 28 were having medium length, 17 were long while 7 were short. (Fig 4.16).

#### **4.1.17 Leaf: width of blade**

The analysis of accessions of rice showed that out of 52 accessions, 27 had narrow while 25 had medium width of blade. (Fig 4.17).

#### **4.1.18 Culm: attitude**

The analysis of rice accessions revealed that 18 of the 52 accessions had an open type culm attitude, 17 had a semi erect attitude, 13 had an erect attitude, and four had a spreading type culm attitude. (Fig 4.18).

#### **4.1.19 Time of heading**

The analysis of accessions of rice showed that out of 52 accessions, 21 were medium, 16 were late, and 14 were early while only 1 was very late. (Fig 4.19).

#### **4.1.20 Spikelet: density of pubescence of lemma**

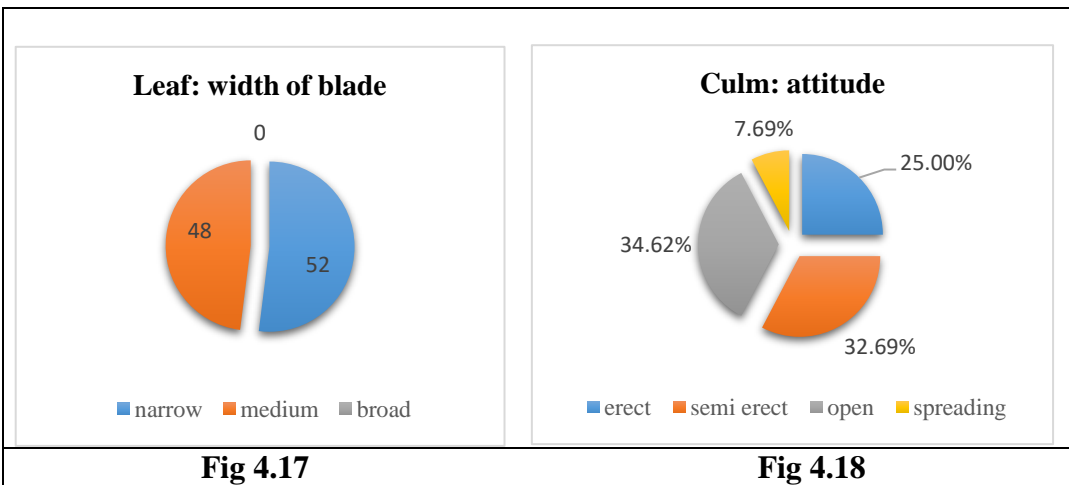
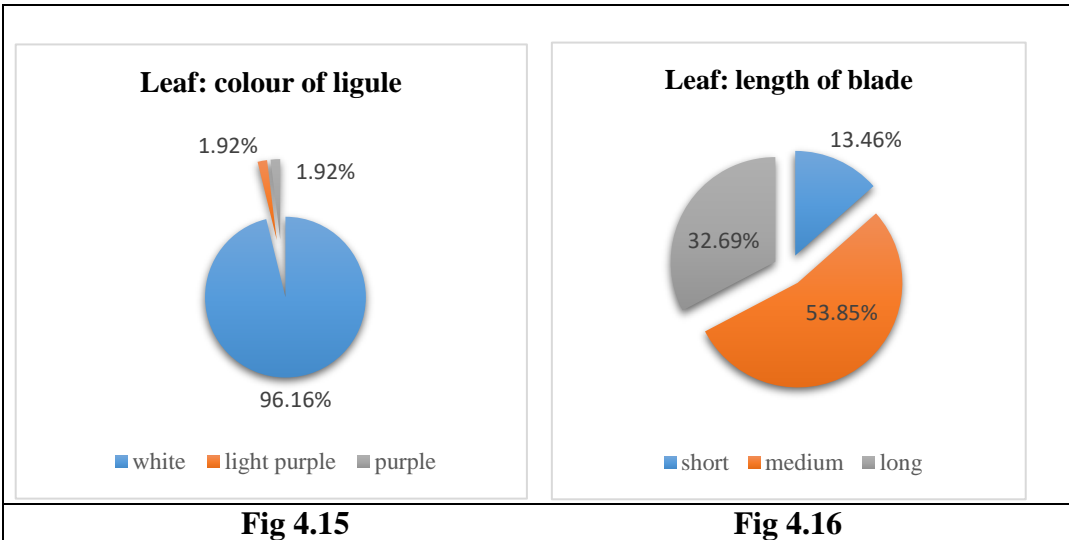
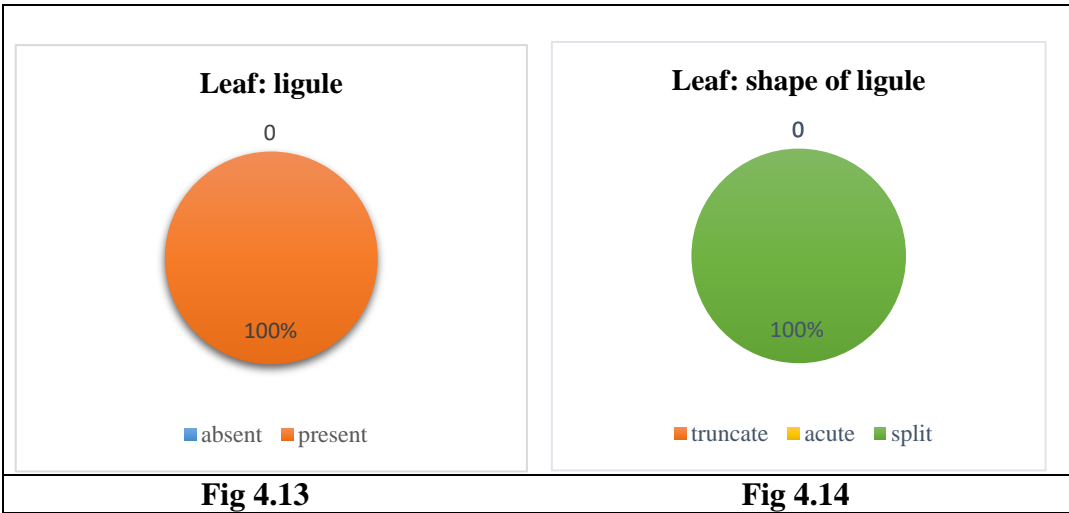
The findings of the analysis reflected that 26 out of 52 accessions were medium, 13 were weak and 13 were strong. (Fig 4.20).

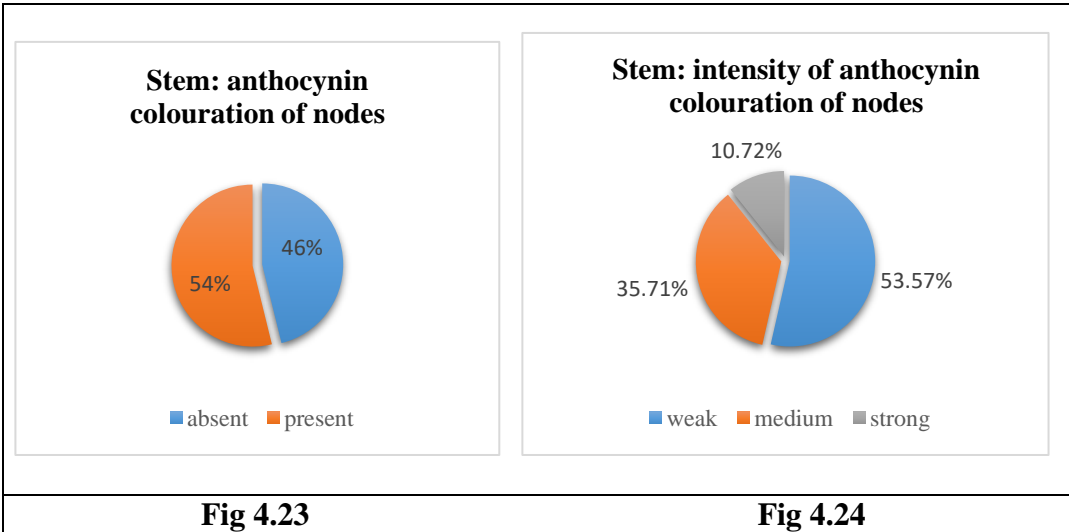
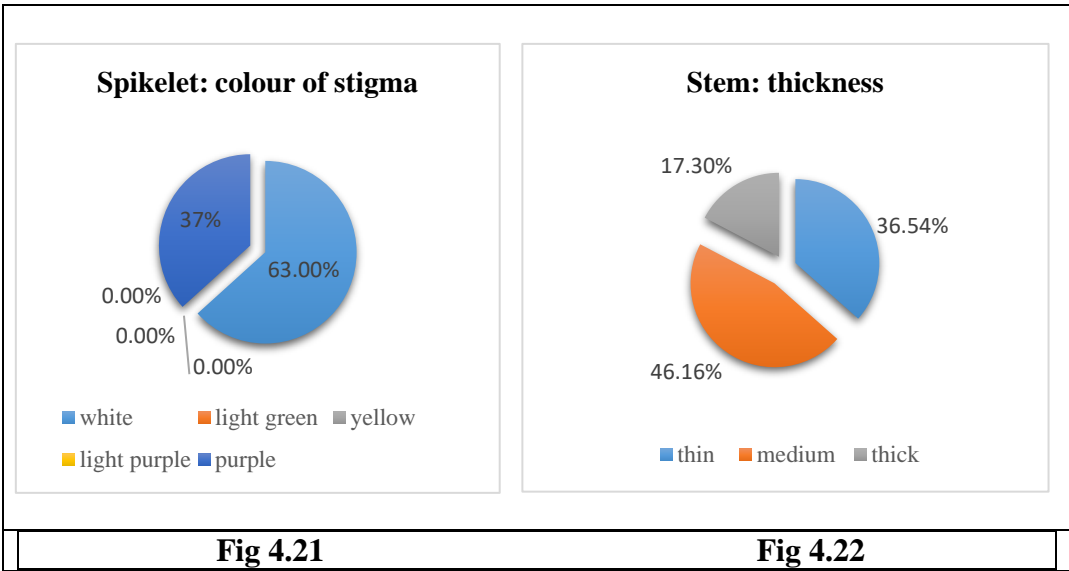
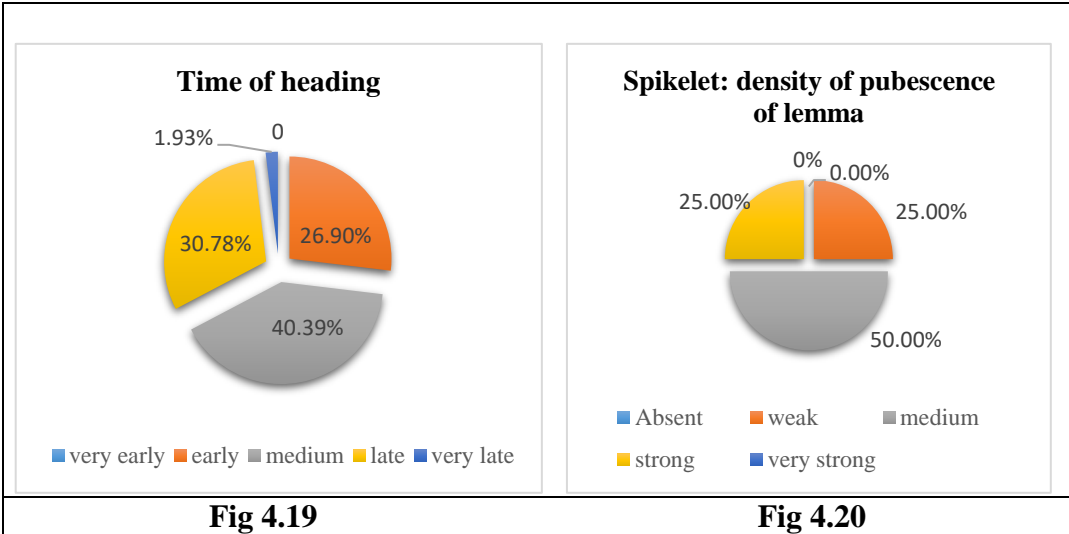
#### **4.1.21 Spikelet: colour of stigma**

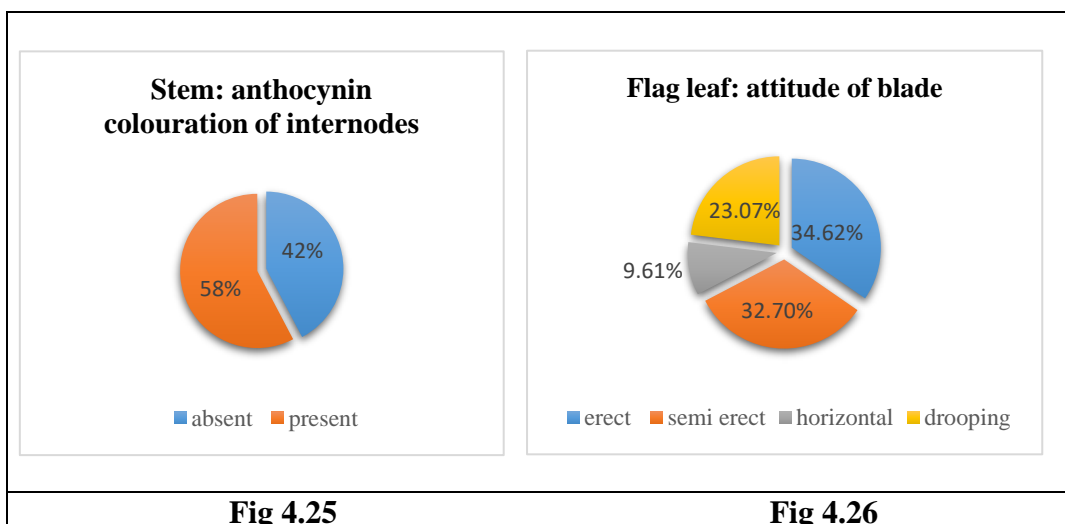
The analysis of accessions of rice showed that out of 52 accessions, 33 were white and 19 were purple. (Fig. 4.21).

#### **4.1.22 Stem: thickness**

Results reflects that out of 52 accessions, 19 accessions were thin, 24 accessions were medium and 9 accessions were thick. (Fig. 4.22).







#### 4.1.23 Stem: anthocyanin coloration of nodes

Out of 52 rice accessions studied, 24 accessions had no anthocyanin coloration of nodes while 28 accessions had anthocyanin coloration. (Fig. 4.23).

#### 4.1.24 Stem: intensity of anthocyanin coloration of nodes

The findings of rice accessions revealed that out of 52 accessions only 28 accessions had anthocyanin coloration out of which 15 accessions were having weak, 10 were having medium while 3 were having strong anthocyanin coloration. (Fig. 4.24).

#### 4.1.25 Stem: anthocyanin coloration of internodes

The analysis of accessions of rice showed that out of 52 accessions, internode of 22 accessions had no anthocyanin coloration while 30 had anthocyanin coloration of internodes. (Fig. 4.25).

#### 4.1.26 Flag leaf: attitude of blade

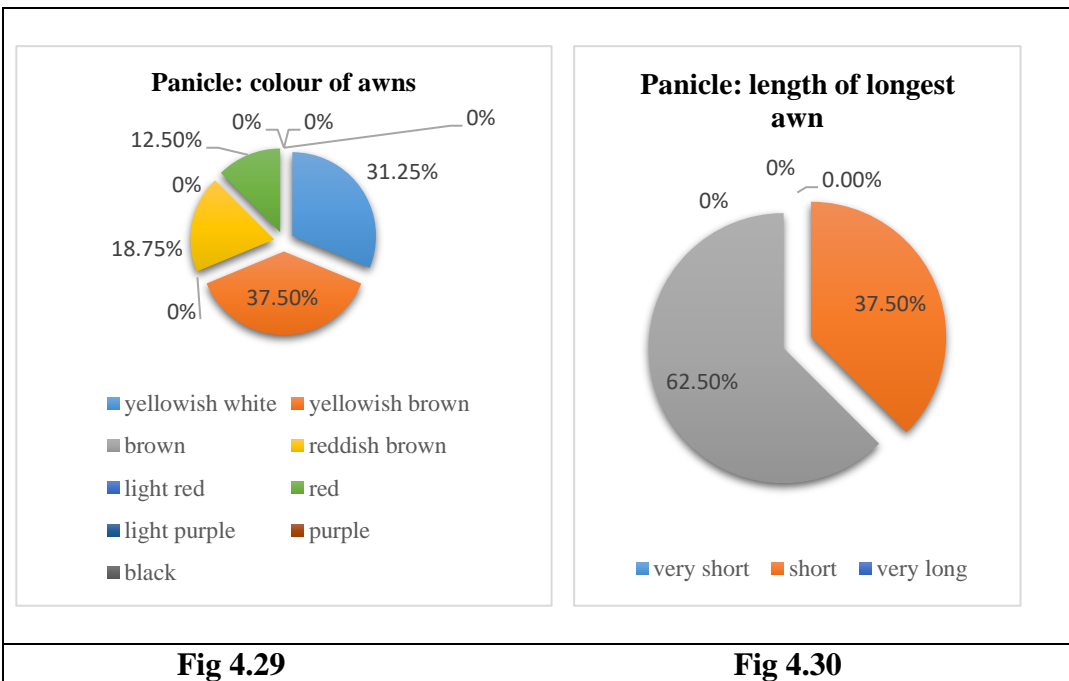
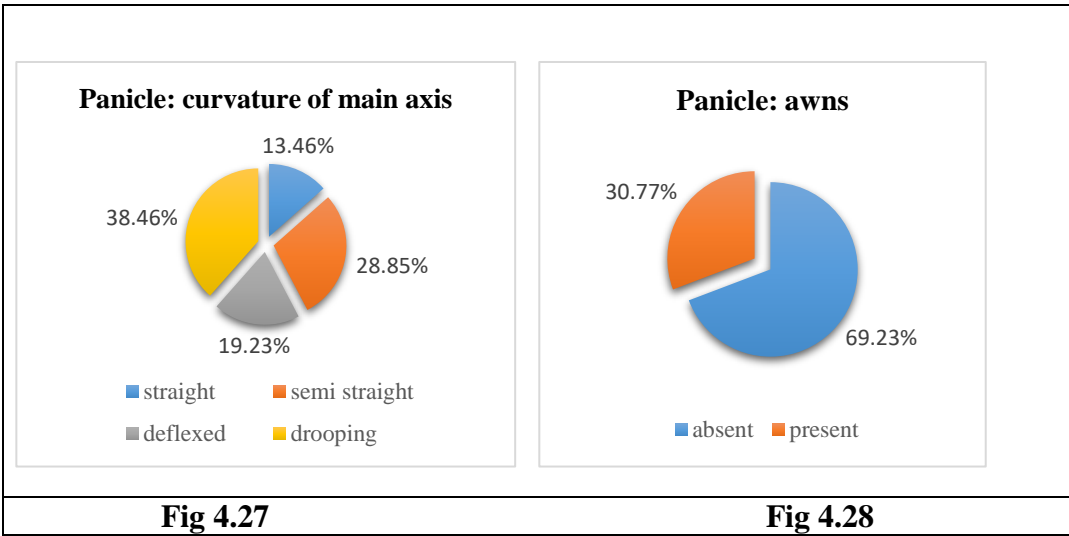
Out of 52 rice accessions studied, 18 were erect, 17 were semi erect, 12 were drooping while 5 were horizontal. (Fig. 4.26).

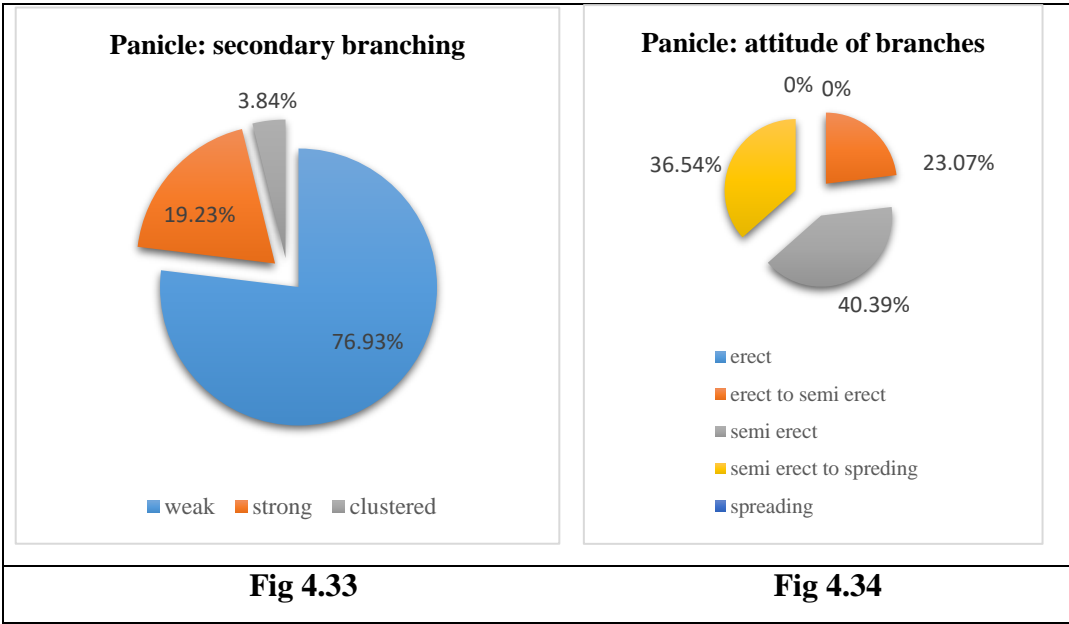
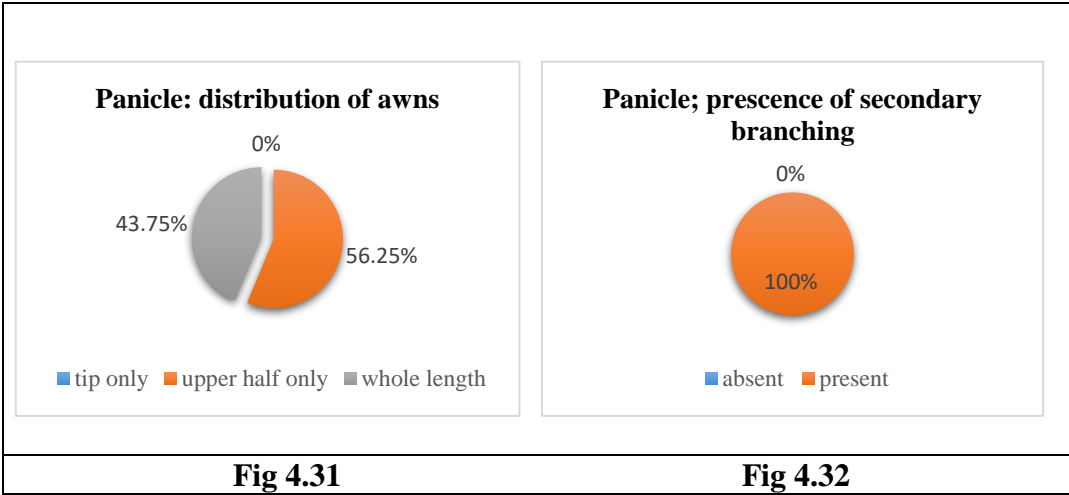
#### 4.1.27 Panicle: curvature of main axis

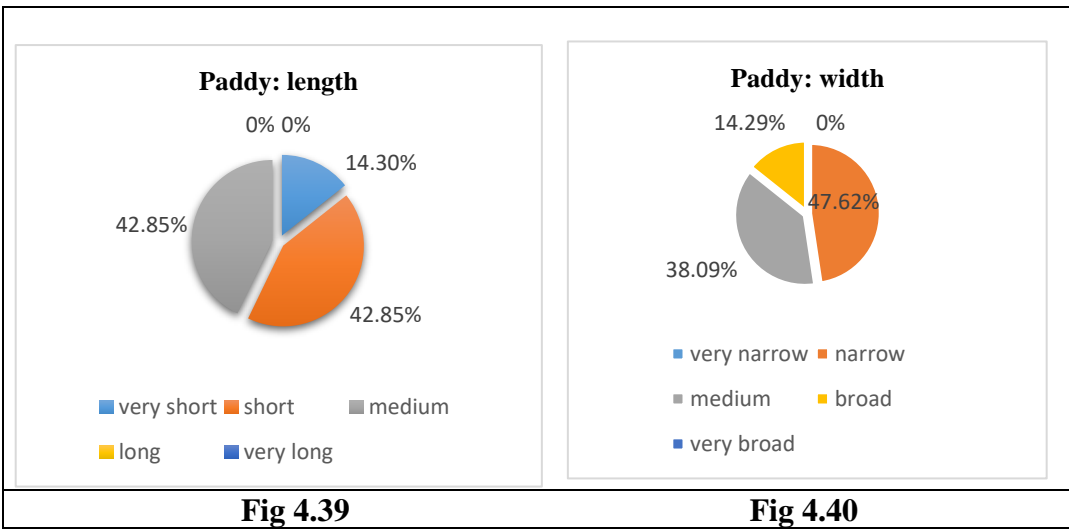
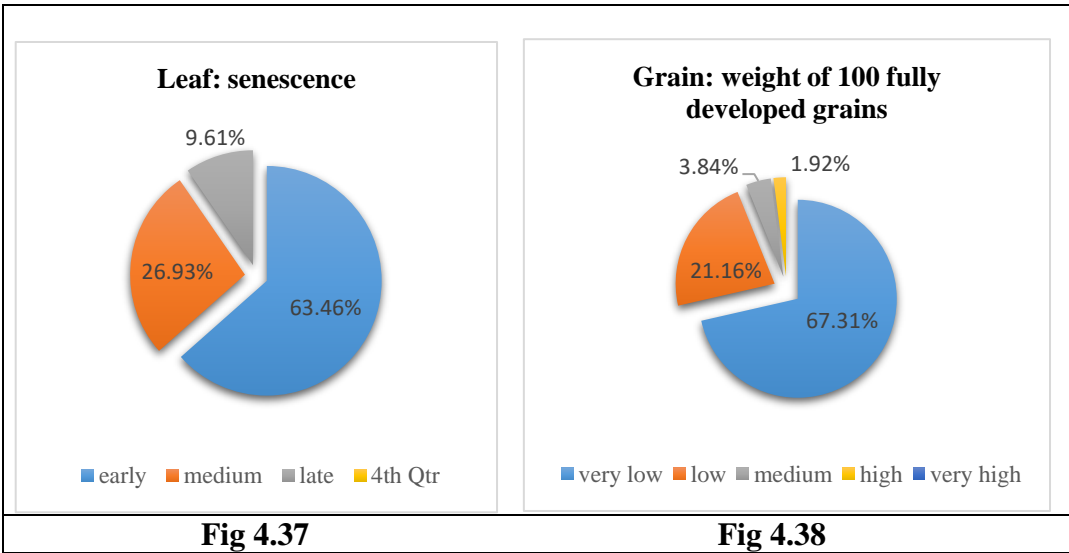
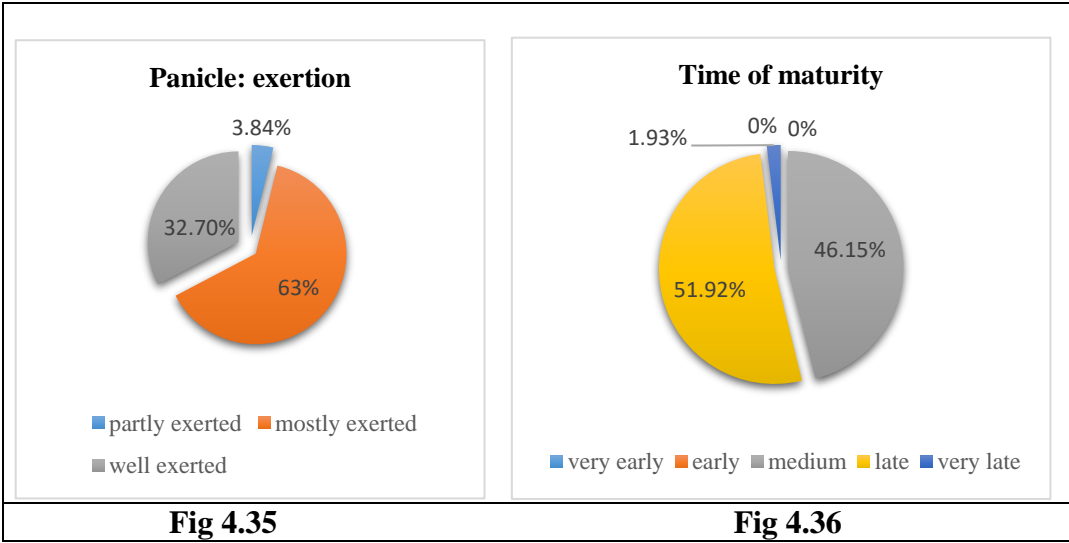
Results showed that out of 52 accessions, 20 had drooping, 15 had semi straight, 10 had deflexed while 7 had straight curvature of main axis of panicle. (Fig. 4.27).

#### 4.1.28 Panicle: awns

Results revealed that out of 52 accessions, only 16 accessions had awns while awns was absent in remaining 36 accessions. (Fig 4.28).







**Table 4.1: Frequency distribution as well as percentage value of agro morphological & quality traits for rice accessions.**

S.no	Traits	Categories or type	No. of accessions	Frequency
1.	<b>Coleoptile: Colour</b>	Colourless	0	0.0
		Green	50	96.16
		Purple	2	3.84
2.	<b>Basal leaf: Sheath colour</b>	Green	26	50
		Light purple	2	3.84
		Purple lines	23	44.23
		Uniform purple	1	1.93
3.	<b>Leaf: Intensity of green colour</b>	Light	12	23.07
		Medium	30	57.7
		Dark	10	19.23
4.	<b>Leaf: Anthocyanin colouration</b>	Absent	48	92.3
		Present	4	7.7
5.	<b>Leaf: distribution of anthocyanin colouration</b>	On tips only	0	0.0
		On margins only	4	100
		In blotches only	0	0.0
		Uniform	0	0.0
6.	<b>Leaf sheath: anthocyanin colouration</b>	Absent	27	52
		Present	25	48
7.	<b>Leaf sheath: intensity of anthocyanin colouration</b>	Very weak	13	52
		Weak	7	28
		Medium	0	0.0
		Strong	4	16
		Very strong	1	4
8.	<b>Leaf: pubescence of blade surface</b>	Absent	4	7.69
		Weak	25	48.07
		Medium	18	34.61
		Strong	5	9.62
		Very strong	0	0.0
9.	<b>Leaf: auricles</b>	Absent	0	0.0
		Present	52	100
10.	<b>Leaf: anthocyanin colouration of auricles</b>	Colourless	13	25
		Light purple	32	61.53
		Purple	7	13.47
11.	<b>Leaf: collar</b>	Absent	0	0.0
		Present	52	100
12.	<b>Leaf: anthocyanin colouration of collar</b>	Absent	44	84.61
		Present	8	15.39
13.	<b>Leaf: ligule</b>	Absent	0	0.0
		Present	52	100
14.	<b>Leaf: shape of ligule</b>	Truncate	0	0.0
		Acute	0	0.0

		Split	52	100
15.	<b>Leaf: colour of ligule</b>	White	50	96.16
		Light purple	1	1.92
		Purple	1	1.92
16.	<b>Leaf: length of blade</b>	Short (45 cm)	7	13.46
		Medium (30-45 cm)	28	53.85
		Long (more than 45 cm)	17	32.69
17.	<b>Leaf: width of blade</b>	Narrow (2 cm)	27	52
		Medium (1-2 cm)	25	48
		Broad (more than 2 cm)	0	0.0
18	<b>Culm: attitude</b>	Erect	13`	25
		Semi-erect	17	32.69
		Open	18	34.62
		Spreading	4	7.69
19.	<b>Time of heading/ flowering</b>	Very early (<71 days)	0	0.0
		Early (71-90 days)	14	26.9
		Medium (91-110 days)	21	40.39
		Late (111-130 days)	16	30.78
		Very late (more than 131 days)	1	1.93
20.	<b>Spikelet: density of pubescence of lemma</b>	Absent	0	0.0
		Weak	13	25
		Medium	26	50
		Strong	13	25
		Very strong	0	0.0
21.	<b>Spikelet: colour of stigma</b>	White	33	63
		light green	0	0.0
		yellow	0	0.0
		light purple	0	0.0
		Purple	19	37
22.	<b>Stem: thickness</b>	Thin (0.55 cm)	19	36.54
		Medium (0.40-0.55 cm)	24	46.16
		Thick (more than 0.55 cm)	9	17.3
23.	<b>Stem: anthocyanin coloration of nodes</b>	Absent	24	46
		Present	28	54
24.	<b>Stem: intensity of anthocyanin colouration of nodes</b>	Weak	15	53.57
		Medium	10	35.71
		Strong	3	10.72
25	<b>Stem: anthocyanin colouration of inter nodes</b>	Absent	22	42
		Present	30	58
26.	<b>Flag leaf :attitude of blade</b>	Erect	18	34.62
		Semi-erect	17	32.7
		Horizontal	5	9.61

		Drooping	12	23.07
<b>27.</b>	<b>Panicle: curvature of main axis</b>	Straight	7	13.46
		Semi-straight	15	28.85
		Deflexed	10	19.23
		Drooping	20	38.46
<b>28</b>	<b>Panicle: awns</b>	Absent	36	69.23
		Present	16	30.77
<b>29</b>	<b>Panicle: colour of awns</b>	Yellowish White	5	31.25
		Yellowish Brown	6	37.5
		Brown	0	0.0
		Reddish brown	3	18.75
		Light red	0	0.0
		Red	2	12.5
		Light purple	0	0.0
		Purple	0	0.0
		Black	0	0.0
<b>30.</b>	<b>Panicle: length of longest awn</b>	Very short	0	0.0
		Short	6	37.5
		Medium	10	62.5
		Long	0	0.0
		Very long	0	0.0
<b>31.</b>	<b>Panicle: distribution of awns</b>	Tip only	0	0.0
		Upper half only	9	56.25
		Whole length	7	43.75
<b>32.</b>	<b>Panicle: presence of secondary branching</b>	Absent	0	0.0
		Present	52	100
<b>33.</b>	<b>Panicle: secondary branching</b>	Weak	40	76.93
		Strong	10	19.23
		Clustered	2	3.84
<b>34.</b>	<b>Panicle: attitude of branches</b>	Erect	0	0.0
		Erect to semi-Erect	12	23.07
		Semi-erect	21	40.39
		Semi-erect to spreading	19	36.54
		Spreading	0	0.0
<b>35.</b>	<b>Panicle: exertion</b>	Partly exerted	2	3.84
		Mostly exerted	33	63.46
		Well exerted	17	32.7
<b>36.</b>	<b>Time of maturity (days)</b>	Very early (less than 100)	0	0.0
		Early (101-120)	0	0.0
		Medium (121-140)	24	46.15
		Late (141-160)	27	51.92
		Very late (more than 160)	1	1.93

<b>37.</b>	<b>Leaf: senescence</b>	Early Medium Late	33 14 5	63.46 26.93 9.61
<b>38.</b>	<b>Grain: Weight of 100 fully developed grains</b>	Very low (less than 15g) Low (15-20 g) Medium. (21-25 g) High (26-30) Very high (more than 30 g)	35 11 2 1 3	67.31 21.16 3.84 1.92 5.77
<b>39.</b>	<b>Grain: Length</b>	Very short (<6mm) Short (6.1-8.5 mm) Medium (8.6-10.5 mm) Long (10.6-12.5 mm) Very long (more than 12.5 mm)	3 9 9 0 0	14.3 42.85 42.85 0.0 0.0
<b>40.</b>	<b>Grain: Width</b>	Very narrow (<2mm) Narrow (2.1-2.5 mm) Medium (2.6-3.0 mm) Broad (3.1-3.5 mm) Very broad (more than 3.5 mm)	0 10 8 3 0	0.0 47.62 38.09 14.29 0.0
<b>41.</b>	<b>Decorticated grain: Length</b>	Short Medium Long Long* (Long for Basmati type) Extra long	11 10 0 0 0	52.38 47.62 0.0 0.0 0.0
<b>42.</b>	<b>Decorticated grain: Width</b>	Narrow (2.5 mm) Medium (2.0-2.5 mm) Broad (more than 2.5 mm)	5 13 3	23.8 61.9 14.3
<b>43.</b>	<b>Endosperm: Presence of amylose</b>	Absent Present	0 21	0.0 100
<b>44.</b>	<b>Endosperm: Content of amylose</b>	Very low (less than 10%) Low (10-19%) amylose Medium (20-25%) High (26-30%) Very high (more than 30%)	0 0 5 4 12	0.0 0.0 23.8 19.05 57.15
<b>45.</b>	<b>Gelatinization temperature through alkali spreading value</b>	Low Medium High medium High	4 12 5 0	19.05 57.15 23.8 0.0

#### **4.1.29 Panicle: colour of awns**

The findings of accessions of rice reflected that out of 52 accessions, 6 accessions had yellowish brown awn, 5 had yellowish white awn, 3 had reddish brown awns while only 2 accessions had red awn. (Fig 4.29).

#### **4.1.30 Panicle: length of longest awn**

Results reflected that out of 52 accessions, 10 had medium while only 6 had short awns. (Fig 4.30).

#### **4.1.31 Panicle: distribution of awns**

The analysis of accessions of rice showed that out of 52 accessions, 9 accessions had awns up to upper half only while 7 accessions had awn in their whole length. (Fig 4.31).

#### **4.1.32 Panicle: presence of secondary branching**

Out of 52 accessions, all of them had secondary branching. (Fig 4.32).

#### **4.1.33 Panicle: secondary branching**

The analysis of accessions of rice showed that out of 52 accessions, 40 accessions had weak secondary branching, 10 had strong while only 2 had clustered secondary branching. (Fig 4.33)

#### **4.1.34 Panicle: attitude of branches**

The results reflect that out of 52 accessions, 21 accessions were semi erect, 19 accessions were semi erect to spreading while 12 accessions were of erect to semi erect type. (Fig 4.34)

#### **4.1.35 Panicle: exertion**

The results showed that out of 52 accessions, 33 accessions were mostly exerted, 17 were well exerted while 2 were partly exerted. (Fig 4.35)

#### **4.1.36 Time of maturity**

The analysis of accessions of rice showed that out of 52 accessions, 27 were late, 24 were medium while only 1 had very late maturity. (Fig 4.36).

#### **4.1.37 Leaf: senescence**

Out of a total of 52 accessions, 33 were early, 14 were medium and 5 were late in terms of senescence of leaf. (Fig 4.37).

#### **4.1.38 Grain: weight of 100 fully developed grains**

The results reflected that out of 52 accessions, 35 accessions had very low, 11 had

low, 2 had medium, and 1 had high while 3 had very high 100 grain weight. (Fig 4.38).

#### **4.1B Quality characterization**

Characterization for quality traits were performed on 21 accessions including 6 checks. Distribution of frequency as well as percentage value of quality traits are shown in table 4.1.

##### **4.1.39 Paddy: length**

The results reflects that out of 21 accessions, 9 had medium, 9 had short while 3 had very short grain length. (Fig 4.39).

##### **4.1.40 Paddy: width**

The analysis of accessions of rice showed that out of 21 accessions, 10 accessions had narrow grain width, 8 had medium while 3 had broad grain width. (Fig 4.40).

##### **4.1.41 Brown rice: length**

The analysis of accessions of rice showed that out of 21 accessions, 11 accessions had short while 10 accessions had medium decorticated grain length. (Fig 4.41).

##### **4.1.42 Brown rice: width**

The findings of accessions of rice showed that out of 21 accessions, 13 had medium, 5 had narrow while 3 had broad decorticated grain width. (Fig 4.42).

##### **4.1.43 Endosperm: presence of amylose**

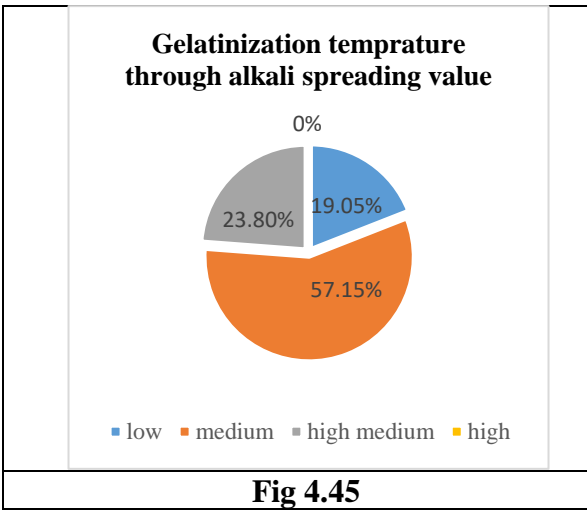
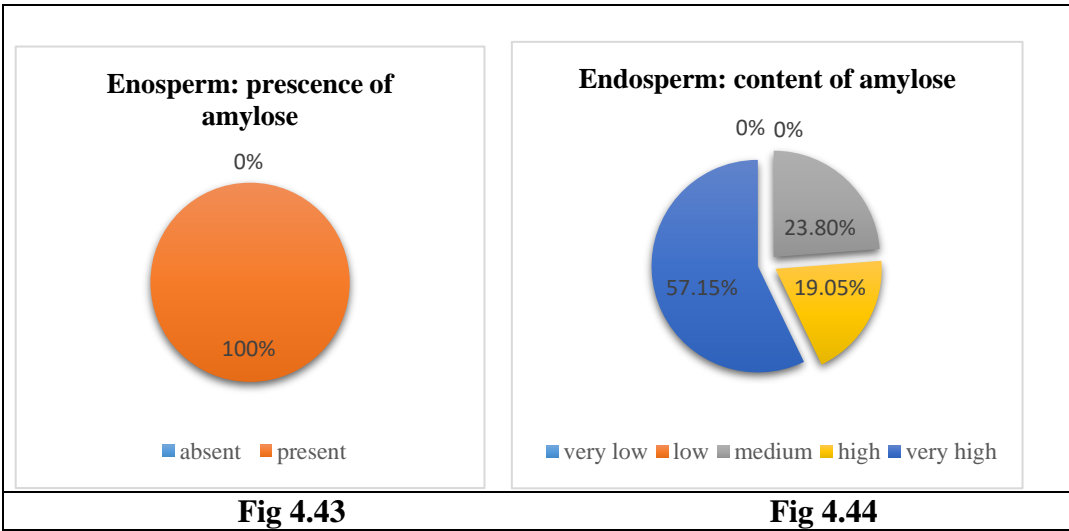
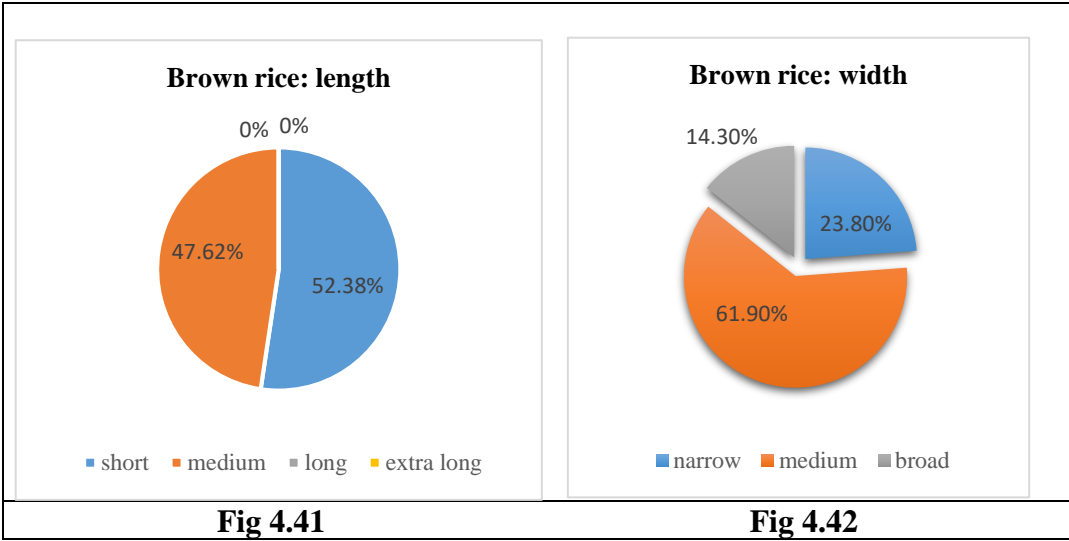
All 21 accessions exhibited presence of amylose. (Fig 4.43).

##### **4.1.44 Endosperm: content of amylose**

Out of 21 accessions, 12 accessions had very high, 4 showed high while 5 accessions showed medium content of amylose. (Fig 4.44).

##### **4.1.45 Gelatinization temperature through alkali spreading value**

The results reflect that out of 21 accessions, 12 accessions had medium, 5 had high medium while 4 had low gelatinization temperature. (Fig 4.45).



## **4.2 Analysis of variance (ANOVA)**

### **4.2.1 Yield and its contributing traits**

Each and every character were found to be highly significant (1 percent level of significance) in the analysis of variance, including days to 50% flowering, plant height, effective tillers plant<sup>-1</sup>, panicle length, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, 100 grain weight, biological yield plant<sup>-1</sup>, harvest index, and grain yield plant<sup>-1</sup>. This substantial diversity could be attributed to the diverse rice accessions employed in this investigation.

Similar results were observed by Babu *et al.* (2012), Sreedhar (2017), Hemlatha *et al.* (2018) and Nanda *et al.* (2021) for the characters days to 50 per cent flowering, plant height, panicle length, number of filled grains panicle<sup>-1</sup> & grain yield plant<sup>-1</sup>

Fiyaz *et al.* (2011) reported same findings for the traits days to 50% flowering, plant height, panicle length, harvest index & yield plant<sup>-1</sup>.

Similar observations were obtained by Tiwari *et al.* (2019) for the traits plant height, thousand grain weight & grain yield.

**Table 4.2 ANOVA for 10 yield & yield contributing characters**

<b>Source of variation</b>	<b>Df</b>	<b>Days to 50 percent flowering</b>	<b>Plant height (cm)</b>	<b>Effective tillers per plant</b>	<b>Panicle length (cm)</b>	<b>Number of filled grains per panicle</b>	<b>Number of unfilled grains per panicle</b>	<b>100 seed wt. (g)</b>	<b>Biological yield per plant (g)</b>	<b>Harvesting index (%)</b>	<b>Grain yield per plant (g)</b>
<b>Replication</b>	<b>1</b>	49.846	10.959	0.087	1.572	153.843	47.088	0.001	22.283	1.895	2.527
<b>Treatment</b>	<b>51</b>	313.354**	1592.208**	8.86**	35.59**	2694.929**	96.857**	0.878**	325.079**	97.023**	84.182**
<b>Error</b>	<b>51</b>	3.376	11.099	0.871	1.332	77.286	10.958	0.001	6.114	1.927	0.373

Note: - \*\* significant at 1 percent level of probability

\* Significant at 5 percent level of probability

#### 4.2.2 Quality traits

The results of the analysis of variance for quality traits revealed that all of the characters were highly significant at 1 percent level of significance including hulling percent, milling percent, paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice width, brown rice L/B, kernel length, kernel width, kernel L/B ratio, elongation value, alkali spreading value, gel consistency, amylose content and head rice recovery . Table 4.3 displays the results. The presence of enough amount of variation among the genotypes for the characters under investigation was reflected by the high and significant values for mean sum of square of different quality characters used in the current investigation, which could be due to the diverse rice germplasm accessions used under study.

For considering the rice to be of best quality, the gel consistency should be medium (41-60 mm), amylose content should be around 20-25%, alkali spreading value must be 4-5 (medium) while elongation value should always be on higher side (1.70 minimum) where the increase in the height after cooking should be greater in proportion to increase in the width.

The above findings is an accordance with the observations of Babu *et al.* (2012) for the traits like head rice recovery, kernel length, kernel breath, alkali spreading value, amylose content, gel consistency while Hemlatha *et al.* (2018) recorded similar findings for the traits hulling %, milling %, kernel length, kernel breadth, gel consistency, amylose content and head rice recovery .

Similar observations were obtained by Chowdhury *et al.* (2016) for the traits hulling %, milling %, gel consistency, elongation ratio, alkali spreading value, amylose content, head rice recovery while by Shahidullah *et al.* (2009) for the traits *viz.*, kernel length, milling %, amylose content , elongation ratio, paddy breadth and paddy length .



**Table 4.3 ANOVA for 16 quality characters**

Source of variation	DF	Hulling %	Milling %	Paddy length	Paddy breadth	Paddy L/B ratio	Brown rice length	Brown rice width	Brown rice L/B ratio
<b>Replication</b>	<b>1</b>	0.010689	0.016403	0.00381	0.000952	0.002752	0.002143	0.002143	0.00161
<b>Treatment</b>	<b>20</b>	48.222517**	52.88522**	4.107238**	0.343167**	0.865012**	2.541643**	0.183452**	0.619332**
<b>Error</b>	<b>20</b>	0.002483	0.003927	0.03381	0.004452	0.007562	0.005643	0.183452	0.00682

Source of variation	DF	Kernel length	Kernel width	Kernel L/B ratio	Elongation ratio	Alkali spreading value	GC	Amylose content	HRR
<b>Replication</b>	<b>1</b>	0.00	0.002143	0.007467	0.000467	0.095238	0.619287	0.029867	0.243809
<b>Treatment</b>	<b>20</b>	1.47631**	0.206738**	0.255272**	0.491936**	2.27381**	89.28095**	65.85654**	37.00395**
<b>Error</b>	<b>20</b>	0.0115	0.001643	0.004427	0.001372	0.045238	0.294286	0.250912	0.38781

### **4.3 Assessment of Genetic Parameters**

#### **4.3.1 Description of means & variability parameters for various yield and its contributing traits**

Mean performance of 52 rice accessions along with 6 checks are given in table 4.4 & 4.5.

##### **4.3.1.1 Days to 50 percent flowering**

The average days to 50% flowering was 100.596 days, with values ranging from 74.5 days to 132.5 days. The maximum days to 50% flowering was exhibited by the accession IC0449908 (132.5 days) and minimum was exhibited by the accession IC0578975 (74.5 days).

##### **4.3.1.2 Plant height**

Plant height varied from 73.08 cm to 174.95 cm with a mean of 128.722 cm. Maximum plant height was recorded in accession IC0449608 (174.95cm) and minimum in accession IC0565343 (73.08 cm).

##### **4.3.1.3 Effective tillers per plant**

Effective tillers plant<sup>-1</sup> extended from 4.5 to 13 with an average value of 7.375. Maximum effective tillers plant<sup>-1</sup> was observed in accession IC0565346 (13) while minimum in accessions IC0301123, IC0377173, EC0497077 (4.5).

##### **4.3.1.4 Panicle length**

The average panicle length was 26.971 cm, with values ranging from 16.65 cm to 37.55 cm. The highest panicle length was obtained for the accession IC0449608 (37.55 cm) while lowest was observed in the case of accession IC0449908 (16.65 cm).

##### **4.3.1.5 Number of filled grains per panicle**

Number of filled grains panicle<sup>-1</sup> showed variation from 102.5 to 260.5 with an average value of 163.558. The maximum was obtained for accession IC0459649 (260.5) while minimum was recorded in accession IC0449608 (102.5).

##### **4.3.1.6 Number of unfilled grains per panicle**

The average number of unfilled grains per panicle was 23.583, with values ranging 7.165 to 38. The maximum was obtained for the accession Acc 2992 (38) while minimum was observed for the accession IC0375799 (7.165).

#### **4.3.1.7 100 seed weight**

Hundred seed weight extended from 0.475 g to 3.195 g with an average of 1.305 g. The maximum hundred seed weight was observed in check Indira aerobic (3.195 g) while minimum was recorded in accession Acc 2986 (0.475 g).

#### **4.3.1.8 Biological yield**

Biological yield varied from 32.83 g to 84.08 g with a mean value of 50.218 g. The maximum biological yield was observed in check Indira aerobic (84.08 g) and the minimum was recorded in accession Acc 2971 (32.83 g).

#### **4.3.1.9 Harvest index**

Harvest index extended from 12.3% to 39.8% with a mean value of 25.772%. The maximum harvest index was observed in accession IC0300191 (39.85) while minimum value was recorded in IC0299989 (12.3%).

#### **4.3.1.10 Grain yield per plant**

Grain yield per plant showed variation from 5.7 g to 31.695 g with a mean value of 13.682 g. The maximum grain yield per plant was observed for the check Indira aerobic (31.696 g) while minimum value was recorded for the accession Acc 2971 (5.7 g).

### **4.3.2 Description of means and variability parameters for different quality traits.**

#### **4.3.2.1 Hulling %**

Hulling percentages ranged from 60.80 percent to 80.89 percent, with an average of 73.64 percent. The highest hulling percent was found in accession Acc 2971 (80.89%), while the lowest hulling percent was found in accession IC0449608 (60.80 percent).

#### **4.3.2.2 Milling %**

Milling % ranged from 52.50% to 72.60% with an average value of 65.39%. The maximum milling % was attained for the accession Acc 2971 (72.60%) and minimum was observed for the accession IC0459649 (52.50%).

#### **4.3.2.3 Paddy length**

The average paddy length was 7.78 mm, with values ranging from 5.35 mm to 10.00 mm. The maximum paddy length was recorded for the check maheshwari (10.00 mm) while minimum was recorded for the accession Acc 2991(5.35 mm).

#### **4.3.2.4 Paddy breadth**

Paddy breadth extended from 2.00 mm to 3.25 mm with an average of 2.53 mm. The maximum paddy breadth was observed for the accession IC0463875 (3.25 mm) and minimum was observed for the accession IC045964 (2.00 mm).

#### **4.3.2.5 Paddy L/B ratio**

The average paddy L/B ratio found out to be 3.12, with values ranging from 1.95 to 4.15. The maximum paddy L/B ratio was obtained for check Chhattisgarh devbhog (4.15) and minimum was recorded for the accession IC0463875 and Acc 2991 (1.95).

#### **4.3.2.6 Brown rice length**

Brown rice length extended from 4.05 mm to 7.30 mm with a mean value of 5.71 mm. The maximum brown rice length was exhibited by the check maheshwari (7.30 mm) and minimum was recorded for the accession Acc 2991 (4.05 mm).

#### **4.3.2.7 Brown rice width**

Brown rice width extended from 1.75 mm to 2.85 mm with a mean value of 2.19 mm. The maximum brown rice width was obtained for the accession IC0463875 (2.85 mm) while minimum was observed for the accession IC0300822 (1.75 mm).

#### **4.3.2.8 Brown rice L/B ratio**

The mean value for brown rice L/B ratio was 2.64 mm, with values ranging from 1.59 mm to 3.48 mm. The maximum brown rice L/B ratio was exhibited by the check IR 64 (3.48 mm) while minimum was observed for the accession IC0463875 (1.59 mm).

#### **4.3.2.9 Kernel length**

Kernel length reflected a variation from 3.45 mm to 6.15 mm with a mean of 4.51 mm. The maximum kernel length was observed for the check maheshwari (6.15 mm) while minimum was observed for the accession IC0459649 and Acc 2992 (3.45 mm).

#### **4.3.2.10 Kernel width**

Kernel width extended from 1.60 mm to 2.65 mm with an average of 2.07 mm. The maximum kernel width was obtained for the accession IC0463875 (2.65 mm) while minimum was observed for the accession IC0449608 (1.60 mm).

#### **4.3.2.11 Kernel L/B ratio**

The average kernel L/B ratio was 2.20 mm, with values ranging from 1.45 mm to

3.00 mm. The maximum kernel L/B ratio was exhibited by the check Chhattisgarh devbhog (3.00 mm) while minimum was observed for the accession IC0463875 (1.45 mm).

#### **4.3.2.12 Elongation ratio**

The average elongation ratio was 2.50, with values ranging from 1.74 to 3.67. The check Chhattisgarh devbhog (3.67) had the greatest elongation value, while the accession IC0463875 had the lowest (1.74).

#### **4.3.2.13 Alkali spreading value**

Alkali spreading value extended from 3.00 to 6.00 with an average of 4.48. The highest alkali spreading value was obtained for the accessions IC0463073, IC0300822, Acc 2971, Acc 2992, (6.00) while minimum was observed for the accessions IC0459649, IC0301123, IC0565346, IC0375799 and Acc 3367 (3.00).

#### **4.3.2.14 Gel consistency**

The average gel consistency was 51.99, with values ranging from 36.50 to 67.25. The maximum gel consistency was observed for the check Chhattisgarh devbhog (67.25) while minimum gel consistency was observed for the accession IC0459649 (36.50).

#### **4.3.2.15 Amylose content**

Amylose content extended from 21.50 to 39.90 with a mean value of 31.41. The maximum amylose content was obtained for the accession Acc 2971 (39.90) while minimum was observed for the accession IC0459649 (21.50).

#### **4.3.2.16 Head rice recovery**

Head rice recovery extended from 49.50 to 67.55 with a mean value of 56.90. The maximum head rice recovery was observed for the check Chhattisgarh devbhog (67.55) while minimum was observed for the accession IC0459649 (49.50).

In the present study, genotypes exhibited average alkali spreading value (4-5), intermediate amylose content (20-25), intermediate gel consistency (41-60 mm) coupled with the high head rice recovery % namely IC0577803, IC0300822, IC0301123, IC0565343, IC0565344, IC0449608 and Acc 2991.

The above identified germplasm accessions were used as donors for development of superior grain quality variances in rice improvement programme.

### 4.3.3 Genotypic and phenotypic coefficient of variation

The presence of variation within a population is required for crop enhancement programmes. Any breeding material with genetic variability provides a basis for selection as well as crucial information for the selection of parents with diversity for use in future programmes for hybridization. The coefficient of variation is a measure of how variable distinct traits are.

In present investigation, calculated values of GCV and PCV are shown in the table 4.4 for yield & its contributing characters & in table 4.5 for quality traits. Analysis reflected that PCV was higher than GCV for all the quantitative traits included in the investigation. From the above results, it can be inferred the variation that are observed are due to both genotype as well as environmental influence.

Classification of PCV and GCV was suggested by Sivasubramanian and Madhavamenon (1973) as low (< 10%), moderate (10-20%) and high (> 20 %).

Based on the genetic analysis, among 10 yield contributing traits highest amount of PCV as well as GCV got for hundred seed weight (50.766 and 50.731) followed by grain yield (47.524 and 47.314), number of unfilled grains per panicle (31.134 and 27.790), effective tillers per plant (29.909 and 27.101), harvest index (27.292 and 26.756), biological yield (25.625 and 25.148), number of filled grains panicle<sup>-1</sup> (22.763 and 22.119) and plant height (21.996 and 21.843).

Moderate amount of PCV and GCV was recorded for panicle length (15.931 and 15.345) and days to 50% flowering (12.510 and 12.376). None of the traits had low PCV as well as GCV.

Among 16 quality traits, highest magnitude of PCV and GCV was noted for alkali spreading value (27.062 and 23.221) followed by paddy L/B ratio (22.180 and 20.044).

Moderate amount of PCV and GCV was obtained for elongation value (19.995 and 18.718), brown rice length (19.837 and 18.616), kernel length (19.707 and 18.418), paddy length (19.476 and 17.674), amylose content (18.835 and 17.612), kernel L/B ratio (17.592 and 15.306), paddy breadth (16.815 and 14.762), kernel width (16.007 and 14.692), brown rice width (14.367 and 12.072) and gel consistency (13.325 and 12.465).

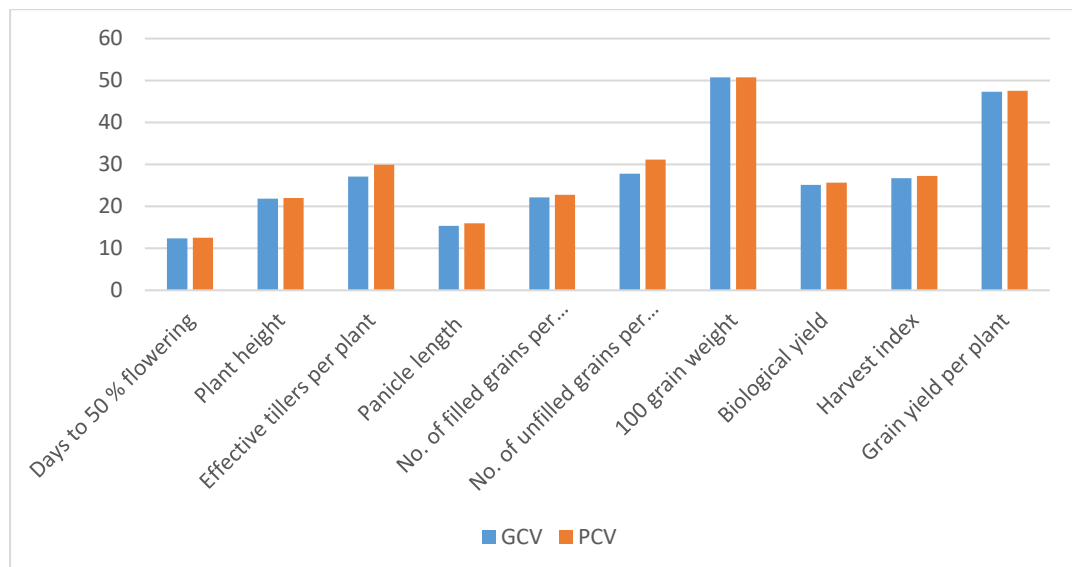
Low amount of PCV and GCV was obtained for milling % (8.090 and 7.661),

head rice recovery (7.859 and 7.029) and hulling % (6.724 and 6.369).

The high magnitude of GCV for grain yield was in accordance with Tuhina-Khatun *et al.* (2015) while presence of high PCV as well as GCV for the trait number of filled grains panicle<sup>-1</sup> and low magnitude of PCV and GCV for milling % and head rice recovery has similarity with the observations of Babu *et al.* (2012).

Moderate magnitude of PCV as well as GCV for amylose content and low amount of PCV and GCV for hulling percent, milling percent, & head rice recovery is in accordance with the results of Chowdhury *et al.* (2016).

Findings of Loitongbam *et al.* (2020) have similarity with the present investigation for the traits i.e. effective tillers plant<sup>-1</sup>, number of filled grains per panicle and number of unfilled grains per panicle<sup>-1</sup>.



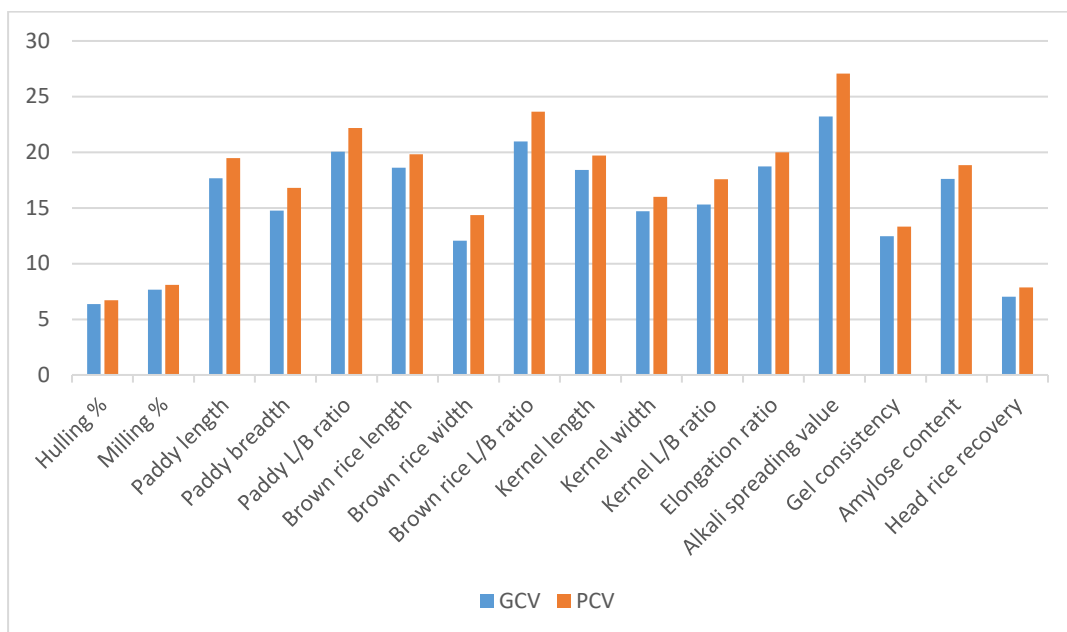
**Fig 4.46 Graphical comparison of GCV % PCV for 10 yield & yield contributing traits.**

**Table 4.4 Estimates of genetic variability of grain yield & its contributing characters**

S.no	Traits	Mean	Range		GCV (%)	PCV (%)	h <sup>2</sup> bs (%)	GA	GA as % of mean
			Min	Max					
1	<b>Days to 50 percent flowering</b>	100.596	74.5	132.5	12.376	12.51	97.868	25.371	25.221
2	<b>Plant height (cm)</b>	128.722	73.08	174.95	21.843	21.996	98.616	57.518	44.684
3	<b>Effective tillers per plant</b>	7.375	4.5	13	27.101	29.909	82.102	3.731	50.585
4	<b>Panicle length (cm)</b>	26.971	16.65	37.55	15.345	15.931	92.783	8.212	30.449
5	<b>Number of filled grains per panicle</b>	163.558	102.5	260.5	22.119	22.763	94.424	72.418	44.277
6	<b>Number of unfilled grains per panicle</b>	23.583	7.165	38	27.79	31.134	79.672	12.05	51.098
7	<b>100 seed weight (g)</b>	1.305	0.475	3.195	50.731	50.766	99.261	1.363	104.434
8	<b>Biological yield per plant (g)</b>	50.218	32.83	84.08	25.148	25.625	96.308	25.53	50.839
9	<b>Harvest index (%)</b>	25.772	12.3	39.8	26.756	27.292	96.105	13.925	54.032
10	<b>Grain yield per plant (g)</b>	13.682	5.7	31.695	47.314	47.524	99.017	13.276	97.035

**Table 4.5 Estimates of genetic variability of quality characters**

S.no	Traits	Mean	Range		GCV (%)	PCV (%)	h <sup>2</sup> <sub>bs</sub> (%)	GA	GA as percent of mean
			Min	Max					
1	Hulling %	73.64	60.80	80.89	6.369	6.724	89.7	12.962	17.601
2	Milling %	65.39	52.50	72.60	7.661	8.090	89.6	13.574	20.76
3	Paddy length	7.78	5.35	10.00	17.674	19.476	82.7	3.736	48.024
4	Paddy breadth	2.53	2.00	3.25	14.762	16.815	77	1.072	42.333
5	Paddy L/B ratio	3.12	1.95	4.15	20.044	22.180	81.6	1.713	54.955
6	Brown rice length	5.71	4.05	7.30	18.616	19.837	88	2.966	51.973
7	Brown rice width	2.19	1.75	2.85	12.072	14.367	70.6	0.769	35.174
8	Brown rice L/B ratio	2.64	1.59	3.48	20.963	23.652	78.5	1.445	54.833
9	Kernel length	4.51	3.45	6.15	18.418	19.707	87.3	2.241	49.712
10	Kernel width	2.07	1.60	2.65	14.692	16.007	84.2	0.838	40.536
11	Kernel L/B ratio	2.20	1.45	3.00	15.306	17.592	75.7	0.918	41.731
12	Elongation ratio	2.50	1.74	3.67	18.718	19.995	87.7	1.303	52.243
13	Alkali spreading value	4.48	3.00	6.00	23.221	27.062	73.6	2.731	61.031
14	Gel consistency	51.99	36.50	67.25	12.465	13.325	87.5	17.551	33.761
15	Amylose content	31.41	21.50	39.90	17.612	18.835	87.4	15.062	47.953
16	Head rice recovery	56.90	49.50	67.55	7.029	7.859	80	11.178	19.643



**Fig 4.47 Graphical comparison of GCV & PCV for 16 quality traits.**

#### **4.3.4 Heritability and genetic advance as percent of mean**

Heritability measures how much variation in a phenotypic character in a population is due to genetic variation between individuals in that population . It determines how much of a trait's variation may be attributable to genetic factors rather than environmental factors. It's a useful indicator of how characters change from parents to offspring. Selection parameters such as heritability and genetic advance are crucial. Heritability estimates combined with genetic advance are more beneficial than heritability alone in estimating the gain under selection. Heritability estimates are often divided into three categories: low (less than 50%), medium (50-70%), and high (more than 70%).

Broad sense heritability was estimated and obtained in terms of percentage. Their values are presented in table 4.4 for grain yield & yield contributing characters & in table 4.5 for quality characters. High heritability estimates were obtained for all the yield and its contributing traits under investigation. The maximum heritability was obtained for hundred seed weight (99.261%) followed by grain yield (99.017%), plant height (98.616%), days to 50% flowering (97.868), biological yield (96.308), harvest index (96.105%), number of filled grains panicle<sup>-1</sup> (94.424%), panicle length (92.783%), effective tillers plant<sup>-1</sup> (82.102%) and number of unfilled grains panicle<sup>-1</sup> (79.672%) .

High heritability obtained for all the quality characters used in present experiment. The highest heritability was recorded for hulling % (89.7%) and milling % (89.6%) followed by brown rice length (88%), elongation value (87.7%), gel consistency (87.5%), amylose content (87.4%), kernel length (87.3%), kernel width (84.2%), paddy length (82.7%), paddy L/B ratio (81.6%), head rice recovery (80%), brown rice L/B ratio (78.5%), paddy breadth (77%), kernel L/B ratio (75.7%), alkali spreading value (73.6%) and brown rice width (70.6%).

In case of yield contributing traits, the highest value for genetic advance as a percent of mean was obtained for 100 seed weight (104.434) followed by grain yield (97.035), harvest index (54.032), number of unfilled grains per panicle (51.098), biological yield (50.839), effective tillers plant<sup>-1</sup> (50.585), plant height (44.684), number of filled grains panicle<sup>-1</sup> (44.277) & panicle length (30.449).

Moderate magnitude for genetic advance as a percent of mean was obtained for days to 50 percent flowering (25.221).

For quality traits, the highest value for genetic advance as a percent of mean was recorded for alkali spreading value (61.031) followed by paddy L/B ratio (54.955), brown rice L/B (54.833), elongation value (52.243), brown rice length (51.973), kernel length (49.712), paddy length (48.024), amylose content (47.953), paddy breadth (42.333), kernel L/B ratio (41.731), kernel width (40.536), brown rice width (35.174) and gel consistency (33.761)'.

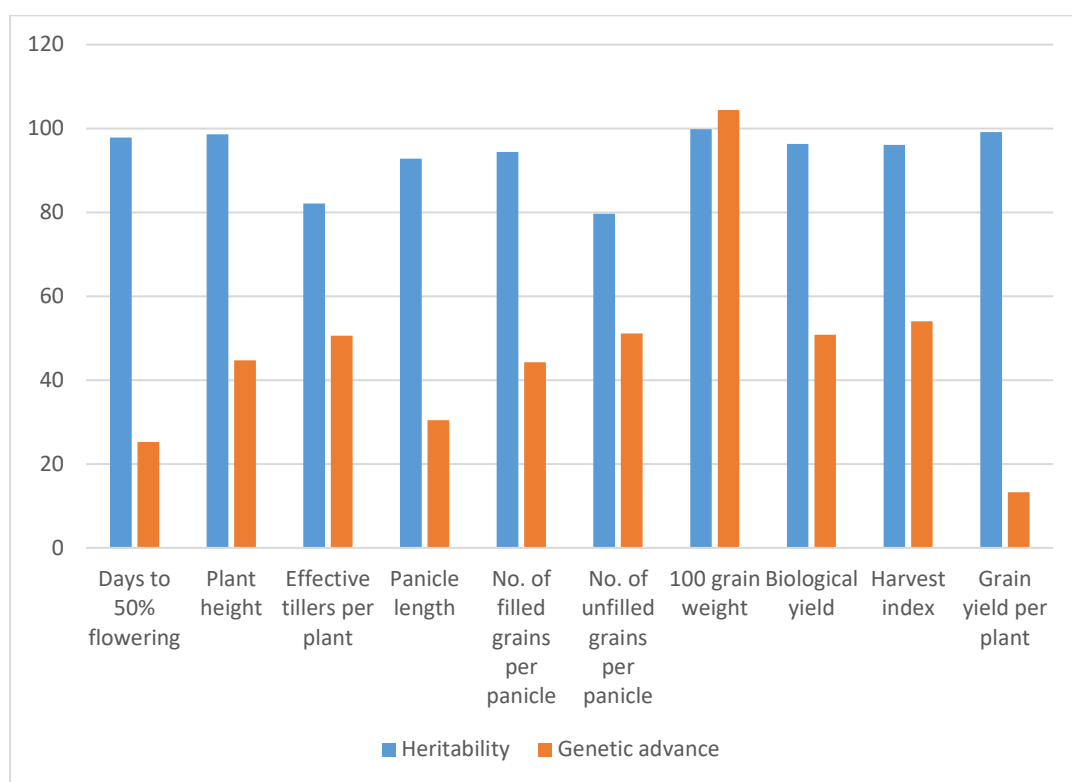
Moderate magnitude for genetic advance as a percent of mean was obtained for milling % (20.76), head rice recovery (19.643) and hulling % (17.601).

High heritability as well as high genetic advance as a percent of mean was recorded for yield & quality characters *viz.*, days to 50% flowering, plant height, effective tillers per plant, panicle length, number of filled grains per panicle, number of unfilled grains panicle<sup>-1</sup>, hundred seed weight, biological yield plant<sup>-1</sup>, harvest index, grain yield plant<sup>-1</sup>, milling %, paddy length, paddy breadth, paddy L/B ratio, brown rice length, brown rice width, brown rice L/B, kernel length, kernel width, kernel L/B ratio, elongation value, alkali spreading value, gel consistency, amylose content and head rice recovery (Fig 4.47 and 4.48) shows that the selection for these traits may be beneficial as heritability is mainly due to additive gene action.

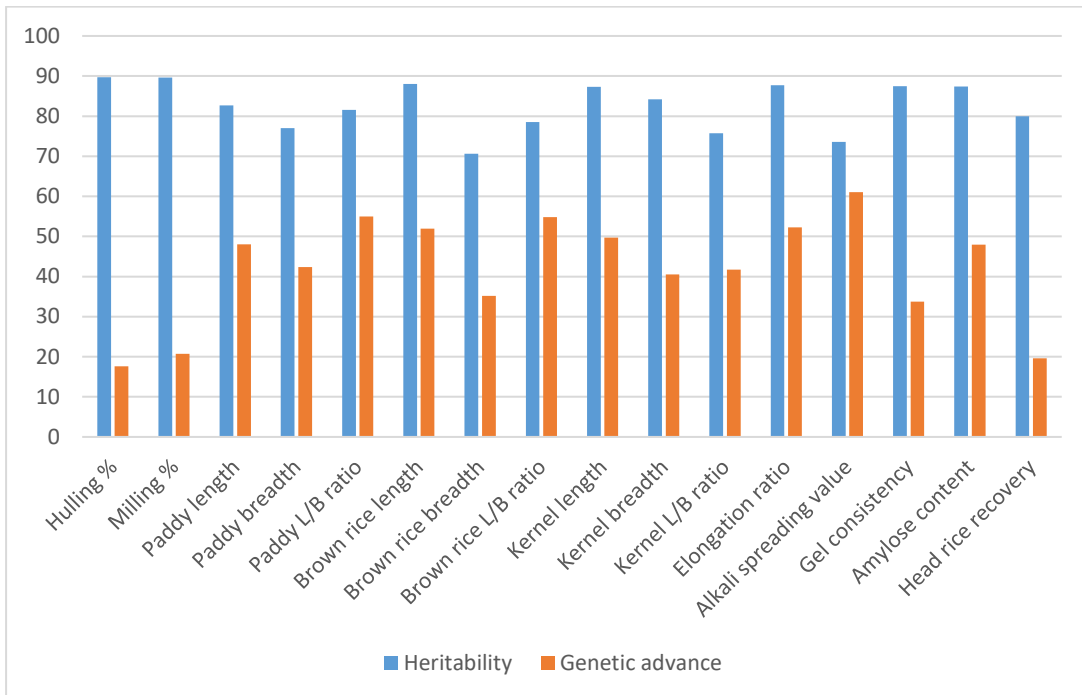
The above findings of present study similar to earlier workers *viz.*, Babu *et al.*

(2012) reported for trait number of filled grains panicle<sup>-1</sup> while with Rashmi *et al.* (2017) for the characters i.e. days to 50% flowering, plant height, panicle length and number of filled grains panicle<sup>-1</sup>. Saidon *et al.* (2020) reported similar findings for paddy length.

Loitongbam *et al.* (2020) reported findings in agreement with the present investigation for the characters *viz.*, days to 50% flowering, effective tillers plant<sup>-1</sup>, plant height, panicle length, number of filled grains panicle<sup>-1</sup> and number of unfilled grains panicle<sup>-1</sup> while Ghosh and. Sharma (2012) observed similar results for the traits like thousand seed weight, grain yield plant<sup>-1</sup> and head rice recovery (%) .



**Fig 4.48 Graphical comparison of heritability and genetic advance for 10 yield and yield contributing traits**



**Fig 4.49 Graphical comparison of heritability and genetic advance for 16 quality traits**

#### **4.4 Association analysis**

##### **4.4.1 Correlation analysis**

Correlation analysis can be used to investigate the strength of the selected trait's relationship with yield and other traits. While planning and evaluating breeding programmes, it is critical to estimate genotypic and phenotypic correlation among characters. When two attributes have a positive association, one benefits indirectly from the improvement of the other.

Correlation coefficient analysis is critical for evaluating the mutual relationship between characters as well as finding component characters for genetic improvement. These have been dealt in every combination possible for crucial traits at genotypic as well as phenotypic level and are shown in table 4.6 (for yield & its contributing traits) and in table 4.7 (for quality traits).

##### **4.4.1.1 Yield and its contributing traits**

###### **4.4.1.1.1 Days to 50% flowering**

Days to 50 percent flowering exhibited positive & significant correlation both at level of phenotype as well as genotype for the traits *viz.*, plant height (0.493), panicle

length (0.209), number of filled grains per panicle (0.556) and number of unfilled grains per panicle (0.237) while negative and highly significant correlation noted for effective tiller per plant (-0.547).

#### **4.4.1.1.2 Plant height**

Plant height exhibited positive and significant association with panicle length (0.751) and number of filled grains per panicles (0.437) while it exhibited negative as well as highly significant correlation with effective tillers per plant<sup>-1</sup> (-0.541).

#### **4.4.1.1.3 Effective tillers per plant**

It had negative and highly significant correlation with panicle length (-0.397), number of filled grains panicles<sup>-1</sup> (-0.610) and number of unfilled grains panicles<sup>-1</sup> (-0.445).

#### **4.4.1.1.4 Panicle length**

Panicle length did not show significant correlation with any of the traits.

#### **4.4.1.1.5 Number of filled grains per panicles**

Number of filled grains per panicles reflected a positive & significant correlation with number of unfilled grains panicles<sup>-1</sup> (0.599) while it exhibited a negative and significant correlation with hundred seed weight (-0.217) as well as harvest index (-0.222).

#### **4.4.1.1.6 Number of unfilled grains per panicles**

Number of unfilled grains panicles<sup>-1</sup> did not exhibit significant correlation with any of the traits.

#### **4.4.1.1.7 100 seed weight**

Hundred seed weight showed a positive as well as significant correlation with biological yield (0.850), harvest index (0.842) and grain yield per plant (0.943).

#### **4.4.1.1.8 Biological yield**

It exhibited a positive as well as significant correlation with harvest index (0.660) and grain yield plant<sup>-1</sup> (0.905).

#### **4.4.1.1.9 Harvest index**

Harvest index exhibited a positive & significant correlation with grain yield plant<sup>-1</sup>. (0.872).

Traits like hundred seed weight (0.943), biological yield (0.905) & harvest index (0.872) showed a positive and significant correlation with grain yield plant<sup>-1</sup>.

Positive & significant correlation of grain yield plant<sup>-1</sup> with harvest index is in accordance with the observations of Madhavilatha *et al.* (2005); Chakraborty *et al.* (2010); Ambili and Radhakrishnan (2011) and Vanisree *et al.* (2013).

Positive & significant correlation of grain yield plant<sup>-1</sup> with biological yield plant<sup>-1</sup> is in accordance with the findings of Verma and Shrivastava (2004).

Positive as well as significant correlation of grain yield plant<sup>-1</sup> with 100 grain weight is in agreement with the results of Verma and Shrivastava (2004); Madhavilatha *et al.* (2005); Muthuswamy and Anandakumar (2006) and Rashid *et al.* (2014).

**Table 4.6 Genotypic and phenotypic correlation coefficient among grain yield and yield contributing traits**

Character		2	3	4	5	6	7	8	9	10
1	G	0.493**	-0.547**	0.209*	0.556**	0.237*	-0.054	-0.183	-0.017	-0.103
	P	0.481**	-0.495**	0.198*	0.534**	0.218*	-0.052	-0.178	-0.010	-0.098
2	G		-0.541**	0.751**	0.437**	0.134	-0.080	-0.179	-0.072	-0.145
	P		-0.500**	0.732**	0.428**	0.120	-0.080	-0.178	-0.077	0.147
3	G			-0.397**	-0.610**	-0.445**	-0.192	0.013	-0.042	-0.041
	P			-0.366**	-0.584**	-0.368**	-0.176	0.013	-0.015	-0.025
4	G				0.158	0.061	0.013	-0.068	0.002	-0.049
	P				0.160	0.059	0.013	-0.067	0.004	-0.047
5	G					0.599**	-0.217*	-0.176	-0.222*	-0.150
	P					0.554**	-0.208*	-0.168	-0.213*	-0.147
6	G						0.037	0.163	-0.026	0.136
	P						0.036	0.126	0.000	0.125
7	G							0.850**	0.842**	0.943**
	P							0.834**	0.827**	0.939**
8	G								0.660**	0.905**
	P								0.616**	0.891**
9	G									0.872**
	P									0.861**
10	G									
	P									

Here, 1= Days to 50 percent flowering, 2= Plant height, 3= Effective tillers per plant, 4= Panicle length, 5= No. of filled grains per panicle, 6= No. of unfilled grains per panicle, 7= Hundred Seed weight, 8= Biological yield, 9= Harvest index, 10= Grain yield/ plant . (\* = at 5 percent level of significance, \*\* = at 1percent level of significance)

#### **4.4.1.2 Quality traits**

##### **4.4.1.2.1 Hulling %**

Hulling % exhibited positive and significant correlation reported with milling % & gel consistency both at genotypic as well as phenotypic level and with amylose content at only phenotypic level.

##### **4.4.1.2.2 Milling %**

Milling % reflected positive & significant correlation with panicle length (0.442), panicle width (0.373), kernel length (0.329), gel consistency (0.644), amylose content (0.534), and head rice recovery (0.462) at the level of both phenotype and genotype while with brown rice length (0.302) at phenotypic level only.

##### **4.4.1.2.3 Paddy length**

Paddy length had a positive and significant correlation with paddy L/B ratio (0.686), brown rice length (0.912), brown rice L/B ratio (0.782), kernel Length (0.780), kernel L/B ratio (0.590), elongation Ratio (0.519) and gel consistency (0.583).

##### **4.4.1.2.4 Paddy breadth**

Paddy breadth exhibited positive and significant correlation with brown rice width (0.863), kernel width (0.833) while a negative and significant correlation with paddy L/B ratio (-0.551), kernel L/B ratio (-0.556), elongation Ratio (-0.399) at both genotypic as well as phenotypic level while with brown rice L/B ratio (-0.403) at genotypic level only.

##### **4.4.1.2.5 Paddy L/B ratio**

Paddy L/B ratio exhibited positive and significant correlation with brown rice length (0.705), brown rice L/B ratio (0.962), kernel length (0.547), kernel L/B ratio (0.898), elongation Ratio (0.741) and gel consistency (0.460) while it had a negative & significant correlation with brown rice (-0.550) width and kernel width (-0.367).

##### **4.4.1.2.6 Brown rice length**

Brown rice length had a positive & significant correlation with brown rice width (0.828), kernel length (0.863), kernel width (0.320), kernel L/B ratio (0.620), elongation ratio (0.588) and gel consistency (0.552).

##### **4.4.1.2.7 Brown rice width**

Brown rice width had a positive and significant correlation with kernel width (0.921) while it had a negative and significant correlation with brown rice L/B

(-0.444), kernel L/B ratio (-0.568) and elongation ratio (-0.434).

#### **4.4.1.2.8 Brown rice L/B ratio**

Brown rice L/B ratio had positive and significant correlation with kernel length (0.669), kernel L/B ratio (0.875), elongation ratio (0.795) and gel consistency (0.529).

#### **4.4.1.2.9 Kernel length**

Kernel Length exhibited positive & significant correlation with kernel width (0.470), kernel L/B ratio (0.654), elongation ratio (0.742), and gel consistency (0.704,) while it had a negative & significant correlation with amylose content (-0.477).

#### **4.4.1.2.10 Kernel breadth**

Kernel Width exhibited a negative & significant correlation with kernel L/B ratio (-0.352).

#### **4.4.1.2.11 Kernel L/B ratio**

Kernel L/B had a positive & significant correlation with elongation ratio (0.907) and gel consistency (0.622) at the level of both phenotype as well as genotype while with head rice recovery (0.314) at phenotypic level only. It exhibited a negative and significant correlation with amylose content (-0.465).

#### **4.4.1.2.12 Elongation ratio**

Elongation Ratio exhibited positive as well as significant correlation with gel consistency (0.666), while it showed a negative and significant correlation with amylose content (-0.623).

#### **4.4.1.2.13 Alkali spreading value**

Alkali Spreading Value neither showed positive nor negative and significant correlation with any of the trait.

#### **4.4.1.2.14 Gel consistency**

Gel Consistency showed positive and significant correlation with head rice recovery (0.668).

#### **4.4.1.2.15 Amylose content**

Amylose Content reflected positive and significant correlation with head rice recovery (0.449).

#### **4.4.1.2.16 Head rice recovery**

Head rice recovery reflected positive and significant correlation with milling %

(0.462), gel consistency (0.668), amylose content (0.449) while it showed only positive and significant genotypic correlation with kernel L/B (0.314).

The attributes milling percent, gel consistency, amylose content, and kernel L/B ratio have a positive & significant correlation with head rice recovery percent, which indicates that selecting these traits would be crucial for enhancing head rice recovery.

The above findings of present investigation is similar to earlier workers *viz.*, Abdala *et al.* (2016) Chowdhury *et al.* (2016), Devi *et al.* (2017), Hemlatha *et al.* (2018) reported for the trait milling %.

Positive and significant correlation of hulling % with milling %, paddy length with brown rice length, kernel length and of brown rice length with kernel length in present investigation has similarity with the findings of Adhimoolam *et al.* (2010).

**Table 4.7 Genotypic and Phenotypic correlation coefficient among quality traits**

		2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	G	0.647**	0.101	0.279	-0.178	0.02	0.205	-0.143	0.121	0.163	-0.052	-0.177	-0.128	0.313*	0.327	0.296
	P	0.647**	0.1	0.276	-0.177	0.021	0.2	-0.142	0.12	0.162	-0.051	-0.176	-0.126	0.311*	0.326*	0.293
2	G		0.442**	0.373*	0.055	0.302*	0.201	0.116	0.329*	0.24	0.112	-0.001	0.078	0.644**	0.534**	0.462**
	P		0.438**	0.367*	0.055	0.301	0.196	0.114	0.327*	0.238	0.111	-0.001	0.076	0.642**	0.532**	0.457**
3	G			0.213	0.686**	0.912**	0.052	0.782**	0.780**	0.258	0.590**	0.519**	-0.159	0.583**	-0.046	0.252
	P			0.214	0.681**	0.906**	0.066	0.759**	0.771**	0.255	0.573**	0.511**	-0.154	0.573**	-0.05	0.252
4	G				-0.551**	0.101	0.863**	-0.403**	0.156	0.833**	-0.556**	-0.399**	-0.101	0.064	0.298	-0.024
	P				-0.554**	0.102	0.837**	-0.4	0.155	0.816**	-0.536**	-0.394**	-0.11	0.059	0.29	-0.019
5	G					0.705**	-0.550**	0.962**	0.547**	-0.367*	0.898**	0.741**	-0.029	0.460**	-0.283	0.252
	P					0.699**	-0.529**	0.943**	0.537**	-0.359*	0.871**	0.734**	-0.016	0.455**	-0.28	0.25
6	G						0.118	0.828**	0.863**	0.320*	0.620**	0.588**	-0.228	0.552**	-0.232	0.159
	P						0.122	0.817**	0.854**	0.320*	0.603**	0.585**	-0.223	0.547**	-0.231	0.159
7	G							-0.444**	0.186	0.921**	-0.568**	-0.434**	-0.236	-0.022	0.109	-0.191
	P							-0.455**	0.177	0.900**	-0.560**	-0.423**	-0.216	-0.026	0.104	-0.184
8	G								0.669**	-0.215	0.875**	0.795**	-0.027	0.529**	-0.293	0.277
	P								0.660**	-0.213	0.858**	0.785**	-0.033	0.524**	-0.287	0.273
9	G									0.470**	0.654**	0.742**	-0.039	0.704**	-0.477**	0.108
	P									0.462**	0.654**	0.730**	-0.051	0.696**	-0.473**	0.103
10	G										-0.352*	-0.125	-0.125	0.18	-0.072	-0.19
	P										-0.355*	-0.122	-0.12	0.176	-0.071	-0.181
11	G											0.907**	0.076	0.622**	-0.465**	0.314*
	P											0.884**	0.055	0.613**	-0.452**	0.297
12	G												0.142	0.666**	-0.623**	0.233
	P												0.14	0.663**	-0.617**	0.231
13	G													0.185	-0.035	0.221
	P													0.179	-0.039	0.221
14	G														-0.021	0.668**
	P														-0.015	0.657**
15	G															0.449**
	P															0.439**
16	G															
	P															

1= Hulling percent, 2= Milling percent, 3= Paddy length, 4= Paddy width, 5= Paddy L/B ratio, 6= Brown rice length, 7= Brown rice width, 8= Brown rice L/B ratio, 9= Kernel length, 10= Kernel width, 11= Kernel L/B ratio, 12= Elongation ratio, 13=Alkali spreading value, 14= Gel consistency, 15= Amylose content, 16= Head rice recovery. (\* = at five percent level of significance, \*\* = at one percent level of significance)

#### **4.4.2 Path analysis**

Using a standardised partial regression coefficient, path coefficient analysis divides the total correlation coefficient into direct & indirect effects, in such a manner that the sum of direct effects of independent traits on dependent characters and all possible indirect effects via all other independent traits equals total genotypic or phenotypic correlations. As a result, path analysis is extremely useful as it allows plant breeders to assess the impact of various characters on dependent traits.

In this investigation, grain yield plant<sup>-1</sup> was used as the dependent variable while the remaining 9 traits were used as independent characters. The genotypic correlation coefficient between grain yield plant<sup>-1</sup> & other yield attributing characters were divided into direct and indirect effects and are shown in table 4.8 for yield and its contributing traits. For the quality traits, head rice recovery % was used as the dependent variable while the remaining 15 traits were used as independent characters. The genotypic correlation coefficient between head rice recovery percent and other characters were divided into direct & indirect effects and are shown in table 4.9.

#### **4.4.1 Yield and its contributing traits**

The character days to 50% flowering exerted negligible negative direct effect (-0.019) on grain yield plant<sup>-1</sup>. It also exhibited a low negative indirect effect on grain yield plant<sup>-1</sup> via effective tillers plant<sup>-1</sup> (-0.11448).

Plant height showed negligible negative direct effect (-0.023) on grain yield plant<sup>-1</sup>. It also exhibited a low negative indirect effect on grain yield plant<sup>-1</sup> via effective tillers plant<sup>-1</sup> (-0.11320).

Effective tillers per plant exerted low negative direct effect (-0.11448) on grain yield plant<sup>-1</sup>. Effective tillers per plant also exhibited a moderate positive indirect effect on grain yield per plant via effective tillers per plant (0.20915). It also exhibited a low negative indirect effect on grain yield plant<sup>-1</sup> via 100 seed weight (-0.11203) and number of filled grains panicle<sup>-1</sup> (-0.10823).

**Table 4.8 Direct & indirect effect of 10 grain yield and its contributing traits over 52 germplasm accessions.**

	<b>DF</b>	<b>PH</b>	<b>ET</b>	<b>PL</b>	<b>NFG</b>	<b>NUFG</b>	<b>SW</b>	<b>BY</b>	<b>HI</b>	<b>Correlation With GY</b>
<b>DF</b>	<b>-0.01928</b>	-0.01151	-0.11448	0.00642	0.09866	0.01757	-0.03163	-0.04449	-0.00464	-0.103
<b>PH</b>	-0.00951	<b>-0.02334</b>	-0.1132	0.02312	0.07765	0.00997	-0.04662	-0.04361	-0.01937	-0.145
<b>ET</b>	0.01055	0.01263	<b>0.20915</b>	-0.0122	-0.10823	-0.03299	-0.11203	0.00327	-0.01136	-0.041
<b>PL</b>	-0.00402	-0.01753	-0.08293	<b>0.03077</b>	0.0281	0.00453	0.00763	-0.01654	0.00066	-0.049
<b>NFG</b>	-0.01071	-0.01021	-0.12748	0.00487	<b>0.17757</b>	0.04438	-0.12632	-0.04275	-0.05961	-0.150
<b>NUFG</b>	-0.00457	-0.00314	-0.09305	0.00188	0.10628	<b>0.07415</b>	0.02143	0.0397	-0.00689	0.136
<b>SW</b>	0.00105	0.00187	-0.04019	0.0004	-0.03847	0.00273	<b>0.58302</b>	0.20668	0.22582	0.943**
<b>BY</b>	0.00353	0.00418	0.00281	-0.00209	-0.03121	0.0121	0.49542	<b>0.24322</b>	0.17698	0.905**
<b>HI</b>	0.00033	0.00169	-0.00887	0.00008	-0.03949	-0.00191	0.49118	0.16058	<b>0.26805</b>	0.872**

Residual effect = 0.01789 (Direct effect are represented in bold)

Here, DF= Days to 50 percent flowering, PH= Plant height, ET= Effective tillers per plant, PL= Panicle length, NFG= No. of filled grains per panicle, NUGF= No. of unfilled grains per panicle, SW= Hundred Seed weight, BY= Biological yield, HI= Harvest index, GY= Grain yield per plant

(\* = at five percent level of significance, \*\* = at one percent level of significance)

Panicle length exerted negligible positive direct effect (0.031) on grain yield plant<sup>-1</sup>. Effective tillers per plant also exhibited negligible positive and negative indirect effect on grain yield plant<sup>-1</sup>.

Number of filled grains per panicle exerted positive direct effect (0.178) on grain yield per plant. It also exhibited a negative indirect effect on grain yield per plant via effective tillers per plant (-0.12748) and 100 seed weight (-0.12632).

Number of unfilled grains per panicle exerted negligible positive direct effect (0.074) on grain yield per plant. It also exhibited a positive indirect effect on grain yield per plant through number of filled grains per panicle (0.10628).

100 seed weight showed positive direct effect (0.583) on grain yield per plant. It also exhibited a positive indirect effect on grain yield plant<sup>-1</sup> via harvest index (0.22582) and biological yield (0.20668).

Biological yield exerted positive direct effect (0.243) on grain yield per plant. It also exhibited a positive indirect effect on grain yield per plant via 100 seed weight (0.49542) and harvest index (0.17698).

Harvest index exerted positive direct effect (0.268) on grain yield per plant. It also exhibited a positive indirect effect on grain yield per plant via 100 seed weight (0.49118) and biological yield (0.16058).

Exhibition of positive direct effect of harvest index on grain yield per plant is in accordance with the results of Nandan *et al.* (2010), Solomon *et al.* (2016). Exhibition of high positive direct effects on grain yield per plant by biological yield per plant followed by harvest index is in accordance with the observations of Hamsa *et al.* (2018).

Path analysis reflected that 100 seed weight, biological yield & harvest index exhibited positive direct effect as well as positive and significant correlation with grain yield per plant which clearly shows that directly selecting these traits will be highly beneficial for enhancing grain yield per plant. Low residual effect of 0.01789 reveals that the number of traits taken for the observation in the investigation are sufficient for the investigation.

The above results are in agreement with the observations of Kumar *et al.* (2016) for the traits panicle length and number of filled grains per panicle with Ravindra *et al.* (2012) for panicle length while with Nagaraju *et al.* (2013) for

number of filled grains per panicle<sup>-1</sup>.

Positive direct effect of number of filled grains per panicle over grain yield was also reported by Devi *et al.* (2017).

#### **4.4.2 Quality traits**

Hulling % exerted positive direct effect (0.381) on head rice recovery. It also showed a positive indirect effect on head rice recovery via amylose content (0.601), paddy width (0.365), brown rice width (0.196), kernel length (0.117) while negative indirect effect on head rice recovery via milling % (-0.659), kernel width (-0.240), elongation ratio (-0.204), paddy L/B (-0.195), paddy length (-0.149).

Milling % exerted negative direct effect (-1.017) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery across amylose content (0.981), paddy width (0.488), kernel length (0.318), hulling % (0.246), brown rice width (0.193), brown rice length (0.135) while negative indirect effect on head rice recovery across paddy length (-0.654), kernel width (-0.353).

Character Paddy length had a negative direct effect (-1.480) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery across kernel length (0.754), paddy L/B ratio (0.751), elongation ratio (0.601), brown rice length (0.407), kernel L/B (0.309), paddy width (0.278) while negative indirect effect on head rice recovery through brown rice L/B ratio(-0.561), milling % (-0.450), kernel width (-0.379).

Paddy width exerted positive direct effect (1.307) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery via brown rice width (0.827), amylose content (0.549), brown rice L/B ratio (0.289), kernel length (0.151) and hulling % (0.106) while negative indirect effect on head rice recovery via kernel width (-1.226), paddy L/B ratio (-0.603), elongation ratio (-0.463), milling % (-0.380), paddy length (-0.315) and kernel L/B ratio (-0.291).

Character Paddy L/B ratio showed positive direct effect (1.095) on head rice recovery. It also had a positive indirect effect on head rice recovery through elongation ratio (0.859), kernel width (0.540), kernel length (0.529), kernel L/B ratio (0.470 and brown rice length (0.315) while negative indirect effect on head rice recovery through paddy length (-1.015), paddy width (-0.720), brown rice L/B ratio (-0.690), brown rice width (-0.528) and amylose content (-0.521).

Brown rice length exerted positive direct effect (0.447) on head rice recovery. It also showed a positive indirect effect on head rice recovery across kernel length (0.834), paddy L/B ratio (0.772), elongation ratio (0.681), kernel L/B ratio (0.325) and paddy width (0.132) while negative indirect effect on head rice recovery via paddy length (-1.350), brown rice L/B ratio (-0.594), kernel width (-0.471), amylose content (-0.426) and milling % (-0.307).

Brown rice width showed positive direct effect (0.959) on head rice recovery. It also exerted a positive indirect effect on head rice recovery across paddy width (1.127), brown rice L/B ratio (0.318), amylose content (0.201) and kernel length (0.180) while negative indirect effect on head rice recovery through kernel width (-1.355), paddy L/B ratio (-0.602), elongation ratio (-0.502), kernel L/B ratio (-0.297) and milling % (-0.204).

Brown rice L/B ratio exerted negative direct effect (-0.717) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery through paddy L/B ratio (1.053), elongation ratio (0.921), kernel length (0.646), kernel L/B ratio (0.458), brown rice length (0.370) & kernel width (0.317) while negative indirect effect on head rice recovery via paddy length (-1.158), amylose content (-0.538), paddy width (-0.527), brown rice width (-0.426) and milling % (-0.118).

Kernel length exhibited a positive direct effect (0.966) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery through elongation ratio (0.859), paddy L/B ratio (0.599), brown rice length (0.385), kernel L/B ratio (0.342), paddy width (0.204) and brown rice width (0.179) while negative indirect effect on head rice recovery via paddy length (-1.155), amylose content (-0.878), kernel width (-0.692), brown rice L/B ratio (-0.479) and milling % (-0.335)

Kernel width exerted negative direct effect (-1.471) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery through paddy width (1.089), brown rice width (0.883), kernel length (0.454), brown rice L/B ratio (0.155) and brown rice length (0.143) while negative indirect effect on head rice recovery across paddy L/B ratio (-0.401), paddy length (-0.382), milling % (-0.244), kernel L/B ratio (-0.184), elongation ratio (-0.145) and amylose content (-0.133).

Kernel L/B ratio exerted positive direct effect (0.524) on head rice recovery. It also exerted a positive indirect effect on head rice recovery via elongation ratio

(1.051), paddy L/B ratio (0.983), kernel length (0.632), kernel width (0.518) and brown rice length (0.277) while negative indirect effect on head rice recovery via paddy length (-0.873), amylose content (-0.854), paddy width (-0.726), brown rice L/B ratio (-0.627), brown rice width (-0.544), milling % (-0.114).

Elongation ratio showed a positive direct effect (1.158) on head rice recovery. It also exerted a positive indirect effect on head rice recovery across paddy L/B ratio (0.811), kernel length (0.717), kernel L/B ratio (0.475), brown rice length (0.263) and kernel width (0.184) while negative indirect effect on head rice recovery via amylose content (-1.145), paddy length (-0.768), brown rice L/B ratio (-0.570), paddy width (-0.522) and brown rice width (-0.416).

Alkali spreading value exerted positive direct effect (0.280) on head rice recovery. It also showed a positive indirect effect on head rice recovery through paddy length (0.2358), kernel width (0.185) and elongation ratio (0.164) while negative indirect effect on head rice recovery via brown rice width (-0.226), paddy width (-0.132), brown rice length (-0.102).

Gel consistency showed positive direct effect (0.109) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery across elongation ratio (0.771), kernel length (0.680), paddy L/B ratio (0.503), kernel L/B ratio (0.326), brown rice length (0.246) & hulling percent (0.119) while negative indirect effect on head rice recovery via paddy length (-0.863), milling % (-0.655), brown rice L/B ratio (-0.380) and kernel width (-0.265).

Amylose content had a positive direct effect (1.839) on head rice recovery. It also exhibited a positive indirect effect on head rice recovery through paddy width (0.390), brown rice L/B ratio (0.210), hulling % (0.124), kernel width (0.106) and brown rice width (0.105) while negative indirect effect on head rice recovery via elongation ratio (-0.721), milling percent (-0.543), Kernel length (-0.461), paddy L/B ratio (-0.310), kernel L/B ratio (-0.243) and brown rice length (-0.103).

Gel consistency, amylose content, kernel L/B ratio showed positive and significant correlation as well as positive direct effect over head rice recovery % while traits hulling %, paddy width, paddy L/B ratio, brown rice length, brown rice width, kernel length, elongation ratio, alkali spreading value only exerted positive direct effect over head rice recovery %. Thus, selection for the traits gel consistency,

amylose content, kernel L/B ratio would surely be beneficial in increasing head rice recovery %.

Positive direct effect of hulling % and brown rice length over head rice recovery % has similarity with the observations of Adhimoolam *et al.* (2010) while Devi *et al.* (2017) had similar findings for positive direct effect of kernel length over head rice recovery %.

**Table 4.9 Direct and indirect effect of 16 quality traits over 52 germplasm accession**

Traits	Hulling percent	Milling percent	Paddy length	Paddy width	Paddy L/B ratio	BR Length	BR Width	BR L/B ratio	Kernel Length	Kernel Width
Hulling %	<b>0.381</b>	-0.659	-0.149	0.365	-0.195	0.009	0.196	0.103	0.117	-0.240
Milling %	0.246	<b>-1.017</b>	-0.654	0.488	0.060	0.135	0.193	-0.083	0.318	-0.353
Paddy length	0.038	-0.450	<b>-1.480</b>	0.278	0.751	0.407	0.050	-0.561	0.754	-0.379
Paddy width	0.106	-0.380	-0.315	<b>1.307</b>	-0.603	0.045	0.827	0.289	0.151	-1.226
Paddy L/B ratio	-0.068	-0.056	-1.015	-0.720	<b>1.095</b>	0.315	-0.528	-0.690	0.529	0.540
BR Length	0.008	-0.307	-1.350	0.132	0.772	<b>0.447</b>	0.113	-0.594	0.834	-0.471
BR Width	0.078	-0.204	-0.077	1.127	-0.602	0.053	<b>0.959</b>	0.318	0.180	-1.355
BR L/W ratio	-0.055	-0.118	-1.158	-0.527	1.053	0.370	-0.426	<b>-0.717</b>	0.646	0.317
Kernel Length	0.046	-0.335	-1.155	0.204	0.599	0.385	0.179	-0.479	<b>0.966</b>	-0.692
Kernel Width	0.062	-0.244	-0.382	1.089	-0.401	0.143	0.883	0.155	0.454	<b>-1.471</b>
Kernel L/B ratio	-0.020	-0.114	-0.873	-0.726	0.983	0.277	-0.544	-0.627	0.632	0.518
Elongation Ratio	-0.067	0.001	-0.768	-0.522	0.811	0.263	-0.416	-0.570	0.717	0.184
Alkali Spreading Value	-0.049	-0.079	0.236	-0.132	-0.032	-0.102	-0.226	0.019	-0.037	0.185
GC	0.119	-0.655	-0.863	0.084	0.503	0.246	-0.021	-0.380	0.680	-0.265
Amylose	0.124	-0.543	0.068	0.390	-0.310	-0.103	0.105	0.210	-0.461	0.106

**Table 4.9 Direct and indirect effect of 16 quality traits over 21 germplasm accessions (continues.)**

Traits	Kernel Length	Kernel Width	Kernel L/B ratio	Elongation Ratio	Alkali Spreading Value	GC	Amylose
Hulling %	0.117	-0.240	-0.027	-0.204	-0.036	0.034	0.601
Milling %	0.318	-0.353	0.059	-0.001	0.022	0.070	0.981
Paddy length	0.754	-0.379	0.309	0.601	-0.045	0.063	-0.085
Paddy width	0.151	-1.226	-0.291	-0.463	-0.028	0.007	0.549
Paddy L/B ratio	0.529	0.540	0.470	0.859	-0.008	0.050	-0.521
BR Length	0.834	-0.471	0.325	0.681	-0.064	0.060	-0.426
BR Width	0.180	-1.355	-0.297	-0.502	-0.066	-0.002	0.201
BR L/W ratio	0.646	0.317	0.458	0.921	-0.007	0.058	-0.538
Kernel Length	<b>0.966</b>	-0.692	0.342	0.859	-0.011	0.077	-0.878
Kernel Width	0.454	<b>-1.471</b>	-0.184	-0.145	-0.035	0.020	-0.133
Kernel L/B ratio	0.632	0.518	<b>0.524</b>	1.051	0.021	0.068	-0.854
Elongation Ratio	0.717	0.184	0.475	<b>1.158</b>	0.040	0.072	-1.145
Alkali Spreading Value	-0.037	0.185	0.040	0.164	<b>0.280</b>	0.020	-0.065
GC	0.680	-0.265	0.326	0.771	0.052	<b>0.109</b>	-0.038
Amylose	-0.461	0.106	-0.243	-0.721	-0.010	-0.002	<b>1.839</b>

Residual effect = 0.1428

Bold values shows direct and normal values shows indirect effects.

#### 4.5 Genetic Divergence analysis

The genetic divergence was assessed using mahalanobis  $D^2$  statistics on 52 genotypes over 10 yield and yield contributing traits and on 21 genotypes over 16 quality traits.

##### 4.5.1 Yield and yield contributing traits

###### 4.5.1.1 Clustering pattern

The relative magnitude of  $D^2$  statistics was used to divide 52 rice genotypes into 8 clusters. Cluster I had the most genotypes, with 23 germplasm accessions after that cluster IV with 8 genotypes, cluster VI with 6 genotypes, cluster III with 5 genotypes, cluster VII with 4 genotypes & cluster II, V, and VIII with 2 genotypes each.

**Table 4.10 Clustering pattern of 52 germplasm accessions.**

Cluster no.	No. of germplasm	Name of germplasm accession
I	23	ICO577803, ICO577396, ICO463073, IC0463190, EC0497166, IC0301119, IC0301123, IC0301206, IC0256817, IC0377173, IC0377238, EC0491242, EC0491282, ECO491353, EC0491389, IC0463875, ICO577148, IC0449608, Acc 2955, Acc 2971, Acc 2986, Acc 2991, Acc 3349
II	2	ICO578975, IC0300191
III	5	ICO578996, ICO578999, IC0565343, IC0565344, IC0449908
IV	8	ICO577396, IC0326451, IC0384190, IC0565346, IC0565360, IC0375799, Acc 2980, Acc 2992
V	2	IC0299989, IC0300822
VI	6	EC0497077, EC0497100, IC0382568, Acc 3236, Acc 3251, Acc 3367
VII	4	Indira Aerobic, Maheshwari, Rajeshwari, IR 64
VIII	2	Samleshwari, Chhattisgarh Devbhog

###### 4.5.1.2 Intra and Inter cluster distance

Highest intra cluster distance was obtained for cluster IV (66.097) having 8 genotypes which was followed by cluster II (42.167) having 2 genotypes, cluster VI (30.235) having 6 genotypes, cluster V (30.072) having 2 genotypes, cluster I

(30.007) having 23 genotypes, cluster III (28.985) having 5 genotypes, cluster VII (21.577) having 6 genotypes while cluster VIII (8.882) had 2 genotypes.

**Table 4.11 Intra and Inter cluster distance**

Cluster	I	II	III	IV	V	VI	VII	VIII
<b>I</b>	<b>30.007</b>	37.313	69.567	32.516	36.006	45.574	64.199	66.284
<b>II</b>		<b>42.167</b>	48.767	29.063	63.541	54.179	39.693	62.239
<b>III</b>			<b>28.985</b>	42.652	86.999	57.107	42.929	61.142
<b>IV</b>				<b>66.097</b>	47.238	27.645	51.692	52.471
<b>V</b>					<b>30.072</b>	41.313	93.826	80.406
<b>VI</b>						<b>30.235</b>	72.996	52.386
<b>VII</b>							<b>21.577</b>	54.292
<b>VIII</b>								<b>8.882</b>

Highest inter cluster distance was recorded between cluster VII & V (93.826) followed by cluster V & III (86.999), cluster VIII & V (80.406), cluster VII & VI (72.996) while lowest inter cluster distance was observed between cluster VI & IV (27.645).

#### **4.5.1.3 Cluster mean**

Wide differences were observed among different clusters for cluster mean values for all the traits under investigation. For the trait, days to 50% flowering, highest cluster mean recorded 104.848 for cluster I followed by 103.200 for cluster III, 98.375 for cluster VII while the lowest cluster mean was recorded 92.000 for cluster II.

Highest cluster mean for the trait plant height was 153.228 for the cluster V followed by 149.582 for the cluster I and 128.640 for cluster II while the lowest cluster mean was recorded 84.761 for cluster III.

Highest value of cluster mean for the trait effective tillers per plant was 10.000 for the cluster IV followed by 9.500 for cluster VIII and 8.400 for cluster III while the lowest cluster mean was recorded 6.083 for cluster VI.

The trait panicle length had the highest cluster mean value 29.988 for cluster V followed by 29.465 for cluster I and 27.165 for cluster II while the lowest cluster mean was recorded 24.015 for cluster VIII.

For the trait number of filled grains per panicle maximum cluster mean value recorded was 193.500 for the cluster V followed by 190.165 for cluster VI and 180.090 for cluster VIII while the minimum cluster mean was recorded 128.138 for

cluster VII.

Maximum value of cluster mean for the trait number of unfilled grains per panicle 32.250 for cluster II followed by 31.000 for cluster VIII & 18.222 for cluster VI while the minimum cluster mean was recorded 26.580 for cluster V.

For the trait 100 seed weight maximum cluster mean value recorded was 2.950 for cluster VII followed by 2.368 for cluster VIII and 1.388 for cluster II while the minimum cluster mean was recorded 0.793 for cluster V.

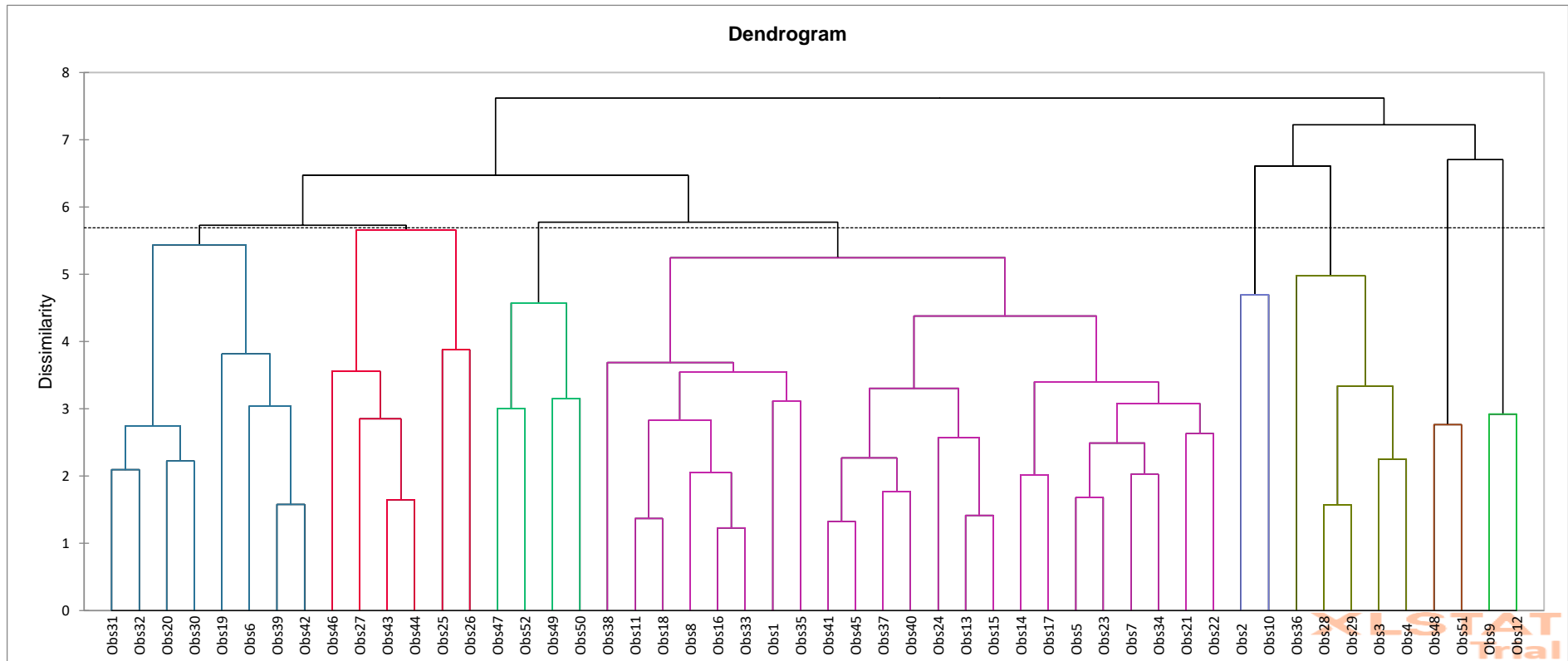
Highest value of cluster mean for the trait biological yield was recorded 80.228 for the cluster VIII followed by 70.229 for cluster VII and 51.151 for cluster I while the lowest cluster mean was 35.250 recorded for cluster V.

For the trait harvest index maximum cluster mean value recorded was 39.150 for cluster VIII followed by 38.113 for cluster VII and 25.389 for cluster I while the minimum cluster mean was obtained for 13.350 for cluster V.

Highest value of cluster mean for the trait grain yield plant<sup>-1</sup> was recorded 31.425 for cluster VIII followed by 26.776 for cluster VII and 15.650 for cluster II while the minimum cluster mean was recorded 8.225 for cluster V.

**Table 4.12 Cluster mean of 10 grain yield and its contributing characters**

<b>Class</b>	<b>Days to 50 percent flowering</b>	<b>Plant height</b>	<b>Effective tillers per plant</b>	<b>Panicle length</b>	<b>No. of filled grains per panicle</b>	<b>No. of unfilled grains per panicle</b>	<b>100 seed wt.</b>	<b>Biological yield</b>	<b>Harvest index</b>	<b>Grain yield per plant</b>
<b>I</b>	104.848	149.582	6.630	29.465	165.195	22.652	1.295	51.151	25.389	13.180
<b>II</b>	92.000	128.640	7.250	27.165	141.250	32.250	1.388	46.000	34.600	15.650
<b>III</b>	103.200	84.761	8.400	23.103	142.266	24.132	0.900	46.332	20.410	9.250
<b>IV</b>	94.625	120.209	10.000	24.743	163.874	22.729	0.908	44.476	23.499	10.656
<b>V</b>	98.250	153.228	6.250	29.988	193.500	26.580	0.793	35.250	13.350	8.225
<b>VI</b>	97.167	114.356	6.083	24.478	190.165	21.694	0.908	40.583	23.253	9.850
<b>VII</b>	98.375	105.118	6.625	25.535	128.138	23.250	2.950	70.229	38.113	26.776
<b>VIII</b>	94.750	98.658	9.500	24.015	180.090	31.000	2.368	80.228	39.150	31.425



**Fig 4.50 Dendrogram showing genetic relationship among 52 accessions along with 6 checks of rice.**

## 4.5.2 Quality traits

### 4.5.2.1 Clustering pattern

Twenty-one rice genotypes were divided into five groups based on the relative magnitude of  $D^2$  statistics. Cluster V had the most genotypes, with six germplasm accessions, followed by clusters I and IV, which had 5 genotypes each, cluster III, which had 4 genotypes, and cluster II, which had only 1 genotype.

**Table 4.13 Clustering pattern of 21 germplasm accessions.**

Cluster number	Number of germplasm	Name of germplasm accession
I	5	IC0577803, IC0565344, Maheshwari, Chhattisgarh devbhog
II	1	IC0459649
III	4	IC0463073, IC0565343, IC0463875, Acc. 2971
IV	5	IC0300822, IC0301123, IC0449608, Acc.2991, Indira aerobic
V	6	IC0565346, IC0375799, Acc. 2992, Acc 3367, Samleshwari, Rajeshwari

### 4.5.2.2 Intra and Inter cluster distance

Highest Intra cluster distance was obtained for cluster IV (10.790) having 5 genotypes followed by cluster I (10.375) which had 5 genotypes, cluster III (7.500) had 4 genotypes, cluster V had 6 genotypes while cluster II had only 1 genotype.

Highest inter cluster distance was exhibited between cluster V & II (28.539) followed by cluster III & II (26.526), cluster II & I (25.122) while lowest inter cluster distance was observed between cluster V & III (5.044).

**Table 4.14 Intra and Inter cluster distance**

Cluster	I	II	III	IV	V
I	<b>10.375</b>	25.122	11.925	8.255	11.331
II		<b>0.000</b>	26.526	22.607	28.539
III			<b>7.500</b>	7.438	5.044
IV				<b>10.790</b>	9.481
V					<b>7.100</b>

#### **4.5.2.3 Cluster mean**

Wide differences were observed among different clusters for cluster mean values for all the traits under investigation. For the trait hulling % highest cluster mean recorded 76.990 for cluster V followed by 75.880 for cluster III while the lowest cluster mean was recorded 70.375 for cluster I.

For the trait milling % maximum cluster mean value recorded was 69.057 for cluster V followed by 66.741 for cluster III while the minimum cluster mean was recorded 52.500 for cluster II.

Highest value of cluster mean for the trait paddy length was recorded 9.050 for cluster I followed by 7.692 for cluster V while the minimum cluster mean was recorded 5.450 for cluster II.

Maximum value of cluster mean for the trait paddy width was 2.863 for cluster III followed by 2.500 for cluster I while the minimum cluster mean was recorded 2.000 for cluster II

Highest value of cluster mean for the trait paddy L/B ratio was recorded 3.682 for cluster I followed by 3.075 for cluster V while the minimum cluster mean was recorded 2.725 for cluster II.

For the trait brown rice length, maximum cluster mean value recorded was 6.860 for cluster I followed by 5.675 for cluster V while the minimum cluster mean was recorded 4.150 for cluster II.

Maximum value of cluster mean for the trait brown rice width was 2.388 for cluster III followed by 2.192 for cluster V while the minimum cluster mean was recorded 1.850 for cluster II.

Maximum value of cluster mean for the trait brown rice L/B ratio was 3.224 for cluster I followed by 2.567 for cluster V while the minimum cluster mean recorded was 2.240 for cluster II. Highest value of cluster mean for the trait Kernel length was recorded 5.340 for cluster I followed by 4.558 for cluster V while the minimum cluster mean was recorded 3.450 for cluster II.

Highest value of cluster mean for the trait kernel length was recorded 5.340 for cluster I followed by 4.558 for cluster V while the minimum cluster mean was recorded 3.450 for cluster II.

For the trait, kernel width maximum cluster mean value recorded was 2.225 for cluster III followed by 2.140 for cluster I while the minimum cluster mean was recorded 1.650 for cluster II.

Highest value of cluster mean for the trait kernel L/B ratio recorded was 2.510 for cluster I followed by 2.216 for cluster V while the minimum cluster mean was recorded 1.860 for cluster III.

Maximum value of cluster mean for the trait elongation ratio was 3.027 for cluster I followed by 2.453 for cluster V while the minimum cluster mean recorded was 2.081 for cluster III.

For the trait, alkali spreading value maximum cluster mean value recorded was 5.250 for cluster III followed by 4.600 for cluster IV while the minimum cluster mean was recorded 3.000 for cluster II.

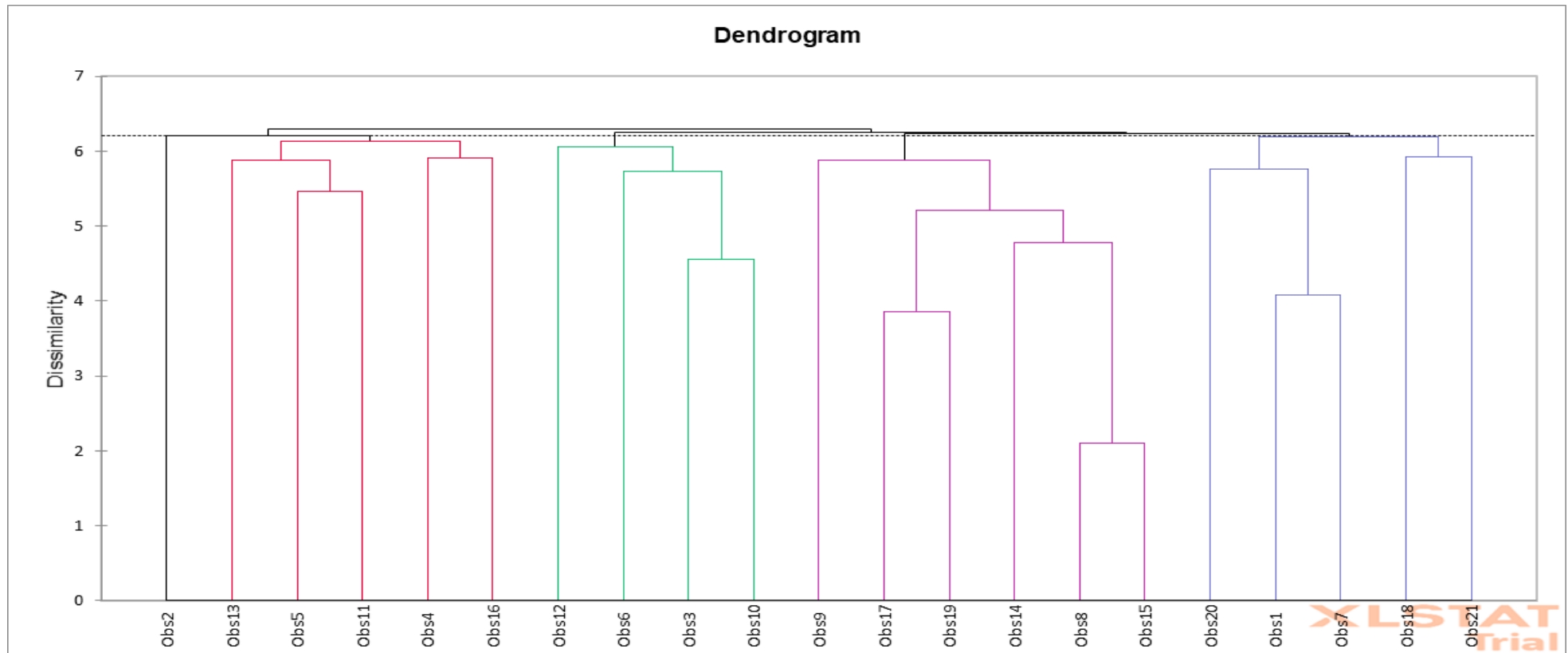
Highest value of cluster mean for the trait gel consistency was recorded 55.350 for cluster I followed by 54.500 for cluster V while the minimum cluster mean was recorded 36.500 for cluster II.

Maximum value of cluster mean for the trait amylose content was 35.538 for cluster III followed by 33.626 for cluster V while the minimum cluster mean recorded was 21.500 for cluster II.

For the trait, head rice recovery % maximum cluster mean value recorded was 58.275 for cluster V followed by 57.640 for cluster I while the minimum cluster mean was recorded 49.500 for cluster II.

**Table 4.15 Cluster mean of quality traits for different clusters.**

<b>Class</b>	<b>Hulling %</b>	<b>Milling %</b>	<b>Paddy length</b>	<b>Paddy width</b>	<b>Paddy L/B ratio</b>	<b>BR Length</b>	<b>BR Width</b>	<b>BR L/B ratio</b>	<b>Kernel Length</b>	<b>Kernel Width</b>	<b>Kernel L/B ratio</b>	<b>Elongation Ratio</b>	<b>Alkali Spreading Value</b>	<b>GC</b>	<b>Amylose</b>	<b>HRR</b>
<b>I</b>	70.325	62.927	9.050	2.500	3.682	6.860	2.140	3.224	5.340	2.140	2.510	3.027	4.500	55.350	27.287	57.640
<b>II</b>	76.495	52.500	5.450	2.000	2.725	4.150	1.850	2.240	3.450	1.650	2.090	2.315	3.000	36.500	21.500	49.500
<b>III</b>	75.880	66.741	7.575	2.863	2.751	5.200	2.388	2.288	4.025	2.225	1.860	2.081	5.250	51.125	35.538	58.275
<b>IV</b>	70.583	64.931	7.250	2.470	2.978	5.310	2.140	2.486	4.220	1.970	2.173	2.384	4.600	49.400	31.560	56.260
<b>V</b>	76.990	69.057	7.692	2.483	3.075	5.675	2.192	2.567	4.558	2.058	2.216	2.453	4.083	54.500	33.626	57.150



**Fig. 4.51 Dendrogram showing genetic relationship among 21 accessions along with 6 checks of rice**

## CHAPTER - V

# SUMMARY AND CONCLUSION

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### 5.1 Summary

The present experiment titled: “**Quantitative & qualitative characterization and quality assessment of rice (*Oryza sativa L.*) genotypes**” was executed at the research and instructional farm, Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh (India) during *Kharif* 2020. Randomised block design along with 2 replications was used to conduct the investigation. Examination of plants at varying stages of growth for diagnosis of stable descriptors of each accessions in each population. Aside from agro- morphological, quality investigation was additionally administered. To identify noble plant type with alluring traits i.e. mean, range, PCV & GCV, heritability, genetic advance as well as genetic advance as a percent of mean were also exercised.

The rice hereditary diversity that has been studied so far suggests that India has a large hereditary base. The landraces accessible today save the richness of alleles. Commercial cultivars have a homogeneous hereditary structure, whereas landraces have a composite hereditary structure. Fifty two accessions were chosen for this investigation and the outcomes are outlined underneath:

DUS characterization was used for finding out the agro morphological variation present in the accessions. In present study all the qualitative characters served as morphological markers due to insignificant environmental effect. In the current experiment, among the qualitative characters observed, basal leaf sheath colour, leaf intensity of green colour, leaf: pubescence of blade surface, leaf: anthocyanin colouration of auricles, panicle: colour of awns and flag leaf: attitude of blade showed wide diversity amongst accessions.

According to the analysis of variance, the mean sum of square values for the genotypes for all the yield as well as quality traits were found significant which suggested that there is a lot of variation among the 52 rice germplasm accessions. Environment had a crucial role in character’s expression as phenotypic coefficient of variance is higher as compared to genotypic coefficient of variance in this investigation.

PCV as well as GCV were observed higher for traits like hundred seed weight, grain yield plant<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, effective tillers plant<sup>-1</sup>, harvest index, biological yield, number of filled grains panicle<sup>-1</sup>, Plant height among quantitative traits while alkali spreading value, brown rice L/B ratio and paddy L/B ratio among quality traits.

Among 10 quantitative traits hundred seed weight, grain yield, harvest index, number of unfilled grains panicle<sup>-1</sup>, biological yield, effective tillers plant<sup>-1</sup>, plant height, number of filled grains panicle<sup>-1</sup>, panicle length and among 16 quality characters alkali spreading value, paddy L/B ratio, brown rice L/B ratio, elongation ratio, brown rice length, kernel length, paddy length, amylose content, paddy breadth, kernel L/B ratio, kernel width, brown rice width, gel consistency exhibited high heritability along with high genetic advance.

Traits hundred seed weight, biological yield and harvest index showed positive as well as significant correlation with grain yield plant<sup>-1</sup> while milling %, gel consistency, amylose content, kernel L/B ratio showed positive and significant correlation with head rice recovery %. High genotypic correlation between concerned traits (independent variable) and dependent variable (head rice recovery % as well as grain yield plant<sup>-1</sup>) depicts that direct selection for the concerned character will essentially enhance grain yield per plant.

Path analysis revealed that hundred seed weight, biological yield and harvest index, number of filled grains panicle<sup>-1</sup>, number of unfilled grains panicle<sup>-1</sup>, panicle length showed positive direct effect over grain yield plant<sup>-1</sup> and hulling %, paddy width, paddy L/B ratio, brown rice length, brown rice width, kernel length, kernel L/B ratio, elongation ratio, alkali spreading value, gel consistency and amylose content exhibited positive direct effect on the head rice recovery percent.

The analysis of genetic divergence was carried out using mahalanobis D<sup>2</sup> method. For grain yield and its contributing traits, 52 accessions were divided into 8 clusters. The distribution of different accessions into different clusters was uneven. Highest number of genotypes were present in cluster I including 23 germplasm accessions which was followed by cluster IV having 8 genotypes, cluster VI having 6 genotypes, cluster III having 5 genotypes, 4 genotypes were grouped under cluster VII while cluster II, V and VIII each had 2 genotypes. The pattern of group

constellation demonstrated that there is a lot of variation.

The intra cluster distance was found to be maximum for cluster IV and among cluster VII & V maximum inter cluster distance was noted while minimum inter cluster distance was noted between cluster VI & IV. Selection of parents should be done from cluster VI and IV in order to realize much variability as well as high heterotic effect. For all of the traits studied, the mean values for clusters showed a broad range of variation. Cluster I showed highest mean values for days to 50 percent flowering, while cluster II showed highest mean values for number of unfilled grains panicle<sup>-1</sup>, highest mean values in case of cluster IV was observed for effective tillers plant<sup>-1</sup>. Mean values were maximum for the traits plant height, panicle length and number of filled grains panicle<sup>-1</sup> in case of cluster V. Mean values were highest for the trait 100 seed weight for cluster VII and cluster VIII showed highest mean values for the traits biological yield, harvest index, grain yield per plant while cluster III and VI did not exhibit highest mean values for any of the traits.

For Quality traits, 21 accessions were divided into 5 clusters, in which cluster V containing 6 germplasm accessions had maximum genotypes cluster I and IV had 5 genotypes, cluster III had 4 genotypes while cluster II had only 1 genotype. Intra cluster distance was found to be highest for cluster IV while cluster V & II had maximum inter cluster distance and cluster V & III had minimum inter cluster distance. For all of the traits studied, the values for cluster mean showed large amount of variation. Highest mean values was observed for paddy length, paddy L/B ratio, brown rice length, brown rice L/B ratio, kernel length, kernel L/B ratio, elongation ratio, gel consistency in case of cluster I, while cluster III showed highest mean values for paddy width, brown rice width, kernel width, alkali spreading value and amylose content. Cluster V showed highest mean values for the traits hulling %, milling %, head rice recovery % while genotypes present in cluster II and IV did not exhibit highest mean values for any of the trait.

## **5.2 Conclusions**

- In the characterization of rice germplasm accessions, qualitative traits might be regarded morphological markers. Characterization of germplasm accessions establishes distinctiveness on the basis of morphological markers. It is not only

important for utilizing the appropriate attribute based donors in breeding program, but also essential in the present era for protecting the unique rice.

- Significant magnitude of the genetic variability was recorded for many of the quantitative characters. The available genetic variability present in the material may be exploited for the improvement of existing genotypes. The significant genetic variability in any breeding substance is a condition as it does not only produce a basis for selection but also produce some useful knowledge concerning selection of various characters.
- For all of the traits studied, the analysis of variance revealed a broad range of variation among genotypes. It suggested that each character had enough variation.
- High heritability as well as high genetic advance as a % of mean was observed for 100 seed weight, grain yield, harvest index, number of unfilled grains per panicle, biological yield, effective tillers per plant, plant height, number of filled grains per panicle, panicle length, alkali spreading value, paddy L/B ratio, brown rice L/B , elongation ratio, brown rice length, kernel length, paddy length, amylose content, paddy breadth, kernel L/B ratio, kernel width, brown rice width, gel consistency suggesting that these character are governed by additive genes and selection for these traits will be beneficial in increasing grain yield.
- Association of correlation reflected significant and positive association of grain yield per plant with 100 seed weight, biological yield and harvest index and significant and positive association of milling percent, gel consistency, amylose content and kernel L/B ratio with head rice recovery %. Positive correlation among helpful characters is approvable because it helps in synchronic development of both the traits.
- Path coefficient analysis for positive direct effect on grain yield  $\text{plant}^{-1}$  observed with 100 seed weight, biological yield and harvest index, number of filled grains  $\text{panicle}^{-1}$ , number of unfilled grains  $\text{panicle}^{-1}$ , panicle length while positive direct effect on head rice recovery % with hulling %, paddy width, paddy L/B ratio, brown rice length, brown rice width, kernel length, kernel L/B ratio, elongation ratio, alkali spreading value, gel consistency, amylose content. Hence these traits could be employed as a criteria for selection for further enhancement in the grain yield  $\text{plant}^{-1}$ .

- Mahalonobis D2 analysis for genetic divergence arranged 52 accessions into 8 clusters for grain yield and its contributing traits and 21 accessions into 5 clusters for quality traits. Parents should be selected from cluster VII and V among grain yield and its contributing traits and from V and II among quality traits as they had highest intercluster distance in order to realize much variability as well as high heterotic effect.
- Among yield and its contributing characters, promising germplasm accessions are IC0300191, EC0497166, IC0301119, IC0301123, IC0301206, IC0377173, IC0377238, EC0491282, EC0491389, IC0463875, IC0449608, Acc. 2971, ICO577803 and ICO463073. Among Quality traits, promising germplasm accessions are, IC0463073, IC0565343, IC0463875, Acc. 2971, IC0565346, IC0375799, Acc. 2992, Acc. 3367, IC0577803, IC0565344, IC0300822, IC0301123, IC0449608, Acc. 2991, IC0565346, IC0375799, Acc. 2992 and Acc. 3367.

Germplasm accessions which are outstanding among both yield and its contributing characters as well as among quality traits are IC0301123, ICO577803, IC0463073, IC0463875, IC0449608 and Acc 2971. Thus, selecting these accessions would be highly beneficial for increasing yield as well as quality in future rice breeding programmes.

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**Appendix A**

**Table: Weekly meteorological data during crop growth period of rice (*Kharif 2020*)**

Weak No.	Date	Max. Temp. (°C)	Min. Temp (°C)	Rainfall (mm)	Rainy days	Relative Humidity (%)		Vapour Pressure (mm of Hg)		Wind Velocity (Kmph)	Evaporation (mm)	Sun shine (hours)
						I	II	I	II			
	July											
<b>27</b>	02-08	33.6	25.8	95.0	3	88	66	23.7	24.6	7.5	28.9	5.4
<b>28</b>	09-15	33.4	25.0	67.5	3	88	74	23.3	24.0	7.2	25.5	2.8
<b>29</b>	16-22	33.0	26.1	39.8	3	86	71	23.5	24.5	5.9	24.9	4.4
<b>30</b>	23-29	32.3	25.9	29.9	2	86	68	23.2	23.5	5.5	22.8	3.8
<b>31</b>	30-05	33.3	26.0	23.6	2	89	69	23.9	24.8	5.9	26.7	3.3
	Aug											
<b>32</b>	06-12	30.5	25.5	81.6	3	92	77	23.3	24.3	7.1	22.9	1.5
<b>33</b>	13-19	28.4	25.1	71.2	4	93	86	22.8	23.8	10.4	13.9	0.5
<b>34</b>	20-26	31.0	25.5	29.8	3	89	74	23.0	23.2	7.8	19.9	2.0
<b>35</b>	27-02	29.8	24.6	235.8	4	93	75	22.6	22.9	8.2	19.9	3.7
	Sep											
<b>36</b>	03-09	32.9	26.0	8.0	2	91	74	24.3	24.8	3.0	22.5	4.9
<b>37</b>	10-16	33.2	26.0	64.0	2	91	67	24.2	23.4	3.4	24.6	6.0
<b>38</b>	17-23	32.7	25.8	16.4	2	89	71	23.1	24.5	2.9	19.5	3.6

<b>39</b>	24-30	32.8	25.3	0.0	0	90	59	22.9	20.4	5.1	24.1	5.3
	Oct											
<b>40</b>	01-07	31.8	25.0	12.8	1	90	63	22.3	21.6	2.6	20.5	4.0
<b>41</b>	08-14	32.5	25.3	0.0	0	90	66	23.0	22.6	4.4	22.4	5.0
<b>42</b>	15-21	31.9	24.4	7.0	1	90	60	22.4	20.4	5.0	23.3	6.5
<b>43</b>	22-28	32.6	20.1	0.0	0	87	35	16.8	12.7	2.1	24.1	8.0
<b>44</b>	29-04	31.8	17.4	0.0	0	82	30	14.0	10.3	2.2	24.9	7.6
	Nov											
<b>45</b>	05-11	30.3	12.5	0.0	0	87	28	10.8	8.7	2.1	23.5	8.5
<b>46</b>	12-18	32.7	18.9	0.0	0	87	37	15.7	13.6	2.9	24.9	8.5
<b>47</b>	19-25	31.0	15.9	0.4	0	88	35	13.4	11.0	2.8	23.1	7.4
<b>48</b>	26-02	28.6	14.7	0.0	0	81	35	11.2	9.9	4.0	22.4	6.2
	Dec											
<b>49</b>	03-09	30.7	11.9	0.0	0	89	33	9.9	9.6	1.3	22.2	7.3
<b>50</b>	10-16	30.2	15.8	0.0	0	86	37	12.5	11.4	2.4	20.1	3.7
<b>51</b>	17-23	27.7	10.3	0.0	0	87	27	9.4	7.1	2.5	22.7	5.0
<b>52</b>	24-31	28.4	10.3	0.0	0	87	28	8.8	7.8	1.8	24.6	4.8

**Appendix B****Table: Description of morphological characters**

S. No	Genotypes	1	2	3	4	5	6	7
1	ICO577803	Green	Purple line	Light	Absent	--	Present	Very weak
2	ICO578975	Green	Purple line	Medium	Absent	--	Present	Weak
3	ICO578996	Green	Green	Medium	Absent	--	Absent	--
4	ICO578999	Green	Green	Dark	Absent	--	Absent	--
5	ICO577396	Green	Purple line	Light	Absent	--	Present	Very weak
6	ICO459649	Green	Purple line	Light	Absent	--	Present	Very weak
7	ICO463073	Green	Purple line	Medium	Absent	--	Present	Very weak
8	IC0463190	Green	Purple line	Light	Absent	--	Present	Weak
9	IC0299989	Green	Green	Light	Absent	--	Absent	--
10	IC0300191	Green	Light purple	Medium	Absent	--	Present	Weak
11	EC0497166	Green	Green	Medium	Absent	--	Absent	--
12	IC0300822	Green	Green	Medium	Absent	--	Absent	--
13	IC0301119	Green	Green	Dark	Absent	--	Absent	--
14	IC0301123	Green	Purple line	Medium	Absent	--	Present	Very weak
15	IC0301206	Green	Purple line	Dark	Absent	--	Present	Very weak
16	IC0256817	Green	Green	Light	Absent	--	Absent	--
17	IC0377173	Green	Purple line	Medium	Absent	--	Present	Weak
18	IC0377238	Green	Uniform purple	Medium	Present	On margins only	Present	Strong
19	IC0326451	Green	Green	Medium	Absent	--	Absent	--

S. No	Genotypes	1	2	3	4	5	6	7
20	IC0384190	Green	Purple line	Light	Absent	--	Present	Very weak
21	EC0491242	Green	Purple line	Medium	Absent	--	Present	Weak
22	EC0491282	Purple	Purple line	Dark	Absent	--	Present	Very weak
23	ECO491353	Green	Purple line	Medium	Absent	--	Present	Very weak
24	EC0491389	Green	Green	Medium	Absent	--	Absent	--
25	EC0497077	Green	Green	Medium	Absent	--	Absent	--
26	EC0497100	Green	Green	Medium	Absent	--	Absent	--
27	IC0382568	Green	Green	Medium	Absent	--	Absent	--
28	IC0565343	Green	Purple line	Medium	Absent	--	Present	Very weak
29	IC0565344	Green	Green	Medium	Absent	--	Absent	--
30	IC0565346	Green	Purple line	Medium	Absent	--	Present	Very weak
31	IC0565360	Green	Green	Medium	Absent	--	Absent	--
32	IC0375799	Purple	Purple line	Light	Absent	--	Present	Weak
33	IC0463875	Green	Green	Light	Absent	--	Absent	--
34	ICO577148	Green	Purple line	Medium	Absent	--	Present	Very weak
35	IC0449608	Green	Green	Medium	Absent	--	Absent	--
36	IC0449908	Green	Green	Dark	Absent	--	Absent	--
37	Acc 2955	Green	Purple line	Medium	Present	On margins only	Present	Strong
38	Acc 2971	Green	Purple line	Light	Absent	--	Present	Very weak
39	Acc 2980	Green	Green	Medium	Absent	--	Absent	--
40	Acc 2986	Green	Purple line	Medium	Present	On margins only	Present	Strong
41	Acc 2991	Green	Green	Light	Absent	--	Absent	--
42	Acc 2992	Green	Green	Light	Absent	--	Absent	--
43	Acc 3236	Green	Light purple	Medium	Absent	--	Present	Weak
44	Acc 3251	Green	Green	Medium	Absent	--	Absent	--
45	Acc 3349	Green	Green	Medium	Absent	--	Absent	--
46	Acc 3367	Green	Green	Dark	Absent	--	Absent	--
47	Indira Aerobic	Green	Green	Dark	Absent	--	Absent	--
48	Samleshwari	Green	Purple line	Dark	Absent	--	Absent	--

<b>S. No</b>	<b>Genotypes</b>	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>
49	Maheshwari	Green	Purple line	Dark	Present	On margin only	Present	Strong
50	Rajeshwari	Green	Purple line	Medium	Absent	--	Present	Very strong
51	Chhattisgarh Devbhog	Green	Green	Dark	Absent	--	Absent	--
52	IR 64	Green	Green	Medium	Absent	--	Absent	--

1 = Coleoptile colour, 2 = Basal leaf sheath colour, 3 = Leaf: Intensity of green colour, 4 = Leaf: Anthocyanin colouration, 5 = Leaf: Distribution of anthocyanin colouration, 6 = Leaf sheath: Anthocyanin colouration, 7 = Leaf sheath: Intensity of anthocyanin colouration

S. No.	Genotypes	8	9	10	11	12	13	14
1	ICO577803	Medium	present	Light purple	present	Absent	present	Split
2	ICO578975	Medium	present	Light purple	present	Absent	present	Split
3	ICO578996	Weak	present	Light purple	present	Absent	present	Split
4	ICO578999	Weak	present	Colourless	present	Absent	present	Split
5	ICO577396	Absent	present	Colourless	present	Absent	present	Split
6	ICO459649	Medium	present	Colourless	present	Absent	present	Split
7	ICO463073	Strong	present	Light purple	present	Absent	present	Split
8	IC0463190	Weak	present	Colourless	present	Absent	present	Split
9	IC0299989	Weak	present	Light purple	present	Absent	present	Split
10	IC0300191	Medium	present	Light purple	present	Absent	present	Split
11	EC0497166	Medium	present	Colourless	present	Absent	present	Split
12	IC0300822	Medium	present	Colourless	present	Absent	present	Split
13	IC0301119	Medium	present	Colourless	present	Absent	present	Split
14	IC0301123	Medium	present	Colourless	present	Absent	present	Split
15	IC0301206	Weak	present	Light purple	present	Absent	present	Split
16	IC0256817	Strong	present	Light purple	present	Absent	present	Split
17	IC0377173	Strong	present	Light purple	present	Absent	present	Split
18	IC0377238	Weak	present	Purple	present	Absent	present	Split
19	IC0326451	Strong	present	Light purple	present	Absent	present	Split
20	IC0384190	Medium	present	Light purple	present	Absent	present	Split
21	EC0491242	Strong	present	Purple	present	Absent	present	Split
22	EC0491282	Absent	present	Light purple	present	Absent	present	Split
23	ECO491353	Weak	present	Light purple	present	Absent	present	Split
24	EC0491389	Weak	present	Light purple	present	Absent	present	Split
25	EC0497077	Absent	present	Light purple	present	Absent	present	Split
26	EC0497100	Absent	present	Light purple	present	Absent	present	Split
27	IC0382568	Medium	present	Light purple	present	Absent	present	Split
28	IC0565343	Weak	present	Light purple	present	Absent	present	Split
29	IC0565344	Medium	present	Light purple	present	Absent	present	Split

S. No.	Genotypes	8	9	10	11	12	13	14
30	IC0565346	Weak	present	Light purple	present	Absent	present	Split
31	IC0565360	Medium	present	Light purple	present	Absent	present	Split
32	IC0375799	Weak	present	Light purple	present	Absent	present	Split
33	IC0463875	Weak	present	Purple	present	Absent	present	Split
34	ICO577148	Medium	present	Purple	present	Absent	present	Split
35	IC0449608	Weak	present	Light purple	present	Absent	present	Split
36	IC0449908	Weak	present	Purple	present	Present	present	Split
37	Acc 2955	Medium	present	Purple	present	Present	present	Split
38	Acc 2971	Weak	present	Colourless	present	Absent	present	Split
39	Acc 2980	Weak	present	Light purple	present	Absent	present	Split
40	Acc 2986	Weak	present	Light purple	present	Present	present	Split
41	Acc 2991	Weak	present	Light purple	present	Absent	present	Split
42	Acc 2992	Weak	present	Light purple	present	Absent	present	Split
43	Acc 3236	Medium	present	Light purple	present	Present	present	Split
44	Acc 3251	Medium	present	Light purple	present	Present	present	Split
45	Acc 3349	Weak	present	Light purple	present	Present	present	Split
46	Acc 3367	Weak	present	Light purple	present	Absent	present	Split
47	Indira Aerobic	Weak	present	Colourless	present	Absent	present	Split
48	Samleshwari	Weak	present	Colourless	present	Absent	present	Split
49	Maheshwari	Medium	present	Light purple	present	Present	present	Split
50	Rajeshwari	Medium	present	Purple	present	Present	present	Split
51	Chhattisgarh Devbhog	Weak	present	Colourless	present	Absent	present	Split
52	IR 64	Weak	present	Colourless	present	Absent	present	Split

8 = Leaf: pubescence of blade surface, 9 = Leaf: auricles, 10 = Leaf: anthocyanin colouration of auricles, 11 = Leaf: collar, 12 = Leaf: anthocyanin colouration of collar, 13 = Leaf: Ligule, 14 = Leaf: Shape of Ligule.

S. No.	Genotypes	15	16	17	18	19	20	21
1	ICO577803	White	Medium	Narrow	Semi erect	Early	Medium	White
2	ICO578975	White	Short	Narrow	Erect	Early	Weak	Purple
3	ICO578996	White	Short	Narrow	Semi erect	Medium	Medium	White
4	ICO578999	White	Short	Narrow	Erect	Medium	Medium	White
5	ICO577396	White	Medium	Narrow	Semi erect	Early	Weak	Purple
6	ICO459649	White	Medium	Narrow	open	Late	Medium	Purple
7	ICO463073	White	Long	Medium	Erect	Early	Strong	White
8	IC0463190	White	Long	Narrow	open	Late	Weak	Purple
9	IC0299989	White	Medium	Narrow	open	Early	Medium	White
10	IC0300191	White	Long	Medium	open	Late	Medium	Purple
11	EC0497166	White	Short	Narrow	open	Late	Medium	White
12	IC0300822	White	Medium	Narrow	open	Medium	Weak	Purple
13	IC0301119	White	Medium	Narrow	open	Late	Strong	White
14	IC0301123	White	Medium	Narrow	open	Late	Weak	Purple
15	IC0301206	White	Long	Medium	Spreading	Late	Strong	White
16	IC0256817	White	Long	Narrow	open	Late	Medium	Purple
17	IC0377173	White	Long	Medium	open	Late	Strong	Purple
18	IC0377238	White	Medium	Narrow	open	Late	Medium	Purple
19	IC0326451	White	Medium	Narrow	Semi erect	Early	Medium	White
20	IC0384190	White	Medium	Narrow	Semi erect	Early	Strong	White
21	EC0491242	White	Medium	Medium	Semi erect	Early	Medium	White
22	EC0491282	White	Medium	Medium	open	Early	Strong	White
23	EC0491353	White	Short	Narrow	open	Medium	Medium	Purple
24	EC0491389	White	Medium	Medium	Semi erect	Late	Strong	White
25	EC0497077	White	Long	Medium	Spreading	Medium	Medium	Purple
26	EC0497100	White	Long	Medium	Erect	Medium	Weak	White
27	IC0382568	White	Medium	Medium	Erect	Medium	Strong	White
28	IC0565343	White	Medium	Medium	open	Early	Strong	White
29	IC0565344	White	Medium	Medium	Semi erect	Medium	Medium	White

S. No.	Genotypes	15	16	17	18	19	20	21
30	IC0565346	White	Medium	Narrow	Spreading	Early	Weak	White
31	IC0565360	White	Medium	Narrow	Semi erect	Early	Medium	White
32	IC0375799	White	Long	Narrow	Spreading	Early	Weak	Purple
33	IC0463875	White	Long	Narrow	Erect	Late	Strong	White
34	ICO577148	White	Long	Medium	Erect	Early	Medium	White
35	IC0449608	White	Medium	Narrow	Semi erect	Late	Weak	White
36	IC0449908	White	Medium	Medium	Erect	Very late	Medium	Purple
37	Acc 2955	Light purple	Medium	Medium	Semi erect	Medium	Medium	White
38	Acc 2971	White	Medium	Narrow	Semi erect	Medium	Weak	White
39	Acc 2980	White	Long	Narrow	Semi erect	Medium	Medium	Purple
40	Acc 2986	Purple	Long	Medium	open	Medium	Medium	Purple
41	Acc 2991	White	Medium	Narrow	Erect	Late	Strong	White
42	Acc 2992	White	Long	Narrow	Semi erect	Late	Medium	White
43	Acc 3236	White	Long	Medium	Erect	Medium	Weak	White
44	Acc 3251	White	Short	Narrow	Semi erect	Medium	Medium	Purple
45	Acc 3349	White	Long	Medium	open	Late	Strong	White
46	Acc 3367	White	Long	Narrow	Erect	Medium	Medium	White
47	Indira Aerobic	White	Short	Medium	Erect	Medium	Weak	White
48	Samleshwari	White	Medium	Medium	Semi erect	Medium	Weak	White
49	Maheshwari	White	Medium	Medium	Semi erect	Medium	Medium	Purple
50	Rajeshwari	White	Medium	Medium	Open	Medium	Medium	Purple
51	Chhattisgarh Devbhog	White	Medium	Medium	Erect	Medium	Medium	White
52	IR 64	White	Medium	Medium	Open	Medium	Strong	White

15 = Leaf: colour of Ligule, 16 = Leaf: Length of blade, 17 = Leaf: width of blade, 18 = Culm: Attitude, 19 = Time of heading, 20 = Spikelet; density of pubescence of lemma, 21=Spikelet; colour of stigma

S. No.	Genotypes	22	23	24	25	26	27	28
1	ICO577803	Medium	Present	Weak	Present	Horizontal	Deflexed	Present
2	ICO578975	Thin	Present	Weak	Present	Semi erect	Semi straight	Absent
3	ICO578996	Medium	Absent	--	Absent	Erect	Straight	Present
4	ICO578999	Medium	Present	Weak	Present	Erect	Drooping	Absent
5	ICO577396	Medium	Absent	--	Present	Drooping	Deflexed	Absent
6	ICO459649	Thin	Absent	--	Present	Horizontal	Deflexed	Absent
7	ICO463073	Thin	Present	Weak	Absent	Semi erect	Semi straight	Absent
8	IC0463190	Thin	Present	Medium	Absent	Semi erect	Drooping	Present
9	IC0299989	Thin	Absent	--	Absent	Semi erect	Semi straight	Absent
10	IC0300191	Thick	Present	Medium	Present	Drooping	Drooping	Present
11	EC0497166	Thick	Absent	--	Absent	Erect	Drooping	Present
12	IC0300822	Thin	Present	Strong	Present	Semi erect	Drooping	Absent
13	IC0301119	Thick	Absent	--	Present	Erect	Drooping	Present
14	IC0301123	Medium	Absent	--	Present	Erect	Straight	Present
15	IC0301206	Medium	Present	Weak	Absent	Erect	Semi straight	Present
16	IC0256817	Thin	Present	Medium	Present	Semi erect	Deflexed	Absent
17	IC0377173	Medium	Absent	--	Absent	Erect	Drooping	Present
18	IC0377238	Thin	Absent	--	Absent	Erect	Drooping	Present
19	IC0326451	Thin	Absent	--	Present	Semi erect	Drooping	Absent
20	IC0384190	Thin	Present	Weak	Present	Erect	Semi straight	Absent
21	EC0491242	Thick	Absent	--	Absent	Drooping	Drooping	Absent
22	EC0491282	Thick	Present	Weak	Present	Drooping	Deflexed	Absent
23	ECO491353	Medium	Absent	--	Present	Semi erect	Drooping	Absent
24	EC0491389	Medium	Present	Weak	Absent	Semi erect	Straight	Absent
25	EC0497077	Medium	Absent		Absent	Semi erect	Deflexed	Absent
26	EC0497100	Thick	Present	Weak	Present	Semi erect	Semi straight	Absent
27	IC0382568	Medium	Present	Weak	Absent	Erect	Drooping	Present
28	IC0565343	Thin	Present	Medium	Present	Erect	Drooping	Absent
29	IC0565344	Medium	Present	Weak	Present	Erect	Semi straight	Absent

S. No.	Genotypes	22	23	24	25	26	27	28
30	IC0565346	Thin	Present	Strong	Present	Erect	Deflexed	Absent
31	IC0565360	Thin	Present	Medium	Present	Erect	Straight	Absent
32	IC0375799	Thin	Present	Weak	Present	Semi erect	Drooping	Present
33	IC0463875	Medium	Absent	--	Absent	Horizontal	Semi straight	Absent
34	ICO577148	Thin	Absent		Present	Drooping	Drooping	Absent
35	IC0449608	Medium	Absent	--	Absent	Drooping	Semi straight	Absent
36	IC0449908	Medium	Absent	--	Present	Erect	Semi straight	Absent
37	Acc 2955	Thick	Present	Medium	Absent	Semi erect	Semi straight	Present
38	Acc 2971	Thin	Absent	--	Absent	Drooping	Deflexed	Absent
39	Acc 2980	Thin	Absent	--	Absent	Drooping	Deflexed	Absent
40	Acc 2986	Thick	Present	Weak	Present	Drooping	Drooping	Present
41	Acc 2991	Medium	Absent	--	Present	Horizontal	Drooping	Absent
42	Acc 2992	Thick	Absent		Present	Drooping	Drooping	Absent
43	Acc 3236	Medium	Present	Medium	Present	Drooping	Straight	Absent
44	Acc 3251	Medium	Absent	--	Present	Drooping	Drooping	Absent
45	Acc 3349	Thin	Present	Medium	Present	Semi erect	Drooping	Absent
46	Acc 3367	Thin	Present	Strong	Absent	Semi erect	Semi straight	Absent
47	Indira Aerobic	Medium	Present	Weak	Absent	Semi erect	Deflexed	Absent
48	Samleshwari	Medium	Present	Medium	Absent	Erect	Straight	Absent
49	Maheshwari	Medium	Absent		Absent	Erect	Semi straight	Present
50	Rajeshwari	Medium	Present	Medium	Present	Erect	Semi straight	Absent
51	Chhattisgarh Devbhog	Medium	Present	Weak	Absent	Semi erect	Semi straight	Present
52	IR 64	Medium	Absent		Present	Horizontal	Straight	Absent

22 = Stem: Thickness, 23 = Stem: Anthocyanin colouration of nodes, 24 = Stem: Intensity of Anthocyanin colouration of nodes, 25 = Anthocyanin colouration of internodes, 26 = Flag leaf: Attitude of blade, 27 = Panicle: curvature of main axis, 28 = Panicle: Awns,

S. No.	Genotypes	29	30	31	32	33	34	35
1	IC0577803	Yellowish white	Medium	Upper half only	present	weak	Semi erect to spreading	Well exerted
2	IC0578975	--		--	present	weak	Semi erect to spreading	Well exerted
3	IC0578996	Yellowish white	Medium	Whole length	present	weak	Semi erect	Mostly exerted
4	IC0578999	--	--	--	present	weak	Erect to semi erect	Mostly exerted
5	IC0577396	--	--	--	present	weak	Semi erect	Mostly exerted
6	IC0459649	--	--	--	present	weak	Semi erect to spreading	Well exerted
7	IC0463073	--	--	--	present	weak	Semi erect	Mostly exerted
8	IC0463190	Reddish brown	Medium	Upper half only	present	weak	Erect to semi erect	Mostly exerted
9	IC0299989	--	--	--	present	weak	Semi erect	Mostly exerted
10	IC0300191	Red	Short	Upper half only	present	weak	Erect to semi erect	Well exerted
11	EC0497166	Yellowish white	Short	Whole length	present	Strong	Semi erect	Mostly exerted
12	IC0300822	--	--	--	present	weak	Semi erect to spreading	Well exerted
13	IC0301119	Yellowish white	Short	Upper half only	present	weak	Erect to semi erect	Mostly exerted
14	IC0301123	Yellowish brown	Medium	Whole length	present	weak	Semi erect	Mostly exerted
15	IC0301206	Yellowish brown	Short	Upper half only	present	weak	Semi erect to spreading	Mostly exerted
16	IC0256817	--	--	--	present	weak	Semi erect to spreading	Well exerted
17	IC0377173	Yellowish white	Short	Whole length	present	Strong	Semi erect	Mostly exerted
18	IC0377238	Yellowish brown	Medium	Upper half only	present	weak	Erect to semi erect	Mostly exerted
19	IC0326451	--	--	--	present	weak	Semi erect to spreading	Well exerted
20	IC0384190	--	--	--	present	weak	Semi erect	Partly exerted
21	EC0491242	--	--	--	present	Strong	Erect to semi erect	Mostly exerted
22	EC0491282	--	--	--	present	weak	Semi erect	Mostly exerted
23	ECO491353	--	--	--	present	weak	Semi erect to spreading	Well exerted
24	EC0491389	--	--	--	present	Strong	Semi erect	Mostly exerted
25	EC0497077	--	--	--	present	weak	Erect to semi erect	Well exerted
26	EC0497100	--	--	--	present	Clustered	Semi erect to spreading	Mostly exerted
27	IC0382568	Reddish brown	Medium	Whole length	present	weak	Erect to semi erect	Mostly exerted
28	IC0565343	--	--	--	present	weak	Semi erect	Mostly exerted
29	IC0565344	--	--	--	present	weak	Semi erect to spreading	Mostly exerted

S. No.	Genotypes	29	30	31	32	33	34	35
30	IC0565346	--	--	--	present	weak	Semi erect to spreading	Well exerted
31	IC0565360	--	--	--	present	weak	Semi erect	Mostly exerted
32	IC0375799	Yellowish brown	Medium	Whole length	present	weak	Semi erect to spreading	Mostly exerted
33	IC0463875	--	--	--	present	weak	Semi erect	Mostly exerted
34	ICO577148	--	--	--	present	Clustered	Semi erect	Partly exerted
35	IC0449608	--	--	--	present	weak	Erect to semi erect	Well exerted
36	IC0449908	--	--	--	present	weak	Semi erect to spreading	Mostly exerted
37	Acc 2955	Reddish brown	Short	Upper half only	present	Strong	Erect to semi erect	Mostly exerted
38	Acc 2971	--	--	--	present	weak	Semi erect	Well exerted
39	Acc 2980	--	--	--	present	weak	Semi erect to spreading	Well exerted
40	Acc 2986	Red	Medium	Whole length	present	weak	Semi erect	Mostly exerted
41	Acc 2991	--	--	--	present	weak	Semi erect to spreading	Well exerted
42	Acc 2992	--	--	--	present	Strong	Semi erect	Well exerted
43	Acc 3236	--	--	--	present	Strong	Semi erect to spreading	Mostly exerted
44	Acc 3251	--	--	--	present	weak	Semi erect to spreading	Mostly exerted
45	Acc 3349	--	--	--	present	weak	Semi erect	Well exerted
46	Acc 3367	--	--	--	present	weak	Semi erect to spreading	Mostly exerted
47	Indira Aerobic	--	--	--	present	weak	Erect to semi erect	Mostly exerted
48	Samleshwari	--	--	--	present	Strong	semi erect	Mostly exerted
49	Maheshwari	Yellowish brown	Medium	Upper half only	present	Strong	Semi erect	Mostly exerted
50	Rajeshwari	--	--	--	present	Strong	Semi erect	Well exerted
51	Chhattisgarh Devbhog	Yellowish brown	Medium	Upper half only	present	weak	Semi erect to spreading	Mostly exerted
52	IR 64	--	--	--	present	weak	Erect to semi erect	Mostly exerted

29 = Panicle: colour of awns, 30 = Panicle: length of longest awn, 31 = Panicle: Distribution of Awns, 32 = Panicle: Presence of secondary branching, 33 = Panicle: Secondary branching, 34 = Panicle: Attitude of branches, 35 = Panicle: Exertion

<b>S. No.</b>	<b>Genotypes</b>	<b>36</b>	<b>37</b>					
1	ICO577803	Medium	Medium					
2	ICO578975	Medium	Early					
3	ICO578996	Medium	Medium					
4	ICO578999	Medium	Early					
5	ICO577396	Medium	Medium					
6	ICO459649	Late	Early					
7	ICO463073	Late	Early					
8	IC0463190	Late	Early					
9	IC0299989	Late	Early					
10	IC0300191	Late	Early					
11	EC0497166	Late	Early					
12	IC0300822	Late	Early					
13	IC0301119	Late	Medium					
14	IC0301123	Late	Early					
15	IC0301206	Late	Medium					
16	IC0256817	Late	Early					
17	IC0377173	Late	Early					
18	IC0377238	Late	Early					
19	IC0326451	Medium	Medium					
20	IC0384190	Medium	Early					
21	EC0491242	Late	Medium					
22	EC0491282	Medium	Medium					
23	ECO491353	Medium	Early					
24	EC0491389	Late	Early					
25	EC0497077	Medium	Medium					
26	EC0497100	Medium	Early					
27	IC0382568	Medium	Early					
28	IC0565343	Medium	Early					
29	IC0565344	Medium	Medium					

<b>S. No.</b>	<b>Genotypes</b>	<b>36</b>	<b>37</b>					
30	IC0565346	Medium	Medium					
31	IC0565360	Late	Early					
32	IC0375799	Medium	Early					
33	IC0463875	Late	Medium					
34	ICO577148	Very late	Early					
35	IC0449608	Late	Early					
36	IC0449908	Late	Medium					
37	Acc 2955	Late	Late					
38	Acc 2971	Late	Early					
39	Acc 2980	Late	Late					
40	Acc 2986	Late	Early					
41	Acc 2991	Medium	Late					
42	Acc 2992	Medium	Late					
43	Acc 3236	Late	Late					
44	Acc 3251	Late	Early					
45	Acc 3349	Medium	Early					
46	Acc 3367	Medium	Early					
47	Indira Aerobic	Medium	Early					
48	Samleshwari	Medium	Early					
49	Maheshwari	Late	Early					
50	Rajeshwari	Late	Early					
51	Chhattisgarh Devbhog	Medium	Medium					
52	IR 64	Medium	Early					

36 = Time of maturity, 37 = Leaf: Senescence.

**APPENDIX - C**

**Table: Mean performance of 52 genotypes for 10 yield and its contributing traits**

S. No.	Genotypes	Days to 50% flowering	Plant height	Effective tillers per plant	Panicle length	Filled grains/ panicle	Unfilled grains/ panicle	100 seed weight (g)	Biological yield (g)	Harvest Index (%)	Total grain weight (g)
1	ICO577803	89.500	151.480	7.000	34.095	131.330	24.500	1.210	45.330	27.600	12.500
2	ICO578975	74.500	98.930	8.500	24.650	118.500	35.500	1.110	51.000	29.350	14.950
3	ICO578996	104.500	93.480	8.500	26.215	140.000	24.000	0.785	54.000	15.250	8.250
4	ICO578999	95.000	87.965	11.000	22.460	99.330	19.000	0.855	51.000	17.750	8.800
5	ICO577396	89.500	121.345	7.000	25.695	154.000	28.500	0.885	51.000	17.550	8.950
6	ICO459649	118.500	145.665	5.500	26.430	260.500	35.165	0.900	46.500	19.850	9.300
7	ICO463073	83.000	125.230	9.500	28.445	131.830	20.500	0.980	53.000	18.800	9.950
8	IC0463190	113.500	156.095	6.500	32.760	155.000	12.000	1.065	40.830	26.180	10.700
9	IC0299989	89.000	151.845	6.500	31.010	165.000	27.500	0.705	34.500	12.300	7.250
10	IC0300191	109.500	158.350	6.000	29.680	164.000	29.000	1.665	41.000	39.850	16.350
11	EC0497166	112.000	158.800	6.000	30.765	161.500	19.500	1.870	50.500	36.600	18.500
12	IC0300822	107.500	154.610	6.000	28.965	222.000	25.660	0.880	36.000	14.400	9.200
13	IC0301119	113.000	154.280	5.000	28.145	168.500	25.000	1.665	61.500	26.550	16.350
14	IC0301123	111.500	163.280	4.500	31.495	208.000	36.500	1.705	64.500	25.950	16.750
15	IC0301206	112.500	151.795	7.000	27.950	147.500	20.000	1.780	66.000	27.085	17.850
16	IC0256817	119.000	152.830	7.000	29.365	163.665	19.500	0.800	40.500	21.075	8.550
17	IC0377173	112.000	165.015	4.500	29.760	197.000	29.000	1.880	63.000	30.050	18.900
18	IC0377238	112.500	166.215	5.500	33.580	175.000	24.330	1.870	54.500	33.750	18.400
19	IC0326451	96.000	123.965	11.000	26.295	182.665	26.500	1.000	47.500	30.550	14.550
20	IC0384190	76.500	105.045	12.000	20.215	107.500	9.500	1.335	53.000	26.000	13.800
21	EC0491242	88.500	150.350	5.500	28.615	172.500	22.000	1.630	64.000	25.200	16.150
22	EC0491282	94.500	117.130	5.500	28.600	185.000	26.000	1.835	68.000	27.050	18.400
23	ECO491353	89.500	131.865	6.500	28.215	156.500	23.000	1.130	49.000	22.750	11.150
24	EC0491389	112.000	159.065	7.000	23.645	182.000	22.000	1.605	60.660	27.250	16.550
25	EC0497077	102.500	121.895	4.500	20.715	247.500	32.000	0.735	38.000	14.220	7.500
26	EC0497100	98.500	99.365	7.000	17.060	151.830	25.665	1.105	44.000	24.900	10.950

27	IC0382568	91.500	116.495	6.500	32.130	168.665	16.000	0.930	42.500	22.900	9.750
28	IC0565343	90.500	73.080	9.000	25.095	143.000	21.830	1.015	46.495	22.350	10.500
29	IC0565344	93.500	87.380	8.000	25.095	139.000	25.830	1.020	44.665	22.950	10.250
30	IC0565346	77.500	83.495	13.000	20.130	115.000	16.500	1.030	56.830	24.750	14.050
31	IC0565360	82.000	81.745	12.000	20.865	103.165	13.000	0.865	39.500	23.100	9.150
32	IC0375799	87.500	119.715	12.500	25.045	102.500	7.165	1.125	43.650	26.800	11.650
33	IC0463875	112.500	131.630	8.000	28.715	143.000	17.665	0.965	41.000	24.270	9.950
34	ICO577148	88.000	154.050	6.500	32.895	161.665	25.500	1.565	59.995	26.200	15.750
35	IC0449608	113.500	174.950	7.500	37.550	163.830	23.500	1.115	44.000	25.900	11.400
36	IC0449908	132.500	81.900	5.500	16.650	190.000	30.000	0.825	35.500	23.750	8.450
37	Acc 2955	99.500	137.200	7.500	26.380	139.500	17.500	0.975	39.995	24.700	9.900
38	Acc 2971	109.500	145.050	8.500	28.780	132.330	17.500	0.550	32.830	17.300	5.700
39	Acc 2980	105.000	145.715	6.500	29.580	214.000	36.000	0.530	34.830	17.845	6.250
40	Acc 2986	108.500	157.050	6.000	26.165	178.500	24.500	1.270	46.830	27.450	12.850
41	Acc 2991	113.000	162.680	7.500	28.800	186.000	18.000	0.875	43.000	23.540	10.200
42	Acc 2992	114.000	156.330	7.500	29.380	225.665	38.000	0.475	34.000	19.095	6.500
43	Acc 3236	92.000	129.200	5.000	27.330	194.500	21.500	0.850	35.500	23.900	8.500
44	Acc 3251	95.000	124.000	6.000	28.130	182.000	14.500	1.115	42.000	26.750	11.250
45	Acc 3349	114.500	153.000	7.000	27.280	205.330	24.500	0.550	36.500	21.150	7.750
46	Acc 3367	103.500	95.180	7.500	21.500	196.495	20.500	0.715	41.500	26.850	11.150
47	Indira Aerobic	102.000	100.365	6.500	25.483	156.550	27.500	3.195	84.080	37.650	31.695
48	Samleshwari	95.000	101.075	8.500	26.130	172.580	28.500	2.550	78.195	39.100	30.595
49	Maheshwari	91.000	112.775	5.500	25.170	106.250	24.000	3.145	66.380	38.800	25.780
50	Rajeshwari	103.500	106.005	6.000	24.195	133.450	13.000	3.095	64.500	38.950	25.155
51	Chhattisgarh Devbhog	94.500	96.240	10.500	21.900	187.600	33.500	2.185	82.260	39.200	32.255
52	IR 64	97.000	101.325	8.500	27.290	116.300	28.500	2.365	65.955	37.050	24.475

**APPENDIX - D Mean performance of 21 genotypes for 16 quality traits**

S.No.	Genotypes	H %	M %	PL (mm)	PB (mm)	PL/BR	Br L (mm)	Br B (mm)	Br L/B ratio	KL (mm)	KB (mm)	KL/B ratio	ER	ASV	GC	AC (%)	HRR (%)
1	IC0577803	74.47	63.61	8.95	2.95	3.03	6.75	2.45	2.76	4.95	2.30	2.15	2.22	4.00	48.00	32.90	57.50
2	IC0459649	76.50	52.50	5.45	2.00	2.73	4.15	1.85	2.24	3.45	1.65	2.09	2.32	3.00	36.50	21.50	49.50
3	IC0463073	73.79	62.05	6.05	3.05	1.97	4.55	2.75	1.65	3.95	2.55	1.55	1.82	6.00	47.00	32.25	55.60
4	IC0300822	74.00	67.07	6.15	2.05	3.00	4.45	1.75	2.54	3.85	1.70	2.26	2.40	6.00	51.50	35.50	58.60
5	IC0301123	75.30	70.03	9.50	3.15	3.01	6.95	2.55	2.73	4.95	2.40	2.06	2.14	3.00	53.00	37.80	61.50
6	IC0565343	74.40	68.28	8.95	2.20	4.07	6.85	2.00	3.43	4.35	1.90	2.26	2.43	5.00	52.50	36.50	59.50
7	IC0565344	66.79	60.21	8.85	2.25	3.93	6.75	2.10	3.20	4.45	1.90	2.34	2.45	4.00	45.50	30.50	52.50
8	IC0565346	75.20	67.80	7.85	2.45	3.21	5.95	2.15	2.75	4.15	1.95	2.13	2.38	3.00	52.50	36.85	57.35
9	IC0375799	74.48	67.80	7.75	2.55	2.96	5.05	2.25	2.24	4.25	2.15	2.07	2.21	3.00	52.00	36.75	55.50
10	IC0463875	74.45	64.04	6.35	3.25	1.95	4.55	2.85	1.59	3.85	2.65	1.45	1.74	4.00	49.00	33.50	54.50
11	IC0449608	60.80	57.40	7.35	2.05	3.58	5.05	1.85	2.73	3.65	1.60	2.30	2.47	5.00	42.50	27.50	51.70
12	Acc 2971	80.89	72.60	8.95	2.95	3.03	4.85	1.95	2.49	3.95	1.80	2.19	2.34	6.00	56.00	39.90	63.50
13	Acc 2991	65.90	60.82	5.35	2.75	1.95	4.05	2.30	1.76	3.55	2.15	1.70	2.19	5.00	44.50	29.50	53.35
14	Acc 2992	75.05	67.05	5.55	2.05	2.71	4.15	1.85	2.24	3.45	1.65	2.09	2.29	6.00	52.00	36.90	60.95
15	Acc 3367	78.90	70.52	7.55	2.75	2.71	5.65	2.25	2.47	4.05	2.00	2.03	2.22	3.00	54.50	39.25	59.50
16	Indira Aerobic	76.93	69.35	7.90	2.35	3.36	6.05	2.25	2.69	5.10	2.00	2.55	2.73	4.00	55.50	27.50	56.15
17	Samleshwari	78.06	69.61	8.70	2.35	3.70	6.25	2.15	2.91	5.40	2.10	2.57	2.82	4.50	57.50	27.50	55.45
18	Maheshwari	70.61	67.81	10.00	3.00	3.33	7.30	2.25	3.24	6.15	2.50	2.46	3.30	5.00	58.50	24.20	52.15
19	Rajeshwari	80.27	71.57	8.75	2.75	3.18	7.00	2.50	2.80	6.05	2.50	2.42	2.81	5.00	58.50	24.51	54.15
20	Chhattisgarh devbhog	70.38	62.50	8.50	2.05	4.15	6.55	1.90	3.46	5.40	1.80	3.00	3.67	5.00	67.25	24.48	67.55
21	IR64	69.40	60.51	8.95	2.25	3.98	6.95	2.00	3.48	5.75	2.20	2.61	3.51	4.50	57.50	24.36	58.50

H% = Hulling percent, M% = Milling percent, PL = Paddy length, PB= Paddy breadth, PL/B ratio = Paddy length/ breadth ratio, Br L= Brown rice length, Br B= Brown rice breadth, Br L/B = Brown rice length/ breadth ratio, KL= Kernel length, KB= Kernel breadth, KL/B ratio= Kernel length/ breadth ratio, ER= Elongation ratio, ASV= Alkali spreading value, GC= Gel consistency, AC= Amylose content, HRR= Head rice recovery

## RESUME

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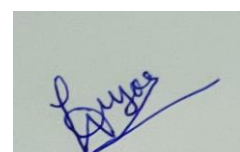
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Member of any Professional  
Society (if any)

Awards/ Recognition

Publications (if any): in numbers  
only



Signature