

**GENETICAL STUDIES, PHENOTYPING AND
MOLECULAR PROFILING OF DIVERSE
GERMPLASM OF RICE (*Oryza sativa* L.)**

By

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M.Sc. (Ag.) GPB



**DEPARTMENT OF AGRICULTURAL BOTANY,
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DAPOLI, DIST. RATNAGIRI-415712, (M.S.) INDIA
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A thesis submitted to the

**DR. BALASAHEB SAWANT KONKAN KRISHI
VIDYAPEETH, DAPOLI**

(Agricultural University)

Dist. Ratnagiri (Maharashtra State), India

in partial fulfillment of the requirements for the degree of

Doctor of Philosophy
(Agriculture)

in

GENETICS AND PLANT BREEDING

by

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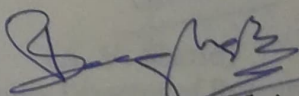
RARS, Karjat, Raigad

CERTIFICATE

This is to certify that the thesis entitled "**GENETICAL STUDIES, PHENOTYPING AND MOLECULAR PROFILING OF DIVERSE GERMPLASM OF RICE (*Oryza sativa* L.)**" submitted to the Faculty of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Dist. Ratnagiri, Maharashtra State in partial fulfillment of the requirements for the degree of **DOCTOR OF PHILOSOPHY (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, embodies the results of the piece of *bona-fide* research carried out by **Mr. SANDEEP GOVINDAPPA SHINDE** (Regd. No. ADPD/19/0312) under my guidance and supervision. No part of this thesis has been submitted for any other degree or diploma and published in other form. All the assistance and help received during the course of investigation and the sources of literature have been duly acknowledged by him.

Place: Dapoli

Date: 6-10-2022



(B. D. Waghmode)

Chairman,
Advisory committee
and
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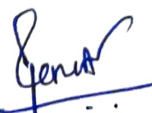
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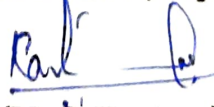


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*Dedicated With Love
To*



My God Shri. Govind and Goddess Sou. Rekha



*My soul
Kumari Shreeja*

*My heart
Kumar Prem*

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ABSTRACT

The present investigation entitled as '**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**' was undertaken with the objectives of characterization of 95 diverse rice germplasm by 62 DUS morphological descriptors, supplemented with molecular profiling by using simple sequence repeat markers and its subsequent evaluation for distinctiveness, uniformity and stability. The nature and extent of variability, heritability, genetic advance and diversity present among the germplasm based on yield and yield contributing parameters was studied to identify potential parents/donors for the hybridization programme. The trials were conducted in two subsequent and independent *Kharif* seasons of 2020 and 2021 at experimental farms of Agricultural Research Station, Shirgaon and Regional Agricultural Research Station, Karjat respectively. Data was recorded for 27 metric characters inclusive of 14 measurable DUS traits and 62 DUS descriptors of rice as per PPV & FRA guidelines. Whereas molecular profiling of 95 rice genotypes using 17 SSR primers was carried out at Plant Biotechnology Center, College of Agriculture, Dapoli.

A perusal of genetic parameters *viz.*, phenotypic and genotypic coefficients of variation revealed less influence of environment on the characters under study for both two seasons and locations. Therefore, response to direct selection may be effective in improving these traits.

All the characters under study for both the locations exhibited high heritability except alkali spreading value which showed lowest heritability: Implying that these characters were under control of additive gene action and direct selection of these traits would be effective for crop improvement.

Divergence studies through D^2 statistics indicated the presence of substantial diversity by forming large number of clusters (22 clusters at Shirgaon and 20 clusters at Karjat) with wide range of inter-cluster distances.

Seventeen SSR primers were used in this study of which all were amplified and showed the polymorphism in rice genotypes. A total of 139 loci were generated by 17 primers. Each primer thus produced on an average 8.17 loci in the size ranging from 132 bp to 884 bp in the 95 rice genotypes in relation to diversity assessment. Among 17 SSR markers, all the primers showed 100 per cent polymorphism. The PIC values of primers ranged from 0.70 in SSR primer RM 7 to 0.92 in SSR primer RM 8225 with an average PIC value of 0.83. The Jaccard's pair wise similarity values ranged from 0.027 to 0.994. Dendrogram was constructed using Jaccard's similarity coefficient and rice genotypes were grouped into two clusters based on SSR markers.

Among the total 62 DUS descriptors, 9 were monomorphic, 15 were dimorphic and 37 were polymorphic in nature. COY-D analysis with respect to 14 measurable traits indicated that all the genotypes were distinct from each other during both the years. All the visually assessed characteristics did not show any variation in their states of expression over the years of study and hence considered to be uniform. All the varieties studied for 62 assessed DUS descriptors exhibited the

same state of expression over the two years and thus considered stable. It may be concluded from the present investigation that the morphological DUS descriptors can be effectively used for identification and grouping of the varieties. Application of biochemical and molecular markers may help in establishing distinctiveness to support morphological marker. The varieties studied for DUS descriptors can be registered with PPV & FR Authority, New Delhi for protection under breeder's rights and farmer's right.

Key words: DUS, PPV & FR, SSR, RBD, D², PIC.

CHAPTER-I

INTRODUCTION

“Rice is life” was the famous theme of International Year of Rice, 2004 denoting its overwhelming importance as an item of food, commerce and the close connection between rice-based systems and many cultures and people worldwide, in particular the poor in developing nations. Devoting an International Year to a single crop is unprecedented in the world history. Today rice is grown and harvested on every continent except Antarctica. Rice remains a staple food for more than half of the world population and forms the cheapest source of food, energy and protein. More than two thirds of the world relies on the nutritional benefit of rice (Pandey and Anurag, 2010).

Rice (*Oryza sativa* L.) ($2n = 24$) is the most important cereal crop which serves as a staple food for over 60 per cent of the world's population (Singh and Singh, 2008). Approximately 90 per cent of rice grown on the planet is produced and consumed in Asia (Singh *et al.*, 2015). India is the world's second largest rice producer and consumer next to China, about 90 per cent of all rice grown in the world is produced and consumed in Asian region. In the world, rice is cultivated on about 167.13 million hectares of area with total production of 782.01 million tonnes and productivity is 3.228 tonnes/ha. Rice has unique position in Indian economy. India ranks second in rice production followed by China. In India, rice occupies an area of 43.79 million hectares with annual production of 116.42 million tonnes and productivity is 2.65 tonnes/ha. (Anonymous, 2021).

In Maharashtra, the total area occupied by this crop was about 1.465 million hectares with annual production of 3.276 lakh tonnes and average productivity of the state was about 2.24 t/ha, (Anonymous, 2021). In Konkan region, rice occupies an area of about 0.387 million hectares with an annual production of around 1.031 million tonnes and average productivity of the konkan was about 2.66 t/ha. The area under rice in konkan region is 26.41 % of the total area in Maharashtra (0.387 million hectares). (Anonymous, 2021).

It is grown in *kharif* and *rabi* season. The per hectare productivity of rice is 2.59 tonnes and 2.73 tonnes in *kharif* and *rabi* season respectively. The major rice growing districts in Maharashtra are Thane, Raigad, Ratnagiri and Sindhudurg along with the West coast and Bhandara, Gadchiroli and Chandrapur in the Eastern parts of the states and minor areas are Tuljapur, Parbhani, Western Ghat of Pune, Nashik, Sangli, Satara, Kolhapur and parts of Nanded. Maximum productivity is observed in Konkan region and it contributes 31.48 per cent of total rice production in the state. Vidarbha region covers large area under rice cultivation than other regions but it has low productivity than Konkan and Western Maharashtra regions.

India, being the part of center of origin, rice is bestowed with wide range of germplasm which encompasses landraces, obsolete cultivars, wild or weedy species, improved varieties and so forth, which led to the tremendous genetic diversity. The genus *Oryza* has 24 species, comprising of 22 wild species and two cultivated species *i.e.*, *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice). *Oryza sativa* has been further classified into five sub-species *viz.*, *japonica* (low amylose content, sticky, short grained and adapted to temperate regions), *indica* (high amylose content, non-

sticky, long-grained and adapted to the tropics), the intermediate *javanica* is designated as *tropical japonica*, *aus* (deep water rice) and *aromatic* (Basmati, Jasmine, Joha etc.) (Garris *et al.*, 2005).

Rice is grown under diverse eco-geographical conditions in various tropical and subtropical countries. Rice yield growth has fallen from 2.3% per year during 1970–1990 to 1.5% during 1990's and to <1.0% during the first decade of present century. Global rice demand is estimated to rise from 676 million tons in 2010 to 763 million tons by 2020 and further increase to 852 million tonnes by 2035. This clearly indicates that an overall increase of 26% or 176 million tons of rice is required in the next 25 years. However, area planted with rice in major production countries has been decreasing because of industrialization and urbanization. Hence, increasing rice yields on existing land remains the primary strategy for increasing production, to meet the future demand for food, anticipated from the projected world population increase. To produce 176 million tons additional rice by 2035, the yield potential of rice needs to be increased from 10 to 12.3 tonnes per hectare (FAOSTAT, 2021).

Green revolution has considerably improved the production of food grains in India and its role in achieving the status of self-sufficiency in food grains is beyond any doubt. But high yielding varieties, which are the back bone of green revolution, reached their yield plateau. So, there is an urgent need to broaden the genetic base of the varieties by introgression of genes from diverse sources. Thus, there is a need to collect, exploit and evaluate the untapped germplasm.

Rice has the largest germplasm collections in the world. This accessible collection of diverse cultivated varieties, landraces and

related wild species has made great contributions to rice breeding. Landraces harbour a great deal of useful traits with genetic potential for rice improvement and they played a very important role in the local food security and sustainable development of agriculture, in addition to their significance as genetic resource for rice genetic improvement (Tang *et al.*., 2021).

Evaluation and characterization of existing landraces of rice is important due to increasing needs of varietal improvement. Characterization is the technique used to evaluate the phenotypic diversity through agro-morphological traits. It has been successfully used in recent years to help in identifying elite individual genotypes. It is an indispensable tool for selecting varieties or lines based on agronomical, morphological, genetic or physiological characters. Characterization of accessions is used to evaluate the phenotypic diversity through agro-morphological traits that are essential for the gene bank management to protect the unique rice (Bajracharya *et al.*, 2020).

The landraces maintained by farmers are endowed with tremendous genetic variability, as they are not subjected to subtle selection over a long period of time. This aids in the adaptation of landraces to wide agro-ecological conditions. This rich variability of complex quantitative traits with respect to maturity, growing adaptation and their physicochemical and organoleptic properties still remains unexploited. Land-races are also important genetic resources for resistance to pests and diseases; they provide “adaptability genes” for specific environmental conditions. Incorporation of adaptability genes from landraces could ensure optimum grain yield for the region (Vijayakumar *et al.*, 2020).

The success of plant breeding depends on the extent of genetic variability present in a crop. Knowledge on the nature and

magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement. A critical analysis of genetic variability present in the germplasm of a crop and its estimation is a prerequisite for initiating any crop improvement programme as well as adopting appropriate selection techniques.

It is very difficult to judge whether observed variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations.

Moreover, knowledge of heritability is also essential for selection of component traits for yield improvement. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

Genetic diversity is a ubiquitous feature of all species in nature. Genetic diversity is an inherited variation among and between populations, created, activated and maintained by evolution. It is a fundamental characteristic without which breeders are very limited and powerless in plant breeding. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different characters and ultimately for a rational use of genetic resources. Genetic diversity can be evaluated with morphological traits, biochemical markers and DNA markers. Morphological and agronomic traits have long been the means of studying variability among population and species. The breeders are interested to evaluate genetic diversity based on morphological traits because they are

inexpensive, rapid and simple to score. The study of these traits needs neither sophisticated method nor complicated equipment. Agro-morphological properties of rice cultivars determine their yield potential, local agronomic suitability and ability to escape from or tolerate biotic and abiotic stresses.

The varieties released from India have shown profound impact in the global rice production. After the initiation of All India Coordinated Rice Improvement Programme (AICRIP), the development and release of rice varieties have been increased tremendously; as of now more than 1200 varieties have been released for various agro-ecosystems in India. Development of new varieties is an expensive task which involves more skill, infrastructure and genetic resources and above all it is a time-consuming process which takes around ten years to release a variety through pedigree breeding, the most commonly used method of variety development. After development of a new variety by painstaking research by the breeders, it is necessary to register newly bred varieties. The protection of ownership of new varieties is of paramount importance to prevent their unauthorized utilization. There are different ways to protect a variety and provide exclusive rights to the breeder. Among them Plant Variety Protection (PVP) through International Union for the Protection of New Varieties of Plants (UPOV) provides Intellectual Property Rights (IPR) to Plant Breeders' Rights (PBR). According to UPOV's PVP system, new variety must satisfy three criteria to be eligible for protection. The first criterion is that the new variety must be Distinct (D) from any other Common Knowledge Varieties (CKVs) in at least one morphological trait. The second criterion is that the variety should be sufficiently Uniform (U) in relevant characteristics depending on reproduction system of the species and finally the distinctive traits

should show Stable (S) expression after two independently growing cycles. Thus, the DUS test provides foundation for plant variety protection and to identify a new variety from already released varieties (also called as reference collection). In India, the plant variety protection is resolved through an authorized *sui generis* enactment of Protection of Plant Varieties and Farmers' Rights Act, 2001 (PPV & FRA), though it is through UPOV (International Union for the Protection of New Varieties of Plants) at international level.

The DUS testing involves comparison of a number of phenotypic characters called descriptors by growing the varieties side by side. Under PPV and FR Act, DUS testing is performed with morpho- physiological descriptors (Anonymous, 2007) and (Rao *et al.*, 2013) which have been capable for distinguishing genetic material in different crops.

However, this technique has now become less reliable for separation and recognition of commercial varieties (Rahman *et al.*, 2020) as there might be minimal morphological variation among cultivars with related pedigrees which often creates ambiguity in identification. Besides, with ever increasing number of varieties every year, conducting DUS test is becoming increasingly expensive. In addition, majority of the characters utilized are multigenic or quantitative and their expression is altered by several environmental factors (Kumar *et al.*, 2018) which ultimately makes DUS testing a tedious and most expensive procedure which demands large area of land and skilled manpower to formulate subjective decisions. These circumstances prompt us to find quick, stable and cost-effective strategies to assist DUS testing.

The wide accessibility and cost-effectiveness of DNA-based markers in recent years makes them appealing alternatives to

investigate their utilization to complement the existing morphological based identification as they are free from environmental impacts (Noli *et al.*, 2018) and they could be applied at any phase of plant development. Even UPOV also endorsed the utilization of molecular markers as the standard method of varietal identification in crops. The potentiality of molecular markers has been demonstrated in several aspects such as genetic purity testing during hybrid seed production, detection and quantification of the adulteration in Basmati rice (Vemireddy *et al.*, 2019) etc. Additionally, Vemireddy *et al.* (2019) developed varietal specific allele profiles for major Indian rice varieties employing hyper variable microsatellite markers.

Compared to the conventional morpho-physiological traits, the molecular markers are more powerful tools for the assessment of genetic variation and elucidation of genetic relationships within and among species (Thomson *et al.*, 2007). Molecular Marker based Genetic Diversity Analysis (MMGDA) has the potential for assessing changes in genetic diversity over time and space (Duwick, 1984). Among DNA-based molecular markers, microsatellites, also called SSRs, are highly polymorphic, as they possess co-dominant inheritance, high abundance, enormous extent of allelic diversity and high reproducibility (Modini *et al.*, 2021). Molecular markers like SSRs (Simple Sequence Repeats) (Sarao *et al.*, 2021), have been tested to complement DUS testing in rice and they were found to be able to distinguish varieties unambiguously and establish level of uniformity and stability. Although there are several QTLs and cloned genes identified in rice, very few gene-specific markers are available to assist DUS descriptors. As per the national guidelines for the conduct of DUS tests in rice, there are 62 DUS related traits (Rani *et al.*, 2006) and (Rao *et al.*, 2013).

Prominent research stations *viz.*, ARS, Shirgaon, RARS, Karjat and KRS, Panvel under the jurisdiction of Dr. Balasaheb Konkan Krishi Vidyapeeth, Dapoli, District Ratnagiri, Maharashtra State, India had released more than 30 varieties and 5 rice hybrids over the years, which have been popular among local farmers and across the state and few across the nation. But many prominent parental lines used for this breeding programme across various groups such as red kernel lines, restorer lines, aromatic lines and lines responsive to biotic and abiotic stress are not yet been characterized by DUS method along with molecular profiling. These lines are used in breeding programme as parent for long time now, having distinct characters. DUS descriptors along with SSR markers will aid to characterize these diverse germplasm lines which can be used to choose elite donor parent for future breeding programme. Such type of attempt will be of its first of kind to study large number of parental germplasm used for Konkan region, to generate passport characterization data of genotypes.

Considering the above perspective, the present investigation entitled, “**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**” was undertaken with the following objectives;

1. Phenotypic characterization and estimation of genetical parameters of diverse rice genotypes for yield and yield parameters.
2. Establishment of DNA profiles of rice genotypes using SSR markers.
3. Generate database of diverse genotypes of rice based on DUS guidelines.



REVIEW OF LITERATURE



CHAPTER – II

REVIEW OF LITERATURE

The spread of modern high yielding varieties in intensive agriculture has posed a great threat to the security of the age old practice of growing traditional varieties and landraces which may have immense potential for different important traits. In order to prevent any further gene erosion, collection and conservation of such invaluable genetic resources of rice is essential.

The exploitation of genetic diversity for crop improvement should be the ultimate objective of exploration and conservation of genetic resources. It is important to ensure that plant genetic resources are adequately safeguarded for future generations. It can be done by identification, characterization and evaluation of important local and parental lines, germplasm in line with DUS descriptors along with molecular profiling. The vital stages of evaluation and incorporation of valuable characters into new varieties are the justifications of genetic resource activities.

For a successful plant breeding programme to improve genetic potential in any crop, variability is the basic requirement. The estimates of different genetic parameters are important for better understanding of the nature and magnitude of genetic variability available in the breeding material along with the association of different yield and quality attributing characters.

The available literature as of now in line with on objectives of present investigation is summarized below:

2.2.1 Studies on genetical parameters studies *viz.*, Variability, Heritability and Genetic Advance

2.2.2 Germplasm characterization using Molecular Markers

2.2.3 Characterization of germplasm using morphological DUS descriptors

2.2.4 Genetic Diversity Analysis Using Both DUS Descriptors and Molecular Markers

2.1 Need for the identification of rice varieties

The identification of varieties is a vital step during the breeding and registration process, seed production, trade and inspection in crops. The rapid identification and characterization of cultivars or varieties would therefore, provide valuable information for their introduction and genetic improvement. Plant cultivar or variety identification is a critical field as more and more varieties or cultivars are developed; the need to identify them unambiguously also increases.

2.2 Methods of identification of rice varieties

The rice varieties are identified employing several conventional and advanced methods. Previously, physical appearance or cooking quality traits were used for cultivar identification. However, the DUS descriptors and molecular markers are being used widely to distinguish rice genotypes. Recently, rice varieties are being identified using artificial intelligence-based neural network and machine learning classifiers. Further, spectroscopy was also used for cultivar identification. The important strides in this aspect are described hereunder.

2.2.1 DUS Testing

India has a rich and wide range of genetic wealth of rice. It has been estimated from various surveys that nearly 50,000 accessions of rice are being grown in the country. A large number of new varieties are being released every year, but not all of these

have been widely accepted, as many of them have been considered to be merely forms of acknowledged varieties. In order to release a new variety commercially, it is essential to register it, which largely relies on the DUS (Distinctness, Uniformity and Stability) test (Anonymous, 2001). Therefore, DUS test has been established to be the foundation of plant variety protection and also to identify a new variety from reference collection (Sharma and Singh, 2018).

A plant variety qualifies for protection when it meets the following essential criteria.

- (i) **Distinctness** –It means that a variety is clearly distinguishable by at least one essential characteristic from any other variety, whose existence is a matter of common knowledge. An essential characteristic is a heritable trait which is determined by one or more genes or the heritable determinants that contribute to the principle features, performance or value of plant variety (Rani *et al.*, 2006).
- (ii) **Uniformity**- It implies that the variety should be sufficiently uniform in its essential characteristics if subjected to variation that may be expected from the particular features of its propagation (Rani *et al.*, 2006).
- (iii) **Stability**- A variety is deemed to be stable when its characteristics remain unchanged after repeated propagation (Rani *et al.*, 2006).
- (iv) **Novelty** - According to section 15 of the Act (PPV and FRA), “Novelty” means commercial novelty *i.e.*, the propagating or harvested material of the variety should not have been sold or otherwise disposed off earlier than one year in India, from the date of filing of application of registration or outside India, not earlier than six years in the case of trees or wines or not

earlier than four years in any other case (new in commercial sense) and a unique and unambiguous denomination (name of the new variety).

Being a signatory to the General Agreement on Trade and Tariffs (GAAT), Government of India has enacted its *sui generis* system, Protection of Plant Varieties and Farmers' Right Act (PPV and FRA), 2001 for protection of plant varieties based on Distinctness, Uniformity and Stability (DUS) test, apart from novelty, as the existing UPOV models of plant variety protection was not suitable for Indian requirements.

The process of variety identification includes several steps such as identification of a variety, confirmation of the variety, distinctness of the variety from all other reference collections, purity of the variety and characterization of the variety which enumerates its full descriptors. The concept of distinctness, uniformity and stability are thus fundamental to the characterization of a variety as a unique creation. Registration is allowed for three types of plant varieties, new varieties bred by breeders, extant varieties and farmers' varieties subject to their fulfilling the conditions of Distinctness, Uniformity and Stability and Novelty in case of breeder's variety. The first step to implement our PPV and FR Act provisions is formulation of National Test Guidelines for conducting DUS tests. The new variety should pass legal examinations to be commercialized and receive the certificate for the Plant Breeders' Rights, a part of which consists of DUS tests according to morphological characteristics.

The new varieties will be subjected to DUS testing by PPV and FR Authority located in New Delhi. The PPV and FR Authority had developed and published in its journal, guidelines for DUS test for each crop (Anonymous, 2007) for the registration and protection of

newly developed varieties from unauthorized utilization. The tests are envisaged to generate comprehensive data on the attributes of a variety so as to compare these with the varieties of common knowledge or similar existing varieties. These shall be based on multi-location field trials conducted for at least two crop seasons (Anonymous, 2007) at minimum two location, along with special chemical laboratory tests (Section 29, PPV and FR rules).

As per the 1991 Act of UPOV, protection granted for the new variety authorizes the breeder with the exclusive right to commercially exploit the variety by direct sale or by licensing to others for sale. Nevertheless, the UPOV Act, 1991 also provides for the protection of Essentially Derived Varieties (EDV) in which the breeder of an Essentially Derived Variety (EDV) needs to obtain authorization of the breeder of the original variety for commercial exploitation of the new variety. Farmers' rights were available to the farmers in the UPOV Act, 1978, but UPOV Act 1991 deprives farmers of their rights to reuse their produce as a seed.

2.1.1 Genetical Parameters *viz.*, Variability, Heritability and Genetic Advance

The relative estimates of variability and their heritable components for yield contributing characters in the germplasm are of immense value in any breeding programme in achieving higher yields. The phenotype of quantitative trait is a combined product of genotype, environment and their interaction. Therefore, the success of any breeding activity depends on the extent of genetic variability available for utilization in crop improvement.

Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present

in relation to observed variation. Basic information on heritability is a prerequisite for planning any breeding programme. High heritability indicates that it should be easy to conduct effective selection for the trait. Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population. Johnson *et al.* (1955) reported that though the heritable estimates give useful indication of relative values of selection based on phenotypic expression. The genetic gain should also be considered to arrive at a more reliable conclusion.

Shanthi and Singh (2001) evaluated 16 rice mutants to study the variability. High GCV and PCV were recorded for number of grains per panicle and grain yield plant⁻¹. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height, number of grains per plant and 1000 grain weight.

The extent of genetic variation in 16 parents and 48 hybrids was studied by Subbaiah *et al.* (2011) for yield and its components and 25 quality characters. High GCV and PCV were recorded for harvest index, total number of productive tillers per plant and gelatinization temperature in parents.

Babu *et al.* (2012) carried out a study of genetic parameters for yield, yield attributing, quality and nutritional characters in 21 rice hybrids. The characters *viz.*, number of filled grains per panicle, number of chaffy grains per panicle and iron content exhibited high GCV and PCV. The characters *viz.*, number of filled grains per panicle and water uptake exhibited high heritability coupled with high genetic advance.

Pratap *et al.* (2012) evaluated 100 high yielding rice genotypes for variability studies. High estimates of heritability, genetic advance, genotypic and phenotypic coefficients of variation were recorded for panicle hill⁻¹, flag leaf area and grain yield hill⁻¹.

Aditya and Bhartiya (2013) evaluated 18 rice genotypes for genetic parameter studies of 15 quantitative traits. The estimates of GCV and PCV were highest for grain yield plot⁻¹. The broad sense heritability was highest for plant height.

Gangashetty *et al.* (2013) used 42 rice genotypes to know the extent of genetic variability. High GCV and PCV were observed for plant height, number of tillers per plant, number of productive tillers per plant, panicle weight, grain length, test weight, iron and zinc content and grain yield plant⁻¹. High heritability with high genetic advance was observed for all traits except days to 50 per cent flowering.

Veni *et al.* (2013) assessed 70 rice genotypes for genetic variability. High GCV and PCV were recorded for water uptake (26.28), grain yield plant⁻¹ (26.18) and test weight (20.35). High heritability coupled with high genetic advance as per of mean was observed for grain yield plant⁻¹, water uptake, test weight and productive tillers per plant.

Dhurai *et al.* (2014) conducted genetic variability studies in 32 rice varieties. The higher magnitude of PCV and GCV was recorded for number of grains per panicle and grain yield plant⁻¹. High heritability coupled with high genetic advance as per cent mean was recorded for plant height, number of effective tillers per plant, panicle length, number of grains per panicle, kernel elongation ratio, kernel length after cooking, 1000-grain weight, harvest index and grain yield plant⁻¹.

Islam *et al.* (2015) evaluated 23 rice genotypes for genetic variability. High GCV and PCV were recorded for plant height, number of filled grains per panicle, days to 50% flowering, 1000 grain weight, grain width and grain yield.

Senapati and Kumar (2015) evaluated 22 Recombinant Inbred Lines (RIL's) for genetic variability, heritability and genetic advance. High PCV and GCV were observed for grain yield plant⁻¹, 1000 grain weight, L/B ratio, grain breadth and panicle weight. High heritability coupled with moderate to high genetic advance as per cent of mean was recorded for plant height, panicle weight, grain length, grain L/B ratio, 1000 grain weight and yield plant⁻¹.

Devi *et al.* (2016) assessed PCV, GCV, heritability and genetic advance in 27 rice genotypes. Higher estimates of PCV and GCV were observed for yield plant⁻¹ and filled seeds per panicle. High heritability in broad sense and high genetic advance as percent of mean were exhibited by effective tillers, plant height, flag leaf length, filled seeds per panicle, test weight, yield plant⁻¹, head rice recovery and length/breadth ratio.

The extent of genetic variation in 36 rice genotypes was studied by Abebe *et al.* (2017). High to medium heritability coupled with high GCV and high genetic advance as percentage of means were exhibited for plant height and grain yield.

Bhinda *et al.* (2017) studied genetic variability for in 42 advanced breeding lines of rice for 15 characters. Alkali spreading value exhibited highest GCV (19.44%) and PCV (21.07%) followed by filled grains per panicle (GCV 14.83% and PCV 19.90%). High heritability coupled with high genetic advance was reported for gel-consistency, plant height, filled grains per panicle, number of grains per panicle and days to 50% flowering.

Umarani *et al.* (2017b) carried out an experiment to assess the variability, heritability and genetic advance in 70 landraces of rice for 16 agro- morphological and grain quality parameters. Among all the characters, total number of grains per panicle

exhibited highest PCV and GCV, whereas lowest PCV and GCV were recorded for spikelet fertility.

Chuchert *et al.* (2018) evaluated 22 rice genotypes for genetic variability in nine traits. High phenotypic and genetic coefficients of variation were observed for yield plant⁻¹, number of panicles per plant, and number of spikelets per panicle. High broad-sense heritability was recorded for yield plant⁻¹.

Gyawali *et al.* (2018) evaluated seven rice genotypes for genetic variability. Genotypic and phenotypic coefficients of variation were high for effective tillers per m², 1000 grain weight, grain yield, harvest index. The highest heritability was recorded by the character, anthesis days (0.97) and genetic advance was found highest for effective tillers per m² (33.80).

Ranjith *et al.* (2018) assessed GCV, PCV, heritability and genetic advance in 30 rice genotypes using 12 characters. High PCV and GCV were observed for fertile grains, flag leaf area and tillers per hill. High heritability coupled with high genetic advance was recorded for plant height.

Singh and Verma (2018) estimated genetic variability, heritability and genetic advance for 15 characters. High genotypic and phenotypic coefficients of variation were observed for flag leaf area and panicle bearing tillers per plant. High heritability coupled with high genetic advance as per cent of mean was observed for grains per panicle, panicle bearing tillers per plant, spikelet per panicle and plant height.

Aravind *et al.* (2019) evaluated 45 mutant lines for genetic variability of 12 characters. High GCV and PCV were observed for number of productive tillers and single plant yield. The traits *viz.*, number of productive tillers, leaf blade width, 1000 grain weight,

LB ratio and single plant yield has high heritability along with genetic advance as percent of mean.

Rahangdale *et al.* (2019) evaluated 67 rice genotypes for 28 morphological and quality traits. High GCV and PCV were obtained for number of spikelets per panicle, spikelet density, grain yield plant⁻¹, fertile spikelets per panicle, biological yield plant⁻¹ and panicle weight plant⁻¹. High heritability accompanied with high genetic advance was observed for the traits 1000 grain weight (g), head rice recovery (%), spikelet fertility (%), harvest index (%), number of spikelets per panicle, fertile spikelets per panicle, spikelet density, grain yield plant⁻¹ (g), panicle weight plant⁻¹ (g), number of tillers per plant and number of productive tillers per plant.

Sao *et al.* (2019) observed high PCV and GCV for number of filled grains per panicle, number of unfilled grains per panicle, total spikelets per panicle, grain weight per plant, panicle weight and harvest index using 47 rice genotypes. High heritability with high genetic advance as percent mean was observed for all yield attributing traits like grain weight per plant, harvest index %, number of filled grains per panicle, panicle weight.

Bhargavi *et al.* (2022) observed significant differences among 52 genotypes for all the traits studied. High PCV and GCV were recorded for the traits *viz.*, panicle number per plant, weight of 1000 fully developed grains and grain yield plant⁻¹ indicating that large amount of variation was present among the genotypes for these characters. Whereas, low PCV and GCV were recorded for the traits *viz.*, grain length, decorticated grain length and length/breadth ratio indicating that the variability for these characters among the genotypes was meagre. The variability studies indicated

that the estimates of PCV were slightly higher than the corresponding GCV for all the characters indicating that the characters were less influenced by the environment. High heritability coupled with high genetic advance as per cent of mean was recorded for time of heading, stem length, panicle number per plant, weight of 1000 fully developed grains, decorticated grain width and grain yield plant⁻¹ indicating that these traits were mostly under the control of additive gene action and direct selection of these traits would be effective for crop improvement. While high heritability coupled with moderate genetic advance as per cent of mean was observed for the traits *viz.*, panicle length of main axis, time of maturity, grain length, grain width, decorticated grain length and length/breadth ratio.

Kushwaha *et al.* (2022) reported that, analysis of variance revealed significant differences among genotypes for all the characters. Brasali was the highest yielder suggesting that it can be used for crossing programme for improvement in yield. High values of GCV, PCV, heritability and genetic advance as percent of mean were observed for grain yield per plant, 1000 grain weight and plant height indicating that these traits can be used as selection indices for yield improvement. Grain length, root volume, panicle length of main axis, number of panicles, showed positive significant correlation with grain yield per plant. Hence, selection for any one of these characters would ultimately bring improvement of in grain yield. Grain length, root volume, panicle length of main axis and leaf length showed high direct effect on grain yield per plant. Hence, selection based on these characters would be more effective for yield improvement.

Table 2.1 List of previous studies on molecular characterization of rice genotypes

Marker system	DUS test	Key message	References
SSRs	D	13 rice cultivars (four commercial traditional Basmati, six cross-bred Basmati and three non-Basmati varieties) were evaluated using 35 SSRs. SSR analysis generated polymorphism sufficient to differentiate all the 13 rice genotypes	Pal <i>et al.</i> (2004)
SSRs	D, U, S	Mapped SSRs of 12 rice linkage groups could differentiate all 23 aromatic varieties. No variation was seen in the analysis of 20 individuals of all seed classes of “Pusa Basmati 1” using 55 SSRs, hence suggesting SSRs for uniformity and stability tests	Singh <i>et al.</i> (2004)
SSRs	D	Suggested the usage of SSR markers in genotype identification, monitoring purity and adulteration and plant variety protection	Siwach <i>et al.</i> (2004)
SSRs	D	The DNA fingerprinting helped to distinctly identify and characterize nine varieties using 18 different RM primers	Chakravarthi and Naravaneni (2006)
SSRs	D	Microsatellite markers could efficiently identify indigenous non- Basmati aromatic rice genotypes and support Intellectual Property Protection	Joshi and Behara (2017)
SSRs	D	A high degree of polymorphism obtained among eight rice genotypes using 14 SSRs suggested that SSRs would also be useful in variety fingerprinting and identification	Malky <i>et al.</i> (2007)

Marker system	DUS test	Key message	References
SSRs	D	SSRs separated rice varieties into Basmati and non-Basmati group	Sarao <i>et al.</i> (2009)
SSRs	D	The microsatellite markers employed for DNA fingerprinting were able to differentiate the parental lines of respective hybrids included under study and also useful for variety identification	Tamilkumar <i>et al.</i> (2009)
SSRs	D	Identified three varietal specific alleles, RM-11/147, RM-151/289, RM-153/178 for BR-11, Badshabhog and BR-19 cultivars using SSRs and suggested that a meaningful data could be obtained through DNA fingerprinting using SSRs	Rahman <i>et al.</i> (2010)
SSRs	D	The highly polymorphic SSRs could be used for quick and reliable detection of specific genotype	Singh and Singh (2012)
SSRs	D	SSRs can efficiently complement morphological descriptors as they are useful for identification of closely related cultivars through fingerprinting	Zhu <i>et al.</i> (2012)
SSRs	U	A set of SSRs was defined to allow the identification and certification of <i>O. sativa</i> varieties including INIA and foreign varieties. Thus, SSRs could be a good complement to the existing agro-morphological data when varieties are closely related	Becerra <i>et al.</i> (2015)
SSRs	S	A combination of five polymorphic SSRs were successful in differentiating 40 varieties, suggesting these SSRs as useful set for complementing DUS tests for stability analysis.	Pourabed <i>et al.</i> (2015)

Marker system	DUS test	Key message	References
SSRs	D	The SSRs (RM206, RM21, RM55, RM258 and RM433) were found robust enough to distinguish the duplicate and similar named rice germplasm for their higher PIC values (> 0.86)	Ahmed <i>et al.</i> (2016)
SSRs	D	The allelic diversity revealed by 45 SSR primers was sufficient enough to distinguish the tested 120 aus rice genotypes through DNA fingerprinting	Islam <i>et al.</i> (2017)
SSRs	D	The average similarity index of 0.65 for morphological data and 0.35 for SSR data apparently defines the advantage of SSR over morphology in unambiguous and quick identification of closely related varieties	Vigneshwari <i>et al.</i> (2017)
SSRs	S	69 SSR markers were used for their molecular characterization and discrimination of 24 entries of rice. The molecular markers showing PIC value >0.5 can be used to distinguish NILs from their respective parents apart from gene linked markers of targeted trait	Reddy and Rani (2018)
SSRs	D, U, S	Out of 25 gene-specific markers used for screening, 18 were polymorphic. The number of alleles of the polymorphic markers ranged from two to three with an average of 2.05 alleles per locus. The PIC values of these gene-specific markers ranged from 0.037 to 0.369 with an average of 0.212. Varietal specific fingerprints were generated using these 18 markers	Bhargavi <i>et al.</i> (2022)

Marker system	DUS test	Key message	References
SSRs	D, U, S	A total of 15 loci were assigned to the fifteen primer pairs. Altogether 33 allelic variants were detected among the twenty-two cultivars with an average of 2.2 alleles per locus. A total of 33 shared and 3 unique allelic variants were generated in the form of amplified products. Average PIC values observed was 0.71.	Kushwaha <i>et al.</i> (2022)

Simple Sequence Repeats; PIC: Polymorphism Information Content; D: Distinctness; U: Uniformity; S: Stability.

2.1.2 Germplasm characterization using molecular markers

The variety identification serves the important goals such as mitigating legal claims, confirming Intellectual Property Rights and maintenance of genetic purity (Patra *et al.*, 2010). The current plant variety identification for their protection relies on morphological description of plant varieties. However, establishing identity of varieties based on the DUS descriptors is quite problematic and difficult due to their limited number, stage specificity and environmental influence which complicate their evaluation (Nuel *et al.*, 2021 and Cooke and Reeves, 2021).

In contrast, DNA or molecular markers are free from the environmental effects and could be applied at different stages of plant growth (Noli *et al.*, 2018).

The increased availability and cost-efficiency of DNA-based markers in recent years makes them an attractive option to explore their use to supplement or even ultimately replace the existing morphological and protein-based approaches (Jamali *et al.*, 2019). Among the DNA based markers, Microsatellite or Simple Sequence Repeat (SSR) markers were mostly used by many of the scientists to identify the rice genotypes. However, employment of gene- specific markers is more reliable in identification of a variety as these markers are tightly linked to the gene controlling the phenotypic expression.

DNA fingerprinting or profiling developed by using molecular markers to describe the combined use of several single locus detection systems is being used as a versatile tool for characterization of rice genotypes. Owing to these reasons, the International Union for the Protection of New Varieties of Plants (UPOV), an intergovernmental organization whose system of plant

variety protection is intended to encourage innovation in the field of plant breeding (Jordens, 2018) has called for the adoption of a DNA-based system that will enable examiners to deploy trait-specific DNA markers in DUS testing (Jamali *et al.*, 2019).

2.1.3 Characterization of germplasm using morphological DUS descriptors

Plant morphological characters have been recognized as the universally undisputed descriptors for DUS testing and varietal characterization of crop varieties. Use of morphological descriptors in sequential fashion is useful and convenient to discriminate different varieties (Patra *et al.*, 2010). The morphological DUS descriptors can be effectively used for identification and grouping of varieties and varieties satisfying the DUS criteria for these morphological descriptors could be registered under the PPV and FR Act for obtaining Plant Breeder's and Farmer's rights. There are 62 DUS descriptors (29 essential and 33 additional) in rice as per the national guidelines for the conduct of tests for Distinctness, Uniformity and Stability. Out of 62 DUS traits, the 29 essential traits should be examined and included in the description of varieties, which would be useful for identification of rice genotypes. A brief resume of work done in India and abroad with reference to this is discussed below:

Patra *et al.* (2010) assessed 60 morphological DUS descriptors of 18 Basmati rice varieties. Among these, 26 were monomorphic, 11 were dimorphic and seven were polymorphic indicating their potential for varietal characterization and distinctiveness.

Joshi *et al.* (2011) characterized 20 indigenous aromatic rice varieties using 60 morphological DUS descriptors. Out of these, 46 traits were visually assessed and 14 were measurable traits. Among 46 morphological characters, 24 were monomorphic, 17 were dimorphic and five were polymorphic.

Chakravorty and Ghosh (2012) characterized 51 landraces of rice using 46 agro-morphological traits following DUS test. Out of 51 varieties studied, 27 were found to be distinctive on the basis of 22 essential and 24 additional characters.

Characterization of 65 landraces of rice was done by Rao *et al.* (2013) using 43 DUS descriptors. Out of 65 landraces, 32 were found to be distinctive on the basis of 22 essential and 24 additional characters.

Characterization of 20 landraces of rice was done by Sinha and Mishra (2017) using DUS test. Out of these 20 investigated varieties, 11 varieties were distinctive for five essential and 18 additional characters.

Umarani *et al.* (2017a) characterized 70 landraces of rice using 14 DUS characters. Out of 14 characters, stem anthocyanin colouration of node was dimorphic, three were trimorphic, six were tetramorphic, lemma anthocyanin colouration of apex and amylose content showed five states of expression. Based on decorticated grain colour six groups were made.

Vigneshwari *et al.* (2017) characterized 13 commercially cultivated rice varieties of Tamil Nadu using 31 morphological traits. The level of discrimination was high in quantitative grain characters compared to qualitative characters.

Kumar *et al.* (2018) characterized 55 rice genotypes following the DUS guidelines. Significant variation was observed for the

characters like coleoptile colour, intensity of leaf green colour, culm attitude, flag leaf attitude, stem length, lemma and palea colour, grain length and test weight.

Manjunatha *et al.* (2018) assessed 25 DUS descriptors to characterize 60 landraces of rice including the aromatic genotypes collected from different parts of Wayanad, Kerala. Out of these, three characteristics were monomorphic, seven were dimorphic, six were trimorphic, seven were tetramorphic, decorticated grain shape showed five states of expression and lemma and palea colour recorded six states of expression.

Varietal identification of four rice varieties from Chhattisgarh was carried out through DUS Characterization by Tiwari *et al.* (2019) and stated that the morphological DUS descriptors could be effectively used for identification and grouping of varieties.

Mondal *et al.* (2019) characterized 21 rice varieties using 60 DUS descriptors (46 qualitative and 14 quantitative). Time to 50% heading, decorticated grain shape, colour of lemma and palea were the descriptors showing more discrimination. Eight qualitative and eight quantitative traits exhibited uniformity as determined by the recommended level.

DUS testing of 66 rice varieties was done by Raghavendra *et al.* (2021) using 27 morphological descriptors. This study demonstrated the effective use of DUS testing in varietal identification.

Patel and Srivastava (2015) characterized the aromatic rice varieties of Chhattisgarh using 45 morphological DUS descriptors. All the 45 unique morphological traits exhibited variability except ligule colour. The traits like grain size, grain shape and plant height contributed towards more diversity.

Sanyal and Joshi (2020) characterized 61 extant varieties of Basmati and non-Basmati groups of rice using 55 DUS descriptors. Their study revealed that six characters were monomorphic, nine were dimorphic and 40 were polymorphic.

Komala *et al.* (2020) characterized eight rice genotypes using 56 morphological DUS descriptors. Among 56 characters studied, the variation was observed in 37 characters.

Rawte and Saxena (2021) used 19 qualitative and 11 quantitative agro- morphological traits to characterize 100 rice accessions. The descriptors offering the most discrimination were time to 50% heading, time to maturity days, 1000 grain weight, stem length, grain length and width.

Banshidhar *et al.* (2019) worked on DUS characterisation of advanced recombinant lines of Kalanamak rice for 47 visually assessed characters and 15 quantitative characters. Out of these characters studied, 27 were monomorphic, 18 were dimorphic and two were polymorphic.

The agro-morphological characterization of aromatic *Harinakhuri* rice landrace was done by Ghosh *et al.* (2021). The lemma and palea of matured grain was straw coloured with purple spot at tip and sterile lemma in purple colour.

Gour *et al.* (2021) characterized 83 indigenous rice lines based on 31 morphological DUS descriptors. Basal leaf sheath colour, colour of tip of lemma, lemma and palea colour showed highest variation in germplasm.

Bhargavi *et al.* (2022) identified 52 rice varieties using 22 DUS descriptors. Out of 22 morphological DUS descriptors studied, four were monomorphic, nine were dimorphic and the remaining nine were polymorphic. Of these 18 traits (both dimorphic and polymorphic), only 10 were essential traits.

Kushwah *et al.* (2022) evaluated 22 local lowland rice cultivars employing DUS based descriptors. Out of 36 DUS descriptors taken under study, no variation was found in traits 9 traits while 13 were dimorphic and 14 showed polymorphic variation.

2.1.4 Genetic diversity analysis using both DUS descriptors and molecular markers

The analysis of genetic variation within and among elite breeding materials is of fundamental interest to plant breeders. Diversity based on phenological and morphological characters usually varies with environments and evaluation of these traits requires growing the plants to full maturity prior to identification. Molecular markers in addition to morphological characters have proven to be powerful tool in the assessment of genetic variation and in the elucidation of genetic relationships within and among species. Several molecular markers have been widely used in genetic diversity studies *viz.*, SSRs (Simple Sequence Repeats) (McCouch *et al.*, 2018; Garriss *et al.*, 2019; Chuang *et al.*, 2021; Kanawapee *et al.*, 2021), providing greater confidence for the assessment of genetic diversity and relationships. Information regarding genetic variability at molecular level could be used to help, identify and develop genetically unique germplasm that compliments existing cultivars. A brief resume of work done in India and abroad with reference to this is discussed below.

Genetic relationship was assessed among 24 rice genotypes by UPGMA clustering using 50 SSRs by Siwach *et al.* (2004). This study revealed that three traditional Basmati varieties were closely related.

Chakravarthi and Naravaneni (2006) worked on the genetic

diversity analysis of 15 elite rice genotypes using 30 SSR primers. Cluster analysis grouped the rice genotypes into 10 classes in which japonica types DH-1 (Azucena) and Moroborekan clustered separately from *indica* types. Mahalingam *et al.* (2016) estimated genetic diversity among 51 restorer and five CMS lines in hybrid rice breeding. Cluster analysis using NTSYS generated dendrogram divided all the 56 parental lines into 13 different clusters with 80 per cent coefficient of similarity.

Islam *et al.* (2017) worked on the allelic diversity and the relationship among 120 *aus* rice landraces through DNA fingerprinting using microsatellite (SSR) markers. The genetic distance-based results obtained in the un-rooted neighbor joining tree clustering revealed nine genetic groups.

Vigneshwari *et al.* (2017) characterized 13 rice varieties of Tamil Nadu using 31 morphological traits and more than 200 SSR markers. Out these SSR markers, 88 showed polymorphism. Cluster analysis based on morphological characters grouped the varieties of medium and long slender grain type in one cluster and short bold grain type into another cluster at about 65 per cent similarity level. The cluster analysis of SSR markers grouped the varieties into four major clusters at a similar level of 35 per cent.

Aljumaili *et al.* (2018) worked on genetic diversity among 53 aromatic rice accessions using 32 SSR markers. The dendrogram based on UPGMA and Nei's genetic distance classified these 53 rice accessions into 10 clusters.

Jalaluddin *et al.* (2017) analysed genetic diversity of 22 *indica* rice cultivars through DNA fingerprinting using five microsatellite markers (RM1, RM3, RM168, RM226 and OSR19). The highest

genetic diversity (GD), 0.6336 was detected in locus RM168 and the lowest (0.2496) on locus OSR19. Average GD was 0.4446, indicating a moderate level of genetic diversity existing among the tested cultivars.

Joshi *et al.* (2017) characterized 19 rice varieties considering 52 DUS traits. High difference between PCV and GCV values for panicle number per plant shows high environmental effect. The varieties were grouped into different clusters based on the eight grouping characters of National DUS testing guidelines.

Reddy and Rani (2018) have done molecular and morphological characterization of 24 Near Isogenic Lines (NILs) of rice developed for major abiotic stresses. Results of molecular characterization showed genetic diversity among 24 entries. Cluster analysis grouped 24 entries into two distinct clusters at similarity coefficient of 33 per cent.

Herrera *et al.* (2018) studied the genetic relationship of some Venezuelan rice cultivars by SSR markers and found low genetic diversity among them.

Joshi *et al.* (2020) studied 20 indigenous aromatic rice varieties using 60 morphological DUS descriptors. On the basis of grouping characteristics seven varieties showed unique profiles.

Hossain *et al.* (2020) determined the allelic diversity and relationship of 12 elite aromatic rice cultivars using 24 SSR markers. The genetic distance- based results seen in the un-rooted neighbour-joining tree and UPGMA clustering revealed five genetic groups in which closely related genotypes were clustered together.

Alice *et al.* (2020) evaluated 195 rice accessions for diversity pattern among them. The genotypes were grouped into 10 clusters. The inter-cluster distance is higher than intra-cluster indicating

wide genetic diversity among the genotypes. The highest inter-cluster distance was observed between cluster VI and VII.

Choudhary *et al.* (2021) performed genetic diversity studies using 64 SSRs in 100 rice genotypes. Of 64 rice SSR primers studied, 52 showed polymorphism. A total of 184 alleles was identified averaging 3.63 alleles per locus. Cluster analysis grouped the 100 genotypes into five clusters.

Rabey *et al.* (2021) used AFLP and SSR markers to study the genetic diversity of eight rice cultivars. The Polymorphism Information Content value for the two types of assays was 0.825 and 0.967 for SSR and AFLP markers respectively. Cluster analysis was used to address relationship between the rice cultivars based on the SSRs and AFLP data.

Raghavendra *et al.* (2021) worked on DUS testing and genetic diversity analysis of 66 rice varieties using 27 morphological descriptors. Genetic similarities among genotypes varied from 0.11 to 1.0 with an average of 0.36. The cluster analysis grouped all the genotypes into two major clusters at 0.21 level of genetic similarity.

Roy and Sharma (2021) worked on assessment of genetic diversity in 84 rice cultivars of West Bengal through DUS characterization and a dendrogram constructed showed genetic diversity among 84 cultivars by grouping them into five major clusters. All the descriptors evaluated in this study have showed that there is enough genetic diversity among cultivars.

Samal *et al.* (2021) characterized 48 traditional aromatic rice varieties using 24 ISSR markers and morphological markers. The genetic diversity was evaluated using UPGMA cluster dendrogram which identified two clusters with a similarity coefficient of 53%.

The genetic diversity and phylogenetic relationship of six

improved African lowland rice varieties *viz.*, BW-348-1, FARO-44, FARO-57, NERICA-L-19, NERICA-L-34 and WITA-4 was investigated using 129 SSR primers distributed on 12 chromosomes of rice by Adegbaaju *et al.* (2015). The SSR based dendrogram generated clustered two genotypes BW348-1 and FARO-44 together and three genotypes FARO-57, NERICA-L-19 and WITA-4 together.

Kunusoth *et al.* (2021) worked on genetic diversity assessment of 24 elite Indian rice varieties using 24 agro-morphological traits and 86 SSR markers. Genetic diversity assessment based on SSR markers displayed genetic similarity coefficients and grouped the varieties into five major clusters.

Singh and Sengar (2021) have done DNA fingerprinting using SSR, ISSR and RAPD markers to evaluate the genetic divergence of 30 rice varieties. The dendrogram developed for aroma and quality traits by UPGMA showed that the genotypes with common phylogeny and geographical orientation tend to cluster together.

Bhargavi *et al.* (2022) worked on 52 rice varieties using 25 gene specific SSR markers to evaluate genetic divergence. Out of 25, 18 SSR markers count to be polymorphic. PIC values ranged from 0.037 to 0.369 with an average of 0.42.

Khushwaha *et al.* (2022) studied genetic diversity of 22 rice genotypes using 15 SSR markers. Average 22 alleles per locus were found and average PIC value 0.563 reported.



MATERIAL & METHODS

CHAPTER-III

MATERIAL AND METHODS

The field experiments of present investigation “**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**” were conducted in the two independent *Kharif* seasons of 2020 and 2021 on experimental farm at Agricultural Research Station, Shirgaon, District- Ratnagiri and experimental farm at Regional Agricultural Research Station, Karjat, District- Raigad respectively. The molecular marker analysis was carried out at Plant Biotechnology Centre, College of Agriculture, Dapoli. The biochemical analysis *viz.*, amylose, calcium content and alkali spreading value was done at biochemistry laboratory of Soil Science and Agricultural Chemistry section, Regional Agricultural Research Station, Karjat District- Raigad. Micronutrient analysis particularly Zinc and Iron content was carried out by using atomic absorption flame spectrophotometer unit available at Khar-land Research Station, Panvel, District- Raigad.

3.1 Climate and weather:

Geographically experimental farm of Agricultural Research Station, Shirgaon is situated between 17°01'28.3"N latitude and 73°17'51.7"E longitudes at 46 meter above mean sea level; which falls under South Konkan Coastal Zone (MH-1) as per agro climatic zone (NARP) whereas experimental farm of Regional Agricultural Research Station, Karjat, District- Raigad is situated between 18°30'56.71" N latitude and 94°15'37.25" E longitudes at 38 meter above mean sea level which falls under North Konkan Coastal Zone (MH-2) as per agro climatic zone (NARP).

3.2 Experimental details:

Total two experiments were conducted and observations recorded accordingly to fulfill the three objectives of present investigation as follows.

Table 3.1 Objective wise experimental details:

SN	Objectives	Experiment conducted	Observations recorded
1.	Phenotypic characterization and estimation of genetical parameters of diverse rice genotypes	Experiment No. 1 Field experiment conducted at ARS, Shirgaon and RARS, Karjat during two independent <i>Kharif</i> seasons of 2020 and 2021 respectively.	As per Table 3.4
2.	Establishment of DNA profiles of rice genotypes using SSR markers.	Experiment No. 2 95 genotypes sown in individual pots to collect leaf samples for DNA isolation and PCR amplification was done for 17 SSR primers.	As per Table 3.13
3.	Generate database of diverse genotypes of rice based DUS guidelines.	Observations for DUS descriptors were recorded from the field and laboratory experiments conducted for Experiment No. 1 and Experiment No. 2 respectively.	As per Table 3.7 and 3.8

Table 3.2 Experimental design and layout (Experiment No. 1) :

Particulars	<i>Kharif 2020, ARS, Shirgaon</i>	<i>Kharif 2021, RARS, Karjat</i>
Date of sowing	12 June 2020	12 June 2021
Date of transplanting	8 July 2020	8 July 2021
Design and Layout	RBD	RBD
Number of Genotypes	95	95
Replications	03	03
Row length	6 m	6 m
Spacing	20cm x 15cm	20cm x 15cm

3.3 Experimental material:

The 95 genotypes were obtained from various sources as details given below.

Table 3.3 Experimental material along with source:-

SN	Genotype	Source	SN	Genotype	Source
I	Red kernel local lines		II	Restorer lines	
1	MO-6	ARS, Moncomba	25	KJT-1R	ARS, Karjat
2	MO-8		26	KJT-2R	
3	MO-13		27	KJT-3R	
4	MO-17		28	KJT-4R	
5	MO-19		29	PR-114	IIRR, Hyderabad
6	Khara Rata	KRS, Panvel	30	RTN 11-2-1-3	ARS, Shirgaon
7	Mayekar Bhat	ARS, Karjat	31	PR-118	IIRR, Hyderabad
8	Munga	ARS, Shirgaon	32	DRR-215	
9	Mahsad		33	RTN-69-1-1	ARS, Shirgaon
10	Waksal-207		34	NAUR-1	NAU, Navsari
11	Barmil		35	BL-184AR	ARS, Karjat
12	Jyoti		36	Gurjari	NAU, Navsari
13	Patani-6		37	DRR-50-12	IIRR, Hyderabad
14	Bhadas-79		38	DRR-363-5	
15	Pandy		39	DRR-50-13	
16	Dular		40	DRR-50-10	
17	Try-1		41	DRR-86-8	
18	Kochari		42	IR-63879-195-2-2-3-2	IRRI, Manila,
19	Lal Patani		43	RTN-27-1-1-2	ARS, Shirgaon
20	Dodak		44	RTN-214-1-1-1-2	

SN	Genotype	Source	SN	Genotype	Source
21	Karhad	ARS, Shirgaon	45	VDN-9-10-1	ARS, Vadgaon
22	Ratnagiri 7		46	VDN-10-18	
23	Bela		47	RTN-35-1-1	ARS, Shirgaon
24	Valai		48	Sahyadri 5 R	
49			HRTMS-61		
50			CR-3993-2-24-45-2	IIRR, Hyderabad	
III	Aromatic lines		IV	Lines responsive to biotic and abiotic stresses	
51	P Basmati	IARI, N. Delhi	70	RS-1113	IIRR, Hyderabad
52	S Basmati		71	RP Bio 197	
53	Kothambir Sal	ARS, Karjat	72	RP-BIO-226	
54	Chinoor	PDKV, Akola	73	Ajaya	
55	P Sugandha-1	IARI, N. Delhi	74	KJT 1	ARS, Karjat
56	P Sugandha-3		75	KJT 2	
57	P Sugandha-4		76	IR-64	IRRI, Manila
58	P Sugandha-5		77	MUDGO	
59	Bhadasbhog	IIRR, Hyderabad	78	MILYANG 46	
60	CR2713-180		79	PTB 33	RARS, Pattambi
61	Kalanamak		80	MTU1010	RARS, Maruteru
62	NDR6315		81	BG 367-2	IRRI, Manila
63	P Samruddhi	MPKV, Rahuri	82	MILYANG 63	
64	Indrayani	ARS, Vadgaon	83	FL 478	
65	Dhanesal	IIRR, Hyderabad	84	MUT NS 1	
66	Ambemohar	ARS, Vadgaon	85	RATHU HEENATI	
67	K Shatabdi	ARS, Karjat	86	SINNA SIVAPPU	
68	Bhogwati	ARS, Radhanagari	87	IRRI 190	
69	Sugandha	VNMKV, Parbhani	88	IRRI 193	
			89	ARC 10550	
			90	S MAHSURI	IIRR, Hyderabad
			91	IRRI 123	IRRI, Manila
			92	IRRI 104	
			93	IRRI 192	
			94	Sonsali	IIRR, Hyderabad
	95	TN-1			

3.4 Brief cultural practices

Nursery beds were prepared by applying 15 Kg N as urea, 20 Kg P₂O₅ as single super phosphate and 2 Kg K₂O as murate of potash per 1000 m² of nursery bed. FYM @ 10t/ha was also added.

Seeds were sown and 25 days old seedlings were transplanted in plots with a basal dose of 50 Kg N, 50 Kg P₂O₅ as, 50 Kg K₂O as 3.3 kg/Guntha Suphala (15:15:15). Twenty five Kg each of nitrogen was then applied at 30 days after transplanting and at 65 days after transplanting. The crop was grown in shallow submergence of 2.5 cm during tillering and water was drained off seven days before harvest.

3.5 Sampling procedure

The observations were made on 30 plants or parts of 30 plants, which were divided among 3 replications (10 plants in each replication) as per the guidelines of PPV & FR Authority (Anonymous, 2009).

Table 3.4 Observations recorded on 27 yield and yield contributing characters, including 14 measurable DUS descriptors along with abbreviations (Objective 1)

SN	Character	Abbreviation	Remark
1	Days to 50% Flowering (Nos.)	DFF (Nos.)	Measurable DUS descriptor No. 20
2	Plant Height (cm)	PHT (cm)	Yield and yield contributing character
3	Stem Length Excluding Panicle (cm)	SLEP (cm)	Measurable DUS descriptor No. 29
4	Number of Tillers Plant ⁻¹	TLPP (Nos.)	Yield and yield contributing character
5	Panicle Length of Main Axis (cm)	PLMA (cm)	Measurable DUS descriptor No. 33
6	Number of Spikelets Panicle ⁻¹	SPP (Nos.)	Yield and yield contributing character
7	Fertility (%)	Fertility (%)	Yield and yield contributing character
8	Days to Maturity (Nos.)	DM (Days)	Measurable DUS descriptor No. 47

SN	Character	Abbreviation	Remark
9	Test Weight of 1000 Grains (g)	TW (g)	Measurable DUS descriptor No. 50
10	Grain Length (mm)	GL (mm)	Measurable DUS descriptor No. 51
11	Grain Width (mm)	GW (mm)	Measurable DUS descriptor No. 52
12	Grain Yield Plant ⁻¹ (g)	GYPP(g)	Yield and yield contributing character
13	Straw Yield Plant ⁻¹ (g)	SYPP (g)	Yield and yield contributing character
14	Grain Yield/ Straw Yield Ratio	G/S	Yield and yield contributing character
15	Straw Yield/ Grain Yield Ratio	S/G	Yield and yield contributing character
16	Leaf Length (cm)	LL (cm)	Measurable DUS descriptor No. 16
17	Leaf Breadth (cm)	LB (cm)	Measurable DUS descriptor No. 17
18	Stem Thickness (cm)	ST (cm)	Measurable DUS descriptor No. 28
19	Number of Panicles Plant ⁻¹	PPP (Nos.)	Measurable DUS descriptor No. 36
20	Decorticated Grain Length (mm)	DGL (mm)	Measurable DUS descriptor No. 54
21	Decorticated Grain Breadth (mm)	DGB (mm)	Measurable DUS descriptor No. 55
22	DGL/DGB Ratio	L/B	Grain type determining character
23	Amylose Content (%)	AC (%)	Measurable DUS descriptor No. 59 and Biochemical Character
24	Zinc Content (ppm)	Zn (ppm)	Biochemical Character
25	Iron Content (ppm)	Fe (ppm)	Biochemical Character
26	Calcium Content (ppm)	Ca (ppm)	Biochemical Character
27	Alkali Spreading Value	ASV	Biochemical Character and cooking quality assessment Character

3.5.1 Methodology for assessment of biochemical quality parameters for experiment number 1 (Objective 1)

3.5.1.1 Amylose content (%)

The simplified procedure (auto analyzer and manual method) of Juliano (1971) is used for the amylose content analysis.

The 100 mg of rice powder is put into a 100 ml volumetric flask and 1 ml of 95% ethanol and 9 ml of 1N sodium hydroxide are added. The contents are heated on a boiling water bath to gelatinize the starch. After cooling for one hour, distilled water is added and contents are mixed well. For each set of samples run, low, intermediate and high amylose standard varieties are included to serve as checks. Five ml of the starch solution is put in a 100 ml volumetric flask with a pipette. One ml of 1N acetic acid, 2 ml of iodine solution (0.2 g iodine and 2.0 g potassium iodide in 100 ml of aqueous solution) is added and volume is made up with distilled water. Contents are shaken well and let stand for 20 minutes. Absorbance of the solution is measured at 620 nm with a spectrophotometer. Amylose content is determined by using a conversion factor and the results are expressed on a dry weight basis.

For the standard curve, 40 mg of potato amylose (Sigma Chemical Co. or Stein Hall and Co. Inc. of known moisture content) are wet with 1 ml ethanol and 9 ml 1N sodium hydroxide. Heated for 5-10 minutes in a boiling water bath, cooled and made up to volume. 1, 2, 3, 4, 5 ml of solution are placed with a pipette in 100 ml volumetric flasks. The solution is acidified with 1N acetic acid (0.2, 0.4, 0.6, 0.8, and 1.0 ml, respectively and treated as above. The absorbance values are plotted at 620 nm, against the concentration of anhydrous amylose (mg) and the conversion factor is determined. The dilution factor of 20 for the samples is included

in the conversion factor. Starch solutions (100 mg/100 ml) prepared by the manual method may be automatically analyzed with an Auto Analyzer. Portions of the starch solutions are transferred into the sample cups of the Auto Analyzer and run at 70 samples/hour. A standard curve is made using rice samples of predetermined amylose content by the simplified manual method at 620 nm. A fresh working iodine solution (1.0 ml 1N acetic acid and 3.0 ml stock iodine solution diluted to 100 ml) is prepared daily. Results are expressed as per cent apparent amylose content in milled rice weight. Apparent amylose content is used since at amylose concentration of more than 25%, amylopectin shows increased iodine binding instead of amylose (Perez and Juliano 1978). They proposed a constant factor of 2.0% to convert apparent amylose content to absolute amylose content based on methanol defeating. After estimating amylose content, the samples were classified as follows.

Term	Amylose (%)	Characteristics when cooked
Waxy	0-7	Absorbed little water and therefore have little volume expansion.
Low amylose	8-20	On cooking tend to be moist, sticky and glossy, split if over cooked.
Intermediate amylose	21-25	Cook fluffy, moist tender and do not become hard upon cooling remains soft. (Most acceptable range for eating)
High amylose	> 25	Become hard when cool, Resist disintegration during boiling

3.5.1.2 Zinc and Iron content ($\mu\text{g g}^{-1}$)

Seeds of individual rice genotypes were harvested and threshed manually. The seeds were de-husked using clean pestle and mortar. The grains were washed quickly with double distilled water to remove any surface contaminants and dried in hot air oven at 70° C for 72 hours. 12.5 ml of 70% concentrated Nitric acid

was added to 0.2 g powdered grain samples and the mixture was incubated overnight. Next day, 10 ml of di-acid mixture (Nitric acid: Per-chloric acid in the ratio of 2:1) was added to the incubated sample. The mixture was then placed on the electric hot plate, allowing evaporation of acid in the form of white fumes, until white precipitate was formed at the base of the flask. The digested sample was left to cool for an hour and the volume was made up to 50 ml using double distilled water. Calibration of an instrument for estimation of an element was done using five standard solutions with appropriate dilutions. A suitable blank was run simultaneously to account for contamination from the reagents. Zinc and iron concentrations in the grain samples of rice were estimated using Atomic Absorption Spectrophotometer (AAS) at 213.86 nm for zinc and 248.33 nm for iron and expressed as $\mu\text{g g}^{-1}$ of grain and data shown in ppm.

Classification scale for zinc and iron content ($\mu\text{g g}^{-1}$)

S.N.	Characters	Categories
1.	Iron	Low (0-9)
		Moderate (9.1-12)
		High (12.1-20)
2.	Zinc	Low (0-15)
		Moderate (15.1-22)
		High (22.1-34)

3.5.1.3 Calcium content ($\mu\text{g g}^{-1}$)

- Weigh 5 g of 2 mm sieved sample in 250 ml conical flask.
- Add extractant in proportion of 1:5 (Extractant = Neutral ammonium acetate 77.1 g in 1 liter distilled water and adjust pH to 7.0).
- Shake for 5 minutes.

- Filter it through Whatsman paper No. 1.
- Collect the filtrate free from sediments and use for estimation of Calcium.
- Pipette out 5 ml of extract in porcelain dish or in 100 ml conical flask, add 5-10 ml distilled water, add 2-3 crystals of sodium dithiocarbamate to avoid interference of heavy metals.
- Add 0.2 g ammonium purpurate to conical flask (red colour at this stage) by adding few drops of 16% NaOH (buffer) and titrate against standard EDTA till colour changes from orange red to purple.

3.5.1.4 Procedure for phenol reaction

Seeds of fifteen varieties were soaked in water for 16 hrs. at ambient temperature and then 50 seeds are placed in petri-plates containing the 1.5% phenol. The reaction takes place with the seed coat. Discoloration does not occur in the enzyme active cells of aleurone. Phenol does not react on seeds as a solution. Its vapors turn the solution producing color reaction.

3.5.1.5 Polished grain: expression of white core

The milled rice sample were observed for White back, White Centre and White belly for the expression of white core or degree of chalkiness and documented into absent, small, medium, large and fully chalky.

3.5.1.6 Gelatinization temperature through Alkali spreading value

Gelatinization temperature through alkali spreading value and clearing scale were determined as per procedure described by Little *et al.*, 1958 is as follow:

Duplicate sets of six whole milled kernels without cracks are selected and placed in plastic boxes (2" × 2" × 1"). Half kernels can be used in the absence of whole kernels. 10 ml of 1.7% (0.3035 N) potassium hydroxide (KOH) solution is added. The samples are arranged to provide enough space between kernels to allow for spreading. The boxes are covered and incubated for 23 hours at 30°C in an oven or by use of ambient temperature. Starchy endosperm is rated visually based on a 7 point numerical spreading scale (Table 3.5 and 3.6).

Table 3.5 Numerical scale for scoring Alkali spreading value along with Gelatinization temperature classification

Score	Spreading scale	Clearing Scale	Alkali digestion	Gelatinization temperature
1	Kernel not affected	Kernel chalky	Low	High
2	Kernel swollen	Kernel chalky collar powdery	Low	High
3	Kernel swollen, collar incomplete and narrow	Kernel chalky collar cottony or cloudy	Low-Intermediate	High-Intermediate
4	Kernel swollen, collar complete and wide	Center cottony, collar cloudy	Intermediate	Intermediate
5	Kernel split or segmented, collar complete and wide	Center cottony, collar clearing	Intermediate	Intermediate
6	Kernel dispersed, merging with collar	Center cloudy collar clear	High	Low
7	All kernel dispersed and inter mingled	Center and collar clear	High	Low

Table 3.6: Alkali spreading value and Gelatinization temperature classification

Alkali Spreading Value	Classification	Gelatinization temperature	Note
6 – 7	High	Low	1
4 – 5	Medium	Intermediate	3
3	Low, Medium	High, Medium	5
1 – 2	Low	High	7

3.5.1.7 Determination of aroma

By applying the standard procedure developed at International Rice Research Institute, Philippines (Jennings et al., 1979) aroma was estimated. In this process the test tube filed with 20 to 30 freshly harvested milled along with distilled and mouth closed by stopper was put on the water bath for 10-20 minutes following cooling and selling for aroma.

3.5.2 Observations recorded on DUS descriptors for experiment number 3 to generate data base of diverse rice germplasm (Objective 3)

Observations were recorded at different growth stages as mentioned in Table 3.7 as per DUS test guidelines of PPV and FR Authority for 62 agro-morphological descriptors as mentioned in Tables 3.8 (Anonymous, 2009). Four types of assessments were followed.

VS: Visual assessment by observations of individual plants or parts of plants

VG: Visual assessment by a single observation of a group of plants or parts of plants

MS: Measurement of a number of individual plants or parts of plants

MG: Measurement by a single observation of a group of plants or parts of plants

Table 3.7 Decimal Code for the Growth Stage

Code	Growth stage
10	After germination, emergence of first leaf through coleoptile / second leaf visible (less than 1 cm)
40	Booting : the increase in the size of the young panicle and its inward extension inside the upper leaf sheaths detectable as a bulge in the rapidly elongating culm
50	1st spikelet of inflorescence just visible
55	½ of inflorescence emerged
60	Beginning of anthesis : it begins with the protrusion of the first dehiscing anthers in the terminal spikelets on the panicle branches
65	Anthesis half way
70	Milk development stage: formation of white milky sap within the spikelets.
80	Dough development (spikelets become hard)
90	Ripening (terminal spikelets ripened)
92	Caryopsis hard (can be no longer be dented by thumbnail and over 90% spikelets ripened)

Table 3.8 Details of DUS descriptors observations

SN	Characteristics	States	Note	Stage of observation	Type of assessment
1	2	3	4	5	6
1. (+)	Coleoptile: Colour	Colourless	1	10	VS
		Green	2		
		Purple	3		
2. (*)	Basal leaf: Sheath colour	Green	1	40	VS
		Light purple	2		
		Purple lines	3		
		Uniform purple	4		
3.	Leaf: Intensity of green colour	Light	3	40	VG
		Medium	5		
		Dark	7		
4.	Leaf: Anthocyanin colouration	Absent	1	40	VG
		Present	9		
5.	Leaf: Distribution of anthocyanin colouration	On tips only	1	40	VG
		On margins only	2		
		In blotches only	3		
		Uniform	4		
6. (+)	Leaf Sheath: Anthocyanin colouration	Absent	1	40	VG
		Present	9		
7.	Leaf sheath: Intensity of anthocyanin colouration	Very weak	1	40	VG
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
8. (*)	Leaf: Pubescence of blade surface	Absent	1	40	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
9. (*)	Leaf: Auricles	Absent	1	40	VS
		Present	9		
10. (*)	Leaf: Anthocyanin colouration of auricles	Colourless	1	40	VS
		Light purple	2		
		Purple	3		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
11. (+)	Leaf: Collar	Absent	1	40	VS
		Present	9		
12.	Leaf: Anthocyanin colouration of collar	Absent	1	40	VS
		Present	9		
13. (+)	Leaf: Ligule	Absent	1	40	VS
		Present	9		
14. (*) (+)	Leaf: Shape of ligule	Truncate	1	40	VS
		Acute	2		
		Split	3		
15. (*)	Leaf: Colour of ligule	White	1	40	VS
		Light purple	2		
		Purple	3		
16.	Leaf: Length of	Short (<30 cm)	3	40	MS
		Medium	5		
		(30-45 cm)			
		Long (>45 cm)	7		
17.	Leaf: Width of blade	Narrow (<1 cm)	3	40	MS
		Medium (1-2 cm)	5		
		Broad (>2 cm)	7		
18.	Culm: Attitude (for floating rice only)	Non procumbent	1	40	VS
		Procumbent	9		
19.	Culm: attitude	Erect	1	40	VS
		Semi-erect	3		
		Open	5		
		Spreading	7		
20.	Time of heading with panicles)	Very early (<71 days)	1	55	VG
		Early (71-90 days)	3		
		Medium (91-110 days)	5		
		Late (111-130 days)	7		
		Very late (> 131 days)	9		
21. (*)	Flag leaf: Attitude of blade (early)	Erect	1	60	VG
		Semi-erect	3		
		Horizontal	5		
		Drooping	7		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
22. (*)	Spikelet: Density of pubescence of lemma	Absent/ Weak	1	60-80	VS
		Medium	3		
		Strong	5		
		Very strong	7		
23.	Male sterility	Absent	1	65	VG
		Present	9		
24. (+)	Lemma: Anthocyanin colouration of keel	Absent or very Weak	1	65	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
25. (+)	Lemma: Anthocyanin colouration of area below apex	Absent	1	65	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
26. (*)(+)	Lemma: Anthocyanin colouration of apex	Absent	1	65	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
27. (*)(+)	Spikelet: Colour of stigma	White	1	65	VS
		Light green	2		
		Yellow	3		
		Light purple	4		
		Purple	5		
28.	Stem: Thickness	Thin (<0.40 cm)	3	70	MS
		Medium(0.40-0.55 cm)	5		
		Thick (>0.55 cm)	7		
29.	Stem: Length (excluding floating rice)	Very short(<91 cm)	1	70	MS
		Short (91-110 cm)	3		
		Medium(111-130 cm)	5		
		Long (131-150 cm)	7		
		Very long (>150 cm)	9		
30. (*)	Stem: Anthocyanin colouration of nodes	Absent	1	70	VS
		Present	9		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
31.	Stem: Intensity of anthocyanin coloration of Nodes	Weak	3	70	VS
		Medium	5		
		Strong	7		
32.	Stem: Anthocyanin colouration of internodes	Absent	1	70	VS
		Present	9		
33. (*)(+)	Panicle: Length of main axis	Very short(<16cm)	1	70-90	MS
		Short (16-20 cm)	3		
		Medium (21-25 cm)	5		
		Long (26-30 cm)	7		
		Very long (>30 cm)	9		
34. (*)	Flag leaf: Attitude of blade	Erect	1	90	VG
		Semi-erect	3		
		Horizontal	5		
		Deflexed	7		
35. (*)(+)	Panicle: Curvature of main axis	Straight	1	90	VG
		Semi-straight	3		
		Deflexed	5		
		Dropping	7		
36.	Panicle: Number per plant	Few (<11)	3	80-90	MS
		Medium (11-20)	5		
		Many (>20)	7		
37. (*)	Spikelet: Colour of tip of lemma	White	1	80-90	VS
		Yellowish	2		
		Brown	3		
		Red	4		
		Purple	5		
		Black	6		
38 (+)	Lemma and Palea: Colour	Straw	1	80-90	VG
		Gold and gold furrows on straw background	2		
		Brown spots on straw	3		
		Brown furrows on straw	4		
		Brown (tawny)	5		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
		Reddish to light purple	6		
		Purple spots / furrows on straw	7		
		Purple	8		
		Black	9		
39. (*) (+)	Panicle: Awns	Absent	1	90	VG
		Present	9		
40. (*)	Panicle: Colour of awns (late observation)	Yellowish White	1	90	VS
		Yellowish Brown	2		
		Brown	3		
		Reddish brown	4		
		Light red	5		
		Red	6		
		Light purple	7		
		Purple	8		
		Black	9		
41.	Panicle: Length of longest awn	Very short	1	90	VG-MS
		Short	3		
		Medium	5		
		Long	7		
		Very long	9		
42. (*)	Panicle: Distribution Of awns	Tip only	1	90	VS
		Upper half only	3		
		Whole length	5		
43. (+)	Panicle : Presence of secondary branching	Absent	1	90	VG
		Present	9		
44. (+)	Panicle: Secondary branching	Weak	1	90	VG
		Strong	2		
		Clustered	3		
45. (*)(+)	Panicle: Attitude of branches	Erect	1	90	VG
		Erect to semi-Erect	3		
		Semi-erect	5		
		Semi-erect to spreading	7		
		Spreading	9		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
46. (*)(+)	Panicle: Exertion	Partly exerted	3	90	VG
		Mostly exerted	5		
		Well exerted	7		
47.	Time maturity	Very early (<100)	1	90	VG
		Early (101-120)	3		
		Medium (121-140)	5		
		Late (141-160)	7		
		Very late (>160)	9		
48.	Leaf: Senescence	Early	3	92	VG
		Medium	5		
		Late	7		
49. (*)(+)	Sterile lemma: Colour	Straw	1	92	VS
		Gold	2		
		Red	3		
		Purple	4		
50.	Grain: Weight of 1000 fully developed grains	Very low (<15 g)	1	92	MG
		Low (15-20 g)	3		
		Medium (21-25g)	5		
		High (26-30)	7		
		Very high (>30 g)	9		
51.	Grain: Length	Very short (<6.0 mm)	1	92	MS
		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		
52.	Grain: Width	Very narrow (<2.0 mm)	1	92	MS
		Narrow (2.1-2.5 mm)	3		
		Medium (2.6-3.0 mm)	5		
		Broad (3.1-3.5 mm)	7		
		Very broad (>3.5 mm)	9		
53. (+)	Grain: Phenol reaction of lemma	Absent	1	92	VG
		Present	9		
54. (*)(+)	Decorticated grain: Length	Short	1	92	MS
		Medium	3		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
		Long	5		
		Long*(Long for Basmati type)	7		
		Extra long	9		
55. (+)	Decorticated grain:	Narrow (<2.0 mm)	3	92	MS
		Medium (2.0-2.5 mm)	5		
		Broad (>2.5 mm)	7		
56. (*) (+)	Decorticated grain: Shape (in lateral view)	Short slender	1	92	MS
		Short bold	2		
		Medium slender	3		
		Long bold	4		
		Long slender	5		
		Long slender*(For Basmati type)	5		
		Extra long slender	6		
57. (*)	Decorticated grain: Colour	White	1	92	VG
		Light brown	2		
		Variegated brown	3		
		Dark brown	4		
		Light red	5		
		Red	6		
		Variegated purple	7		
		Purple	8		
58. (+)	Endosperm: Presence of amylose	Absent	1	92	MG
		Present	9		
59. (*) (+)	Endosperm:Content of amylose	Very low (<10%)	1	92	MG
		Low (10-19%)	3		
		Medium (20-25%)	5		
		High (26-30%)	7		
		Very high (>30%)	9		
60 (+)	Varieties with endosperm of amylose absentonly Polished grain: Expression of white core	Absent or	1	90	MG
		very small			
		Small	3		
		Medium	5		
		Large	7		
		Fully chalky	9		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
61. (+)	Gelatinization temperature through alkali spreading value	Low	1	92	MG
		Medium	3		
		High medium	5		
		High	7		
62. (*)(+)	Decorticated grain: Aroma	Absent	1	92	MG
		Present	9		

(*) Characteristics that can be observed during every growing season in all varieties and shall always be included in the description of the variety, except when the state of expression of any of these characters is rendered impossible by a preceding phonological characteristic or by the environmental conditions of the testing region. Under such exceptional situation, adequate explanation shall be provided.

(+) The plant parts on which the observations to be taken are given in the explanation or figure(s) in section VIII of the guideline for the conduct of test for Distinctiveness, Uniformity and Stability on Rice (*Oryza sativa* L.) published by PPV & FR Authority, Govt. of India.

3.6 Statistical Analysis

The mean data in respect of various 27 characters were subjected to the following statistical techniques using INDOSTAT software.

3.6.1 Analysis of variance

The analysis of variance for each character was calculated as per the standard statistical procedure given by Panse and Sukhatme (1967).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij}	=	Performance of the j^{th} genotype in the i^{th} block
μ	=	General mean
b_i	=	True effect of i^{th} block
t_j	=	True effect of j^{th} genotype

e_{ij} = Random error associates with j^{th} genotype and i^{th} block

The structure of analysis of variance was as follows.

Table 3.9 ANOVA Table for Randomized Complete Block Design

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	Expected Mean Sum of Squares	'F' calculated Value
Replications	(r-1)	RSS	M_r	$\sigma^2_e + t \sigma^2_r$	M_r/M_e
Treatments	(t-1)	TrSS	M_t	$\sigma^2_e + r \sigma^2_g$	M_t/M_e
Error	(r-1) (t-1)	ESS	M_e	σ^2_e	
Total	(rt-1)	TSS			

Where,

r = Number of replications

t = Number of treatments

M_r = Mean sum of square of replication

M_t = Mean sum of square of treatment

M_e = Mean sum of square of error

σ^2_e = Environmental variance

σ^2_r = Variance due to replications

σ^2_g = Variance due to genotypes

Test of significance for each character was carried out against the corresponding error degrees of freedom using 'F' table values given by Fisher and Yates (1963).

3.6.1.1 Estimation of Genetic Parameters Phenotypic and genotypic variance

Phenotypic and genotypic variances were estimated using the following formula

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + M_e = \frac{M_t - M_e}{r} + M_e$$

3.6.1.2 Coefficient of Variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton and Devane. (1953).

a. Genotypic coefficient of variation (GCV)

$$\text{GCV} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

b. Phenotypic coefficient of variation (PCV)

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{X})} \times 100$$

The GCV and PCV values were classified as described by Subramanian and Menon (1973).

Classification	GCV/ PCV
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.6.1.3 Heritability

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability in broad sense } (h^2_{bs}) = \frac{\text{GV } (\sigma^2_g)}{\text{PV } (\sigma^2_p)} \times 100$$

Heritability in broad sense was categorized as per the classification given by Johnson *et al.* (1955)

Classification	Heritability
Low	Less than 30%
Moderate	30 – 60%
High	More than 60%

3.6.1.4 Expected genetic advance

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

$$\text{Expected genetic advance (GA)} = K \times \sigma_p \times h^2$$

Where,

K = Selection differential at 5% selection intensity (2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

3.6.1.5 Genetic advance as per cent of mean (GAM)

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

Where,

GA = Genetic advance

X = Grand mean of the character

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

Classification	GAM
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.7 Genetic Divergence

3.7.1 Mahalanobis' D² analysis

The data collected on different yield contributing characters was analysed using Mahalanobis' D² analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1936).

3.7.2 Test of significance

Variances were calculated for all the characters studied and test of significance was done. For the character pairs analysis of covariance was estimated on the basis of mean values (Panse & Sukhatme, 1967). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion.

The sum of squares and sum of products of error and error + variety, variance- covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\Lambda = \frac{|E|}{|E+V|}$$

Where,

Λ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E+V|$ = Determinant of error + variety matrix

$V_{(stat.)}$ = $-m \log_e \Lambda$ (at pq degrees of freedom)

Where,

$$m = n - (p + q + 1)/2$$

n = degree of freedom for error + varieties

p = number of variables /characters

q = number of varieties –1 (or degrees of freedom)

$V_{(stat.)}$ is distributed as χ^2 with pq degrees of freedom

3.7.3 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation of the differences in the mean values of various characters of the two genotypes *i.e.*, Σd^2_{ij} . Therefore transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.7.4 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.*, $Y_{it} - Y_{jt}$ for $t=1, 2, \dots, p$ variables are computed and the D^2 values were calculated as,

$$D^2_{ij} = \sum_{t=1}^p (y^t_i - y^t_j)^2$$

Where,

y^t_i is uncorrelated mean value of i^{th} genotype for character ' t '

y^t_j is uncorrelated mean value of j^{th} genotype for character ' t '

D^2_{ij} is D^2 between i^{th} and j^{th} genotypes

3.7.5 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for p degrees of freedom, where p is the number of characters considered *i.e.* 27 in the present study.

3.7.6 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using Agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1979).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.7.7 Average intra-cluster distance

For the measurement of intra-cluster distances, the formula used was $\Sigma D^2_i/n$ where, ΣD^2_i was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.7.8 Average inter-cluster distance

Clusters were taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the numbers of one cluster to each of the number of other cluster divided by the product of number of genotypes in both the clusters under consideration.

The square root of the average D^2 value gave the genetic distance between the clusters. Based on D^2 values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average inters cluster distance} = \frac{D^2}{n_1 \times n_2}$$

Where,

D^2 = difference in the mean values between two populations
when all the character are considered simultaneously.
 n_1 and n_2 are number of genotypes of two clusters

Scale of divergence based on D values

Category	“D” values
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

3.8 Material and methodology for molecular profiling using SSR primers

3.8.1 Extraction of genomic DNA

3.8.1.1 Plant material

For the present investigation, all 95 genotypes of rice were sown in the pots and kept in greenhouse. The leaf samples were collected from 10-12 days old seedlings for the isolation of genomic DNA.

3.8.1.2 Preparation of stock solutions for reagents and buffers for DNA isolation.

The buffers and reagents for DNA extraction were prepared as per Sambrook Maniatis (1989). The composition and procedure for preparation of different stock solutions and buffers are given in the Table 3.10.

Table No. 3.10 : Preparation of solutions for DNA isolation

a) Extraction buffer			
Extraction buffer stock solutions: For 100ml. (g)	SN	Chemicals	Qty. required
	1.	200 mM Tris-HCl,	2.423
	2.	25 mM EDTA	0.831
	3.	250 mM NaCl	1.461
	1.	0.5M Glucose	0.9
	2.	0.5% SDS	0.05
	3.	3% PVP	0.3
	4.	0.4% Sodium Bisulphite	0.04
	5.	5% Sarcosyl	500 µl
b) 70% Ethanol For 100ml.	1.	Absolute ethyl alcohol	70ml
	2.	Distilled water	30ml
c) Chloroform: Isoamyl alcohol(24:1) For 100ml	1.	Chloroform	96ml
	2.	Isoamyl alcohol	4ml
d) TAE Buffer (50X) (Add 50 times double distilled water to 50X Buffer to make 1X- TAE buffer.) For 1000ml	1.	TrisHCl	242.5 g
	2.	Glacial acetic acid	57.1 ml
	3.	0.5 M EDTA (pH 8.0)	200ml
e) Ethidium Bromide (Final concentration was thus made 10 mg/ml. It was then stored in dark bottle at room temperature.)	1.	EthidiumBromide	0.1 g
	2.	Distilled water	10 l

3.8.1.3 Procedure for extraction of genomic DNA

The DNA was isolated by following the protocol of Edwards *et al.*, 1991 with the slight modifications of buffer composition and concentration. The young newly flushing 10-12 days old leaves were collected and sterilized with 70% ethanol to avoid the contamination. The isolation of genomic DNA was done using the following protocol.

- Leaf tissue (100 mg) were collected and cut into small pieces then kept in 1.5 ml eppendorf tube which leads to ensure uniform size of sample.
- Collected tissue was macerated by micro pestle at room temperature without buffer for 20 sec.
- Extraction buffer (500 μ l) was added and leaf tissue macerated gently for 30 seconds and kept in hot water bath for 45 minutes at 65°C.
- The sample was cooled down at room temperature and centrifuged at 10,000 rpm for 10 minutes.
- Aqueous layer was transferred to fresh eppendorf tube and 200 μ l of CIA (24:1) was added and mixed by gentle inversion for 5-6 times. The contents were then centrifuged at 10,000 rpm for 10 minutes.
- Again aqueous layer was transferred to fresh Eppendorff tube and 200 μ l of CIA (24:1) was added and mixed by gentle inversion for 5-6 times. The contents were then centrifuged at 10,000 rpm for 10 minutes.
- Supernatant was mixed with double volume of chilled Iso-propanol and incubated at -20°C for overnight.
- On the next day the solution was centrifuged at 10,000 rpm for 10 minutes and pellet was collected.

- Pellet was washed with 100 µl of 70 per cent ethanol followed by centrifugation at 10,000 rpm for 10 minutes.
- Pellet was dried and re-suspended in 50 µl of 1x TE buffer.
- Incubated at 37°C in a water bath for 10 minutes and stored at -20°C till further use.

3.8.1.4 DNA purification

Purification of DNA in samples was done to remove RNA, proteins and polysaccharides which were the major contaminants. RNA was removed by RNase enzyme treatment. RNase was added to the DNA sample @100 µg ml⁻¹ and incubated at 37°C for 1 hour.

3.8.1.5 DNA quantification through agarose gel electrophoresis

Concentration of DNA in the sample was obtained after agarose gel electrophoresis with standard DNA on 0.8 per cent agarose gel and by comparison of the intensity of staining with ethidium bromide.

3.8.1.6 Dilution of crude extract of DNA

The isolated DNA from all the rice genotypes was in varying concentrations. While preparing the working DNA samples it was diluted in such a manner as detailed in Table 3.10, so as it maintains the DNA content in all the samples in similar concentration.

Table No. 3.11 Sample wise dilution of the isolated DNA

SN.	Dilution ratio	Quantity of DNA (µl)	Quantity of D/W (µl)
1.	1:10	2	20
2.	1:15	2	30
3.	1:20	2	40

3.9 Screening of rice genotypes using SSR molecular markers:

The rice genotypes were screened for biotic and abiotic resistance using 20 SSR primers over different chromosomes for different biotic and abiotic stress resistance genes. The SSR primers were obtained from the GRAMENE database (Release #39, <http://archive.gramene.org/markers/microsat/all-ssr.tab>)

Details of the primers used are appended in Table 3.13.

3.9.1 Requirements:

Table No. 3.12:

Stock solutions	Source
Taq. assay buffer	M/s Bangalore Genei Pvt. Ltd., Bangalore
MgCl ₂	M/s Bangalore Genei Pvt. Ltd., Bangalore
dNTPs	M/s Bangalore Genei Pvt. Ltd., Bangalore
Primers (Fw./Rev.)	Bio-resource Biotech Pvt. Ltd., Pune.
Taq. DNA Polymerase	M/s Bangalore Genei Pvt. Ltd., Bangalore

Thermal cycler: Eppendorf, Master cycler gradient supplied by Eppendorf gradient, 2231, Hamburg Germany was used for cyclic amplification of DNA.

3.9.2 Preparation of master mixture

Since the pipetting of small volumes is difficult and often inaccurate, a master mix was prepared where constituents common to all the reactions were combined in one tube multiplying the volume for one reaction with total number of samples. Later, the appropriate amount of master mix was dispensed to each tube and template DNA was added separately in each tube. Details are appended in Table 3.14.

Table No. 3.13 List of microsatellite primers with their sequences and linked gene.

S N	Primer	Sequence Forward primer	Sequence Reverse Primer	Ch. No.	Linked gene
1.	RM 140	TGCCTCTTCCCTGGCTCCCCTG	GGCATGCCGAATGAAATGCATG	1	<i>Saltol</i>
2.	RM 1287	CCATTTGCAGTATGAACCATGC	ATCATGCAATAGCCGGTAGAGG	1	<i>Saltol</i>
3.	RM 3412	AAAGCAGGTTTTCTCCTCC	CCCATGTGCAATGTGTCTTC	1	<i>Saltol</i>
4.	RM234	ACAGTATCCAAGGCCCTGG'	CACGTGAGACAAAGACGGAG	7	Glb 1
5.	RM 6775	AATTGATGCAGGTTCAAGCAAGC	GGAAATGTGGTTGAGAGTTGAGAGC	6	<i>Bph25</i>
6.	RM 309	CACGCACCTTTCTGGCTTTCAGC	AGCAACCTCCGACGGGAGAAGG	12	<i>Bph26</i>
7.	RM 8225	GCGTGTTCAAGAAATTAGGATACGG	GATCTCGCCACGTAATTGTTGC	6	<i>Pi-z</i>
8.	RM 212	AAGGTCAAGGAAACAGGGACTGG	AGCCACGAATTCCACTTTCAGC	1	<i>Dr</i>
9.	RM 302	TGCAGGTAGAACTTGAAGC	AGTGGATGTTAGGTGTAACAGG	1	<i>Dr</i>
10.	RM 201	CTCGTTTATTACCTACAGTACC	CTACCTCCTTTCTAGACCGATA	9	<i>Dr</i>
11.	PTA 248	AGACGCGGAAGGGTGGTTCCTCGGA	AGACCGGGTAAT CGAAAGATGAAA	11	<i>Xa21</i>
12.	RM 122	GAGTCGATGTAATGTCATCAGTGC	GAAGGAGGTATCGCTTTGTTGGAC	5	<i>Xa5</i>
13.	RM 22709	CGCGTGGGCGAGACTAATCG	CCTTGACTCCGAGGATTCATTGTCC	8	<i>Gm8</i>
14.	RM 547	TTGTCAAGATCATCCTCGTAGC	GTCATTCTGCAACCTGAGATCC	8	<i>Gm4</i>
15.	RM 7	TTCGCCATGAAGTCTCTCG	CCTCCCATCATTTTCGTTGTT	3	<i>Tgw</i>
16.	RM 42	ATCCTACCGCTGACCATGAG	TTTGGTCTACGTGGCGTACA	6	<i>Wx</i>
17.	RM276	CTCAACGTTGACACCTCGTG-3'	TCCTCCATCGAGCAGTATCA	6	<i>Wx</i>

Table No. 3.14 Master mixture for polymerase chain reaction (PCR).

Components	Stock concentration	Vol. for one reaction/10 µl
Taq buffer	10X	1.25µl
MgCl ₂	25 mM	0.25µl
dNTP mix	10 mM	0.5µl
Primer- F	25picomole/µl	0.5µl
Primer- R	25picomole/µl	0.5µl
TaqDNA polymerase	3 U/µl	0.25µl
Template DNA	30-50 ng	1.0µl
Sterile Distilled water	--	5.75 µl
Total	--	10 µl

3.9.3 Thermal cycling

- Sterile micro centrifuge tubes were numbered from 1 to 34.
- 1.0 µl of diluted template DNA from individual rice genotype was added to each tube.
- 9 µl of master mix was added to each tube and was given short spin to mix the contents.
- The tubes were placed in the thermal cycler for 35 cycles of PCR. Samples were held at 4°C in the thermal cycler until the contents were loaded on to the gel for electrophoresis. (Table No. 3.15)

Table No. 3.15 Thermo Profile

Steps	Temp. (°C)	Period (min.)	
Initial Denaturation	94°C	5 min.	
Denaturation	94°C	20sec	35 Cycle
Annealing	53°C - 63°C*	30sec	
Extension	72°C	45 sec	
Final extension	72°C	7 min.	
Hold	4°C	--	

(*Note: - Annealing temperature based on T_m value of each primer)

3.9.4. Optimization of annealing temperature for gene specific primers by PCR amplification studies

Gradient PCR amplification of gene specific primers was carried out so as to determine the annealing temperature of each primer. The PCR programme was set in Thermal Cycler Eppendorf, Master Cycler Gradient, made in Germany.

The annealing temperature of each primer was standardized based on T_m value of each forward and reverse primer and standardized temperature was used for further amplification (Table 3.16).

Table No. 3.16 Annealing temperatures of SSR markers used in the study.

SN	Primer	Amplification size for resistance	Standardized Annealing temperature (°C)
1.	RM 140	260	62.1
2.	RM 1287	160	56.7
3	RM-3412	211	62.8
4	RM 234	255	56.5
5	RM 6775	192	58.7
6	RM 309	152	66.9
7	RM 8225	221	58.7
8	RM 212	135	62.9
9	RM 302	140	61.7
10	RM 201	220	52.1
11	pTA248	1040	54.0
12	RM 122	240-250	61.5
13	RM 22709	160-170	65.9
14	RM 547	270	56.1
15	RM 7	245	58.9
16	RM 42	155	61.3
17	RM 276	223	62.3

3.9.5 Separation of amplified product by agarose gel electrophoresis

- **Requirements:**

- a) Electrophoretic unit (Gel casting tray, gel comb, power pack)
- b) Gel documentation system
- c) Agarose
- d) Tracking dye (Bromophenol blue)
- e) Ethidium Bromide ($1\ \mu\text{g ml}^{-1}$)
- f) 50X TAE buffer.
- g) DNA ladder

- **Procedure**

The amplified products in SSR reaction were separated by agarose gel electrophoresis in 2 per cent agarose gel (Merck, India) containing ethidium bromide in 1X TAE Buffer (pH 8.0) and separation was carried out by applying constant voltage of 70 volts for 100 minutes.

3.9.6 Visualization, photography and gel documentation

The gels were photographed under UV light using Pentax K 312 nm camera. The photographs of gel was taken by the documentation systems (Uvi-Tech, Fire reader, Cambridge, England) and saved in computer for further analysis.

3.9.7 Molecular screening of genotypes

The gels were carefully analyzed and amplicons which obtained only once for a particular variety were marked which contained the band for that particular variety. Additionally, the

fragments present in two genotypes were also marked, which in combination with other bands produced with other primers would constitute the screenings.

3.8 Scoring and Data Analysis

Each amplification product as a dominant expression was considered as SSR marker and was scored across all the samples. Bands were scored as present (+/1) or absent (-/0). The size of each allele was determined by running simultaneously a DNA ladder by using software (Uvitec, Fire-reader software version 15.12). The data was used for similarity based analysis using the programme MVSP-A (Multivariate Statistical Package - 5785 Version 3.1). Similarity coefficients were used to construct UPGMA (Un-weighted Pair Group Method with Average) to generate Dendrogram.

Distance matrix and dendrogram was constructed based on diversity coefficient generated from pooled data by using Un-weighted Pair Group Method of Arithmetic Means (UPGMA), a computer programme for distance estimation. The percentage polymorphism of the obtained bands was calculated by using following formula,

$$\text{Per cent polymorphism} = \frac{\text{Total number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

3.9 Polymorphism Information Content

Polymorphism Information Content (PIC) value were calculated as per formula developed by Powell *et al.*, (1996).

Where,

$$PIC = 1 - \sum P_{ij}^2$$

- P_{ij} is the frequency of i^{th} and j^{th} locus, summed across the entire locus over all lines.
- PIC values range from 0 (monomorphic) to 1 (very highly discriminative, with many alleles each in equal and low frequency) were estimated for each profile generated across 95 rice genotypes



EXPERIMENTAL RESULTS

CHAPTER-IV

EXPERIMENTAL FINDINGS

Ninety five genotypes of rice were evaluated for Twenty seven characters including grain yield per plant in order to estimate various genetic parameters. The results were obtained from the observation after statistical analysis are presented and discussed under the following headings:

- 4.1 Genetical studies for 27 yield and yield contributing traits.
- 4.2 Molecular profiling of rice germplasm using SSR markers.
- 4.3 Morphological characterization of rice germplasm based on DUS guidelines

4.1 Genetical studies for 27 yield and yield contributing traits.

4.1.1 Analysis of variance (ANOVA)

Analysis of variance for 27 quantitative characters including grain yield plant⁻¹ revealed significant differences among the genotypes for these characters under study indicating the presence of greater variability among the genotypes. The details pertaining to ANOVA for experiments carried out at ARS, Shirgaon and RARS, Karjat are furnished under Table Number 4.1 and 4.2 respectively.

4.1.2 Mean performance along with range of 95 rice genotypes for various 27 traits

The mean performance of 95 genotypes for grain yield plant⁻¹ and its component traits for experiment carried out at Shirgaon and Karjat are presented in the Table 4.3 and 4.4, respectively.

4.1.2.1 Mean performance of rice genotypes for various 27 traits

4.1.2.1.1 Days to 50% Flowering (Nos.) days)

The number of days to 50% of flowering at Shirgaon location, ranged from 73.00 to 112.00 days with a general mean of 91.48 days. Among all the genotypes IRRI 104 (73.00 days) was found to be earliest while Kalanamak (112.00 days) was found to be late.

However the number of days to 50% flowering at Karjat location ranged from 72.33 to 111.33 days with a general mean of 90.41 days. Among all the genotypes IRRI 104 (72.33 days) was found to be earliest while Kalanamak (111.33 days) was found to be late.

4.1.2.1.2 Plant height (cm)

For this trait at Shirgaon location, the genotypes exhibited a range of 78.37 to 192.33 cm with a general mean of 123.67 cm. The shortest genotype was MO-8 (78.37 cm) and the longest genotype was NDR6315 (123.67 cm).

Whereas at Karjat location, the genotypes exhibited a range of 77.14 to 193.22 cm with a general mean of 123.91 cm. The shortest genotype was MO-8 (77.14 cm) and the longest genotype was NDR6315 (193.22 cm).

4.1.2.1.3 Stem length (excluding panicle; excluding floating rice) (cm)

At Shirgaon location, for this trait, the genotypes exhibited a range of 54.83 cm to 156.67 cm with a general mean of 96.86 cm. The shortest genotype was MO-8 (54.83 cm) and the longest genotype was NDR6315 (156.67 cm).

However at Karjat location, the genotypes exhibited a range of 53.03 cm to 156.75 cm with a general mean of 96.63 cm. The shortest genotype was MO-8 (53.03 cm) and the longest genotype was NDR6315 (156.75 cm).

4.1.2.1.4 Number of Tillers Plant⁻¹ (Nos.)

The number of tillers per plant at Shirgaon location, ranged from 8.93 (Mahsad) to 21.73 (TN-1) panicles with a general mean of 11.56.

Whereas at Karjat location, the number of tillers per plant ranged from 9.60 (Mahsad) to 22.38 (TN-1) panicles with a general mean of 12.20.

4.1.2.1.5 Panicle length of main axis (cm)

The panicle length at Shirgaon ranged from 22.13 to 35.67 cm with a general mean of 26.87 cm. The genotype IRRI 104 had shorter panicle length of 22.13 cm while the genotype NDR6315 exhibited highest value of to 35.67 cm which was almost 13.54 cm longer than IRRI 104.

While, the panicle length at Karjat ranged from 22.21 to 36.47 cm with a general mean of 27.28 cm. The genotype Gurjari had shorter panicle length of 22.21 cm while the genotype NDR6315 exhibited highest value of to 36.47 cm which was almost 14.26 cm longer than Gurjari.

4.1.2.1.6 Number of Spikelets Panicle⁻¹ (Nos.)

The number of panicles per plant at Shirgaon ranged from 55.31 (IRRI 190) to 300.48 (Ajaya) panicles with a general mean of 131.45.

However at Karjat, the number of panicles per plant ranged from 55.50 (Dodak) to 30.1.00 (Ajaya) panicles with a general mean of 131.61.

4.1.2.1.7 Fertility (%)

At Shigaon, the fertility (%) was within the range of 57.54 to 98.07 % with a general mean of 86.00 %. The maximum fertility was recorded for IRRI 192 (57.54%) and the minimum fertility was recorded for Try-1 (98.07%).

Whereas at Karjat, the fertility (%) was within the range of 57.54 to 98.34 % with a general mean of 86.06 %. The maximum fertility was recorded for IRRI-192 (98.34 %) and the minimum fertility was recorded for Try-1 (57.54 %).

4.1.2.1.8 Days to Maturity (Nos.) (days)

The time of maturity was within the range of 103.00 to 142.00 days at Shirgaon, with a general mean of 121.48 days. Among all the genotypes, IRRI 104 (103.00 days) was found to be earliest, while Kalanamak (142.00 days) was found to be late.

Whereas at Karjat, the time of maturity was within the range of 102.33 to 141.33 days with a general mean of 120.41 days. Among all the genotypes, IRRI 104 (102.33 days) was found to be earliest, while Kalanamak (141.33 days) was found to be late.

4.1.2.1.9 Test weight (g)

At Shirgaon the general mean of weight of 1000 fully developed grains was 21.83 g and the values ranged from 11.22 to 29.13 g Among the genotypes studied, Bela (29.13g) recorded highest 1000 grain weight and the lowest 1000 grain weight was recorded for Bhadasbhog (11.22 g).

However at Karjat, the general mean of weight of 1000 fully developed grains was 21.71 g and the values ranged from 10.74 to 29.29 g. Among the genotypes studied, Bela (29.29 g) recorded highest 1000 grain weight and the lowest 1000 grain weight was recorded for Bhadasbhog (10.74 g).

4.1.2.1.10 Grain length (mm)

At Shirgaon, the general mean of grain length was 9.42 mm and the values ranged from 5.99 to 11.65 mm. Among the genotypes used, Sugandha (11.65 mm) recorded the maximum grain length and the minimum grain length was recorded by Kothambir Sal (5.99 mm).

Whereas at Karjat, the general mean of grain length was 9.42 mm and the values ranged from 6.03 to 11.65 mm. Among the genotypes used, Sugandha (11.65 mm) recorded the maximum grain length and the minimum grain length was recorded by Kothambir Sal (6.03 mm).

4.1.2.1.11 Grain width (mm)

The grain width was within the range of 2.23 to 3.90 mm with a general mean of 2.87 mm. The maximum grain width was recorded for Kochari (3.90 mm) while the minimum grain width was recorded for Samba Mahsuri (2.23 mm).

However at Karjat, the grain width was within the range of 2.07 to 3.91 mm with a general mean of 2.84 mm. The maximum grain width was recorded for Kothari (3.91 mm) while the minimum grain width was recorded for Samba Mahsuri (2.07 mm).

4.1.2.1.12 Grain yield plant⁻¹ (g)

At Shirgaon, grain yield plant⁻¹ ranged from 9.22 g (Dular) to 32.27 g (PR-118) with a general mean of 17.11 g.

Whereas at Karjat, it was ranged from 9.24 g (Dular) to 30.64 g (PR-118) with a general mean of 16.94 g

4.1.2.1.13 Straw yield plant⁻¹ (g)

The straw yield plant⁻¹ falls within the range of 12.33 to 46.33 g with a general mean of 23.35 mm at Shirgaon. The highest and lowest values for this trait were recorded by PR-118 (46.33 g) and Dular (12.33 g) respectively.

Whereas at Karjat, it falls within the range of 8.60 to 46.50 g with a general mean of 22.70 g. The highest and lowest values for this trait were recorded by PR-118 (46.50 g) and Bhadas-79 (8.60 g) respectively.

4.1.2.1.14 Grain yield plant⁻¹ to Straw yield plant⁻¹ ratio

At Shirgaon, the ratio for grain yield plant⁻¹ to straw yield plant⁻¹ ranged from 0.51 (Chinoor) to 0.94 (Gurjari) with a general mean of 0.74.

However at Karjat, the ratio for grain yield plant⁻¹ to straw yield plant⁻¹ ranged from 0.59 (HRTMS-61) to 00.88 (RTN214-1-1-1-2) with a general mean of 0.84.

4.1.2.1.15 Straw yield plant⁻¹ to Grain yield plant⁻¹ ratio

The ratio for straw yield plant⁻¹ to grain yield plant⁻¹ ranged from 1.07 (Gurjari) to 1.96 (Chinoor) with a general mean of 1.37 at Shigaon.

Whereas at Karjat, this ratio ranged from 0.84 (Bhadas-79) to 1.73 (HRTMS-61) with a general mean of 1.34.

4.1.2.1.16 Leaf length (cm)

At Shigaon, the general mean of leaf length was 49.62 and the values ranged from 30.37 cm to 71.60 cm. Among the

genotypes studied, Patani-6 (71.60 cm) recorded the maximum leaf length and the minimum leaf length was recorded by RTN-214-1-1-1-2 (30.37 cm).

However at Karjat the general mean of leaf length was 49.52 and the values ranged from 30.40 cm to 71.69 cm. Among the genotypes studied, Patani-6 (71.69 cm) recorded the maximum leaf length and the minimum leaf length was recorded by RTN-214-1-1-1-2 (30.40 cm).

4.1.2.1.17 Leaf breadth (cm)

The general mean of leaf breadth was 1.10 cm and the values ranged from 0.70 cm to 1.50 cm. at Shirgaon. Among the genotypes studied, CR-3993-2-24-45-2 (1.50 cm) recorded the maximum leaf breadth and the minimum leaf breadth was recorded by Bhadas-79 (0.70 cm).

Whereas at Karjat, the general mean of leaf breadth was 1.07 cm and the values ranged from 0.47 cm to 1.58 cm. Among the genotypes studied, CR-3993-2-24-45-2 (1.58 cm) recorded the maximum leaf breadth and the minimum leaf breadth was recorded by RTN-214-1-1-1-2 (0.47cm).

4.1.2.1.18 Stem thickness (cm)

For this trait, at Shirgaon, the genotypes exhibited a range of 0.50 cm to 1.00 cm with a general mean of 0.74 cm. The thinnest genotype for stem was RTN-214-1-1-1-2 (0.50 cm) and the thickest genotype was Patani-6 (1.00 cm).

However, for this trait, the genotypes exhibited a range of 0.51 cm to 1.06 cm with a general mean of 0.76 cm. The thinnest genotype was RTN-214-1-1-1-2 (0.51 cm) and the thickest genotype was RP-BIO-226 (1.06 cm).

4.1.2.1.19 Panicle number plant⁻¹ (cm)

At Shirgaon, the number of panicles per plant ranged from 7.93 (Mahsad) to 20.73 (TN-1) panicles with a general mean of 10.56.

Whereas at Karjat, the number of panicles per plant ranged from 7.98 (Mahsad) to 21.38 (TN-1) panicles with a general mean of 11.05.

4.1.2.1.20 Decorticated grain length (mm)

At Shirgaon, the decorticated grain length falls within the range of 4.03 to 9.68 mm with a general mean of 6.76 mm. The highest and lowest values for this trait were recorded by Sugnadha (8.17 mm) and Kothambir Sal (4.03 mm), respectively.

However at Karjat, the decorticated grain length falls within the range of 4.01 to 8.14 mm with a general mean of 6.78 mm. The highest and lowest values for this trait were recorded by Sugandha (9.71 mm) and Kothambir Sal (4.01 mm), respectively.

4.1.2.1.21 Decorticated grain width (mm)

The decorticated grain width was within the range of 1.61 to 3.11 mm with a general mean of 2.42 mm at Shirgaon. The genotype Bela (3.11 mm) recorded maximum decorticated grain width and the genotypes, HRTMS-61 (1.80 mm) recorded minimum decorticated grain width.

Whereas at Karjat, the decorticated grain width was within the range of 1.61 to 3.11 mm with a general mean of 2.42 mm. The genotype Bela (3.11 mm) recorded maximum decorticated grain width and the genotypes, HRTMS-61 (1.63 mm) recorded minimum decorticated grain width.

4.1.2.1.21 Length/breadth ratio

At Shirgaon, this trait values were calculated by dividing decorticated grain length (mm) with decorticated grain width (mm). This trait varied from 1.41 to 4.30 with a general mean of 2.85. The genotype P. Basmati (4.69) recorded maximum length/breadth ratio and the genotype Kothambir Sal (1.41) recorded minimum length/breadth ratio.

However at Karjat, this trait varied from 1.41 to 4.34 with a general mean of 2.85. The genotype P. Basmati (4.66) recorded maximum length/breadth ratio and the genotype Kothambir Sal (1.41) recorded minimum length/breadth ratio.

4.1.2.1.22 Amylose content (%)

At Shirgaon, the amylose content (%) was within the range of 11.67 to 34.99 % with a general mean of 23.15 %. The maximum amylose content was recorded for Ajaya (34.99%) and the minimum amylose content was recorded for MUDGO (11.67 %).

However at Karjat, the amylose content (%) was within the range of 11.86 to 35.01 % with a general mean of 23.01 %. The maximum amylose content was recorded for Ajaya (35.01%) and the minimum amylose content was recorded for MUDGO (11.86 %).

4.1.2.1.23 Zinc content (ppm)

At Shirgaon, this trait was varied from 1.09 ppm to 22.62 ppm with a general mean of 11.95 ppm. The genotype PTB 33 (22.62 ppm) recorded maximum zinc content and the genotype KJT-2R (1.09 ppm) recorded minimum zinc content.

However, this trait was varied from 1.12 ppm to 22.59 ppm with a general mean of 11.99 ppm. The genotype PTB 33 (22.59

ppm) recorded maximum zinc content and the genotype KJT-2R (1.12 ppm) recorded minimum zinc content.

4.1.2.1.24 Fe content (ppm)

Values for this trait ranged from 1.70 ppm to 28.00 ppm with a general mean of 13.11 ppm. The genotype Kalanamak (28.00 ppm) recorded maximum Fe content and the genotype Mahsad (1.70 ppm) recorded minimum.

Fe content whereas at Karjat, values for this trait ranged from 1.83 ppm to 28.12 ppm with a general mean of 13.16 ppm. The genotype Kalanamak (28.12 ppm) recorded maximum Fe content and the genotype RP-BIO-226 (1.83 ppm) recorded minimum Fe content.

4.1.2.1.25 Calcium content (ppm)

At Shirgaon, calcium content falls within the range from 3.63 ppm to 102.00 ppm with a general mean of 53.53 ppm. The genotype Bhogwati (102.00 ppm) recorded maximum calcium content and the genotype Sugandha (3.63 ppm) recorded minimum calcium content.

However, at Karjat, calcium content falls within the range from 3.86 ppm to 102.68 ppm with a general mean of 54.06 ppm. The genotype BG-367-2 (102.68ppm) recorded maximum calcium content and the genotype Sugandha (3.86 ppm) recorded minimum calcium content.

4.1.2.1.26 Alkali spreading value (Nos.)

Scores for alkali spreading value ranged from 3.00 (Jyoti, Try-1, Dodak, Karhad, NDR6315, Ambemohar and Sugandha,) to 5.33 (RP-BIO-226) panicles with a general mean of 4.59 at Shirgaon.

However at Karjat, scores for alkali spreading value ranged from 3.00 (Jyoti, Try-1, Dodak, Karhad, NDR6315, Ambemohar and Sugandha,) to 5.33(RP-BIO-226) panicles with a general mean of 4.59

4.1.3 Genetic variability, Heritability and Genetic advance

The genotypic and phenotypic coefficients of variation, heritability (broad sense) and genetic advance as per cent of mean were estimated for 95 rice genotypes during first year at Shirgaon and second year at Karjat, respectively. Results are furnished in Table 4.5 and Table 4.6 for PCV, GCV, heritability (broad sense) and genetic advance as per cent of mean, respectively.

4.1.3.1 Variability

In the present study, experiment carried out at ARS, Shirgaon during *Kharif*, 2020 the GCV values ranged from 5.82 to 45.67 per cent whereas, PCV values ranged from 5.91 to 46.02 per cent.

Whereas, at Karjat during *Kharif*, 2021, the GCV values ranged from 5.95 to 45.64 per cent whereas, PCV values ranged from 6.08 to 46.06 per cent.

4.1.3.1.1 Low GCV and low PCV (Below 10%)

At Shirgaon, The GCV and PCV values were lowest for the traits *viz.*, days to maturity (5.82 and 5.91 %), followed by days to 50% flowering (7.72 and 7.85 %), panicle length of main axis (8.51 and 9.46 %) and fertility % (9.14 and 9.19 %).

While at Karjat, the GCV and PCV values were lowest for the traits *viz.*, days to maturity (5.95 and 6.08 %), followed by days to 50% flowering (7.93 and 8.10 %), panicle length of main axis (8.33 and 9.41 %) and fertility % (9.18 and 9.23 %) indicating that the variability of these characters among the genotypes was meager at both locations.

4.1.3.1.2 Moderate GCV and moderate PCV (10- 20%)

At Shirgaon, moderate GCV and PCV values were observed for the traits *viz.*, Number of Tillers Plant⁻¹ (14.57 and 15.82 %), test weight of 1000 grains (19.34 and 20.08%), grain length, grain width, grain yield/ straw yield ratio, straw yield/ grain yield ratio, leaf length, leaf breadth, stem thickness, Number of panicles plant⁻¹, decorticated grain length and decorticated grain breath.

However at Karjat, moderate GCV and PCV values were observed for the traits *viz.*, Number of Tillers Plant⁻¹ (13.84 and 15.13 %), grain length, grain width, grain yield/ straw yield ratio, straw yield/ grain yield ratio, leaf breadth, stem thickness, number of panicles plant⁻¹, decorticated grain length, decorticated grain breath and alkali spreading value.

4.1.3.1.3 High GCV and high PCV (Above 20%)

At Shirgaon, high GCV and PCV values were observed for the traits *viz.*, zinc content (45.67 and 46.02%), plant height (cm), stem length excluding panicle, number of spikelets panicle⁻¹, grain yield per plant, straw yield per plant L/B ratio, amylose content (%), iron content (ppm) and calcium content (ppm).

Whereas at Karjat, high GCV and PCV values were observed for the traits *viz.*, zinc content (45.64 and 46.06%), plant height (cm), stem length excluding panicle, number of spikelets panicle⁻¹, test weight, grain yield plant⁻¹, grain yield plant⁻¹, straw yield plant⁻¹, leaf length, L/B ratio, amylose content (%), Fe content (ppm), and calcium content (ppm) indicating that large amount of variation is present among the genotypes for both locations.

4.1.3.2 Heritability (broad sense)

In the present study all the characters *viz.*, showed high heritability (broad sense) (>60%) except alkali spreading value which showed lowest heritability (<30%) i.e. (29.00 %) at Shirgaon.

Whereas at Karjat, all the characters *viz.*, showed high heritability (broad sense) (>60%) except alkali spreading value which showed lowest heritability (broad sense) (<30%) i.e. (28.00 %).

4.1.3.3 Genetic advance as per cent of mean

At Shirgaon, the genetic advance as per cent of mean was high (>20%) for the characters *viz.*, plant height, stem length excluding panicle, number of spikelets per panicle and calcium content. On the other hand, moderate genetic advance (10-20%) as per cent of mean was noted for days to 50% flowering, fertility %, days to maturity, straw yield per plant, leaf length and zinc content. Remaining seventeen characters showed low genetic advance (<10%) as per cent of mean.

High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was observed for the traits *viz.*, plant height, stem length excluding panicle length, Number of spikelets panicle⁻¹ and calcium content. High heritability (>60%) coupled with moderate genetic advance (10-20%) as per cent of mean was observed for the traits *viz.*, days to 50% flowering, fertility (%), days to maturity, straw yield plant⁻¹, leaf length and zinc content.

Whereas at Karjat, the genetic advance as per cent of mean was high (>20 %) for the characters *viz.*, plant height, stem length excluding panicle, number of spikelets per panicle, leaf length and calcium content. On the other hand, moderate genetic advance (10-20 %) as per cent of mean was noted for days to 50% flowering,

fertility %, days to maturity, straw yield per plant and zinc content. Rest of the seventeen characters showed low genetic advance as per cent of mean (<10%).

High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was reported for plant height, stem length excluding panicle, number of spikelets panicle⁻¹, leaf length and calcium content. High heritability (>60%) coupled with moderate genetic advance as per cent of mean (10-20%) was observed for the traits *viz.*, days to 50% flowering, fertility (%), leaf length and calcium content.

4.1.4 Genetic diversity

The 95 rice genotypes were assessed for genetic divergence by adopting Mahalanobis D² statistic for 27 yield and yield contributing parameters over two locations *viz.*, during *Kharif*, 2020 and *Kharif*, 2021 at ARS, Shirgaon and RARS, Karjat respectively.

4.1.4.1 Grouping of genotypes into various clusters

At Shirgaon, the 95 genotypes were categorized into 22 clusters based on D² values using agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The genotypes belonging to same cluster had an average smaller D² values than those belonging to different clusters. The distribution of genotypes into various clusters is furnished in Table 4.7 and Fig. 1 (Tocher's method). Cluster I was largest out of the twenty two clusters which comprises of 57 genotypes followed by cluster IV with 32 genotypes. Remaining clusters constitutes of one genotype respectively. The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster.

However at Karjat, the 95 genotypes were categorized into 20 clusters based on D^2 values using agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is furnished in Table 4.8 and Fig. 2 (Tochers method). Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters are mono-genotypic.

4.1.4.2 Average intra and inter cluster distances

At Shirgaon, intra cluster D^2 values ranged from 0.00 (all clusters except cluster I and IV) to 723.08 (cluster IV). Maximum intra cluster distance was observed in cluster IV (723.05) followed by cluster I (587.10) The details of inter and intra cluster distances are presented in Table 4.9 The inter-cluster D^2 values ranged from 147.10 (cluster II and III) to 3111.77 (cluster XIX and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (3111.77), followed by cluster XVIII and XX (3076.24), cluster XX and XXI (3018.86), cluster XXI and XXII (2771.82), cluster X and cluster XXII (2405.44), cluster XIII and XX (2344.39). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.10. Cluster I comprises 57 genotypes. It was nearest to cluster VIII (766.88) and was farthest from the cluster XXII (1624.67).

Whereas at Karjat, intra cluster D^2 values ranged from 0.00 (all clusters except cluster I, V and X) to 607.76 (cluster X). Maximum intra cluster distance was observed in cluster X (607.76)

followed by cluster I (437.13). The details of inter and intra cluster distances are presented in Table 4.11.

The inter-cluster D^2 values ranged from 232.22 (cluster IX and XI) to 2259.27 (clusters XIV and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (2259.27), followed by cluster XV and XX (1920.54), cluster VI and XX (1830.75), cluster X and XIX (1730.06). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.12. Cluster I comprises 58 genotypes. It was nearest to cluster IV (552.11) and was farthest from the cluster XX(1407.0).

4.1.4.3 Cluster mean values

The cluster means values at Shirgaon, for all the 27 characters are presented in Table 4.13. Cluster mean values for days to 50% flowering ranged from 78.00 days (cluster XII) to 108.33 days (cluster XII). Plant height ranged from 81.33cm in cluster XVI to 173.60 cm in cluster XXII, stem length excluding panicle was ranged from 57.33 cm in cluster XVI to 142.87 cm in cluster XXII. Number of tillers plant⁻¹ was ranged from 9.43 in cluster XII to 14.87 in cluster XXI. Panicle length of main axis was ranged from 22.40 cm in cluster XIII to 30.73 cm in cluster XXII. Number of spikelets panicle⁻¹ ranged from 55.32 in cluster XIX to 187.77 in cluster VII. Fertility % ranged from 57.54% in cluster XXII to 97.30 % in cluster X. Days to maturity ranged from 108.00 days in cluster XII to 138.33 days in cluster XVII. Test weight was ranged from 11.98 g in cluster XVI to 27.26 in cluster VI. Grain length ranged from 5.99 cm in cluster XX to 12.84 cm in cluster XVIII. Grain width was ranged from 2.23 cm in cluster XVI to 3.50 cm in cluster XXII. Grain yield plant⁻¹ was ranged from 11.20 g in

cluster II to 25.00 g in cluster XVII. Straw yield plant⁻¹ was ranged from 14.35 g in cluster XXII to 32.33 g in cluster XV. Grain yield to straw yield ratio ranged from 0.63 in cluster XXI to 0.94 in cluster XIII. Straw yield to grain yield ratio was ranged from 1.07 in cluster XIII to 1.59 in cluster XXI. Leaf length was ranged from 30.37cm in cluster VII to 67.23 cm in cluster III. Leaf breadth was ranged from 0.72 cm in cluster XV to 1.40 cm in cluster X. Stem thickness was ranged from 0.50 cm in cluster VII to 0.87 cm in cluster III. Number of panicles plant⁻¹ was ranged from 8.43 in cluster XII to 13.87 in cluster XXI. Decorticated grain length was ranged from 4.03 mm in cluster XX to 9.68 mm in cluster XVIII. Decorticated grain breath was ranged from 1.87 mm in cluster IX to 3.10 mm in cluster XXII. L/B Ratio was ranged from 1.41 in cluster XX to 4.69 in cluster XVIII. Amylose content was ranged from 14.33% in cluster VI to 29.42 % in cluster XIV. Zinc content was ranged from 1.09 ppm in cluster IX to 29.13 ppm in cluster XX. Iron content was ranged from 5.53 ppm in cluster XXII to 21.42 ppm in cluster X. Calcium content was ranged from 3.63 ppm in cluster XXI to 102.00 ppm in cluster IX. Alkali spreading value was ranged from 3.00 in cluster XXII to 5.00 in cluster XX.

However at Karjat the cluster means values for all the 27 characters are presented in Table 4.14 Cluster mean values for days to 50% flowering ranged from 72.33 days (cluster 8) to 107.00 days (cluster III). Plant height ranged from 85.83 cm in cluster VIII to 167.46 cm in cluster XX. Stem length excluding panicle was ranged from 63.41cm in cluster VIII to 136.15 cm in cluster XX. Number of tillers plant⁻¹ was ranged from 10.10 in cluster XI to 15.48 in cluster XV. Panicle length of main axis was ranged from 22.21cm in cluster XVII to 32.33 cm in cluster XVI. Number of spikelets panicle⁻¹ ranged from 55.50 in cluster VII to 178.78 in

cluster XVIII. Fertility % ranged from 57.54% in cluster XX to 97.16 % in cluster XIV. Days to maturity ranged from 102.33days in cluster VIII to 137.00 days in cluster III. Test weight was ranged from 13.36 g in cluster II to 27.83 in cluster IX. Grain length ranged from 7.50 cm in cluster XIII to 12.83 cm in cluster XIX. Grain width was ranged from 2.07 cm in cluster VI to 3.51 cm in cluster XX. Grain yield plant⁻¹ was ranged from 10.99 g in cluster II to 30.64 g in cluster XVI. Straw yield plant⁻¹ was ranged from 14.31 g in cluster XX to 46.50 g in cluster XVI. Grain yield to straw yield ratio ranged from 0.63 in cluster XV to 0.89 in cluster I. Straw yield to grain yield ratio was ranged from 1.18 in cluster 3 to 1.58 in cluster XV. Leaf length was ranged from 32.65 cm in cluster III to 66.35 cm in cluster II. Leaf breadth was ranged from 0.71 cm in cluster XIII to 1.39 cm in cluster XV. Stem thickness was ranged from 0.52 cm in cluster VII to 0.95 cm in cluster XVI. Number of panicles plant⁻¹ was ranged from 8.48 in cluster XI to 14.48 in cluster XV. Decorticated grain length was ranged from 5.24 mm in cluster XIII to 9.71 mm in cluster XIX. Decorticated grain breath was ranged from 1.85 mm in cluster VI to 3.09 mm in cluster XX. L/B ratio was ranged from 1.88 in cluster XIII to 4.66 in cluster XIX. Amylose content was ranged from 12.39 % in cluster VIII to 29.55 % in cluster XI. Zinc content was ranged from 2.02 ppm in cluster VII to 18.52 ppm in cluster XI. Iron content was ranged from 5.68 ppm in cluster XX to 21.39 ppm in cluster XIV. Calcium content was ranged from 3.86 ppm in cluster XV to 102.68 ppm in cluster XII. Alkali spreading value was ranged from 3.00 in cluster XX to 5.00 in cluster XII

4.1.4.4 Wilk`s ‘V’ criterion test

Wilk`s ‘V’ (Statistical) criterion was used to test the significant differences between the groups based on the pooled

effects for all the characters in the present study. The X^2 test at 281 degrees of freedom was conducted to study the significance of 'V' (Statistical) value. Highly significant 'V' statistic value indicating, that there was significant difference among the genotypes when all the characters were considered simultaneously.

The 95 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect for all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.1.4.5 Per cent contribution of character towards total genetic diversity

At Shirgaon, per cent contribution of 27 characters and towards total genetic divergence was found maximum for leaf length (cm) (26.00%) followed by calcium content (ppm) (23.23%), Number of panicles plant⁻¹ (cm) (19.42%), fertility (%) (9.09%), zinc and iron content ppm (5.69), decorticated grain length (mm) (5.46%), days to maturity (Nos.) (1.63%), Number of spikelets panicle⁻¹ (1.05%), plant height (cm) (Nos.) (0.63%), days to 50% flowering (Nos.) (0.56%), grain width (mm) (0.43%), amylose content (0.34 %), straw yield plant⁻¹ (g) (0.31%), grain yield plant⁻¹ (g) (0.25%), grain yield/ straw yield ratio (0.13%), Number of tillers plant⁻¹ and test weight of 1000 grains (g) (0.04%). It has been presented in the Table 4.15.

Character contribution was to total divergence was based on number of times character ranked first. From the table it was observed that for leaf length ranked 1st maximum times (1161) followed by calcium content (1037), Number of panicles plant⁻¹ (867) and the Number of tillers plant⁻¹ and test weight ranked 1st minimum times (2).

Whereas at Karjat, per cent contribution of 27 characters and

towards total genetic divergence was found maximum for calcium content (ppm) (26.32%) followed by leaf length (cm) (26.0%), fertility (%) (14.58%), decorticated grain length (mm) (9.97%), zinc content (ppm) (9.07%), Iron content (ppm) (6.29%), Number of spikelets Panicle⁻¹ (2.46%), plant height (cm) (1.39%), amylose content (%) (1.21%), days to 50% flowering (Nos.) (0.87%), grain yield plant⁻¹ (g) (0.74%), Number of tillers plant⁻¹ (0.31%), test weight (g) (0.27 %), panicle length of main axis (cm) (0.25%), straw yield plant⁻¹ (g) (0.13%), days to maturity (Nos.) and grain length (mm) (0.02%). It has been presented in the Table 4.16.

Character contribution was to total divergence was based on number of times character ranked first. From the table it was observed that for calcium content ranked 1st for maximum times (1175) followed by leaf length (1165), fertility% (651) and days to maturity (Nos.) and grain length (mm) ranked 1st for minimum times(1).

4.2 Molecular profiling of rice germplasm using SSR markers.

In the present study, 17 SSR markers were used to screen 95 rice genotypes. (Table 3.13).

4.2.1 DNA isolation

The standard procedure of DNA isolation along with slight modification of buffer components and their quality were employed (data not shown). The good quality and desired quantity of DNA was obtained (Plate Number1).

4.2.2 Standardization of annealing temperature:

The SSR markers having OD 25 nm were diluted at a concentration of 5pm/μl and employed for standardization of annealing temperature. The T_m value of reverse and forward primer was taken into consideration and programme was set accordingly. The data obtained is presented in T17. Each primer has shown different annealing temperature. It has been observed that, the

lowest annealing temperature was recorded in primer pTA-248 (54°C) whereas, maximum annealing temperature was recorded in primer RM 309 (66.9°C).

Table 4.17 : Optimization of annealing temperature of various SSR markers.

SN	Primer	Repeat motif	Size (bp)	Standardised AT (°C)
1	RM 140	(CT)12	261	62.1
2	RM 1287	(AG)17	162	56.7
3	RM 3412	(CT)17	211	62.8
4	RM 234	(CT)25	156	56.5
5	RM 6775	(TCC)8	192	58.7
6	RM 309	(GT)13	169	66.9
7	RM 8225	A11N(AAG)14	221	58.7
8	RM 212	(CT)24	136	62.9
9	RM 302	(GT)30(AT)8	156	61.7
10	RM 201	(CT)17	158	52.1
11	pTA 248	-	950	54.0
12	RM 122	(GA)7A(GA)2A(GA)11	227	61.5
13	RM 22709	-	160-170	65.9
14	RM 547	(ATT)19	235	56.1
15	RM 7	(GA)19	180	58.9
16	RM 42	(AG)6-(AG)(2T(GA)5	166	61.3
17	RM 276	(AG)8A3(GA)33	149	58.5

4.2.3 Genetic diversity

4.2.3.1 Polymorphism percentage:

The polymorphism percentage for individual primer was calculated by the ratio of number of polymorphic bands obtained over the total number of bands produced across the 95 rice genotypes. A total of 17 SSR primer pairs distributed across the genome were used for molecular analysis of 95 rice genotypes. All the 17 microsatellite markers used were found to be polymorphic and showed 100 per cent polymorphism. The overall size of amplified products ranged from 132 bp to 884 bp. A total of 139

alleles were obtained using 17 SSR primer pairs with an average of 8.17 alleles per primer. The number of alleles amplified for each primer pair ranged from 3 to 14.

4.2.3.2 Polymorphic Information Content (PIC):

The PIC values of primers ranged from 0.70 in SSR primer RM 7 to 0.92 in SSR primer RM 8225 with an average PIC value of 0.83. Further, it was observed that, there was no correlation between per cent polymorphism and PIC values as SSR primers RM 7 showed minimum PIC value but were 100 per cent polymorphic. The higher the PIC value, the more informative is the SSR marker. Hence, primers RM 825, RM 1287, pTA-248, RM 201, RM 122 and RM 22709 were found to be highly informative.

Table 4.18: Molecular polymorphism, PIC values, number of alleles and size of loci revealed by SSR primers

Primer	Size (bp)	Amplicons	Polymorphism %	PIC
RM 140	261	13	100	0.84
RM 1287	162	10	100	0.87
RM 3412	211	3	100	0.83
RM 234	156	6	100	0.86
RM 6775	192	12	100	0.72
RM 309	169	8	100	0.75
RM 8225	221	6	100	0.92
RM 212	136	3	100	0.86
RM 302	156	11	100	0.76
RM 201	158	14	100	0.89
PTA 248	950	7	100	0.87
RM 122	227	5	100	0.87
RM 22709	160-170	10	100	0.87
RM 547	235	4	100	0.84
RM 7	180	12	100	0.70
RM 42	166	11	100	0.74
RM 276	149	4	100	0.84
Average				0.83

Table 4.19 : Amplification of gene specific alleles with linked SSR markers for biotic and abiotic stresses resistance/tolerance.

SN	Traits	Primers	Resistance/ Tolerance genotypes
1	Blast	RM 8225	Try-1, Kochari, Lal Patani, Karhad, Ratnagiri 7, Phule Samruddhi, Ambemohar, Rathu Heenati, Sinna Sivappu, IRRI 190, IRRI 193, ARC10550, Samba Mahsuri, IRRI 123
2	Salt	RM 140	MO-17, MO-19, KJT-2R, RTN 11-2-1-3, Pak Basmati, Super Basmati,, Chinoor, Pusa Sugandha-1, Pusa Sugandha-3, Pusa Sugandha-4, Bhogwati, RP Bio 197, RP-BIO-226, Ajaya, Karjat 1
		RM 1287	VDN-9-10-1, HRTMS-61,
3	Brown plant hopper	RM 6775	Pusa Sugandha-4, Pusa Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, Phule Samruddhi
		RM 309	Kala Rata, Try-1, Kochari, BG 367-2, FL 478, MUT NS 1, Rathu Heenati, Sinna Sivappu
4	Drought	RM 212	BG 367-2, Milyang 63, FL 478, MUT NS 1, IRRI 192
		RM 201	Dhanesal, Ambemohar, Bhogwati, Sugandha
5	Gall midge	RM 22709	MO-6, MO-8, Munga, Patni-6, Pandya, NAUR-1, DRR-50-12, DRR-363-5, DRR-50-10, IR-63879-195-2-2-3-2, RTN-214-1-1-1-2, Chinoor, RP Bio 197, RP-BIO-226, Ajaya, Karjat 2, IR-64,
6	Amylose	RM 42	Try-1, KJT-1R, Gurjari, RTN-214-1-1-1-2, HRTMS-61, Phule Samruddhi, Indrayani, Dhanesal, Ambemohar, Karjat Shatabdi, RS-1113,

4.2.4 Genetic distance:

The diversity observed in the Ninety five rice genotypes mainly attributed to the genetic dissimilarities. The Jaccard's similarity coefficient values among the rice genotypes are presented in (Table 4.20). The pair wise similarity values ranged from 0.027 to 0.994.

4.2.4.1 Cluster analysis and Dendrogram construction:

UPGMA cluster analysis was performed using Jaccard's similarity coefficient matrices calculated from SSR markers to generate a dendrogram for 95 rice genotypes (Table 4.20). The UPGMA based dendrogram of 95 rice genotypes generated with Multivariate Statistical Package (MVSP). It was observed that, there are two major clusters. The first major cluster consists of four sub clusters. Two rice genotypes CR-3993-2-24-45-2 and HRTMS-61 formed the independent first sub cluster (IAa). Second sub cluster (IAb) consists of ten genotypes *viz.*, VDN-10-18, RTN-35-1-1, Sahyadri 5R, VDN-9-19-1, DRR-86-8, RTN-27-1-1-2, DRR-50-13, RTN-214-1-1-1-2, DRR-363-5, DRR-50-12. Third sub cluster (IBa) consists of seven genotypes *viz.*, BL-184AR, Gurjari, NAUR-1, IR 63879-195-2-2-3-2, DRR-50-10, RTN69-1-1, DRR-215. While fourth sub cluster (IBb) consists of four genotypes *viz.*, PR-118, RTN 11-2-1-3, PR-114, KJT-4R.

The second major cluster consists of four sub clusters. First sub cluster (IIAa) consist of five rice genotypes *viz.*, Sugandha, Bhogwati, Ambemohar, Karjat Shatabdi, Dhanesal. Second sub cluster (IIAb) consist of three rice genotypes *viz.*, Indrayani, NDR6315, Bhadasbhog. Third sub cluster (IIBa) consist of fourteen rice genotypes *viz.*, FL 478, Milyang 63, BG367, IRRI 193, Sinna Sivappu, Tathu Heenati, MUT NS 1, MTU1010, IRRI 192, IRRI 104, IRRI 123, Samba Mahsuri, ARC 10550, MUDGO. Third sub cluster (IIBb) consist of fifty rice genotypes *viz.*, TN1, Sonsali, Munga, Bela,

Ratnagiri 7, Valai, Kahad, Dodak, Kochari, Lal Patani, Try-1, Bhadas, Pandya, Patani-6, IRRI 190, Bamil, Jyoti, Waksa-207, Mahasad, Dular, Mayekar Bhat, Khara Rata, PTB 33, Milyang 46, Karjat 1, IR 64, Ajaya, RP BIO 226, RS 1113, RP BIO 197, Super Basmati, Kothambir Sal, Phule Samruddhi, Kalanamak, CR2713-180, Pusa Sugandha-5, Pusa Sugandha-3, KJT-1R, MO-19, MO-17, MO-13, KJT-3R, KJT-2R, Karjat 2, Pusa Sugandha 4, Chinoor, Pusa Sugandha-1, MO-8, Pak Basmati, MO-6.

Table 4.21: Clustering pattern of 95 rice genotypes.

Cluster			Number of Genotypes	Name of the genotypes
I	IA	IAa	02	CR-3993-2-24-45-2, HRTMS-61
		IAb	10	VDN-10-18, RTN-35-1-1, Sahyadri 5R, VDN-9-19-1, DRR-86-8, RTN-27-1-1-2, DRR-50-13, RTN-214-1-1-1-2, DRR-363-5, DRR-50-12
	IB	IBa	07	BL-184AR, Gurjari, NAUR-1, IR 63879-195-2-2-3-2, DRR-50-10, RTN69-1-1, DRR-215
		IBb	04	PR-118, RTN 11-2-1-3, PR-114, KJT-4R
II	IIA	IIAa	05	Sugandha, Bhogwati, Ambemohar, Karjat Shatabdi, Dhanesal
		IIAb	03	Indrayani, NDR6315, Bhadasbhog
	IIB	IIBa	14	FL 478, Milyang 63, BG367, IRRI 193, Sinna Sivappu, Tathu Heenati, MUT NS 1, MTU1010, IRRI 192, IRRI 104, IRRI 123, Samba Mahsuri, ARC 10550, MUDGO
		IIBb	50	TN1, Sonsali, Munga, Bela, Ratnagiri 7, Valai, Kahad, Dodak, Kochari, Lal Patani, Try-1, Bhadas, Pandy, Patani-6, IRRI 190, Bamil, Jyoti, Waksa-207, Mahasad, Dular, Mayekar Bhat, Kala Rata, PTB 33, Milyang 46, Karjat 1, IR 64, Ajaya, RP BIO 226, RS 1113, RP BIO 197, Super Basmati, Kothambir Sal, Phule Samruddhi, Kalanamak, CR2713-180, Pusa Sugandha-5, Pusa Sugandha-3, KJT-1R, MO-19, MO-17, MO-13, KJT-3R, KJT-2R, Karjat 2, Pusa Sugandha 4, Chinoor, Pusa Sugandha-1, MO-8, Pak Basmati, MO-6
		Total	95 genotypes	

4.3 Morphological characterization of rice germplasm based on DUS guidelines

In the present investigation 95 rice germplasm were characterized using 62 DUS descriptors over two independent *Kharif* seasons of 2020 and 2021 at two different locations ARS, Shiragon and RARS, Karjat, respectively.

4.3.1 DUS Descriptors in Rice Varieties

In rice, in total, 62 DUS descriptors have been notified by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA) in India for conducting DUS test. In the present study, 95 germplasm were characterized using 62 DUS descriptors. The varietal-specific DUS traits (62 traits) of 95 genotypes recorded in the present study as per DUS guidelines are presented in the table 4.22 and 4.23. Observations for all 62 descriptors were found to be similar over both the locations.

4.3.1.1 Coleoptile colour

This character was found to be polymorphic and exhibited three variations among 95 genotypes *viz.*, maximum 85 genotypes found to be colourless, 9 purple and only one genotype (Karhad) exhibited green coleoptile.

4.3.1.2 Basal Leaf: Sheath colour

This character was also found to be polymorphic and shown four types of variants among 95 genotypes *viz.*, highest number of 82 genotypes exhibited green for basal leaf sheath colour followed by 9 having light purple colour, 3 shown uniform purple and only one genotype (Mahasad) have purple lines.

4.3.1.3 Leaf: Intensity of green colour

Out of 95 genotypes light, medium and dark green leaves were observed on 32, 33 and 30 genotypes respectively. Hence this character found to be polymorphic in line with first two characters.

4.3.1.4 Leaf: Anthocyanin colouration

Out of 95 genotypes studied only 3 genotypes exhibited presence of leaf anthocyanin colouration *viz.*, Mahasad, Waksal-207 and Barmil, whereas leaf anthocyanin colouration in remaining 92 genotypes were found to be absent. Hence this trait can be categorized as dimorphic.

4.3.1.5 Leaf: Distribution of Anthocyanin Coloration

Out of 95 genotypes 2 genotypes *viz.*, Mahasad and Barmil exhibited uniform distribution of anthocyanin colouration and only one genotype Waksal-207 shows anthocyanin colouration on leaf margins. For rest of 92 genotypes this descriptor is not applicable as leaf anthocyanin coloration is absent. This trait is dimorphic.

4.3.1.6 Leaf Sheath: Anthocyanin Coloration

14 genotypes were showing presence of anthocyanin coloration on leaf sheath, whereas anthocyanin coloration on leaf sheath is absent in remaining 81 genotypes out of total 95. This descriptor can be described as dimorphic.

4.3.1.7 Leaf Sheath: Intensity of Anthocyanin Coloration

This character is polymorphic in nature as it shows five variations among 95 genotypes. Intensity anthocyanin coloration was found to be very weak, weak, medium, strong and very strong in 4,4,2,2 and 2 genotypes respectively whereas, for remaining 81 genotypes categorization for this trait was not applicable.

4.3.1.8 Leaf: Pubescence of blade surface

Stronger pubescence of leaf surface is not-preferred by insect pests. Hence presence of this trait in stronger range implies morphological resistance against pests. Out of 95 germplasm 22 were weak, while 40, 22 and 6 were seen to have medium, strong and very strong pubescence of leaf blade surface. This trait is polymorphic.

4.3.1.9 Leaf auricles

Auricles are hinge like structures that function to project the leaf away from the vertical axis of the plant. Among the 95 genotypes studied, all genotypes exhibited presence of leaf auricle. Hence this descriptor is monomorphic.

4.3.1.10 Leaf: Anthocyanin colouration of auricles

Colourless auricles were present in 86 genotypes, whereas light purple and purple auricles were present in 2 and 7 genotypes respectively, showing polymorphic nature for this trait.

4.3.1.11 Leaf collar

There was no variation in the genotypes for this character. All the 95 genotypes (100%) included in the present study showed presence of leaf collar. Thus this descriptor is monomorphic by nature.

4.3.1.12 Leaf collar: Anthocyanin colouration of collar

There was dimorphic variation in the genotypes for this character. Among total 95 genotypes included in the present study only 5 showed presence of anthocyanin colouration on leaf collar while rest of 90 genotypes were devoid of the same.

4.3.1.13 Leaf ligule

The ligule appears to be a continuation of the leaf sheath and encircles or clasps the stem as does the leaf sheath. Traditionally, it has been assumed in protecting the culm and leaves that it encloses from the entry of water, dust and harmful spores. There was no variation in the genotypes for this character. All the 95 genotypes showed presence of leaf ligule concluding the trait is monomorphic.

4.3.1.14 Leaf: Shape of ligule:

All the genotypes included under this study reported split shape of leaf ligule. Accordingly this descriptor falls under monomorphic class.

4.3.1.15 Colour of leaf ligule

Only one genotype (Dhanesal) exhibited light purple coloured ligule and the remaining 94 genotypes exhibited white coloured ligule. This trait is dimorphic in nature.

4.3.1.16 Leaf: Length of Blade

This measurable trait showed two variations viz., 40 genotypes found to be medium for length of leaf blade and remaining 55 have long leaf blade. Hence this character is dimorphic by nature.

4.3.1.17 Leaf: Width of Blade

This measurable trait showed similar dimorphic variation in line with the previous one. Out of 95 genotypes, 26 exhibited narrow leaf blade for its width while 69 were medium for the same.

4.3.1.18 Culm: Attitude (for floating rice only)

This trait was not applicable for the genotypes under study as it does not fall under floating rice category.

4.3.1.19 Culm: Attitude

Erect culms were observed in 84 genotypes while semi erect culm was seen in 11 genotypes showing dimorphic variation for the trait.

4.3.1.20 Time of heading (50% of plants with panicles) (days)

The experimental material was categorized into three classes based on this trait. The time of heading of 42 genotypes early type with the duration ranging from 71-90 days, 52 genotypes were found to be medium with 91-110 days to heading. 10 genotypes were found to be late with 111-130 days to heading and the remaining only one genotype (Kalanamak) exhibited late with duration of more than 131 days. Accordingly this trait is polymorphic.

4.3.1.21 Flag leaf: Attitude of blade (Early observation):

Polymorphic variation is observed the trait as erect flag leaf was observed in 79 genotypes while semi erect and horizontal flag leaves were observed in 14 and 2 genotypes respectively.

4.3.1.22 Spikelet: Density of pubescence of lemma

95 genotypes were classified in to weak (10), medium (23), strong (25) and very strong (37) based on density of pubescence of lemma exhibiting polymorphic variation.

4.3.1.23 Male sterility

All the 95 genotypes under study were found negative for male sterility attributing monomorphic nature.

4.3.1.24 Lemma: Anthocyanin colouration of keel

Out of 95 genotypes 90 genotypes were having very weak or no anthocyanin colouration of keel of lemma while 2 genotypes were found to have strong colouration and 3 genotypes exhibited very strong colouration. Thus this trait is polymorphic.

4.3.1.25 Lemma: Anthocyanin colouration of area below apex

This character was found to be polymorphic and exhibited three variations. Among the 95 genotypes studied, 90 genotypes showed absence of anthocyanin colouration and only one genotype (Kochari) showed presence of anthocyanin colouration of area below apex of lemma with medium note, whereas 4 genotypes have very strong colouration.

4.3.1.26 Lemma: Anthocyanin colouration of apex

The 95 genotypes were classified in to absent (81), strong (9) and very strong (5) exhibiting polymorphic variation.

4.3.1.27 Spikelet: Colour of Stigma

White stigma was found in 84 genotypes while purple were found in 11 genotypes. Moreover no light green, yellow and light purple colour stigma was seen.

4.3.1.28 Stem thickness

All 95 genotypes under study showed thick stem attributing monomorphic trait.

4.3.1.29 Stem length (excluding panicle; excluding floating rice) (cm)

Based on the stem length, the experimental material was grouped into four classes attributing polymorphic variation. Very short stem length (< 91 cm) was recorded by 46 genotypes, 16

genotypes were found to have medium stem length ranging from 110-130 cm, and 20 genotypes recorded short stem length ranging from 91-110 cm whereas 13 genotypes exhibited long stem length (>150cm).

4.3.1.30 Stem: Anthocyanin colouration of nodes

This trait showed dimorphic variation. In 91 genotypes anthocyanin colouration was absent in nodes while rest 4 genotypes it was present on the nodes.

4.3.1.31 Stem: Intensity of anthocyanin colouration of nodes

The anthocyanin colouration of nodes was found to be weak and medium 3 and 1 (Gurjari) genotypes respectively. For remaining 91 genotypes this trait is not applicable as colouration is absent. Thus the variation the said character is dimorphic.

4.3.1.32 Stem: Anthocyanin colouration of internodes

Out of 95 genotypes anthocyanin was present in 2 genotypes and absent in 93 genotypes at internode attributing monomorphic variation.

4.3.1.33 Panicle length of main axis (cm)

This trait exhibited polymorphic variation and according to panicle length of main axis, the genotypes were categorized into three groups, dominated by 63 genotypes with long sized panicles (26-30 cm), followed by 22 genotypes having medium sized panicles (21-25 cm) and remaining 10 genotypes had very long panicles (> 30 cm).

4.3.1.34 Flag leaf: Attitude of blade (late observation)

67 genotypes were having erect flag leaf while 20 and 7 were having semi-erect and horizontal flag leaf. Remaining only one

genotype (NDR-6315) showed deflexed flag leaf. Variation for the said character found to be polymorphic.

4.3.1.35 Panicle: Curvature of main axis

95 genotypes were classified in to straight (28), semi-straight (33), deflexed (24) and drooping (10) for panicle curvature attributed polymorphic variation for the said descriptor.

4.3.1.36 Panicle number plant⁻¹

The experimental material in the present study was polymorphic for this character. Out of 95 genotypes, 55 genotypes possessed fewer panicles per plant (<11), 39 genotypes have medium number of panicles (11-20) and remaining only one genotype *viz.*, TN-1 possessed many number (>20) of panicles.

4.3.1.37 Spikelet: Colour of tip of lemma:

95 genotypes were classified in to White (69), Yellowish (12), Brown (3), Purple (7) and Black (4) for tip colour of lemma as this trait exhibited polymorphic nature.

4.3.1.38 Lemma and palea colour:

Lemma and palea colour was observed under eight categories; straw (77), brown spots on straw (3), brown furrows on straw (3), brown tawny (6), reddish to light purple (3), purple spots/furrows (1), purple (1) and black (1) exhibiting polymorphic variation.

4.3.1.39 Panicle awns

Among the 95 genotypes, 34 genotypes possessed awns and the remaining 61 genotypes were awn-less, showing dimorphic variation.

4.3.1.40 Panicle: Colour of awns (late observation)

The colour of awns was Yellowish white (24), Yellowish brown (3), Reddish brown (1), Light red (1), Red (1) Light purple (3) and black (1). Traits not applicable for remaining 61 genotypes as those are awn less. Polymorphic variation is seen for the said character.

4.3.1.41 Panicle: Length of longest awns

Out of 95 genotypes studied 34 were awned and among these 20 genotypes had short awns, 11 showed medium length of awns and 3 were having very long awns (Khara rata, P. Basmati and Kalanamak). Polymorphic variation is observed for the said descriptor.

4.3.1.42 Panicle distribution of awns

Out of 95, 34 genotypes possessed awns. Out of these 34, 23 genotypes possessed awns at tip only, 6 genotypes have awns on upper half of panicle and the remaining 5 genotypes possessed awns throughout the whole length of panicle.

4.3.1.43 Presence of panicle secondary branching

Out of 95 genotypes studied 79 showed presence of secondary branching of the panicles whereas in 16 genotypes it was absent. There was dimorphic variation in the genotypes with respect to this character.

4.3.1.44 Panicle: Secondary branching

The experimental material in the present study was dimorphic for this character. Out of 95 genotypes, 21 genotypes possessed strong secondary branches and 58 genotypes possessed weak secondary branches.

4.3.1.45 Panicle: Attitude of branches:

95 genotypes were classified in to erect to semi-erect (9), semi- erect (13), spreading (4), semi-erect to spreading (6) and erect (47) for panicle branch attitude. Variation for the said trait is polymorphic.

4.3.1.46 Panicle: Exertion:

88 genotypes were having well exerted panicle while 6 and only 1 (CR-3993-2-24-45-2) genotypes were having mostly exerted and partly exerted panicle respectively. This character is found to be polymorphic by nature.

4.3.1.47 Time of maturity (days)

The genotypes in the present study were categorized into three classes based on this character. The time of maturity of 40 genotypes were early with the duration ranging from 101- 120 days, 54 genotypes were of medium duration ranging from 121- 140 days to maturity and only one genotype (Kalanamak) was found to be late with 141-160 days to maturity. Hence this trait is polymorphic.

4.3.1.48 Leaf: Senescence:

95 genotypes were grouped in to early (77), medium (15) and late (3) on the basis of leaf senescence. Thus it showed polymorphic variation.

4.3.1.49 Sterile lemma: Colour

95 genotypes were grouped in to five classes for colour of this trait *viz.*, straw (16), gold (3), red (8), purple (6) and white (62) exhibiting polymorphic variation.

4.3.1.50 Weight of 1000 fully developed grains (g)

Based on this character, the genotypes in the present study were categorized into four classes. Very low 1000 grain weight (<15 g) was recorded by 5 genotypes, 26 genotypes recorded low 1000 grain weight ranging from 15-20 g, 46 genotypes recorded medium 1000 grain weight ranging from 21-25 g. Whereas, 18 genotypes recorded high 1000 grain weight ranging from 26-30 g and the remaining 46 genotypes recorded medium 1000 grain weight ranging from 21-25 g.

4.3.1.51 Grain length (mm)

This trait was observed to be polymorphic. Out of 95 genotypes, 1 genotype (Kothimbir Sal) had very short (<6.0 mm) sized grain length, 13 genotypes had short grains (6.1-8.5 mm), 70 genotypes exhibiting medium sized grains (8.6-10.5 mm), 10 showed long length for the trait and the remaining only one genotype had very long grain length (Sugandha)

4.3.1.52 Grain width (mm)

The genotypes in the present study were categorized into four classes with respect to width of the grain. 6 genotypes were narrow (2.1-2.5 mm), 57 genotypes had medium grain width (2.6-3.0 mm), 28 genotypes had broad grain width (3.1-3.5 mm) and remaining 4 genotypes were found to be very broad (>3.5 mm) for width of grain. Hence polymorphic variation is observed for the said trait.

4.3.1.53 Grain: Phenol reaction of lemma:

Out of 95 genotypes 72 were having positive response whereas 23 were showing negative response for phenol reaction of lemma.

4.3.1.54 Decorticated grain length (mm)

In the present study, decorticated grain length of 52 genotypes was categorized into five groups showing polymorphic variation. 15 genotypes were short (< 6.0 mm), 4 genotypes found to be medium (< 6.00 mm)), 63 genotypes were long (6.0-6.6 mm), 11 genotypes were long for Basmati type (> 6.61 mm) and only two genotype (P. Basamti and S. Basmati) exhibited Extra-long length (>7.5 mm).

4.3.1.55 Decorticated grain width (mm)

The expression of this character among the genotypes was polymorphic *viz.*, narrow (<2.0 mm) in 4 genotypes, broad (> 2.5 mm) in 32 genotypes and medium (2.0-2.5 mm) in the remaining 59 genotypes.

4.3.1.56 Decorticated grain shape (in lateral view)

In the present study, decorticated grain shape of the genotypes was categorized into seven groups for shape of decorticated grain *viz.*, 2 genotypes had short slender (KL < 6.0 mm; LB ratio > 3.0 mm) shape, 13 genotypes showed short bold (KL < 6.0 mm; LB ratio < 2.5 mm) shape, 4 had medium slender (KL < 6.0 mm; LB ratio = 2.5 -3.0 mm) shape, 31 exhibited long bold (KL > 6.0 mm; LB ratio < 3.0 mm) shape, 31 showed long slender (KL > 6.0 mm; LB ratio > 3.0 mm) shape, Long Slender (Basmati type) (KL > 6.61 mm; LB ratio > 3.0 mm) and only 2 genotype possessed (P. Basmati and S. basmati) extra-long slender (KL > 7.5 mm; LB ratio > 3.0 mm) shape. Variation for the said character is polymorphic.

4.3.1.57 Decorticated grain: Colour

95 genotypes were classified in to White (72), Light red (5) and Red (18) on the basis of decorticated grain colour, thus showing polymorphic variation.

4.3.1.58 Endosperm: Presence of amylose

All 95 genotypes were having amylose exhibiting monomorphic variation.

4.3.1.59 Endosperm: Content of amylose

95 genotypes were classified in to four groups for the content of amylose *viz.*, 19 were having Low amylose (10-19%), 48 having medium (20-25%), 26 exhibited high (26-30%) and only 2 genotypes (Ajaya and Milyang-63) having very high (>30%) amylose. Polymorphic variation was observed for this trait

4.3.1.60 Varieties with endosperm of amylose absent only polished grain: Expression of white core

All the 95 genotypes were negative for the said character showing monomorphic variation.

4.3.1.61 Gelatinization temperature through alkali spreading value

Based on the scale of this trait all 95 genotypes were classified into three groups *viz.*, only one genotype (KJT-3R) exhibited low gelatinization temperature (55-69 °C), 33 genotypes were having medium GT (70-74 °C) and 61 showing high-medium GT (74-79° C) variation for the said descriptor were polymorphic.

4.3.1.62 Decorticated grain: Aroma

Out of 95 genotypes only 19 genotypes were having aroma while 76 were negative for aroma, thus depicting dimorphic variation.

4.3.2. Identification of 95 rice genotypes using DUS Descriptors

In the present study, out of 62 DUS descriptors one descriptor *viz.*, culm attitude (for floating rice only) was not

applicable for the genotypes under study as none of the genotypes was floating rice, rest 61 descriptors were recorded in 95 rice germplasm. Out of 95 genotypes 9 were monomorphic, 15 were dimorphic and remaining 37 were polymorphic

4.3.3 Analysis of distinctiveness, uniformity and distinctiveness by DUSTNT and mJRA software

The data recorded on 95 genotypes based on DUS guidelines were analyzed by DUSTNT and mJRA software and results are presented as follows.

4.3.3.1 Analysis of Distinctiveness

The data were recorded on 14 measurable characteristics and subjected to COY-D analysis at 0.1% level of significance (Table 4.25). The analysis revealed that all the genotypes were showing distinctiveness with respect to each other. COY-D analysis using MJRA was also carried out for all the rice genotypes and the results are given in the Table 4.26. The MJRA model for measurable characters took account of systematic annual increase or decrease in character expression across all varieties by fitting extra terms, one for each year in the analysis of variance. Each term represented the linear regression of the observations for the year against the variety means overall years (Digby, 1979). The MJRA analysis revealed F_1 ratio which takes into account the variety mean square and variety x year mean square. It was found to be highly significant for all the measurable characters under the study except for leaf width, stem thickness, grain width and decorticated grain width at 1% probability. It indicated that all the 95 varieties under study were quite distinct from each other except for leaf width, stem thickness, grain width and decorticated grain width.

A perusal of MJRA analysis revealed that the F_2 ratio which takes into account the variety x year mean square and variety x replication mean square was found to be non-significant for all the measurable characteristics at 1% probability except days to 50% flowering character. It indicated that the environment has a greater influence on days to 50% flowering. The slope of mJRA curve for all the characters for both the years calculated by the DUSTNT software was more than zero (ranged from 0.949 to 1.276) and regression probability was also more than zero (i.e. 1.147) weight of fully developed 1000 grains to 68.34 for time maturity which indicates that the characteristics under the study were not completely independent from the environment. Euclidian proximity matrix generated using DUSTNT software is shown in Table 4.27.

4.3.1.7.2 Analysis of uniformity

Sixty two characteristics were studied during the *kharif* seasons of 2020 and 2021 at ARS, Shirgaon and RARS, Karjat respectively. According to DUS guidelines of PPV&FR Authority forty six characteristics were visually assessed. These characteristics did not exhibit any variation in their state of expression during the two years of study. Further no off type plants were observed. There were 14 measurable characteristics which were subjected to COY-U analysis for assessment of uniformity using DUSTNT software (Table 4.28.) A candidate variety will be considered to be sufficiently uniform, if using a COY-U analysis the standard deviation for each characteristic is not greater than the mean standard deviation for the same characteristics in comparable varieties at 1% probability level. COY-U test compared within plot standard deviation between treatments, so if there is no within plot variations this test cannot be performed (Dey *et. al.* 2013) and (Mondal *et. al.*, 2019)

In the present study, the standard deviation was found to be zero for the characters leaf width, stem thickness, grain length, grain width, decorticated grain length and decorticated grain width. So, for these characters there is no within plot variation between varieties and COY-U test could not be performed.

The variety Waksal-207 and Bhogawati for character grain length; Try-1 and Valai for days to maturity, Samba Mahsuri for stem length excluding panicle and Bhadasbhog for amylose content were found to be not uniform as the standard deviation exceeded over-years criterion with 1% probability. Jyoti , KJT-3R, KJT-4R were found to be non-uniform for the character stem length (excluding panicle) as the within-years standard deviation exceeded once the UPOV criterion. In general, most of the varieties showed uniformity except for non-uniformity of one or two characters in some of the varieties. In that case varieties should be grown for one or two years to bring sufficient level of uniformity.

4.3.1.7.3 Analysis of stability

46 visually assessed characteristics exhibited stable performance on both the years of experiment as there was no variation in the state of expression of the characteristics over the years. Fourteen measurable characters were subjected to statistical analysis for stability by comparison of respective values of PCV and GCV based on pooled morphological data. Genetic parameters for measurable characteristics are presented in Table 4.29. Phenotypic Coefficient of Variation (PCV) is the resultant of combined action of genotype and environment over a genotype. Genotypic Coefficient of Variation (GCV), a component of total variation reflects the heritable portion. In the present study, the GCV values for 14 measurable DUS characters ranged from 5.89

to 25.09 per cent whereas, PCV values ranged from 6.00 to 25.41 per cent. As the PCV estimates were slightly higher than the corresponding GCV for the characters studied, it indicates that the characters were less influenced by the environment. Thus it indicates that environmental factors are not affecting the expression of these characters.

Thus increasing the soil nutrients and or any change in environmental factors will not affect the any of the 14 characters studied. Thus all these 14 descriptors are genetically regulated characters and can be used as varietal differentiation and identification.

Therefore, phenotypic selection would be effective for the improvement of these traits.

High heritability and genetic advance was observed for all the characters indicating that the characters are governed by additive and/ or additive x additive gene action.



DISCUSSION



CHAPTER-V

DISCUSSIONS

Identification of DUS traits is vital for protection of rice varieties under PPV and FRA and also during the trade and seed production. There are two strategies commonly used for cultivar identification such as morphological descriptors and molecular or DNA markers. Traditionally, morphological descriptors are used for testing Distinctness, Uniformity and Stability (DUS), as they are less expensive and easy to measure without having sophisticated laboratory facilities. However, limited number, stage-specific and inconsistent expression due to the environmental influence, renders DUS descriptors unsuitable to exploit extensively for rapid identification of cultivars. Furthermore, they failed to distinguish large number of varieties or breeding lines with slight variation in agronomic traits- a common phenomenon in recently released varieties. These problems of the morphological descriptors can be solved efficiently by molecular markers as they are stable, abundant with high discriminating power, although expensive.

Taking consideration of above facts, in the present investigation, 95 diverse rice germplasm were assessed for qualitative and quantitative traits and data obtained were analyzed to find out variation among different cultivars for different characters. Mean performance of the genotypes for the various traits were under taken for estimation of genetic coefficient of variation, heritability, genetic advance, among character and genetic divergence through D^2 statistic. Along with this diversity analysis using SSR marker was also done, morphological characterization based on DUS guidelines was carried out and both results obtained were compared to draw valuable inference.

5.1 Analysis of variance:

The Analysis of variance for the quantitative characters revealed that mean sum of square of genotypes for all 27 characters studied, revealed that genotypes were significantly different for all the characters under study indicating the presence of greater variability among the genotypes.

5.1.1 Variability:

In any plant breeding programme variability and selection are indispensable. Success of plant breeding programme depends on extent of variability present in the material under study. More the variability better is the chance of selection.

In the present study wide range of variability was observed among the genotypes for all character under the study.

Phenotypic Coefficient of Variation (PCV) is the resultant of combined action of genotype and environment over a genotype. Genotypic Coefficient of Variation (GCV), a component of total variation reflects the heritable portion. In the present study, experiment carried out at ARS, Shirgaon, the GCV values ranged from 5.82 to 45.67 per cent whereas, PCV values ranged from 5.91 to 46.02 per cent, similarly for experiment carried out at RARS, Karjat during *Kharif*, 2021, the GCV values ranged from 5.95 to 45.64 per cent whereas, PCV values ranged from 6.08 to 46.06 per cent.

As the PCV estimates were slightly higher than the corresponding GCV for the characters studied at both locations, it indicates that the characters were less influenced by the environment. Therefore, phenotypic selection would be effective for the improvement of these traits.

The results were in accordance with finding of Vanisree *et al.* (2013) and Lingaiah *et al.* (2015), Similar findings were reported by Senapati and Kumar (2015) and Bhinda *et al.* (2017) for grain length, Babu *et al.* (2012), Pratap *et al.* (2012), Dhurai *et al.* (2014) and Aravind *et al.* (2019) for decorticated grain length and Subbaiah *et al.* (2011) and Dhurai *et al.* (2014) for length/breadth ratio.

5.1.2 Mean performance:

Study of per se performance of individual genotypes suggests the importance of material under study and it becomes first-hand information for the breeders. The mean of different quantitative characters including grain yield plant⁻¹, suggests that selection of desirable genotypes based on the traits evaluated can be effective.

5.1.3 Interpretation of results obtained for grain yield and important 9 metric traits

Important 9 yield associated metric characters along with grain yield were studied for 95 germplasm in the present investigation. The results obtained for this study are further summarized based on genotypes falling under desirable note for farmer and scientific community and presented in table 5.1 Interpretation of these results is discussed as below.

5.1.3.1 Number of spikelets panicle⁻¹/ (SPP)

Highest number of spikelets panicle⁻¹ were observed for 13 genotypes out of 95 studied *viz.*, Ajaya (300.48), followed by Bela (263.62), MO-6 (206.28), Mahsad (198.61), RTN-214-1-1-1-2 (187.77), IR-64 (185.96), RTN-69-1-1 (182.72), P Sugandha-3 (182.50), BL-184AR (179.30), KJT-3R (178.35), KJT 2 (178.06), Sahyadri 5 R (176.75) and CR-3993-2-24-45-2 (176.67). These 13 genotypes can be included in crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.2 Fertility (%)

Out of 95 germplasm lines studied, 34 were found to have highest fertility i.e. above 90% viz., Ambemohar (93.34), ARC 10550 (96.61), Barmil (91.52), BG 367-2 (90.39), Bhadas-79 (90.13), Bhogwati (90.30), BL-184AR (93.46), Dhanesal (92.59), DRR-86-8 (96.83), FL 478 (96.25), IR-63879-195-2-2-3-2 (94.59), IRRI 192 (98.07), IRRI 193 (95.49), IRRI 193 (95.08), K Shatabdi (91.02), KJT-3R (92.89), Mahsad (90.11), MILYANG 63 (90.73), MO-6 (93.76), MUDGO (93.72), Munga (94.48), P Basmati (93.80), P Sugandha-1 (96.37), P Sugandha-3 (94.14), Pandya (92.75), Patani-6 (92.59), PR-114 (93.40), Ratnagiri 7 (92.18), RP Bio 197 (92.25), RP-BIO-226(91.96), Sahyadri 5 R (97.30), Sugandha (91.09), Valai (93.91) and VDN-9-10-1 (90.44). Thus these 34 genotypes can be included in crop improvement programme since fertility % is positively associated with the yield. Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.3 Grain yield plant⁻¹ (g)/ (GYPP)

Out 95 genotypes, 22 exhibited the highest grain yield plant⁻¹ (g) viz., BG 367-2 (23.57), CR 2713-180 (22.57), CR-3993-2-24-45-2 (21.57), DRR-50-10 (23.33), DRR-50-12 (21.93), DRR-50-13 (22.87), Gurjari (23.07), IR-64 (24.37), Jyoti (22.50), KJT 2 (25.00), KJT-1R (29.00), KJT-2R (21.70), KJT-3R (21.50), MILYANG 63 (21.30), MTU1010 (23.90), NDR6315 (25.27), PR-118 (32.27), PTB 33 (20.43), S Basmati (22.53), S SIVAPPU (22.85), Sahyadri 5 R (24.28) and Sonsali (21.18). These 22 genotypes were found to be highest yielders, hence can be included in the crop improvement programme as donor parents. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.4 Number of panicles plant⁻¹ (Nos.) / (PPP)

Among 95 genotypes studied, 45 showed highest number of panicles plant⁻¹. *viz.*, TN-1 (20.73), S Basmati (15.80), DRR-215 (15.07), Bhadasbhog (14.33), Sugandha (13.87), Kalanamak (13.27), Dhanesal (12.80), PR-118 (12.60), Ambemohar (12.47), DRR-50-13 (12.33), CR2713-180 (11.87), RTN-35-1-1 (11.80), VDN-9-10-1 (11.60), Kothambir Sal (11.53), Bhogwati (11.53), MO-19 (11.50), KJT 1 (11.47), PR-114 (11.40), NAUR-1 (11.20), VDN-10-18 (11.20), P Samruddhi (11.07), IR-64 (11.00), IRRI 192 (11.00), RTN 11-2-1-3 (10.87), IR-63879-195-2-2-3-2 (10.87), P Sugandha-3 (10.87), BG 367-2 (10.87), MILYANG 46 (10.80), PTB 33 (10.80), IRRI 104 (10.80), Mayekar Bhat (10.76), KJT-1R (10.73), Sahyadri 5 R (10.73), IRRI 190 (10.73), DRR-86-8 (10.67), RS-1113 (10.67), MO-6 (10.65), Munga (10.63), Chinoor (10.60), K Shatabdi (10.60), KJT 2 (10.60), BL-184AR (10.53), P Basmati (10.53), MUT NS 1 (10.53) and R HEENATI (10.53), thus these 45 genotypes can be used donor parent in crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.3.5 Panicle length of main axis (cm) / (PLMA)

Among all 95 germplasm lines studied, only 12 genotypes showed longest panicle length of main axis *viz.*, NDR6315 (35.67), PR-118 (32.60), Kochari (32.47), DRR-215 (32.33), CR2713-180 (31.60), Ambemohar (31.13), KJT-1R (30.80), Try-1 (30.73), Bhadasbhog (30.73), MUT NS 1 (30.27), DRR-50-13 (30.13). Panicle length positively correlated with yield, thus these 12 genotypes must be used as donor parent for crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.3.6 Stem length excluding panicle (cm) / (SLEP)

Out 95 genotypes, 62 exhibited lowest stem length i.e. below 110 cm and hence these 62 genotypes were found to be of dwarf and semi-dwarf stature, which is a climate smart growth habit. Such genotypes are lodging resistant and fertilizer responsive. Thus these genotypes should be incorporated in crop ideotype and crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.7 Zinc content ppm / (Zn)

Out 95 genotypes, only 4 genotypes *viz.*, PTB 33 (22.62), IRRI 123 (21.40), DRR-50-12 (20.70) and Ambemohar (20.08) exhibited zinc content around national standard i. e. 24 ppm, hence these 4 genotypes are desirable to include in development of bio- fortified varieties. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.1.3.8 Iron content ppm / (Fe)

Out of 95, 76 genotypes exhibited highest Fe content i.e. above 10% which is around national standard of 10%. Hence these 76 genotypes should be included in crop improvement for development of bio-fortified varieties. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.9 Calcium content (ppm) / (Ca)

Out of 95 genotypes, the 10 genotypes showed highest calcium content *viz.*, Bhogwati (102.00), BG 367-2 (101.33), RTN-214-1-1-1-2 (92.57), Ambemohar (87.67), RTN-27-1-1-2 (84.23), MILYANG 46 (84.00), VDN-9-10-1 (83.57), RS-1113 (83.33), KJT 2 (82.00) and IR-64 (80.67). Thus these 10 genotypes will better serves as donor parent for development of bio-fortified varieties.

This finding was also confirmed by Sanyal and Joshi (2016). Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.3.10 Amylose content / (AC)

Out of 95 genotypes studied, 33 genotypes showed medium (20-25%) amylose content *viz.*, Chinoor, P Sugandha-4, Karhad, Bhadas-79, TN-1, KJT 1, P Basmati, Bhogwati, Ratnagiri 7, Kothambir Sal, KJT-1R, Patani-6, P Sugandha-5, Kala Rata, IRRI 192, DRR-215, Valai, S Basmati, CR-3993-2-24-45-2, PTB 33, RTN-69-1-1, P Sugandha-1, IRRI 190, R. HEENATI , RTN 11-2-1-3, DRR-50-12, MO-13, BL-184AR, Sahyadri 5 R, Gurjari, MO-6, S SIVAPPU, and PR-114 This medium range of amylose content is desirable as grains on cooking become soft yet separated and widely preferred by consumers. Hence these 33 genotypes will better serves as donor parent for crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.4 Genotypic and phenotypic variances:

It is well known that variability in the biological population is an outcome of genetic constitution of individuals present in that population and its interaction in the prevailing environment. In the present investigation, the phenotypic variance was higher than corresponding genotypic variances for all the characters studied at both the locations, but the difference between genotypic and phenotypic variance was quite low, indicating that variability assessed is mainly due to stable performance of the genotypes over environments.

5.1.5 Genotypic and phenotypic coefficient of variation:

Phenotypic coefficient of variation was found to be higher than their corresponding genotypic coefficient variation for all the traits under study at both the locations. The relative difference between phenotypic coefficient of variation and genotypic coefficient of variation was narrow for all the 27 characters evaluated, suggesting that these traits were less influenced by environmental effect. Hence selection for these traits may be effective based on their phenotypic values.

For ARS, Shirgaon location, High GCV and PCV values were observed for the traits viz., zinc content, plant height, stem length excluding panicle, number of spikelets panicle per panicle, grain width, decorticated grain breath, L/B ratio, amylose content, iron content, calcium content and grain yield plant-⁻¹ indicating that large amount of variation is present among the genotypes, whereas for RARS, Karjat location, High GCV and PCV values were observed for the traits viz., zinc content, plant height, stem length excluding panicle, number of spikelets per panicle, weight of 1000 grains, grain yield plant⁻¹, straw yield plant⁻¹, leaf length, L/B ratio, amylose content, iron content, calcium content and grain yield plant⁻¹ indicating that large amount of variation is present among the genotypes. Similar results were obtained by for panicle number per plant, Gangashetty *et al.* (2013) and Veni *et al.* (2013) for No. of spikelets panicle per panicle, and Gangashetty *et al.* (2013), Veni *et al.* (2013), Dhurai *et al.* (2014), Gyawali *et al.* (2018), Chuchert *et al.* (2018) and Arvind *et al.* (2019) and Bhargavi *et al.* (2022) for grain yield plant⁻¹.

5.1.6 Heritability and genetic advance:

Heritability measures the transmission of character from one generation to next generation. Heritability also separates the portion of environmental variability from phenotypic variability, so

utilizing in making effective selection. Thus, presence of higher magnitude of genetic variability along with the degree to which it is transmitted from one generation to another is equally important for effective selection. (Burton and Devane, 1953).

Johnson *et al.* (1955) suggested that heritability and the genetic advance when calculated together would prove more useful in predicting the resultant effect of selection based on phenotypic expression. He further emphasized that without genetic advance; the estimates of heritability will not be of practical value and suggested the concurrent use of genetic advance along with heritability. High heritability alone is not enough to make sufficient improvement through selection in genetic advance generations. High heritability was obtained all the characters except alkali spreading value for both the locations indicating that these characters were least influenced by environmental effect and selection may be effective. Similar results were found in the results of Sarangi *et al.* (2009), Arvind *et al.*, (2019) and Bhargavi *et al.* (2022).

5.1.7 Genetic advance as percent of mean:

Genetic advance is a measure of genetic gain under selection. The success of genetic advance under selection depends on heritability of the character under consideration. This indicates that though the character is less influenced by environmental effects, the selection for improvement of such trait may not be useful because, heritability is based on total genetic variance which includes fixable (additive) and non-fixable (dominance and epistatic) variance. For ARS, Shirgaon location, the genetic advance as per cent of mean was high for the characters *viz.*, plant height, stem length excluding panicle, number of spikelets per panicle and

calcium content. On the other hand, moderate genetic advance as per cent of mean was noted for days to 50% flowering, fertility %, days to maturity, straw yield per plant, leaf length and zinc content. Rest of the seventeen characters showed low genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean was observed for the traits viz., plant height, stem length excluding panicle length and calcium content, which suggests that these characters are subjected to any selection scheme for exploiting fixable genetic variance will be highly effective. Whereas for location RARS, Karjat. The genetic advance as per cent of mean was high for the characters viz., plant height, stem length excluding panicle, number of spikelets per panicle, leaf length and calcium content. On the other hand, moderate genetic advance as per cent of mean was noted for days to 50% flowering, fertility %, days to maturity, straw yield per plant and zinc content. Rest of the seventeen characters showed low genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean was reported for plant height, stem length excluding panicle, number of spikelets panicle⁻¹, leaf length and calcium implying that these characters were under control of additive gene action and direct selection of these traits would be effective for crop improvement. Similar reports were published by Shanthi and Singh (2001), Babu *et al.* (2012), Aditya and Bhartiya (2013) and Dhurai *et al.* (2015) for straw yield/ grain yield ratio. Dhurai *et al.* (2015) and Islam *et al.* (2015) for days to maturity, Islam *et al.* (2015) and Bindha *et al.* (2017) for grain length, Abebe *et al.* (2017), Singh and Verma (2018) and Ranjith *et al.* (2018) for 50% flowering, Singh and Verma (2018) for fertility (%) and Bhargavi *et al.* (2022).

5.1.8 Genetic diversity:

Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization program. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 95 rice genotypes and to identify the diverse genotypes for future utilization breeding program.

In the present investigation for the experiment conducted at ARS, Shiragon, the genotypes were grouped into 22 clusters on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance. Cluster I comprised of maximum number of genotypes (57) followed by cluster IV with 32 genotypes. Remaining clusters constitutes of each one genotype only. Whereas for the experiment carried out at RARS, Karjat, the genotypes were grouped into 20 clusters on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters constitute of each one genotype only. The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster. The genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters

For location I (Shirgaon) intra cluster D^2 values ranged from 0.00 (all clusters except cluster I and IV) to 723.08 (IV). Maximum intra cluster distance was observed in cluster IV (723.08) followed

by cluster I (587.10). The inter-cluster D^2 values ranged from 147.10 (cluster II and III) to 3111.77 (clusters XIX and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (3111.77), followed by cluster XVIII and XX (3076.24), cluster XX and XXI (3018.86), cluster XXI and XXII (2771.82), cluster X and cluster XXII (2405.44), cluster XIII and XX (2344.39). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.10. Cluster I comprises 57 genotypes. It was nearest to cluster VIII (766.88) indicating genotypes are closely related and was farthest from the cluster XXII (1624.67) implying these genotypes more diversely related conferring intermitting within these genotypes would be useful for crop improvement.

For location II (Karjat), intra cluster D^2 values ranged from 0.00 (all clusters except cluster I, V and X) to 607.76 (cluster X). Maximum intra cluster distance was observed in cluster X (723.05) followed by cluster V (481.62) and cluster I (437.13). The inter-cluster D^2 values ranged from 232.11 (cluster IX and XI) to 2259.27 (clusters XIV and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIV and XX (2259.27), followed by cluster VII and XX (1830.75), cluster XI and XIV (1730.06), cluster III and XX (1730.06), cluster XVIII and cluster XX (1665.85), cluster IV and XIX (1557.16). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.10. Cluster I comprises 58 genotypes. It was nearest to cluster IV (552.11) indicating genotypes are closely related and was farthest from the cluster XX (1407.01) implying these genotypes more diversely related conferring intermitting within these genotypes would be useful for crop improvement.

Similar divergence estimation based on D^2 distances was done by Shivani *et al.* (2018), Kumari *et al.* (2018), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022)

5.1.8.1 Cluster mean analysis:

Cluster means with respect to 27 characters and 95 genotypes was evaluated with help D^2 values for the both the locations. A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The promising landraces from these clusters with high mean values for different traits may be directly used for adaptation or may be used as parents in future hybridization, depending upon the objective of the breeding programme to derive superior transgressive segregants.

5.1.8.2 Per cent contribution of character towards total genetic diversity:

The selection and choice of parents mainly depend upon contribution of characters towards divergence (Dey *et al.*, 2009).

The utility of D^2 statistics as a potential tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence.

For ARS, Shirgaon location, out of the 27 characters studied, 13 characters namely leaf length, calcium content, number of panicles plant⁻¹, fertility %, zinc content, iron content, number of

spikelets panicle⁻¹, plant height, days to 50% flowering, grain width, amylose content, straw yield plant⁻¹ and grain yield plant⁻¹ together contributed maximum (92.69%) to the total genetic divergence. Whereas for RARS, Karjat location out of the 27 characters studied, 11 characters namely leaf length, calcium content, fertility, decorticated grain length, zinc content, iron content, number of spikelets panicle⁻¹, plant height, amylose content, days to 50% flowering and grain yield plant⁻¹ together contributed maximum (98.99%) to the total genetic divergence. Thus, it is suggested that these traits should be given importance in further breeding programmes i.e., during hybridization and selection of segregating populations, using this particular set of landraces, so far not utilized in breeding programmes, which have potential for use in future rice improvement programmes aiming at the development of rice varieties or hybrids with high yield and better grain quality. These findings were in accordance with the finding of Guru *et al.*, (2017), Shivani *et al.* (2018), Kumari *et al.* (2018), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.2 Genetic diversity

Molecular markers have played an increasing role in rice breeding and genetics. Of the different types of molecular markers, microsatellites have been utilized most extensively, because they can be readily amplified by PCR and the large amount of allelic variation at each locus. Microsatellites are also known as Simple Sequence Repeats (SSR), and they are typically composed of 1–6 nucleotide repeats. These markers are abundant, distributed throughout the genome and are highly polymorphic compared with other genetic markers, as well as being species-specific and co-dominant. For these reasons, they have become increasingly important genetic markers in rice breeding programs Gous Miah *et al.* (2013), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.2.1 Polymorphism percentage:

The overall size of amplified products ranged from 132 bp to 884 bp. A total of 139 alleles were obtained using 17 SSR primer pairs with an average of 8.17 alleles per primer. The all 17 SSR primers used in the study were highly polymorphic and distributed throughout the genome of rice. The number of alleles amplified for each primer pair ranged from 3 to 14. The numbers of alleles detected in the present study are also consistent with the earlier reports of (Abdullah *et al.*, 2021) which revealed up to 82 alleles for 7 microsatellite markers across 28 varieties. Earlier (Paul *et al.*, 2022) observed an allelic range of 1-8 with an average of 3.7 alleles per primers.

5.2.2 Polymorphic Information Content (PIC):

The lowest PIC value was 0.70 with RM 7 and highest PIC value was 0.92 with RM 8225 and average PIC value recorded was 0.83. The higher the PIC value, the more informative is the SSR marker. Hence, primers RM 825, RM 1287, pTA-248, RM 201, RM 122 and RM 22709 were found to be highly informative. The current PIC value is higher than the previous reports of (Miah *et al.*, 2021). The high PIC value obtained in the present investigation might be due to high genetic diversity among the rice varieties. The PIC values are usually dependent on the genetic diversity of the accessions chosen (Tang *et al.*, 2022) for the specific study. Markers with PIC values of 0.5 or higher are highly informative for genetic studies and are extremely useful in distinguishing the polymorphism rate of a marker at a specific locus (Jain *et al.*, 2021) and (Hoque *et al.*, 2021). The Polymorphism information content (PIC) values shown by some of the SSRs in the present investigation were found to be higher than the previously reported (Singha *et al.* 2021).

5.2.3 Genetic distance:

The diversity observed in the Ninety five rice genotypes mainly attributed to the genetic dissimilarities. The pair wise similarity values ranged from 0.027 to 0.994. However, genetic diversity detected using molecular markers in the present investigation indicates the high discrimination capacity of SSR markers. This is of major importance for solving the problems concerning the breeding to obtain the heterosis. Similar findings were reported by (Seetharam *et al.* 2019), (Embate *et al.* 2021) and (Rohmawati *et al.* 2021)

5.2.4 Cluster analysis and Dendrogram construction:

The UPGMA based dendrogram of 95 rice genotypes generated with Multivariate Statistical Package (MVSP) revealed that, there are two major clusters. The first major cluster consists of four sub clusters. Two rice genotypes CR-3993-2-24-45-2 and HRTMS-61 formed the independent first sub cluster (IAa). Second sub cluster (IAb) consists of ten genotypes. Third sub cluster (IBa) consists of seven genotypes. Fourth sub cluster (IBb) consists of four genotypes.

The second major cluster consists of four sub clusters. First sub cluster (IIAa) consist of five rice genotypes. Second sub cluster (IIAb) consist of three rice genotypes. Third sub cluster (IIBa) consist of fourteen rice genotypes. Third sub cluster (IIBb) consist of fifty rice genotypes.

This shows the potentiality of SSR markers for the characterization of germplasm accessions.

From these studies, it is revealed that, rice varieties are more divergent indicating that large part of the genome may be

dissimilar among themselves. However, genetic diversity detected using molecular markers in the present investigation indicates the high discrimination capacity of SSR markers. This is of major importance for solving the problems concerning the breeding to obtain the heterosis. (Chuang *et al.*, 2011) and (Liu *et al.*, 2022) reported similar findings.

Because of the poly-allelic nature of SSR markers, they have the advantage of discriminating the individuals more precisely. The SSR marker gave more clusters with fewer genotypes in each cluster and therefore, more variation within each cluster. Similar pattern of population variance was also reported by (Jasim *et al.*, 2019), (Yogi *et al.*, 2020) and (Naaz *et al.*, 2022).

5.2.5. Resistance against biotic and abiotic stresses:

Out of 95 genotypes Try-1, Kochari, Lal Patani, Karhad, Ratnagiri 7, Phule Samruddhi, Ambemohar, Rathu Heenati, Sinna Sivappu, IRRI 190, IRRI 193, ARC10550, Samba Mahsuri, IRRI 123 shown the gene linked with blast resistance is present when amplified with RM 8225 marker.(Gentallan *et al.*, 2021) and (Chakrobarty *et al.*, 2022) also used microsatellite markers to screen the various genotypes for blast resistance.

Salt resistance gene was present in MO-17, MO-19, KJT-2R, RTN 11-2-1-3, Pak Basmati, Super Basmati, Chinoor, Pusa Sugandha-1, Pusa Sugandha-3, Pusa Sugandha-4, Bhogwati, RP Bio 197, RP-BIO-226, Ajaya, Karjat 1. Molecular mapping of genes linked to salt tolerance traits was also carried out by (Krishnendu *et al.*, 2021) and (Li *et al.*, 2022). The gene linked with BPH resistance be present in Pusa Sugandha-4, Pusa Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, Phule Samruddhi, Kala Rata, Try-1, Kochari, BG 367-2, FL 478, MUT NS

1, RATHu Heenati and Sinna Sivappu. Similar results also found by (Li-Hang *et al.*, 2020) and (McClung *et al.*, 2022) where they used different microsatellite markers to screen the rice populations for BPH resistance.

BG 367-2, Milyang 63, FL 478, MUT NS 1, IRRI 192 having gene resistance to drought similarly (Gregorio *et al.*, 2020) and (Mateu-Andres *et al.*, 2022) also used different microsatellite markers to screen the rice populations for drought tolerance.

5.3 Interpretation of results obtained for 62 DUS descriptors

62 DUS descriptors were studied for 95 germplasm in the present investigation. The results obtained for this study are further summarized based on genotypes falling under desirable note for farmer and scientific community and presented in table 5.1. Interpretation of these results is discussed as below.

5.3.1 Coleoptile: Colour (CC)

Coleoptiles are cylindrical organs that en-sheath the first leaf and shoot apex in grass seedlings. Coleoptile functions like a 'snorkel'; the elongated. They help in the emergence of the first leaf (and shoot apex) by protecting it during its passage through the soil. On emergence, the first leaf breaks through the coleoptile tip. (Kordan, 1974). Desirable note for this trait is that variation in colour observed. Among 95 genotypes studied, green (1), purple (9) and remaining 85 were found be white. As polymorphic variation was observed, this trait can be considered as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.3.2 Basal leaf: Sheath colour (BL-SC)

It is an elongated, cylindrical structure that encloses younger parts of the shoot. Its major function is to protect younger shoots

inside of it and to support the whole plant, which explains why there are very few chloroplasts found in the sheath mesophyll. (N Guo *et al.*, 2020). Desirable note for this trait is that polymorphic variation observed in colour i.e. out of 95 germplasm lines studied 82 were found be green followed by light purple(9), purple lines (1), uniform purple (3). Hence this descriptor can serves as morphological marker to distinguish diverse germplasm. Similar results were reported by Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022)

5.3.3 Leaf: Intensity of green colour (L-IGC)

The leaves grow alternately on the stem, with one leaf per node. The leaves are the growth engine of the plant, as they capture solar radiation and produce carbohydrates. The plant breathes and perspires through its leaves. Scale of green coloration serves as the index of nitrogen status of the crop (Giha *et al.*, 2021).Intensity of green colouration is directly correlated with nitrogen uptake and photosynthetic efficiency of plant. Out 95 genotypes, 30 exhibited the dark intensity for green colour of leaf, these 30 genotypes Pandya, KJT-3R, KJT-4R, PR-118, NAUR-1, Gurjari, DRR-363-5, VDN-9-10-1, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, S Basmati, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-5,CR2713-180, Indrayani, Sugandha, RS-1113, RP Bio 197, KJT 1, MUDGO, MILYANG 46,P TB 33, BG 367-2, MILYANG 63, MUT NS 1, Sonsali and TN-1 which photo-synthetically more efficient and thus can be included in crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.4 Leaf: Anthocyanin colouration (L-AC)

Anthocyanin's, a major subclass of flavonoids, are the main secondary metabolites that give color to rice tissues.

Anthocyanin accumulation in plants has diverse functions; including resisting UV radiation, participating in hormone regulation, and responding to biotic and abiotic stress, and are beneficial to human health. (Xia *et al.*, 2021). Presence of anthocyanin colouration is desirable as it acts as morphological mechanism (non-preference by insect-pests) of defense against insect-pests attack. Among 95 genotypes studied, only 3 showed positive note for this descriptor *viz.*, Mahsad, Waksal-207 and Barmil and thus, these genotypes can be best served as potential donor parent for insect-pest resistance breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.4.5 Leaf: Distribution of anthocyanin colouration (L-DAC)

Anthocyanin accumulates in many plant tissues or organs, in rice for example leading to red, purple red and purple phenotypes for protection from damage by biotic and abiotic stresses and for reproduction. Uniformly distributed Purple pigmentation leaves are common in wild rice and landraces and occasionally found in modern cultivars. (Han-shiuan *et al.*, 2020). Among all 95 germplasm lines studied, only 1 genotype (Waksal-207) showed presence for this trait and hence can be used in abiotic stress resistance breeding programme in future. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.4.6 Leaf Sheath: anthocyanin colouration (LS-AC)

Leaf sheath is an elongated, cylindrical structure that encloses younger parts of the shoot. Its major function is to protect younger shoots inside of it and to support the whole plant. (Davis, 2020). Accumulation of anthocyanin pigmentation on basal leaf

sheath in rice highlights the phenotypic defense mechanism against biotic stresses. (E Mackon *et al.*, 2021). Out 95 genotype only 14 exhibited presence of this trait. Hence these 14 genotypes Mahsad, Waksal-207, Barmil, Patani-6, Pandya, Dular, Try-1, Kochari, Bela, Valai, Gurjari, Dhanesal, RP-BIO-226 and IRRI 190 are desirable to include in crop improvement for biotic resistance breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.7 Leaf sheath: Intensity of anthocyanin colouration (LS-IAC)

Darker intensity of anthocyanin pigmentation on leaf sheath indicates more the phenotype is repellent against pests attack (Yamuangmorn *et al.*, 2021). Out 95 genotypes, only 2 genotypes (Dhanesal and IRRI 190) exhibited strong intensity of anthocyanin colouration and other 2 (Try-1 and Bela) showed very strong intensity, hence these 4 genotypes desirable to include in crop improvement for pests resistance breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.4.8 Leaf: Pubescence of Blade Surface (L-PBS)

Pubescence is characterized by tri-chomes gathering on the plant surface, consisting of unicellular or multicellular exogenous substances on leaves, stems, and root surfaces. Pubescence may be related to the development of glandular cells and thus are called glandular hairs. Glandular hairs can accumulate and secrete alkaloids such as nicotine and terpenoids as well as some chemical substances against injurious insect. The hairy surface serves as morphological barrier against sucking pests. (Zeng *et al.*, 2019.) Many plants have pubescence designed to provide a tiny bit of shade to reduce the temperature of the leaves and stems and

protect the leaves from losing too much water from transpiration (Hamaoka *et al.*, 2017). Stronger the pubescence, more the phenotype is non- preferred by sucking pests. As well as stronger pubescence prevent water loss from leaves during transpiration. Out of 95, 27 genotypes exhibited strong pubescence *viz.*, Barmil, Jyoti, Dodak, Karhad, KJT-1R, KJT-3R, PR-114, DRR-215, IR-63879-195-2-2-3-2, RTN-27-1-1-2, Sahyadri 5 R, S Basmati, Chinoor, P Sugandha-4, Bhadasbhog, Sugandha, RS-1113, RP-BIO-226, Ajaya, KJT 1, IR-64, MILYANG 46, PTB 33, MILYANG630, FL 478, S MAHSURI, IRRI 104 and other 6 i.e P Sugandha-1, P Sugandha-3, Kalanamak, KJT 2, SINNA SIVAPPU, IRRI 190 showed very strong note. Hence these 33 genotypes should be included in crop improvement for biotic and abiotic stress breeding as a donor parents. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.9 Leaf: Auricles (L-A)

Auricles are pair of hairy, sickle-shaped appendages located in the junction of the collar and the sheath. The auricles are located at the lower end of the leaf-blade, where it meets the leaf-sheath. They may be extended as a pair of claw-like projections. It keeps the leaf sheath and culm together (Lee *et. al*, 2022). Presence of auricle is desirable which serves as binding agent for leaf sheath and culm. All the 95 genotypes studied showed presence of auricles hence all these genotypes can be used in crop ideotype breeding programme. This finding was also confirmed by Sanyal and Joshi (2016). Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.4.10 Leaf: Anthocyanin colouration of auricles (L-ACA)

Anthocyanins are a group of poly-phenolic pigments that are ubiquitously found in the leaf of rice. In rice, anthocyanin's played a role not only in reproduction, by attracting pollinators and seed dispersers, but also in protection against various abiotic and biotic stresses. (Ying *et al.*, 2018). Dark colouration such as purple is of desirable note as it works as shield against various biotic stresses. Out of 95 genotypes studied, 7 genotypes *viz.*, Barmil, Patani-6, Pandya, Valai, Gurjari, PTB 33 and IRRI 190 showed purple anthocyanin colouration on the leaves, thus these 7 germplasm can be included development of insect-pests resistant lines as a donor parent. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.11 Leaf: Collar (L-C)

It is a white band at the junction of the blade and sheath. All the 95 genotypes were found to be positive for this trait and can be incorporated in crop ideotype breeding programme. This result was in agreement with the findings of Kumar *et al.* (2018), Gour *et al.* (2019), Bharagvi *et al.* (2022) and Lavanya *et al.* (2021).

5.4.12 Leaf: Anthocyanin colouration of collar (L-ACC)

Presence of this trait is of desirable note as it works as shield against various biotic stresses. Out of 95 genotypes studied, only 5 lines *viz.*, Barmil, Patani-6, Pandya, Gurjari, IRRI 190 showed presence of anthocyanin colouration on the leaf collar, thus these 5 germplasm lines can be included development of insect-pests resistant lines as a donor parent. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.13 Leaf: Ligule (L-L)

It is a triangular, papery scale located inside the blade, it looks like a continuation of the sheath. It protects the culm and leaves that it encloses from the entry of water, dust and harmful spores (Davis *et al.*, 2020). Presence of this trait is of desirable note as it works as filter to avoid the entry of water, dust and harmful spores in culm. All the 95 genotypes were found to be positive for this trait and can be incorporated in crop ideotype breeding programme. Similar findings were reported by Sanyal and Joshi (2016), Kumar *et al.* (2018), Gour *et al.* (2019), Lavanya *et al.* (2021) and Bhargavi *et al.* (2022).

5.1.14 Leaf: Shape of ligule (L-SL)

Different shapes serves as morphological markers. Though all the 95 genotypes found to have split shape of ligule, shape of ligule can be used to distinguish diverse germplasm and serves as morphological marker. Similar results were reported by Kumar *et al.* (2018), Gour *et al.* (2019), Lavanya *et al.* (2021) and Bhargavi *et al.* (2022)

5.1.15 Leaf: Colour of ligule (L-CL)

Dark colouration such as purple is of desirable note as it works as shield against various biotic stresses. Out of 95 only one genotype (Dhanesal) showed light purple coloration of ligule, thus this genotype can be used as donor parent in biotic stress tolerance breeding programme. These results were in accordance with Komala *et al.* (2017), Kumar *et al.* (2018), Gour *et al.* (2019), Lavanya *et al.* (2021), Bhargavi *et al.* (2022), and Kushwah *et al.* (2022).

5.1.16 Leaf: Length of blade (L-LB)

It is measured from the tip of the entire leaf down to the base of the lowest leaflets where they meet the leaf stem for the leaf

length. The photosynthetic energy storage and normal life function of rice are directly affected by the leaf. Meanwhile, leaf size is an important part of ideal rice plant type, as well as an important character of rice yield formation (McDonald *et al.*, 2020). Longer leaf length directly correlated with higher photosynthetic efficiency. Out of 95 only 55 genotypes showed long leaf length thus these genotypes can be used as donor parents in crop ideotype breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.17 Leaf: Width of blade (L-WB)

Leaf width corresponds to the longest extension of any two points on the blade edge perpendicular to the leaf length axis, that is the axes connecting leaf apex and base (Shi *et al.*, 2019a). Prior research has found that leaf width not only affects the morphogenesis of leaves, but serves as a primary role in the regulation of grain and panicle traits and more efficient photosynthesis (Fu, 2019). Longer leaf width directly correlated with higher photosynthetic efficiency. Out of 95 only 69 genotypes showed medium leaf width thus these genotype can be used as donor parent in crop ideotype breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.18 Culm: Attitude (for floating rice only) C-A (FR)

This descriptor is not applicable, as none of the genotypes are floating rice under study.

5.1.19 Culm: attitude (C-A)

The jointed stem of rice, called a culm, is made up of a series of nodes and internodes. The node (nodal region) bears a leaf and a

bud. The main role of culm is to support rice plant and helps to transport minerals and water absorbed by roots to upper parts. (Davis *et al.*, 2020). Culm attitude is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for culm attitude. Out of 95, 84 genotypes showed erect culm attitude while 11 had semi-erect culm attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.20 Time of heading (50% of plants with panicles) (TH)

Days to 50% flowering was determined by recording the number of days following transplanting (DAT) until 50% of plants in a plot had at least one open flower. Time for heading to 50% flowering indicates the duration of the genotype for maturity and adaptability for different ecosystems. (Anputhas *et al.*, 2021). Out of 95 genotypes 42 were early indicated their adaptability for upland ecosystem, while 52 showed mid-late duration which are adaptable for midland and rest 1 found be of late duration which is adaptable for lowland. Similar results were reported by Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Arvind *et al.* (2019), Bharagvi *et al.* (2022), Lavanya *et al.* (2021) and Kushwah *et al.* (2022).

5.1.21 Flag leaf: Attitude of blade (early observation) FL-AB (EO)

The flag leaf is the top leaf on a rice stem, closest to the grain-producing panicle. Flag leaves have a major role in providing energy to the developing grain, and any impact on photosynthesis

in the flag leaf can have a dramatic effect on grain productivity.(Davis *et. al.*, 2020). It is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for flag leaf attitude. Out of 95, 79 genotypes showed erect attitude while 14 had semi-erect attitude and rest 1 showed horizontal attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.1.22 Spikelet: Density of pubescence of lemma (S-DBL)

Spikelets are the basic inflorescence units in rice and typically consist of a flower of interlocked lemma and palea forming a husk, two lodicules, six stamens, and one pistil. In rice, the spikelet meristem develops a pair of rudimentary glumes and then produces two lateral floral meristems and one terminal floral meristem. The two lateral floral meristems form one pair of sterile lemmas (degraded lateral florets), and the terminal floral meristem develops one fertile terminal floret (Fu *et. al.*, 2019). Pubescence plays an important role in insect resistance, drought tolerance, and other stresses. Out of 95 genotypes studied 37 *viz.*, MO-19, Mayekar Bhat, Waksal-207, Patani-6, Kochari, Lal Patani, Dodak, Karhad, Valai, PR-114, BL-184AR, Gurjari, DRR-86-8, IR-63879-195-2-2-3-2, RTN-35-1-1, Chinoor, P Sugandha-4, Kalanamak, P Samruddhi, Indrayani, Dhanesal, RS-1113, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali and TN-1 had shown very strong pubescent lemma. Thus these genotypes can be included in biotic stress resistance breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.23 Male sterility (MS)

Male sterility is defined as the failure of plants to produce functional anthers, pollen, or male gametes. The use of male sterility reduces the cost of hybrid seed production for several reasons. It avoids hand emasculation and pollination, accelerating the hybrid breeding programs and allowing the large-scale production of hybrid seeds and the commercial exploitation of hybrid vigour (Laura *et al.*, 2020). For commercial cultivation, absence of male sterility is desirable. All 95 genotypes showed absence of male sterility. Thus all are desirable for commercial cultivation and can be included in crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.24 Lemma: Anthocyanin colouration of keel (L-ACK)

The lemma has a constricted structure at its end called the keel. Presence of this trait is of desirable note as it works as shield against various biotic stresses. Out of 95 genotypes studied, 3 showed very strong anthocyanin colouration on the keel, thus these 3 germplasm (NDR6315, Dhanesal and Ambemohar) can be included development of insect-pests resistant lines as a donor parent. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.25 Lemma: Anthocyanin colouration of area below apex (L-ACABA)

The anthocyanin biosynthesis attracts strong interest due to the potential antioxidant value and as an important morphological marker (Khan *et al.*, 2020). Out of 95 genotypes studied, 4

(Bhadasbhog, NDR6315, Dhanesal and Ambemohar) showed very strong anthocyanin colouration area below apex. Thus these 4 germplasm can be included development of insect-pests resistant lines as a donor parent. As well as this trait can be used morphological marker to distinguish the germplasm. Sanyal and Joshi (2016), Kumar *et al.* (2018), Manjunatha *et al.* (2018), Gour *et al.* (2019) Bharagvi *et al.* (2022), Lavanya *et al.* (2021) and Kushwah *et al.* (2022) have also reported the similar results pertaining to this trait.

5.1.26 Lemma: Anthocyanin colouration of apex (L-ACA)

The anthocyanin biosynthesis attracts strong interest due to the potential antioxidant value and as an important morphological marker (Khan *et al.*, 2020). Out of 95 genotypes studied, 4 (Kala Rata, Bhadasbhog, NDR6315, Dhanesal and Ambemohar) showed very strong anthocyanin colouration area below apex. Thus these 4 germplasm can be included development of insect-pests resistant lines as a donor parent. As well as this trait can be used morphological marker to distinguish the germplasm. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.27 Spikelet: Colour of stigma (S-CS)

In rice, the pistil is the female reproductive organ, and it consists of two stigmas and an ovary. The stigma is capable of receiving pollen grains and guiding pollen tube growth. Furthermore, the stigma color is often regarded as an important trait in variety identification in some crop plants such as rice (Han *et al.*, 2018). Out of 95, 84 genotypes showed white stigma, while rest 11 had purple stigma. Thus this trait can be used as morphological marker to distinguish the germplasm. Lavanya *et al.*

(2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.28 Stem: Thickness (ST)

The stem of rice popularly known as the haulm or the culm, is generally erect, cylindrical, hollow at the internodes and solid at the nodes. The number and length of internodes vary with the different varieties. The stem's main function is to transport water and nutrients and to bring air to the roots. (Davis *et. al.*, 2020).

Thicker stems are preferred as such stems gives support to plants while lodging. All 95 genotype showed thick stem habit. Thus all genotype can be used as donor parent in crop ideotype breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.29 Stem: Length (excluding panicle; excluding floating rice) (S- L (FR))

The lower internodes are shorter than the upper ones. The shorter the lower internodes, the more resistant the plant will be to lodging. Each node has one leaf and one bud that can develop into a tiller. Shorter stem length *viz.*, dwarf and semi- dwarf stature of plant is preferred as these are climate smart structure and they have lodging resistance and are responsive to fertilizers. Stem length in the range of 70-110 cm is considered to be of dwarf to semi-dwarf stature. Out of 95, 46 genotypes were very short and 20 showed short plant type thus these genotypes can be used as donor parent in crop ideotype breeding programme. These results were in accordance with Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Aravind *et al.* (2019), Lavanya *et al.* (2021), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.1.30 Stem: Anthocyanin colouration of nodes (S-CAN)

Accumulation of anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses (Mackon *et al.*, 2021). Out of 95, only 4 (Lal Patani, Gurjari, DRR-86-8, HRTMS-61) genotypes showed presence of anthocyanin colouration of nodes. Thus these genotypes can be included in biotic stress resistance breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.31 Stem: Intensity of anthocyanin coloration of nodes (S-IACN)

Stronger the presence anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (Mackon *et al.*, 2021). Out of 95, only one (Gurjari) genotype showed medium scale intensity of anthocyanin colouration of nodes. Thus this genotype can be included in biotic stress resistance breeding as donor parent. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.32 Stem: Anthocyanin colouration of internodes (S-ACI)

Accumulation of anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (Mackon *et al.*, 2021). Out of 95, only 2 genotypes (Mahsad and Bela) showed presence of anthocyanin colouration of inter nodes. Thus these genotypes can be included in biotic stress resistance breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.33 Panicle: Length of main axis (P-LMA)

Panicles form the rice inflorescence. It is the top part of the rice plant, carried on the last inter-node. Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets. Schematic representation of a rice panicle comprising a main central axis named rachis, to which primary branches are attached; the primary branches bear secondary branches, which in turn bear tertiary branches. Spikelets are attached to the branches by a peduncle. (Antonio *et al.*, 2021). Longer panicles indicated more number of grains and thus length of main axis is directly correlated to the yield. Out of 95, 10 genotypes *viz.*, Try-1, Kochari, KJT-1R, PR-118, DRR-215, DRR-50-13, CR2713-180, NDR6315, Ambemohar and MUT NS-1 showed very long panicles and other 63 *viz.*, MO-6, MO-13, Kala Rata, Barmil, Jyoti, Patani-6, Bhadas-79, Pandya, Lal Patani, Dodak, Bela, Valai, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN 11-2-1-3, RTN-69-1-1, NAUR-1, BL-184AR, DRR-50-12, DRR-363-5, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, Sahyadri-5R, CR-3993-2-24-45-2, P Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, Kalanamak, P Samruddhi, Indrayani, Dhanesal, KShatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, Sonsali had long panicle. Thus these genotypes can be directly released for commercial cultivation or can be used in crop improvement as donor parent. Similar results pertaining to this trait were reported by Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018) and Aravind *et*

al. (2019). Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.34 Flag leaf: Attitude of blade (late observation) FL-AB (LO)

The flag leaf is the top leaf on a rice stem, closest to the grain-producing panicle. Flag leaves have a major role in providing energy to the developing grain, and any impact on photosynthesis in the flag leaf can have a dramatic effect on grain productivity (Davis *et al.*, 2020). It is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for flag leaf attitude. Out of 95, 67 genotypes showed erect attitude, while 20 had semi-erect attitude and 7 had horizontal attitude rest 1 showed deflexed attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding programme as well as this trait can be used morphological marker as polymorphic variation is present. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.35 Panicle: Curvature of main axis (P-CMA)

Over the past 30 years, super rice played an important role in boosting rice yield. The phenotype of erect panicle (EP) architecture controlled by dense and erect panicle 1 (*dep1*) is the typical characteristic of super rice, and the phenotype has been used in rice breeding for nearly a century (Sibo *et al.*, 2022). Bending-type lodging is caused by increase in panicle weight during maturation and occurs over the entire internode of rice during strong wind. Out of 95, 28 genotypes showed straight curvature of panicles, thus these 28 straight type genotypes are suitable to include in crop improvement programme and crop ideotype breeding. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.36 Panicle: Number per plant (P-NP)

Panicles form the rice inflorescence. It is the top part of the rice plant, carried on the last inter-node. Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets. Panicle number is directly correlated with yield. Out of 95, 39 genotypes viz., MO-6, MO-19, Mayekar Bhat, Munga, PR-114, RTN 11-2-1-3, PR-118, DRR-215, NAUR-1, BL-184AR, DRR-50-13, DRR-86-8, IR-63879-195-2-2-3-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, S Basmati, Kothambir Sal, P Sugandha-3, Bhadasbhog, CR2713-180, Kalanamak, P Samruddhi, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, KJT 1, IR-64, MILYANG 46, PTB 33, BG 367-2, MUT NS 1, RATHU HEENATI, IRRI 190, IRRI 104 and IRRI 192 had medium number of panicles and only 1 (TN-1) showed many number of panicles. Thus these genotypes are suitable to include in crop improvement programme. These results were in accordance with the findings of Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Arvind *et al.* (2019), Bhargavi *et al.* (2022), and Kushwaha *et al.* (2022).

5.1.37 Spikelet: Colour of tip of lemma (S-CTL)

More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color viz., Yellowish (2), Brown (3), Purple (5) and Black (6). Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.38 Lemma and Palea: Colour (LP-C)

Lemma is specialized bracts or bracteates. In rice the palea is in bended form and facing towards the lemma. Palea is one of the chaffy scales on the receptacle of many composite plants. The upper bracts that with the lemma encloses the flower in rice. The other scales, the lemma and the palea, occur in pairs. Generally the lemma is larger than the palea, which is hidden between the lemma and the spikelet axis. The lemma and palea surround and protect the flower, and all three of these structures form the floret. (Lombardo *et al.*, 2022) More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.39 Panicle: Awns (P-A)

The fili-form extension of the keel of the lemma is known as awn having bristles or hair like structure. They contribute to grain dispersal and burial and fend off animal predators. But not preferred for modern cultivars as it is inconvenient for mechanical threshing. Out of 95, 61 genotypes were awnless. Thus these genotypes should be included in crop improvement programme. This result was in accordance with the findings of Sanyal and Joshi (2016), Kumar *et al.* (2018), Manjunatha *et al.* (2018), Gour *et al.* (2019), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.1.40 Panicle: Colour of awns (late observation) P-CA (LO)

More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.*

(2022) reported similar findings.

5.1.41 Panicle: Length of longest awn (P-LLA)

Not preferable character for presence of all its notes except absent. Out of 95, these 61 awnless genotypes are desirable and can be included in breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.42 Panicle: Distribution of awns (P-DA)

Not preferable character for presence of all its notes except absent. Out of 95, these 61 awnless genotypes are desirable and can be included in breeding programme. Sanyal and Joshi (2016), Kumar *et al.* (2018), Manjunatha *et al.* (2018), Gour *et al.* (2019), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022) have also reported the similar results.

5.1.43 Panicle: Presence of secondary branching (P-PSB)

Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets. The acquisition of greater secondary branching potential plays an important role in increasing grain yield in cultivated rice (Huang *et al.*, 2021). It is directly correlated with yield. Out of 95, 79 genotypes showed presence of secondary branching. Thus these genotypes are desirable and can be included in breeding programme. Similar results were reported by Sanyal and Joshi (2016), Manjunatha *et al.* (2018), Bhargavi *et al.* (2022 and Kushwaha *et al.* (2022).

5.1.44 Panicle: Secondary branching (P-SB)

Stronger note is desirable for this trait. Out of 95, 21 genotypes *viz.*, Mahsad, Waksal-207, PR-114, DRR-215, BL-184AR, Gurjari, DRR-363-5, DRR-50-13, DRR-50-10, IR-63879-

195-2-2-3-2, P Basmati, Chinoor, P Sugandha-1, Indrayani, RS-1113, RP Bio 197, Ajaya, PTB 33, RATHU HEENATI, SINNA SIVAPPU and IRRI 192 showed presence of strong secondary branching. Thus these genotypes are desirable and can be included in crop ideotype breeding programme. This finding was also reported by Manjunatha *et al.* (2018), Ghosh *et al.* (2019), Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.1.45 Panicle: Attitude of branches (P-AB)

Erect attitude is desirable as it indicates bending resistance. Out of 95, 47 genotypes *viz.*, Pandya, Dular, PR-114, RTN 11-2-1-3, PR-118, DRR-215, DRR-50-12, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-214-1-1-1-2, VDN-10-18, RTN-35-1-1, P Basmati, S Basmati, P Sugandha-4, P Sugandha-5, Kalanamak, P Samruddhi, Indrayani, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192 and Sonsali showed presence of erect attitude of branching. Thus these genotypes are desirable and can be included in crop ideotype development programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.46 Panicle: Exertion (P-E)

Panicle exertion, the distance between the leaf cushion of flag and the neck-panicle node, is an important morphological trait, which has significant impact on hybrid seed production of rice (Yang *et al.*, 2020). Well exerted panicles are meant to be exposed for full sunlight and hence all the grains are fully developed in such genotypes. Out of 95, 88 genotypes showed presence of well

exerted panicles. Thus these genotypes are desirable and can be included in ideotype breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.47 Time maturity (days) (TM)

Time of maturity is the biological cycle of rice (days from seedling to harvest). All notes are preferable for this trait. As early genotypes are suitable for upland ecosystem, mid-late cultures are adaptable for midland ecosystem whereas late lines are good for lowland ecosystem. (Sandhu *et al.*, 2019) and (Anputhas *et al.*, 2021). Out of 95 genotypes 40 were early, indicating their adaptability for upland ecosystem, while 54 showed mid-late duration which are adaptable for midland and one genotype was found be of late duration which is adaptable for lowland. These results were in accordance with Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Arvind *et al.* (2019), Bhargavi *et al.* (2022).

5.1.48 Leaf: Senescence (L-S)

Leaf senescence, which is the last developmental phase of plant growth, is controlled by multiple genetic and environmental factors. Leaf yellowing is a visual indicator of senescence due to the loss of the green pigment chlorophyll. Leaf senescence constitutes the final stage of leaf development and is critical for plants' fitness as nutrient relocation from leaves to reproducing seeds is achieved through this process. (Schipper *et al.*, 2022). Late senescence of leaf is desirable as underdeveloped grain in panicle will get nutritional support even after maturity to get complete development. Late leaf senescence showed by 3 genotypes viz., VDN-10-18, CR-3993-2-24-45-2 and Ambemohar out of 95. Thus these genotypes can be utilized in crop improvement

programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.49 Sterile lemma: Colour (SL-C)

Sterile lemmas are produced between the fertile floret and the rudimentary glumes (Lombardo *et al.*, 2022). More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.50 Grain: Weight of 1000 fully developed grains (TKW)

The 1,000 kernel (1,000 K) weight is a measure of seed size. Thousand kernel weight (TKW) is an important parameter for the evaluation of variety breeding. TKW is not only directly related to the grain yield and milling quality of grain, but also has an impact on the seedling vigor and growth indirectly affecting the yield (Wu *et al.*; 2021). Test weight below 14 g indicates superfine grains, whereas more the test weight, grains will be coarse and bold. Out of 95 genotypes 5 showed very low and 26 had low test weight below 15 g. Thus these grains are super fine and can be used for table purpose, while rest showed high and very high test weight. Thus these genotypes will be considered for flour making, roti making and beaten rice manufacturing. Komala *et al.* (2017), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022) recorded the similar results.

5.1.51 Grain: Length (G-L)

Grain length and width determine rice grain shape. Therefore affect yield and appearance, thus representing two of the most

agronomically important traits in rice breeding (Li and Li, 2021). Extra-long grain and short slender, medium slender size Basmati is preferred for table purpose. While long and medium bold grains are desirable for roti making and other industrial purposes. All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Similar results were reported by Mondal *et al.* (2014), Komala *et al.* (2017), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.1.52 Grain: Width (G-W)

Its significance is same in line with previous descriptor i.e. Grain length *viz.*, Grain length and width determine rice grain size. Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021). All variations for this trait are desirable as per its utility and can be included in crop improvement programme. These results were in agreement with the findings of Komala *et al.* (2017).

5.1.53 Grain: Phenol reaction of lemma (G-PRL)

Phenol colour reaction on grains and glumes is used for characterization of rice varieties for distinctiveness, uniformity and stability (DUS) testing in plant variety protection. According to DUS test guidelines, rice varieties are classified into two groups based on presence and absence of phenol colour reaction on the grains (Sahil *et al.*, 2021) Variation for this trait is used to distinguish germplasm. This trait exhibited di-morphic variation for this trait. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.54 Decorticated grain: Length (DG-L)

Decorticated grain length is length of grain, after de-hulling and before milling. Decorticated grain length was measured in mm and a digital caliper was used for clear visualization. Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021). Extra-long grains and short slender, medium slender size Basmati is preferred for table purpose. While long and medium bold grain s are desirable for roti making and other industrial purposes. All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Mondal *et al.* (2014), Komala *et al.* (2017) and Umarani *et al.* (2017a), Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) have recorded the similar results.

51.55 Decorticated grain: Width (DG-W)

Decorticated grain width (After de-hulling, before milling).Decorticated grain width was measured in mm and a digital caliper was used for clear visualization. Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021). All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Similar results were reported by Mondal *et al.* (2014), Komala *et al.* (2017), Umarani *et al.* (2017a) and Kushwaha *et al.* (2022)

5.1.56 Decorticated grain: Shape (in lateral view) (DG-S)

Common variety gives rise to short bold and long bold rice. Fine variety gives rise to medium slender rice. Super fine variety gives rise to long slender and short slender rice. Short bold and long bold genotypes are utilized for flour roti making. Medium

slender varieties are used for various Chinese, Italian dishes. Short slender and extra-long slender germplasm can be used for table purpose (Hori *et al.*, 2022). Long grain rice tends to cook up light, fluffy and separate when cooked rather than clumping together.-table purpose. Biryanis etc. Medium grain rice tends to cook up moist and tender and used for Chinese, Spanish and Italian cuisine etc., while short grain rice tends to clump together when cooked and forms what is called glutinous rice used for flour (*atta*) roti making. All variations for this trait are desirable as per its utility and can be included in crop improvement programme. The results obtained were similar with Mondal *et al.* (2014), Komala *et al.* (2017), Umarani *et al.* (2017a) and Bhargavi *et al.* (2022).

5.1.57 Decorticated grain: Colour (DG-C)

It's true that most rice (*Oryza sativa* L.) is white, but some varieties offer phytochemicals (mainly polyphenols and anthocyanin's) in the outer bran layer, which not only imbues them with hues of a different color but also boosts their nutrient content (Webb, 2021). Research shows that black rice has the highest antioxidant activity of all the varieties, making it a nutritious choice, followed by brown and then red rice (Kubala, 2019). All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.58 Endosperm: Presence of amylose (E-PA)

Amylose is a polysaccharide made of α -D-glucose units, bonded to each other through α (1→4) glycosidase bonds. It is one of the two components of starch. Starch is the abundant component in rice endosperm, and its microstructure determines the quality and functional properties of rice grain (X fan *et al.*,

2019). Presence of amylose is desirable in medium scale for commercial table purpose use. All 95 genotypes showed presence of amylose. Thus all these genotypes can be included in crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings

5.1.59 Endosperm: Content of amylose (E-CA)

After cooking, the high-amylose and intermediate-amylose rice's are firm and fluffy; while the low-amylose and waxy rice's are soft, moist, and sticky in texture (Chen, 2020). Medium range of amylose content is preferable. Low amylose varieties can be used for Chinese cuisine. Medium amylose varieties are directly used table purpose. While high amylose varieties are used for beaten rice, puffed rice. (*poha and murmura*). Out of 95 genotypes, 48 exhibited medium scale of amylose, which is highly and widely preferred by consumers for table purpose. Thus these genotypes are good donors for crop improvement. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.60 Varieties with endosperm of amylose absent only polished grain: Expression of white core (E-CAWC)

Grain chalkiness reduces the quality of rice (*Oryza sativa*) and is a highly undesirable trait for breeding and marketing (Wu *et al.*, 2022). Absence of chalkiness is desirable for this trait. This trait exhibited monomorphic variation for this trait i.e. expression is absent or very small for all 95 genotypes. Thus all the genotypes are desirable to use in crop improvement programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.61 Gelatinization temperature through alkali spreading value (GT-ASV)

Alkali spreading value (ASV) of whole kernel milled rice is the measure of volume expansion in contact with dilute alkali and also a measure of gelatinization temperature. Again gelatinization temperature is partly associated with the amylose content of the starch (Akuli *et al.*, 2019). It determines the cooking time and energy required for the rice. High-medium note is desirable as requires less cooking time and low energy. ASV is inversely proportional to the GT. Out of 95, 61 genotypes had high-medium ASV. Thus these genotypes can be included in crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.62 Decorticated grain: Aroma (DG-A)

Aroma in scented and basmati rice is due to 2-acetyl-1-pyrroline (Bharati *et al.*, 2020). Makes rice varieties of special value and have wide consumer preference. Presence of aroma is desirable. Out of 95, 19 germplasm *viz.*, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati and Sugandha found to be aromatic and thus can be used in crop improvement programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.3.2 Analysis of variance of 14 measurable characters

Analysis of variance for 14 measurable characteristics for 2020 and 2021 seasons (pooled data) have been presented in Appendix 2. Highly significant differences were observed among the

varieties for all the characters in both the years. The standard error mean for all the characteristics under study were less in both the years which indicated less role of environment for the expression of the characteristics.

5.3.3 Analysis of Distinctiveness

The variations recorded for the morphological traits (both qualitative and quantitative) in the 95 rice germplasm can be used for distinguishing these varieties. To establish distinctiveness among rice genotypes qualitative characters have been used. Qualitative traits are considered as morphological markers in the identification of genotypes of rice because they are less influenced by environment. Thus, characterization of germplasm accessions establishes distinctiveness among rice genotypes.

DUS characterization was carried out for finding out the morphological variation present in the accessions. Results of the present investigation for 62 DUS characters except culm attitude (for floating rice (not applicable character) revealed that,

5.3.3.1 No variation (i.e. 0% variation) was found among the germplasm accessions for the characters: Leaf: Auricles, Leaf: Collar, Leaf: Anthocyanin colouration of collar, Leaf: Ligule, Leaf: Shape of ligule, Male sterility, Stem: Thickness, Endosperm: Presence of amylose and Varieties with endosperm of amylose absent only Polished grain: Expression of white core. These characters were monomorphic due to negligible effect of environment over both the years and locations. Thus these 9 characters served as morphological markers.

5.3.3.2 Moderate variations were found among genotypes for characters *viz.*, Leaf: Anthocyanin colouration, Leaf: Distribution of anthocyanin colouration, Leaf Sheath: anthocyanin colouration, Leaf: Colour of ligule, Leaf: Length of blade, Leaf: Width of blade, Culm: attitude, Spikelet: Colour of stigma, Stem: Anthocyanin colouration of nodes, Stem: Intensity of anthocyanin coloration of nodes, Stem: Anthocyanin colouration of internodes Panicle: Awns, Panicle : Presence of secondary branching, Grain: Phenol reaction of lemma and Decorticated grain: Aroma.

5.3.3.3 Characters exhibiting high variation among experimental material *viz.*, Coleoptile: Colour, Basal leaf: Sheath colour, Leaf: Intensity of green colour, Leaf sheath: Intensity of anthocyanin colouration, Leaf: Pubescence of Blade Surface, Leaf: Anthocyanin colouration of auricles, Time of heading (50% of plants with panicles), Flag leaf: Attitude of blade (early observation), Spikelet: Density of pubescence of lemma, Lemma: Anthocyanin colouration of keel, Lemma: Anthocyanin colouration of area below apex, Lemma: Anthocyanin colouration of apex, Stem: Length (excluding panicle, excluding floating rice), Panicle: Length of main axis, Flag leaf: Attitude of blade (late observation), Panicle: Curvature of main axis, Panicle: Number per plant, Spikelet: Colour of tip of lemma, Lemma and Palea: Colour, Panicle: Colour of awns (late observation), Panicle: Length of longest awn, Panicle: Distribution of awns, Panicle: Secondary branching, Panicle: Attitude of branches, Panicle: Exertion, Time

maturity(days), Leaf: Senescence, Sterile lemma: Colour, Grain: Weight of 1000 fully developed grains, Grain: Length, Grain: Width, Decorticated grain: Length, Decorticated grain: Width, Decorticated grain: Shape (in lateral view), Decorticated grain: Colour, Endosperm: Content of amylose and Gelatinization temperature through alkali spreading value. Thus, 9 characters were monomorphic, 15 were dimorphic and 37 were polymorphic showing wide range of variations. Results in similar pattern were reported by Sajid *et al.* (2015), Pauchauri *et al.* (2017) and Rawte and Saxena (2018).

5.3.3.4 COY-D analysis with respect to 14 measurable traits indicated that all the varieties were distinct from each other during both the years. Similarly other workers also reported distinctiveness among varieties of different crops using MJRA model, in sorghum (Joshi *et al.*, 2009), basmati rice (Patra and Chawla, 2010), aromatic rice (Joshi *et al.*, 2011) French bean (Mall and Chawla, 2012) and rye grass (Ruiz *et al.*, 2011).

5.3.4 Analysis of Uniformity

All the visually assessed characteristics did not show any variation in their states of expression over the years of study and hence considered to be uniform. 14 measurable characteristics were subjected to COY-U analysis for the assessment of uniformity. All the varieties were more or less uniform for measurable characters. 86 genotypes namely MO-6, MO-8, MO-13, MO-17, MO-19, Kala Rata, Mayekar Bhat, Munga, Mahsad, Barmil, Patani-6, Bhadas-79, Pandya, Dular, Kochari, Lal Patani,

Dodak, Karhad, Ratnagiri 7, Bela, KJT-2R, PR-114, RTN11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P. Sugandha-4, Bhadasbhog, CR2713-180, Kalanamak, NDR631, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, I R-64, MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, R HEENATI, S SIVAPPU, IRRI 190, IRRI 193, ARC 10550, IRRI 123, IRRI 104, IRRI 192, Sonsali and T N-1 showed uniformity for all the 14 measurable characters. Remaining 9 genotypes *viz.*, Waksal-207, Jyoti, Try-1, Valai, KJT-3R, KJT-4R, P Sugandha-5, Bhogwati and Sambha Mahsuri showed uniformity for thirteen out of fourteen measurable characters. Such non uniformity by COYU analysis has been reported earlier also in basmati and aromatic rice varieties (Patra and Chawla, 2010) and (Joshi *et al.*, 2011), sorghum varieties (Joshi *et al.*, 2009) and French bean varieties (Mall and Chawla, 2012).

5.3.5 Analysis of stability

All the varieties studied for forty six visually assessed DUS descriptors exhibited the same state of expression over the two years and thus considered stable.

14 measurable characteristics were subjected to statistical analysis for stability by comparison of respective values of PCV and GCV based on pooled morphological data. All the 14 measurable characteristics showed slightly higher magnitude of PCV over GCV.

This indicates that environment influence was less for the expression of these characters and hence 14 measurable characters were stable over the two years and two different environments. (Patra *et al.*, 2010 and Subbaiah *et al.*, 2011) reported similar findings.



SUMMARY & CONCLUSIONS

CHAPTER-VI

SUMMARY AND CONCLUSIONS

The present investigation entitled as '**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**' was undertaken with the objectives of characterization of 95 diverse rice germplasm by 62 DUS morphological descriptors, supplemented with molecular profiling by using simple sequence repeat markers and their subsequent examination for distinctiveness, uniformity and stability. The nature and extent of variability, heritability, genetic advance and diversity present among the germplasm based on yield and yield contributing parameters was studied to identify potential parents/donors for the hybridization programme. RBD trials were conducted in two subsequent and independent *Kharif* seasons of 2020 and 2021 at experimental farms of Agricultural Research Station, Shirgaon and Regional Agricultural Research Station, Karjat respectively. Data was recorded for 27 metric characters inclusive of 14 measurable DUS traits and 62 DUS descriptors of rice as per PPV & FR guidelines. Whereas molecular profiling of 95 rice genotypes using 17 SSR primers was carried out at Plant Biotechnology Center, College of Agriculture, Dapoli. The results from the investigation are summarized and concluded as below:

- Analysis of variance for both seasons and locations revealed the presence of significant differences among the 95 germplasm of rice under study for all the twenty seven metric traits, indicating the presence of considerable genetic variation in the experimental material.

- A perusal of genetic parameters *viz.*, phenotypic and genotypic coefficients of variation revealed less influence of environment on the characters under study for both two seasons and locations. Therefore, response to direct selection may be effective in improving these traits. Among all the characters under study, for location 1 (Shirgaon) zinc content exhibited highest PCV and GCV values followed by calcium content, iron content, number of spikelets per panicle, stem length excluding panicle, plant height, amylose content and decorticated length breadth ratio, whereas lowest PCV and GCV values were reported for days to maturity. While for location II (Karjat) zinc content exhibited highest PCV and GCV values followed by calcium content, iron content, number of spikelets per panicle, straw yield per plant, grain yield per plant, stem length excluding panicle, plant height, amylose content and decorticated length breadth ratio, whereas lowest PCV and GCV values were reported for days to maturity.
- All the characters under study for both the locations exhibited high heritability except alkali spreading value which showed lowest heritability. For ARS, Shirgaon location, high heritability coupled with high genetic advance as per cent of mean was observed for the traits *viz.*, plant height, stem length excluding panicle length and calcium content, which suggests that these characters are subjected to any selection scheme for exploiting fixable genetic variance will be highly effective. Whereas for location RARS, Karjat, high heritability coupled with high genetic advance as per cent of mean was reported for plant height, stem length excluding panicle, number of spikelets panicle⁻¹, leaf length and calcium implying that these characters were under control of additive gene action and direct

selection of these traits would be effective for crop improvement.

- Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. For location I (Shirgaon) all 95 rice germplasm under study were distributed into twenty two clusters based on D^2 values using Tocher's method such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. Out of twenty two clusters, cluster I was the largest comprising of fifty seven genotypes, followed by cluster IV with 32 genotypes. Remaining 20 clusters were mono-genotypic clusters suggesting the existence of high degree of heterogeneity among the genotypes. Whereas for location II (Karjat) the genotypes were grouped into 20 clusters. Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters were mono-genotypic.
- Grouping of most of the genotypes into one cluster (cluster I) for both the locations indicates genetic relatedness between these genotypes. This can be further explained by free flow of genes between these accessions. The clustering pattern showed that the landraces originating from similar geographical regions were categorized into different clusters, indicating that geographical diversity and genetic diversity were not related. Therefore, the kind of genetic diversity found among the genotypes belonging to same geographical region might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions.

- For location I (Shirgaon) maximum intra cluster distance was observed in cluster IV, followed by cluster I, while for location II (Karjat) maximum intra cluster distance was observed in cluster X, followed by cluster V and cluster I indicating that some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean values for the desirable characters. Maximum inter cluster distance for location I (Shirgaon) was exhibited between XIX and XX, followed by cluster XVIII and XX, cluster XX and XXI, cluster XXI and XXII, cluster X and cluster XXII, cluster XIII and XX whereas for location II (Karjat) maximum inter cluster distance was exhibited between cluster XIV and XX, followed by cluster VII and XX, cluster XI and XIV, cluster III and XX, cluster XVIII and cluster XX, cluster IV and XIX. The greater the distance between two clusters, the wider the genetic diversity among the genotypes of those clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. The promising genotypes from these clusters with high mean values as discussed in 4.1.6.5 and 4.1.6.6 for different traits may be directly used for adaptation or may be used as parents in future hybridization, depending upon the objective of the breeding programme to derive superior transgressive segregants.
- For location I (Shirgaon) 13 characters namely leaf length, calcium content, number of panicles plant⁻¹, fertility, zinc content, iron content, number of spikelet's panicle⁻¹, plant height, days to 50% flowering grain width, amylose content, straw yield plant⁻¹ and grain yield plant⁻¹ together contributed

maximum (92.69%) to the total genetic divergence. Whereas for RARS, Karjat location out of the 27 characters studied, 11 characters namely leaf length, calcium content, fertility, decorticated grain length, zinc content, iron content, number of spikelets panicle⁻¹, plant height, amylose content, days to 50% flowering and grain yield plant⁻¹ together contributed maximum (98.99%) to the total genetic divergence. Thus, it is suggested that these traits should be given importance in further breeding programmes i.e., during hybridization and selection of segregating populations, in this particular set of germplasm to develop high yielding rice varieties/hybrids with superior grain quality.

- Seventeen SSR primers were used in this study and all amplified and showed the polymorphism in rice genotypes. A total of 139 loci were generated by 17 primers. Each primer thus produced on an average 8.17 loci in the size ranging from 132 bp to 884 bp in the 95 rice genotypes in relation to diversity assessment.
- Among 17 SSR markers, all the primers showed 100 per cent polymorphism.
- The PIC values of primers ranged from 0.70 in SSR primer RM 7 to 0.92 in SSR primer RM 8225 with an average PIC value of 0.83.
- The Jaccard's pair wise similarity values ranged from 0.027 to 0.994.
- Dendrogram was constructed using Jaccard's similarity coefficient and rice genotypes were grouped into two clusters based on SSR markers.

- SSR primers showed 100% polymorphism which represents the capability of these primers to amplify the less conserved region of the DNA. It also depicted that rice genotypes used in the present screening were divergent which a very important factor in breeding programmes.
- The screening of rice genotype through microsatellites is very important for identifying parental genotypes that will be exploited for MAS breeding of elite lines that are more stable to stresses and this will lead to increase yield in order to feed the growing population.
- Among the total sixty two DUS descriptors, 9 were monomorphic, 15 were dimorphic and 37 were polymorphic in nature
- Among the forty six visually assessed DUS descriptors, 6 were monomorphic, 12 were dimorphic and 26 were polymorphic in nature.
- Out of fourteen measurable characteristics, 3 were monomorphic, 3 were dimorphic and 11 were polymorphic in nature.
- Results of analysis of variance revealed highly significant differences among all the genotypes for all the characteristics in both the years.
- COY-D analysis with respect to 14 measurable traits indicated that all the genotypes were distinct from each other during both the years.
- All the visually assessed characteristics did not show any variation in their states of expression over the years of study and hence considered to be uniform. 14 measurable

characteristics were subjected to COY-U analysis for the assessment of uniformity. All the varieties were more or less uniform for measurable characters. 86 showed uniformity for all the 14 measurable characters whereas remaining 9 genotypes showed uniformity for thirteen out of fourteen measurable characters. All the varieties studied for forty six visually assessed DUS descriptors exhibited the same state of expression over the two years and thus considered stable.

- It may be concluded from the present investigation that the morphological DUS descriptors can be effectively used for identification and grouping of the varieties. Application of biochemical and molecular markers may help in establishing distinctiveness to support morphological marker. The varieties studied for DUS descriptors can be registered with PPV & FR Authority for obtaining breeder's and farmers' rights.

CONCLUSION:

Following conclusions are based on grouping of genotypes falling under early, mid-late and late maturity duration along with dwarf/semi-dwarf stature and high grain yield (above 15 g), high fertility (>90%), number of panicles per plant (> 10), medium to high panicle length (>26 cm), number of spikelets per panicle (>175), medium amylose content (21-25%) and high Ferrous (>10 ppm), Zinc (>20ppm) and Calcium (>80ppm) content. Almost all genotypes recommended here are either at par desirable values given above or nearer to that. Thus following genotypes are observed to be elite among early, mid-late and late group having good combination yield associated traits and with high nutritional value. Thus it is recommended to utilize these lines for further crop improvement and is also useful for farmer's direct cultivation and having consumer's preference too.

- Twelve genotypes found to be of early maturity duration (101-120 days) suitable for upland ecosystem and best utilized for research purpose along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., Jyoti, Ratnagiri-7, KJT-2R, KJT-4R, CR-2713-180, SINNA SIVAPPU, PR-114, MILYANG 63, IRRI 190, PTB 33, P Sugandha-1 and P Sugandha-3.
- Fourteen genotypes falls under Mid-late maturity duration(121-140 days) suitable for mid-land ecosystem along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., KJT-1R, KJT-3R, PR-118, NAUR-1, Gurjari, RTN-35-1-1, CR-3993-2-24-45-2, S Basmati, NDR-6315, KJT 2, IR-64, Bhogwati, ARC 10550 and TN-1.
- One genotype falls under Late maturity duration(141-160 days) suitable for low-land ecosystem along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., Kalanamak.
- One genotype falls under mid-late maturity duration(121-140 days) suitable for mid-land ecosystem and khar-land along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., Khara rata.

❖ **Future line of work**

- ❖ Passport data bulletin of all the 95 genotypes can be released for public domain which will assist rice scientist community to choose better parent as per breeding objectives.
- ❖ QR code (quick response code) should be generated for each genotype inclusive of DUS and molecular fingerprints developed under this study. This will facilitate rapid and easy dissemination of passport data of these genotypes.



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* Original not seen.



APPENDICES



CHAPTER-I

INTRODUCTION

“Rice is life” was the famous theme of International Year of Rice, 2004 denoting its overwhelming importance as an item of food, commerce and the close connection between rice-based systems and many cultures and people worldwide, in particular the poor in developing nations. Devoting an International Year to a single crop is unprecedented in the world history. Today rice is grown and harvested on every continent except Antarctica. Rice remains a staple food for more than half of the world population and forms the cheapest source of food, energy and protein. More than two thirds of the world relies on the nutritional benefit of rice (Pandey and Anurag, 2010).

Rice (*Oryza sativa* L.) ($2n = 24$) is the most important cereal crop which serves as a staple food for over 60 per cent of the world's population (Singh and Singh, 2008). Approximately 90 per cent of rice grown on the planet is produced and consumed in Asia (Singh *et al.*, 2015). India is the world's second largest rice producer and consumer next to China, about 90 per cent of all rice grown in the world is produced and consumed in Asian region. In the world, rice is cultivated on about 167.13 million hectares of area with total production of 782.01 million tonnes and productivity is 3.228 tonnes/ha. Rice has unique position in Indian economy. India ranks second in rice production followed by China. In India, rice occupies an area of 43.79 million hectares with annual production of 116.42 million tonnes and productivity is 2.65 tonnes/ha. (Anonymous, 2021).

In Maharashtra, the total area occupied by this crop was about 1.465 million hectares with annual production of 3.276 lakh tonnes and average productivity of the state was about 2.24 t/ha, (Anonymous, 2021). In Konkan region, rice occupies an area of about 0.387 million hectares with an annual production of around 1.031 million tonnes and average productivity of the konkan was about 2.66 t/ha. The area under rice in konkan region is 26.41 % of the total area in Maharashtra (0.387 million hectares). (Anonymous, 2021).

It is grown in *kharif* and *rabi* season. The per hectare productivity of rice is 2.59 tonnes and 2.73 tonnes in *kharif* and *rabi* season respectively. The major rice growing districts in Maharashtra are Thane, Raigad, Ratnagiri and Sindhudurg along with the West coast and Bhandara, Gadchiroli and Chandrapur in the Eastern parts of the states and minor areas are Tuljapur, Parbhani, Western Ghat of Pune, Nashik, Sangli, Satara, Kolhapur and parts of Nanded. Maximum productivity is observed in Konkan region and it contributes 31.48 per cent of total rice production in the state. Vidarbha region covers large area under rice cultivation than other regions but it has low productivity than Konkan and Western Maharashtra regions.

India, being the part of center of origin, rice is bestowed with wide range of germplasm which encompasses landraces, obsolete cultivars, wild or weedy species, improved varieties and so forth, which led to the tremendous genetic diversity. The genus *Oryza* has 24 species, comprising of 22 wild species and two cultivated species *i.e.*, *Oryza sativa* (Asian rice) and *Oryza glaberrima* (African rice). *Oryza sativa* has been further classified into five sub-species *viz.*, *japonica* (low amylose content, sticky, short grained and adapted to temperate regions), *indica* (high amylose content, non-

sticky, long-grained and adapted to the tropics), the intermediate *javanica* is designated as *tropical japonica*, *aus* (deep water rice) and *aromatic* (Basmati, Jasmine, Joha etc.) (Garris *et al.*, 2005).

Rice is grown under diverse eco-geographical conditions in various tropical and subtropical countries. Rice yield growth has fallen from 2.3% per year during 1970–1990 to 1.5% during 1990's and to <1.0% during the first decade of present century. Global rice demand is estimated to rise from 676 million tons in 2010 to 763 million tons by 2020 and further increase to 852 million tonnes by 2035. This clearly indicates that an overall increase of 26% or 176 million tons of rice is required in the next 25 years. However, area planted with rice in major production countries has been decreasing because of industrialization and urbanization. Hence, increasing rice yields on existing land remains the primary strategy for increasing production, to meet the future demand for food, anticipated from the projected world population increase. To produce 176 million tons additional rice by 2035, the yield potential of rice needs to be increased from 10 to 12.3 tonnes per hectare (FAOSTAT, 2021).

Green revolution has considerably improved the production of food grains in India and its role in achieving the status of self-sufficiency in food grains is beyond any doubt. But high yielding varieties, which are the back bone of green revolution, reached their yield plateau. So, there is an urgent need to broaden the genetic base of the varieties by introgression of genes from diverse sources. Thus, there is a need to collect, exploit and evaluate the untapped germplasm.

Rice has the largest germplasm collections in the world. This accessible collection of diverse cultivated varieties, landraces and

related wild species has made great contributions to rice breeding. Landraces harbour a great deal of useful traits with genetic potential for rice improvement and they played a very important role in the local food security and sustainable development of agriculture, in addition to their significance as genetic resource for rice genetic improvement (Tang *et al.*., 2021).

Evaluation and characterization of existing landraces of rice is important due to increasing needs of varietal improvement. Characterization is the technique used to evaluate the phenotypic diversity through agro-morphological traits. It has been successfully used in recent years to help in identifying elite individual genotypes. It is an indispensable tool for selecting varieties or lines based on agronomical, morphological, genetic or physiological characters. Characterization of accessions is used to evaluate the phenotypic diversity through agro-morphological traits that are essential for the gene bank management to protect the unique rice (Bajracharya *et al.*, 2020).

The landraces maintained by farmers are endowed with tremendous genetic variability, as they are not subjected to subtle selection over a long period of time. This aids in the adaptation of landraces to wide agro-ecological conditions. This rich variability of complex quantitative traits with respect to maturity, growing adaptation and their physicochemical and organoleptic properties still remains unexploited. Land-races are also important genetic resources for resistance to pests and diseases; they provide “adaptability genes” for specific environmental conditions. Incorporation of adaptability genes from landraces could ensure optimum grain yield for the region (Vijayakumar *et al.*, 2020).

The success of plant breeding depends on the extent of genetic variability present in a crop. Knowledge on the nature and

magnitude of genetic variation governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement. A critical analysis of genetic variability present in the germplasm of a crop and its estimation is a prerequisite for initiating any crop improvement programme as well as adopting appropriate selection techniques.

It is very difficult to judge whether observed variability is heritable or not. Heritability indicates the extent of transmissibility of a character into future generations.

Moreover, knowledge of heritability is also essential for selection of component traits for yield improvement. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimates along with genetic advance is normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

Genetic diversity is a ubiquitous feature of all species in nature. Genetic diversity is an inherited variation among and between populations, created, activated and maintained by evolution. It is a fundamental characteristic without which breeders are very limited and powerless in plant breeding. Genetic divergence among the genotypes plays an important role in the selection of parents having wider variability for different characters and ultimately for a rational use of genetic resources. Genetic diversity can be evaluated with morphological traits, biochemical markers and DNA markers. Morphological and agronomic traits have long been the means of studying variability among population and species. The breeders are interested to evaluate genetic diversity based on morphological traits because they are

inexpensive, rapid and simple to score. The study of these traits needs neither sophisticated method nor complicated equipment. Agro-morphological properties of rice cultivars determine their yield potential, local agronomic suitability and ability to escape from or tolerate biotic and abiotic stresses.

The varieties released from India have shown profound impact in the global rice production. After the initiation of All India Coordinated Rice Improvement Programme (AICRIP), the development and release of rice varieties have been increased tremendously; as of now more than 1200 varieties have been released for various agro-ecosystems in India. Development of new varieties is an expensive task which involves more skill, infrastructure and genetic resources and above all it is a time-consuming process which takes around ten years to release a variety through pedigree breeding, the most commonly used method of variety development. After development of a new variety by painstaking research by the breeders, it is necessary to register newly bred varieties. The protection of ownership of new varieties is of paramount importance to prevent their unauthorized utilization. There are different ways to protect a variety and provide exclusive rights to the breeder. Among them Plant Variety Protection (PVP) through International Union for the Protection of New Varieties of Plants (UPOV) provides Intellectual Property Rights (IPR) to Plant Breeders' Rights (PBR). According to UPOV's PVP system, new variety must satisfy three criteria to be eligible for protection. The first criterion is that the new variety must be Distinct (D) from any other Common Knowledge Varieties (CKVs) in at least one morphological trait. The second criterion is that the variety should be sufficiently Uniform (U) in relevant characteristics depending on reproduction system of the species and finally the distinctive traits

should show Stable (S) expression after two independently growing cycles. Thus, the DUS test provides foundation for plant variety protection and to identify a new variety from already released varieties (also called as reference collection). In India, the plant variety protection is resolved through an authorized *sui generis* enactment of Protection of Plant Varieties and Farmers' Rights Act, 2001 (PPV & FRA), though it is through UPOV (International Union for the Protection of New Varieties of Plants) at international level.

The DUS testing involves comparison of a number of phenotypic characters called descriptors by growing the varieties side by side. Under PPV and FR Act, DUS testing is performed with morpho- physiological descriptors (Anonymous, 2007) and (Rao *et al.*, 2013) which have been capable for distinguishing genetic material in different crops.

However, this technique has now become less reliable for separation and recognition of commercial varieties (Rahman *et al.*, 2020) as there might be minimal morphological variation among cultivars with related pedigrees which often creates ambiguity in identification. Besides, with ever increasing number of varieties every year, conducting DUS test is becoming increasingly expensive. In addition, majority of the characters utilized are multigenic or quantitative and their expression is altered by several environmental factors (Kumar *et al.*, 2018) which ultimately makes DUS testing a tedious and most expensive procedure which demands large area of land and skilled manpower to formulate subjective decisions. These circumstances prompt us to find quick, stable and cost-effective strategies to assist DUS testing.

The wide accessibility and cost-effectiveness of DNA-based markers in recent years makes them appealing alternatives to

investigate their utilization to complement the existing morphological based identification as they are free from environmental impacts (Noli *et al.*, 2018) and they could be applied at any phase of plant development. Even UPOV also endorsed the utilization of molecular markers as the standard method of varietal identification in crops. The potentiality of molecular markers has been demonstrated in several aspects such as genetic purity testing during hybrid seed production, detection and quantification of the adulteration in Basmati rice (Vemireddy *et al.*, 2019) etc. Additionally, Vemireddy *et al.* (2019) developed varietal specific allele profiles for major Indian rice varieties employing hyper variable microsatellite markers.

Compared to the conventional morpho-physiological traits, the molecular markers are more powerful tools for the assessment of genetic variation and elucidation of genetic relationships within and among species (Thomson *et al.*, 2007). Molecular Marker based Genetic Diversity Analysis (MMGDA) has the potential for assessing changes in genetic diversity over time and space (Duwick, 1984). Among DNA-based molecular markers, microsatellites, also called SSRs, are highly polymorphic, as they possess co-dominant inheritance, high abundance, enormous extent of allelic diversity and high reproducibility (Modini *et al.*, 2021). Molecular markers like SSRs (Simple Sequence Repeats) (Sarao *et al.*, 2021), have been tested to complement DUS testing in rice and they were found to be able to distinguish varieties unambiguously and establish level of uniformity and stability. Although there are several QTLs and cloned genes identified in rice, very few gene-specific markers are available to assist DUS descriptors. As per the national guidelines for the conduct of DUS tests in rice, there are 62 DUS related traits (Rani *et al.*, 2006) and (Rao *et al.*, 2013).

Prominent research stations *viz.*, ARS, Shirgaon, RARS, Karjat and KRS, Panvel under the jurisdiction of Dr. Balasaheb Konkan Krishi Vidyapeeth, Dapoli, District Ratnagiri, Maharashtra State, India had released more than 30 varieties and 5 rice hybrids over the years, which have been popular among local farmers and across the state and few across the nation. But many prominent parental lines used for this breeding programme across various groups such as red kernel lines, restorer lines, aromatic lines and lines responsive to biotic and abiotic stress are not yet been characterized by DUS method along with molecular profiling. These lines are used in breeding programme as parent for long time now, having distinct characters. DUS descriptors along with SSR markers will aid to characterize these diverse germplasm lines which can be used to choose elite donor parent for future breeding programme. Such type of attempt will be of its first of kind to study large number of parental germplasm used for Konkan region, to generate passport characterization data of genotypes.

Considering the above perspective, the present investigation entitled, “**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**” was undertaken with the following objectives;

1. Phenotypic characterization and estimation of genetical parameters of diverse rice genotypes for yield and yield parameters.
2. Establishment of DNA profiles of rice genotypes using SSR markers.
3. Generate database of diverse genotypes of rice based on DUS guidelines.

CHAPTER – II

REVIEW OF LITERATURE

The spread of modern high yielding varieties in intensive agriculture has posed a great threat to the security of the age old practice of growing traditional varieties and landraces which may have immense potential for different important traits. In order to prevent any further gene erosion, collection and conservation of such invaluable genetic resources of rice is essential.

The exploitation of genetic diversity for crop improvement should be the ultimate objective of exploration and conservation of genetic resources. It is important to ensure that plant genetic resources are adequately safeguarded for future generations. It can be done by identification, characterization and evaluation of important local and parental lines, germplasm in line with DUS descriptors along with molecular profiling. The vital stages of evaluation and incorporation of valuable characters into new varieties are the justifications of genetic resource activities.

For a successful plant breeding programme to improve genetic potential in any crop, variability is the basic requirement. The estimates of different genetic parameters are important for better understanding of the nature and magnitude of genetic variability available in the breeding material along with the association of different yield and quality attributing characters.

The available literature as of now in line with on objectives of present investigation is summarized below:

2.2.1 Studies on genetical parameters studies *viz.*, Variability, Heritability and Genetic Advance

2.2.2 Germplasm characterization using Molecular Markers

2.2.3 Characterization of germplasm using morphological DUS descriptors

2.2.4 Genetic Diversity Analysis Using Both DUS Descriptors and Molecular Markers

2.1 Need for the identification of rice varieties

The identification of varieties is a vital step during the breeding and registration process, seed production, trade and inspection in crops. The rapid identification and characterization of cultivars or varieties would therefore, provide valuable information for their introduction and genetic improvement. Plant cultivar or variety identification is a critical field as more and more varieties or cultivars are developed; the need to identify them unambiguously also increases.

2.2 Methods of identification of rice varieties

The rice varieties are identified employing several conventional and advanced methods. Previously, physical appearance or cooking quality traits were used for cultivar identification. However, the DUS descriptors and molecular markers are being used widely to distinguish rice genotypes. Recently, rice varieties are being identified using artificial intelligence-based neural network and machine learning classifiers. Further, spectroscopy was also used for cultivar identification. The important strides in this aspect are described hereunder.

2.2.1 DUS Testing

India has a rich and wide range of genetic wealth of rice. It has been estimated from various surveys that nearly 50,000 accessions of rice are being grown in the country. A large number of new varieties are being released every year, but not all of these

have been widely accepted, as many of them have been considered to be merely forms of acknowledged varieties. In order to release a new variety commercially, it is essential to register it, which largely relies on the DUS (Distinctness, Uniformity and Stability) test (Anonymous, 2001). Therefore, DUS test has been established to be the foundation of plant variety protection and also to identify a new variety from reference collection (Sharma and Singh, 2018).

A plant variety qualifies for protection when it meets the following essential criteria.

- (i) **Distinctness** –It means that a variety is clearly distinguishable by at least one essential characteristic from any other variety, whose existence is a matter of common knowledge. An essential characteristic is a heritable trait which is determined by one or more genes or the heritable determinants that contribute to the principle features, performance or value of plant variety (Rani *et al.*, 2006).
- (ii) **Uniformity**- It implies that the variety should be sufficiently uniform in its essential characteristics if subjected to variation that may be expected from the particular features of its propagation (Rani *et al.*, 2006).
- (iii) **Stability**- A variety is deemed to be stable when its characteristics remain unchanged after repeated propagation (Rani *et al.*, 2006).
- (iv) **Novelty** - According to section 15 of the Act (PPV and FRA), “Novelty” means commercial novelty *i.e.*, the propagating or harvested material of the variety should not have been sold or otherwise disposed off earlier than one year in India, from the date of filing of application of registration or outside India, not earlier than six years in the case of trees or wines or not

earlier than four years in any other case (new in commercial sense) and a unique and unambiguous denomination (name of the new variety).

Being a signatory to the General Agreement on Trade and Tariffs (GAAT), Government of India has enacted its *sui generis* system, Protection of Plant Varieties and Farmers' Right Act (PPV and FRA), 2001 for protection of plant varieties based on Distinctness, Uniformity and Stability (DUS) test, apart from novelty, as the existing UPOV models of plant variety protection was not suitable for Indian requirements.

The process of variety identification includes several steps such as identification of a variety, confirmation of the variety, distinctness of the variety from all other reference collections, purity of the variety and characterization of the variety which enumerates its full descriptors. The concept of distinctness, uniformity and stability are thus fundamental to the characterization of a variety as a unique creation. Registration is allowed for three types of plant varieties, new varieties bred by breeders, extant varieties and farmers' varieties subject to their fulfilling the conditions of Distinctness, Uniformity and Stability and Novelty in case of breeder's variety. The first step to implement our PPV and FR Act provisions is formulation of National Test Guidelines for conducting DUS tests. The new variety should pass legal examinations to be commercialized and receive the certificate for the Plant Breeders' Rights, a part of which consists of DUS tests according to morphological characteristics.

The new varieties will be subjected to DUS testing by PPV and FR Authority located in New Delhi. The PPV and FR Authority had developed and published in its journal, guidelines for DUS test for each crop (Anonymous, 2007) for the registration and protection of

newly developed varieties from unauthorized utilization. The tests are envisaged to generate comprehensive data on the attributes of a variety so as to compare these with the varieties of common knowledge or similar existing varieties. These shall be based on multi-location field trials conducted for at least two crop seasons (Anonymous, 2007) at minimum two location, along with special chemical laboratory tests (Section 29, PPV and FR rules).

As per the 1991 Act of UPOV, protection granted for the new variety authorizes the breeder with the exclusive right to commercially exploit the variety by direct sale or by licensing to others for sale. Nevertheless, the UPOV Act, 1991 also provides for the protection of Essentially Derived Varieties (EDV) in which the breeder of an Essentially Derived Variety (EDV) needs to obtain authorization of the breeder of the original variety for commercial exploitation of the new variety. Farmers' rights were available to the farmers in the UPOV Act, 1978, but UPOV Act 1991 deprives farmers of their rights to reuse their produce as a seed.

2.1.1 Genetical Parameters *viz.*, Variability, Heritability and Genetic Advance

The relative estimates of variability and their heritable components for yield contributing characters in the germplasm are of immense value in any breeding programme in achieving higher yields. The phenotype of quantitative trait is a combined product of genotype, environment and their interaction. Therefore, the success of any breeding activity depends on the extent of genetic variability available for utilization in crop improvement.

Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present

in relation to observed variation. Basic information on heritability is a prerequisite for planning any breeding programme. High heritability indicates that it should be easy to conduct effective selection for the trait. Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population. Johnson *et al.* (1955) reported that though the heritable estimates give useful indication of relative values of selection based on phenotypic expression. The genetic gain should also be considered to arrive at a more reliable conclusion.

Shanthi and Singh (2001) evaluated 16 rice mutants to study the variability. High GCV and PCV were recorded for number of grains per panicle and grain yield plant⁻¹. High heritability coupled with high genetic advance as per cent of mean was recorded for plant height, number of grains per plant and 1000 grain weight.

The extent of genetic variation in 16 parents and 48 hybrids was studied by Subbaiah *et al.* (2011) for yield and its components and 25 quality characters. High GCV and PCV were recorded for harvest index, total number of productive tillers per plant and gelatinization temperature in parents.

Babu *et al.* (2012) carried out a study of genetic parameters for yield, yield attributing, quality and nutritional characters in 21 rice hybrids. The characters *viz.*, number of filled grains per panicle, number of chaffy grains per panicle and iron content exhibited high GCV and PCV. The characters *viz.*, number of filled grains per panicle and water uptake exhibited high heritability coupled with high genetic advance.

Pratap *et al.* (2012) evaluated 100 high yielding rice genotypes for variability studies. High estimates of heritability, genetic advance, genotypic and phenotypic coefficients of variation were recorded for panicle hill⁻¹, flag leaf area and grain yield hill⁻¹.

Aditya and Bhartiya (2013) evaluated 18 rice genotypes for genetic parameter studies of 15 quantitative traits. The estimates of GCV and PCV were highest for grain yield plot⁻¹. The broad sense heritability was highest for plant height.

Gangashetty *et al.* (2013) used 42 rice genotypes to know the extent of genetic variability. High GCV and PCV were observed for plant height, number of tillers per plant, number of productive tillers per plant, panicle weight, grain length, test weight, iron and zinc content and grain yield plant⁻¹. High heritability with high genetic advance was observed for all traits except days to 50 per cent flowering.

Veni *et al.* (2013) assessed 70 rice genotypes for genetic variability. High GCV and PCV were recorded for water uptake (26.28), grain yield plant⁻¹ (26.18) and test weight (20.35). High heritability coupled with high genetic advance as per of mean was observed for grain yield plant⁻¹, water uptake, test weight and productive tillers per plant.

Dhurai *et al.* (2014) conducted genetic variability studies in 32 rice varieties. The higher magnitude of PCV and GCV was recorded for number of grains per panicle and grain yield plant⁻¹. High heritability coupled with high genetic advance as per cent mean was recorded for plant height, number of effective tillers per plant, panicle length, number of grains per panicle, kernel elongation ratio, kernel length after cooking, 1000-grain weight, harvest index and grain yield plant⁻¹.

Islam *et al.* (2015) evaluated 23 rice genotypes for genetic variability. High GCV and PCV were recorded for plant height, number of filled grains per panicle, days to 50% flowering, 1000 grain weight, grain width and grain yield.

Senapati and Kumar (2015) evaluated 22 Recombinant Inbred Lines (RIL's) for genetic variability, heritability and genetic advance. High PCV and GCV were observed for grain yield plant⁻¹, 1000 grain weight, L/B ratio, grain breadth and panicle weight. High heritability coupled with moderate to high genetic advance as per cent of mean was recorded for plant height, panicle weight, grain length, grain L/B ratio, 1000 grain weight and yield plant⁻¹.

Devi *et al.* (2016) assessed PCV, GCV, heritability and genetic advance in 27 rice genotypes. Higher estimates of PCV and GCV were observed for yield plant⁻¹ and filled seeds per panicle. High heritability in broad sense and high genetic advance as percent of mean were exhibited by effective tillers, plant height, flag leaf length, filled seeds per panicle, test weight, yield plant⁻¹, head rice recovery and length/breadth ratio.

The extent of genetic variation in 36 rice genotypes was studied by Abebe *et al.* (2017). High to medium heritability coupled with high GCV and high genetic advance as percentage of means were exhibited for plant height and grain yield.

Bhinda *et al.* (2017) studied genetic variability for in 42 advanced breeding lines of rice for 15 characters. Alkali spreading value exhibited highest GCV (19.44%) and PCV (21.07%) followed by filled grains per panicle (GCV 14.83% and PCV 19.90%). High heritability coupled with high genetic advance was reported for gel-consistency, plant height, filled grains per panicle, number of grains per panicle and days to 50% flowering.

Umarani *et al.* (2017b) carried out an experiment to assess the variability, heritability and genetic advance in 70 landraces of rice for 16 agro- morphological and grain quality parameters. Among all the characters, total number of grains per panicle

exhibited highest PCV and GCV, whereas lowest PCV and GCV were recorded for spikelet fertility.

Chuchert *et al.* (2018) evaluated 22 rice genotypes for genetic variability in nine traits. High phenotypic and genetic coefficients of variation were observed for yield plant⁻¹, number of panicles per plant, and number of spikelets per panicle. High broad-sense heritability was recorded for yield plant⁻¹.

Gyawali *et al.* (2018) evaluated seven rice genotypes for genetic variability. Genotypic and phenotypic coefficients of variation were high for effective tillers per m², 1000 grain weight, grain yield, harvest index. The highest heritability was recorded by the character, anthesis days (0.97) and genetic advance was found highest for effective tillers per m² (33.80).

Ranjith *et al.* (2018) assessed GCV, PCV, heritability and genetic advance in 30 rice genotypes using 12 characters. High PCV and GCV were observed for fertile grains, flag leaf area and tillers per hill. High heritability coupled with high genetic advance was recorded for plant height.

Singh and Verma (2018) estimated genetic variability, heritability and genetic advance for 15 characters. High genotypic and phenotypic coefficients of variation were observed for flag leaf area and panicle bearing tillers per plant. High heritability coupled with high genetic advance as per cent of mean was observed for grains per panicle, panicle bearing tillers per plant, spikelet per panicle and plant height.

Aravind *et al.* (2019) evaluated 45 mutant lines for genetic variability of 12 characters. High GCV and PCV were observed for number of productive tillers and single plant yield. The traits *viz.*, number of productive tillers, leaf blade width, 1000 grain weight,

LB ratio and single plant yield has high heritability along with genetic advance as percent of mean.

Rahangdale *et al.* (2019) evaluated 67 rice genotypes for 28 morphological and quality traits. High GCV and PCV were obtained for number of spikelets per panicle, spikelet density, grain yield plant⁻¹, fertile spikelets per panicle, biological yield plant⁻¹ and panicle weight plant⁻¹. High heritability accompanied with high genetic advance was observed for the traits 1000 grain weight (g), head rice recovery (%), spikelet fertility (%), harvest index (%), number of spikelets per panicle, fertile spikelets per panicle, spikelet density, grain yield plant⁻¹ (g), panicle weight plant⁻¹ (g), number of tillers per plant and number of productive tillers per plant.

Sao *et al.* (2019) observed high PCV and GCV for number of filled grains per panicle, number of unfilled grains per panicle, total spikelets per panicle, grain weight per plant, panicle weight and harvest index using 47 rice genotypes. High heritability with high genetic advance as percent mean was observed for all yield attributing traits like grain weight per plant, harvest index %, number of filled grains per panicle, panicle weight.

Bhargavi *et al.* (2022) observed significant differences among 52 genotypes for all the traits studied. High PCV and GCV were recorded for the traits *viz.*, panicle number per plant, weight of 1000 fully developed grains and grain yield plant⁻¹ indicating that large amount of variation was present among the genotypes for these characters. Whereas, low PCV and GCV were recorded for the traits *viz.*, grain length, decorticated grain length and length/breadth ratio indicating that the variability for these characters among the genotypes was meagre. The variability studies indicated

that the estimates of PCV were slightly higher than the corresponding GCV for all the characters indicating that the characters were less influenced by the environment. High heritability coupled with high genetic advance as per cent of mean was recorded for time of heading, stem length, panicle number per plant, weight of 1000 fully developed grains, decorticated grain width and grain yield plant⁻¹ indicating that these traits were mostly under the control of additive gene action and direct selection of these traits would be effective for crop improvement. While high heritability coupled with moderate genetic advance as per cent of mean was observed for the traits *viz.*, panicle length of main axis, time of maturity, grain length, grain width, decorticated grain length and length/breadth ratio.

Kushwaha *et al.* (2022) reported that, analysis of variance revealed significant differences among genotypes for all the characters. Brasali was the highest yielder suggesting that it can be used for crossing programme for improvement in yield. High values of GCV, PCV, heritability and genetic advance as percent of mean were observed for grain yield per plant, 1000 grain weight and plant height indicating that these traits can be used as selection indices for yield improvement. Grain length, root volume, panicle length of main axis, number of panicles, showed positive significant correlation with grain yield per plant. Hence, selection for any one of these characters would ultimately bring improvement of in grain yield. Grain length, root volume, panicle length of main axis and leaf length showed high direct effect on grain yield per plant. Hence, selection based on these characters would be more effective for yield improvement.

Table 2.1 List of previous studies on molecular characterization of rice genotypes

Marker system	DUS test	Key message	References
SSRs	D	13 rice cultivars (four commercial traditional Basmati, six cross-bred Basmati and three non-Basmati varieties) were evaluated using 35 SSRs. SSR analysis generated polymorphism sufficient to differentiate all the 13 rice genotypes	Pal <i>et al.</i> (2004)
SSRs	D, U, S	Mapped SSRs of 12 rice linkage groups could differentiate all 23 aromatic varieties. No variation was seen in the analysis of 20 individuals of all seed classes of “Pusa Basmati 1” using 55 SSRs, hence suggesting SSRs for uniformity and stability tests	Singh <i>et al.</i> (2004)
SSRs	D	Suggested the usage of SSR markers in genotype identification, monitoring purity and adulteration and plant variety protection	Siwach <i>et al.</i> (2004)
SSRs	D	The DNA fingerprinting helped to distinctly identify and characterize nine varieties using 18 different RM primers	Chakravarthi and Naravaneni (2006)
SSRs	D	Microsatellite markers could efficiently identify indigenous non- Basmati aromatic rice genotypes and support Intellectual Property Protection	Joshi and Behara (2017)
SSRs	D	A high degree of polymorphism obtained among eight rice genotypes using 14 SSRs suggested that SSRs would also be useful in variety fingerprinting and identification	Malky <i>et al.</i> (2007)

Marker system	DUS test	Key message	References
SSRs	D	SSRs separated rice varieties into Basmati and non-Basmati group	Sarao <i>et al.</i> (2009/21)
SSRs	D	The microsatellite markers employed for DNA fingerprinting were able to differentiate the parental lines of respective hybrids included under study and also useful for variety identification	Tamilkumar <i>et al.</i> (2009)
SSRs	D	Identified three varietal specific alleles, RM-11/147, RM-151/289, RM-153/178 for BR-11, Badshabhog and BR-19 cultivars using SSRs and suggested that a meaningful data could be obtained through DNA fingerprinting using SSRs	Rahman <i>et al.</i> (2010)
SSRs	D	The highly polymorphic SSRs could be used for quick and reliable detection of specific genotype	Singh and Singh (2012)
SSRs	D	SSRs can efficiently complement morphological descriptors as they are useful for identification of closely related cultivars through fingerprinting	Zhu <i>et al.</i> (2012)
SSRs	U	A set of SSRs was defined to allow the identification and certification of <i>O. sativa</i> varieties including INIA and foreign varieties. Thus, SSRs could be a good complement to the existing agro-morphological data when varieties are closely related	Becerra <i>et al.</i> (2015)
SSRs	S	A combination of five polymorphic SSRs were successful in differentiating 40 varieties, suggesting these SSRs as useful set for complementing DUS	Pourabed <i>et al.</i> (2015)

Marker system	DUS test	Key message	References
		tests for stability analysis.	
SSRs	D	The SSRs (RM206, RM21, RM55, RM258 and RM433) were found robust enough to distinguish the duplicate and similar named rice germplasm for their higher PIC values (> 0.86)	Ahmed <i>et al.</i> (2016)
SSRs	D	The allelic diversity revealed by 45 SSR primers was sufficient enough to distinguish the tested 120 aus rice genotypes through DNA fingerprinting	Islam <i>et al.</i> (2017)
SSRs	D	The average similarity index of 0.65 for morphological data and 0.35 for SSR data apparently defines the advantage of SSR over morphology in unambiguous and quick identification of closely related varieties	Vigneshwari <i>et al.</i> (2017)
SSRs	S	69 SSR markers were used for their molecular characterization and discrimination of 24 entries of rice. The molecular markers showing PIC value >0.5 can be used to distinguish NILs from their respective parents apart from gene linked markers of targeted trait	Reddy and Rani (2018)
SSRs	D, U, S	Out of 25 gene-specific markers used for screening, 18 were polymorphic. The number of alleles of the polymorphic markers ranged from two to three with an average of 2.05 alleles per locus. The PIC values of these gene-specific markers ranged from 0.037 to 0.369 with an average of 0.212. Varietal specific fingerprints were generated using these 18 markers	Bhargavi <i>et al.</i> (2022)

Marker system	DUS test	Key message	References
SSRs	D, U, S	A total of 15 loci were assigned to the fifteen primer pairs. Altogether 33 allelic variants were detected among the twenty-two cultivars with an average of 2.2 alleles per locus. A total of 33 shared and 3 unique allelic variants were generated in the form of amplified products. Average PIC values observed was 0.71.	Kushwaha <i>et al.</i> (2022)

Simple Sequence Repeats; PIC: Polymorphism Information Content; D: Distinctness; U: Uniformity; S: Stability.

2.1.2 Germplasm characterization using molecular markers

The variety identification serves the important goals such as mitigating legal claims, confirming Intellectual Property Rights and maintenance of genetic purity (Patra *et al.*, 2010). The current plant variety identification for their protection relies on morphological description of plant varieties. However, establishing identity of varieties based on the DUS descriptors is quite problematic and difficult due to their limited number, stage specificity and environmental influence which complicate their evaluation (Nuel *et al.*, 2021 and Cooke and Reeves, 2021).

In contrast, DNA or molecular markers are free from the environmental effects and could be applied at different stages of plant growth (Noli *et al.*, 2008/18).

The increased availability and cost-efficiency of DNA-based markers in recent years makes them an attractive option to explore their use to supplement or even ultimately replace the existing morphological and protein-based approaches (Jamali *et al.*, 2019). Among the DNA based markers, Microsatellite or Simple Sequence Repeat (SSR) markers were mostly used by many of the scientists to identify the rice genotypes. However, employment of gene- specific markers is more reliable in identification of a variety as these markers are tightly linked to the gene controlling the phenotypic expression.

DNA fingerprinting or profiling developed by using molecular markers to describe the combined use of several single locus detection systems is being used as a versatile tool for characterization of rice genotypes. Owing to these reasons, the International Union for the Protection of New Varieties of Plants (UPOV), an intergovernmental organization whose system of plant

variety protection is intended to encourage innovation in the field of plant breeding (Jordens, 2018) has called for the adoption of a DNA-based system that will enable examiners to deploy trait-specific DNA markers in DUS testing (Jamali *et al.*, 2019).

2.1.3 Characterization of germplasm using morphological DUS descriptors

Plant morphological characters have been recognized as the universally undisputed descriptors for DUS testing and varietal characterization of crop varieties. Use of morphological descriptors in sequential fashion is useful and convenient to discriminate different varieties (Patra *et al.*, 2010). The morphological DUS descriptors can be effectively used for identification and grouping of varieties and varieties satisfying the DUS criteria for these morphological descriptors could be registered under the PPV and FR Act for obtaining Plant Breeder's and Farmer's rights. There are 62 DUS descriptors (29 essential and 33 additional) in rice as per the national guidelines for the conduct of tests for Distinctness, Uniformity and Stability. Out of 62 DUS traits, the 29 essential traits should be examined and included in the description of varieties, which would be useful for identification of rice genotypes. A brief resume of work done in India and abroad with reference to this is discussed below:

Patra *et al.* (2010) assessed 60 morphological DUS descriptors of 18 Basmati rice varieties. Among these, 26 were monomorphic, 11 were dimorphic and seven were polymorphic indicating their potential for varietal characterization and distinctiveness.

Joshi *et al.* (2011) characterized 20 indigenous aromatic rice varieties using 60 morphological DUS descriptors. Out of these, 46 traits were visually assessed and 14 were measurable traits. Among 46 morphological characters, 24 were monomorphic, 17 were dimorphic and five were polymorphic.

Chakravorty and Ghosh (2012) characterized 51 landraces of rice using 46 agro-morphological traits following DUS test. Out of 51 varieties studied, 27 were found to be distinctive on the basis of 22 essential and 24 additional characters.

Characterization of 65 landraces of rice was done by Rao *et al.* (2013) using 43 DUS descriptors. Out of 65 landraces, 32 were found to be distinctive on the basis of 22 essential and 24 additional characters.

Characterization of 20 landraces of rice was done by Sinha and Mishra (2017) using DUS test. Out of these 20 investigated varieties, 11 varieties were distinctive for five essential and 18 additional characters.

Umarani *et al.* (2017a) characterized 70 landraces of rice using 14 DUS characters. Out of 14 characters, stem anthocyanin colouration of node was dimorphic, three were trimorphic, six were tetramorphic, lemma anthocyanin colouration of apex and amylose content showed five states of expression. Based on decorticated grain colour six groups were made.

Vigneshwari *et al.* (2017) characterized 13 commercially cultivated rice varieties of Tamil Nadu using 31 morphological traits. The level of discrimination was high in quantitative grain characters compared to qualitative characters.

Kumar *et al.* (2018) characterized 55 rice genotypes following the DUS guidelines. Significant variation was observed for the

characters like coleoptile colour, intensity of leaf green colour, culm attitude, flag leaf attitude, stem length, lemma and palea colour, grain length and test weight.

Manjunatha *et al.* (2018) assessed 25 DUS descriptors to characterize 60 landraces of rice including the aromatic genotypes collected from different parts of Wayanad, Kerala. Out of these, three characteristics were monomorphic, seven were dimorphic, six were trimorphic, seven were tetramorphic, decorticated grain shape showed five states of expression and lemma and palea colour recorded six states of expression.

Varietal identification of four rice varieties from Chhattisgarh was carried out through DUS Characterization by Tiwari *et al.* (2019) and stated that the morphological DUS descriptors could be effectively used for identification and grouping of varieties.

Mondal *et al.* (2019) characterized 21 rice varieties using 60 DUS descriptors (46 qualitative and 14 quantitative). Time to 50% heading, decorticated grain shape, colour of lemma and palea were the descriptors showing more discrimination. Eight qualitative and eight quantitative traits exhibited uniformity as determined by the recommended level.

DUS testing of 66 rice varieties was done by Raghavendra *et al.* (2019/21) using 27 morphological descriptors. This study demonstrated the effective use of DUS testing in varietal identification.

Patel and Srivastava (2020/15) characterized the aromatic rice varieties of Chhattisgarh using 45 morphological DUS descriptors. All the 45 unique morphological traits exhibited variability except ligule colour. The traits like grain size, grain shape and plant height contributed towards more diversity.

Sanyal and Joshi (2020) characterized 61 extant varieties of Basmati and non-Basmati groups of rice using 55 DUS descriptors. Their study revealed that six characters were monomorphic, nine were dimorphic and 40 were polymorphic.

Komala *et al.* (2020) characterized eight rice genotypes using 56 morphological DUS descriptors. Among 56 characters studied, the variation was observed in 37 characters.

Rawte and Saxena (2021) used 19 qualitative and 11 quantitative agro- morphological traits to characterize 100 rice accessions. The descriptors offering the most discrimination were time to 50% heading, time to maturity days, 1000 grain weight, stem length, grain length and width.

Banshidhar *et al.* (2021/19) worked on DUS characterisation of advanced recombinant lines of Kalanamak rice for 47 visually assessed characters and 15 quantitative characters. Out of these characters studied, 27 were monomorphic, 18 were dimorphic and two were polymorphic.

The agro-morphological characterization of aromatic *Harinakhuri* rice landrace was done by Ghosh *et al.* (2021). The lemma and palea of matured grain was straw coloured with purple spot at tip and sterile lemma in purple colour.

Gour *et al.* (2021) characterized 83 indigenous rice lines based on 31 morphological DUS descriptors. Basal leaf sheath colour, colour of tip of lemma, lemma and palea colour showed highest variation in germplasm.

Bhargavi *et al.* (2022) identified 52 rice varieties using 22 DUS descriptors. Out of 22 morphological DUS descriptors studied, four were monomorphic, nine were dimorphic and the remaining nine were polymorphic. Of these 18 traits (both dimorphic and polymorphic), only 10 were essential traits.

Kushwah *et al.* (2022) evaluated 22 local lowland rice cultivars employing DUS based descriptors. Out of 36 DUS descriptors taken under study, no variation was found in traits 9 traits while 13 were dimorphic and 14 showed polymorphic variation.

2.1.4 Genetic diversity analysis using both DUS descriptors and molecular markers

The analysis of genetic variation within and among elite breeding materials is of fundamental interest to plant breeders. Diversity based on phenological and morphological characters usually varies with environments and evaluation of these traits requires growing the plants to full maturity prior to identification. Molecular markers in addition to morphological characters have proven to be powerful tool in the assessment of genetic variation and in the elucidation of genetic relationships within and among species. Several molecular markers have been widely used in genetic diversity studies *viz.*, SSRs (Simple Sequence Repeats) (McCouch *et al.*, 2018; Garris *et al.*, 2019; Chuang *et al.*, 2021; Kanawapee *et al.*, 2021), providing greater confidence for the assessment of genetic diversity and relationships. Information regarding genetic variability at molecular level could be used to help, identify and develop genetically unique germplasm that compliments existing cultivars. A brief resume of work done in India and abroad with reference to this is discussed below.

Genetic relationship was assessed among 24 rice genotypes by UPGMA clustering using 50 SSRs by Siwach *et al.* (2004). This study revealed that three traditional Basmati varieties were closely related.

Chakravarthi and Naravaneni (2006) worked on the genetic

diversity analysis of 15 elite rice genotypes using 30 SSR primers. Cluster analysis grouped the rice genotypes into 10 classes in which japonica types DH-1 (Azucena) and Moroborekan clustered separately from *indica* types. Mahalingam *et al.* (2016) estimated genetic diversity among 51 restorer and five CMS lines in hybrid rice breeding. Cluster analysis using NTSYS generated dendrogram divided all the 56 parental lines into 13 different clusters with 80 per cent coefficient of similarity.

Islam *et al.* (2017) worked on the allelic diversity and the relationship among 120 *aus* rice landraces through DNA fingerprinting using microsatellite (SSR) markers. The genetic distance-based results obtained in the un-rooted neighbor joining tree clustering revealed nine genetic groups.

Vigneshwari *et al.* (2017) characterized 13 rice varieties of Tamil Nadu using 31 morphological traits and more than 200 SSR markers. Out these SSR markers, 88 showed polymorphism. Cluster analysis based on morphological characters grouped the varieties of medium and long slender grain type in one cluster and short bold grain type into another cluster at about 65 per cent similarity level. The cluster analysis of SSR markers grouped the varieties into four major clusters at a similar level of 35 per cent.

Aljumaili *et al.* (2018) worked on genetic diversity among 53 aromatic rice accessions using 32 SSR markers. The dendrogram based on UPGMA and Nei's genetic distance classified these 53 rice accessions into 10 clusters.

Jalaluddin *et al.* (2017) analysed genetic diversity of 22 *indica* rice cultivars through DNA fingerprinting using five microsatellite markers (RM1, RM3, RM168, RM226 and OSR19). The highest

genetic diversity (GD), 0.6336 was detected in locus RM168 and the lowest (0.2496) on locus OSR19. Average GD was 0.4446, indicating a moderate level of genetic diversity existing among the tested cultivars.

Joshi *et al.* (2017) characterized 19 rice varieties considering 52 DUS traits. High difference between PCV and GCV values for panicle number per plant shows high environmental effect. The varieties were grouped into different clusters based on the eight grouping characters of National DUS testing guidelines.

Reddy and Rani (2018) have done molecular and morphological characterization of 24 Near Isogenic Lines (NILs) of rice developed for major abiotic stresses. Results of molecular characterization showed genetic diversity among 24 entries. Cluster analysis grouped 24 entries into two distinct clusters at similarity coefficient of 33 per cent.

Herrera *et al.* (2018) studied the genetic relationship of some Venezuelan rice cultivars by SSR markers and found low genetic diversity among them.

Joshi *et al.* (2020) studied 20 indigenous aromatic rice varieties using 60 morphological DUS descriptors. On the basis of grouping characteristics seven varieties showed unique profiles.

Hossain *et al.* (2020) determined the allelic diversity and relationship of 12 elite aromatic rice cultivars using 24 SSR markers. The genetic distance- based results seen in the un-rooted neighbour-joining tree and UPGMA clustering revealed five genetic groups in which closely related genotypes were clustered together.

Alice *et al.* (2021/20) evaluated 195 rice accessions for diversity pattern among them. The genotypes were grouped into 10 clusters. The inter-cluster distance is higher than intra-cluster

indicating wide genetic diversity among the genotypes. The highest inter-cluster distance was observed between cluster VI and VII.

Choudhary *et al.* (2021) performed genetic diversity studies using 64 SSRs in 100 rice genotypes. Of 64 rice SSR primers studied, 52 showed polymorphism. A total of 184 alleles was identified averaging 3.63 alleles per locus. Cluster analysis grouped the 100 genotypes into five clusters.

Rabey *et al.* (2021) used AFLP and SSR markers to study the genetic diversity of eight rice cultivars. The Polymorphism Information Content value for the two types of assays was 0.825 and 0.967 for SSR and AFLP markers respectively. Cluster analysis was used to address relationship between the rice cultivars based on the SSRs and AFLP data.

Raghavendra *et al.* (2021) worked on DUS testing and genetic diversity analysis of 66 rice varieties using 27 morphological descriptors. Genetic similarities among genotypes varied from 0.11 to 1.0 with an average of 0.36. The cluster analysis grouped all the genotypes into two major clusters at 0.21 level of genetic similarity.

Roy and Sharma (2021) worked on assessment of genetic diversity in 84 rice cultivars of West Bengal through DUS characterization and a dendrogram constructed showed genetic diversity among 84 cultivars by grouping them into five major clusters. All the descriptors evaluated in this study have showed that there is enough genetic diversity among cultivars.

Samal *et al.* (2021) characterized 48 traditional aromatic rice varieties using 24 ISSR markers and morphological markers. The genetic diversity was evaluated using UPGMA cluster dendrogram which identified two clusters with a similarity coefficient of 53%.

The genetic diversity and phylogenetic relationship of six

improved African lowland rice varieties *viz.*, BW-348-1, FARO-44, FARO-57, NERICA-L-19, NERICA-L-34 and WITA-4 was investigated using 129 SSR primers distributed on 12 chromosomes of rice by Adegbaaju *et al.* (2015). The SSR based dendrogram generated clustered two genotypes BW348-1 and FARO-44 together and three genotypes FARO-57, NERICA-L-19 and WITA-4 together.

Kunusoth *et al.* (2021) worked on genetic diversity assessment of 24 elite Indian rice varieties using 24 agro-morphological traits and 86 SSR markers. Genetic diversity assessment based on SSR markers displayed genetic similarity coefficients and grouped the varieties into five major clusters.

Singh and Sengar (2021) have done DNA fingerprinting using SSR, ISSR and RAPD markers to evaluate the genetic divergence of 30 rice varieties. The dendrogram developed for aroma and quality traits by UPGMA showed that the genotypes with common phylogeny and geographical orientation tend to cluster together.

Bhargavi *et al.* (2022) worked on 52 rice varieties using 25 gene specific SSR markers to evaluate genetic divergence. Out of 25, 18 SSR markers count to be polymorphic. PIC values ranged from 0.037 to 0.369 with an average of 0.42.

Khushwaha *et al.* (2022) studied genetic diversity of 22 rice genotypes using 15 SSR markers. Average 22 alleles per locus were found and average PIC value 0.563 reported.

CHAPTER-III

MATERIAL AND METHODS

The field experiments of present investigation “**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**” were conducted in the two independent *Kharif* seasons of 2020 and 2021 on experimental farm at Agricultural Research Station, Shirgaon, District- Ratnagiri and experimental farm at Regional Agricultural Research Station, Karjat, District- Raigad respectively. The molecular marker analysis was carried out at Plant Biotechnology Centre, College of Agriculture, Dapoli. The biochemical analysis *viz.*, amylose, calcium content and alkali spreading value was done at biochemistry laboratory of Soil Science and Agricultural Chemistry section, Regional Agricultural Research Station, Karjat District- Raigad. Micronutrient analysis particularly Zinc and Iron content was carried out by using atomic absorption flame spectrophotometer unit available at Khar-land Research Station, Panvel, District- Raigad.

3.1 Climate and weather:

Geographically experimental farm of Agricultural Research Station, Shirgaon is situated between 17°01'28.3"N latitude and 73°17'51.7"E longitudes at 46 meter above mean sea level; which falls under South Konkan Coastal Zone (MH-1) as per agro climatic zone (NARP) whereas experimental farm of Regional Agricultural Research Station, Karjat, District- Raigad is situated between 18°30'56.71" N latitude and 94°15'37.25" E longitudes at 38 meter above mean sea level which falls under North Konkan Coastal Zone (MH-2) as per agro climatic zone (NARP).

3.2 Experimental details:

Total two experiments were conducted and observations recorded accordingly to fulfill the three objectives of present investigation as follows.

Table 3.1 Objective wise experimental details:

SN	Objectives	Experiment conducted	Observations recorded
1.	Phenotypic characterization and estimation of genetical parameters of diverse rice genotypes	Experiment No. 1 Field experiment conducted at ARS, Shirgaon and RARS, Karjat during two independent <i>Kharif</i> seasons of 2020 and 2021 respectively.	As per Table 3.4
2.	Establishment of DNA profiles of rice genotypes using SSR markers.	Experiment No. 2 95 genotypes sown in individual pots to collect leaf samples for DNA isolation and PCR amplification was done for 17 SSR primers.	As per Table 3.13
3.	Generate database of diverse genotypes of rice based DUS guidelines.	Observations for DUS descriptors were recorded from the field and laboratory experiments conducted for Experiment No. 1 and Experiment No. 2 respectively.	As per Table 3.7 and 3.8

Table 3.2 Experimental design and layout (Experiment No. 1) :

Particulars	<i>Kharif 2020, ARS, Shirgaon</i>	<i>Kharif 2021, RARS, Karjat</i>
Date of sowing	12 June 2020	12 June 2021
Date of transplanting	8 July 2020	8 July 2021
Design and Layout	RBD	RBD
Number of Genotypes	95	95
Replications	03	03
Row length	6 m	6 m
Spacing	20cm x 15cm	20cm x 15cm

3.3 Experimental material:

The 95 genotypes were obtained from various sources as details given below.

Table 3.3 Experimental material along with source:-

SN	Genotype	Source	SN	Genotype	Source
I	Red kernel local lines		II	Restorer lines	
1	MO-6	ARS, Moncomba	25	KJT-1R	ARS, Karjat
2	MO-8		26	KJT-2R	
3	MO-13		27	KJT-3R	
4	MO-17		28	KJT-4R	
5	MO-19		29	PR-114	IIRR, Hyderabad
6	Khara Rata	KRS, Panvel	30	RTN 11-2-1-3	ARS, Shirgaon
7	Mayekar Bhat	ARS, Karjat	31	PR-118	IIRR, Hyderabad
8	Munga	ARS, Shirgaon	32	DRR-215	
9	Mahsad		33	RTN-69-1-1	ARS, Shirgaon
10	Waksal-207		34	NAUR-1	NAU, Navsari
11	Barmil		35	BL-184AR	ARS, Karjat
12	Jyoti		36	Gurjari	NAU, Navsari
13	Patani-6		37	DRR-50-12	IIRR, Hyderabad
14	Bhadas-79		38	DRR-363-5	
15	Pandy		39	DRR-50-13	
16	Dular		40	DRR-50-10	
17	Try-1		41	DRR-86-8	IRRI, Manila,
18	Kochari		42	IR-63879-195-2-2-3-2	
19	Lal Patani		43	RTN-27-1-1-2	ARS, Shirgaon
20	Dodak		44	RTN-214-1-1-1-2	

SN	Genotype	Source	SN	Genotype	Source
21	Karhad	ARS, Shirgaon	45	VDN-9-10-1	ARS, Vadgaon
22	Ratnagiri 7		46	VDN-10-18	
23	Bela		47	RTN-35-1-1	ARS, Shirgaon
24	Valai		48	Sahyadri 5 R	
49			HRTMS-61		
50			CR-3993-2-24-45-2	IIRR, Hyderabad	
III	Aromatic lines		IV	Lines responsive to biotic and abiotic stresses	
51	P Basmati	IARI, N. Delhi	70	RS-1113	IIRR, Hyderabad
52	S Basmati		71	RP Bio 197	
53	Kothambir Sal	ARS, Karjat	72	RP-BIO-226	
54	Chinoor	PDKV, Akola	73	Ajaya	
55	P Sugandha-1	IARI, N. Delhi	74	KJT 1	ARS, Karjat
56	P Sugandha-3		75	KJT 2	
57	P Sugandha-4		76	IR-64	IRRI, Manila
58	P Sugandha-5		77	MUDGO	
59	Bhadasbhog	IIRR, Hyderabad	78	MILYANG 46	
60	CR2713-180		79	PTB 33	RARS, Pattambi
61	Kalanamak		80	MTU1010	RARS, Maruteru
62	NDR6315		81	BG 367-2	IRRI, Manila
63	P Samruddhi	MPKV, Rahuri	82	MILYANG 63	
64	Indrayani	ARS, Vadgaon	83	FL 478	
65	Dhanesal	IIRR, Hyderabad	84	MUT NS 1	
66	Ambemohar	ARS, Vadgaon	85	RATHU HEENATI	
67	K Shatabdi	ARS, Karjat	86	SINNA SIVAPPU	
68	Bhogwati	ARS, Radhanagari	87	IRRI 190	
69	Sugandha	VNMKV, Parbhani	88	IRRI 193	
			89	ARC 10550	
			90	S MAHSURI	IIRR, Hyderabad
			91	IRRI 123	IRRI, Manila
			92	IRRI 104	
			93	IRRI 192	
			94	Sonsali	IIRR, Hyderabad
	95	TN-1			

3.4 Brief cultural practices

Nursery beds were prepared by applying 15 Kg N as urea, 20 Kg P₂O₅ as single super phosphate and 2 Kg K₂O as murate of potash per 1000 m² of nursery bed. FYM @ 10t/ha was also added.

Seeds were sown and 25 days old seedlings were transplanted in plots with a basal dose of 50 Kg N, 50 Kg P₂O₅ as, 50 Kg K₂O as 3.3 kg/Guntha Suphala (15:15:15). Twenty five Kg each of nitrogen was then applied at 30 days after transplanting and at 65 days after transplanting. The crop was grown in shallow submergence of 2.5 cm during tillering and water was drained off seven days before harvest.

3.5 Sampling procedure

The observations were made on 30 plants or parts of 30 plants, which were divided among 3 replications (10 plants in each replication) as per the guidelines of PPV & FR Authority (Anonymous, 2009).

Table 3.4 Observations recorded on 27 yield and yield contributing characters, including 14 measurable DUS descriptors along with abbreviations (Objective 1)

SN	Character	Abbreviation	Remark
1	Days to 50% Flowering (Nos.)	DFF (Nos.)	Measurable DUS descriptor No. 20
2	Plant Height (cm)	PHT (cm)	Yield and yield contributing character
3	Stem Length Excluding Panicle (cm)	SLEP (cm)	Measurable DUS descriptor No. 29
4	Number of Tillers Plant ⁻¹	TLPP (Nos.)	Yield and yield contributing character
5	Panicle Length of Main Axis (cm)	PLMA (cm)	Measurable DUS descriptor No. 33
6	Number of Spikelets Panicle ⁻¹	SPP (Nos.)	Yield and yield contributing character
7	Fertility (%)	Fertility (%)	Yield and yield contributing character
8	Days to Maturity (Nos.)	DM (Days)	Measurable DUS descriptor No. 47

SN	Character	Abbreviation	Remark
9	Test Weight of 1000 Grains (g)	TW (g)	Measurable DUS descriptor No. 50
10	Grain Length (mm)	GL (mm)	Measurable DUS descriptor No. 51
11	Grain Width (mm)	GW (mm)	Measurable DUS descriptor No. 52
12	Grain Yield Plant ⁻¹ (g)	GYPP(g)	Yield and yield contributing character
13	Straw Yield Plant ⁻¹ (g)	SYPP (g)	Yield and yield contributing character
14	Grain Yield/ Straw Yield Ratio	G/S	Yield and yield contributing character
15	Straw Yield/ Grain Yield Ratio	S/G	Yield and yield contributing character
16	Leaf Length (cm)	LL (cm)	Measurable DUS descriptor No. 16
17	Leaf Breadth (cm)	LB (cm)	Measurable DUS descriptor No. 17
18	Stem Thickness (cm)	ST (cm)	Measurable DUS descriptor No. 28
19	Number of Panicles Plant ⁻¹	PPP (Nos.)	Measurable DUS descriptor No. 36
20	Decorticated Grain Length (mm)	DGL (mm)	Measurable DUS descriptor No. 54
21	Decorticated Grain Breadth (mm)	DGB (mm)	Measurable DUS descriptor No. 55
22	DGL/DGB Ratio	L/B	Grain type determining character
23	Amylose Content (%)	AC (%)	Measurable DUS descriptor No. 59 and Biochemical Character
24	Zinc Content (ppm)	Zn (ppm)	Biochemical Character
25	Iron Content (ppm)	Fe (ppm)	Biochemical Character
26	Calcium Content (ppm)	Ca (ppm)	Biochemical Character
27	Alkali Spreading Value	ASV	Biochemical Character and cooking quality assessment Character

3.5.1 Methodology for assessment of biochemical quality parameters for experiment number 1 (Objective 1)

3.5.1.1 Amylose content (%)

The simplified procedure (auto analyzer and manual method) of Juliano (1971) is used for the amylose content analysis.

The 100 mg of rice powder is put into a 100 ml volumetric flask and 1 ml of 95% ethanol and 9 ml of 1N sodium hydroxide are added. The contents are heated on a boiling water bath to gelatinize the starch. After cooling for one hour, distilled water is added and contents are mixed well. For each set of samples run, low, intermediate and high amylose standard varieties are included to serve as checks. Five ml of the starch solution is put in a 100 ml volumetric flask with a pipette. One ml of 1N acetic acid, 2 ml of iodine solution (0.2 g iodine and 2.0 g potassium iodide in 100 ml of aqueous solution) is added and volume is made up with distilled water. Contents are shaken well and let stand for 20 minutes. Absorbance of the solution is measured at 620 nm with a spectrophotometer. Amylose content is determined by using a conversion factor and the results are expressed on a dry weight basis.

For the standard curve, 40 mg of potato amylose (Sigma Chemical Co. or Stein Hall and Co. Inc. of known moisture content) are wet with 1 ml ethanol and 9 ml 1N sodium hydroxide. Heated for 5-10 minutes in a boiling water bath, cooled and made up to volume. 1, 2, 3, 4, 5 ml of solution are placed with a pipette in 100 ml volumetric flasks. The solution is acidified with 1N acetic acid (0.2, 0.4, 0.6, 0.8, and 1.0 ml, respectively and treated as above. The absorbance values are plotted at 620 nm, against the concentration of anhydrous amylose (mg) and the conversion factor is determined. The dilution factor of 20 for the samples is included

in the conversion factor. Starch solutions (100 mg/100 ml) prepared by the manual method may be automatically analyzed with an Auto Analyzer. Portions of the starch solutions are transferred into the sample cups of the Auto Analyzer and run at 70 samples/hour. A standard curve is made using rice samples of predetermined amylose content by the simplified manual method at 620 nm. A fresh working iodine solution (1.0 ml 1N acetic acid and 3.0 ml stock iodine solution diluted to 100 ml) is prepared daily. Results are expressed as per cent apparent amylose content in milled rice weight. Apparent amylose content is used since at amylose concentration of more than 25%, amylopectin shows increased iodine binding instead of amylose (Perez and Juliano 1978). They proposed a constant factor of 2.0% to convert apparent amylose content to absolute amylose content based on methanol defeating. After estimating amylose content, the samples were classified as follows.

Term	Amylose (%)	Characteristics when cooked
Waxy	0-7	Absorbed little water and therefore have little volume expansion.
Low amylose	8-20	On cooking tend to be moist, sticky and glossy, split if over cooked.
Intermediate amylose	21-25	Cook fluffy, moist tender and do not become hard upon cooling remains soft. (Most acceptable range for eating)
High amylose	> 25	Become hard when cool, Resist disintegration during boiling

3.5.1.2 Zinc and Iron content ($\mu\text{g g}^{-1}$)

Seeds of individual rice genotypes were harvested and threshed manually. The seeds were de-husked using clean pestle and mortar. The grains were washed quickly with double distilled water to remove any surface contaminants and dried in hot air oven at 70° C for 72 hours. 12.5 ml of 70% concentrated Nitric acid

was added to 0.2 g powdered grain samples and the mixture was incubated overnight. Next day, 10 ml of di-acid mixture (Nitric acid: Per-chloric acid in the ratio of 2:1) was added to the incubated sample. The mixture was then placed on the electric hot plate, allowing evaporation of acid in the form of white fumes, until white precipitate was formed at the base of the flask. The digested sample was left to cool for an hour and the volume was made up to 50 ml using double distilled water. Calibration of an instrument for estimation of an element was done using five standard solutions with appropriate dilutions. A suitable blank was run simultaneously to account for contamination from the reagents. Zinc and iron concentrations in the grain samples of rice were estimated using Atomic Absorption Spectrophotometer (AAS) at 213.86 nm for zinc and 248.33 nm for iron and expressed as $\mu\text{g g}^{-1}$ of grain and data shown in ppm.

Classification scale for zinc and iron content ($\mu\text{g g}^{-1}$)

S.N.	Characters	Categories
1.	Iron	Low (0-9) Moderate (9.1-12) High (12.1-20)
2.	Zinc	Low (0-15) Moderate (15.1-22) High (22.1-34)

3.5.1.3 Calcium content ($\mu\text{g g}^{-1}$)

- Weigh 5 g of 2 mm sieved sample in 250 ml conical flask.
- Add extractant in proportion of 1:5 (Extractant = Neutral ammonium acetate 77.1 g in 1 liter distilled water and adjust pH to 7.0).
- Shake for 5 minutes.

- Filter it through Whatman paper No. 1.
- Collect the filtrate free from sediments and use for estimation of Calcium.
- Pipette out 5 ml of extract in porcelain dish or in 100 ml conical flask, add 5-10 ml distilled water, add 2-3 crystals of sodium dithiocarbamate to avoid interference of heavy metals.
- Add 0.2 g ammonium purpurate to conical flask (red colour at this stage) by adding few drops of 16% NaOH (buffer) and titrate against standard EDTA till colour changes from orange red to purple.

3.5.1.4 Procedure for phenol reaction

Seeds of fifteen varieties were soaked in water for 16 hrs. at ambient temperature and then 50 seeds are placed in petri-plates containing the 1.5% phenol. The reaction takes place with the seed coat. Discoloration does not occur in the enzyme active cells of aleurone. Phenol does not react on seeds as a solution. Its vapors turn the solution producing color reaction.

3.5.1.5 Polished grain: expression of white core

The milled rice sample were observed for White back, White Centre and White belly for the expression of white core or degree of chalkiness and documented into absent, small, medium, large and fully chalky.

3.5.1.6 Gelatinization temperature through Alkali spreading value

Gelatinization temperature through alkali spreading value and clearing scale were determined as per procedure described by Little *et al.*, 1958 is as follow:

Duplicate sets of six whole milled kernels without cracks are selected and placed in plastic boxes (2" × 2" × 1"). Half kernels can be used in the absence of whole kernels. 10 ml of 1.7% (0.3035 N) potassium hydroxide (KOH) solution is added. The samples are arranged to provide enough space between kernels to allow for spreading. The boxes are covered and incubated for 23 hours at 30°C in an oven or by use of ambient temperature. Starchy endosperm is rated visually based on a 7 point numerical spreading scale (Table 3.5 and 3.6).

Table 3.5 Numerical scale for scoring Alkali spreading value along with Gelatinization temperature classification

Score	Spreading scale	Clearing Scale	Alkali digestion	Gelatinization temperature
1	Kernel not affected	Kernel chalky	Low	High
2	Kernel swollen	Kernel chalky collar powdery	Low	High
3	Kernel swollen, collar incomplete and narrow	Kernel chalky collar cottony or cloudy	Low-Intermediate	High-Intermediate
4	Kernel swollen, collar complete and wide	Center cottony, collar cloudy	Intermediate	Intermediate
5	Kernel split or segmented, collar complete and wide	Center cottony, collar clearing	Intermediate	Intermediate
6	Kernel dispersed, merging with collar	Center cloudy collar clear	High	Low
7	All kernel dispersed and inter mingled	Center and collar clear	High	Low

Table 3.6: Alkali spreading value and Gelatinization temperature classification

Alkali Spreading Value	Classification	Gelatinization temperature	Note
6 – 7	High	Low	1
4 – 5	Medium	Intermediate	3
3	Low, Medium	High, Medium	5
1 – 2	Low	High	7

3.5.1.7 Determination of aroma

By applying the standard procedure developed at International Rice Research Institute, Philippines (Jennings et al., 1979) aroma was estimated. In this process the test tube filed with 20 to 30 freshly harvested milled along with distilled and mouth closed by stopper was put on the water bath for 10-20 minutes following cooling and selling for aroma.

3.5.2 Observations recorded on DUS descriptors for experiment number 3 to generate data base of diverse rice germplasm (Objective 3)

Observations were recorded at different growth stages as mentioned in Table 3.7 as per DUS test guidelines of PPV and FR Authority for 62 agro-morphological descriptors as mentioned in Tables 3.8 (Anonymous, 2009). Four types of assessments were followed.

VS: Visual assessment by observations of individual plants or parts of plants

VG: Visual assessment by a single observation of a group of plants or parts of plants

MS: Measurement of a number of individual plants or parts of plants

MG: Measurement by a single observation of a group of plants or parts of plants

Table 3.7 Decimal Code for the Growth Stage

Code	Growth stage
10	After germination, emergence of first leaf through coleoptile / second leaf visible (less than 1 cm)
40	Booting : the increase in the size of the young panicle and its inward extension inside the upper leaf sheaths detectable as a bulge in the rapidly elongating culm
50	1st spikelet of inflorescence just visible
55	½ of inflorescence emerged
60	Beginning of anthesis : it begins with the protrusion of the first dehiscing anthers in the terminal spikelets on the panicle branches
65	Anthesis half way
70	Milk development stage: formation of white milky sap within the spikelets.
80	Dough development (spikelets become hard)
90	Ripening (terminal spikelets ripened)
92	Caryopsis hard (can be no longer be dented by thumbnail and over 90% spikelets ripened)

Table 3.8 Details of DUS descriptors observations

SN	Characteristics	States	Note	Stage of observation	Type of assessment
1	2	3	4	5	6
1. (+)	Coleoptile: Colour	Colourless	1	10	VS
		Green	2		
		Purple	3		
2. (*)	Basal leaf: Sheath colour	Green	1	40	VS
		Light purple	2		
		Purple lines	3		
		Uniform purple	4		
3.	Leaf: Intensity of green colour	Light	3	40	VG
		Medium	5		
		Dark	7		
4.	Leaf: Anthocyanin colouration	Absent	1	40	VG
		Present	9		
5.	Leaf: Distribution of anthocyanin colouration	On tips only	1	40	VG
		On margins only	2		
		In blotches only	3		
		Uniform	4		
6. (+)	Leaf Sheath: Anthocyanin colouration	Absent	1	40	VG
		Present	9		
7.	Leaf sheath: Intensity of anthocyanin colouration	Very weak	1	40	VG
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
8. (*)	Leaf: Pubescence of blade surface	Absent	1	40	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
9. (*)	Leaf: Auricles	Absent	1	40	VS
		Present	9		
10. (*)	Leaf: Anthocyanin colouration of auricles	Colourless	1	40	VS
		Light purple	2		
		Purple	3		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
11. (+)	Leaf: Collar	Absent	1	40	VS
		Present	9		
12.	Leaf: Anthocyanin colouration of collar	Absent	1	40	VS
		Present	9		
13. (+)	Leaf: Ligule	Absent	1	40	VS
		Present	9		
14. (*) (+)	Leaf: Shape of ligule	Truncate	1	40	VS
		Acute	2		
		Split	3		
15. (*)	Leaf: Colour of ligule	White	1	40	VS
		Light purple	2		
		Purple	3		
16.	Leaf: Length of	Short (<30 cm)	3	40	MS
		Medium	5		
		(30-45 cm)			
		Long (>45 cm)	7		
17.	Leaf: Width of blade	Narrow (<1 cm)	3	40	MS
		Medium (1-2 cm)	5		
		Broad (>2 cm)	7		
18.	Culm: Attitude (for floating rice only)	Non procumbent	1	40	VS
		Procumbent	9		
19.	Culm: attitude	Erect	1	40	VS
		Semi-erect	3		
		Open	5		
		Spreading	7		
20.	Time of heading with panicles)	Very early (<71 days)	1	55	VG
		Early (71-90 days)	3		
		Medium (91-110 days)	5		
		Late (111-130 days)	7		
		Very late (> 131 days)	9		
21. (*)	Flag leaf: Attitude of blade (early	Erect	1	60	VG
		Semi-erect	3		
		Horizontal	5		
		Drooping	7		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
22. (*)	Spikelet: Density of pubescence of lemma	Absent/ Weak	1	60-80	VS
		Medium	3		
		Strong	5		
		Very strong	7		
23.	Male sterility	Absent	1	65	VG
		Present	9		
24. (+)	Lemma: Anthocyanin colouration of keel	Absent or very Weak	1	65	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
25. (+)	Lemma: Anthocyanin colouration of area below apex	Absent	1	65	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
26. (*)(+)	Lemma: Anthocyanin colouration of apex	Absent	1	65	VS
		Weak	3		
		Medium	5		
		Strong	7		
		Very strong	9		
27. (*)(+)	Spikelet: Colour of stigma	White	1	65	VS
		Light green	2		
		Yellow	3		
		Light purple	4		
		Purple	5		
28.	Stem: Thickness	Thin (<0.40 cm)	3	70	MS
		Medium(0.40-0.55 cm)	5		
		Thick (>0.55 cm)	7		
29.	Stem: Length (excluding floating rice)	Very short(<91 cm)	1	70	MS
		Short (91-110 cm)	3		
		Medium(111-130 cm)	5		
		Long (131-150 cm)	7		
		Very long (>150 cm)	9		
30. (*)	Stem: Anthocyanin colouration of nodes	Absent	1	70	VS
		Present	9		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
31.	Stem: Intensity of anthocyanin coloration of Nodes	Weak	3	70	VS
		Medium	5		
		Strong	7		
32.	Stem: Anthocyanin colouration of internodes	Absent	1	70	VS
		Present	9		
33. (*)(+)	Panicle: Length of main axis	Very short(<16cm)	1	70-90	MS
		Short (16-20 cm)	3		
		Medium (21-25 cm)	5		
		Long (26-30 cm)	7		
		Very long (>30 cm)	9		
34. (*)	Flag leaf: Attitude of blade	Erect	1	90	VG
		Semi-erect	3		
		Horizontal	5		
		Deflexed	7		
35. (*)(+)	Panicle: Curvature of main axis	Straight	1	90	VG
		Semi-straight	3		
		Deflexed	5		
		Dropping	7		
36.	Panicle: Number per plant	Few (<11)	3	80-90	MS
		Medium (11-20)	5		
		Many (>20)	7		
37. (*)	Spikelet: Colour of tip of lemma	White	1	80-90	VS
		Yellowish	2		
		Brown	3		
		Red	4		
		Purple	5		
		Black	6		
38 (+)	Lemma and Palea: Colour	Straw	1	80-90	VG
		Gold and gold furrows on straw background	2		
		Brown spots on straw	3		
		Brown furrows on straw	4		
		Brown (tawny)	5		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
		Reddish to light purple	6		
		Purple spots / furrows on straw	7		
		Purple	8		
		Black	9		
39. (*) (+)	Panicle: Awns	Absent	1	90	VG
		Present	9		
40. (*)	Panicle: Colour of awns (late observation)	Yellowish White	1	90	VS
		Yellowish Brown	2		
		Brown	3		
		Reddish brown	4		
		Light red	5		
		Red	6		
		Light purple	7		
		Purple	8		
		Black	9		
41.	Panicle: Length of longest awn	Very short	1	90	VG-MS
		Short	3		
		Medium	5		
		Long	7		
		Very long	9		
42. (*)	Panicle: Distribution Of awns	Tip only	1	90	VS
		Upper half only	3		
		Whole length	5		
43. (+)	Panicle : Presence of secondary branching	Absent	1	90	VG
		Present	9		
44. (+)	Panicle: Secondary branching	Weak	1	90	VG
		Strong	2		
		Clustered	3		
45. (*)(+)	Panicle: Attitude of branches	Erect	1	90	VG
		Erect to semi-Erect	3		
		Semi-erect	5		
		Semi-erect to spreading	7		
		Spreading	9		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
46. (*)(+)	Panicle: Exertion	Partly exerted	3	90	VG
		Mostly exerted	5		
		Well exerted	7		
47.	Time maturity	Very early (<100)	1	90	VG
		Early (101-120)	3		
		Medium (121-140)	5		
		Late (141-160)	7		
		Very late (>160)	9		
48.	Leaf: Senescence	Early	3	92	VG
		Medium	5		
		Late	7		
49. (*)(+)	Sterile lemma: Colour	Straw	1	92	VS
		Gold	2		
		Red	3		
		Purple	4		
50.	Grain: Weight of 1000 fully developed grains	Very low (<15 g)	1	92	MG
		Low (15-20 g)	3		
		Medium (21-25g)	5		
		High (26-30)	7		
		Very high (>30 g)	9		
51.	Grain: Length	Very short (<6.0 mm)	1	92	MS
		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		
52.	Grain: Width	Very narrow (<2.0 mm)	1	92	MS
		Narrow (2.1-2.5 mm)	3		
		Medium (2.6-3.0 mm)	5		
		Broad (3.1-3.5 mm)	7		
		Very broad (>3.5 mm)	9		
53. (+)	Grain: Phenol reaction of lemma	Absent	1	92	VG
		Present	9		
54. (*)(+)	Decorticated grain: Length	Short	1	92	MS
		Medium	3		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
		Long	5		
		Long*(Long for Basmati type)	7		
		Extra long	9		
55. (+)	Decorticated grain:	Narrow (<2.0 mm)	3	92	MS
		Medium (2.0-2.5 mm)	5		
		Broad (>2.5 mm)	7		
56. (*) (+)	Decorticated grain: Shape (in lateral view)	Short slender	1	92	MS
		Short bold	2		
		Medium slender	3		
		Long bold	4		
		Long slender	5		
		Long slender*(For Basmati type)	5		
		Extra long slender	6		
57. (*)	Decorticated grain: Colour	White	1	92	VG
		Light brown	2		
		Variegated brown	3		
		Dark brown	4		
		Light red	5		
		Red	6		
		Variegated purple	7		
		Purple	8		
58. (+)	Endosperm: Presence of amylose	Absent	1	92	MG
		Present	9		
59. (*) (+)	Endosperm:Content of amylose	Very low (<10%)	1	92	MG
		Low (10-19%)	3		
		Medium (20-25%)	5		
		High (26-30%)	7		
		Very high (>30%)	9		
60 (+)	Varieties with endosperm of amylose absentonly Polished grain: Expression of white core	Absent or	1	90	MG
		very small			
		Small	3		
		Medium	5		
		Large	7		
		Fully chalky	9		

SN	Characteristics	States	Note	Stage of observation	Type of assessment
61. (+)	Gelatinization temperature through alkali spreading value	Low	1	92	MG
		Medium	3		
		High medium	5		
		High	7		
62. (*)(+)	Decorticated grain: Aroma	Absent	1	92	MG
		Present	9		

(*) Characteristics that can be observed during every growing season in all varieties and shall always be included in the description of the variety, except when the state of expression of any of these characters is rendered impossible by a preceding phonological characteristic or by the environmental conditions of the testing region. Under such exceptional situation, adequate explanation shall be provided.

(+) The plant parts on which the observations to be taken are given in the explanation or figure(s) in section VIII of the guideline for the conduct of test for Distinctiveness, Uniformity and Stability on Rice (*Oryza sativa* L.) published by PPV & FR Authority, Govt. of India.

3.6 Statistical Analysis

The mean data in respect of various 27 characters were subjected to the following statistical techniques using INDOSTAT software.

3.6.1 Analysis of variance

The analysis of variance for each character was calculated as per the standard statistical procedure given by Panse and Sukhatme (1967).

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

Y_{ij}	=	Performance of the j^{th} genotype in the i^{th} block
μ	=	General mean
b_i	=	True effect of i^{th} block
t_j	=	True effect of j^{th} genotype

e_{ij} = Random error associates with j^{th} genotype and i^{th} block

The structure of analysis of variance was as follows.

Table 3.9 ANOVA Table for Randomized Complete Block Design

Source of variation	Degrees of freedom	Sum of Squares	Mean Sum of Squares	Expected Mean Sum of Squares	'F' calculated Value
Replications	(r-1)	RSS	M_r	$\sigma^2_e + t \sigma^2_r$	M_r/M_e
Treatments	(t-1)	TrSS	M_t	$\sigma^2_e + r \sigma^2_g$	M_t/M_e
Error	(r-1) (t-1)	ESS	M_e	σ^2_e	
Total	(rt-1)	TSS			

Where,

r = Number of replications

t = Number of treatments

M_r = Mean sum of square of replication

M_t = Mean sum of square of treatment

M_e = Mean sum of square of error

σ^2_e = Environmental variance

σ^2_r = Variance due to replications

σ^2_g = Variance due to genotypes

Test of significance for each character was carried out against the corresponding error degrees of freedom using 'F' table values given by Fisher and Yates (1963).

3.6.1.1 Estimation of Genetic Parameters Phenotypic and genotypic variance

Phenotypic and genotypic variances were estimated using the following formula

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + M_e = \frac{M_t - M_e}{r} + M_e$$

3.6.1.2 Coefficient of Variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton and Devane. (1953).

a. Genotypic coefficient of variation (GCV)

$$\text{GCV} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

b. Phenotypic coefficient of variation (PCV)

$$\text{PCV} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{X})} \times 100$$

The GCV and PCV values were classified as described by Subramanian and Menon (1973).

Classification	GCV/ PCV
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.6.1.3 Heritability

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

$$\text{Heritability in broad sense } (h^2_{bs}) = \frac{\text{GV } (\sigma^2_g)}{\text{PV } (\sigma^2_p)} \times 100$$

Heritability in broad sense was categorized as per the classification given by Johnson *et al.* (1955)

Classification	Heritability
Low	Less than 30%
Moderate	30 – 60%
High	More than 60%

3.6.1.4 Expected genetic advance

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

$$\text{Expected genetic advance (GA)} = K \times \sigma_p \times h^2$$

Where,

K = Selection differential at 5% selection intensity (2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

3.6.1.5 Genetic advance as per cent of mean (GAM)

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

Where,

GA = Genetic advance

X = Grand mean of the character

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

Classification	GAM
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.7 Genetic Divergence

3.7.1 Mahalanobis' D² analysis

The data collected on different yield contributing characters was analysed using Mahalanobis' D² analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1936).

3.7.2 Test of significance

Variances were calculated for all the characters studied and test of significance was done. For the character pairs analysis of covariance was estimated on the basis of mean values (Panse & Sukhatme, 1967). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion.

The sum of squares and sum of products of error and error + variety, variance- covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\Lambda = \frac{|E|}{|E+V|}$$

Where,

Λ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E+V|$ = Determinant of error + variety matrix

$V_{(stat.)}$ = $-m \log_e \Lambda$ (at pq degrees of freedom)

Where,

$$m = n - (p + q + 1)/2$$

n = degree of freedom for error + varieties

p = number of variables /characters

q = number of varieties –1 (or degrees of freedom)

$V_{(stat.)}$ is distributed as χ^2 with pq degrees of freedom

3.7.3 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation of the differences in the mean values of various characters of the two genotypes *i.e.*, Σd^2_{ij} . Therefore transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.7.4 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.*, $Y_{it} - Y_{jt}$ for $t=1, 2 \dots p$ variables are computed and the D^2 values were calculated as,

$$D^2_{ij} = \sum_{t=1}^p (y^t_i - y^t_j)^2$$

Where,

y^t_i is uncorrelated mean value of i^{th} genotype for character ' t '

y^t_j is uncorrelated mean value of j^{th} genotype for character ' t '

D^2_{ij} is D^2 between i^{th} and j^{th} genotypes

3.7.5 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for p degrees of freedom, where p is the number of characters considered *i.e.* 27 in the present study.

3.7.6 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using Agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1979).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster.

The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued till all the genotypes were included into one or other cluster.

3.7.7 Average intra-cluster distance

For the measurement of intra-cluster distances, the formula used was $\Sigma D^2_i/n$ where, ΣD^2_i was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.7.8 Average inter-cluster distance

Clusters were taken one by one and their distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the numbers of one cluster to each of the number of other cluster divided by the product of number of genotypes in both the clusters under consideration.

The square root of the average D^2 value gave the genetic distance between the clusters. Based on D^2 values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average inters cluster distance} = \frac{D^2}{n_1 \times n_2}$$

Where,

D^2 = difference in the mean values between two populations
when all the character are considered simultaneously.
 n_1 and n_2 are number of genotypes of two clusters

Scale of divergence based on D values

Category	“D” values
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

3.8 Material and methodology for molecular profiling using SSR primers

3.8.1 Extraction of genomic DNA

3.8.1.1 Plant material

For the present investigation, all 95 genotypes of rice were sown in the pots and kept in greenhouse. The leaf samples were collected from 10-12 days old seedlings for the isolation of genomic DNA.

3.8.1.2 Preparation of stock solutions for reagents and buffers for DNA isolation.

The buffers and reagents for DNA extraction were prepared as per Sambrook Maniatis (1989). The composition and procedure for preparation of different stock solutions and buffers are given in the Table 3.10.

Table No. 3.10 : Preparation of solutions for DNA isolation

a) Extraction buffer			
Extraction buffer stock solutions: For 100ml. (g)	SN	Chemicals	Qty. required
	1.	200 mM Tris-HCl,	2.423
	2.	25 mM EDTA	0.831
	3.	250 mM NaCl	1.461
	1.	0.5M Glucose	0.9
	2.	0.5% SDS	0.05
	3.	3% PVP	0.3
	4.	0.4% Sodium Bisulphite	0.04
	5.	5% Sarcosyl	500 µl
b) 70% Ethanol For 100ml.	1.	Absolute ethyl alcohol	70ml
	2.	Distilled water	30ml
c) Chloroform: Isoamyl alcohol(24:1) For 100ml	1.	Chloroform	96ml
	2.	Isoamyl alcohol	4ml
d) TAE Buffer (50X) (Add 50 times double distilled water to 50X Buffer to make 1X- TAE buffer.) For 1000ml	1.	TrisHCl	242.5 g
	2.	Glacial acetic acid	57.1 ml
	3.	0.5 M EDTA (pH 8.0)	200ml
e) Ethidium Bromide (Final concentration was thus made 10 mg/ml. It was then stored in dark bottle at room temperature.)	1.	EthidiumBromide	0.1 g
	2.	Distilled water	10 l

3.8.1.3 Procedure for extraction of genomic DNA

The DNA was isolated by following the protocol of Edwards *et al.*, 1991 with the slight modifications of buffer composition and concentration. The young newly flushing 10-12 days old leaves were collected and sterilized with 70% ethanol to avoid the contamination. The isolation of genomic DNA was done using the following protocol.

- Leaf tissue (100 mg) were collected and cut into small pieces then kept in 1.5 ml eppendorf tube which leads to ensure uniform size of sample.
- Collected tissue was macerated by micro pestle at room temperature without buffer for 20 sec.
- Extraction buffer (500 μ l) was added and leaf tissue macerated gently for 30 seconds and kept in hot water bath for 45 minutes at 65°C.
- The sample was cooled down at room temperature and centrifuged at 10,000 rpm for 10 minutes.
- Aqueous layer was transferred to fresh eppendorf tube and 200 μ l of CIA (24:1) was added and mixed by gentle inversion for 5-6 times. The contents were then centrifuged at 10,000 rpm for 10 minutes.
- Again aqueous layer was transferred to fresh Eppendorff tube and 200 μ l of CIA (24:1) was added and mixed by gentle inversion for 5-6 times. The contents were then centrifuged at 10,000 rpm for 10 minutes.
- Supernatant was mixed with double volume of chilled Iso-propanol and incubated at -20°C for overnight.
- On the next day the solution was centrifuged at 10,000 rpm for 10 minutes and pellet was collected.

- Pellet was washed with 100 µl of 70 per cent ethanol followed by centrifugation at 10,000 rpm for 10 minutes.
- Pellet was dried and re-suspended in 50 µl of 1x TE buffer.
- Incubated at 37°C in a water bath for 10 minutes and stored at -20°C till further use.

3.8.1.4 DNA purification

Purification of DNA in samples was done to remove RNA, proteins and polysaccharides which were the major contaminants. RNA was removed by RNase enzyme treatment. RNase was added to the DNA sample @100 µg ml⁻¹ and incubated at 37°C for 1 hour.

3.8.1.5 DNA quantification through agarose gel electrophoresis

Concentration of DNA in the sample was obtained after agarose gel electrophoresis with standard DNA on 0.8 per cent agarose gel and by comparison of the intensity of staining with ethidium bromide.

3.8.1.6 Dilution of crude extract of DNA

The isolated DNA from all the rice genotypes was in varying concentrations. While preparing the working DNA samples it was diluted in such a manner as detailed in Table 3.10, so as it maintains the DNA content in all the samples in similar concentration.

Table No. 3.11 Sample wise dilution of the isolated DNA

SN.	Dilution ratio	Quantity of DNA (µl)	Quantity of D/W (µl)
1.	1:10	2	20
2.	1:15	2	30
3.	1:20	2	40

3.9 Screening of rice genotypes using SSR molecular markers:

The rice genotypes were screened for biotic and abiotic resistance using 20 SSR primers over different chromosomes for different biotic and abiotic stress resistance genes. The SSR primers were obtained from the GRAMENE database (Release #39, <http://archive.gramene.org/markers/microsat/all-ssr.tab>)

Details of the primers used are appended in Table 3.13.

3.9.1 Requirements:

Table No. 3.12:

Stock solutions	Source
Taq. assay buffer	M/s Bangalore Genei Pvt. Ltd., Bangalore
MgCl ₂	M/s Bangalore Genei Pvt. Ltd., Bangalore
dNTPs	M/s Bangalore Genei Pvt. Ltd., Bangalore
Primers (Fw./Rev.)	Bio-resource Biotech Pvt. Ltd., Pune.
Taq. DNA Polymerase	M/s Bangalore Genei Pvt. Ltd., Bangalore

Thermal cycler: Eppendorf, Master cycler gradient supplied by Eppendorf gradient, 2231, Hamburg Germany was used for cyclic amplification of DNA.

3.9.2 Preparation of master mixture

Since the pipetting of small volumes is difficult and often inaccurate, a master mix was prepared where constituents common to all the reactions were combined in one tube multiplying the volume for one reaction with total number of samples. Later, the appropriate amount of master mix was dispensed to each tube and template DNA was added separately in each tube. Details are appended in Table 3.14.

Table No. 3.13 List of microsatellite primers with their sequences and linked gene.

S N	Primer	Sequence Forward primer	Sequence Reverse Primer	Ch. No.	Linked gene
1.	RM 140	TGCCTCTTCCCTGGCTCCCCTG	GGCATGCCGAATGAAATGCATG	1	<i>Saltol</i>
2.	RM 1287	CCATTTGCAGTATGAACCATGC	ATCATGCAATAGCCGGTAGAGG	1	<i>Saltol</i>
3.	RM 3412	AAAGCAGGTTTTCTCCTCC	CCCATGTGCAATGTGTCTTC	1	<i>Saltol</i>
4.	RM234	ACAGTATCCAAGGCCCTGG'	CACGTGAGACAAAGACGGAG	7	Glb 1
5.	RM 6775	AATTGATGCAGGTTCAAGCAAGC	GGAAATGTGGTTGAGAGTTGAGAGC	6	<i>Bph25</i>
6.	RM 309	CACGCACCTTTCTGGCTTTCAGC	AGCAACCTCCGACGGGAGAAGG	12	<i>Bph26</i>
7.	RM 8225	GCGTGTTCAAGAAATTAGGATACGG	GATCTCGCCACGTAATTGTTGC	6	<i>Pi-z</i>
8.	RM 212	AAGGTCAAGGAAACAGGGACTGG	AGCCACGAATTCCACTTTCAGC	1	<i>Dr</i>
9.	RM 302	TGCAGGTAGAACTTGAAGC	AGTGGATGTTAGGTGTAACAGG	1	<i>Dr</i>
10.	RM 201	CTCGTTTATTACCTACAGTACC	CTACCTCCTTTCTAGACCGATA	9	<i>Dr</i>
11.	PTA 248	AGACGCGGAAGGGTGGTTCCTCGGA	AGACCGGGTAAT CGAAAGATGAAA	11	<i>Xa21</i>
12.	RM 122	GAGTCGATGTAATGTCATCAGTGC	GAAGGAGGTATCGCTTTGTTGGAC	5	<i>Xa5</i>
13.	RM 22709	CGCGTGGGCGAGACTAATCG	CCTTGACTCCGAGGATTCATTGTCC	8	<i>Gm8</i>
14.	RM 547	TTGTCAAGATCATCCTCGTAGC	GTCATTCTGCAACCTGAGATCC	8	<i>Gm4</i>
15.	RM 7	TTCGCCATGAAGTCTCTCG	CCTCCCATCATTTTCGTTGTT	3	<i>Tgw</i>
16.	RM 42	ATCCTACCGCTGACCATGAG	TTTGGTCTACGTGGCGTACA	6	<i>Wx</i>
17.	RM276	CTCAACGTTGACACCTCGTG-3'	TCCTCCATCGAGCAGTATCA	6	<i>Wx</i>

Table No. 3.14 Master mixture for polymerase chain reaction (PCR).

Components	Stock concentration	Vol. for one reaction/10 µl
Taq buffer	10X	1.25µl
MgCl ₂	25 mM	0.25µl
dNTP mix	10 mM	0.5µl
Primer- F	25picomole/µl	0.5µl
Primer- R	25picomole/µl	0.5µl
TaqDNA polymerase	3 U/µl	0.25µl
Template DNA	30-50 ng	1.0µl
Sterile Distilled water	--	5.75 µl
Total	--	10 µl

3.9.3 Thermal cycling

- Sterile micro centrifuge tubes were numbered from 1 to 34.
- 1.0 µl of diluted template DNA from individual rice genotype was added to each tube.
- 9 µl of master mix was added to each tube and was given short spin to mix the contents.
- The tubes were placed in the thermal cycler for 35 cycles of PCR. Samples were held at 4°C in the thermal cycler until the contents were loaded on to the gel for electrophoresis. (Table No. 3.15)

Table No. 3.15 Thermo Profile

Steps	Temp. (°C)	Period (min.)	
Initial Denaturation	94°C	5 min.	
Denaturation	94°C	20sec	35 Cycle
Annealing	53°C - 63°C*	30sec	
Extension	72°C	45 sec	
Final extension	72°C	7 min.	
Hold	4°C	--	

(*Note: - Annealing temperature based on T_m value of each primer)

3.9.4. Optimization of annealing temperature for gene specific primers by PCR amplification studies

Gradient PCR amplification of gene specific primers was carried out so as to determine the annealing temperature of each primer. The PCR programme was set in Thermal Cycler Eppendorf, Master Cycler Gradient, made in Germany.

The annealing temperature of each primer was standardized based on T_m value of each forward and reverse primer and standardized temperature was used for further amplification (Table 3.16).

Table No. 3.16 Annealing temperatures of SSR markers used in the study.

SN	Primer	Amplification size for resistance	Standardized Annealing temperature (°C)
1.	RM 140	260	62.1
2.	RM 1287	160	56.7
3	RM-3412	211	62.8
4	RM 234	255	56.5
5	RM 6775	192	58.7
6	RM 309	152	66.9
7	RM 8225	221	58.7
8	RM 212	135	62.9
9	RM 302	140	61.7
10	RM 201	220	52.1
11	pTA248	1040	54.0
12	RM 122	240-250	61.5
13	RM 22709	160-170	65.9
14	RM 547	270	56.1
15	RM 7	245	58.9
16	RM 42	155	61.3
17	RM 276	223	62.3

3.9.5 Separation of amplified product by agarose gel electrophoresis

- **Requirements:**

- a) Electrophoretic unit (Gel casting tray, gel comb, power pack)
- b) Gel documentation system
- c) Agarose
- d) Tracking dye (Bromophenol blue)
- e) Ethidium Bromide ($1\ \mu\text{g ml}^{-1}$)
- f) 50X TAE buffer.
- g) DNA ladder

- **Procedure**

The amplified products in SSR reaction were separated by agarose gel electrophoresis in 2 per cent agarose gel (Merck, India) containing ethidium bromide in 1X TAE Buffer (pH 8.0) and separation was carried out by applying constant voltage of 70 volts for 100 minutes.

3.9.6 Visualization, photography and gel documentation

The gels were photographed under UV light using Pentax K 312 nm camera. The photographs of gel was taken by the documentation systems (Uvi-Tech, Fire reader, Cambridge, England) and saved in computer for further analysis.

3.9.7 Molecular screening of genotypes

The gels were carefully analyzed and amplicons which obtained only once for a particular variety were marked which contained the band for that particular variety. Additionally, the

fragments present in two genotypes were also marked, which in combination with other bands produced with other primers would constitute the screenings.

3.8 Scoring and Data Analysis

Each amplification product as a dominant expression was considered as SSR marker and was scored across all the samples. Bands were scored as present (+/1) or absent (-/0). The size of each allele was determined by running simultaneously a DNA ladder by using software (Uvitec, Fire-reader software version 15.12). The data was used for similarity based analysis using the programme MVSP-A (Multivariate Statistical Package - 5785 Version 3.1). Similarity coefficients were used to construct UPGMA (Un-weighted Pair Group Method with Average) to generate Dendrogram.

Distance matrix and dendrogram was constructed based on diversity coefficient generated from pooled data by using Un-weighted Pair Group Method of Arithmetic Means (UPGMA), a computer programme for distance estimation. The percentage polymorphism of the obtained bands was calculated by using following formula,

$$\text{Per cent polymorphism} = \frac{\text{Total number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

3.9 Polymorphism Information Content

Polymorphism Information Content (PIC) value were calculated as per formula developed by Powell *et al.*, (1996).

Where,

$$PIC = 1 - \sum P_{ij}^2$$

- P_{ij} is the frequency of i^{th} and j^{th} locus, summed across the entire locus over all lines.
- PIC values range from 0 (monomorphic) to 1 (very highly discriminative, with many alleles each in equal and low frequency) were estimated for each profile generated across 95 rice genotypes

CHAPTER-IV

EXPERIMENTAL FINDINGS

Ninety five genotypes of rice were evaluated for Twenty seven characters including grain yield per plant in order to estimate various genetic parameters. The results were obtained from the observation after statistical analysis are presented and discussed under the following headings:

- 4.1 Genetical studies for 27 yield and yield contributing traits.
- 4.2 Molecular profiling of rice germplasm using SSR markers.
- 4.3 Morphological characterization of rice germplasm based on DUS guidelines

4.1 Genetical studies for 27 yield and yield contributing traits.

4.1.1 Analysis of variance (ANOVA)

Analysis of variance for 27 quantitative characters including grain yield plant⁻¹ revealed significant differences among the genotypes for these characters under study indicating the presence of greater variability among the genotypes. The details pertaining to ANOVA for experiments carried out at ARS, Shirgaon and RARS, Karjat are furnished under Table Number 4.1 and 4.2 respectively.

4.1.2 Mean performance along with range of 95 rice genotypes for various 27 traits

The mean performance of 95 genotypes for grain yield plant⁻¹ and its component traits for experiment carried out at Shirgaon and Karjat are presented in the Table 4.3 and 4.4, respectively.

4.1.2.1 Mean performance of rice genotypes for various 27 traits

4.1.2.1.1 Days to 50% Flowering (Nos.) days)

The number of days to 50% of flowering at Shirgaon location, ranged from 73.00 to 112.00 days with a general mean of 91.48 days. Among all the genotypes IRRI 104 (73.00 days) was found to be earliest while Kalanamak (112.00 days) was found to be late.

However the number of days to 50% flowering at Karjat location ranged from 72.33 to 111.33 days with a general mean of 90.41 days. Among all the genotypes IRRI 104 (72.33 days) was found to be earliest while Kalanamak (111.33 days) was found to be late.

4.1.2.1.2 Plant height (cm)

For this trait at Shirgaon location, the genotypes exhibited a range of 78.37 to 192.33 cm with a general mean of 123.67 cm. The shortest genotype was MO-8 (78.37 cm) and the longest genotype was NDR6315 (123.67 cm).

Whereas at Karjat location, the genotypes exhibited a range of 77.14 to 193.22 cm with a general mean of 123.91 cm. The shortest genotype was MO-8 (77.14 cm) and the longest genotype was NDR6315 (193.22 cm).

4.1.2.1.3 Stem length (excluding panicle; excluding floating rice) (cm)

At Shirgaon location, for this trait, the genotypes exhibited a range of 54.83 cm to 156.67 cm with a general mean of 96.86 cm. The shortest genotype was MO-8 (54.83 cm) and the longest genotype was NDR6315 (156.67 cm).

However at Karjat location, the genotypes exhibited a range of 53.03 cm to 156.75 cm with a general mean of 96.63 cm. The shortest genotype was MO-8 (53.03 cm) and the longest genotype was NDR6315 (156.75 cm).

4.1.2.1.4 Number of Tillers Plant⁻¹ (Nos.)

The number of tillers per plant at Shirgaon location, ranged from 8.93 (Mahsad) to 21.73 (TN-1) panicles with a general mean of 11.56.

Whereas at Karjat location, the number of tillers per plant ranged from 9.60 (Mahsad) to 22.38 (TN-1) panicles with a general mean of 12.20.

4.1.2.1.5 Panicle length of main axis (cm)

The panicle length at Shirgaon ranged from 22.13 to 35.67 cm with a general mean of 26.87 cm. The genotype IRRI 104 had shorter panicle length of 22.13 cm while the genotype NDR6315 exhibited highest value of to 35.67 cm which was almost 13.54 cm longer than IRRI 104.

While, the panicle length at Karjat ranged from 22.21 to 36.47 cm with a general mean of 27.28 cm. The genotype Gurjari had shorter panicle length of 22.21 cm while the genotype NDR6315 exhibited highest value of to 36.47 cm which was almost 14.26 cm longer than Gurjari.

4.1.2.1.6 Number of Spikelets Panicle⁻¹ (Nos.)

The number of panicles per plant at Shirgaon ranged from 55.31 (IRRI 190) to 300.48 (Ajaya) panicles with a general mean of 131.45.

However at Karjat, the number of panicles per plant ranged from 55.50 (Dodak) to 30.1.00 (Ajaya) panicles with a general mean of 131.61.

4.1.2.1.7 Fertility (%)

At Shigaon, the fertility (%) was within the range of 57.54 to 98.07 % with a general mean of 86.00 %. The maximum fertility was recorded for IRRI 192 (57.54%) and the minimum fertility was recorded for Try-1 (98.07%).

Whereas at Karjat, the fertility (%) was within the range of 57.54 to 98.34 % with a general mean of 86.06 %. The maximum fertility was recorded for IRRI-192 (98.34 %) and the minimum fertility was recorded for Try-1 (57.54 %).

4.1.2.1.8 Days to Maturity (Nos.) (days)

The time of maturity was within the range of 103.00 to 142.00 days at Shirgaon, with a general mean of 121.48 days. Among all the genotypes, IRRI 104 (103.00 days) was found to be earliest, while Kalanamak (142.00 days) was found to be late.

Whereas at Karjat, the time of maturity was within the range of 102.33 to 141.33 days with a general mean of 120.41 days. Among all the genotypes, IRRI 104 (102.33 days) was found to be earliest, while Kalanamak (141.33 days) was found to be late.

4.1.2.1.9 Test weight (g)

At Shirgaon the general mean of weight of 1000 fully developed grains was 21.83 g and the values ranged from 11.22 to 29.13 g Among the genotypes studied, Bela (29.13g) recorded highest 1000 grain weight and the lowest 1000 grain weight was recorded for Bhadasbhog (11.22 g).

However at Karjat, the general mean of weight of 1000 fully developed grains was 21.71 g and the values ranged from 10.74 to 29.29 g. Among the genotypes studied, Bela (29.29 g) recorded highest 1000 grain weight and the lowest 1000 grain weight was recorded for Bhadasbhog (10.74 g).

4.1.2.1.10 Grain length (mm)

At Shirgaon, the general mean of grain length was 9.42 mm and the values ranged from 5.99 to 11.65 mm. Among the genotypes used, Sugandha (11.65 mm) recorded the maximum grain length and the minimum grain length was recorded by Kothambir Sal (5.99 mm).

Whereas at Karjat, the general mean of grain length was 9.42 mm and the values ranged from 6.03 to 11.65 mm. Among the genotypes used, Sugandha (11.65 mm) recorded the maximum grain length and the minimum grain length was recorded by Kothambir Sal (6.03 mm).

4.1.2.1.11 Grain width (mm)

The grain width was within the range of 2.23 to 3.90 mm with a general mean of 2.87 mm. The maximum grain width was recorded for Kochari (3.90 mm) while the minimum grain width was recorded for Samba Mahsuri (2.23 mm).

However at Karjat, the grain width was within the range of 2.07 to 3.91 mm with a general mean of 2.84 mm. The maximum grain width was recorded for Kothari (3.91 mm) while the minimum grain width was recorded for Samba Mahsuri (2.07 mm).

4.1.2.1.12 Grain yield plant⁻¹ (g)

At Shirgaon, grain yield plant⁻¹ ranged from 9.22 g (Dular) to 32.27 g (PR-118) with a general mean of 17.11 g.

Whereas at Karjat, it was ranged from 9.24 g (Dular) to 30.64 g (PR-118) with a general mean of 16.94 g

4.1.2.1.13 Straw yield plant⁻¹ (g)

The straw yield plant⁻¹ falls within the range of 12.33 to 46.33 g with a general mean of 23.35 mm at Shirgaon. The highest and lowest values for this trait were recorded by PR-118 (46.33 g) and Dular (12.33 g) respectively.

Whereas at Karjat, it falls within the range of 8.60 to 46.50 g with a general mean of 22.70 g. The highest and lowest values for this trait were recorded by PR-118 (46.50 g) and Bhadas-79 (8.60 g) respectively.

4.1.2.1.14 Grain yield plant⁻¹ to Straw yield plant⁻¹ ratio

At Shirgaon, the ratio for grain yield plant⁻¹ to straw yield plant⁻¹ ranged from 0.51 (Chinoor) to 0.94 (Gurjari) with a general mean of 0.74.

However at Karjat, the ratio for grain yield plant⁻¹ to straw yield plant⁻¹ ranged from 0.59 (HRTMS-61) to 00.88 (RTN214-1-1-1-2) with a general mean of 0.84.

4.1.2.1.15 Straw yield plant⁻¹ to Grain yield plant⁻¹ ratio

The ratio for straw yield plant⁻¹ to grain yield plant⁻¹ ranged from 1.07 (Gurjari) to 1.96 (Chinoor) with a general mean of 1.37 at Shigaon.

Whereas at Karjat, this ratio ranged from 0.84 (Bhadas-79) to 1.73 (HRTMS-61) with a general mean of 1.34.

4.1.2.1.16 Leaf length (cm)

At Shigaon, the general mean of leaf length was 49.62 and the values ranged from 30.37 cm to 71.60 cm. Among the

genotypes studied, Patani-6 (71.60 cm) recorded the maximum leaf length and the minimum leaf length was recorded by RTN-214-1-1-1-2 (30.37 cm).

However at Karjat the general mean of leaf length was 49.52 and the values ranged from 30.40 cm to 71.69 cm. Among the genotypes studied, Patani-6 (71.69 cm) recorded the maximum leaf length and the minimum leaf length was recorded by RTN-214-1-1-1-2 (30.40 cm).

4.1.2.1.17 Leaf breadth (cm)

The general mean of leaf breadth was 1.10 cm and the values ranged from 0.70 cm to 1.50 cm. at Shirgaon. Among the genotypes studied, CR-3993-2-24-45-2 (1.50 cm) recorded the maximum leaf breadth and the minimum leaf breadth was recorded by Bhadas-79 (0.70 cm).

Whereas at Karjat, the general mean of leaf breadth was 1.07 cm and the values ranged from 0.47 cm to 1.58 cm. Among the genotypes studied, CR-3993-2-24-45-2 (1.58 cm) recorded the maximum leaf breadth and the minimum leaf breadth was recorded by RTN-214-1-1-1-2 (0.47cm).

4.1.2.1.18 Stem thickness (cm)

For this trait, at Shirgaon, the genotypes exhibited a range of 0.50 cm to 1.00 cm with a general mean of 0.74 cm. The thinnest genotype for stem was RTN-214-1-1-1-2 (0.50 cm) and the thickest genotype was Patani-6 (1.00 cm).

However, for this trait, the genotypes exhibited a range of 0.51 cm to 1.06 cm with a general mean of 0.76 cm. The thinnest genotype was RTN-214-1-1-1-2 (0.51 cm) and the thickest genotype was RP-BIO-226 (1.06 cm).

4.1.2.1.19 Panicle number plant⁻¹ (cm)

At Shirgaon, the number of panicles per plant ranged from 7.93 (Mahsad) to 20.73 (TN-1) panicles with a general mean of 10.56.

Whereas at Karjat, the number of panicles per plant ranged from 7.98 (Mahsad) to 21.38 (TN-1) panicles with a general mean of 11.05.

4.1.2.1.20 Decorticated grain length (mm)

At Shirgaon, the decorticated grain length falls within the range of 4.03 to 9.68 mm with a general mean of 6.76 mm. The highest and lowest values for this trait were recorded by Sugnadha (8.17 mm) and Kothambir Sal (4.03 mm), respectively.

However at Karjat, the decorticated grain length falls within the range of 4.01 to 8.14 mm with a general mean of 6.78 mm. The highest and lowest values for this trait were recorded by Sugandha (9.71 mm) and Kothambir Sal (4.01 mm), respectively.

4.1.2.1.21 Decorticated grain width (mm)

The decorticated grain width was within the range of 1.61 to 3.11 mm with a general mean of 2.42 mm at Shirgaon. The genotype Bela (3.11 mm) recorded maximum decorticated grain width and the genotypes, HRTMS-61 (1.80 mm) recorded minimum decorticated grain width.

Whereas at Karjat, the decorticated grain width was within the range of 1.61 to 3.11 mm with a general mean of 2.42 mm. The genotype Bela (3.11 mm) recorded maximum decorticated grain width and the genotypes, HRTMS-61 (1.63 mm) recorded minimum decorticated grain width.

4.1.2.1.21 Length/breadth ratio

At Shirgaon, this trait values were calculated by dividing decorticated grain length (mm) with decorticated grain width (mm). This trait varied from 1.41 to 4.30 with a general mean of 2.85. The genotype P. Basmati (4.69) recorded maximum length/breadth ratio and the genotype Kothambir Sal (1.41) recorded minimum length/breadth ratio.

However at Karjat, this trait varied from 1.41 to 4.34 with a general mean of 2.85. The genotype P. Basmati (4.66) recorded maximum length/breadth ratio and the genotype Kothambir Sal (1.41) recorded minimum length/breadth ratio.

4.1.2.1.22 Amylose content (%)

At Shirgaon, the amylose content (%) was within the range of 11.67 to 34.99 % with a general mean of 23.15 %. The maximum amylose content was recorded for Ajaya (34.99%) and the minimum amylose content was recorded for MUDGO (11.67 %).

However at Karjat, the amylose content (%) was within the range of 11.86 to 35.01 % with a general mean of 23.01 %. The maximum amylose content was recorded for Ajaya (35.01%) and the minimum amylose content was recorded for MUDGO (11.86 %).

4.1.2.1.23 Zinc content (ppm)

At Shirgaon, this trait was varied from 1.09 ppm to 22.62 ppm with a general mean of 11.95 ppm. The genotype PTB 33 (22.62 ppm) recorded maximum zinc content and the genotype KJT-2R (1.09 ppm) recorded minimum zinc content.

However, this trait was varied from 1.12 ppm to 22.59 ppm with a general mean of 11.99 ppm. The genotype PTB 33 (22.59

ppm) recorded maximum zinc content and the genotype KJT-2R (1.12 ppm) recorded minimum zinc content.

4.1.2.1.24 Fe content (ppm)

Values for this trait ranged from 1.70 ppm to 28.00 ppm with a general mean of 13.11 ppm. The genotype Kalanamak (28.00 ppm) recorded maximum Fe content and the genotype Mahsad (1.70 ppm) recorded minimum.

Fe content whereas at Karjat, values for this trait ranged from 1.83 ppm to 28.12 ppm with a general mean of 13.16 ppm. The genotype Kalanamak (28.12 ppm) recorded maximum Fe content and the genotype RP-BIO-226 (1.83 ppm) recorded minimum Fe content.

4.1.2.1.25 Calcium content (ppm)

At Shirgaon, calcium content falls within the range from 3.63 ppm to 102.00 ppm with a general mean of 53.53 ppm. The genotype Bhogwati (102.00 ppm) recorded maximum calcium content and the genotype Sugandha (3.63 ppm) recorded minimum calcium content.

However, at Karjat, calcium content falls within the range from 3.86 ppm to 102.68 ppm with a general mean of 54.06 ppm. The genotype BG-367-2 (102.68ppm) recorded maximum calcium content and the genotype Sugandha (3.86 ppm) recorded minimum calcium content.

4.1.2.1.26 Alkali spreading value (Nos.)

Scores for alkali spreading value ranged from 3.00 (Jyoti, Try-1, Dodak, Karhad, NDR6315, Ambemohar and Sugandha,) to 5.33 (RP-BIO-226) panicles with a general mean of 4.59 at Shirgaon.

However at Karjat, scores for alkali spreading value ranged from 3.00 (Jyoti, Try-1, Dodak, Karhad, NDR6315, Ambemohar and Sugandha,) to 5.33(RP-BIO-226) panicles with a general mean of 4.59

4.1.3 Genetic variability, Heritability and Genetic advance

The genotypic and phenotypic coefficients of variation, heritability (broad sense) and genetic advance as per cent of mean were estimated for 95 rice genotypes during first year at Shirgaon and second year at Karjat, respectively. Results are furnished in Table 4.5 and Table 4.6 for PCV, GCV, heritability (broad sense) and genetic advance as per cent of mean, respectively.

4.1.3.1 Variability

In the present study, experiment carried out at ARS, Shirgaon during *Kharif*, 2020 the GCV values ranged from 5.82 to 45.67 per cent whereas, PCV values ranged from 5.91 to 46.02 per cent.

Whereas, at Karjat during *Kharif*, 2021, the GCV values ranged from 5.95 to 45.64 per cent whereas, PCV values ranged from 6.08 to 46.06 per cent.

4.1.3.1.1 Low GCV and low PCV (Below 10%)

At Shirgaon, The GCV and PCV values were lowest for the traits *viz.*, days to maturity (5.82 and 5.91 %), followed by days to 50% flowering (7.72 and 7.85 %), panicle length of main axis (8.51 and 9.46 %) and fertility % (9.14 and 9.19 %).

While at Karjat, the GCV and PCV values were lowest for the traits *viz.*, days to maturity (5.95 and 6.08 %), followed by days to 50% flowering (7.93 and 8.10 %), panicle length of main axis (8.33 and 9.41 %) and fertility % (9.18 and 9.23 %) indicating that the variability of these characters among the genotypes was meager at both locations.

4.1.3.1.2 Moderate GCV and moderate PCV (10- 20%)

At Shirgaon, moderate GCV and PCV values were observed for the traits *viz.*, Number of Tillers Plant⁻¹ (14.57 and 15.82 %), test weight of 1000 grains (19.34 and 20.08%), grain length, grain width, grain yield/ straw yield ratio, straw yield/ grain yield ratio, leaf length, leaf breadth, stem thickness, Number of panicles plant⁻¹, decorticated grain length and decorticated grain breath.

However at Karjat, moderate GCV and PCV values were observed for the traits *viz.*, Number of Tillers Plant⁻¹ (13.84 and 15.13 %), grain length, grain width, grain yield/ straw yield ratio, straw yield/ grain yield ratio, leaf breadth, stem thickness, number of panicles plant⁻¹, decorticated grain length, decorticated grain breath and alkali spreading value.

4.1.3.1.3 High GCV and high PCV (Above 20%)

At Shirgaon, high GCV and PCV values were observed for the traits *viz.*, zinc content (45.67 and 46.02%), plant height (cm), stem length excluding panicle, number of spikelets panicle⁻¹, grain yield per plant, straw yield per plant L/B ratio, amylose content (%), iron content (ppm) and calcium content (ppm).

Whereas at Karjat, high GCV and PCV values were observed for the traits *viz.*, zinc content (45.64 and 46.06%), plant height (cm), stem length excluding panicle, number of spikelets panicle⁻¹, test weight, grain yield plant⁻¹, grain yield plant⁻¹, straw yield plant⁻¹, leaf length, L/B ratio, amylose content (%), Fe content (ppm), and calcium content (ppm) indicating that large amount of variation is present among the genotypes for both locations.

4.1.3.2 Heritability (broad sense)

In the present study all the characters *viz.*, showed high heritability (broad sense) (>60%) except alkali spreading value which showed lowest heritability (<30%) i.e. (29.00 %) at Shirgaon.

Whereas at Karjat, all the characters *viz.*, showed high heritability (broad sense) (>60%) except alkali spreading value which showed lowest heritability (broad sense) (<30%) i.e. (28.00 %).

4.1.3.3 Genetic advance as per cent of mean

At Shirgaon, the genetic advance as per cent of mean was high (>20%) for the characters *viz.*, plant height, stem length excluding panicle, number of spikelets per panicle and calcium content. On the other hand, moderate genetic advance (10-20%) as per cent of mean was noted for days to 50% flowering, fertility %, days to maturity, straw yield per plant, leaf length and zinc content. Remaining seventeen characters showed low genetic advance (<10%) as per cent of mean.

High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was observed for the traits *viz.*, plant height, stem length excluding panicle length, Number of spikelets panicle⁻¹ and calcium content. High heritability (>60%) coupled with moderate genetic advance (10-20%) as per cent of mean was observed for the traits *viz.*, days to 50% flowering, fertility (%), days to maturity, straw yield plant⁻¹, leaf length and zinc content.

Whereas at Karjat, the genetic advance as per cent of mean was high (>20 %) for the characters *viz.*, plant height, stem length excluding panicle, number of spikelets per panicle, leaf length and calcium content. On the other hand, moderate genetic advance (10-20 %) as per cent of mean was noted for days to 50% flowering,

fertility %, days to maturity, straw yield per plant and zinc content. Rest of the seventeen characters showed low genetic advance as per cent of mean (<10%).

High heritability (>60%) coupled with high genetic advance as per cent of mean (>20%) was reported for plant height, stem length excluding panicle, number of spikelets panicle⁻¹, leaf length and calcium content. High heritability (>60%) coupled with moderate genetic advance as per cent of mean (10-20%) was observed for the traits *viz.*, days to 50% flowering, fertility (%), leaf length and calcium content.

4.1.4 Genetic diversity

The 95 rice genotypes were assessed for genetic divergence by adopting Mahalanobis D² statistic for 27 yield and yield contributing parameters over two locations *viz.*, during *Kharif*, 2020 and *Kharif*, 2021 at ARS, Shirgaon and RARS, Karjat respectively.

4.1.4.1 Grouping of genotypes into various clusters

At Shirgaon, the 95 genotypes were categorized into 22 clusters based on D² values using agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The genotypes belonging to same cluster had an average smaller D² values than those belonging to different clusters. The distribution of genotypes into various clusters is furnished in Table 4.7 and Fig. 1 (Tocher's method). Cluster I was largest out of the twenty two clusters which comprises of 57 genotypes followed by cluster IV with 32 genotypes. Remaining clusters constitutes of one genotype respectively. The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster.

However at Karjat, the 95 genotypes were categorized into 20 clusters based on D^2 values using agglomerative hierarchical clustering complete linkage based on Mahalanobis distance Berkhin *et al.* (2006). The genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is furnished in Table 4.8 and Fig. 2 (Tochers method). Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters are mono-genotypic.

4.1.4.2 Average intra and inter cluster distances

At Shirgaon, intra cluster D^2 values ranged from 0.00 (all clusters except cluster I and IV) to 723.08 (cluster IV). Maximum intra cluster distance was observed in cluster IV (723.05) followed by cluster I (587.10) The details of inter and intra cluster distances are presented in Table 4.9 The inter-cluster D^2 values ranged from 147.10 (cluster II and III) to 3111.77 (cluster XIX and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (3111.77), followed by cluster XVIII and XX (3076.24), cluster XX and XXI (3018.86), cluster XXI and XXII (2771.82), cluster X and cluster XXII (2405.44), cluster XIII and XX (2344.39). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.10. Cluster I comprises 57 genotypes. It was nearest to cluster VIII (766.88) and was farthest from the cluster XXII (1624.67).

Whereas at Karjat, intra cluster D^2 values ranged from 0.00 (all clusters except cluster I, V and X) to 607.76 (cluster X). Maximum intra cluster distance was observed in cluster X (607.76)

followed by cluster I (437.13). The details of inter and intra cluster distances are presented in Table 4.11.

The inter-cluster D^2 values ranged from 232.22 (cluster IX and XI) to 2259.27 (clusters XIV and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (2259.27), followed by cluster XV and XX (1920.54), cluster VI and XX (1830.75), cluster X and XIX (1730.06). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.12. Cluster I comprises 58 genotypes. It was nearest to cluster IV (552.11) and was farthest from the cluster XX(1407.0).

4.1.4.3 Cluster mean values

The cluster means values at Shirgaon, for all the 27 characters are presented in Table 4.13. Cluster mean values for days to 50% flowering ranged from 78.00 days (cluster XII) to 108.33 days (cluster XII). Plant height ranged from 81.33cm in cluster XVI to 173.60 cm in cluster XXII, stem length excluding panicle was ranged from 57.33 cm in cluster XVI to 142.87 cm in cluster XXII. Number of tillers plant⁻¹ was ranged from 9.43 in cluster XII to 14.87 in cluster XXI. Panicle length of main axis was ranged from 22.40 cm in cluster XIII to 30.73 cm in cluster XXII. Number of spikelets panicle⁻¹ ranged from 55.32 in cluster XIX to 187.77 in cluster VII. Fertility % ranged from 57.54% in cluster XXII to 97.30 % in cluster X. Days to maturity ranged from 108.00 days in cluster XII to 138.33 days in cluster XVII. Test weight was ranged from 11.98 g in cluster XVI to 27.26 in cluster VI. Grain length ranged from 5.99 cm in cluster XX to 12.84 cm in cluster XVIII. Grain width was ranged from 2.23 cm in cluster XVI to 3.50 cm in cluster XXII. Grain yield plant⁻¹ was ranged from 11.20 g in

cluster II to 25.00 g in cluster XVII. Straw yield plant⁻¹ was ranged from 14.35 g in cluster XXII to 32.33 g in cluster XV. Grain yield to straw yield ratio ranged from 0.63 in cluster XXI to 0.94 in cluster XIII. Straw yield to grain yield ratio was ranged from 1.07 in cluster XIII to 1.59 in cluster XXI. Leaf length was ranged from 30.37cm in cluster VII to 67.23 cm in cluster III. Leaf breadth was ranged from 0.72 cm in cluster XV to 1.40 cm in cluster X. Stem thickness was ranged from 0.50 cm in cluster VII to 0.87 cm in cluster III. Number of panicles plant⁻¹ was ranged from 8.43 in cluster XII to 13.87 in cluster XXI. Decorticated grain length was ranged from 4.03 mm in cluster XX to 9.68 mm in cluster XVIII. Decorticated grain breath was ranged from 1.87 mm in cluster IX to 3.10 mm in cluster XXII. L/B Ratio was ranged from 1.41 in cluster XX to 4.69 in cluster XVIII. Amylose content was ranged from 14.33% in cluster VI to 29.42 % in cluster XIV. Zinc content was ranged from 1.09 ppm in cluster IX to 29.13 ppm in cluster XX. Iron content was ranged from 5.53 ppm in cluster XXII to 21.42 ppm in cluster X. Calcium content was ranged from 3.63 ppm in cluster XXI to 102.00 ppm in cluster IX. Alkali spreading value was ranged from 3.00 in cluster XXII to 5.00 in cluster XX.

However at Karjat the cluster means values for all the 27 characters are presented in Table 4.14 Cluster mean values for days to 50% flowering ranged from 72.33 days (cluster 8) to 107.00 days (cluster III). Plant height ranged from 85.83 cm in cluster VIII to 167.46 cm in cluster XX. Stem length excluding panicle was ranged from 63.41cm in cluster VIII to 136.15 cm in cluster XX. Number of tillers plant⁻¹ was ranged from 10.10 in cluster XI to 15.48 in cluster XV. Panicle length of main axis was ranged from 22.21cm in cluster XVII to 32.33 cm in cluster XVI. Number of spikelets panicle⁻¹ ranged from 55.50 in cluster VII to 178.78 in

cluster XVIII. Fertility % ranged from 57.54% in cluster XX to 97.16 % in cluster XIV. Days to maturity ranged from 102.33days in cluster VIII to 137.00 days in cluster III. Test weight was ranged from 13.36 g in cluster II to 27.83 in cluster IX. Grain length ranged from 7.50 cm in cluster XIII to 12.83 cm in cluster XIX. Grain width was ranged from 2.07 cm in cluster VI to 3.51 cm in cluster XX. Grain yield plant⁻¹ was ranged from 10.99 g in cluster II to 30.64 g in cluster XVI. Straw yield plant⁻¹ was ranged from 14.31 g in cluster XX to 46.50 g in cluster XVI. Grain yield to straw yield ratio ranged from 0.63 in cluster XV to 0.89 in cluster I. Straw yield to grain yield ratio was ranged from 1.18 in cluster 3 to 1.58 in cluster XV. Leaf length was ranged from 32.65 cm in cluster III to 66.35 cm in cluster II. Leaf breadth was ranged from 0.71 cm in cluster XIII to 1.39 cm in cluster XV. Stem thickness was ranged from 0.52 cm in cluster VII to 0.95 cm in cluster XVI. Number of panicles plant⁻¹ was ranged from 8.48 in cluster XI to 14.48 in cluster XV. Decorticated grain length was ranged from 5.24 mm in cluster XIII to 9.71 mm in cluster XIX. Decorticated grain breath was ranged from 1.85 mm in cluster VI to 3.09 mm in cluster XX. L/B ratio was ranged from 1.88 in cluster XIII to 4.66 in cluster XIX. Amylose content was ranged from 12.39 % in cluster VIII to 29.55 % in cluster XI. Zinc content was ranged from 2.02 ppm in cluster VII to 18.52 ppm in cluster XI. Iron content was ranged from 5.68 ppm in cluster XX to 21.39 ppm in cluster XIV. Calcium content was ranged from 3.86 ppm in cluster XV to 102.68 ppm in cluster XII. Alkali spreading value was ranged from 3.00 in cluster XX to 5.00 in cluster XII

4.1.4.4 Wilk`s ‘V’ criterion test

Wilk`s ‘V’ (Statistical) criterion was used to test the significant differences between the groups based on the pooled

effects for all the characters in the present study. The X^2 test at 281 degrees of freedom was conducted to study the significance of 'V' (Statistical) value. Highly significant 'V' statistic value indicating, that there was significant difference among the genotypes when all the characters were considered simultaneously.

The 95 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect for all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.1.4.5 Per cent contribution of character towards total genetic diversity

At Shirgaon, per cent contribution of 27 characters and towards total genetic divergence was found maximum for leaf length (cm) (26.00%) followed by calcium content (ppm) (23.23%), Number of panicles plant⁻¹ (cm) (19.42%), fertility (%) (9.09%), zinc and iron content ppm (5.69), decorticated grain length (mm) (5.46%), days to maturity (Nos.) (1.63%), Number of spikelets panicle⁻¹ (1.05%), plant height (cm) (Nos.) (0.63%), days to 50% flowering (Nos.) (0.56%), grain width (mm) (0.43%), amylose content (0.34 %), straw yield plant⁻¹ (g) (0.31%), grain yield plant⁻¹ (g) (0.25%), grain yield/ straw yield ratio (0.13%), Number of tillers plant⁻¹ and test weight of 1000 grains (g) (0.04%). It has been presented in the Table 4.15.

Character contribution was to total divergence was based on number of times character ranked first. From the table it was observed that for leaf length ranked 1st maximum times (1161) followed by calcium content (1037), Number of panicles plant⁻¹ (867) and the Number of tillers plant⁻¹ and test weight ranked 1st minimum times (2).

Whereas at Karjat, per cent contribution of 27 characters and

towards total genetic divergence was found maximum for calcium content (ppm) (26.32%) followed by leaf length (cm) (26.0%), fertility (%) (14.58%), decorticated grain length (mm) (9.97%), zinc content (ppm) (9.07%), Iron content (ppm) (6.29%), Number of spikelets Panicle⁻¹ (2.46%), plant height (cm) (1.39%), amylose content (%) (1.21%), days to 50% flowering (Nos.) (0.87%), grain yield plant⁻¹ (g) (0.74%), Number of tillers plant⁻¹ (0.31%), test weight (g) (0.27 %), panicle length of main axis (cm) (0.25%), straw yield plant⁻¹ (g) (0.13%), days to maturity (Nos.) and grain length (mm) (0.02%). It has been presented in the Table 4.16.

Character contribution was to total divergence was based on number of times character ranked first. From the table it was observed that for calcium content ranked 1st for maximum times (1175) followed by leaf length (1165), fertility% (651) and days to maturity (Nos.) and grain length (mm) ranked 1st for minimum times(1).

4.2 Molecular profiling of rice germplasm using SSR markers.

In the present study, 17 SSR markers were used to screen 95 rice genotypes. (Table 3.13).

4.2.1 DNA isolation

The standard procedure of DNA isolation along with slight modification of buffer components and their quality were employed (data not shown). The good quality and desired quantity of DNA was obtained (Plate Number1).

4.2.2 Standardization of annealing temperature:

The SSR markers having OD 25 nm were diluted at a concentration of 5pm/μl and employed for standardization of annealing temperature. The T_m value of reverse and forward primer was taken into consideration and programme was set accordingly. The data obtained is presented in T17. Each primer has shown different annealing temperature. It has been observed that, the

lowest annealing temperature was recorded in primer pTA-248 (54°C) whereas, maximum annealing temperature was recorded in primer RM 309 (66.9°C).

Table 4.17 : Optimization of annealing temperature of various SSR markers.

SN	Primer	Repeat motif	Size (bp)	Standardised AT (°C)
1	RM 140	(CT)12	261	62.1
2	RM 1287	(AG)17	162	56.7
3	RM 3412	(CT)17	211	62.8
4	RM 234	(CT)25	156	56.5
5	RM 6775	(TCC)8	192	58.7
6	RM 309	(GT)13	169	66.9
7	RM 8225	A11N(AAG)14	221	58.7
8	RM 212	(CT)24	136	62.9
9	RM 302	(GT)30(AT)8	156	61.7
10	RM 201	(CT)17	158	52.1
11	pTA 248	-	950	54.0
12	RM 122	(GA)7A(GA)2A(GA)11	227	61.5
13	RM 22709	-	160-170	65.9
14	RM 547	(ATT)19	235	56.1
15	RM 7	(GA)19	180	58.9
16	RM 42	(AG)6-(AG)(2T(GA)5	166	61.3
17	RM 276	(AG)8A3(GA)33	149	58.5

4.2.3 Genetic diversity

4.2.3.1 Polymorphism percentage:

The polymorphism percentage for individual primer was calculated by the ratio of number of polymorphic bands obtained over the total number of bands produced across the 95 rice genotypes. A total of 17 SSR primer pairs distributed across the genome were used for molecular analysis of 95 rice genotypes. All the 17 microsatellite markers used were found to be polymorphic and showed 100 per cent polymorphism. The overall size of amplified products ranged from 132 bp to 884 bp. A total of 139

alleles were obtained using 17 SSR primer pairs with an average of 8.17 alleles per primer. The number of alleles amplified for each primer pair ranged from 3 to 14.

4.2.3.2 Polymorphic Information Content (PIC):

The PIC values of primers ranged from 0.70 in SSR primer RM 7 to 0.92 in SSR primer RM 8225 with an average PIC value of 0.83. Further, it was observed that, there was no correlation between per cent polymorphism and PIC values as SSR primers RM 7 showed minimum PIC value but were 100 per cent polymorphic. The higher the PIC value, the more informative is the SSR marker. Hence, primers RM 825, RM 1287, pTA-248, RM 201, RM 122 and RM 22709 were found to be highly informative.

Table 4.18: Molecular polymorphism, PIC values, number of alleles and size of loci revealed by SSR primers

Primer	Size (bp)	Amplicons	Polymorphism %	PIC
RM 140	261	13	100	0.84
RM 1287	162	10	100	0.87
RM 3412	211	3	100	0.83
RM 234	156	6	100	0.86
RM 6775	192	12	100	0.72
RM 309	169	8	100	0.75
RM 8225	221	6	100	0.92
RM 212	136	3	100	0.86
RM 302	156	11	100	0.76
RM 201	158	14	100	0.89
PTA 248	950	7	100	0.87
RM 122	227	5	100	0.87
RM 22709	160-170	10	100	0.87
RM 547	235	4	100	0.84
RM 7	180	12	100	0.70
RM 42	166	11	100	0.74
RM 276	149	4	100	0.84
Average				0.83

Table 4.19 : Amplification of gene specific alleles with linked SSR markers for biotic and abiotic stresses resistance/tolerance.

SN	Traits	Primers	Resistance/ Tolerance genotypes
1	Blast	RM 8225	Try-1, Kochari, Lal Patani, Karhad, Ratnagiri 7, Phule Samruddhi, Ambemohar, Rathu Heenati, Sinna Sivappu, IRRI 190, IRRI 193, ARC10550, Samba Mahsuri, IRRI 123
2	Salt	RM 140	MO-17, MO-19, KJT-2R, RTN 11-2-1-3, Pak Basmati, Super Basmati,, Chinoor, Pusa Sugandha-1, Pusa Sugandha-3, Pusa Sugandha-4, Bhogwati, RP Bio 197, RP-BIO-226, Ajaya, Karjat 1
		RM 1287	VDN-9-10-1, HRTMS-61,
3	Brown plant hopper	RM 6775	Pusa Sugandha-4, Pusa Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, Phule Samruddhi
		RM 309	Kala Rata, Try-1, Kochari, BG 367-2, FL 478, MUT NS 1, Rathu Heenati, Sinna Sivappu
4	Drought	RM 212	BG 367-2, Milyang 63, FL 478, MUT NS 1, IRRI 192
		RM 201	Dhanesal, Ambemohar, Bhogwati, Sugandha
5	Gall midge	RM 22709	MO-6, MO-8, Munga, Patni-6, Pandya, NAUR-1, DRR-50-12, DRR-363-5, DRR-50-10, IR-63879-195-2-2-3-2, RTN-214-1-1-1-2, Chinoor, RP Bio 197, RP-BIO-226, Ajaya, Karjat 2, IR-64,
6	Amylose	RM 42	Try-1, KJT-1R, Gurjari, RTN-214-1-1-1-2, HRTMS-61, Phule Samruddhi, Indrayani, Dhanesal, Ambemohar, Karjat Shatabdi, RS-1113,

4.2.4 Genetic distance:

The diversity observed in the Ninety five rice genotypes mainly attributed to the genetic dissimilarities. The Jaccard's similarity coefficient values among the rice genotypes are presented in (Table 4.20). The pair wise similarity values ranged from 0.027 to 0.994.

4.2.4.1 Cluster analysis and Dendrogram construction:

UPGMA cluster analysis was performed using Jaccard's similarity coefficient matrices calculated from SSR markers to generate a dendrogram for 95 rice genotypes (Table 4.20). The UPGMA based dendrogram of 95 rice genotypes generated with Multivariate Statistical Package (MVSP). It was observed that, there are two major clusters. The first major cluster consists of four sub clusters. Two rice genotypes CR-3993-2-24-45-2 and HRTMS-61 formed the independent first sub cluster (IAa). Second sub cluster (IAb) consists of ten genotypes *viz.*, VDN-10-18, RTN-35-1-1, Sahyadri 5R, VDN-9-19-1, DRR-86-8, RTN-27-1-1-2, DRR-50-13, RTN-214-1-1-1-2, DRR-363-5, DRR-50-12. Third sub cluster (IBa) consists of seven genotypes *viz.*, BL-184AR, Gurjari, NAUR-1, IR 63879-195-2-2-3-2, DRR-50-10, RTN69-1-1, DRR-215. While fourth sub cluster (IBb) consists of four genotypes *viz.*, PR-118, RTN 11-2-1-3, PR-114, KJT-4R.

The second major cluster consists of four sub clusters. First sub cluster (IIAa) consist of five rice genotypes *viz.*, Sugandha, Bhogwati, Ambemohar, Karjat Shatabdi, Dhanesal. Second sub cluster (IIAb) consist of three rice genotypes *viz.*, Indrayani, NDR6315, Bhadasbhog. Third sub cluster (IIBa) consist of fourteen rice genotypes *viz.*, FL 478, Milyang 63, BG367, IRRI 193, Sinna Sivappu, Tathu Heenati, MUT NS 1, MTU1010, IRRI 192, IRRI 104, IRRI 123, Samba Mahsuri, ARC 10550, MUDGO. Third sub cluster (IIBb) consist of fifty rice genotypes *viz.*, TN1, Sonsali, Munga, Bela,

Ratnagiri 7, Valai, Kahad, Dodak, Kochari, Lal Patani, Try-1, Bhadas, Pandya, Patani-6, IRRI 190, Bamil, Jyoti, Waksa-207, Mahasad, Dular, Mayekar Bhat, Khara Rata, PTB 33, Milyang 46, Karjat 1, IR 64, Ajaya, RP BIO 226, RS 1113, RP BIO 197, Super Basmati, Kothambir Sal, Phule Samruddhi, Kalanamak, CR2713-180, Pusa Sugandha-5, Pusa Sugandha-3, KJT-1R, MO-19, MO-17, MO-13, KJT-3R, KJT-2R, Karjat 2, Pusa Sugandha 4, Chinoor, Pusa Sugandha-1, MO-8, Pak Basmati, MO-6.

Table 4.21: Clustering pattern of 95 rice genotypes.

Cluster			Number of Genotypes	Name of the genotypes
I	IA	IAa	02	CR-3993-2-24-45-2, HRTMS-61
		IAb	10	VDN-10-18, RTN-35-1-1, Sahyadri 5R, VDN-9-19-1, DRR-86-8, RTN-27-1-1-2, DRR-50-13, RTN-214-1-1-1-2, DRR-363-5, DRR-50-12
	IB	IBa	07	BL-184AR, Gurjari, NAUR-1, IR 63879-195-2-2-3-2, DRR-50-10, RTN69-1-1, DRR-215
		IBb	04	PR-118, RTN 11-2-1-3, PR-114, KJT-4R
II	IIA	IIAa	05	Sugandha, Bhogwati, Ambemohar, Karjat Shatabdi, Dhanesal
		IIAb	03	Indrayani, NDR6315, Bhadasbhog
	IIB	IIBa	14	FL 478, Milyang 63, BG367, IRRI 193, Sinna Sivappu, Tathu Heenati, MUT NS 1, MTU1010, IRRI 192, IRRI 104, IRRI 123, Samba Mahsuri, ARC 10550, MUDGO
		IIBb	50	TN1, Sonsali, Munga, Bela, Ratnagiri 7, Valai, Kahad, Dodak, Kochari, Lal Patani, Try-1, Bhadas, Pandy, Patani-6, IRRI 190, Bamil, Jyoti, Waksa-207, Mahasad, Dular, Mayekar Bhat, Kala Rata, PTB 33, Milyang 46, Karjat 1, IR 64, Ajaya, RP BIO 226, RS 1113, RP BIO 197, Super Basmati, Kothambir Sal, Phule Samruddhi, Kalanamak, CR2713-180, Pusa Sugandha-5, Pusa Sugandha-3, KJT-1R, MO-19, MO-17, MO-13, KJT-3R, KJT-2R, Karjat 2, Pusa Sugandha 4, Chinoor, Pusa Sugandha-1, MO-8, Pak Basmati, MO-6
		Total	95 genotypes	

4.3 Morphological characterization of rice germplasm based on DUS guidelines

In the present investigation 95 rice germplasm were characterized using 62 DUS descriptors over two independent *Kharif* seasons of 2020 and 2021 at two different locations ARS, Shiragon and RARS, Karjat, respectively.

4.3.1 DUS Descriptors in Rice Varieties

In rice, in total, 62 DUS descriptors have been notified by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA) in India for conducting DUS test. In the present study, 95 germplasm were characterized using 62 DUS descriptors. The varietal-specific DUS traits (62 traits) of 95 genotypes recorded in the present study as per DUS guidelines are presented in the table 4.22 and 4.23. Observations for all 62 descriptors were found to be similar over both the locations.

4.3.1.1 Coleoptile colour

This character was found to be polymorphic and exhibited three variations among 95 genotypes *viz.*, maximum 85 genotypes found to be colourless, 9 purple and only one genotype (Karhad) exhibited green coleoptile.

4.3.1.2 Basal Leaf: Sheath colour

This character was also found to be polymorphic and shown four types of variants among 95 genotypes *viz.*, highest number of 82 genotypes exhibited green for basal leaf sheath colour followed by 9 having light purple colour, 3 shown uniform purple and only one genotype (Mahasad) have purple lines.

4.3.1.3 Leaf: Intensity of green colour

Out of 95 genotypes light, medium and dark green leaves were observed on 32, 33 and 30 genotypes respectively. Hence this character found to be polymorphic in line with first two characters.

4.3.1.4 Leaf: Anthocyanin colouration

Out of 95 genotypes studied only 3 genotypes exhibited presence of leaf anthocyanin colouration *viz.*, Mahasad, Waksal-207 and Barmil, whereas leaf anthocyanin colouration in remaining 92 genotypes were found to be absent. Hence this trait can be categorized as dimorphic.

4.3.1.5 Leaf: Distribution of Anthocyanin Coloration

Out of 95 genotypes 2 genotypes *viz.*, Mahasad and Barmil exhibited uniform distribution of anthocyanin colouration and only one genotype Waksal-207 shows anthocyanin colouration on leaf margins. For rest of 92 genotypes this descriptor is not applicable as leaf anthocyanin coloration is absent. This trait is dimorphic.

4.3.1.6 Leaf Sheath: Anthocyanin Coloration

14 genotypes were showing presence of anthocyanin coloration on leaf sheath, whereas anthocyanin coloration on leaf sheath is absent in remaining 81 genotypes out of total 95. This descriptor can be described as dimorphic.

4.3.1.7 Leaf Sheath: Intensity of Anthocyanin Coloration

This character is polymorphic in nature as it shows five variations among 95 genotypes. Intensity anthocyanin coloration was found to be very weak, weak, medium, strong and very strong in 4,4,2,2 and 2 genotypes respectively whereas, for remaining 81 genotypes categorization for this trait was not applicable.

4.3.1.8 Leaf: Pubescence of blade surface

Stronger pubescence of leaf surface is not-preferred by insect pests. Hence presence of this trait in stronger range implies morphological resistance against pests. Out of 95 germplasm 22 were weak, while 40, 22 and 6 were seen to have medium, strong and very strong pubescence of leaf blade surface. This trait is polymorphic.

4.3.1.9 Leaf auricles

Auricles are hinge like structures that function to project the leaf away from the vertical axis of the plant. Among the 95 genotypes studied, all genotypes exhibited presence of leaf auricle. Hence this descriptor is monomorphic.

4.3.1.10 Leaf: Anthocyanin colouration of auricles

Colourless auricles were present in 86 genotypes, whereas light purple and purple auricles were present in 2 and 7 genotypes respectively, showing polymorphic nature for this trait.

4.3.1.11 Leaf collar

There was no variation in the genotypes for this character. All the 95 genotypes (100%) included in the present study showed presence of leaf collar. Thus this descriptor is monomorphic by nature.

4.3.1.12 Leaf collar: Anthocyanin colouration of collar

There was dimorphic variation in the genotypes for this character. Among total 95 genotypes included in the present study only 5 showed presence of anthocyanin colouration on leaf collar while rest of 90 genotypes were devoid of the same.

4.3.1.13 Leaf ligule

The ligule appears to be a continuation of the leaf sheath and encircles or clasps the stem as does the leaf sheath. Traditionally, it has been assumed in protecting the culm and leaves that it encloses from the entry of water, dust and harmful spores. There was no variation in the genotypes for this character. All the 95 genotypes showed presence of leaf ligule concluding the trait is monomorphic.

4.3.1.14 Leaf: Shape of ligule:

All the genotypes included under this study reported split shape of leaf ligule. Accordingly this descriptor falls under monomorphic class.

4.3.1.15 Colour of leaf ligule

Only one genotype (Dhanesal) exhibited light purple coloured ligule and the remaining 94 genotypes exhibited white coloured ligule. This trait is dimorphic in nature.

4.3.1.16 Leaf: Length of Blade

This measurable trait showed two variations viz., 40 genotypes found to be medium for length of leaf blade and remaining 55 have long leaf blade. Hence this character is dimorphic by nature.

4.3.1.17 Leaf: Width of Blade

This measurable trait showed similar dimorphic variation in line with the previous one. Out of 95 genotypes, 26 exhibited narrow leaf blade for its width while 69 were medium for the same.

4.3.1.18 Culm: Attitude (for floating rice only)

This trait was not applicable for the genotypes under study as it does not fall under floating rice category.

4.3.1.19 Culm: Attitude

Erect culms were observed in 84 genotypes while semi erect culm was seen in 11 genotypes showing dimorphic variation for the trait.

4.3.1.20 Time of heading (50% of plants with panicles) (days)

The experimental material was categorized into three classes based on this trait. The time of heading of 42 genotypes early type with the duration ranging from 71-90 days, 52 genotypes were found to be medium with 91-110 days to heading. 10 genotypes were found to be late with 111-130 days to heading and the remaining only one genotype (Kalanamak) exhibited late with duration of more than 131 days. Accordingly this trait is polymorphic.

4.3.1.21 Flag leaf: Attitude of blade (Early observation):

Polymorphic variation is observed the trait as erect flag leaf was observed in 79 genotypes while semi erect and horizontal flag leaves were observed in 14 and 2 genotypes respectively.

4.3.1.22 Spikelet: Density of pubescence of lemma

95 genotypes were classified in to weak (10), medium (23), strong (25) and very strong (37) based on density of pubescence of lemma exhibiting polymorphic variation.

4.3.1.23 Male sterility

All the 95 genotypes under study were found negative for male sterility attributing monomorphic nature.

4.3.1.24 Lemma: Anthocyanin colouration of keel

Out of 95 genotypes 90 genotypes were having very weak or no anthocyanin colouration of keel of lemma while 2 genotypes were found to have strong colouration and 3 genotypes exhibited very strong colouration. Thus this trait is polymorphic.

4.3.1.25 Lemma: Anthocyanin colouration of area below apex

This character was found to be polymorphic and exhibited three variations. Among the 95 genotypes studied, 90 genotypes showed absence of anthocyanin colouration and only one genotype (Kochari) showed presence of anthocyanin colouration of area below apex of lemma with medium note, whereas 4 genotypes have very strong colouration.

4.3.1.26 Lemma: Anthocyanin colouration of apex

The 95 genotypes were classified in to absent (81), strong (9) and very strong (5) exhibiting polymorphic variation.

4.3.1.27 Spikelet: Colour of Stigma

White stigma was found in 84 genotypes while purple were found in 11 genotypes. Moreover no light green, yellow and light purple colour stigma was seen.

4.3.1.28 Stem thickness

All 95 genotypes under study showed thick stem attributing monomorphic trait.

4.3.1.29 Stem length (excluding panicle; excluding floating rice) (cm)

Based on the stem length, the experimental material was grouped into four classes attributing polymorphic variation. Very short stem length (< 91 cm) was recorded by 46 genotypes, 16

genotypes were found to have medium stem length ranging from 110-130 cm, and 20 genotypes recorded short stem length ranging from 91-110 cm whereas 13 genotypes exhibited long stem length (>150cm).

4.3.1.30 Stem: Anthocyanin colouration of nodes

This trait showed dimorphic variation. In 91 genotypes anthocyanin colouration was absent in nodes while rest 4 genotypes it was present on the nodes.

4.3.1.31 Stem: Intensity of anthocyanin colouration of nodes

The anthocyanin colouration of nodes was found to be weak and medium 3 and 1 (Gurjari) genotypes respectively. For remaining 91 genotypes this trait is not applicable as colouration is absent. Thus the variation the said character is dimorphic.

4.3.1.32 Stem: Anthocyanin colouration of internodes

Out of 95 genotypes anthocyanin was present in 2 genotypes and absent in 93 genotypes at internode attributing monomorphic variation.

4.3.1.33 Panicle length of main axis (cm)

This trait exhibited polymorphic variation and according to panicle length of main axis, the genotypes were categorized into three groups, dominated by 63 genotypes with long sized panicles (26-30 cm), followed by 22 genotypes having medium sized panicles (21-25 cm) and remaining 10 genotypes had very long panicles (> 30 cm).

4.3.1.34 Flag leaf: Attitude of blade (late observation)

67 genotypes were having erect flag leaf while 20 and 7 were having semi-erect and horizontal flag leaf. Remaining only one

genotype (NDR-6315) showed deflexed flag leaf. Variation for the said character found to be polymorphic.

4.3.1.35 Panicle: Curvature of main axis

95 genotypes were classified in to straight (28), semi-straight (33), deflexed (24) and drooping (10) for panicle curvature attributed polymorphic variation for the said descriptor.

4.3.1.36 Panicle number plant⁻¹

The experimental material in the present study was polymorphic for this character. Out of 95 genotypes, 55 genotypes possessed fewer panicles per plant (<11), 39 genotypes have medium number of panicles (11-20) and remaining only one genotype *viz.*, TN-1 possessed many number (>20) of panicles.

4.3.1.37 Spikelet: Colour of tip of lemma:

95 genotypes were classified in to White (69), Yellowish (12), Brown (3), Purple (7) and Black (4) for tip colour of lemma as this trait exhibited polymorphic nature.

4.3.1.38 Lemma and palea colour:

Lemma and palea colour was observed under eight categories; straw (77), brown spots on straw (3), brown furrows on straw (3), brown tawny (6), reddish to light purple (3), purple spots/furrows (1), purple (1) and black (1) exhibiting polymorphic variation.

4.3.1.39 Panicle awns

Among the 95 genotypes, 34 genotypes possessed awns and the remaining 61 genotypes were awn-less, showing dimorphic variation.

4.3.1.40 Panicle: Colour of awns (late observation)

The colour of awns was Yellowish white (24), Yellowish brown (3), Reddish brown (1), Light red (1), Red (1) Light purple (3) and black (1). Traits not applicable for remaining 61 genotypes as those are awn less. Polymorphic variation is seen for the said character.

4.3.1.41 Panicle: Length of longest awns

Out of 95 genotypes studied 34 were awned and among these 20 genotypes had short awns, 11 showed medium length of awns and 3 were having very long awns (Khara rata, P. Basmati and Kalanamak). Polymorphic variation is observed for the said descriptor.

4.3.1.42 Panicle distribution of awns

Out of 95, 34 genotypes possessed awns. Out of these 34, 23 genotypes possessed awns at tip only, 6 genotypes have awns on upper half of panicle and the remaining 5 genotypes possessed awns throughout the whole length of panicle.

4.3.1.43 Presence of panicle secondary branching

Out of 95 genotypes studied 79 showed presence of secondary branching of the panicles whereas in 16 genotypes it was absent. There was dimorphic variation in the genotypes with respect to this character.

4.3.1.44 Panicle: Secondary branching

The experimental material in the present study was dimorphic for this character. Out of 95 genotypes, 21 genotypes possessed strong secondary branches and 58 genotypes possessed weak secondary branches.

4.3.1.45 Panicle: Attitude of branches:

95 genotypes were classified in to erect to semi-erect (9), semi- erect (13), spreading (4), semi-erect to spreading (6) and erect (47) for panicle branch attitude. Variation for the said trait is polymorphic.

4.3.1.46 Panicle: Exertion:

88 genotypes were having well exerted panicle while 6 and only 1 (CR-3993-2-24-45-2) genotypes were having mostly exerted and partly exerted panicle respectively. This character is found to be polymorphic by nature.

4.3.1.47 Time of maturity (days)

The genotypes in the present study were categorized into three classes based on this character. The time of maturity of 40 genotypes were early with the duration ranging from 101- 120 days, 54 genotypes were of medium duration ranging from 121- 140 days to maturity and only one genotype (Kalanamak) was found to be late with 141-160 days to maturity. Hence this trait is polymorphic.

4.3.1.48 Leaf: Senescence:

95 genotypes were grouped in to early (77), medium (15) and late (3) on the basis of leaf senescence. Thus it showed polymorphic variation.

4.3.1.49 Sterile lemma: Colour

95 genotypes were grouped in to five classes for colour of this trait *viz.*, straw (16), gold (3), red (8), purple (6) and white (62) exhibiting polymorphic variation.

4.3.1.50 Weight of 1000 fully developed grains (g)

Based on this character, the genotypes in the present study were categorized into four classes. Very low 1000 grain weight (<15 g) was recorded by 5 genotypes, 26 genotypes recorded low 1000 grain weight ranging from 15-20 g, 46 genotypes recorded medium 1000 grain weight ranging from 21-25 g. Whereas, 18 genotypes recorded high 1000 grain weight ranging from 26-30 g and the remaining 46 genotypes recorded medium 1000 grain weight ranging from 21-25 g.

4.3.1.51 Grain length (mm)

This trait was observed to be polymorphic. Out of 95 genotypes, 1 genotype (Kothimbir Sal) had very short (<6.0 mm) sized grain length, 13 genotypes had short grains (6.1-8.5 mm), 70 genotypes exhibiting medium sized grains (8.6-10.5 mm), 10 showed long length for the trait and the remaining only one genotype had very long grain length (Sugandha)

4.3.1.52 Grain width (mm)

The genotypes in the present study were categorized into four classes with respect to width of the grain. 6 genotypes were narrow (2.1-2.5 mm), 57 genotypes had medium grain width (2.6-3.0 mm), 28 genotypes had broad grain width (3.1-3.5 mm) and remaining 4 genotypes were found to be very broad (>3.5 mm) for width of grain. Hence polymorphic variation is observed for the said trait.

4.3.1.53 Grain: Phenol reaction of lemma:

Out of 95 genotypes 72 were having positive response whereas 23 were showing negative response for phenol reaction of lemma.

4.3.1.54 Decorticated grain length (mm)

In the present study, decorticated grain length of 52 genotypes was categorized into five groups showing polymorphic variation. 15 genotypes were short (< 6.0 mm), 4 genotypes found to be medium (< 6.00 mm)), 63 genotypes were long (6.0-6.6 mm), 11 genotypes were long for Basmati type (> 6.61 mm) and only two genotype (P. Basamti and S. Basmati) exhibited Extra-long length (>7.5 mm).

4.3.1.55 Decorticated grain width (mm)

The expression of this character among the genotypes was polymorphic *viz.*, narrow (<2.0 mm) in 4 genotypes, broad (> 2.5 mm) in 32 genotypes and medium (2.0-2.5 mm) in the remaining 59 genotypes.

4.3.1.56 Decorticated grain shape (in lateral view)

In the present study, decorticated grain shape of the genotypes was categorized into seven groups for shape of decorticated grain *viz.*, 2 genotypes had short slender (KL < 6.0 mm; LB ratio > 3.0 mm) shape, 13 genotypes showed short bold (KL < 6.0 mm; LB ratio < 2.5 mm) shape, 4 had medium slender (KL < 6.0 mm; LB ratio = 2.5 -3.0 mm) shape, 31 exhibited long bold (KL > 6.0 mm; LB ratio < 3.0 mm) shape, 31 showed long slender (KL > 6.0 mm; LB ratio > 3.0 mm) shape, Long Slender (Basmati type) (KL > 6.61 mm; LB ratio > 3.0 mm) and only 2 genotype possessed (P. Basmati and S. basmati) extra-long slender (KL > 7.5 mm; LB ratio > 3.0 mm) shape. Variation for the said character is polymorphic.

4.3.1.57 Decorticated grain: Colour

95 genotypes were classified in to White (72), Light red (5) and Red (18) on the basis of decorticated grain colour, thus showing polymorphic variation.

4.3.1.58 Endosperm: Presence of amylose

All 95 genotypes were having amylose exhibiting monomorphic variation.

4.3.1.59 Endosperm: Content of amylose

95 genotypes were classified in to four groups for the content of amylose *viz.*, 19 were having Low amylose (10-19%), 48 having medium (20-25%), 26 exhibited high (26-30%) and only 2 genotypes (Ajaya and Milyang-63) having very high (>30%) amylose. Polymorphic variation was observed for this trait

4.3.1.60 Varieties with endosperm of amylose absent only polished grain: Expression of white core

All the 95 genotypes were negative for the said character showing monomorphic variation.

4.3.1.61 Gelatinization temperature through alkali spreading value

Based on the scale of this trait all 95 genotypes were classified into three groups *viz.*, only one genotype (KJT-3R) exhibited low gelatinization temperature (55-69 °C), 33 genotypes were having medium GT (70-74 °C) and 61 showing high-medium GT (74-79° C) variation for the said descriptor were polymorphic.

4.3.1.62 Decorticated grain: Aroma

Out of 95 genotypes only 19 genotypes were having aroma while 76 were negative for aroma, thus depicting dimorphic variation.

4.3.2. Identification of 95 rice genotypes using DUS Descriptors

In the present study, out of 62 DUS descriptors one descriptor *viz.*, culm attitude (for floating rice only) was not

applicable for the genotypes under study as none of the genotypes was floating rice, rest 61 descriptors were recorded in 95 rice germplasm. Out of 95 genotypes 9 were monomorphic, 15 were dimorphic and remaining 37 were polymorphic

4.3.3 Analysis of distinctiveness, uniformity and distinctiveness by DUSTNT and mJRA software

The data recorded on 95 genotypes based on DUS guidelines were analyzed by DUSTNT and mJRA software and results are presented as follows.

4.3.3.1 Analysis of Distinctiveness

The data were recorded on 14 measurable characteristics and subjected to COY-D analysis at 0.1% level of significance (Table 4.25). The analysis revealed that all the genotypes were showing distinctiveness with respect to each other. COY-D analysis using MJRA was also carried out for all the rice genotypes and the results are given in the Table 4.26. The MJRA model for measurable characters took account of systematic annual increase or decrease in character expression across all varieties by fitting extra terms, one for each year in the analysis of variance. Each term represented the linear regression of the observations for the year against the variety means overall years (Digby, 1979). The MJRA analysis revealed F_1 ratio which takes into account the variety mean square and variety x year mean square. It was found to be highly significant for all the measurable characters under the study except for leaf width, stem thickness, grain width and decorticated grain width at 1% probability. It indicated that all the 95 varieties under study were quite distinct from each other except for leaf width, stem thickness, grain width and decorticated grain width.

A perusal of MJRA analysis revealed that the F_2 ratio which takes into account the variety x year mean square and variety x replication mean square was found to be non-significant for all the measurable characteristics at 1% probability except days to 50% flowering character. It indicated that the environment has a greater influence on days to 50% flowering. The slope of mJRA curve for all the characters for both the years calculated by the DUSTNT software was more than zero (ranged from 0.949 to 1.276) and regression probability was also more than zero (i.e. 1.147) weight of fully developed 1000 grains to 68.34 for time maturity which indicates that the characteristics under the study were not completely independent from the environment. Euclidian proximity matrix generated using DUSTNT software is shown in Table 4.27.

4.3.1.7.2 Analysis of uniformity

Sixty two characteristics were studied during the *kharif* seasons of 2020 and 2021 at ARS, Shirgaon and RARS, Karjat respectively. According to DUS guidelines of PPV&FR Authority forty six characteristics were visually assessed. These characteristics did not exhibit any variation in their state of expression during the two years of study. Further no off type plants were observed. There were 14 measurable characteristics which were subjected to COY-U analysis for assessment of uniformity using DUSTNT software (Table 4.28.) A candidate variety will be considered to be sufficiently uniform, if using a COY-U analysis the standard deviation for each characteristic is not greater than the mean standard deviation for the same characteristics in comparable varieties at 1% probability level. COY-U test compared within plot standard deviation between treatments, so if there is no within plot variations this test cannot be performed (Dey *et. al.* 2013) and (Mondal *et. al.*, 2019)

In the present study, the standard deviation was found to be zero for the characters leaf width, stem thickness, grain length, grain width, decorticated grain length and decorticated grain width. So, for these characters there is no within plot variation between varieties and COY-U test could not be performed.

The variety Waksal-207 and Bhogawati for character grain length; Try-1 and Valai for days to maturity, Samba Mahsuri for stem length excluding panicle and Bhadasbhog for amylose content were found to be not uniform as the standard deviation exceeded over-years criterion with 1% probability. Jyoti , KJT-3R, KJT-4R were found to be non-uniform for the character stem length (excluding panicle) as the within-years standard deviation exceeded once the UPOV criterion. In general, most of the varieties showed uniformity except for non-uniformity of one or two characters in some of the varieties. In that case varieties should be grown for one or two years to bring sufficient level of uniformity.

4.3.1.7.3 Analysis of stability

46 visually assessed characteristics exhibited stable performance on both the years of experiment as there was no variation in the state of expression of the characteristics over the years. Fourteen measurable characters were subjected to statistical analysis for stability by comparison of respective values of PCV and GCV based on pooled morphological data. Genetic parameters for measurable characteristics are presented in Table 4.29. Phenotypic Coefficient of Variation (PCV) is the resultant of combined action of genotype and environment over a genotype. Genotypic Coefficient of Variation (GCV), a component of total variation reflects the heritable portion. In the present study, the GCV values for 14 measurable DUS characters ranged from 5.89

to 25.09 per cent whereas, PCV values ranged from 6.00 to 25.41 per cent. As the PCV estimates were slightly higher than the corresponding GCV for the characters studied, it indicates that the characters were less influenced by the environment. Thus it indicates that environmental factors are not affecting the expression of these characters.

Thus increasing the soil nutrients and or any change in environmental factors will not affect the any of the 14 characters studied. Thus all these 14 descriptors are genetically regulated characters and can be used as varietal differentiation and identification.

Therefore, phenotypic selection would be effective for the improvement of these traits.

High heritability and genetic advance was observed for all the characters indicating that the characters are governed by additive and/ or additive x additive gene action.

CHAPTER-V

DISCUSSIONS

Identification of DUS traits is vital for protection of rice varieties under PPV and FRA and also during the trade and seed production. There are two strategies commonly used for cultivar identification such as morphological descriptors and molecular or DNA markers. Traditionally, morphological descriptors are used for testing Distinctness, Uniformity and Stability (DUS), as they are less expensive and easy to measure without having sophisticated laboratory facilities. However, limited number, stage-specific and inconsistent expression due to the environmental influence, renders DUS descriptors unsuitable to exploit extensively for rapid identification of cultivars. Furthermore, they failed to distinguish large number of varieties or breeding lines with slight variation in agronomic traits- a common phenomenon in recently released varieties. These problems of the morphological descriptors can be solved efficiently by molecular markers as they are stable, abundant with high discriminating power, although expensive.

Taking consideration of above facts, in the present investigation, 95 diverse rice germplasm were assessed for qualitative and quantitative traits and data obtained were analyzed to find out variation among different cultivars for different characters. Mean performance of the genotypes for the various traits were under taken for estimation of genetic coefficient of variation, heritability, genetic advance, among character and genetic divergence through D^2 statistic. Along with this diversity analysis using SSR marker was also done, morphological characterization based on DUS guidelines was carried out and both results obtained were compared to draw valuable inference.

5.1 Analysis of variance:

The Analysis of variance for the quantitative characters revealed that mean sum of square of genotypes for all 27 characters studied, revealed that genotypes were significantly different for all the characters under study indicating the presence of greater variability among the genotypes.

5.1.1 Variability:

In any plant breeding programme variability and selection are indispensable. Success of plant breeding programme depends on extent of variability present in the material under study. More the variability better is the chance of selection.

In the present study wide range of variability was observed among the genotypes for all character under the study.

Phenotypic Coefficient of Variation (PCV) is the resultant of combined action of genotype and environment over a genotype. Genotypic Coefficient of Variation (GCV), a component of total variation reflects the heritable portion. In the present study, experiment carried out at ARS, Shirgaon, the GCV values ranged from 5.82 to 45.67 per cent whereas, PCV values ranged from 5.91 to 46.02 per cent, similarly for experiment carried out at RARS, Karjat during *Kharif*, 2021, the GCV values ranged from 5.95 to 45.64 per cent whereas, PCV values ranged from 6.08 to 46.06 per cent.

As the PCV estimates were slightly higher than the corresponding GCV for the characters studied at both locations, it indicates that the characters were less influenced by the environment. Therefore, phenotypic selection would be effective for the improvement of these traits.

The results were in accordance with finding of Vanisree *et al.* (2013) and Lingaiah *et al.* (2015), Similar findings were reported by Senapati and Kumar (2015) and Bhinda *et al.* (2017) for grain length, Babu *et al.* (2012), Pratap *et al.* (2012), Dhurai *et al.* (2014) and Aravind *et al.* (2019) for decorticated grain length and Subbaiah *et al.* (2011) and Dhurai *et al.* (2014) for length/breadth ratio.

5.1.2 Mean performance:

Study of per se performance of individual genotypes suggests the importance of material under study and it becomes first-hand information for the breeders. The mean of different quantitative characters including grain yield plant⁻¹, suggests that selection of desirable genotypes based on the traits evaluated can be effective.

5.1.3 Interpretation of results obtained for grain yield and important 9 metric traits

Important 9 yield associated metric characters along with grain yield were studied for 95 germplasm in the present investigation. The results obtained for this study are further summarized based on genotypes falling under desirable note for farmer and scientific community and presented in table 5.1 Interpretation of these results is discussed as below.

5.1.3.1 Number of spikelets panicle⁻¹/ (SPP)

Highest number of spikelets panicle⁻¹ were observed for 13 genotypes out of 95 studied *viz.*, Ajaya (300.48), followed by Bela (263.62), MO-6 (206.28), Mahsad (198.61), RTN-214-1-1-1-2 (187.77), IR-64 (185.96), RTN-69-1-1 (182.72), P Sugandha-3 (182.50), BL-184AR (179.30), KJT-3R (178.35), KJT 2 (178.06), Sahyadri 5 R (176.75) and CR-3993-2-24-45-2 (176.67). These 13 genotypes can be included in crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.2 Fertility (%)

Out of 95 germplasm lines studied, 34 were found to have highest fertility i.e. above 90% viz., Ambemohar (93.34), ARC 10550 (96.61), Barmil (91.52), BG 367-2 (90.39), Bhadas-79 (90.13), Bhogwati (90.30), BL-184AR (93.46), Dhanesal (92.59), DRR-86-8 (96.83), FL 478 (96.25), IR-63879-195-2-2-3-2 (94.59), IRRI 192 (98.07), IRRI 193 (95.49), IRRI 193 (95.08), K Shatabdi (91.02), KJT-3R (92.89), Mahsad (90.11), MILYANG 63 (90.73), MO-6 (93.76), MUDGO (93.72), Munga (94.48), P Basmati (93.80), P Sugandha-1 (96.37), P Sugandha-3 (94.14), Pandya (92.75), Patani-6 (92.59), PR-114 (93.40), Ratnagiri 7 (92.18), RP Bio 197 (92.25), RP-BIO-226(91.96), Sahyadri 5 R (97.30), Sugandha (91.09), Valai (93.91) and VDN-9-10-1 (90.44). Thus these 34 genotypes can be included in crop improvement programme since fertility % is positively associated with the yield. Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.3 Grain yield plant⁻¹ (g)/ (GYPP)

Out 95 genotypes, 22 exhibited the highest grain yield plant⁻¹ (g) viz., BG 367-2 (23.57), CR 2713-180 (22.57), CR-3993-2-24-45-2 (21.57), DRR-50-10 (23.33), DRR-50-12 (21.93), DRR-50-13 (22.87), Gurjari (23.07), IR-64 (24.37), Jyoti (22.50), KJT 2 (25.00), KJT-1R (29.00), KJT-2R (21.70), KJT-3R (21.50), MILYANG 63 (21.30), MTU1010 (23.90), NDR6315 (25.27), PR-118 (32.27), PTB 33 (20.43), S Basmati (22.53), S SIVAPPU (22.85), Sahyadri 5 R (24.28) and Sonsali (21.18). These 22 genotypes were found to be highest yielders, hence can be included in the crop improvement programme as donor parents. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.4 Number of panicles plant⁻¹ (Nos.) / (PPP)

Among 95 genotypes studied, 45 showed highest number of panicles plant⁻¹. *viz.*, TN-1 (20.73), S Basmati (15.80), DRR-215 (15.07), Bhadasbhog (14.33), Sugandha (13.87), Kalanamak (13.27), Dhanesal (12.80), PR-118 (12.60), Ambemohar (12.47), DRR-50-13 (12.33), CR2713-180 (11.87), RTN-35-1-1 (11.80), VDN-9-10-1 (11.60), Kothambir Sal (11.53), Bhogwati (11.53), MO-19 (11.50), KJT 1 (11.47), PR-114 (11.40), NAUR-1 (11.20), VDN-10-18 (11.20), P Samruddhi (11.07), IR-64 (11.00), IRRI 192 (11.00), RTN 11-2-1-3 (10.87), IR-63879-195-2-2-3-2 (10.87), P Sugandha-3 (10.87), BG 367-2 (10.87), MILYANG 46 (10.80), PTB 33 (10.80), IRRI 104 (10.80), Mayekar Bhat (10.76), KJT-1R (10.73), Sahyadri 5 R (10.73), IRRI 190 (10.73), DRR-86-8 (10.67), RS-1113 (10.67), MO-6 (10.65), Munga (10.63), Chinoor (10.60), K Shatabdi (10.60), KJT 2 (10.60), BL-184AR (10.53), P Basmati (10.53), MUT NS 1 (10.53) and R HEENATI (10.53), thus these 45 genotypes can be used donor parent in crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.3.5 Panicle length of main axis (cm) / (PLMA)

Among all 95 germplasm lines studied, only 12 genotypes showed longest panicle length of main axis *viz.*, NDR6315 (35.67), PR-118 (32.60), Kochari (32.47), DRR-215 (32.33), CR2713-180 (31.60), Ambemohar (31.13), KJT-1R (30.80), Try-1 (30.73), Bhadasbhog (30.73), MUT NS 1 (30.27), DRR-50-13 (30.13). Panicle length positively correlated with yield, thus these 12 genotypes must be used as donor parent for crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.3.6 Stem length excluding panicle (cm) / (SLEP)

Out 95 genotypes, 62 exhibited lowest stem length i.e. below 110 cm and hence these 62 genotypes were found to be of dwarf and semi-dwarf stature, which is a climate smart growth habit. Such genotypes are lodging resistant and fertilizer responsive. Thus these genotypes should be incorporated in crop ideotype and crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.7 Zinc content ppm / (Zn)

Out 95 genotypes, only 4 genotypes *viz.*, PTB 33 (22.62), IRRI 123 (21.40), DRR-50-12 (20.70) and Ambemohar (20.08) exhibited zinc content around national standard i. e. 24 ppm, hence these 4 genotypes are desirable to include in development of bio- fortified varieties. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.1.3.8 Iron content ppm / (Fe)

Out of 95, 76 genotypes exhibited highest Fe content i.e. above 10% which is around national standard of 10%. Hence these 76 genotypes should be included in crop improvement for development of bio-fortified varieties. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.3.9 Calcium content (ppm) / (Ca)

Out of 95 genotypes, the 10 genotypes showed highest calcium content *viz.*, Bhogwati (102.00), BG 367-2 (101.33), RTN-214-1-1-1-2 (92.57), Ambemohar (87.67), RTN-27-1-1-2 (84.23), MILYANG 46 (84.00), VDN-9-10-1 (83.57), RS-1113 (83.33), KJT 2 (82.00) and IR-64 (80.67). Thus these 10 genotypes will better serves as donor parent for development of bio-fortified varieties.

This finding was also confirmed by Sanyal and Joshi (2016). Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.3.10 Amylose content / (AC)

Out of 95 genotypes studied, 33 genotypes showed medium (20-25%) amylose content *viz.*, Chinoor, P Sugandha-4, Karhad, Bhadas-79, TN-1, KJT 1, P Basmati, Bhogwati, Ratnagiri 7, Kothambir Sal, KJT-1R, Patani-6, P Sugandha-5, Kala Rata, IRRI 192, DRR-215, Valai, S Basmati, CR-3993-2-24-45-2, PTB 33, RTN-69-1-1, P Sugandha-1, IRRI 190, R. HEENATI , RTN 11-2-1-3, DRR-50-12, MO-13, BL-184AR, Sahyadri 5 R, Gurjari, MO-6, S SIVAPPU, and PR-114 This medium range of amylose content is desirable as grains on cooking become soft yet separated and widely preferred by consumers. Hence these 33 genotypes will better serves as donor parent for crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.4 Genotypic and phenotypic variances:

It is well known that variability in the biological population is an outcome of genetic constitution of individuals present in that population and its interaction in the prevailing environment. In the present investigation, the phenotypic variance was higher than corresponding genotypic variances for all the characters studied at both the locations, but the difference between genotypic and phenotypic variance was quite low, indicating that variability assessed is mainly due to stable performance of the genotypes over environments.

5.1.5 Genotypic and phenotypic coefficient of variation:

Phenotypic coefficient of variation was found to be higher than their corresponding genotypic coefficient variation for all the traits under study at both the locations. The relative difference between phenotypic coefficient of variation and genotypic coefficient of variation was narrow for all the 27 characters evaluated, suggesting that these traits were less influenced by environmental effect. Hence selection for these traits may be effective based on their phenotypic values.

For ARS, Shirgaon location, High GCV and PCV values were observed for the traits viz., zinc content, plant height, stem length excluding panicle, number of spikelets panicle per panicle, grain width, decorticated grain breath, L/B ratio, amylose content, iron content, calcium content and grain yield plant-indicating that large amount of variation is present among the genotypes, whereas for RARS, Karjat location, High GCV and PCV values were observed for the traits viz., zinc content, plant height, stem length excluding panicle, number of spikelets per panicle, weight of 1000 grains, grain yield plant⁻¹, straw yield plant⁻¹, leaf length, L/B ratio, amylose content, iron content, calcium content and grain yield plant⁻¹ indicating that large amount of variation is present among the genotypes. Similar results were obtained by for panicle number per plant, Gangashetty *et al.* (2013) and Veni *et al.* (2013) for No. of spikelets panicle per panicle, and Gangashetty *et al.* (2013), Veni *et al.* (2013), Dhurai *et al.* (2014), Gyawali *et al.* (2018), Chuchert *et al.* (2018) and Arvind *et al.* (2019) and Bhargavi *et al.* (2022) for grain yield plant⁻¹.

5.1.6 Heritability and genetic advance:

Heritability measures the transmission of character from one generation to next generation. Heritability also separates the portion of environmental variability from phenotypic variability, so

utilizing in making effective selection. Thus, presence of higher magnitude of genetic variability along with the degree to which it is transmitted from one generation to another is equally important for effective selection. (Burton and Devane, 1953).

Johnson *et al.* (1955) suggested that heritability and the genetic advance when calculated together would prove more useful in predicting the resultant effect of selection based on phenotypic expression. He further emphasized that without genetic advance; the estimates of heritability will not be of practical value and suggested the concurrent use of genetic advance along with heritability. High heritability alone is not enough to make sufficient improvement through selection in genetic advance generations. High heritability was obtained all the characters except alkali spreading value for both the locations indicating that these characters were least influenced by environmental effect and selection may be effective. Similar results were found in the results of Sarangi *et al.* (2009), Arvind *et al.*, (2019) and Bhargavi *et al.* (2022).

5.1.7 Genetic advance as percent of mean:

Genetic advance is a measure of genetic gain under selection. The success of genetic advance under selection depends on heritability of the character under consideration. This indicates that though the character is less influenced by environmental effects, the selection for improvement of such trait may not be useful because, heritability is based on total genetic variance which includes fixable (additive) and non-fixable (dominance and epistatic) variance. For ARS, Shirgaon location, the genetic advance as per cent of mean was high for the characters *viz.*, plant height, stem length excluding panicle, number of spikelets per panicle and

calcium content. On the other hand, moderate genetic advance as per cent of mean was noted for days to 50% flowering, fertility %, days to maturity, straw yield per plant, leaf length and zinc content. Rest of the seventeen characters showed low genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean was observed for the traits viz., plant height, stem length excluding panicle length and calcium content, which suggests that these characters are subjected to any selection scheme for exploiting fixable genetic variance will be highly effective. Whereas for location RARS, Karjat. The genetic advance as per cent of mean was high for the characters viz., plant height, stem length excluding panicle, number of spikelets per panicle, leaf length and calcium content. On the other hand, moderate genetic advance as per cent of mean was noted for days to 50% flowering, fertility %, days to maturity, straw yield per plant and zinc content. Rest of the seventeen characters showed low genetic advance as per cent of mean. High heritability coupled with high genetic advance as per cent of mean was reported for plant height, stem length excluding panicle, number of spikelets panicle⁻¹, leaf length and calcium implying that these characters were under control of additive gene action and direct selection of these traits would be effective for crop improvement. Similar reports were published by Shanthi and Singh (2001), Babu *et al.* (2012), Aditya and Bhartiya (2013) and Dhurai *et al.* (2015) for straw yield/ grain yield ratio. Dhurai *et al.* (2015) and Islam *et al.* (2015) for days to maturity, Islam *et al.* (2015) and Bindha *et al.* (2017) for grain length, Abebe *et al.* (2017), Singh and Verma (2018) and Ranjith *et al.* (2018) for 50% flowering, Singh and Verma (2018) for fertility (%) and Bhargavi *et al.* (2022).

5.1.8 Genetic diversity:

Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization program. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 95 rice genotypes and to identify the diverse genotypes for future utilization breeding program.

In the present investigation for the experiment conducted at ARS, Shiragon, the genotypes were grouped into 22 clusters on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance. Cluster I comprised of maximum number of genotypes (57) followed by cluster IV with 32 genotypes. Remaining clusters constitutes of each one genotype only. Whereas for the experiment carried out at RARS, Karjat, the genotypes were grouped into 20 clusters on the basis of D^2 matrix which was based on D^2 values and Ward minimum variance Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters constitute of each one genotype only. The genotypes present in different clusters showed high degree of diversity than the genotypes present in the same cluster. The genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters

For location I (Shirgaon) intra cluster D^2 values ranged from 0.00 (all clusters except cluster I and IV) to 723.08 (IV). Maximum intra cluster distance was observed in cluster IV (723.08) followed

by cluster I (587.10). The inter-cluster D^2 values ranged from 147.10 (cluster II and III) to 3111.77 (clusters XIX and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIX and XX (3111.77), followed by cluster XVIII and XX (3076.24), cluster XX and XXI (3018.86), cluster XXI and XXII (2771.82), cluster X and cluster XXII (2405.44), cluster XIII and XX (2344.39). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.10. Cluster I comprises 57 genotypes. It was nearest to cluster VIII (766.88) indicating genotypes are closely related and was farthest from the cluster XXII (1624.67) implying these genotypes more diversely related conferring intermitting within these genotypes would be useful for crop improvement.

For location II (Karjat), intra cluster D^2 values ranged from 0.00 (all clusters except cluster I, V and X) to 607.76 (cluster X). Maximum intra cluster distance was observed in cluster X (723.05) followed by cluster V (481.62) and cluster I (437.13). The inter-cluster D^2 values ranged from 232.11 (cluster IX and XI) to 2259.27 (clusters XIV and XX) indicating high diversity among the genotypes of these clusters. The highest inter cluster distance was observed between cluster XIV and XX (2259.27), followed by cluster VII and XX (1830.75), cluster XI and XIV (1730.06), cluster III and XX (1730.06), cluster XVIII and cluster XX (1665.85), cluster IV and XIX (1557.16). The nearest and the farthest cluster from each cluster based on D^2 values were given in Table 4.10. Cluster I comprises 58 genotypes. It was nearest to cluster IV (552.11) indicating genotypes are closely related and was farthest from the cluster XX (1407.01) implying these genotypes more diversely related conferring intermitting within these genotypes would be useful for crop improvement.

Similar divergence estimation based on D^2 distances was done by Shivani *et al.* (2018), Kumari *et al.* (2018), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022)

5.1.8.1 Cluster mean analysis:

Cluster means with respect to 27 characters and 95 genotypes was evaluated with help D^2 values for the both the locations. A critical appraisal of the observations indicated that none of the clusters contained genotypes with all the desirable traits which could be directly selected and utilized. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The promising landraces from these clusters with high mean values for different traits may be directly used for adaptation or may be used as parents in future hybridization, depending upon the objective of the breeding programme to derive superior transgressive segregants.

5.1.8.2 Per cent contribution of character towards total genetic diversity:

The selection and choice of parents mainly depend upon contribution of characters towards divergence (Dey *et al.*, 2009).

The utility of D^2 statistics as a potential tool to quantify the extent of divergence in biological populations at genetic level is further enhanced by its applicability to estimate the relative contribution of the various plant characters to total genetic divergence.

For ARS, Shirgaon location, out of the 27 characters studied, 13 characters namely leaf length, calcium content, number of panicles plant⁻¹, fertility %, zinc content, iron content, number of

spikelets panicle⁻¹, plant height, days to 50% flowering, grain width, amylose content, straw yield plant⁻¹ and grain yield plant⁻¹ together contributed maximum (92.69%) to the total genetic divergence. Whereas for RARS, Karjat location out of the 27 characters studied, 11 characters namely leaf length, calcium content, fertility, decorticated grain length, zinc content, iron content, number of spikelets panicle⁻¹, plant height, amylose content, days to 50% flowering and grain yield plant⁻¹ together contributed maximum (98.99%) to the total genetic divergence. Thus, it is suggested that these traits should be given importance in further breeding programmes i.e., during hybridization and selection of segregating populations, using this particular set of landraces, so far not utilized in breeding programmes, which have potential for use in future rice improvement programmes aiming at the development of rice varieties or hybrids with high yield and better grain quality. These findings were in accordance with the finding of Guru *et al.*, (2017), Shivani *et al.* (2018), Kumari *et al.* (2018), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.2 Genetic diversity

Molecular markers have played an increasing role in rice breeding and genetics. Of the different types of molecular markers, microsatellites have been utilized most extensively, because they can be readily amplified by PCR and the large amount of allelic variation at each locus. Microsatellites are also known as Simple Sequence Repeats (SSR), and they are typically composed of 1–6 nucleotide repeats. These markers are abundant, distributed throughout the genome and are highly polymorphic compared with other genetic markers, as well as being species-specific and co-dominant. For these reasons, they have become increasingly important genetic markers in rice breeding programs Gous Miah *et al.* (2013), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.2.1 Polymorphism percentage:

The overall size of amplified products ranged from 132 bp to 884 bp. A total of 139 alleles were obtained using 17 SSR primer pairs with an average of 8.17 alleles per primer. The all 17 SSR primers used in the study were highly polymorphic and distributed throughout the genome of rice. The number of alleles amplified for each primer pair ranged from 3 to 14. The numbers of alleles detected in the present study are also consistent with the earlier reports of (Abdullah *et al.*, 2021) which revealed up to 82 alleles for 7 microsatellite markers across 28 varieties. Earlier (Paul *et al.*, 2022) observed an allelic range of 1-8 with an average of 3.7 alleles per primers.

5.2.2 Polymorphic Information Content (PIC):

The lowest PIC value was 0.70 with RM 7 and highest PIC value was 0.92 with RM 8225 and average PIC value recorded was 0.83. The higher the PIC value, the more informative is the SSR marker. Hence, primers RM 825, RM 1287, pTA-248, RM 201, RM 122 and RM 22709 were found to be highly informative. The current PIC value is higher than the previous reports of (Miah *et al.*, 2021). The high PIC value obtained in the present investigation might be due to high genetic diversity among the rice varieties. The PIC values are usually dependent on the genetic diversity of the accessions chosen (Tang *et al.*, 2022) for the specific study. Markers with PIC values of 0.5 or higher are highly informative for genetic studies and are extremely useful in distinguishing the polymorphism rate of a marker at a specific locus (Jain *et al.*, 2021) and (Hoque *et al.*, 2021). The Polymorphism information content (PIC) values shown by some of the SSRs in the present investigation were found to be higher than the previously reported (Singha *et al.* 2021).

5.2.3 Genetic distance:

The diversity observed in the Ninety five rice genotypes mainly attributed to the genetic dissimilarities. The pair wise similarity values ranged from 0.027 to 0.994. However, genetic diversity detected using molecular markers in the present investigation indicates the high discrimination capacity of SSR markers. This is of major importance for solving the problems concerning the breeding to obtain the heterosis. Similar findings were reported by (Seetharam *et al.* 2019), (Embate *et al.* 2021) and (Rohmawati *et al.* 2021)

5.2.4 Cluster analysis and Dendrogram construction:

The UPGMA based dendrogram of 95 rice genotypes generated with Multivariate Statistical Package (MVSP) revealed that, there are two major clusters. The first major cluster consists of four sub clusters. Two rice genotypes CR-3993-2-24-45-2 and HRTMS-61 formed the independent first sub cluster (IAa). Second sub cluster (IAb) consists of ten genotypes. Third sub cluster (IBa) consists of seven genotypes. Fourth sub cluster (IBb) consists of four genotypes.

The second major cluster consists of four sub clusters. First sub cluster (IIAa) consist of five rice genotypes. Second sub cluster (IIAb) consist of three rice genotypes. Third sub cluster (IIBa) consist of fourteen rice genotypes. Third sub cluster (IIBb) consist of fifty rice genotypes.

This shows the potentiality of SSR markers for the characterization of germplasm accessions.

From these studies, it is revealed that, rice varieties are more divergent indicating that large part of the genome may be

dissimilar among themselves. However, genetic diversity detected using molecular markers in the present investigation indicates the high discrimination capacity of SSR markers. This is of major importance for solving the problems concerning the breeding to obtain the heterosis. (Chuang *et al.*, 2011) and (Liu *et al.*, 2022) reported similar findings.

Because of the poly-allelic nature of SSR markers, they have the advantage of discriminating the individuals more precisely. The SSR marker gave more clusters with fewer genotypes in each cluster and therefore, more variation within each cluster. Similar pattern of population variance was also reported by (Jasim *et al.*, 2019), (Yogi *et al.*, 2020) and (Naaz *et al.*, 2022).

5.2.5. Resistance against biotic and abiotic stresses:

Out of 95 genotypes Try-1, Kochari, Lal Patani, Karhad, Ratnagiri 7, Phule Samruddhi, Ambemohar, Rathu Heenati, Sinna Sivappu, IRRI 190, IRRI 193, ARC10550, Samba Mahsuri, IRRI 123 shown the gene linked with blast resistance is present when amplified with RM 8225 marker.(Gentallan *et al.*, 2021) and (Chakrobarty *et al.*, 2022) also used microsatellite markers to screen the various genotypes for blast resistance.

Salt resistance gene was present in MO-17, MO-19, KJT-2R, RTN 11-2-1-3, Pak Basmati, Super Basmati, Chinoor, Pusa Sugandha-1, Pusa Sugandha-3, Pusa Sugandha-4, Bhogwati, RP Bio 197, RP-BIO-226, Ajaya, Karjat 1. Molecular mapping of genes linked to salt tolerance traits was also carried out by (Krishnendu *et al.*, 2021) and (Li *et al.*, 2022). The gene linked with BPH resistance be present in Pusa Sugandha-4, Pusa Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, Phule Samruddhi, Kala Rata, Try-1, Kochari, BG 367-2, FL 478, MUT NS

1, RATHu Heenati and Sinna Sivappu. Similar results also found by (Li-Hang *et al.*, 2020) and (McClung *et al.*, 2022) where they used different microsatellite markers to screen the rice populations for BPH resistance.

BG 367-2, Milyang 63, FL 478, MUT NS 1, IRRI 192 having gene resistance to drought similarly (Gregorio *et al.*, 2020) and (Mateu-Andres *et al.*, 2022) also used different microsatellite markers to screen the rice populations for drought tolerance.

5.3 Interpretation of results obtained for 62 DUS descriptors

62 DUS descriptors were studied for 95 germplasm in the present investigation. The results obtained for this study are further summarized based on genotypes falling under desirable note for farmer and scientific community and presented in table 5.1. Interpretation of these results is discussed as below.

5.3.1 Coleoptile: Colour (CC)

Coleoptiles are cylindrical organs that en-sheath the first leaf and shoot apex in grass seedlings. Coleoptile functions like a 'snorkel'; the elongated. They help in the emergence of the first leaf (and shoot apex) by protecting it during its passage through the soil. On emergence, the first leaf breaks through the coleoptile tip. (Kordan, 1974). Desirable note for this trait is that variation in colour observed. Among 95 genotypes studied, green (1), purple (9) and remaining 85 were found be white. As polymorphic variation was observed, this trait can be considered as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.3.2 Basal leaf: Sheath colour (BL-SC)

It is an elongated, cylindrical structure that encloses younger parts of the shoot. Its major function is to protect younger shoots

inside of it and to support the whole plant, which explains why there are very few chloroplasts found in the sheath mesophyll. (N Guo *et al.*, 2020). Desirable note for this trait is that polymorphic variation observed in colour i.e. out of 95 germplasm lines studied 82 were found be green followed by light purple(9), purple lines (1), uniform purple (3). Hence this descriptor can serves as morphological marker to distinguish diverse germplasm. Similar results were reported by Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022)

5.3.3 Leaf: Intensity of green colour (L-IGC)

The leaves grow alternately on the stem, with one leaf per node. The leaves are the growth engine of the plant, as they capture solar radiation and produce carbohydrates. The plant breathes and perspires through its leaves. Scale of green coloration serves as the index of nitrogen status of the crop (Giha *et al.*, 2021).Intensity of green colouration is directly correlated with nitrogen uptake and photosynthetic efficiency of plant. Out 95 genotypes, 30 exhibited the dark intensity for green colour of leaf, these 30 genotypes Pandya, KJT-3R, KJT-4R, PR-118, NAUR-1, Gurjari, DRR-363-5, VDN-9-10-1, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, S Basmati, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-5,CR2713-180, Indrayani, Sugandha, RS-1113, RP Bio 197, KJT 1, MUDGO, MILYANG 46,P TB 33, BG 367-2, MILYANG 63, MUT NS 1, Sonsali and TN-1 which photo-synthetically more efficient and thus can be included in crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.4 Leaf: Anthocyanin colouration (L-AC)

Anthocyanin's, a major subclass of flavonoids, are the main secondary metabolites that give color to rice tissues.

Anthocyanin accumulation in plants has diverse functions; including resisting UV radiation, participating in hormone regulation, and responding to biotic and abiotic stress, and are beneficial to human health. (Xia *et al.*, 2021). Presence of anthocyanin colouration is desirable as it acts as morphological mechanism (non-preference by insect-pests) of defense against insect-pests attack. Among 95 genotypes studied, only 3 showed positive note for this descriptor *viz.*, Mahsad, Waksal-207 and Barmil and thus, these genotypes can be best served as potential donor parent for insect-pest resistance breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.4.5 Leaf: Distribution of anthocyanin colouration (L-DAC)

Anthocyanin accumulates in many plant tissues or organs, in rice for example leading to red, purple red and purple phenotypes for protection from damage by biotic and abiotic stresses and for reproduction. Uniformly distributed Purple pigmentation leaves are common in wild rice and landraces and occasionally found in modern cultivars. (Han-shiuan *et al.*, 2020). Among all 95 germplasm lines studied, only 1 genotype (Waksal-207) showed presence for this trait and hence can be used in abiotic stress resistance breeding programme in future. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.4.6 Leaf Sheath: anthocyanin colouration (LS-AC)

Leaf sheath is an elongated, cylindrical structure that encloses younger parts of the shoot. Its major function is to protect younger shoots inside of it and to support the whole plant. (Davis, 2020). Accumulation of anthocyanin pigmentation on basal leaf

sheath in rice highlights the phenotypic defense mechanism against biotic stresses. (E Mackon *et al.*, 2021). Out 95 genotype only 14 exhibited presence of this trait. Hence these 14 genotypes Mahsad, Waksal-207, Barmil, Patani-6, Pandya, Dular, Try-1, Kochari, Bela, Valai, Gurjari, Dhanesal, RP-BIO-226 and IRRI 190 are desirable to include in crop improvement for biotic resistance breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.7 Leaf sheath: Intensity of anthocyanin colouration (LS-IAC)

Darker intensity of anthocyanin pigmentation on leaf sheath indicates more the phenotype is repellent against pests attack (Yamuangmorn *et al.*, 2021). Out 95 genotypes, only 2 genotypes (Dhanesal and IRRI 190) exhibited strong intensity of anthocyanin colouration and other 2 (Try-1 and Bela) showed very strong intensity, hence these 4 genotypes desirable to include in crop improvement for pests resistance breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.4.8 Leaf: Pubescence of Blade Surface (L-PBS)

Pubescence is characterized by tri-chomes gathering on the plant surface, consisting of unicellular or multicellular exogenous substances on leaves, stems, and root surfaces. Pubescence may be related to the development of glandular cells and thus are called glandular hairs. Glandular hairs can accumulate and secrete alkaloids such as nicotine and terpenoids as well as some chemical substances against injurious insect. The hairy surface serves as morphological barrier against sucking pests. (Zeng *et al.*, 2019.) Many plants have pubescence designed to provide a tiny bit of shade to reduce the temperature of the leaves and stems and

protect the leaves from losing too much water from transpiration (Hamaoka *et al.*, 2017). Stronger the pubescence, more the phenotype is non-preferred by sucking pests. As well as stronger pubescence prevent water loss from leaves during transpiration. Out of 95, 27 genotypes exhibited strong pubescence *viz.*, Barmil, Jyoti, Dodak, Karhad, KJT-1R, KJT-3R, PR-114, DRR-215, IR-63879-195-2-2-3-2, RTN-27-1-1-2, Sahyadri 5 R, S Basmati, Chinoor, P Sugandha-4, Bhadasbhog, Sugandha, RS-1113, RP-BIO-226, Ajaya, KJT 1, IR-64, MILYANG 46, PTB 33, MILYANG630, FL 478, S MAHSURI, IRRI 104 and other 6 i.e P Sugandha-1, P Sugandha-3, Kalanamak, KJT 2, SINNA SIVAPPU, IRRI 190 showed very strong note. Hence these 33 genotypes should be included in crop improvement for biotic and abiotic stress breeding as a donor parents. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.9 Leaf: Auricles (L-A)

Auricles are pair of hairy, sickle-shaped appendages located in the junction of the collar and the sheath. The auricles are located at the lower end of the leaf-blade, where it meets the leaf-sheath. They may be extended as a pair of claw-like projections. It keeps the leaf sheath and culm together (Lee *et al.*, 2022). Presence of auricle is desirable which serves as binding agent for leaf sheath and culm. All the 95 genotypes studied showed presence of auricles hence all these genotypes can be used in crop ideotype breeding programme. This finding was also confirmed by Sanyal and Joshi (2016). Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.4.10 Leaf: Anthocyanin colouration of auricles (L-ACA)

Anthocyanins are a group of poly-phenolic pigments that are ubiquitously found in the leaf of rice. In rice, anthocyanin's played a role not only in reproduction, by attracting pollinators and seed dispersers, but also in protection against various abiotic and biotic stresses. (Ying *et al.*, 2018). Dark colouration such as purple is of desirable note as it works as shield against various biotic stresses. Out of 95 genotypes studied, 7 genotypes *viz.*, Barmil, Patani-6, Pandya, Valai, Gurjari, PTB 33 and IRRI 190 showed purple anthocyanin colouration on the leaves, thus these 7 germplasm can be included development of insect-pests resistant lines as a donor parent. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.4.11 Leaf: Collar (L-C)

It is a white band at the junction of the blade and sheath. All the 95 genotypes were found to be positive for this trait and can be incorporated in crop ideotype breeding programme. This result was in agreement with the findings of Kumar *et al.* (2018), Gour *et al.* (2019), Bharagvi *et al.* (2022) and Lavanya *et al.* (2021).

5.4.12 Leaf: Anthocyanin colouration of collar (L-ACC)

Presence of this trait is of desirable note as it works as shield against various biotic stresses. Out of 95 genotypes studied, only 5 lines *viz.*, Barmil, Patani-6, Pandya, Gurjari, IRRI 190 showed presence of anthocyanin colouration on the leaf collar, thus these 5 germplasm lines can be included development of insect-pests resistant lines as a donor parent. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.13 Leaf: Ligule (L-L)

It is a triangular, papery scale located inside the blade, it looks like a continuation of the sheath. It protects the culm and leaves that it encloses from the entry of water, dust and harmful spores (Davis *et al.*, 2020). Presence of this trait is of desirable note as it works as filter to avoid the entry of water, dust and harmful spores in culm. All the 95 genotypes were found to be positive for this trait and can be incorporated in crop ideotype breeding programme. Similar findings were reported by Sanyal and Joshi (2016), Kumar *et al.* (2018), Gour *et al.* (2019), Lavanya *et al.* (2021) and Bhargavi *et al.* (2022).

5.1.14 Leaf: Shape of ligule (L-SL)

Different shapes serves as morphological markers. Though all the 95 genotypes found to have split shape of ligule, shape of ligule can be used to distinguish diverse germplasm and serves as morphological marker. Similar results were reported by Kumar *et al.* (2018), Gour *et al.* (2019), Lavanya *et al.* (2021) and Bhargavi *et al.* (2022)

5.1.15 Leaf: Colour of ligule (L-CL)

Dark colouration such as purple is of desirable note as it works as shield against various biotic stresses. Out of 95 only one genotype (Dhanesal) showed light purple coloration of ligule, thus this genotype can be used as donor parent in biotic stress tolerance breeding programme. These results were in accordance with Komala *et al.* (2017), Kumar *et al.* (2018), Gour *et al.* (2019), Lavanya *et al.* (2021), Bhargavi *et al.* (2022), and Kushwah *et al.* (2022).

5.1.16 Leaf: Length of blade (L-LB)

It is measured from the tip of the entire leaf down to the base of the lowest leaflets where they meet the leaf stem for the leaf

length. The photosynthetic energy storage and normal life function of rice are directly affected by the leaf. Meanwhile, leaf size is an important part of ideal rice plant type, as well as an important character of rice yield formation (McDonald *et al.*, 2020). Longer leaf length directly correlated with higher photosynthetic efficiency. Out of 95 only 55 genotypes showed long leaf length thus these genotypes can be used as donor parents in crop ideotype breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.17 Leaf: Width of blade (L-WB)

Leaf width corresponds to the longest extension of any two points on the blade edge perpendicular to the leaf length axis, that is the axes connecting leaf apex and base (Shi *et al.*, 2019a). Prior research has found that leaf width not only affects the morphogenesis of leaves, but serves as a primary role in the regulation of grain and panicle traits and more efficient photosynthesis (Fu, 2019). Longer leaf width directly correlated with higher photosynthetic efficiency. Out of 95 only 69 genotypes showed medium leaf width thus these genotype can be used as donor parent in crop ideotype breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.18 Culm: Attitude (for floating rice only) C-A (FR)

This descriptor is not applicable, as none of the genotypes are floating rice under study.

5.1.19 Culm: attitude (C-A)

The jointed stem of rice, called a culm, is made up of a series of nodes and internodes. The node (nodal region) bears a leaf and a

bud. The main role of culm is to support rice plant and helps to transport minerals and water absorbed by roots to upper parts. (Davis *et al.*, 2020). Culm attitude is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for culm attitude. Out of 95, 84 genotypes showed erect culm attitude while 11 had semi-erect culm attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.20 Time of heading (50% of plants with panicles) (TH)

Days to 50% flowering was determined by recording the number of days following transplanting (DAT) until 50% of plants in a plot had at least one open flower. Time for heading to 50% flowering indicates the duration of the genotype for maturity and adaptability for different ecosystems. (Anputhas *et al.*, 2021). Out of 95 genotypes 42 were early indicated their adaptability for upland ecosystem, while 52 showed mid-late duration which are adaptable for midland and rest 1 found be of late duration which is adaptable for lowland. Similar results were reported by Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Arvind *et al.* (2019), Bharagvi *et al.* (2022), Lavanya *et al.* (2021) and Kushwah *et al.* (2022).

5.1.21 Flag leaf: Attitude of blade (early observation) FL-AB (EO)

The flag leaf is the top leaf on a rice stem, closest to the grain-producing panicle. Flag leaves have a major role in providing energy to the developing grain, and any impact on photosynthesis

in the flag leaf can have a dramatic effect on grain productivity.(Davis *et. al.*, 2020). It is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for flag leaf attitude. Out of 95, 79 genotypes showed erect attitude while 14 had semi-erect attitude and rest 1 showed horizontal attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.1.22 Spikelet: Density of pubescence of lemma (S-DBL)

Spikelets are the basic inflorescence units in rice and typically consist of a flower of interlocked lemma and palea forming a husk, two lodicules, six stamens, and one pistil. In rice, the spikelet meristem develops a pair of rudimentary glumes and then produces two lateral floral meristems and one terminal floral meristem. The two lateral floral meristems form one pair of sterile lemmas (degraded lateral florets), and the terminal floral meristem develops one fertile terminal floret (Fu *et. al.*, 2019). Pubescence plays an important role in insect resistance, drought tolerance, and other stresses. Out of 95 genotypes studied 37 *viz.*, MO-19, Mayekar Bhat, Waksal-207, Patani-6, Kochari, Lal Patani, Dodak, Karhad, Valai, PR-114, BL-184AR, Gurjari, DRR-86-8, IR-63879-195-2-2-3-2, RTN-35-1-1, Chinoor, P Sugandha-4, Kalanamak, P Samruddhi, Indrayani, Dhanesal, RS-1113, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali and TN-1 had shown very strong pubescent lemma. Thus these genotypes can be included in biotic stress resistance breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.23 Male sterility (MS)

Male sterility is defined as the failure of plants to produce functional anthers, pollen, or male gametes. The use of male sterility reduces the cost of hybrid seed production for several reasons. It avoids hand emasculation and pollination, accelerating the hybrid breeding programs and allowing the large-scale production of hybrid seeds and the commercial exploitation of hybrid vigour (Laura *et al.*, 2020). For commercial cultivation, absence of male sterility is desirable. All 95 genotypes showed absence of male sterility. Thus all are desirable for commercial cultivation and can be included in crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.24 Lemma: Anthocyanin colouration of keel (L-ACK)

The lemma has a constricted structure at its end called the keel. Presence of this trait is of desirable note as it works as shield against various biotic stresses. Out of 95 genotypes studied, 3 showed very strong anthocyanin colouration on the keel, thus these 3 germplasm (NDR6315, Dhanesal and Ambemohar) can be included development of insect-pests resistant lines as a donor parent. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.25 Lemma: Anthocyanin colouration of area below apex (L-ACABA)

The anthocyanin biosynthesis attracts strong interest due to the potential antioxidant value and as an important morphological marker (Khan *et al.*, 2020). Out of 95 genotypes studied, 4

(Bhadasbhog, NDR6315, Dhanesal and Ambemohar) showed very strong anthocyanin colouration area below apex. Thus these 4 germplasm can be included development of insect-pests resistant lines as a donor parent. As well as this trait can be used morphological marker to distinguish the germplasm. Sanyal and Joshi (2016), Kumar *et al.* (2018), Manjunatha *et al.* (2018), Gour *et al.* (2019) Bharagvi *et al.* (2022), Lavanya *et al.* (2021) and Kushwah *et al.* (2022) have also reported the similar results pertaining to this trait.

5.1.26 Lemma: Anthocyanin colouration of apex (L-ACA)

The anthocyanin biosynthesis attracts strong interest due to the potential antioxidant value and as an important morphological marker (Khan *et al.*, 2020). Out of 95 genotypes studied, 4 (Kala Rata, Bhadasbhog, NDR6315, Dhanesal and Ambemohar) showed very strong anthocyanin colouration area below apex. Thus these 4 germplasm can be included development of insect-pests resistant lines as a donor parent. As well as this trait can be used morphological marker to distinguish the germplasm. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.27 Spikelet: Colour of stigma (S-CS)

In rice, the pistil is the female reproductive organ, and it consists of two stigmas and an ovary. The stigma is capable of receiving pollen grains and guiding pollen tube growth. Furthermore, the stigma color is often regarded as an important trait in variety identification in some crop plants such as rice (Han *et al.*, 2018). Out of 95, 84 genotypes showed white stigma, while rest 11 had purple stigma. Thus this trait can be used as morphological marker to distinguish the germplasm. Lavanya *et al.*

(2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.28 Stem: Thickness (ST)

The stem of rice popularly known as the haulm or the culm, is generally erect, cylindrical, hollow at the internodes and solid at the nodes. The number and length of internodes vary with the different varieties. The stem's main function is to transport water and nutrients and to bring air to the roots. (Davis *et. al.*, 2020).

Thicker stems are preferred as such stems gives support to plants while lodging. All 95 genotype showed thick stem habit. Thus all genotype can be used as donor parent in crop ideotype breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.29 Stem: Length (excluding panicle; excluding floating rice) (S- L (FR))

The lower internodes are shorter than the upper ones. The shorter the lower internodes, the more resistant the plant will be to lodging. Each node has one leaf and one bud that can develop into a tiller. Shorter stem length *viz.*, dwarf and semi- dwarf stature of plant is preferred as these are climate smart structure and they have lodging resistance and are responsive to fertilizers. Stem length in the range of 70-110 cm is considered to be of dwarf to semi-dwarf stature. Out of 95, 46 genotypes were very short and 20 showed short plant type thus these genotypes can be used as donor parent in crop ideotype breeding programme. These results were in accordance with Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Aravind *et al.* (2019), Lavanya *et al.* (2021), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.1.30 Stem: Anthocyanin colouration of nodes (S-CAN)

Accumulation of anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses (*Mackon et al.*, 2021). Out of 95, only 4 (Lal Patani, Gurjari, DRR-86-8, HRTMS-61) genotypes showed presence of anthocyanin colouration of nodes. Thus these genotypes can be included in biotic stress resistance breeding programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.31 Stem: Intensity of anthocyanin coloration of nodes (S-IACN)

Stronger the presence anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (*Mackon et al.*, 2021). Out of 95, only one (Gurjari) genotype showed medium scale intensity of anthocyanin colouration of nodes. Thus this genotype can be included in biotic stress resistance breeding as donor parent. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.32 Stem: Anthocyanin colouration of internodes (S-ACI)

Accumulation of anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (*Mackon et al.*, 2021). Out of 95, only 2 genotypes (Mahsad and Bela) showed presence of anthocyanin colouration of inter nodes. Thus these genotypes can be included in biotic stress resistance breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.33 Panicle: Length of main axis (P-LMA)

Panicles form the rice inflorescence. It is the top part of the rice plant, carried on the last inter-node. Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets. Schematic representation of a rice panicle comprising a main central axis named rachis, to which primary branches are attached; the primary branches bear secondary branches, which in turn bear tertiary branches. Spikelets are attached to the branches by a peduncle. (Antonio *et al.*, 2021). Longer panicles indicated more number of grains and thus length of main axis is directly correlated to the yield. Out of 95, 10 genotypes *viz.*, Try-1, Kochari, KJT-1R, PR-118, DRR-215, DRR-50-13, CR2713-180, NDR6315, Ambemohar and MUT NS-1 showed very long panicles and other 63 *viz.*, MO-6, MO-13, Kala Rata, Barmil, Jyoti, Patani-6, Bhadas-79, Pandya, Lal Patani, Dodak, Bela, Valai, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN 11-2-1-3, RTN-69-1-1, NAUR-1, BL-184AR, DRR-50-12, DRR-363-5, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, Sahyadri-5R, CR-3993-2-24-45-2, P Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, Kalanamak, P Samruddhi, Indrayani, Dhanesal, KShatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, Sonsali had long panicle. Thus these genotypes can be directly released for commercial cultivation or can be used in crop improvement as donor parent. Similar results pertaining to this trait were reported by Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018) and Aravind *et*

al. (2019). Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.34 Flag leaf: Attitude of blade (late observation) FL-AB (LO)

The flag leaf is the top leaf on a rice stem, closest to the grain-producing panicle. Flag leaves have a major role in providing energy to the developing grain, and any impact on photosynthesis in the flag leaf can have a dramatic effect on grain productivity (Davis *et al.*, 2020). It is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for flag leaf attitude. Out of 95, 67 genotypes showed erect attitude, while 20 had semi-erect attitude and 7 had horizontal attitude rest 1 showed deflexed attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding programme as well as this trait can be used morphological marker as polymorphic variation is present. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.35 Panicle: Curvature of main axis (P-CMA)

Over the past 30 years, super rice played an important role in boosting rice yield. The phenotype of erect panicle (EP) architecture controlled by dense and erect panicle 1 (*dep1*) is the typical characteristic of super rice, and the phenotype has been used in rice breeding for nearly a century (Sibo *et al.*, 2022). Bending-type lodging is caused by increase in panicle weight during maturation and occurs over the entire internode of rice during strong wind. Out of 95, 28 genotypes showed straight curvature of panicles, thus these 28 straight type genotypes are suitable to include in crop improvement programme and crop ideotype breeding. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.36 Panicle: Number per plant (P-NP)

Panicles form the rice inflorescence. It is the top part of the rice plant, carried on the last inter-node. Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets. Panicle number is directly correlated with yield. Out of 95, 39 genotypes viz., MO-6, MO-19, Mayekar Bhat, Munga, PR-114, RTN 11-2-1-3, PR-118, DRR-215, NAUR-1, BL-184AR, DRR-50-13, DRR-86-8, IR-63879-195-2-2-3-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, S Basmati, Kothambir Sal, P Sugandha-3, Bhadasbhog, CR2713-180, Kalanamak, P Samruddhi, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, KJT 1, IR-64, MILYANG 46, PTB 33, BG 367-2, MUT NS 1, RATHU HEENATI, IRRI 190, IRRI 104 and IRRI 192 had medium number of panicles and only 1 (TN-1) showed many number of panicles. Thus these genotypes are suitable to include in crop improvement programme. These results were in accordance with the findings of Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Arvind *et al.* (2019), Bhargavi *et al.* (2022), and Kushwaha *et al.* (2022).

5.1.37 Spikelet: Colour of tip of lemma (S-CTL)

More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color viz., Yellowish (2), Brown (3), Purple (5) and Black (6). Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.38 Lemma and Palea: Colour (LP-C)

Lemma is specialized bracts or bracteates. In rice the palea is in bended form and facing towards the lemma. Palea is one of the chaffy scales on the receptacle of many composite plants. The upper bracts that with the lemma encloses the flower in rice. The other scales, the lemma and the palea, occur in pairs. Generally the lemma is larger than the palea, which is hidden between the lemma and the spikelet axis. The lemma and palea surround and protect the flower, and all three of these structures form the floret. (Lombardo *et al.*, 2022) More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.39 Panicle: Awns (P-A)

The fili-form extension of the keel of the lemma is known as awn having bristles or hair like structure. They contribute to grain dispersal and burial and fend off animal predators. But not preferred for modern cultivars as it is inconvenient for mechanical threshing. Out of 95, 61 genotypes were awnless. Thus these genotypes should be included in crop improvement programme. This result was in accordance with the findings of Sanyal and Joshi (2016), Kumar *et al.* (2018), Manjunatha *et al.* (2018), Gour *et al.* (2019), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.1.40 Panicle: Colour of awns (late observation) P-CA (LO)

More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.*

(2022) reported similar findings.

5.1.41 Panicle: Length of longest awn (P-LLA)

Not preferable character for presence of all its notes except absent. Out of 95, these 61 awnless genotypes are desirable and can be included in breeding programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.42 Panicle: Distribution of awns (P-DA)

Not preferable character for presence of all its notes except absent. Out of 95, these 61 awnless genotypes are desirable and can be included in breeding programme. Sanyal and Joshi (2016), Kumar *et al.* (2018), Manjunatha *et al.* (2018), Gour *et al.* (2019), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022) have also reported the similar results.

5.1.43 Panicle: Presence of secondary branching (P-PSB)

Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets. The acquisition of greater secondary branching potential plays an important role in increasing grain yield in cultivated rice (Huang *et al.*, 2021). It is directly correlated with yield. Out of 95, 79 genotypes showed presence of secondary branching. Thus these genotypes are desirable and can be included in breeding programme. Similar results were reported by Sanyal and Joshi (2016), Manjunatha *et al.* (2018), Bhargavi *et al.* (2022 and Kushwaha *et al.* (2022).

5.1.44 Panicle: Secondary branching (P-SB)

Stronger note is desirable for this trait. Out of 95, 21 genotypes *viz.*, Mahsad, Waksal-207, PR-114, DRR-215, BL-184AR, Gurjari, DRR-363-5, DRR-50-13, DRR-50-10, IR-63879-

195-2-2-3-2, P Basmati, Chinoor, P Sugandha-1, Indrayani, RS-1113, RP Bio 197, Ajaya, PTB 33, RATHU HEENATI, SINNA SIVAPPU and IRRI 192 showed presence of strong secondary branching. Thus these genotypes are desirable and can be included in crop ideotype breeding programme. This finding was also reported by Manjunatha *et al.* (2018), Ghosh *et al.* (2019), Lavanya *et al.* (2021) and Kushwaha *et al.* (2022).

5.1.45 Panicle: Attitude of branches (P-AB)

Erect attitude is desirable as it indicates bending resistance. Out of 95, 47 genotypes *viz.*, Pandya, Dular, PR-114, RTN 11-2-1-3, PR-118, DRR-215, DRR-50-12, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-214-1-1-1-2, VDN-10-18, RTN-35-1-1, P Basmati, S Basmati, P Sugandha-4, P Sugandha-5, Kalanamak, P Samruddhi, Indrayani, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192 and Sonsali showed presence of erect attitude of branching. Thus these genotypes are desirable and can be included in crop ideotype development programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.46 Panicle: Exertion (P-E)

Panicle exertion, the distance between the leaf cushion of flag and the neck-panicle node, is an important morphological trait, which has significant impact on hybrid seed production of rice (Yang *et al.*, 2020). Well exerted panicles are meant to be exposed for full sunlight and hence all the grains are fully developed in such genotypes. Out of 95, 88 genotypes showed presence of well

exerted panicles. Thus these genotypes are desirable and can be included in ideotype breeding programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.47 Time maturity (days) (TM)

Time of maturity is the biological cycle of rice (days from seedling to harvest). All notes are preferable for this trait. As early genotypes are suitable for upland ecosystem, mid-late cultures are adaptable for midland ecosystem whereas late lines are good for lowland ecosystem. (Sandhu *et al.*, 2019) and (Anputhas *et al.*, 2021). Out of 95 genotypes 40 were early, indicating their adaptability for upland ecosystem, while 54 showed mid-late duration which are adaptable for midland and one genotype was found to be of late duration which is adaptable for lowland. These results were in accordance with Kalyan *et al.* (2017), Umarani *et al.* (2017a), Rawte and Saxena (2018), Arvind *et al.* (2019), Bhargavi *et al.* (2022).

5.1.48 Leaf: Senescence (L-S)

Leaf senescence, which is the last developmental phase of plant growth, is controlled by multiple genetic and environmental factors. Leaf yellowing is a visual indicator of senescence due to the loss of the green pigment chlorophyll. Leaf senescence constitutes the final stage of leaf development and is critical for plants' fitness as nutrient relocation from leaves to reproducing seeds is achieved through this process. (Schipper *et al.*, 2022). Late senescence of leaf is desirable as underdeveloped grain in panicle will get nutritional support even after maturity to get complete development. Late leaf senescence showed by 3 genotypes viz., VDN-10-18, CR-3993-2-24-45-2 and Ambemohar out of 95. Thus these genotypes can be utilized in crop improvement

programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.49 Sterile lemma: Colour (SL-C)

Sterile lemmas are produced between the fertile floret and the rudimentary glumes (Lombardo *et al.*, 2022). More variation in colour for this trait serves morphological marker. This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.50 Grain: Weight of 1000 fully developed grains (TKW)

The 1,000 kernel (1,000 K) weight is a measure of seed size. Thousand kernel weight (TKW) is an important parameter for the evaluation of variety breeding. TKW is not only directly related to the grain yield and milling quality of grain, but also has an impact on the seedling vigor and growth indirectly affecting the yield (Wu *et al.*; 2021). Test weight below 14 g indicates superfine grains, whereas more the test weight, grains will be coarse and bold. Out of 95 genotypes 5 showed very low and 26 had low test weight below 15 g. Thus these grains are super fine and can be used for table purpose, while rest showed high and very high test weight. Thus these genotypes will be considered for flour making, roti making and beaten rice manufacturing. Komala *et al.* (2017), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022) recorded the similar results.

5.1.51 Grain: Length (G-L)

Grain length and width determine rice grain shape. Therefore affect yield and appearance, thus representing two of the most

agronomically important traits in rice breeding (Li and Li, 2021). Extra-long grain and short slender, medium slender size Basmati is preferred for table purpose. While long and medium bold grains are desirable for roti making and other industrial purposes. All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Similar results were reported by Mondal *et al.* (2014), Komala *et al.* (2017), Bhargavi *et al.* (2022) and Kushwaha *et al.* (2022).

5.1.52 Grain: Width (G-W)

Its significance is same in line with previous descriptor i.e. Grain length *viz.*, Grain length and width determine rice grain size. Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021). All variations for this trait are desirable as per its utility and can be included in crop improvement programme. These results were in agreement with the findings of Komala *et al.* (2017).

5.1.53 Grain: Phenol reaction of lemma (G-PRL)

Phenol colour reaction on grains and glumes is used for characterization of rice varieties for distinctiveness, uniformity and stability (DUS) testing in plant variety protection. According to DUS test guidelines, rice varieties are classified into two groups based on presence and absence of phenol colour reaction on the grains (Sahil *et al.*, 2021) Variation for this trait is used to distinguish germplasm. This trait exhibited di-morphic variation for this trait. Thus this trait can be used as morphological marker to distinguish diverse germplasm. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings.

5.1.54 Decorticated grain: Length (DG-L)

Decorticated grain length is length of grain, after de-hulling and before milling. Decorticated grain length was measured in mm and a digital caliper was used for clear visualization. Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021). Extra-long grains and short slender, medium slender size Basmati is preferred for table purpose. While long and medium bold grain s are desirable for roti making and other industrial purposes. All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Mondal *et al.* (2014), Komala *et al.* (2017) and Umarani *et al.* (2017a), Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) have recorded the similar results.

51.55 Decorticated grain: Width (DG-W)

Decorticated grain width (After de-hulling, before milling).Decorticated grain width was measured in mm and a digital caliper was used for clear visualization. Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021). All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Similar results were reported by Mondal *et al.* (2014), Komala *et al.* (2017), Umarani *et al.* (2017a) and Kushwaha *et al.* (2022)

5.1.56 Decorticated grain: Shape (in lateral view) (DG-S)

Common variety gives rise to short bold and long bold rice. Fine variety gives rise to medium slender rice. Super fine variety gives rise to long slender and short slender rice. Short bold and long bold genotypes are utilized for flour roti making. Medium

slender varieties are used for various Chinese, Italian dishes. Short slender and extra-long slender germplasm can be used for table purpose (Hori *et al.*, 2022). Long grain rice tends to cook up light, fluffy and separate when cooked rather than clumping together.-table purpose. Biryanis etc. Medium grain rice tends to cook up moist and tender and used for Chinese, Spanish and Italian cuisine etc., while short grain rice tends to clump together when cooked and forms what is called glutinous rice used for flour (*atta*) roti making. All variations for this trait are desirable as per its utility and can be included in crop improvement programme. The results obtained were similar with Mondal *et al.* (2014), Komala *et al.* (2017), Umarani *et al.* (2017a) and Bhargavi *et al.* (2022).

5.1.57 Decorticated grain: Colour (DG-C)

It's true that most rice (*Oryza sativa* L.) is white, but some varieties offer phytochemicals (mainly polyphenols and anthocyanin's) in the outer bran layer, which not only imbues them with hues of a different color but also boosts their nutrient content (Webb, 2021). Research shows that black rice has the highest antioxidant activity of all the varieties, making it a nutritious choice, followed by brown and then red rice (Kubala, 2019). All variations for this trait are desirable as per its utility and can be included in crop improvement programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.58 Endosperm: Presence of amylose (E-PA)

Amylose is a polysaccharide made of α -D-glucose units, bonded to each other through α (1→4) glycosidase bonds. It is one of the two components of starch. Starch is the abundant component in rice endosperm, and its microstructure determines the quality and functional properties of rice grain (X fan *et al.*,

2019). Presence of amylose is desirable in medium scale for commercial table purpose use. All 95 genotypes showed presence of amylose. Thus all these genotypes can be included in crop improvement programme. Lavanya *et al.* (2021) and Kushwaha *et al.* (2022) reported similar findings

5.1.59 Endosperm: Content of amylose (E-CA)

After cooking, the high-amylose and intermediate-amylose rice's are firm and fluffy; while the low-amylose and waxy rice's are soft, moist, and sticky in texture (Chen, 2020). Medium range of amylose content is preferable. Low amylose varieties can be used for Chinese cuisine. Medium amylose varieties are directly used table purpose. While high amylose varieties are used for beaten rice, puffed rice. (*poha and murmura*). Out of 95 genotypes, 48 exhibited medium scale of amylose, which is highly and widely preferred by consumers for table purpose. Thus these genotypes are good donors for crop improvement. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.60 Varieties with endosperm of amylose absent only polished grain: Expression of white core (E-CAWC)

Grain chalkiness reduces the quality of rice (*Oryza sativa*) and is a highly undesirable trait for breeding and marketing (Wu *et al.*, 2022). Absence of chalkiness is desirable for this trait. This trait exhibited monomorphic variation for this trait i.e. expression is absent or very small for all 95 genotypes. Thus all the genotypes are desirable to use in crop improvement programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.61 Gelatinization temperature through alkali spreading value (GT-ASV)

Alkali spreading value (ASV) of whole kernel milled rice is the measure of volume expansion in contact with dilute alkali and also a measure of gelatinization temperature. Again gelatinization temperature is partly associated with the amylose content of the starch (Akuli *et al.*, 2019). It determines the cooking time and energy required for the rice. High-medium note is desirable as requires less cooking time and low energy. ASV is inversely proportional to the GT. Out of 95, 61 genotypes had high-medium ASV. Thus these genotypes can be included in crop improvement programme. Similar findings were reported by Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.1.62 Decorticated grain: Aroma (DG-A)

Aroma in scented and basmati rice is due to 2-acetyl-1-pyrroline (Bharati *et al.*, 2020). Makes rice varieties of special value and have wide consumer preference. Presence of aroma is desirable. Out of 95, 19 germplasm *viz.*, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati and Sugandha found to be aromatic and thus can be used in crop improvement programme. Results were in accordance with the findings of Lavanya *et al.* (2021) and Kushwaha *et al.* (2022)

5.3.2 Analysis of variance of 14 measurable characters

Analysis of variance for 14 measurable characteristics for 2020 and 2021 seasons (pooled data) have been presented in Appendix 2. Highly significant differences were observed among the

varieties for all the characters in both the years. The standard error mean for all the characteristics under study were less in both the years which indicated less role of environment for the expression of the characteristics.

5.3.3 Analysis of Distinctiveness

The variations recorded for the morphological traits (both qualitative and quantitative) in the 95 rice germplasm can be used for distinguishing these varieties. To establish distinctiveness among rice genotypes qualitative characters have been used. Qualitative traits are considered as morphological markers in the identification of genotypes of rice because they are less influenced by environment. Thus, characterization of germplasm accessions establishes distinctiveness among rice genotypes.

DUS characterization was carried out for finding out the morphological variation present in the accessions. Results of the present investigation for 62 DUS characters except culm attitude (for floating rice (not applicable character) revealed that,

5.3.3.1 No variation (i.e. 0% variation) was found among the germplasm accessions for the characters: Leaf: Auricles, Leaf: Collar, Leaf: Anthocyanin colouration of collar, Leaf: Ligule, Leaf: Shape of ligule, Male sterility, Stem: Thickness, Endosperm: Presence of amylose and Varieties with endosperm of amylose absent only Polished grain: Expression of white core. These characters were monomorphic due to negligible effect of environment over both the years and locations. Thus these 9 characters served as morphological markers.

5.3.3.2 Moderate variations were found among genotypes for characters *viz.*, Leaf: Anthocyanin colouration, Leaf: Distribution of anthocyanin colouration, Leaf Sheath: anthocyanin colouration, Leaf: Colour of ligule, Leaf: Length of blade, Leaf: Width of blade, Culm: attitude, Spikelet: Colour of stigma, Stem: Anthocyanin colouration of nodes, Stem: Intensity of anthocyanin coloration of nodes, Stem: Anthocyanin colouration of internodes Panicle: Awns, Panicle : Presence of secondary branching, Grain: Phenol reaction of lemma and Decorticated grain: Aroma.

5.3.3.3 Characters exhibiting high variation among experimental material *viz.*, Coleoptile: Colour, Basal leaf: Sheath colour, Leaf: Intensity of green colour, Leaf sheath: Intensity of anthocyanin colouration, Leaf: Pubescence of Blade Surface, Leaf: Anthocyanin colouration of auricles, Time of heading (50% of plants with panicles), Flag leaf: Attitude of blade (early observation), Spikelet: Density of pubescence of lemma, Lemma: Anthocyanin colouration of keel, Lemma: Anthocyanin colouration of area below apex, Lemma: Anthocyanin colouration of apex, Stem: Length (excluding panicle, excluding floating rice), Panicle: Length of main axis, Flag leaf: Attitude of blade (late observation), Panicle: Curvature of main axis, Panicle: Number per plant, Spikelet: Colour of tip of lemma, Lemma and Palea: Colour, Panicle: Colour of awns (late observation), Panicle: Length of longest awn, Panicle: Distribution of awns, Panicle: Secondary branching, Panicle: Attitude of branches, Panicle: Exertion, Time

maturity(days), Leaf: Senescence, Sterile lemma: Colour, Grain: Weight of 1000 fully developed grains, Grain: Length, Grain: Width, Decorticated grain: Length, Decorticated grain: Width, Decorticated grain: Shape (in lateral view), Decorticated grain: Colour, Endosperm: Content of amylose and Gelatinization temperature through alkali spreading value. Thus, 9 characters were monomorphic, 15 were dimorphic and 37 were polymorphic showing wide range of variations. Results in similar pattern were reported by Sajid *et al.* (2015), Pauchauri *et al.* (2017) and Rawte and Saxena (2018).

5.3.3.4 COY-D analysis with respect to 14 measurable traits indicated that all the varieties were distinct from each other during both the years. Similarly other workers also reported distinctiveness among varieties of different crops using MJRA model, in sorghum (Joshi *et al.*, 2009), basmati rice (Patra and Chawla, 2010), aromatic rice (Joshi *et al.*, 2011) French bean (Mall and Chawla, 2012) and rye grass (Ruiz *et al.*, 2011).

5.3.4 Analysis of Uniformity

All the visually assessed characteristics did not show any variation in their states of expression over the years of study and hence considered to be uniform. 14 measurable characteristics were subjected to COY-U analysis for the assessment of uniformity. All the varieties were more or less uniform for measurable characters. 86 genotypes namely MO-6, MO-8, MO-13, MO-17, MO-19, Kala Rata, Mayekar Bhat, Munga, Mahsad, Barmil, Patani-6, Bhadas-79, Pandya, Dular, Kochari, Lal Patani,

Dodak, Karhad, Ratnagiri 7, Bela, KJT-2R, PR-114, RTN11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P. Sugandha-4, Bhadasbhog, CR2713-180, Kalanamak, NDR631, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, I R-64, MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, R HEENATI, S SIVAPPU, IRRI 190, IRRI 193, ARC 10550, IRRI 123, IRRI 104, IRRI 192, Sonsali and T N-1 showed uniformity for all the 14 measurable characters. Remaining 9 genotypes *viz.*, Waksal-207, Jyoti, Try-1, Valai, KJT-3R, KJT-4R, P Sugandha-5, Bhogwati and Sambha Mahsuri showed uniformity for thirteen out of fourteen measurable characters. Such non uniformity by COYU analysis has been reported earlier also in basmati and aromatic rice varieties (Patra and Chawla, 2010) and (Joshi *et al.*, 2011), sorghum varieties (Joshi *et al.*, 2009) and French bean varieties (Mall and Chawla, 2012).

5.3.5 Analysis of stability

All the varieties studied for forty six visually assessed DUS descriptors exhibited the same state of expression over the two years and thus considered stable.

14 measurable characteristics were subjected to statistical analysis for stability by comparison of respective values of PCV and GCV based on pooled morphological data. All the 14 measurable characteristics showed slightly higher magnitude of PCV over GCV.

This indicates that environment influence was less for the expression of these characters and hence 14 measurable characters were stable over the two years and two different environments. (Patra *et al.*, 2010 and Subbaiah *et al.*, 2011) reported similar findings.

CHAPTER-VI

SUMMARY AND CONCLUSIONS

The present investigation entitled as '**Genetical studies, phenotyping and molecular profiling of diverse germplasm of rice (*Oryza sativa* L.)**' was undertaken with the objectives of characterization of 95 diverse rice germplasm by 62 DUS morphological descriptors, supplemented with molecular profiling by using simple sequence repeat markers and their subsequent examination for distinctiveness, uniformity and stability. The nature and extent of variability, heritability, genetic advance and diversity present among the germplasm based on yield and yield contributing parameters was studied to identify potential parents/donors for the hybridization programme. RBD trials were conducted in two subsequent and independent *Kharif* seasons of 2020 and 2021 at experimental farms of Agricultural Research Station, Shirgaon and Regional Agricultural Research Station, Karjat respectively. Data was recorded for 27 metric characters inclusive of 14 measurable DUS traits and 62 DUS descriptors of rice as per PPV & FR guidelines. Whereas molecular profiling of 95 rice genotypes using 17 SSR primers was carried out at Plant Biotechnology Center, College of Agriculture, Dapoli. The results from the investigation are summarized and concluded as below:

- Analysis of variance for both seasons and locations revealed the presence of significant differences among the 95 germplasm of rice under study for all the twenty seven metric traits, indicating the presence of considerable genetic variation in the experimental material.

- A perusal of genetic parameters *viz.*, phenotypic and genotypic coefficients of variation revealed less influence of environment on the characters under study for both two seasons and locations. Therefore, response to direct selection may be effective in improving these traits. Among all the characters under study, for location 1 (Shirgaon) zinc content exhibited highest PCV and GCV values followed by calcium content, iron content, number of spikelets per panicle, stem length excluding panicle, plant height, amylose content and decorticated length breadth ratio, whereas lowest PCV and GCV values were reported for days to maturity. While for location II (Karjat) zinc content exhibited highest PCV and GCV values followed by calcium content, iron content, number of spikelets per panicle, straw yield per plant, grain yield per plant, stem length excluding panicle, plant height, amylose content and decorticated length breadth ratio, whereas lowest PCV and GCV values were reported for days to maturity.
- All the characters under study for both the locations exhibited high heritability except alkali spreading value which showed lowest heritability. For ARS, Shirgaon location, high heritability coupled with high genetic advance as per cent of mean was observed for the traits *viz.*, plant height, stem length excluding panicle length and calcium content, which suggests that these characters are subjected to any selection scheme for exploiting fixable genetic variance will be highly effective. Whereas for location RARS, Karjat, high heritability coupled with high genetic advance as per cent of mean was reported for plant height, stem length excluding panicle, number of spikelets panicle⁻¹, leaf length and calcium implying that these characters were under control of additive gene action and direct

selection of these traits would be effective for crop improvement.

- Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. For location I (Shirgaon) all 95 rice germplasm under study were distributed into twenty two clusters based on D^2 values using Tocher's method such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. Out of twenty two clusters, cluster I was the largest comprising of fifty seven genotypes, followed by cluster IV with 32 genotypes. Remaining 20 clusters were mono-genotypic clusters suggesting the existence of high degree of heterogeneity among the genotypes. Whereas for location II (Karjat) the genotypes were grouped into 20 clusters. Cluster I was largest out of the 20 clusters which comprises of 58 genotypes followed by cluster V with 14 genotypes and cluster X with 6 genotypes. Remaining clusters were mono-genotypic.
- Grouping of most of the genotypes into one cluster (cluster I) for both the locations indicates genetic relatedness between these genotypes. This can be further explained by free flow of genes between these accessions. The clustering pattern showed that the landraces originating from similar geographical regions were categorized into different clusters, indicating that geographical diversity and genetic diversity were not related. Therefore, the kind of genetic diversity found among the genotypes belonging to same geographical region might be due to differences in adaptation, selection criteria, selection pressure and environmental conditions.

- For location I (Shirgaon) maximum intra cluster distance was observed in cluster IV, followed by cluster I, while for location II (Karjat) maximum intra cluster distance was observed in cluster X, followed by cluster V and cluster I indicating that some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean values for the desirable characters. Maximum inter cluster distance for location I (Shirgaon) was exhibited between XIX and XX, followed by cluster XVIII and XX, cluster XX and XXI, cluster XXI and XXII, cluster X and cluster XXII, cluster XIII and XX whereas for location II (Karjat) maximum inter cluster distance was exhibited between cluster XIV and XX, followed by cluster VII and XX, cluster XI and XIV, cluster III and XX, cluster XVIII and cluster XX, cluster IV and XIX. The greater the distance between two clusters, the wider the genetic diversity among the genotypes of those clusters. Such highly divergent, high performing genotypes would be of great use in recombination breeding programme in order to get high heterotic recombinants. The promising genotypes from these clusters with high mean values as discussed in 4.1.6.5 and 4.1.6.6 for different traits may be directly used for adaptation or may be used as parents in future hybridization, depending upon the objective of the breeding programme to derive superior transgressive segregants.
- For location I (Shirgaon) 13 characters namely leaf length, calcium content, number of panicles plant⁻¹, fertility, zinc content, iron content, number of spikelet's panicle⁻¹, plant height, days to 50% flowering grain width, amylose content, straw yield plant⁻¹ and grain yield plant⁻¹ together contributed

maximum (92.69%) to the total genetic divergence. Whereas for RARS, Karjat location out of the 27 characters studied, 11 characters namely leaf length, calcium content, fertility, decorticated grain length, zinc content, iron content, number of spikelets panicle⁻¹, plant height, amylose content, days to 50% flowering and grain yield plant⁻¹ together contributed maximum (98.99%) to the total genetic divergence. Thus, it is suggested that these traits should be given importance in further breeding programmes i.e., during hybridization and selection of segregating populations, in this particular set of germplasm to develop high yielding rice varieties/hybrids with superior grain quality.

- Seventeen SSR primers were used in this study and all amplified and showed the polymorphism in rice genotypes. A total of 139 loci were generated by 17 primers. Each primer thus produced on an average 8.17 loci in the size ranging from 132 bp to 884 bp in the 95 rice genotypes in relation to diversity assessment.
- Among 17 SSR markers, all the primers showed 100 per cent polymorphism.
- The PIC values of primers ranged from 0.70 in SSR primer RM 7 to 0.92 in SSR primer RM 8225 with an average PIC value of 0.83.
- The Jaccard's pair wise similarity values ranged from 0.027 to 0.994.
- Dendrogram was constructed using Jaccard's similarity coefficient and rice genotypes were grouped into two clusters based on SSR markers.

- SSR primers showed 100% polymorphism which represents the capability of these primers to amplify the less conserved region of the DNA. It also depicted that rice genotypes used in the present screening were divergent which a very important factor in breeding programmes.
- The screening of rice genotype through microsatellites is very important for identifying parental genotypes that will be exploited for MAS breeding of elite lines that are more stable to stresses and this will lead to increase yield in order to feed the growing population.
- Among the total sixty two DUS descriptors, 9 were monomorphic, 15 were dimorphic and 37 were polymorphic in nature
- Among the forty six visually assessed DUS descriptors, 6 were monomorphic, 12 were dimorphic and 26 were polymorphic in nature.
- Out of fourteen measurable characteristics, 3 were monomorphic, 3 were dimorphic and 11 were polymorphic in nature.
- Results of analysis of variance revealed highly significant differences among all the genotypes for all the characteristics in both the years.
- COY-D analysis with respect to 14 measurable traits indicated that all the genotypes were distinct from each other during both the years.
- All the visually assessed characteristics did not show any variation in their states of expression over the years of study and hence considered to be uniform. 14 measurable

characteristics were subjected to COY-U analysis for the assessment of uniformity. All the varieties were more or less uniform for measurable characters. 86 showed uniformity for all the 14 measurable characters whereas remaining 9 genotypes showed uniformity for thirteen out of fourteen measurable characters. All the varieties studied for forty six visually assessed DUS descriptors exhibited the same state of expression over the two years and thus considered stable.

- It may be concluded from the present investigation that the morphological DUS descriptors can be effectively used for identification and grouping of the varieties. Application of biochemical and molecular markers may help in establishing distinctiveness to support morphological marker. The varieties studied for DUS descriptors can be registered with PPV & FR Authority for obtaining breeder's and farmers' rights.

CONCLUSION:

Following conclusions are based on grouping of genotypes falling under early, mid-late and late maturity duration along with dwarf/semi-dwarf stature and high grain yield (above 15 g), high fertility (>90%), number of panicles per plant (> 10), medium to high panicle length (>26 cm), number of spikelets per panicle (>175), medium amylose content (21-25%) and high Ferrous (>10 ppm), Zinc (>20ppm) and Calcium (>80ppm) content. Almost all genotypes recommended here are either at par desirable values given above or nearer to that. Thus following genotypes are observed to be elite among early, mid-late and late group having good combination yield associated traits and with high nutritional value. Thus it is recommended to utilize these lines for further crop improvement and is also useful for farmer's direct cultivation and having consumer's preference too.

- Twelve genotypes found to be of early maturity duration (101-120 days) suitable for upland ecosystem and best utilized for research purpose along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., Jyoti, Ratnagiri-7, KJT-2R, KJT-4R, CR-2713-180, SINNA SIVAPPU, PR-114, MILYANG 63, IRRI 190, PTB 33, P Sugandha-1 and P Sugandha-3.
- Fourteen genotypes falls under Mid-late maturity duration(121-140 days) suitable for mid-land ecosystem along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., KJT-1R, KJT-3R, PR-118, NAUR-1, Gurjari, RTN-35-1-1, CR-3993-2-24-45-2, S Basmati, NDR-6315, KJT 2, IR-64, Bhogwati, ARC 10550 and TN-1.
- One genotype falls under Late maturity duration(141-160 days) suitable for low-land ecosystem along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., Kalanamak.
- One genotype falls under mid-late maturity duration(121-140 days) suitable for mid-land ecosystem and khar-land along with dwarf /semi-dwarf stature (which is lodging resistant and fertilizer responsive) viz., Khara rata.

❖ **Future line of work**

- ❖ Passport data bulletin of all the 95 genotypes can be released for public domain which will assist rice scientist community to choose better parent as per breeding objectives.
- ❖ QR code (quick response code) should be generated for each genotype inclusive of DUS and molecular fingerprints developed under this study. This will facilitate rapid and easy dissemination of passport data of these genotypes.

LITERATURE CITED

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* Original not seen.

Table 4.1 : Analysis of variance 27 yield and yield contributing traits in 95 rice genotypes ARS, Shirgaon Year I

SN	Character	Mean sum of squares		
		Replications (df : 2)	Genotypes (df : 94)	Error (df : 188)
1	Days to 50% Flowering (Nos.)	3.232	151.367**	1.650
2	Plant Height (cm)	662.394	1966.888**	16.209
3	Stem Length Excluding Panicle (cm)	489.905	1802.479**	15.098
4	Number of Tillers Plant ⁻¹	24.521	9.029**	0.507
5	Panicle Length of Main Axis (cm)	17.348	16.923**	1.230
6	Number of Spikelets Panicle ⁻¹	2052.790	5021.236**	58.318
7	Fertility (%)	15.762	186.044**	0.622
8	Days to Maturity (Nos.)	3.232	151.367**	1.650
9	Test Weight (g)	0.096	54.883**	1.391
10	Grain Length (mm)	0.131	3.216**	0.068
11	Grain Width (mm)	0.215	0.395**	0.005
12	Grain Yield Plant ⁻¹ (g)	3.494	56.835**	1.006
13	Straw Yield Plant ⁻¹ (g)	17.180	112.182**	1.852
14	Grain Yield/ Straw Yield Ratio	0.001	0.020**	0.002
15	Straw Yield/ Grain Yield Ratio	0.009	0.080**	0.009
16	Leaf: Length of Blade (cm)	32.821	292.421**	0.572
17	Leaf: Width of Blade (cm))	0.120	0.092**	0.010
18	Stem Thickness (cm)	0.793	0.041**	0.006
19	Number of Panicles Plant ⁻¹	24.521	9.029**	0.507
20	Decorticated Grain Length (mm)	0.097	2.332**	0.010
21	Decorticated Grain Breath (mm)	0.238	0.299**	0.014
22	DGL/DGB Ratio	0.309	1.053**	0.038
23	Amylose Content (%)	89.014	68.911**	1.147
24	Zinc Content (ppm)	56.125	89.797**	0.465
25	Iron Content (ppm)	59.745	69.368**	0.422
26	Calcium Content (ppm)	295.100	1185.430**	2.603
27	Alkali Spreading Value	0.497	1.280**	0.570

**and *: Significant at 1 per cent and 5 per cent level

Table F value @ 5% is 1.929

Table F value @ 1% is 1.499

Table 4.2 Analysis of variance for 27 yield and yield contributing traits in 95 rice genotypes RARS, Karjat Year II

SN	Character	Mean sum of squares		
		Replications (df : 2)	Genotypes (df : 94)	Error (df : 188)
1	Days to 50% Flowering (Nos.)	2.782	156.267**	2.247
2	Plant Height (cm)	376.688	1931.494**	17.206
3	Stem Length Excluding Panicle(cm)	243.177	1760.981**	15.163
4	Number of Tillers Plant ⁻¹	23.908	9.115**	0.555
5	Panicle Length of Main Axis (cm)	14.563	16.902**	1.429
6	Number of Spikelets Panicle ⁻¹	1392.820	5027.046**	61.097
7	Fertility (%)	27.812	187.892**	0.616
8	Days to Maturity (Nos.)	2.782	156.267**	2.247
9	Test Weight (g)	2.616	57.574**	1.439
10	Grain Length (mm)	0.048	3.225**	0.065
11	Grain Width (mm)	0.014	0.447**	0.018
12	Grain Yield Plant ⁻¹ (g)	0.681	54.583**	1.022
13	Straw Yield Plant ⁻¹ (g)	4.343	111.945**	2.179
14	Grain Yield/ Straw Yield Ratio	1.985	2.236**	2.196
15	Straw Yield/ Grain Yield Ratio	0.017	0.055**	0.013
16	Leaf: Length of Blade (cm)	38.534	298.735**	0.743
17	Leaf: Width of Blade (cm))	1.319	0.122**	0.046
18	Stem Thickness (cm)	0.770	0.042**	0.006
19	Number of Panicles Plant ⁻¹	18.611	10.190**	0.644
20	Decorticated Grain Length (mm)	0.091	2.313**	0.010
21	Decorticated Grain Breath (mm)	0.132	0.297**	0.015
22	DGL/DGB Ratio	0.195	1.044**	0.039
23	Amylose Content (%)	89.434	69.076**	1.191
24	Zinc Content (ppm)	56.809	90.304**	0.553
25	Iron Content (ppm)	48.103	69.114**	0.521
26	Calcium Content (ppm)	229.938	1194.773**	3.655
27	Alkali Spreading Value	2.897	1.280**	0.545

**and *: Significant at 1 per cent and 5 per cent level

Table F value @ 5% is 1.929

Table F value @ 1% is 1.499

Table 4.3 Mean performance for grain yield and its component traits of 95 rice genotypes, location 1, year 1, ARS, Shirgaon Part 1/2

SN	Character Genotype	DFP (Nos.)	PHT (cm)	SLEP (cm)	TLPP (Nos)	PLMA (cm)	SPP (Nos.)	Fertility (%)	DM (Days)	TW (gm)	GL (mm)	GW (mm)	GYP (gm)	SYPP (gm)	G/S	S/G
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	MO-6	91.67	90.20	62.47	11.65	27.73	206.28	93.76	121.67	21.21	8.16	3.16	18.43	27.64	0.67	1.51
2	MO-8	86.00	78.37	54.83	11.44	23.53	132.90	85.00	116.00	18.37	8.66	2.78	12.62	22.56	0.56	1.79
3	MO-13	91.00	114.67	88.93	10.87	25.73	114.39	84.32	121.00	18.62	8.74	3.02	17.79	21.97	0.82	1.24
4	MO-17	82.67	102.85	79.59	11.07	23.27	126.74	83.52	112.67	25.13	8.16	3.25	14.05	17.26	0.81	1.23
5	MO-19	83.00	88.33	64.60	12.50	23.73	117.52	82.30	113.00	22.37	9.49	2.97	15.33	19.76	0.78	1.29
6	Khara Rata	92.00	140.47	111.47	10.87	29.00	72.88	77.20	122.00	26.83	9.03	3.48	11.39	14.91	0.77	1.31
7	Mavekar Bhat	87.00	136.53	111.47	11.77	25.07	102.68	87.66	117.00	26.30	8.47	3.18	9.62	13.00	0.74	1.35
8	Munga	97.67	145.00	120.27	11.63	24.73	121.57	94.48	127.67	24.29	8.48	3.41	14.27	17.93	0.80	1.25
9	Mahsad	90.00	161.39	136.25	8.93	25.13	198.61	90.11	120.00	25.00	9.12	3.45	17.75	22.43	0.79	1.27
10	Waksal-207	86.00	141.95	116.95	9.83	25.00	112.09	80.17	116.00	23.77	9.34	3.46	15.02	19.59	0.77	1.31
11	Barmil	93.00	161.01	133.01	10.33	28.00	166.09	91.52	123.00	27.41	9.15	3.44	18.11	22.16	0.82	1.22
12	Jyoti	88.33	134.33	108.53	10.40	25.80	124.58	82.59	118.33	27.01	7.58	3.21	22.50	32.33	0.70	1.44
13	Patani-6	92.00	162.73	136.33	9.70	26.40	139.73	92.59	122.00	23.40	8.40	3.75	19.29	24.18	0.80	1.25
14	Bhadas-79	91.00	145.33	117.93	10.83	27.40	131.14	90.13	121.00	22.93	7.64	2.93	10.68	13.45	0.79	1.26
15	Pandy	93.00	160.65	134.25	9.83	26.40	139.60	92.75	123.00	23.77	9.04	3.52	14.04	17.26	0.81	1.23
16	Dular	92.00	97.97	74.43	9.80	23.53	95.63	88.90	122.00	24.83	9.34	3.15	9.22	12.33	0.75	1.34
17	Try-1	93.67	173.60	142.87	10.50	30.73	97.08	57.54	123.67	23.76	10.16	3.50	11.73	14.35	0.81	1.23
18	Kochari	81.00	169.27	136.80	11.20	32.47	99.44	88.19	111.00	26.68	10.24	3.90	16.47	25.33	0.65	1.54
19	Lal Patani	78.00	108.83	82.97	9.43	25.87	101.56	63.87	108.00	24.43	10.42	2.71	12.30	16.97	0.73	1.38
20	Dodak	78.33	94.57	68.10	10.47	26.47	55.32	77.84	108.33	26.61	9.89	2.51	16.26	20.21	0.81	1.24
21	Karhad	77.33	90.00	67.33	10.50	22.67	92.64	79.64	107.33	26.77	9.81	3.12	13.45	17.79	0.76	1.32
22	Ratnagiri 7	88.67	104.37	80.10	10.77	24.27	131.69	92.18	118.67	25.54	8.49	3.14	20.43	25.23	0.81	1.24
23	Bela	95.00	155.27	128.27	10.00	27.00	263.62	87.41	125.00	29.13	9.18	3.51	11.40	17.76	0.64	1.56
24	Valai	96.67	161.73	136.13	10.83	25.60	163.68	93.91	126.67	25.62	9.44	3.53	13.37	22.04	0.61	1.65
25	KJT-1R	98.33	133.80	103.00	11.73	30.80	133.95	86.55	128.33	28.55	9.82	2.64	29.00	33.47	0.87	1.16
26	KJT-2R	85.67	132.47	104.47	10.40	28.00	140.80	84.25	115.67	21.20	10.16	2.70	21.70	31.03	0.70	1.43
27	KJT-3R	97.67	136.07	108.47	9.73	27.60	178.35	92.89	127.67	25.06	10.51	2.33	21.50	26.33	0.82	1.22
28	KJT-4R	86.00	109.87	84.07	11.40	25.80	152.00	79.32	116.00	23.45	10.67	2.55	15.20	21.47	0.71	1.42
29	PR-114	84.33	126.07	99.47	12.40	26.60	154.13	93.40	114.33	18.68	10.02	2.71	17.83	24.27	0.74	1.36
30	RTN 11-2-1-3	93.00	99.87	70.80	11.87	29.07	173.84	76.17	123.00	16.99	10.18	2.47	14.67	20.37	0.72	1.39
31	PR-118	99.00	141.40	108.80	13.60	32.60	164.16	82.52	129.00	20.75	11.08	2.64	32.27	46.33	0.70	1.44
32	DRR-215	96.67	160.27	127.93	16.07	32.33	129.18	82.71	126.67	22.07	10.06	2.52	15.27	17.73	0.86	1.16
33	RTN-69-1-1	87.33	144.93	117.73	11.40	27.20	182.72	77.74	117.33	23.47	9.99	2.61	16.80	21.65	0.77	1.29
34	NAUR-1	94.00	113.53	87.27	12.20	26.27	139.86	65.41	124.00	28.23	9.34	2.72	18.80	26.50	0.71	1.41
35	BL-184AR	90.33	115.80	87.87	11.53	27.93	179.30	93.46	120.33	14.88	9.55	3.12	12.40	15.47	0.80	1.25
36	Gurjari	96.00	114.73	92.33	9.87	22.40	170.51	68.21	126.00	26.91	9.39	3.24	23.07	24.70	0.94	1.07
37	DRR-50-12	97.33	142.20	114.67	10.73	27.53	114.76	83.77	127.33	19.84	8.88	2.79	21.93	31.90	0.69	1.45
38	DRR-363-5	98.67	141.53	112.87	9.87	28.67	143.49	81.26	128.67	23.80	8.46	3.01	19.97	24.80	0.80	1.24
39	DRR-50-13	98.00	141.87	111.73	13.33	30.13	111.33	83.84	128.00	22.03	8.65	2.29	22.87	36.00	0.64	1.57
40	DRR-50-10	99.33	138.13	109.60	10.80	28.53	120.15	84.44	129.33	23.07	8.65	3.04	23.33	29.93	0.78	1.28
41	DRR-86-8	91.00	129.33	99.73	11.67	29.60	160.55	96.83	121.00	24.76	9.98	2.60	15.67	20.33	0.77	1.30
42	IR-63879-195-2-2-	86.00	111.73	85.47	11.87	26.27	104.05	94.59	116.00	18.61	10.80	2.56	16.50	24.53	0.67	1.49
43	RTN-27-1-1-2	86.67	123.20	98.47	10.67	24.73	77.30	65.45	116.67	21.78	9.50	2.59	11.73	18.17	0.65	1.55
44	RTN-214-1-1-1-2	92.00	124.53	99.67	10.67	24.87	187.77	86.24	122.00	18.80	9.34	2.49	17.57	19.33	0.91	1.10
45	VDN-9-10-1	91.67	130.13	104.87	12.60	25.27	120.44	90.44	121.67	24.51	8.56	2.97	17.18	26.07	0.66	1.52
46	VDN-10-18	99.00	129.53	103.20	12.20	26.33	164.68	89.33	129.00	13.70	9.36	2.58	14.97	19.40	0.77	1.30
47	RTN-35-1-1	100.00	127.43	102.37	12.80	25.07	102.95	77.20	130.00	17.51	10.01	2.61	20.40	28.60	0.71	1.40
48	Sahyadri 5 R	97.00	154.53	128.80	11.73	25.73	176.75	97.30	127.00	27.17	8.94	3.15	24.28	32.13	0.76	1.33
49	HRTMS-61	101.00	139.13	113.73	10.87	25.40	166.33	84.34	131.00	16.39	9.96	2.50	15.78	26.57	0.59	1.69
50	CR-3993-2-24-45-2	101.00	101.00	75.33	10.87	25.67	176.67	72.95	131.00	20.73	9.33	3.20	21.57	28.55	0.76	1.32
51	P Basmati	99.67	128.20	101.33	11.53	26.87	162.29	93.80	129.67	23.03	8.55	2.79	14.90	23.27	0.64	1.56
52	S Basmati	107.67	121.70	104.07	16.80	23.07	126.14	83.51	137.67	21.37	9.78	2.85	22.53	35.83	0.63	1.59
53	Kothambir Sal	106.33	162.47	135.53	12.53	26.93	106.35	87.51	136.33	12.06	5.99	3.26	12.34	18.10	0.68	1.48
54	Chinoor	93.00	95.40	68.60	11.60	26.80	115.00	83.56	123.00	14.75	10.29	2.46	11.17	22.00	0.51	1.96
55	P Sugandha-1	87.00	98.67	71.20	10.87	27.47	107.80	96.37	117.00	23.50	10.58	2.81	17.68	27.70	0.64	1.57
56	P Sugandha-3	85.67	107.33	79.87	11.87	27.47	182.50	94.14	115.67	25.47	10.18	2.85	18.80	26.30	0.72	1.40
57	P Sugandha-4	92.00	93.67	67.07	11.27	26.60	78.16	79.18	122.00	25.27	9.21	2.92	13.13	20.57	0.64	1.57
58	P Sugandha-5	88.67	126.53	100.07	11.47	26.47	110.84	86.06	118.67	27.37	9.35	3.23	16.07	21.43	0.75	1.34
59	Bhadasbhog	88.00	179.27	148.53	15.33	30.73	127.05	85.40	118.00	11.22	10.06	2.47	14.06	21.50	0.66	1.53
60	CR2713-180	80.00	130.87	99.27	12.87	31.60	108.52	79.25	110.00	16.87	9.97	2.47	22.57	43.20	0.52	1.91
61	Kalanamak	112.00	172.00	143.47	14.27	28.53	156.30	82.37	142.00	20.83	8.37	2.91	14.24	18.28	0.78	1.29
62	NDR6315	96.33	192.33	156.67	11.33	35.67	81.85	88.30	126.33	15.35	8.21	2.75	25.27	31.17	0.81	1.23
63	P Samraddhi	91.00	116.00	87.33	12.07	28.67	162.76	89.36	121.00	17.95	10.83	2.66	16.07	23.40	0.69	1.46
64	Indrayani	91.00	106.07	79.40	11.47	26.67	163.49	88.91	121.00	16.02	10.49	2.68	12.63	18.27	0.69	1.45
65	Dhanesal	83.00	163.20	135.07	13.80	28.13	129.66	92.59	113.00	13.84	10.40	2.57	11.20	15.00	0.75	1.34
66	Ambemohar	96.00	142.20	111.07	13.47	31.13	157.55	93.34	126.00	13.57	6.95	2.95	14.63	20.50	0.71	1.41
67	K Shatabdi	89.67	104.93	79.13	11.60	25.80	108.05	91.02	119.67	13.79	7.36	3.09	16.68	20.10	0.83	1.21
68	Bhogwati	92.00	107.67	81.27	12.53	26.40	105.63	90.30	122.00	22.53	11.06	2.30	17.99	27.67	0.65	1.54
69	Sugandha	87.33	107.40	81.80	14.87	25.60	125.77	91.09	117.33	24.58	11.65	2.51	16.93	26.83	0.63	1.59
70	RS-1113	81.00	115.73	89.20	11.67	26.53	91.50	85.37	111.00	13.49	8.24	2.25	15.50	23.93	0.65	1.54
71	RP Bio 197	88.00	113.33													

Table 4.3 Mean performance for grain yield and its component traits of 95 rice genotypes, location 1, year 1, ARS, Shirgaon Part2/2													
SN	Character Genotype	LL (cm)	LB (cm)	ST (cm)	PPP (Nos.)	DGL (mm)	DGB (mm)	L/B	AC (%)	Zn (ppm)	Fe (ppm)	Ca (ppm)	ASV
		16	17	18	19	20	21	22	23	24	25	26	27
1	MO-6	49.33	1.00	0.78	10.65	5.77	2.79	2.07	24.38	12.73	12.65	40.03	5.00
2	MO-8	53.70	1.10	0.70	10.44	6.38	2.47	2.58	26.03	3.00	11.33	19.23	5.00
3	MO-13	57.50	0.97	0.80	9.87	6.20	2.52	2.46	23.78	10.65	20.72	18.50	5.00
4	MO-17	59.33	1.00	0.90	10.07	5.97	2.75	2.17	28.60	6.74	13.33	34.37	5.00
5	MO-19	44.37	1.03	0.70	11.50	6.86	2.50	2.75	28.66	15.40	9.87	24.37	5.00
6	Khara Rata	69.30	1.20	0.80	9.87	6.18	2.66	2.33	22.50	16.93	11.43	48.60	5.00
7	Mayekar Bhat	54.57	1.00	0.70	10.77	6.18	3.07	2.01	28.45	18.82	11.68	52.83	3.33
8	Munga	61.30	0.82	0.53	10.63	6.16	3.06	2.01	25.61	13.48	5.85	33.57	5.00
9	Mahsad	67.27	1.10	0.63	7.93	6.48	3.00	2.16	27.02	9.57	1.70	43.60	5.00
10	Waksal-207	62.77	1.13	0.63	8.83	6.46	2.96	2.18	28.46	10.70	19.33	73.67	5.00
11	Barnill	58.67	1.17	0.73	9.33	6.09	2.89	2.11	25.34	9.76	17.43	28.37	5.00
12	Jyoti	47.53	0.72	0.63	9.40	5.20	2.79	1.86	26.99	3.87	18.27	28.53	3.00
13	Patani-6	71.60	1.03	1.00	8.70	5.94	3.08	1.93	21.67	7.30	14.23	48.13	5.00
14	Bhadas-79	46.83	0.70	0.80	9.83	5.53	2.56	2.16	20.72	13.53	9.99	52.83	5.00
15	Pandy	48.47	0.80	0.90	8.83	6.39	2.82	2.27	25.42	11.60	12.63	38.70	5.00
16	Dular	44.37	1.00	0.70	8.80	6.85	2.84	2.41	27.16	4.63	2.45	53.60	5.00
17	Try-1	62.93	1.10	0.83	9.50	6.98	3.10	2.26	17.72	2.15	5.53	68.47	3.00
18	Kochari	61.63	0.93	0.70	10.20	5.46	2.27	2.41	26.85	4.97	2.00	28.67	5.00
19	Lal Patani	41.13	1.00	0.60	8.43	7.61	2.25	3.38	29.40	18.53	8.83	63.50	5.00
20	Dodak	36.17	0.95	0.53	9.47	7.04	2.18	3.24	27.24	2.03	8.33	38.33	3.00
21	Karhad	45.43	1.17	0.80	9.50	7.10	2.84	2.50	20.35	6.67	18.17	43.47	3.00
22	Ratnagiri 7	52.77	1.20	0.90	9.77	5.70	2.81	2.03	21.30	17.54	15.72	34.20	5.00
23	Bela	60.43	1.17	0.90	9.00	6.46	3.11	2.08	19.49	9.35	10.68	63.60	5.00
24	Valai	57.57	1.00	1.00	9.83	6.42	3.10	2.07	22.73	5.58	15.52	58.47	5.00
25	KJT-1R	47.47	1.30	0.60	10.73	7.24	2.64	2.74	21.62	5.00	15.50	62.70	5.00
26	KJT-2R	43.40	0.90	0.60	9.40	7.03	2.28	3.08	27.39	1.09	11.50	72.57	5.00
27	KJT-3R	52.57	1.10	0.80	8.73	7.47	2.33	3.21	25.37	8.68	14.42	39.10	5.00
28	KJT-4R	43.17	1.33	0.70	10.40	7.64	2.24	3.41	25.49	5.90	16.35	32.90	4.33
29	PR-114	46.27	1.30	0.97	11.40	7.13	2.29	3.12	24.97	7.92	18.58	38.50	4.33
30	RTN 11-2-1-	41.30	0.93	0.90	10.87	7.68	2.23	3.44	23.64	18.42	17.47	32.90	4.33
31	PR-118	55.00	1.30	0.90	12.60	7.32	2.28	3.22	14.46	14.67	17.78	32.60	4.00
32	DRR-215	52.00	1.20	0.83	15.07	7.24	2.24	3.24	22.59	16.35	22.25	38.27	5.00
33	RTN-69-1-1	60.40	1.00	0.80	10.40	7.08	2.10	3.37	23.36	13.80	12.68	48.13	4.33
34	NAUR-1	54.23	1.20	0.80	11.20	7.00	2.31	3.03	19.43	13.37	12.58	44.23	4.33
35	BL-184AR	51.27	1.23	0.70	10.53	5.81	2.17	2.68	23.80	17.83	13.25	42.87	4.33
36	Gurjari	32.97	1.10	0.77	8.87	7.23	2.67	2.70	24.36	17.83	10.10	28.67	3.67
37	DRR-50-12	69.07	1.17	0.77	9.73	6.57	2.36	2.79	23.67	20.70	17.28	28.37	5.00
38	DRR-363-5	65.53	1.20	0.87	8.87	6.27	2.64	2.38	30.76	12.60	21.32	28.00	5.00
39	DRR-50-13	56.63	1.00	0.83	12.33	6.18	2.04	3.03	28.53	18.40	12.53	68.93	5.00
40	DRR-50-10	55.63	0.93	0.77	9.80	6.21	2.37	2.62	25.70	12.40	5.83	73.60	5.00
41	DRR-86-8	51.47	1.10	0.57	10.67	7.16	2.28	3.14	29.45	18.15	17.58	74.00	3.67
42	IR-63879-19	38.00	1.10	0.60	10.87	8.01	2.03	3.94	29.65	13.58	15.12	79.13	5.00
43	RTN-27-1-1-	39.47	1.10	0.80	9.67	6.86	2.19	3.14	29.42	15.43	16.52	84.23	4.33
44	RTN-214-1-3	30.37	0.80	0.50	9.67	6.92	2.22	3.11	28.60	9.40	21.28	92.57	3.67
45	VDN-9-10-1	52.43	1.03	0.77	11.60	5.54	2.24	2.47	28.20	9.03	6.28	83.57	3.67
46	VDN-10-18	67.23	1.10	0.87	11.20	6.87	2.04	3.36	27.64	13.65	18.30	59.10	5.00
47	RTN-35-1-1	53.93	1.10	0.70	11.80	7.22	2.29	3.15	25.29	8.97	15.20	73.67	5.00
48	Sahyadri 5 R	33.43	1.40	0.57	10.73	6.81	2.65	2.57	23.97	8.47	21.42	64.00	5.00
49	HRTMS-61	59.37	1.30	0.50	9.87	5.76	1.61	3.57	25.09	9.67	5.05	28.60	5.00
50	CR-3993-2-2	54.33	1.50	0.80	9.87	6.85	2.69	2.55	22.86	6.65	13.35	63.33	5.00
51	P Basmati	64.43	1.10	0.80	10.53	7.61	1.77	4.30	21.25	17.80	11.25	48.47	5.00
52	S Basmati	45.50	1.30	0.80	15.80	7.80	1.81	4.31	22.74	12.62	13.17	67.20	5.00
53	Kothambir Sa	53.60	0.80	0.77	11.53	4.03	2.87	1.41	21.47	19.13	13.27	79.10	5.00
54	Chinoor	37.17	1.30	0.77	10.60	7.17	2.08	3.45	20.06	6.90	15.27	62.73	5.00
55	P Sugandha-1	43.00	1.10	0.70	9.87	8.02	2.19	3.67	23.38	7.25	14.33	31.70	5.00
56	P Sugandha-3	43.00	1.13	0.63	10.87	8.02	2.35	3.41	19.80	11.20	19.08	69.07	5.00
57	P Sugandha-4	40.60	1.30	0.63	10.27	7.83	2.67	2.93	20.33	11.42	17.98	38.50	3.33
58	P Sugandha-5	50.23	1.10	0.70	10.47	7.63	2.28	3.35	22.46	5.00	9.32	40.07	5.00
59	Bhadasbhog	61.20	1.00	0.70	14.33	7.19	2.15	3.34	25.18	14.33	12.38	57.40	5.00
60	CR2713-180	54.53	1.30	0.60	11.87	6.84	2.16	3.17	19.53	16.75	15.60	47.33	5.00
61	Kalnamak	53.33	0.87	0.70	13.27	5.79	2.43	2.38	26.61	13.20	28.00	69.00	5.00
62	NDR6315	67.63	0.70	0.70	10.33	5.90	2.45	2.40	16.99	18.22	14.17	55.00	3.00
63	P Samruddhi	39.43	1.13	0.80	11.07	7.24	2.39	3.03	19.46	13.95	10.42	69.43	5.00
64	Indrayani	47.43	0.90	0.70	10.47	7.25	2.26	3.20	16.73	13.67	17.32	41.67	5.00
65	Dhanesal	66.20	1.03	0.70	12.80	7.18	2.41	2.98	23.80	13.73	12.75	63.00	5.00
66	Ambemohar	51.60	0.93	0.60	12.47	4.91	2.40	2.05	21.52	20.08	9.45	87.67	3.00
67	K Shatabdi	41.37	1.00	0.60	10.60	5.02	2.47	2.03	19.24	12.60	16.45	43.33	5.00
68	Bhogwati	38.40	0.90	0.70	11.53	8.04	1.87	4.29	21.26	15.82	18.25	102.00	5.00
69	Sugandha	51.30	1.33	0.80	13.87	8.17	2.39	3.42	17.15	8.00	5.72	3.63	3.00
70	RS-1113	44.83	1.50	0.70	10.67	5.86	1.85	3.17	14.61	19.02	11.33	83.33	5.00
71	RP Bio 197	50.47	1.10	0.90	9.33	7.10	2.26	3.14	29.31	17.40	11.40	42.67	5.00
72	RP-BIO-226	52.57	1.40	1.00	9.07	6.90	2.35	2.94	29.97	17.90	1.92	40.33	5.33
73	Ajaya	51.63	1.30	0.93	9.73	5.81	2.25	2.58	34.99	10.27	13.13	55.33	4.33
74	KJT 1	57.47	0.97	0.77	11.47	5.63	2.35	2.39	21.17	9.62	10.78	72.67	4.33
75	KJT 2	33.17	1.10	0.80	10.60	7.19	2.03	3.55	18.50	7.68	10.67	82.00	4.33
76	IR-64	36.70	1.20	0.70	11.00	7.17	2.22	3.23	19.68	4.93	10.47	80.67	4.00
77	MUDGO	49.37	1.40	0.60	10.40	7.13	2.25	3.16	11.67	7.18	8.80	67.67	5.00
78	MILYANG 4	40.83	1.10	0.70	10.80	7.16	2.28	3.14	12.49	2.17	10.32	84.00	4.33
79	PTB 33	51.00	1.33	0.80	10.80	7.62	2.29	3.33	23.27	22.62	13.45	63.00	4.33
80	MTU1010	41.50	0.90	0.70	9.93	7.42	2.33	3.19	27.66	6.88	11.58	57.67	4.33
81	BG 367-2	44.17	1.20	0.70	10.87	7.99	2.18	3.66	14.33	4.50	8.67	101.33	3.67
82	MILYANG 6	33.17	1.20	0.70	8.60	7.46	2.58	2.89	30.79	16.23	11.48	76.33	5.00
83	FL 478	57.13	1.17	0.93	8.33	6.83	2.86	2.39	29.12	19.23	14.95	72.00	5.00
84	MUT NS 1	50.43	1.20	0.83	10.53	6.23	2.56	2.44	25.70	12.52	12.00	38.00	5.00
85	R HEENATI	36.93	1.10	0.73	10.53	6.92	2.70	2.56	23.46	6.83	10.52	38.67	5.00
86	S SIVAPPU	43.30	1.00	0.70	10.33	8.01	2.49	3.21	24.76	14.67	21.50	45.67	3.67
87	IRRI 190	34.43	1.23	0.70	10.73	7.07	2.60	2.72	23.45	8.00	11.12	42.00	5.00
88	IRRI 193	41.37	0.80	0.90	9.07	7.42	2.30	3.22	16.28	19.22	16.25	57.67	4.33
89	ARC 10550	44.53	0.80	0.60	9.87	7.48	2.28	3.28	15.96	16.50	10.48	36.00	3.67

Table 4.4 Mean performance for grain yield and its component traits of 95 rice genotypes, location 2, year 2, RARS, Karjat Part 1/2

SN	Character Genotype	DFF (Nos.) 1	PHT (cm) 2	SLEP (cm) 3	TLPP (Nos.) 4	PLMA (cm) 5	SPP (Nos.) 6	Fertility (%) 7	DM (Days) 8	TW (gm) 9	GL (mm) 10	GW (mm) 11	GYP (gm) 12	SYPP (gm) 13	G/S 14	S/G 15
1	MO-6	90.00	91.59	63.29	12.32	28.30	206.46	93.76	120.00	21.36	8.15	3.16	18.46	23.53	0.79	1.28
2	MO-8	85.00	77.14	53.03	12.11	24.10	133.08	85.01	115.00	18.53	8.68	2.79	12.65	19.83	0.64	1.57
3	MO-13	89.67	112.69	86.38	11.54	26.30	114.57	84.32	119.67	18.78	8.78	3.03	17.81	21.93	0.82	1.23
4	MO-17	87.00	101.82	77.98	11.74	23.84	126.91	83.53	117.00	25.29	8.22	3.25	14.08	17.22	0.82	1.22
5	MO-19	81.67	88.44	64.14	13.17	24.30	117.69	82.30	111.67	22.52	9.50	2.97	15.36	19.72	0.78	1.28
6	Khara Rata	91.00	143.16	113.59	11.54	29.57	73.06	77.21	121.00	26.99	9.03	3.49	11.42	14.87	0.77	1.30
7	Mayekar Bhat	85.00	140.88	115.24	12.44	25.64	102.85	87.66	115.00	26.45	8.49	3.18	9.65	12.96	0.74	1.34
8	Munga	96.00	141.75	116.45	12.30	25.30	121.75	94.48	126.00	24.45	8.52	3.41	14.30	17.89	0.80	1.25
9	Mahsad	90.00	162.44	136.74	9.60	25.70	198.78	90.11	120.00	25.16	9.16	3.45	17.78	22.39	0.79	1.26
10	Waksal-207	85.00	140.13	114.56	10.50	25.57	112.27	80.17	115.00	23.92	9.35	3.46	15.05	19.55	0.77	1.30
11	Barmil	93.00	161.35	132.78	11.00	28.57	166.26	91.52	123.00	27.57	9.17	3.44	18.13	22.16	0.82	1.22
12	Jyoti	83.00	133.88	107.51	11.07	26.37	124.76	82.60	113.00	27.16	7.50	3.21	22.53	32.30	0.70	1.44
13	Patani-6	94.33	161.64	134.67	10.37	26.97	139.91	92.59	124.33	23.56	8.30	3.75	19.32	24.14	0.80	1.25
14	Bhadas-79	92.67	145.34	117.37	11.50	27.97	131.32	90.13	122.67	23.09	7.83	2.93	10.71	8.60	0.74	0.84
15	Pandya	91.00	158.94	131.97	10.50	26.97	139.77	92.76	121.00	23.92	9.00	3.52	14.07	17.22	0.82	1.22
16	Dular	91.00	97.37	73.26	10.47	24.10	95.81	88.90	121.00	24.99	9.33	3.16	9.24	12.30	0.75	1.33
17	Try-1	91.67	167.46	136.15	11.17	31.30	97.25	57.54	121.67	23.92	10.20	3.51	11.76	14.31	0.82	1.22
18	Kochari	79.00	166.19	133.15	11.87	33.04	99.62	88.19	109.00	26.84	10.28	3.91	16.49	25.30	0.65	1.54
19	Lal Patani	76.00	105.09	78.66	10.10	26.44	101.74	63.88	106.00	24.59	10.66	2.71	12.33	16.93	0.73	1.38
20	Dodak	74.33	90.72	63.68	11.14	27.04	55.50	77.84	104.33	26.76	9.85	2.51	16.28	20.17	0.81	1.23
21	Karhad	73.33	89.60	66.36	11.17	23.24	92.82	79.65	103.33	26.92	9.92	3.12	13.48	17.75	0.76	1.32
22	Ratnagiri 7	85.00	107.07	82.23	11.44	24.84	131.87	92.18	115.00	25.69	8.40	3.14	20.46	25.17	0.81	1.23
23	Bela	93.67	157.95	130.38	10.67	27.57	263.79	87.42	123.67	29.29	9.10	3.52	11.43	14.26	0.80	1.25
24	Vajai	95.00	158.46	132.29	11.50	26.17	163.86	93.91	125.00	25.78	9.12	3.54	13.39	17.53	0.77	1.31
25	KJT-1R	97.33	133.09	102.62	12.12	30.47	134.38	86.40	127.33	28.15	9.81	2.68	28.57	33.51	0.85	1.17
26	KJT-2R	85.00	132.58	104.09	10.79	28.49	141.23	84.11	115.00	20.79	10.15	2.74	21.49	31.17	0.69	1.46
27	KJT-3R	96.33	136.03	108.09	10.12	27.95	178.78	92.74	126.33	24.65	10.49	2.27	21.90	27.36	0.80	1.25
28	KJT-4R	85.00	109.09	83.69	11.79	25.40	152.43	79.17	115.00	23.04	10.61	2.49	15.64	21.38	0.73	1.37
29	PR-114	83.00	125.41	99.09	12.79	26.32	154.55	93.25	113.00	18.28	10.01	2.76	16.73	24.24	0.69	1.45
30	RTN 11-2-1-3	92.00	97.98	70.42	12.25	27.56	174.26	76.02	122.00	16.58	10.17	2.52	14.63	20.59	0.71	1.41
31	PR-118	98.00	140.75	108.42	13.99	32.33	164.58	82.38	128.00	20.34	11.07	2.69	30.64	46.50	0.66	1.52
32	DRR-215	95.33	159.93	127.55	16.45	32.38	129.60	82.56	125.33	21.66	10.05	2.57	15.29	18.09	0.84	1.19
33	RTN-69-1-1	86.33	144.78	117.35	11.79	27.43	183.14	77.60	116.33	23.06	9.98	2.65	16.59	21.78	0.76	1.31
34	NAUR-1	93.00	113.72	86.89	12.59	26.84	140.28	65.26	123.00	27.83	9.33	2.77	18.88	26.01	0.72	1.38
35	BL-184AR	90.00	115.13	87.49	11.92	27.64	179.72	93.31	120.00	14.48	9.54	3.16	13.00	15.74	0.83	1.21
36	Gurjari	95.00	114.16	91.95	10.25	22.21	170.94	68.06	125.00	26.50	9.38	3.28	22.93	27.51	0.83	1.20
37	DRR-50-12	95.33	142.03	114.29	11.12	27.74	115.18	83.62	125.33	19.44	8.87	2.83	21.99	31.12	0.71	1.41
38	DRR-363-5	97.00	141.28	112.49	10.25	28.80	143.91	81.12	127.00	23.39	8.45	3.05	20.68	23.96	0.86	1.16
39	DRR-50-13	97.00	141.87	111.35	13.72	30.51	111.75	83.69	127.00	21.62	8.64	2.33	23.14	35.77	0.65	1.55
40	DRR-50-10	97.67	137.67	109.22	11.19	28.45	120.57	84.29	127.67	22.66	8.64	3.08	23.03	29.64	0.78	1.29
41	DRR-86-8	88.67	128.30	99.35	12.05	28.95	160.97	96.68	118.67	24.35	9.97	2.65	15.74	21.94	0.72	1.39
42	IR-63879-195-2-2-3-2	83.00	111.85	85.09	12.25	26.76	104.47	94.44	113.00	18.21	10.79	2.61	17.07	24.93	0.69	1.46
43	RTN-27-1-1-2	85.00	122.83	98.09	11.05	24.74	77.72	65.30	115.00	21.37	9.49	2.64	12.08	17.89	0.68	1.49
44	RTN-214-1-1-1-2	91.00	124.51	99.29	11.05	25.23	188.19	86.09	121.00	18.39	9.33	2.53	17.83	20.42	0.88	1.14
45	VDN-9-10-1	90.33	129.92	104.49	12.99	25.43	121.07	90.30	120.33	24.10	8.55	3.01	17.25	26.18	0.66	1.52
46	VDN-10-18	96.67	129.09	102.82	12.59	26.27	164.86	89.19	126.67	13.29	9.35	2.63	14.72	17.85	0.82	1.21
47	RTN-35-1-1	98.33	127.36	101.99	13.19	25.37	103.37	77.06	128.33	17.10	10.00	2.66	20.79	26.97	0.77	1.30
48	Sahyadri 5 R	95.67	154.59	128.42	12.12	26.17	177.17	97.16	125.67	26.76	8.93	3.20	23.93	32.33	0.74	1.36
49	HRTMS-61	99.33	138.98	113.35	11.25	25.62	166.76	84.20	129.33	15.98	9.95	2.54	15.60	26.80	0.59	1.73
50	CR-3993-2-24-45-2	100.00	100.36	74.95	11.25	25.41	177.09	72.81	130.00	20.32	9.32	3.24	20.98	28.74	0.73	1.38
51	P Basmati	99.00	129.30	101.52	12.47	27.78	161.56	94.06	129.00	22.55	8.59	2.56	14.69	22.88	0.64	1.56
52	S Basmati	107.00	127.93	104.11	17.58	23.83	125.41	83.62	137.00	20.89	9.82	2.63	22.33	35.44	0.63	1.59
53	Kothambir Sal	105.67	163.03	135.46	13.20	27.58	105.62	87.50	135.67	11.58	6.03	3.03	12.13	17.71	0.69	1.47
54	Chinoor	92.33	95.93	68.51	12.25	27.43	114.27	83.54	122.33	14.27	10.33	2.24	10.96	15.61	0.71	1.43
55	P Sugandha-1	86.33	99.45	71.23	11.64	28.22	107.07	96.47	116.33	23.02	10.62	2.59	17.48	27.31	0.64	1.57
56	P Sugandha-3	85.00	107.53	79.61	12.35	27.93	181.77	93.95	115.00	24.99	10.22	2.63	18.59	25.91	0.72	1.39
57	P Sugandha-4	91.33	94.51	67.13	12.07	27.38	77.43	79.31	121.33	24.79	9.25	2.69	12.93	20.18	0.64	1.56
58	P Sugandha-5	88.00	127.41	100.15	12.29	27.27	110.11	86.21	118.00	26.89	9.39	3.00	15.86	21.04	0.75	1.33
59	Bhadasbhog	87.33	179.90	148.49	16.03	31.41	126.32	85.43	117.33	10.74	10.10	2.24	13.85	21.11	0.66	1.52
60	CR2713-180	79.33	131.77	99.36	13.70	32.41	107.79	79.42	109.33	16.39	10.01	2.25	22.36	32.81	0.68	1.47
61	Kalanamak	111.33	173.12	143.67	15.21	29.45	155.57	82.64	141.33	20.35	8.41	2.69	14.03	18.04	0.78	1.29
62	NDR6315	95.67	193.22	156.75	12.16	36.47	81.12	88.45	125.67	14.87	8.25	2.52	25.06	30.78	0.82	1.23
63	P Samrudhi	90.33	116.71	87.33	12.81	29.38	162.03	89.42	120.33	17.47	10.87	2.44	15.86	23.01	0.69	1.45
64	Indrayani	90.33	106.91	79.46	12.27	27.45	162.76	89.04	120.33	15.54	10.53	2.46	12.43	17.88	0.69	1.44
65	Dhanesal	82.33	164.39	135.30	14.78	29.09	128.93	92.90	112.33	13.36	10.44	2.34	10.99	14.61	0.75	1.33
66	Ambemohar	95.33	143.02	111.12	14.26	31.90	156.82	93.46	125.33	13.09	6.99	2.72	14.43	20.11	0.71	1.40
67	K Shatabdi	89.00	105.89	79.25	12.46	26.64	107.32	91.21	119.00	13.31	7.40	2.86	16.48	19.71	0.84	1.20
68	Bhogwati	91.33	108.95	81.55	13.56	27.40	104.90	90.66	121.33	22.05	11.10	2.07	17.78	27.28	0.66	1.54
69	Sugandha	86.67	107.85	81.67	15.48	26.19	125.04	91.03	116.67	24.10	11.69	2.28	16.73	26.44	0.63	1.58
70	RS-1113	80.00	117.03	90.01	12.49	27.02	92.02	85.65	110.00	13.68	8.20	2.24	15.12	19.63	0.77	1.30
71	RP Bio 197	87.33	114.67	87.49	11.17	27.17	1									

Table 4.4 Mean performance for grain yield and its component traits of 95 rice genotypes, location 2, year 2, RARS, Karjat Part 2/2														
SN	Character	LL (cm)	LB (cm)	ST (cm)	PPP (Nos.)	DGL (mm)	DGB (mm)	L/B	AC (%)	Zn (ppm)	Fe (ppm)	Ca (ppm)	ASV	
	Genotype	16	17	18	19	20	21	22	23	24	25	26	27	
1	MO-6	49.42	0.99	0.77	10.70	5.81	2.79	2.08	24.53	12.72	12.79	40.47	5.00	
2	MO-8	53.79	1.09	0.68	10.49	6.42	2.47	2.60	26.18	2.99	11.48	19.49	5.00	
3	MO-13	57.59	0.96	0.78	9.92	6.24	2.52	2.48	23.92	10.64	20.86	18.82	5.00	
4	MO-17	59.42	0.99	0.88	10.12	6.01	2.74	2.19	28.74	6.73	13.48	34.69	5.00	
5	MO-19	44.46	1.03	0.68	11.55	6.90	2.49	2.77	28.81	15.39	10.01	24.63	5.00	
6	Khara Rata	69.39	1.19	0.78	9.92	6.22	2.65	2.34	22.65	16.92	11.58	48.85	5.00	
7	Mayekar Bhat	54.66	0.99	0.68	10.82	6.22	3.07	2.03	28.59	18.81	11.83	53.34	3.33	
8	Munga	61.39	0.81	0.52	10.68	6.20	3.06	2.03	25.76	13.47	5.99	33.94	5.00	
9	Mahsad	67.36	1.09	0.62	7.98	6.52	3.00	2.17	27.16	9.56	1.85	44.06	5.00	
10	Waksal-207	62.86	1.13	0.62	8.88	6.50	2.96	2.20	28.60	10.69	19.48	74.17	5.00	
11	Barmil	58.76	1.16	0.72	9.38	6.13	2.89	2.12	25.49	9.75	17.58	28.88	5.00	
12	Jyoti	47.62	0.71	0.62	9.45	5.24	2.79	1.88	27.14	3.86	18.41	28.97	3.00	
13	Patani-6	71.69	1.03	0.98	8.75	5.93	3.07	1.93	21.82	7.29	14.38	48.39	5.00	
14	Bhadas-79	46.92	0.69	0.78	9.88	5.57	2.55	2.18	20.86	13.52	10.13	53.16	5.00	
15	Pandy	48.56	0.79	0.88	8.88	6.43	2.81	2.29	25.57	11.59	12.78	39.14	5.00	
16	Dular	44.46	0.99	0.68	8.85	6.83	2.84	2.41	27.31	4.62	2.59	54.07	5.00	
17	Try-1	63.02	1.09	0.82	9.55	7.02	3.09	2.27	17.87	2.14	5.68	68.82	3.00	
18	Kochari	61.72	0.93	0.68	10.25	5.50	2.27	2.43	27.00	4.96	2.14	29.10	5.00	
19	Lal Patani	41.22	0.99	0.58	8.48	7.65	2.25	3.40	29.55	18.52	8.98	63.75	5.00	
20	Dodak	36.26	0.94	0.52	9.52	7.08	2.17	3.26	27.39	2.02	8.48	38.66	3.00	
21	Karhad	45.52	1.16	0.78	9.55	7.14	2.83	2.52	20.50	6.66	18.31	43.73	3.00	
22	Ratnagiri 7	52.86	1.19	0.88	9.82	5.74	2.80	2.05	21.45	17.53	15.86	34.45	5.00	
23	Bela	60.52	1.16	0.88	9.05	6.50	3.11	2.09	19.64	9.34	10.83	63.92	5.00	
24	Valai	57.66	0.99	0.98	9.88	6.46	3.10	2.09	22.88	5.57	15.66	58.84	5.00	
25	KJT-1R	47.69	1.29	0.59	11.12	7.27	2.66	2.73	21.18	5.01	15.43	62.80	5.00	
26	KJT-2R	43.47	0.93	0.61	9.79	7.06	2.30	3.07	26.96	1.12	11.45	72.69	5.00	
27	KJT-3R	52.52	0.82	0.84	9.12	7.45	2.31	3.23	24.98	8.75	14.39	39.25	5.00	
28	KJT-4R	43.10	1.04	0.70	10.79	7.58	2.21	3.43	25.06	5.92	16.29	33.01	4.33	
29	PR-114	46.33	1.13	0.96	11.79	7.17	2.31	3.11	24.53	7.93	18.51	38.60	4.33	
30	RTN 11-2-1-3	41.07	0.47	0.90	11.25	7.71	2.25	3.43	23.20	18.44	17.40	33.01	4.33	
31	PR-118	55.09	1.16	0.95	12.99	7.36	2.30	3.20	14.08	14.74	17.77	32.76	4.00	
32	DRR-215	52.11	1.08	0.87	15.45	7.28	2.26	3.22	22.19	16.40	22.22	38.41	5.00	
33	RTN-69-1-1	60.39	0.76	0.82	10.79	7.11	2.12	3.36	22.95	13.84	12.64	48.26	4.33	
34	NAUR-1	54.36	1.09	0.79	11.59	7.03	2.33	3.02	18.99	13.38	12.51	44.33	4.33	
35	BL-184AR	51.50	1.23	0.69	10.92	5.85	2.19	2.67	23.35	17.84	13.17	42.96	4.33	
36	Gurjari	33.08	0.98	0.83	9.25	7.26	2.69	2.70	23.99	17.92	10.10	28.84	3.67	
37	DRR-50-12	69.09	0.96	0.81	10.12	6.61	2.38	2.78	23.28	20.76	17.26	28.52	5.00	
38	DRR-363-5	65.62	1.06	0.93	9.25	6.31	2.66	2.37	30.39	12.68	21.31	28.17	5.00	
39	DRR-50-13	56.90	1.03	0.89	12.72	6.21	2.06	3.02	28.15	18.47	12.52	69.09	5.00	
40	DRR-50-10	55.71	0.78	0.76	10.19	6.25	2.39	2.62	25.25	12.41	5.76	73.70	5.00	
41	DRR-86-8	51.61	1.02	0.59	11.05	7.20	2.30	3.12	29.04	18.19	17.54	74.13	3.67	
42	IR-63879-195-2-2-3-2	38.31	1.18	0.64	11.25	8.11	2.05	3.95	29.26	13.65	15.09	79.28	5.00	
43	RTN-27-1-1-2	39.36	0.77	0.83	10.05	6.90	2.21	3.13	29.01	15.49	16.48	84.37	4.33	
44	RTN-214-1-1-1-2	30.40	0.61	0.51	10.05	6.95	2.24	3.10	28.17	9.43	21.23	92.69	3.67	
45	VDN-9-10-1	52.68	1.05	0.78	11.99	5.58	2.26	2.47	27.78	9.07	6.23	83.69	3.67	
46	VDN-10-18	67.27	0.91	0.86	11.59	6.91	2.06	3.35	27.19	13.66	18.23	59.20	5.00	
47	RTN-35-1-1	53.82	0.75	0.70	12.19	7.26	2.31	3.14	24.85	8.99	15.14	73.78	5.00	
48	Sahyadri 5 R	33.45	1.19	0.61	11.12	6.85	2.67	2.57	23.57	8.53	21.39	64.15	5.00	
49	HRTMS-61	59.51	1.22	0.55	10.25	5.80	1.63	3.55	24.71	9.74	5.04	28.76	5.00	
50	CR-3993-2-24-45-2	54.65	1.58	0.79	10.25	6.89	2.71	2.54	22.41	6.66	13.27	63.43	5.00	
51	P Basmati	64.54	1.12	0.82	11.47	7.60	1.75	4.34	20.71	18.05	11.37	48.70	5.00	
52	S Basmati	45.45	1.34	0.84	16.58	7.81	1.80	4.34	22.20	12.87	13.28	67.43	5.00	
53	Kothambir Sal	53.44	0.87	0.84	12.20	4.01	2.85	1.41	20.94	19.38	13.38	79.33	5.00	
54	Chinoor	36.99	1.33	0.80	11.25	7.15	2.06	3.47	19.53	7.15	15.38	62.96	5.00	
55	P Sugandha-1	42.95	1.12	0.72	10.64	8.00	2.17	3.69	22.85	7.50	14.45	31.93	5.00	
56	P Sugandha-3	42.65	1.16	0.66	11.35	8.00	2.33	3.43	19.26	11.45	19.20	69.30	5.00	
57	P Sugandha-4	40.57	1.38	0.71	11.07	7.81	2.65	2.95	19.79	11.67	18.10	38.73	3.33	
58	P Sugandha-5	50.23	1.16	0.76	11.29	7.61	2.26	3.37	21.92	5.25	9.43	40.30	5.00	
59	Bhadasbhog	61.07	1.05	0.75	15.03	7.16	2.13	3.36	24.64	14.58	12.50	57.63	5.00	
60	CR2713-180	54.54	1.32	0.62	12.70	6.82	2.14	3.19	18.99	17.00	15.72	47.56	5.00	
61	Kalanamak	53.45	0.88	0.71	14.21	5.76	2.41	2.39	26.08	13.45	28.12	69.23	5.00	
62	NDR6315	67.63	0.79	0.79	11.16	5.88	2.43	2.42	16.46	18.47	14.28	55.23	3.00	
63	P Samuddhi	39.34	1.20	0.87	11.81	7.22	2.37	3.05	18.92	14.20	10.53	69.66	5.00	
64	Indrayani	47.41	0.99	0.79	11.27	7.22	2.24	3.22	16.19	13.92	17.43	41.90	5.00	
65	Dhanesal	66.35	1.11	0.78	13.78	7.15	2.39	2.99	23.26	13.98	12.87	63.23	5.00	
66	Ambemohar	51.56	0.95	0.62	13.26	4.89	2.38	2.05	20.98	20.33	9.57	87.90	3.00	
67	K Shatabdi	41.40	1.05	0.65	11.46	4.99	2.45	2.04	18.70	12.85	16.57	43.56	5.00	
68	Bhogwati	38.60	0.97	0.77	12.56	8.01	1.85	4.32	20.72	16.07	18.37	102.23	5.00	
69	Sugandha	51.08	1.39	0.86	14.48	8.14	2.37	3.44	16.62	8.25	5.83	3.86	3.00	
70	RS-1113	44.31	1.50	0.71	11.49	5.84	1.83	3.20	14.92	19.08	11.52	84.79	5.00	
71	RP Bio 197	49.96	1.12	0.93	10.17	7.08	2.24	3.16	29.46	17.32	11.43	43.97	5.00	
72	RP-BIO-226	52.09	1.45	1.06	9.90	6.88	2.33	2.96	30.01	17.70	1.83	41.52	5.33	
73	Ajaya	51.12	1.31	0.96	10.53	5.79	2.23	2.59	35.01	10.05	13.03	56.50	4.33	
74	KJT 1	56.94	0.97	0.78	12.19	5.61	2.33	2.41	21.32	9.53	10.81	73.96	4.33	
75	KJT 2	32.65	1.11	0.82	11.26	7.17	2.01	3.57	18.35	7.30	10.40	83.00	4.33	
76	IR-64	36.24	1.26	0.77	11.71	7.15	2.20	3.25	19.85	4.87	10.52	81.99	4.00	
77	MUDGO	48.88	1.44	0.65	11.16	7.11	2.23	3.18	11.86	7.14	8.87	69.01	5.00	
78	MILYANG 46	40.34	1.13	0.74	11.55	7.14	2.26	3.16	12.56	2.00	10.27	85.22	4.33	
79	PTB 33	50.48	1.34	0.81	11.42	7.60	2.27	3.35	23.48	22.59	13.54	64.36	4.33	
80	MTU1010	40.97	0.90	0.71	10.65	7.40	2.31	3.21	27.97	6.96	11.78	59.13	4.33	
81	BG 367-2	43.71	1.27	0.78	11.66	7.97	2.16	3.68	14.52	4.46	8.74	102.68	3.67	
82	MILYANG 63	32.69	1.25	0.76	9.47	7.44	2.56	2.90	30.90	16.11	11.47	77.59	5.00	
83	FL 478	56.68	1.24	1.02	9.12	6.81	2.84	2.40	29.29	19.17	15.00	73.32	5.00	
84	MUT NS 1	49.97	1.26	0.91	11.31	6.21	2.54	2.45	26.05	12.63	12.23	39.50	5.00	
85	R HEENATI	36.41	1.10	0.75	11.15	6.90	2.68	2.57	23.62	6.76	10.56	39.98	5.00	
86	S SIVAPPU	42.81	1.03	0.74	10.98	7.99	2.47	3.23	24.99	14.66	21.61	47.05	3.67	
87	IRRI 190	33.96	1.29	0.76	11.50	7.05	2.58	2.73	23.84	8.16	11.39	43.55	5.00	
88	IRRI 193	40.88	0.84	0.95	9.93	7.40	2.28	3.24	16.26	18.96	16.11	58.80	4.33	
89	ARC 10550	44.03	0.82	0.63	10.58	7.46	2.26	3.30						

Table 4.5 Genetic parameters of yeild and 27 yield contributing characters Location-1 Year-1 Kharif 2020 ARS, Shirgaon

SN	Characters	$\bar{X}$	Range				Variance/ σ^2			Coefficient of Variance			h^2 (bs)	GAM (5%)	SE $\pm$	CD (5%)	CV %
			Min.	Name	Max.	Name	σ^2_g	σ^2_p	σ^2_e	GCV %	PCV %	ECV %					
1	DFF (Nos.)	91.48	73.00	IRRI-104	112.00	Kalanamak	49.91	51.56	1.65	7.72	7.85	1.40	97.00	14.32	0.74	2.07	1.40
2	PHT (cm)	123.67	78.37	MO-8	192.33	NDR6315	650.23	666.44	16.21	20.62	20.87	3.26	98.00	51.89	2.32	6.48	3.26
3	SLEP (cm)	96.86	54.83	MO-8	156.67	NDR6315	595.79	610.89	15.10	25.20	25.52	4.01	98.00	49.66	2.24	6.26	4.01
4	TLPP (Nos.)	11.56	8.93	Mahsad	21.73	TN-1	2.84	3.35	0.51	14.57	15.82	6.16	85.00	3.20	0.41	1.15	6.16
5	PLMA (cm)	26.87	22.13	IRRI-104	35.67	NDR6315	5.23	6.46	1.23	8.51	9.46	4.13	81.00	4.24	0.64	1.79	4.13
6	SPP (Nos.)	131.45	55.31	IRRI-190	300.48	Ajaya	1654.31	1712.62	58.32	30.94	31.48	5.81	97.00	82.35	4.41	12.30	5.81
7	Fertility (%)	86.00	57.54	Try-1	98.07	IRRI-192	61.81	62.43	0.62	9.14	9.19	0.92	99.00	16.11	0.46	1.27	0.92
8	DM (Days)	121.48	103.00	IRRI-104	142.00	Kalanamak	49.91	51.56	1.65	5.82	5.91	1.06	97.00	14.32	0.74	2.07	1.06
9	TW (g)	21.83	11.22	Bhadasbhog	29.13	Bela	17.83	19.22	1.39	19.34	20.08	5.40	93.00	8.38	0.68	1.90	5.40
10	GL (mm)	9.42	5.99	Kothimbir sal	11.65	Sugandha	1.05	1.12	0.07	10.83	11.18	2.76	94.00	2.05	0.15	0.42	2.76
11	GW (mm)	2.87	2.23	S. Mahsuri	3.90	Kochari	0.13	0.14	0.01	12.55	12.79	2.48	96.00	0.73	0.04	0.11	2.48
12	GYPP(g)	17.11	9.22	Dular	32.27	PR-118	18.61	19.62	1.01	25.21	25.88	5.86	95.00	8.66	0.58	1.62	5.86
13	SYPP (g)	23.35	12.33	Dular	46.33	PR-118	36.78	38.63	1.85	25.98	26.62	5.83	95.00	12.19	0.79	2.19	5.83
14	G/S ratio	0.74	0.51	Chinoor	0.94	Gurjari	0.01	0.01	0.00	10.23	12.25	6.75	70.00	0.13	0.03	0.08	6.75
15	S/G ratio	1.37	1.07	Gurjari	1.96	Chinoor	0.02	0.03	0.01	11.23	13.13	6.80	73.00	0.27	0.05	0.15	6.80
16	LL (cm)	49.62	30.37	RTN-214-1-1-1-2	71.60	Patni-6	97.28	97.86	0.57	19.88	19.94	1.52	99.00	20.26	0.44	1.22	1.52
17	LB (cm)	1.10	0.70	Bhadas-79	1.50	CR-3993-2-24-45-2	0.03	0.04	0.01	15.04	17.64	9.22	73.00	0.29	0.06	0.16	9.22
18	ST (cm)	0.74	0.50	RTN-214-1-1-1-2	1.00	Patni-6	0.01	0.02	0.01	14.48	17.89	10.51	66.00	0.18	0.04	0.13	10.51
19	PPP (Nos.)	10.56	7.93	Mahsad	20.73	TN-1	2.84	3.35	0.51	15.95	17.32	6.74	85.00	3.20	0.41	1.15	6.74
20	DGL (mm)	6.76	4.03	Kothimbir sal	8.17	Sugandha	0.77	0.78	0.01	12.94	13.03	1.48	99.00	1.80	0.06	0.16	1.48
21	DGB (mm)	2.42	1.61	HRTMS-61	3.11	Bela	0.10	0.11	0.01	12.68	13.59	4.89	87.00	0.59	0.07	0.19	4.89
22	L/B ratio	2.85	1.41	Kothimbir sal	4.30	P. Basmati	0.34	0.38	0.04	20.29	21.41	6.83	90.00	1.14	0.11	0.32	6.83
23	AC (%)	23.15	11.67	MUDGO	34.99	Ajaya	22.59	23.74	1.15	20.53	21.04	4.63	95.00	9.55	0.62	1.73	4.63
24	Zn (ppm)	11.95	1.09	KJT-2R	22.62	PTB-33	29.78	30.24	0.47	45.67	46.02	5.71	99.00	11.15	0.39	1.10	5.71
25	Fe (ppm)	13.11	1.70	Mahsad	28.00	Kalanamak	22.98	23.40	0.42	36.58	36.91	4.96	98.00	9.79	0.38	1.05	4.96
26	Ca (ppm)	53.53	3.63	Sugandha	102.00	Bhogawati	394.28	396.88	2.60	37.09	37.22	3.01	99.00	40.77	0.93	2.60	3.01
27	ASV (Nos.)	4.59	3.00	Jyoti	5.33	RP-BIO226	0.24	0.81	0.57	10.60	19.57	16.45	29.00	0.54	0.44	1.22	16.45

Note- Red - Lowest, Blue- Highest, Orange- Low, Yelllow- Moderate and Green- High

Table 4.6 Genetic parameters of yield and 27 yield contributing characters Location-2 Year-2 Kharif 2021 RARS, Karjat

SN	Characters	$\bar{X}$	Range				Variance/ σ^2			Coefficient of Variance			σ^2 (bs)	GAM (5%)	SE±	CD (5%)	CV %
			Min.	Name	Max.	Name	σ^2_g	σ^2_p	σ^2_e	GCV %	PCV %	ECV %					
1	DFF (Nos.)	90.41	72.33	IRRI-104	111.33	Kalanamak	51.34	53.59	2.25	7.93	8.10	1.66	96.00	14.45	0.87	2.41	1.66
2	PHT (cm)	123.91	77.14	MO-8	193.22	NDR6315	638.10	655.30	17.21	20.39	20.66	3.35	97.00	51.35	2.39	6.68	3.35
3	SLEP (cm)	96.63	53.03	MO-8	156.75	NDR6315	581.94	597.10	15.16	24.97	25.29	4.03	98.00	49.06	2.25	6.27	4.03
4	TLPP (Nos.)	12.20	9.60	Mahsad	22.38	TN-1	2.85	3.41	0.56	13.84	15.13	6.11	84.00	3.18	0.43	1.20	6.11
5	PLMA (cm)	27.28	22.21	Gurjari	36.47	NDR6315	5.16	6.59	1.43	8.33	9.41	4.38	78.00	4.14	0.69	1.93	4.38
6	SPP (Nos.)	131.61	55.50	Dodak	301.00	Ajaya	1655.32	1716.41	61.10	30.92	31.48	5.94	96.00	82.31	4.51	12.59	5.94
7	Fertility (%)	86.06	57.54	Try-1	98.34	IRRI-192	62.43	63.04	0.62	9.18	9.23	0.91	99.00	16.20	0.45	1.26	0.91
8	DM (Days)	120.41	102.33	IRRI-104	141.33	Kalanamak	51.34	53.59	2.25	5.95	6.08	1.25	96.00	14.45	0.87	2.41	1.24
9	TW (g)	21.71	10.74	Bhadasbhog	29.29	Bela	18.71	20.15	1.44	19.92	20.67	5.53	93.00	8.59	0.69	1.93	5.53
10	GL (mm)	9.42	6.03	Kothimbir sal	11.65	Sugandha	1.05	1.12	0.07	10.86	11.19	2.70	94.00	2.05	0.15	0.41	2.70
11	GW (mm)	2.84	2.07	S. Mahsuri	3.91	Kochari	0.14	0.16	0.02	13.32	14.13	4.73	89.00	0.73	0.08	0.22	4.73
12	GYPP(g)	16.94	9.24	Dular	30.64	PR-118	17.85	18.88	1.02	24.95	25.65	5.97	95.00	8.47	0.58	1.63	5.97
13	SYPP (g)	22.70	8.60	Bhdas-79	46.50	PR-118	36.59	38.77	2.18	26.65	27.43	6.50	94.00	12.11	0.85	2.38	6.50
14	G/S ratio	0.84	0.59	HRTMS-61	0.88	RTN-214-1-1-1-2	0.01	2.21	2.20	13.86	17.31	17.77	91.00	0.02	0.86	0.02	6.77
15	S/G ratio	1.34	0.84	Bhdas-79	1.73	HRTMS-61	0.01	0.03	0.01	10.11	12.27	8.49	52.00	0.18	0.07	0.18	8.49
16	LL (cm)	49.52	30.40	RTN-214-1-1-1-2	71.69	Patni-6	99.33	100.07	0.74	20.13	20.20	1.74	99.00	20.46	0.50	1.39	1.74
17	LB (cm)	1.07	0.47	RTN-214-1-1-1-2	1.58	CR-3993-2-24-45-2	0.03	0.07	0.05	14.76	24.91	20.07	75.00	0.19	0.12	0.35	20.07
18	ST (cm)	0.76	0.51	RTN-214-1-1-1-2	1.06	RP-BIO-226	0.01	0.02	0.01	14.42	17.66	10.21	67.00	0.19	0.05	0.13	10.21
19	PPP (Nos.)	11.05	7.98	Mahsad	21.38	TN-1	3.18	3.83	0.64	16.15	17.71	7.27	83.00	3.35	0.46	1.29	7.27
20	DGL (mm)	6.78	4.01	Kothimbir sal	8.14	Sugandha	0.77	0.78	0.01	12.87	12.96	1.46	99.00	1.79	0.06	0.16	1.46
21	DGB (mm)	2.42	1.61	HRTMS-61	3.11	Bela	0.09	0.11	0.02	12.67	13.61	4.97	87.00	0.59	0.07	0.19	4.97
22	L/B ratio	2.85	1.41	Kothimbir sal	4.34	P. Basmati	0.34	0.37	0.04	20.14	21.27	6.84	90.00	1.13	0.11	0.32	6.84
23	AC (%)	23.01	11.86	MUDGO	35.01	Ajaya	22.63	23.82	1.19	20.67	21.21	4.74	95.00	9.55	0.63	1.76	4.74
24	Zn (ppm)	11.99	1.12	KJT-2R	22.59	PTB-33	29.92	30.47	0.55	45.64	46.06	6.20	98.00	11.17	0.43	1.20	6.20
25	Fe (ppm)	13.16	1.83	RP-BIO-226	28.12	Kalanamak	22.87	23.39	0.52	36.32	36.73	5.48	98.00	9.74	0.42	1.16	5.48
26	Ca (ppm)	54.06	3.86	Sugandha	102.68	BG-367-2	397.04	400.70	3.66	36.86	37.03	3.54	99.00	40.86	1.10	3.08	3.54
27	ASV (Nos.)	4.59	3.00	Jyoti	5.33	RP-BIO-226	0.25	0.79	0.55	10.79	19.36	16.08	28.00	0.57	0.43	1.19	16.08

Note- Red - Lowest, Blue- Highest, Orange- Low, Yellow- Moderate and Green- High

Table 4.7 Clustering pattern of 95 genotypes studied at ARS, Shirgaon Year *Kharif*, 2020 based on D² analysis

Cluster Number	Number of genotypes	Genotype number	Genotypes name
I	57	1, 2, 3, 4, 5, 7, 10, 11, 14, 15, 16, 21, 22, 25, 29, 30, 31, 32, 34, 35, 39, 41, 42, 47, 50, 52, 54, 55, 56, 57, 58, 59, 60, 63, 64, 70, 71, 72, 74, 76, 77, 78, 79, 80, 82, 83, 84, 85, 86, 87, 88, 89, 91, 92, 93, 94 and 95	MO-6, MO-8, MO-13, MO-17, MO-19, Mayekar Bhat, Waksal207, Barmil, Bhadas-79, Pandy, Dular, Karhad, Ratnagiri 7, KJT-1R, PR-114, RTN 11-2-1-3, PR-118, DRR-215, NAUR-1, BL-184AR, DRR-50-13, DRR-86-8, IR-63879-195-2-2-3-2, RTN-35-1-1, CR-3993-2-24-45-2, S Basmati, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, P Samruddhi, Indrayani, RS-1113, RP Bio 197, RP-BIO-226, KJT 1, IR-64, MUDGO, MILYANG 46, PTB 33, MTU1010,MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, IRRI 123, IRRI 104, IRRI 192, Sonsali and TN-1
II	1	65	Dhanesal
III	1	46	VDN-10-18
IV	32	6, 8 ,9, 13, 18, 23, 24, 33, 37, 38, 40, 45, 49, 51, 61, 62, 66 and 73	Khara Rata, Munga, Mahsad,, Patani-6, Kochari, Bela , Valai , RTN-69-1-1, DRR-50-12, DRR-363-5, DRR-50-10, VDN-9-10-1, HRTMS-61, P Basmati, Kalanamak, NDR6315, Ambemohar and Ajaya
V	1	67	K Shatabdi
VI	1	81	BG 367-2
VII	1	44	RTN-214-1-1-1-2
VIII	1	26	KJT-2R
IX	1	68	Bhogwati
X	1	48	Sahyadri 5 R
XI	1	27	KJT-3R
XII	1	19	Lal Patani
XIII	1	36	Gurjari
XIV	1	43	RTN-27-1-1-2
XV	1	12	Jyoti
XVI	1	90	S MAHSURI
XVII	1	75	KJT 2
XVIII	1	28	KJT-4R
XIX	1	20	Dodak
XX	1	53	Kothambir Sal
XXI	1	69	Sugandha
XXII	1	17	Try-1

Table 4.8 Clustering patterns of 95 genotypes studied at RARS, Karjat Year *Kharif*, 2021 based on D² analysis

Cluster Number	Number of genotypes	Genotype number	Genotypes name
I	58	1, 2, 3, 4, 5, 7, 8, 11, 14, 15, 16, 21, 22, 24, 25, 26, 29, 30, 32, 33, 35, 39, 40, 41, 42, 47, 50, 51, 52, 54, 55, 56, 57, 58, 59, 60, 63, 64, 67, 71, 72, 74, 76, 77, 78, 79, 80, 82, 84, 85, 86, 87, 88, 89, 91, 93, 94 and 95	MO-6, MO-8, MO-13, MO-17, MO-19, Mayekar Bhat, Munga, Barmil, Bhadas-79, Pandy, Dular, Karhad, Ratnagiri 7, Valai , KJT-1R, KJT-2R, PR-114, RTN 11-2-1-3, DRR-215, RTN-69-1-1, BL-184AR, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-35-1-1, CR-3993-2-24-45-2, P Basmati, S Basmati, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, P Samruddhi, Indrayani, K Shatabdi, RP Bio 197, RP-BIO-226, KJT 1, IR-64, MUDGO, MILYANG-46, PTB 33, MTU1010, MILYANG 63, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, IRRI 123, IRRI 192, Sonsali and TN-1,
II	1	65	Dhanesal
III	1	75	KJT 2
IV	1	45	VDN-9-10-1
V	14	6, 9, 10, 13, 18, 23, 37, 38, 46, 49, 61, 62 and 73	Khara Rata, Mahsad, Waksal-207, Patani-6, Kochari, Bela , DRR-50-12, DRR-363-5, VDN-10-18, HRTMS-61, Kalanamak, NDR6315 and Ajaya
VI	1	68	Bhogwati
VII	1	20	Dodak
VIII	1	92	IRRI 104
IX	1	34	NAUR-1
X	6	43, 44, 53, 66, 70 and 90	RTN-27-1-1-2, RTN-214-1-1-1-2, Kothambir Sal, Ambemohar, RS-1113 and S MAHSURI
XI	1	19	Lal Patani
XII	1	81	BG 367-2
XIII	1	12	Jyoti
XIV	1	48	Sahyadri 5 R
XV	1	69	Sugandha
XVI	1	31	PR-118
XVII	1	36	Gurjari
XVIII	1	27	KJT-3R
XIX	1	28	KJT-4R
XX	1	17	Try-1

Table 4.9 Intra and Intra cluster distances among cluster groups at ARS, Shiragon (Year I Location I)																							
	SN	C L U S T E R D I S T A N C E S																					
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX	XXI	XII
C L U S T E R D I S T A N C E S	I	587.1																					
	II	792.91	0																				
	III	783.45	147.1	0																			
	IV	899.78	532.08	493.74	723.08																		
	V	837.77	1361.03	1250.82	1217.24	0																	
	VI	934.32	911.79	1094.47	1247.34	1694.8	0																
	VII	781.98	1239.14	1240.97	1375.37	1114.04	558.98	0															
	VIII	766.88	914.47	979.18	1020.59	721.25	715.73	809.74	0														
	IX	774.98	913.59	977.29	1224.85	1050.38	363.17	355.94	555.95	0													
	X	790.25	1346.64	1338.69	1349.94	709.23	908.74	440.15	667.87	494.26	0												
	XI	781.14	732.49	685.19	992.05	1134.72	1159.31	1291.51	548.02	832.33	855.81	0											
	XII	772.3	1193.81	1243.27	1238.48	1236.06	1131.62	918.65	822.79	938.51	1392.91	1121.13	0										
	XIII	877.41	1889.74	1741.74	1592.49	1070.06	1743.98	1079.21	1219.09	1382.91	1087.56	1187.07	447.59	0									
	XIV	878.39	1175.54	1166.9	1224.34	894.77	1020.66	786.14	500.52	609.98	1086.32	1128.6	303.76	862.03	0								
	XV	863.62	1392.06	1308.11	1246.97	1296.68	1496.35	1004.64	1454.15	1678.79	1174.38	1647.2	1136.88	946.68	1536.24	0							
	XVI	828.35	1091.2	935.63	1086.17	1063.63	1066.52	728.41	1337.38	921.19	1291.48	1608.17	885.27	1136.78	1039.03	980.83	0						
	XVII	996.59	1502.02	1366.77	1437.69	1181.12	746.59	627.73	687.91	702.98	991.05	1238.45	840.82	985.25	634.92	1580.03	1164.32	0					
	XVIII	878.13	1413.75	1425.12	1614.92	1576.66	1333.07	1135.18	964.17	1144.34	1094.09	527.88	722.06	638.59	1140.08	1220.66	1733.74	1230.29	0				
	XIX	1157.8	1967.47	2089	1972.05	1985.19	1372.62	1115.92	1648.77	1781.66	1707.11	1927.18	882.02	950.9	1603.53	513.87	1267.51	1558.49	924.56	0			
	XX	1421.04	1002.5	935.07	1039.05	1019.8	1649.25	1500.74	1447.52	1380.77	1563.59	2060.97	1919.89	2344.39	1308.49	1948.56	1183.92	1398.47	3076.24	3111.2	0		
	XXI	1083.06	1450.02	1528.41	1635.36	1964.67	1736.59	1736.66	1812.48	2004.43	1773.37	1190.4	1341.19	1099.13	2163.85	864.77	1759.33	1727.15	670.28	719.58	3018.86	0	
	XXII	1624.67	1151.53	1255.29	1292.64	2140.34	1589.48	2172.29	1081.59	1816.52	2405.44	1536.41	1073.68	1962.01	954.21	2188.83	1865.41	1798.23	1905.07	2472.34	1923.25	2771.82	0

Table 4.10 The nearest and farthest clusters from each cluster based on D² value in 95 rice genotypes at Shiragaon

SN	Clusters	Inter cluster distance	
		Farthest cluster	Nearest cluster
1	Cluster I	XXII	VIII
Intra cluster distances	587.1	1624.67	766.88
2	Cluster II	XIX	III
Intra cluster distances	0	1967.47	147.1
3	Cluster III	XIX	IV
Intra cluster distances	0	2089	493.74
4	Cluster IV	XIX	XXI
Intra cluster distances	723.08	1972.05	992.05
5	Cluster V	XXII	X
Intra cluster distances	0	2140.34	709.23
6	Cluster VI	XIII	IX
Intra cluster distances	0	1743.98	363.17
7	Cluster VII	XXII	IX
Intra cluster distances	0	2172.29	355.94
8	Cluster VIII	XXI	XIV
Intra cluster distances	0	1812.48	500.52
9	Cluster IX	XXI	X
Intra cluster distances	0	2004.43	494.26
10	Cluster X	XXII	XI
Intra cluster distances	0	2405.44	855.81
11	Cluster XI	XX	XVIII
Intra cluster distances	0	2060.97	527.88
12	Cluster XII	XX	XIV
Intra cluster distances	0	1919.89	303.76
13	Cluster XIII	XX	XVIII
Intra cluster distances	0	2344.39	638.59
14	Cluster XIV	XXI	XVII
Intra cluster distances	0	2163.85	634.92
15	Cluster XV	XXII	XIX
Intra cluster distances	0	2188.83	513.87
16	Cluster XVI	XXII	XVII
Intra cluster distances	0	1865.41	1164.32
17	Cluster XVII	XXII	XVIII
Intra cluster distances	0	1798.23	1230.29
18	Cluster XVIII	XX	XXI
Intra cluster distances	0	3076.24	670.28
19	Cluster XIX	XX	XXI
Intra cluster distances	0	3111.17	719.58
20	Cluster XX	XXI	XXII
Intra cluster distances	0	3018.86	1923.25
21	Cluster XXI	XX	XII
Intra cluster distances	0	3018.86	1341.19
22	Cluster XXII	XXI	XIV
Intra cluster distances	0	2771.82	954.21

Table 4.11 Intra and Intra cluster distances among cluster groups at RARS, Karjat (Year II Location II)

	SN	C L U S T E R D I S T A N C E S																			
		I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX	XX
C L U S T E R D I S T A N C E S	I	437.13																			
	II	595.43	0																		
	III	594.98	1025.04	0																	
	IV	552.11	452.62	553.16	0																
	V	647.61	392.85	950.07	500.98	481.62															
	VI	612.23	680.31	432.09	539.86	963.61	0														
	VII	695.5	1380.22	769.19	1063.29	1230.1	1197.97	0													
	VIII	572.67	1156.24	500.78	856.04	1128.59	781.82	255.97	0												
	IX	644.78	820.82	598.2	846.54	678.47	1075.02	641.68	633.82	0											
	X	742.24	784.04	666.01	486.15	835.42	658.73	1308.17	887.95	973.58	607.76										
	XI	729.07	1088.4	593.92	943.1	998.74	966.24	483.78	465.97	232.22	991.29	0									
	XII	712.72	729.94	403.26	450.59	991.15	250.75	1085.47	767.1	1089.3	869.28	1069.01	0								
	XIII	571.23	1030.61	881.02	772.34	755.71	1221.71	415.6	527.98	607.68	990.12	822.61	1249.35	0							
	XIV	603.46	1017.97	622.66	752.29	1050	433.15	997.82	737.58	1301.15	886.66	1277.62	650.09	695.64	0						
	XV	670.69	981.44	1112.44	1262.93	1074.67	1217.19	550.78	753.8	770.57	1573.92	969.79	1274.18	756.52	1064.4	0					
	XVI	596.78	731.47	766.29	1005.34	744.5	881.88	959.3	873.95	489.83	1147.64	901.38	1007.55	634.24	834.72	518.62	0				
	XVII	745.65	1501.01	611.12	1260.16	1201.56	1192.61	508.62	510.09	411.75	1190.68	326.25	1426.5	639.66	972.02	719.28	692.36	0			
	XVIII	577.86	591.03	796.05	896.08	778.06	664.83	929.11	1018.53	763.25	1280.21	968.59	778.12	937.06	681.26	366.2	461.56	894.16	0		
	XIX	816.95	1188.34	908.97	1557.16	1308.42	1065.3	541.86	728.18	722.05	1730.06	692.56	1108.87	976.38	1011.67	408.86	645.69	636.93	405.57	0	
	XX	1407.01	1086.44	1213.26	1152.83	1062.82	1830.75	1435.33	1437.53	617.68	1548.93	850.34	1355.28	1418.62	2259.3	1920.54	1469.58	1541.53	1665.85	1579.3	0

Table 4.12 The nearest and farthest clusters from each cluster based on D2 value in 95 rice genotypes at Karjat

S. No.	Clusters	Inter cluster distance	
		Farthest cluster	Nearest cluster
1	Cluster I	XX	IV
Intra cluster distances	437.13	1407.01	552.11
2	Cluster II	XVII	V
Intra cluster distances	0	1501.01	392.85
3	Cluster III	XX	XII
Intra cluster distances	0	1213.26	403.26
4	Cluster IV	XIX	XII
Intra cluster distances	0	1557.16	450.59
5	Cluster V	XIX	IX
Intra cluster distances	481.62	1308.42	678.47
6	Cluster VI	XX	XII
Intra cluster distances	0	1830.75	250.75
7	Cluster VII	XX	VIII
Intra cluster distances	0	1435.33	255.97
8	Cluster VIII	XX	XI
Intra cluster distances	0	1437.53	465.97
9	Cluster IX	XIV	XI
Intra cluster distances	0	1301.15	232.22
10	Cluster X	XIX	XII
Intra cluster distances	607.76	1730.06	869.28
11	Cluster XI	XIV	XVII
Intra cluster distances	0	1277.62	326.25
12	Cluster XII	XVII	XIV
Intra cluster distances	0	1426.5	650.09
13	Cluster XIII	XX	XVI
Intra cluster distances	0	1418.62	634.24
14	Cluster XIV	XX	XVIII
Intra cluster distances	0	2259.27	681.26
15	Cluster XV	XX	XVIII
Intra cluster distances	0	1920.54	366.2
16	Cluster XVI	XX	XVIII
Intra cluster distances	0	1469.58	461.56
17	Cluster XVII	XX	XIX
Intra cluster distances	0	1541.53	636.93
18	Cluster XVIII	XX	XIX
Intra cluster distances	0	1665.85	405.57
19	Cluster XIX	XX	XVIII
Intra cluster distances	0	1730.06	405.57
20	Cluster XX	III	IX
Intra cluster distances	0	1213.26	617.68

Table 4.13 Cluster means values of 22 (I to XXII) cluster groups for 27 different quantitative characters at ARS, Shiragon (Year I Location I)																												
	SN	C H A R A C T E R S																										
		1 DFE	2 PHT	3 SLEP	4 TLPP	5 PLMA	6 SPP	7 FERT	8 DM	9 TW	10 GL	11 GW	12 GYPP	13 SYPP	14 G/S	15 S/G	16 LL	17 LB	18 ST	19 PPP	20 DGL	21 DGB	22 L/B	23 AC	24 Zn	25 Fe	26 Ca	27 ASV
C L U S T E R M E A N S	I	89.95	115.89	89.24	11.78	26.74	125.00	87.00	119.95	21.81	9.60	2.85	17.09	23.43	0.74	1.38	47.62	1.13	0.75	10.78	6.94	2.44	2.90	22.59	12.34	13.55	51.53	4.70
	II	83.00	163.20	135.07	13.80	28.13	129.66	92.59	113.00	13.84	10.40	2.57	11.20	15.00	0.75	1.34	66.20	1.03	0.70	12.80	7.18	2.41	3.03	23.80	13.73	12.75	63.00	5.00
	III	99.00	129.53	103.20	12.20	26.33	164.44	89.33	129.00	13.70	9.36	2.58	14.97	19.40	0.77	1.30	67.23	1.10	0.87	11.20	6.87	2.04	3.37	27.64	13.65	18.30	59.10	5.00
	IV	95.74	148.79	120.94	11.15	27.86	153.67	87.06	125.74	22.46	8.79	3.09	16.70	23.21	0.72	1.41	61.12	1.04	0.76	10.15	6.11	2.52	2.51	24.67	12.50	11.44	51.69	4.63
	V	89.67	104.93	79.13	11.60	25.80	108.05	91.02	119.67	13.79	7.36	3.09	16.68	20.10	0.83	1.21	41.37	1.00	0.60	10.60	5.02	2.47	2.03	19.24	12.60	16.45	43.33	5.00
	VI	93.00	107.33	79.00	11.87	28.33	71.89	90.39	123.00	27.26	10.27	2.61	23.57	31.47	0.75	1.34	44.17	1.20	0.70	10.87	7.99	2.18	3.67	14.33	4.50	8.67	101.33	3.67
	VII	92.00	124.53	99.67	10.67	24.87	187.77	86.24	122.00	18.80	9.34	2.49	17.57	19.33	0.91	1.10	30.37	0.80	0.50	9.67	6.92	2.22	3.12	28.60	9.40	21.28	92.57	3.67
	VIII	85.67	132.47	104.47	10.40	28.00	140.80	84.25	115.67	21.20	10.16	2.70	21.70	31.03	0.70	1.43	43.40	0.90	0.60	9.40	7.03	2.28	3.08	27.39	1.09	11.50	72.57	5.00
	IX	92.00	107.67	81.27	12.53	26.40	105.63	90.30	122.00	22.53	11.06	2.30	17.99	27.67	0.65	1.54	38.40	0.90	0.70	11.53	8.04	1.87	4.30	21.26	15.82	18.25	102.00	5.00
	X	97.00	154.53	128.80	11.73	25.73	176.75	97.30	127.00	27.17	8.94	3.15	24.28	32.13	0.76	1.33	33.43	1.40	0.57	10.73	6.81	2.65	2.58	23.97	8.47	21.42	64.00	5.00
	XI	97.67	136.07	108.47	9.73	27.60	178.35	92.89	127.67	25.06	11.68	2.31	21.50	26.33	0.82	1.22	52.57	1.10	0.80	8.73	8.87	2.09	4.24	25.37	8.68	14.42	39.10	5.00
	XII	78.00	108.83	82.97	9.43	25.87	101.56	63.87	108.00	24.43	10.42	2.71	12.30	16.97	0.73	1.38	41.13	1.00	0.60	8.43	7.61	2.25	3.38	29.40	18.53	8.83	63.50	5.00
	XIII	96.00	114.73	92.33	9.87	22.40	170.51	68.21	126.00	26.91	9.39	3.24	23.07	24.70	0.94	1.07	32.97	1.10	0.77	8.87	7.23	2.67	2.70	24.36	17.83	10.10	28.67	3.67
	XIV	86.67	123.20	98.47	10.67	24.73	77.30	65.45	116.67	21.78	9.50	2.59	11.73	18.17	0.65	1.55	39.47	1.10	0.80	9.67	6.86	2.19	3.14	29.42	15.43	16.52	84.23	4.33
	XV	88.33	134.33	108.53	10.40	25.80	124.58	82.59	118.33	27.01	7.58	3.21	22.50	32.33	0.70	1.44	47.53	0.72	0.63	9.40	5.20	2.79	1.87	26.99	3.87	18.27	28.53	3.00
	XVI	102.67	81.33	57.33	10.27	24.00	144.82	81.42	132.67	11.98	7.75	2.23	14.61	19.30	0.76	1.32	40.30	1.00	0.60	9.27	5.49	1.87	2.94	18.50	18.55	10.45	71.67	3.67
	XVII	108.33	94.47	67.07	11.60	27.40	178.06	74.53	138.33	20.64	9.47	2.51	25.00	29.57	0.84	1.18	33.17	1.10	0.80	10.60	7.19	2.03	3.57	18.50	7.68	10.67	82.00	4.33
	XVIII	86.00	109.87	84.07	11.40	25.80	152.00	79.32	116.00	23.45	12.84	2.60	15.20	21.47	0.71	1.42	43.17	1.33	0.70	10.40	9.68	2.07	4.69	25.49	5.90	16.35	32.90	4.33
	XIX	78.33	94.57	68.10	10.47	26.47	55.32	77.84	108.33	26.61	9.89	2.51	16.26	20.21	0.81	1.24	36.17	0.95	0.53	9.47	7.04	2.18	3.24	27.24	2.03	8.33	38.33	3.00
	XX	106.33	162.47	135.53	12.53	26.93	106.35	87.51	136.33	12.06	5.99	3.26	12.34	18.10	0.68	1.48	53.60	0.80	0.77	11.53	4.03	2.87	1.41	21.47	19.13	13.27	79.10	5.00
	XXI	87.33	107.40	81.80	14.87	25.60	125.77	91.09	117.33	24.58	11.65	2.51	16.93	26.83	0.63	1.59	51.30	1.33	0.80	13.87	8.17	2.39	3.45	17.15	8.00	5.72	3.63	3.00
	XXII	93.67	173.60	142.87	10.50	30.73	97.08	57.54	123.67	23.76	10.16	3.50	11.73	14.35	0.81	1.23	62.93	1.10	0.83	9.50	6.98	3.10	2.25	17.72	2.15	5.53	68.47	3.00

Table 4.14 Cluster means values of 20 (I to XX) cluster groups for 27 different quantitative characters at RARS, Karjat (Year II Location II)																												
	SN	C H A R A C T E R S																										
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
C L U S T E R M E A N S	I	89.85	117.59	90.45	12.39	27.14	128.16	87.84	119.85	21.73	9.52	2.83	16.76	22.49	0.89	1.34	47.97	1.09	0.77	11.24	6.91	2.43	2.89	22.89	12.05	13.25	51.48	4.72
	II	82.33	164.39	135.30	14.78	29.09	128.93	92.90	112.33	13.36	10.44	2.34	10.99	14.61	0.75	1.33	66.35	1.11	0.78	13.78	7.15	2.39	3.05	23.26	13.98	12.87	63.23	5.00
	III	107.00	95.45	67.72	12.26	27.73	178.57	74.81	137.00	20.83	9.44	2.50	24.63	29.13	0.84	1.18	32.65	1.11	0.82	11.26	7.17	2.01	3.60	18.35	7.30	10.40	83.00	4.33
	IV	90.33	129.92	104.49	12.99	25.43	121.07	90.30	120.33	24.10	8.55	3.01	17.25	26.18	0.66	1.52	52.68	1.05	0.78	11.99	5.58	2.26	2.47	27.78	9.07	6.23	83.69	3.67
	V	93.55	152.27	123.89	11.34	28.38	150.98	86.08	123.55	21.99	8.99	3.12	16.26	21.43	0.77	1.32	63.14	1.06	0.80	10.08	6.22	2.55	2.52	25.66	12.62	13.75	50.53	4.81
	VI	91.33	108.95	81.55	13.56	27.40	104.90	90.66	121.33	22.05	11.10	2.07	17.78	27.28	0.66	1.54	38.60	0.97	0.77	12.56	8.01	1.85	4.33	20.72	16.07	18.37	102.23	5.00
	VII	74.33	90.72	63.68	11.14	27.04	55.50	77.84	104.33	26.76	9.85	2.51	16.28	20.17	0.81	1.23	36.26	0.94	0.52	9.52	7.08	2.17	3.26	27.39	2.02	8.48	38.66	3.00
	VIII	72.33	85.83	63.41	12.42	22.42	95.59	79.09	102.33	20.87	9.32	2.74	15.86	18.94	0.84	1.20	34.09	1.31	0.72	11.42	6.76	2.58	2.62	12.39	5.73	10.18	59.45	5.00
	IX	93.00	113.72	86.89	12.59	26.84	140.28	65.26	123.00	27.83	9.33	2.77	18.88	26.01	0.72	1.38	54.36	1.09	0.79	11.59	7.03	2.33	3.02	18.99	13.38	12.51	44.33	4.33
	X	93.06	125.49	98.67	12.18	26.82	127.62	83.29	123.06	15.05	7.96	2.56	14.31	18.95	0.75	1.35	43.15	0.95	0.69	11.18	5.68	2.23	2.64	22.14	17.06	13.81	83.70	4.11
	XI	76.00	105.09	78.66	10.10	26.44	101.74	63.88	106.00	24.59	10.66	2.71	12.33	16.93	0.73	1.38	41.22	0.99	0.58	8.48	7.65	2.25	3.40	29.55	18.52	8.98	63.75	5.00
	XII	92.00	108.57	79.78	12.66	28.79	72.40	90.67	122.00	27.44	10.24	2.60	23.26	31.09	0.75	1.33	43.71	1.27	0.78	11.66	7.97	2.16	3.70	14.52	4.46	8.74	102.68	3.67
	XIII	83.00	133.88	107.51	11.07	26.37	124.76	82.60	113.00	27.16	7.50	3.21	22.53	32.30	0.70	1.44	47.62	0.71	0.62	9.45	5.24	2.79	1.88	27.14	3.86	18.41	28.97	3.00
	XIV	95.67	154.59	128.42	12.12	26.17	177.17	97.16	125.67	26.76	8.93	3.20	23.93	32.33	0.74	1.36	33.45	1.19	0.61	11.12	6.85	2.67	2.57	23.57	8.53	21.39	64.15	5.00
	XV	86.67	107.85	81.67	15.48	26.19	125.04	91.03	116.67	24.10	11.69	2.28	16.73	26.44	0.63	1.58	51.08	1.39	0.86	14.48	8.14	2.37	3.46	16.62	8.25	5.83	3.86	3.00
	XVI	98.00	140.75	108.42	13.99	32.33	164.58	82.38	128.00	20.34	11.07	2.69	30.64	46.50	0.66	1.52	55.09	1.16	0.95	12.99	7.36	2.30	3.21	14.08	14.74	17.77	32.76	4.00
	XVII	95.00	114.16	91.95	10.25	22.21	170.94	68.06	125.00	26.50	9.38	3.28	22.93	27.51	0.83	1.20	33.08	0.98	0.83	9.25	7.26	2.69	2.70	23.99	17.92	10.10	28.84	3.67
	XVIII	96.33	136.03	108.09	10.12	27.95	178.78	92.74	126.33	24.65	11.67	2.35	21.90	27.36	0.80	1.25	52.52	0.82	0.84	9.12	8.91	2.11	4.22	24.98	8.75	14.39	39.25	5.00
	XIX	85.00	109.09	83.69	11.79	25.40	152.43	79.17	115.00	23.04	12.83	2.65	15.64	21.38	0.73	1.37	43.10	1.04	0.70	10.79	9.71	2.09	4.66	25.06	5.92	16.29	33.01	4.33
	XX	91.67	167.46	136.15	11.17	31.30	97.25	57.54	121.67	23.92	10.20	3.51	11.76	14.31	0.82	1.22	63.02	1.09	0.82	9.55	7.02	3.09	2.27	17.87	2.14	5.68	68.82	3.00

Table 4.15 Ranking and per cent contribution of 27 characters towards total divergence (ARS, Shiragon) based on Wilks' V test			
SN	Character	Times ranked first	Per cent contribution
1	Days to 50% Flowering (Nos.)	25	0.56%
2	Plant Height (cm)	28	0.63%
3	Stem Length Excluding Panicle (cm)	0	0.00%
4	No. of Tillers Plant-1	2	0.04%
5	Panicle Length of Main Axis (cm)	0	0.00%
6	No. of Spikelets Panicle-1	47	1.05%
7	Fertility (%)	406	9.09%
8	Days to Maturity (Nos.)	73	1.63%
9	Test Weight of 1000 Grains (gm)	2	0.04%
10	Grain Length (mm)	0	0.00%
11	Grain Width (mm)	19	0.43%
12	Grain Yield Plant-1 (gm)	11	0.25%
13	Straw Yield Plant-1 (gm)	14	0.31%
14	Grain Yield/ Straw Yield Ratio	6	0.13%
15	Straw Yield/ Grain Yield Ratio	0	0.00%
16	Leaf Length (cm)	1161	26.00%
17	Leaf Breadth (cm)	0	0.00%
18	Stem Thickness (cm)	0	0.00%
19	No. of Panicles Plant-1	867	19.42%
20	Decorticated Grain Length (mm)	244	5.46%
21	Decorticated Grain Breath (mm)	0	0.00%
22	DGL/DGB Ratio	0	0.00%
23	Amylose Content (%)	15	0.34%
24	Zinc Content (ppm)	254	5.69%
25	Iron Content (ppm)	254	5.69%
26	Calcium Content (ppm)	1037	23.23%
27	Alkali Spreading Value	0	0.00%

Table 4.16 Ranking and per cent contribution of 27 characters towards total divergence (RARS, Karjat) based on Wilks' V test

SN	Character	Times ranked first	Per cent contribution
1	Days to 50% Flowering (Nos.)	39	0.87%
2	Plant Height (cm)	62	1.39%
3	Stem Length Excluding Panicle (cm)	0	0.00%
4	No. of Tillers Plant-1	14	0.31%
5	Panicle Length of Main Axis (cm)	11	0.25%
6	No. of Spikelets Panicle-1	110	2.46%
7	Fertility (%)	651	14.58%
8	Days to Maturity (Nos.)	1	0.02%
9	Test Weight of 1000 Grains (gm)	12	0.27%
10	Grain Length (mm)	1	0.02%
11	Grain Width (mm)	0	0.00%
12	Grain Yield Plant-1 (gm)	33	0.74%
13	Straw Yield Plant-1 (gm)	6	0.13%
14	Grain Yield/ Straw Yield Ratio	0	0.00%
15	Straw Yield/ Grain Yield Ratio	0	0.00%
16	Leaf Length (cm)	1165	26.09 %
17	Leaf Breadth (cm)	0	0.00%
18	Stem Thickness (cm)	0	0.00%
19	No. of Panicles Plant-1	0	0.00%
20	Decorticated Grain Length (mm)	445	9.97%
21	Decorticated Grain Breath (mm)	0	0.00%
22	DGL/DGB Ratio	0	0.00%
23	Amylose Content (%)	54	1.21%
24	Zinc Content (ppm)	405	9.07%
25	Iron Content (ppm)	281	6.29%
26	Calcium Content (ppm)	1175	26.32%
27	Alkali Spreading Value	0	0.00%

Table 4.20 Similarity matrix based on dendrogram by using 17 SSR primers on 95 rice genotypes.

[illegible]

Table No 4.22: Frequency distribution of 95 genotypes for various notes of 62 DUS descriptors.

SN	CH	States	N	FN	F%	Genotypes
1	CC	NA	0	0	0.00	NIL
		Colourless	1	85	89.47	MO-6, MO-8, MO-13, MO-17,MO-19,Khara Rata,MayekarBhat,Munga, Jyoti, Bhadas-79, Pandy, Dular, Try-1, LalPatani, Dodak, Ratnagiri 7, KJT-1R, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN 11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati , Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar,K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO,MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU EENATI SINNA SIVAPPU IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali, TN-1
		Green	2	1	1.05	Karhad
		Purple	3	9	9.47	Mahsad, Waksal-207, Barmil, Patani-6, Kochari, Bela, Valai, Gurjari, IRRI 190
		Total		95	100.00	NIL
2	BL-SC	NA	0	0	0.00	NIL
		Green	1	82	86.32	MO-6, MO-8, MO-13, MO-17, MO-19, Khara Rata, MayekarBhat, Munga,Jyoti, Dular, LalPatani, Dodak, Karhad, Ratnagiri 7, KJT-1R, KJT-2R,KJT-3R ,KJT-4R ,PR-114, RTN 11-2-1-3, PR-118, DRR-215, RTN-69-1-1,NAUR-1 , BL-184AR, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, , HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha- 1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315, P Samruddhi, Indrayani,Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, Ajaya, KJT 1, KJT 2, IR-64MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190,IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali, TN-1
		Light Purple	2	9	9.47	Waksal-207, Barmil, Patani-6 , Bhadas-79, Pandy, Kochari, Valai, Gurjari, RP-BIO-226
		Purple Lines	3	1	1.05	Mahsad
		Uniform Purple	4	3	3.16	Try-1, Bela, Dhanesal
		Total		95	100.00	NIL

SN	CH	States	N	FN	F%	Genotypes
3	L-IGC	NA	0	0	0.00	NIL
		Light	3	32	33.68	MO-8,MO-13,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri7,Bela ,Valai ,KJT-1R,RTN 11-2-1-3,DRR-50-13,DRR-50-10,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-10-18,Kothambir Sal,NDR6315,Dhanesal,RP-BIO-226,SINNA SIVAPPU ,IRRI 190,IRRI 192
		Medium	5	33	34.74	MO-6,MO-17,MO-19,Dular,Try-1,KJT-2R,PR-114,DRR-215,RTN-69-1-1,BL-184AR,DRR-50-12,DRR-86-8,IR-63879-195-2-2-3-2,CR-3993-2-24-45-2,Basmati,PSugandha-4,Bhadasbhog,Kalanamak,PSamruddhi,Ambemohar,KShatabdi,Bhogwati,Ajaya,KJT 2,IR-64,MTU1010,FL 478,RATHU HEENATI ,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,
		Dark	7	30	31.58	Pandy,KJT-3R,KJT-4R,PR-118,NAUR-1,Gurjari,DRR-363-5,VDN-9-10-1,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,S Basmati,Chinoor,P Sugandha-1, P Sugandha-3,P Sugandha-5,CR2713-180,Indrayani,Sugandha,RS-1113,RP Bio 197,KJT 1,MUDGO ,MILYANG 46,PTB 33,BG 367-2,MILYANG 63,MUT NS 1,Sonsali ,TN-1,
		Total		95	100.00	NIL
4	L-AC	NA	0	0	0.00	NIL
		Absent	1	92	96.84	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Kochari,Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1, BL-184AR, Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, KothambirSal, Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,KShatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP- BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192,Sonsali, TN-1
		Present	9	3	3.16	Mahsad,Waksal-207,Barmil
		Total		95	100.00	NIL
5	L-DAC					MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Kochari,Lal Patani,Dodak,Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18, RTN-35-1-

SN	CH	States	N	FN	F%	Genotypes
		NA	0	92	96.84	1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, KothambirSal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4, P Sugandha-5, Bhadasbhog,CR2713-180, Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,KShatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP- BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		On tips only	1	0	0.00	NIL
		On marginsonly	2	1	1.05	Waksal-207
		In blotches only	3	0	0.00	NIL
		Uniform	4	2	2.11	Mahsad, Barmil
		Total		95	100.00	NIL
6	LS-AC	NA	0	0	0.00	NIL
		Absent	1	81	85.26	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Bhadas-79,Lal Patani,Dodak,Karhad,Ratnagiri 7,KJT- 1R,KJT-2R,KJT-3R, KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5, DRR-50-13,DRR-50-10,DRR-86-8, IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2, P Basmati,S Basmati ,KothambirSal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,Ajaya,KJT 1,KJT 2, IR-64,MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Present	9	14	14.74	Mahsad,Waksal-207,Barmil,Patani-6,Pandy,Dular,Try-1,Kochari,Bela,Valai, Gurjari,Dhanesal,RP-BIO-226,IRRI 190
		Total		95	100.00	NIL
7	LS-IAC					MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Bhadas-79,Lal Patani,Dodak,Karhad,Ratnagiri 7,KJT- 1R,KJT-2R,KJT-3R, KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-

SN	CH	States	N	FN	F%	Genotypes
		NA	0	81	85.26	10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati, S Basmati, KothambirSal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315, P Samruddhi, Indrayani, Ambemohar, K Shatabdi, Bhogwati,Sugandha,RS-1113,RP Bio 197,Ajaya,KJT 1,KJT 2,IR-64,MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 193, ARC 10550 , S MAHSURI, IRRI-123, IRRI 104, IRRI 192, Sonsali , TN-1
		Very Weak	1	4	4.21	Barmil, Pandy, Valai, R-BIO-226
		Weak	3	4	4.21	Waksal-207,Patani-6,Dular,Gurjari
		Medium	5	2	2.11	Mahsad, Kochari
		Strong	7	2	2.11	Dhanesal,IRRI 190
		Very Strong	9	2	2.11	Try-1, Bela
		Total		95	100.00	NIL
8	L-PBS	NA	0	0	0.00	NIL
		Absent	1	0	0.00	NIL
		Weak	3	22	23.15	MO-6,MO-13,MO-17,Khara Rata,Mayekar Bhat,Munga,Mahsad,Bhadas-79, Dular, Kochari,Valai ,PR-118,Gurjari,DRR-50- 13,DRR-50-10,VDN-10-18, HRTMS-61,CR-3993-2-24-45-2,Kothambir Sal,KShatabdi,P Sugandha-5,IRRI 193
		Medium	5	40	42.11	MO-8,MO-19,Waksal-207,Patani-6,Pandy,Try-1, Lal Patani, Ratnagiri 7,Bela ,KJT-2R,KJT-4R,RTN 11-2-1-3,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-86-8,RTN-214-1-1-1-2,VDN-9-10-1,RTN-35-1-1,P Basmati,CR2713180,NDR6315,P Samruddhi, Indrayani,Dhanesal,Ambemohar,Bhogwati,RP Bio 197, MUDGO, MTU1010,BG 367-2,MUT NS 1,RATHU HEENATI, ARC 10550 ,IRRI 123,IRRI 192,Sonsali ,TN-1
		Strong	7	27	28.42	Barmil,Jyoti,Dodak,Karhad,KJT-1R,KJT-3R,PR-114,DRR-215,IR-63879-195-2-2-3-2,RTN-27-1-1-2,Sahyadri 5 R,S Basmati ,Chinoor, P Sugandha-4, Bhadasbhog,Sugandha,RS-1113,RP-BIO-226,Ajaya,KJT 1,IR-64,MILYANG 46,PTB 33,MILYANG630, FL 478,S MAHSURI,IRRI 104
		Very Strong	9	6	6.32	P Sugandha-1,P Sugandha-3,Kalanamak,KJT 2,SINNA SIVAPPU ,IRRI 190
		Total		95	100.00	NIL
9	L-A	NA	0	0	0.00	NIL

SN	CH	States	N	FN	F%	Genotypes
		Absent	1	0	0.00	NIL
		Present	9	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Try-1, Kochari, LalPatani, Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1, NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2, VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,KothambirSal,Chinoor,P Sugandha-1, P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IIRI 190, IIRI 193, ARC 10550 , S MAHSURI, IIRI 123, IIRI 104, IIRI 192, Sonsali , TN-1
		Total		95	100.00	NIL
10	L-ACA	NA	0	0	0.00	NIL
		Colourless	1	86	90.53	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Jyoti,Bhadas-79,Dular,Try- 1,Kochari,Lal Patani,Dodak, Karhad,Ratnagiri 7,Bela ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR- 215,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12, DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1, Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, KothambirSal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180, Kalanamak, NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar, KShatabdi,Bhogwati,Sugandha, RS-1113, RP Bio 197,RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , ARC 10550 , S MAHSURI, IIRI 123, IIRI 104, IIRI 192, Sonsali , TN-1
		Light Purple	2	2	2.11	MILYANG 46,IIRI 193
		Purple	3	7	7.37	Barmil,Patani-6,Pandy,Valai ,Gurjari,PTB 33,IIRI 190
		Total		95	100.00	NIL
11	L-C	NA	0	0	0.00	NIL
		Absent	1	0	0.00	NIL
						MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79, Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114, RTN 11- 2-1-

SN	CH	States	N	FN	F%	Genotypes
		Present	9	95	100.00	3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10, DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,KothambirSal, Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4, P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanelal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Total		95	100.00	NIL
12	L-ACC	NA	0	0	0.00	NIL
		Absent	1	90	94.74	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Jyoti,Bhadas-79,Dular,Try- 1,Kochari,Lal Patani,Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR- 118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18, RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, Kalanamak, NDR6315,P Samruddhi, Indrayani, Dhanelal, Ambemohar,KShatabdi,Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali ,TN-1
		Present	9	5	5.26	Barmil,Patani-6,Pandy,Gurjari,IRRI 190,
		Total		95	100.00	NIL
13	L-L	NA	0	0	0.00	NIL
		Absent	1	0	0.00	NIL
		Present	9	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215, RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5, DRR-50-13, DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2, P Basmati,S Basmati, Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315, P Samruddhi,Indrayani, Dhanelal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113, RP Bio 197, RP-BIO-226, Ajaya,

SN	CH	States	N	FN	F%	Genotypes
						KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRR1 190, IRR1 193, ARC 10550 , S MAHSURI, IRR1 123, IRR1 104, IRR1 192, Sonsali , TN-1
		Total		95	100.00	NIL
14	L-SL	NA	0	0	0.00	NIL
		Truncate	1	0	0.00	NIL
		Acute	2	0	0.00	NIL
		Split	3	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy, Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118, DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati , Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak, NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRR1 190, IRR1 193, ARC 10550 , S MAHSURI, IRR1 123, IRR1 104, IRR1 192, Sonsali , TN-1
		Total		95	100.00	NIL
15	L-CL	NA	0	0	0.00	NIL
		White	1	94	98.95	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,ayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1, Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113,RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63,FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRR1 190, IRR1 193, ARC 10550 , S MAHSURI, IRR1 123, IRR1 104, IRR1 192, Sonsali , TN-1,
		Light Purple	2	1	1.05	Dhanesal
		Purple	3	0	0.00	NIL

SN	CH	States	N	FN	F%	Genotypes
		Total		95	100.00	NIL
16	L-LB	NA	0	0	0.00	NIL
		Short (<30 cm)	3	0	0.00	NIL
		Medium (30-45cm)	5	40	42.11	MO-19,Dular,Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-2R,KJT-4R,RTN 11-2-1-3,Gurjari,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,Sahyadri 5 R,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Samruddhi,K Shatabdi, Bhogwati, RS-1113,KJT 2,IR-64,MILYANG 46,MTU1010,BG 367-2,MILYANG 63,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550,S MAHSURI,IRRI 123,IRRI 104,RRI 192,Sonsali
		Long (>45cm)	7	55	57.89	MO-6,MO-8,MO-13,MO-17,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207, Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Try-1,Kochari,KJT-1R,KJT-3R,PR-114, PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-50-13, DRR-50-10,DRR-86-8,VDN-9-10-1,VDN-10-18,RTN-35-1-1,HRTMS-61, CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,P Sugandha-5,Bhadasbhog, CR2713-180,Kalanamak, NDR6315, Indrayani, Dhanesal, Ambemohar,Sugandha, RP Bio 197,RP-BIO-226,Ajaya,KJT 1,MUDGO ,PTB 33,FL 478,MUT NS 1,TN-1
		Total		95	100.00	NIL
17	L-WB	NA	0	0	0.00	NIL
		Narrow (<1cm)	3	26	27.37	MO-6,MO-13, MO-17, Munga, Jyoti, Bhadas-79, Pandey, Dular,Kochari,Lal Patani, Dodak,Valai, KJT-2R, RTN 11-2-1-3,DRR-50-13,RTN-214-1-1-1-2,Kothambir Sal, Kalanamak,NDR6315,Indrayani, Ambemohar,Bhogwati,KJT 1,MTU1010,IRRI 190,IRRI 193,
		Medium (1-2cm)	5	69	72.63	MO-8,MO-19,Khara Rata,Mayekar Bhat,Mahsad,Waksal-207,Barmil,Patani-6,Try-1,Karhad,Ratnagiri 7,Bela ,KJT-1R,KJT-3R, KJT-4R,PR-114,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-10,DRR-86-8, IR-63879-195-2-2-3-2,RTN-27-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2, P Basmati,S Basmati ,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, P Samruddhi, Dhanesal,K Shatabdi,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 2,IR-64,MUDGO , MILYANG 46,PTB 33,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,ARC 10550 ,S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Broad (> 2 cm)	7	0	0.00	NIL
		Total		95	100.00	NIL
18	C-A (FR)					MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-

SN	CH	States	N	FN	F%	Genotypes
		NA	0	95	100.00	207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy, Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela ,alai ,KJT-1R,KJT-2R,KJT-3R,JT-4R,PR-114,RTN 11-2- 1-3,PR-118, DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati, Basmati, Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3, P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, Kalanamak, NDR6315, Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Non procumbent	1	0	0.00	NIL
		Procumbent	9	0	0.00	NIL
		Total		95	100.00	NIL
19	C-A	NA	0	0	0.00	NIL
		Erect	1	84	88.42	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat, Munga, Mahsad, Barmil, Bhadas-79,Dular,Dodak,Karhad,Ratnagiri 7, KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari, DRR-50- 12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2, VDN-9-10-1,VDN-10- 18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati , Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak, NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya, KJT 1, KJT 2, IR-64, UDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali
		Semi- erect	3	11	11.58	Waksal-207,Jyoti,Patani-6,Pandy,Try-1,Kochari,Lal Patani,Bela ,Valai ,FL 478, TN-1,
		Open	5	0	0.00	NIL
		Spreading	7	0	0.00	NIL
		Total		95	100.00	NIL
20	TH	NA	0	0	0.00	NIL
		Very early (<71)	1	0	0.00	NIL

SN	CH	States	N	FN	F%	Genotypes
		Early (71-90)	3	42	42.21	MO-8,MO-17,MO-19,Mayekar Bhat,Mahsad,Waksal-207,Jyoti,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,KJT-2R,KJT-4R,PR-114, RTN-69-1-1,NAUR-1,BL-184AR,RTN-214-1-1-1-2,VDN-9-10-1,P Sugandha-1,P Sugandha-3,P Sugandha-5, Bhadasbhog,CR2713-180, Dhanesal,K Shatabdi,Sugandha,RS-1113,RP Bio 197,KJT 1,MUDGO ,MILYANG 46,PTB 33,MILYANG 63,FL 478, RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,IRRI 104,IRRI 192
		Medium (91-110)	5	52	54.74	MO-13,Khara Rata,Munga,Barmil,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Bela ,Valai , KJT-1R,KJT-3R,RTN 11-2-1-3,PR-118,DRR-215, Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-4,NDR6315,P Samruddhi,Indrayani, Ambemohar,Bhogwati,RP-BIO-226,Ajaya,KJT 2,IR-64,MTU1010,BG 367-2,MUT NS 1,ARC 10550 ,S MAHSURI,IRRI 123,Sonsali ,TN-1,
		Late (111-130)	7	1	1.05	Kalanamak
		Very late(>131)	9	0	0.00	NIL
		Total		95	100.00	NIL
						NIL
21	FL-AB (EO)	NA	0	0	0.00	NIL
		Erect	1	79	83.16	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat,Munga,Mahsad,Barmil,Jyoti,Patani-6, Bhadas-79, Pandi,Dular,Kochari,Lal Patani, Dodak,Karhad,Bela ,alai ,KJT-1R,KJT-2R, KJT-3R,KJT-4R,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL- 184AR, Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN- 10-18,RTN-35-1-1, Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,P Samruddhi, Indrayani,Dhaneasal,K Shatabdi,Bhogwati,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46, PTB 33, BG 367-2, MILYANG 63, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190,IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Semi-erect	3	14	14.74	Khara Rata,Waksal-207,Try-1,Ratnagiri 7,PR-114,IR-63879-195-2-2-3-2,S Basmati , Kothambir Sal, CR2713-180,Kalanamak,NDR6315, Ambemohar,MTU1010,FL 478
		Horizontal	5	2	2.11	Bhadasbhog, Sugandha
		Drooping	7	0	0.00	NIL
		Total		95	100.00	NIL

SN	CH	States	N	FN	F%	Genotypes
22	S-DBL	NA	0	0	0.00	NIL
		Absent	1	0	0.00	NIL
		Weak	3	10	10.53	Khara Rata,Jyoti,Dular,KJT-1R,KJT-3R,RTN-69-1-1,Sahyadri 5 R, Bhadasbhog, Ambemohar,Ajaya,
		Medium	5	23	24.21	MO-6,MO-13,MO-17,Munga,Mahsad,Barmil,Bhadas-79,Bela ,KJT-2R,RTN 11-2-1-3,PR-118,DRR-215,DRR-363-5,DRR-50-13,P Basmati,S Basmati, Kothambir Sal, NDR6315, Bhogwati,RP-BIO-226,KJT 1,KJT 2,ARC 10550
		Strong	7	25	26.32	MO-8,Pandy,Try-1,Ratnagiri 7,KJT-4R,NAUR-1,DRR-50-12,DRR-50-10,RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,HRTMS-61,CR-3993-2-24-45-2,P Sugandha-1,P Sugandha-3,P Sugandha-5,CR2713-180,K Shatabdi, Sugandha, RP Bio 197,IR-64,MUDGO ,MILYANG 46,PTB 33,
		Very Strong	9	37	38.95	MO-19,Mayekar Bhat,Waksal-207,Patani-6,Kochari,Lal Patani,Dodak,Karhad,Valai ,PR-114,BL-184AR,Gurjari,DRR-86-8,IR-63879-195-2-2-3-2,RTN-35-1-1,Chinoor,P Sugandha-4, Kalanamak,P Samruddhi,Indrayani,Dhanesal,RS-1113,MTU1010,BG 367-2,MILYANG 63, FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali,TN-1,
		Total		95	100.00	NIL
23	MS	NA	0	0	0.00	NIL
		Absent	1	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79, Pandy, Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,ela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713- 180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197,RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192,Sonsali , TN-1
		Present		0	0.00	NIL

SN	CH	States	N	FN	F%	Genotypes
		Total		95	100.00	NIL
24	L-ACK	NA	0	0	0.00	NIL
		Absent/ Veryweak	1	90	94.74	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy, Dular,Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215, RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor, P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak, P Samruddhi, Indrayani, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1,
		Weak	3	0	0.00	NIL
		Medium	5	0	0.00	NIL
		Strong	7	2	2.11	Try1, Kochari
		Very Strong	9	3	3.16	NDR6315, Dhanesal. Ambemohar
		Total		95	100.00	NIL
25	L-ACABA	NA	0	0	0.00	NIL
		Absent	1	90	94.74	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela, Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1- 3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal, Chinoor, P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,CR2713- 180,Kalanamak,P Samruddhi,Indrayani,K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Weak	3	0	0.00	NIL

SN	CH	States	N	FN	F%	Genotypes
		Medium	5	1	1.05	Kochari
		Strong	7	0	0.00	NIL
		Very Strong	9	4	4.21	Bhadasbhog, NDR6315, Dhanesal, Ambemohar
		Total		95	100.00	NIL
26	L-ACA	NA	0	0	0.00	NIL
		Absent	1	81	85.26	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat,Munga,Waksal-207,Jyoti,Bhadas-79,Dular,ry-1,Lal Patani,Dodak,Karhad,Ratnagiri 7,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,L-184AR, Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati, S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3, Sugandha-4,P Sugandha-5,CR2713-180,Kalanamak,P Samruddhi, Indrayani, K Shatabdi, Bhogwati, Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IIRI 193, ARC 10550 , S MAHSURI, IIRI 123, IIRI 104, IIRI 192, Sonsali , TN-1
		Weak	3	0	0.00	NIL
		Medium	5	0	0.00	Mahasad
		Strong	7	9	9.47	NIL
		Very Strong	9	5	5.26	Khara Rata
		Total		95	100.00	NIL
		NA	0	0	0.00	NIL
		White	1	84	88.42	MO-6,MO-8,O-13,MO-17,MO-19,Mayekar Bhat,Munga,Waksal-207,Jyoti,Bhadas-79,Dular, Try-1,Lal Patani,Dodak,Karhad, KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IIRI 193, ARC 10550 , S MAHSURI, IIRI 123, IIRI 104, IIRI 192, Sonsali , TN-1
27	S-CS	NA	0	0	0.00	NIL
		White	1	84	88.42	MO-6,MO-8,O-13,MO-17,MO-19,Mayekar Bhat,Munga,Waksal-207,Jyoti,Bhadas-79,Dular, Try-1,Lal Patani,Dodak,Karhad, KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IIRI 193, ARC 10550 , S MAHSURI, IIRI 123, IIRI 104, IIRI 192, Sonsali , TN-1

SN	CH	States	N	FN	F%	Genotypes
		Light green	2	0	0.00	NIL
		Yellow	3	0	0.00	NIL
		Light Purple	4	0	0.00	NIL
		Purple	5	11	11.58	Khara Rata,Mahsad,Barmil,Patani-6,Pandy,Kochari,Ratnagiri 7,Bela ,Valai ,NAUR-1,IRRI 190,
		Total		95	100.00	NIL
28	ST	NA	0	0	0.00	NIL
		Thin (<0.40 cm)	3	0	0.00	NIL
		Med. (0.4-0.55 cm)	5	0	0.00	NIL
		Thick (>0.55cm)	7	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,ochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Total		95	100.00	NIL
29	S- L (FR)	NA	0	0	0.00	NIL
		V. Short(<91 cm)	1	46	48.42	MO-6,MO-8,MO-13,MO-17,MO-19,Dular,Lal Patani,Dodak,Karhad,Ratnagiri 7,KJT-4R,RTN 11-2-1-3,NAUR-1,BL-184AR,RTN-27-1-1-2,CR-3993-2-24-45-2,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Samruddhi, Indrayani, KShatabdi, Bhogwati, Sugandha,RS-1113,RP Bio 197,Ajaya,KJT 2,IR-64,UDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI104,IRRI 192
		Short (91-110 cm)	3	20	21.05	Jyoti,KJT-1R,KJT-2R,KJT-3R,PR-114,PR-118,Gurjari,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,P Basmati,S Basmati ,P Sugandha-5,CR2713-180,RP-BIO-226,KJT 1,TN-1

SN	CH	States	N	FN	F%	Genotypes
		Med. (111-130 cm)	5	16	16.84	Khara Rata, Mayekar Bhat,Munga,Waksal-207,Bhadas-79,Bela ,DRR-215,RTN-69-1-1,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,HRTMS-61, Ambemohar, Sonsali
		Long (131-150 cm)	7	13	13.68	Mahsad,Barmil,Patani-6,Pandy,Try-1,Kochari,Valai ,Kothambir Sal, Bhadasbhog, Kalanamak,NDR6315,Dhanesal,FL 478
		V .Long (>150 cm)	9	0	0.00	NIL
		Total		95	100.00	NIL
30	S-CAN	NA	0	0	0.00	NIL
		Absent	1	91	95.79	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari, Dodak,Karhad, Ratnagiri 7, Bela, Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-80,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal,Ambemohar, K Shatabdi,Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI ,SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Present	9	4	4.21	Lal Patani,Gurjari,DRR-86-8,HRTMS-61
		Total		95	100.00	NIL
31	S-IACN	NA	0	91	95.79	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari, Dodak, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-80,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi,Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI ,SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1

SN	CH	States	N	FN	F%	Genotypes
		Weak	3	3	3.16	Lal Patani, DRR-86-8, HRTMS-61
		Medium	5	1	1.05	Gurjari
		Strong	7	0	0.00	NIL
		Total		95	100.00	NIL
32	S-ACI	NA	0	0	0.00	NIL
		Absent	1	93	97.89	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Waksal-207,Barmil, Jyoti,Patani-6,Bhadas-79,Pandy,Dular, Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR- 215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati, S Basmati, Kothambir Sal, Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Present	9	2	2.11	Mahsad, Bela
		Total		95	100.00	NIL
33	P-LMA	NA	0	0	0.00	NIL
		Very short(<16 cm)	1	0	0.00	NIL
		Short (16-20cm)	3	0	0.00	NIL
		Med. (21-25cm)	5	22	23.16	MO-8,MO-17,MO-19,Mayekar Bhat,Munga,Mahsad,Waksal-207,Dular, Karhad, Ratnagiri 7,Gurjari, RTN-35-1-1,HRTMS-61,S Basmati ,MUDGO, MILYANG 46,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,TN-1
		Long (26-30cm)	7	63	66.32	MO-6,MO-13,Khara Rata,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Lal Patani, Dodak, Bela ,Valai ,KJT-2R,KJT-3R,KJT-4R,PR- 114,RTN 11-2-1-3,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,Sahyadri 5 R,CR-3993-2-24-45-2, P Basmati, Kothambir Sal, Chinoor,PSugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, Kalanamak, P Samruddhi, Indrayani, Dhanesal, KShatabdi, Bhogwati, Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,PTB 33,MTU1010,BG 367- 2,MILYANG 63,FL 478,RATHU HEENATI ,SINNA SIVAPPU ,IRRI

SN	CH	States	N	FN	F%	Genotypes
						190,IRRI 193,Sonsali
		V. Long(>30cm)	9	10	10.53	Try-1,Kochari,KJT-1R,PR-118,DRR-215,DRR-50-13,CR2713-180, NDR6315, Ambemohar, MUT NS 1
		Total		95	100.00	NIL
34	FL-AB (LO)	NA	0	0	0.00	NIL
		Erect	1	67	70.53	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat, Munga,Mahsad, Barmil,Jyoti, Patani-6,Bhadas-79,Pandy,Dular,Kochari,Lal Patani,Karhad,Ratnagiri 7,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,HRTMS-61,CR-3993-2-24-45-2,Dhanesal,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550 ,IRRI 123, IRRI 104, Sonsali , TN-1
		Semi-erect	3	20	21.05	Khara Rata,Waksal-207,Try-1,Dodak,Bela ,Valai ,VDN-9-10-1,Sahyadri 5 R,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-4,CR2713-180, Kalanamak, Indrayani, Ambemohar, K Shatabdi,Sugandha,S MAHSURI,IRRI 192
		Horizontal	5	7	7.37	P Basmati,S Basmati ,P Sugandha-3,P Sugandha-5, Bhadasbhog,P Samruddhi,Bhogwati
		Deflexed	7	1	1.05	NDR6315
		Total		95	100.00	NIL
35	P-CMA	NA	0	0	0.00	NIL
		Straight	1	28	29.47	Khara Rata,Mayekar Bhat,Munga,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Dodak,Bela ,Valai ,P Sugandha-4,P Sugandha-5,RS-1113, RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,MTU1010,BG 367-2,MILYANG 63,IRRI 190,IRRI 193,ARC 10550 ,IRRI104,Sonsali ,TN-1
		Semi- straight	3	33	34.74	MO-13,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,P Basmati, Bhadasbhog,CR2713-180,NDR6315,P Samruddhi, Ambemohar, IR-64, MUDGO, MILYANG 46, RATHU HEENATI,SINNA SIVAPPU ,S MAHSURI
		Deflexed	5	24	25.26	MO-6,MO-8,MO-17,MO-19,Mahsad,Waksal-207,Barmil,Jyoti,Kochari,Lal Patani, Karhad, Ratnagiri 7, CR-3993-2-24-45- 2, Chinoor,P Sugandha-1,P Sugandha-3 ,Indrayani,K Shatabdi, Sugandha, PTB 33,FL 478,MUT NS 1,IRRI 123,IRRI 192
		Drooping	7	10	10.53	VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,S Basmati, Kothambir Sal, Kalanamak,Dhanesal,Bhogwati,

SN	CH	States	N	FN	F%	Genotypes
		Total		95	100.00	NIL
36	P-NP	NA	0	0	0.00	NIL
		Few (<11)	3	55	57	MO-8,MO-13,MO-17,Khara Rata,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Kochari,Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,RTN-69-1-1,Gurjari,DRR-50-12,DRR-363-5,DRR-50-10,RTN-27-1-1-2,RTN-214-1-1-1-2,HRTMS-61,CR-3993-2-24-45-2,P Basmati, Chinoor, P Sugandha-1, P Sugandha-4,P Sugandha-5,NDR6315,Indrayani,RS-1113,RP Bio 197,RP-BIO-226,Ajaya, KJT 2,MUDGO ,MTU1010,MILYANG 63,FL 478,SINNA SIVAPPU ,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,Sonsali
		Medium (11-20)	5	39	41.05	MO-6,MO-19,Mayekar Bhat,Munga,PR-114,RTN 11-2-1-3,PR-118,DRR-215,NAUR-1,BL-184AR,DRR-50-13,DRR-86-8,IR-63879-195-2-2-3-2,VDN-9-10-1,VDN-10-18, RTN-35-1-1,Sahyadri 5 R,S Basmati ,Kothambir Sal,P Sugandha-3,Bhadasbhog,CR2713-180,Kalanamak,P Samruddhi,Dhanesal,Ambemohar,K Shatabdi, Bhogwati,Sugandha,KJT 1,IR-64,MILYANG 46,PTB 33,BG 367-2,MUT NS 1, RATHU HEENATI ,IRRI 190,IRRI 104,IRRI 192
		Many (>20)	7	1	1.05	TN-1
		Total		95	100.00	NIL
37	S-CTL	NA	0	0	0.00	NIL
		White	1	69	72.63	MO-6,MO-8,MO-13,MO-17,Khara Rata,Mayekar Bhat,Mahsad,Barmil,Patani-6,Dular,Try-1,Dodak,Karhad,Ratnagiri 7,KJT- 1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,VDN-9-10-1,VDN-10-18,P Basmati,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha- 5,P Samruddhi,Indrayani,K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI190,IRRI 193,ARC 10550 ,S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Yellowish	2	12	12.63	Lal Patani,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,S Basmati , Kothambir Sal,CR2713-180,Kalanamak
		Brown	3	3	3.16	Munga,Kochari,Dhanesal
		Red	4	0	0.00	NIL
		Purple	5	7	7.37	Waksal-207,Jyoti,Bhadas-79,Pandy,Bela ,Valai ,RTN-69-1-1

SN	CH	States	N	FN	F%	Genotypes
		Black	6	4	4.21	MO-19, Bhadasbhog,NDR6315,Ambemohar
		Total		95	100.00	NIL
38	LP-C	NA	0	0	0.00	NIL
		Straw	1	77	81.05	MO-6,MO-8,MO-13,MO-17,Khara Rata,Munga,Barmil,Patani-6,Dular,Try-1,Lal Patani, Dodak,Karhad,Ratnagiri 7,KJT-1R,KJT- 2R,KJT-3R,JT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180,P Samruddhi,Indrayani,K Shatabdi,Bhogwati,Sugandha,RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR- 64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2, MILYANG 63, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, TN-1
		Gold & gold furrows on straw background	2	0	0.00	NIL
		Brown spots on straw	3	3	3.16	Bela,Valai, Kalanamak
		Brown furrows on straw	4	3	3.16	Mahsad,CR-3993-2-24-45-2,Sonsali
		Brown(tawny)	5	6	6.32	MO-19,Waksal-207,Jyoti,Bhadas-79,Pandy,RP Bio 197
		Reddish to light purple	6	3	3.16	Kochari, Dhanesal, FL 478
		Purple spots/ furrows on straw	7	1	1.05	Mayekar Bhat
		Purple	8	1	1.05	Ambemohar
		Black	9	1	1.05	NDR6315
		Total		95	100.00	NIL
39	P-A	NA	0	0	0.00	NIL
						MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat,Munga,Waksal-207,Barmil,Jyoti,Patani-

SN	CH	States	N	FN	F%	Genotypes
		Absent	1	61	64.21	6,Bhadas- 79,Pandy,Dular,Dodak,Karhad,Ratnagiri 7,Valai ,KJT-1R,KJT-2R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1, VDN-10-18,RTN-35-1-1, Chinoor, P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,NDR6315, Ambemohar,K Shatabdi, Bhogwati, RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,MILYANG 46,PTB 33,MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali ,TN-1
		Present	9	34	35.79	Khara Rata,Mahsad,Try-1,Kochari,Lal Patani,Bela ,KJT-3R,KJT-4R,NAUR-1,DRR-363-5,DRR-86-8,RTN-27-1-1-2,Sahyadri 5R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal, Bhadasbhog,CR2713-180,Kalanamak,P Samruddhi, Indrayani, Dhanelal, Sugandha,RP Bio 197, IR-64,MUDGO ,MTU1010,BG 367-2,MUT NS 1,SINNA SIVAPPU, IRRI190,IRRI 193
		Total		95	100.00	NIL
40	P-CA (LO)	NA	0	61	64.21	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat,Munga,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Dodak, Karhad,Ratnagiri 7,Valai ,KJT-1R,KJT-2R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12, DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, NDR6315, Ambemohar,K Shatabdi,Bhogwati,RS-1113,RP-BIO-226,Ajaya,KJT 1, KJT 2,MILYANG 46,PTB 33,MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali ,TN-1
		Yellowish White	1	24	25.26	Try-1,Lal Patani,KJT-3R,KJT-4R,DRR-363-5,DRR-86-8,RTN-27-1-1-2,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,P Samruddhi, Indrayani, Dhanelal, RP Bio 197,IR-64,MUDGO ,MTU1010,BG 367-2,MUT NS 1,SINNA SIVAPPU, IRRI 193
		Yellowish brown	2	3	3.16	Kochari,Kalanamak,Sugandha
		Brown	3	0	0.00	NIL
		ReddishBrown	4	1	1.05	Bhadasbhog
		Light red	5	1	1.05	NAUR-1
		Red	6	1	1.05	Mahsad
		Light Purple	7	3	3.16	Khara Rata,CR2713-180,IRRI 190

SN	CH	States	N	FN	F%	Genotypes
		Purple	8	0	0.00	NIL
		Black	9	1	1.05	Bela
		Total		95	100.00	NIL
41	P-LLA	NA	0	61	64.21	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat,Munga,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Dodak, Karhad,Ratnagiri 7,Valai ,KJT-1R,KJT-2R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12, DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, NDR6315, Ambemohar,K Shatabdi,Bhogwati,RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,MILYANG 46,PTB 33, MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali ,TN-1
		Very short	1	0	0.00	NIL
		Short	3	20	21.05	Mahsad,Try-1,Bela ,KJT-4R,NAUR-1,DRR-363-5,DRR-86-8,RTN-27-1-1-2,Sahyadri 5 R,HRTMS-61,S Basmati ,Kothambir Sal,CR2713-180,P Samruddhi, Indrayani, Sugandha, RP Bio 197,SINNA SIVAPPU ,IRRI 190,IRRI 193
		Medium	5	11	11.58	Kochari,Lal Patani,KJT-3R,CR-3993-2-24-45-2, Bhadasbhog,Dhanesal,IR-64,MUDGO ,MTU1010,BG 367-2,MUT NS 1
		Long	7	0	0.00	NIL
		Very long	9	3	3.16	Khara Rata,P Basmati,Kalanamak
		Total		95	100.00	NIL
42	P-DA	NA	0	60	63.16	MO-6,MO-8,MO-13,MO-17,MO-19,Munga,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Dodak,Karhad,Ratnagiri 7,Valai ,KJT-1R,KJT-2R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Chinoor,P Sugandha-1, P Sugandha-3,P Sugandha-4,P Sugandha-5,NDR6315, Ambemohar, K Shatabdi, Bhogwati,RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,MILYANG 46,PTB 33, MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali ,TN-1
		Tip only	1	23	24.21	Mahsad,Kochari,Bela ,KJT-4R,NAUR-1,DRR-363-5,DRR-86-8,RTN-27-1-1-2,Sahyadri 5 R,HRTMS-61,S Basmati ,Kothambir Sal,CR2713-180,P Samruddhi, Indrayani, Dhanesal,Sugandha,RP Bio 197,BG 367-2,MUT NS 1,SINNA SIVAPPU ,IRRI 190,IRRI193
		Upper halfonly	3	6	6.32	Khara Rata,Try-1,Lal Patani, Bhadasbhog,IR-64,MUDGO

SN	CH	States	N	FN	F%	Genotypes
43	P-PSB	Whole length	5	6	6.32	Mayekar Bhat,KJT-3R,CR-3993-2-24-45-2,P Basmati,Kalanamak,MTU1010,
		Total		95	100.00	NIL
		NA	0	0	0.00	NIL
		Absent	1	16	16.84	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Patani-6,Try-1,KJT-1R,KJT-2R,KJT-3R,KJT-4R,NAUR-1
		Present	9	79	83.16	Mahsad,Waksal-207,Barmil,Bhadas-79,Pandy,Dular,Kochari,Lal Patani ,Dodak, Karhad, Ratnagiri 7, Bela, Valai, PR-114,RTN 11-2- 1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP- BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRR1 190, IRR1 193, ARC 10550 , S MAHSURI, IRR1 123, IRR1 104, IRR1 192, Sonsali ,TN-1
		Total		95	100.00	NIL
44	P-SB	NA	0	16	16.84	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Patani-6,Try-1,KJT-1R,KJT-2R,KJT-3R,KJT-4R,NAUR-1
		Weak	1	58	61.05	Barmil,Bhadas-79,Pandy,Dular,Kochari,Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,RTN 11-2-1-3,PR-118,RTN-69-1- 1,DRR-50-12,DRR-86-8,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,S Basmati, Kothambir Sal,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713- 180,Kalanamak,NDR6315,P Samruddhi, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RP-BIO-226,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,IRRI 190,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,Sonsali ,TN-1
		Strong	2	21	22.11	Mahsad,Waksal-207,PR-114,DRR-215,BL-184AR,Gurjari,DRR-363-5,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,P Basmati,Chinoor,P Sugandha-1,Indrayani,RS-1113,RP Bio 197,Ajaya,PTB 33,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 192
		Clustered	3	0	0.00	NIL
		Total		95	100.00	NIL
45	P-AB	NA	0	16	16.84	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Patani-6,Try-

SN	CH	States	N	FN	F%	Genotypes
						1,KJT-1R,KJT-2R,KJT-3R,KJT-4R,NAUR-1
		Erect	1	47	49.47	Pandy,Dular,PR-114,RTN 11-2-1-3,PR-118,DRR-215,DRR-50-12,DRR-50-13,DRR-50-10,DRR-86-8, IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,P Basmati,S Basmati ,P Sugandha-4,P Sugandha-5,Kalanamak,P Samruddhi, Indrayani, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64, MILYANG46,PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,IRRI 190,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali
		Erect to semi Erect	3	9	9.47	Barmil,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,RTN-69-1-1,DRR-363-5,RS-1113
		Semi-erect	5	13	13.68	Bhadas-79,VDN-9-10-1,HRTMS-61,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3, Bhadasbhog,CR2713-180,NDR6315,Dhanesal,MUDGO, SINNA SIVAPPU
		Semi- erectto spreading	7	6	6.32	Mahsad,Kochari,Lal Patani,RTN-27-1-1-2,Sahyadri 5 R,CR-3993-2-24-45-2
		Spreading	9	4	4.21	Waksal-207,BL-184AR,Gurjari,TN-1
		Total		95	100.00	NIL
46	P-E	NA	0	0	0.00	NIL
		Partly exerted	3	1	1.05	CR-3993-2-24-45-2
		Mostly exerted	5	6	6.32	MO-17,Khara Rata,Jyoti,Dular,KJT-1R,P Sugandha-1
		Well exerted	7	88	92.83	MO-6,MO-8,MO-13,MO-19,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Patani-6,Bhadas-79,Pandy,Try-1,Kochari,Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal,Ambemohar,K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Total		95	100.00	NIL
47	TM	NA	0	0	0.00	NIL
		Very early(<100)	1	0	0.00	NIL

SN	CH	States	N	FN	F%	Genotypes
		Early (101-120)	3	40	2.11	MO-8,MO-17,MO-19,Mayekar Bhat,Mahsad,Waksal-207,Jyoti,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,KJT-2R,KJT-4R,PR- 114,RTN-69-1-1,BL-184AR,IR-63879-195-2-2-3-2,RTN-27-1-1-2,P Sugandha-1,P Sugandha-3,P Sugandha-5, Bhadasbhog,CR2713-180,Dhanesal,K Shatabdi,RS-1113,RP Bio 197,KJT 1,MUDGO ,MILYANG 46,PTB 33,MILYANG 63,FL478,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,IRRI 104,IRRI 192
		Medium (121-140)	5	54	56.84	MO-6,MO-13,Khara Rata,Munga,Barmil,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Bela ,Valai ,KJT-1R,KJT-3R,RTN 11-2-1-3,PR-118,DRR-215,NAUR-1,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha 4,NDR6315,P Samruddhi, Indrayani, Ambemohar, Bhogwati, Sugandha,RP-BIO-226,Ajaya,KJT 2,IR-64,MTU1010,BG 367-2,MUTNS 1,ARC 10550 ,S MAHSURI,IRRI 123,Sonsali ,TN-1
		Late (141 -160)	7	1	1.05	Kalanamak
		Very late (>160)	9	0	0.00	NIL
		Total		95	100.00	NIL
48	L-S	NA	0	0	0.00	NIL
		Early	3	77	81.05	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7, Bela ,Valai ,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-27-1-1-2,P Basmati,S Basmati ,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,P Samruddhi,Indrayani,K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Medium	5	15	15.79	KJT-1R,KJT-2R,KJT-3R,DRR-86-8,RTN-214-1-1-1-2,VDN-9-10-1,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,Kothambir Sal, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,Dhanesal
		Late	7	3	3.16	VDN-10-18,CR-3993-2-24-45-2,Ambemohar
		Total		95	100.00	NIL
49	SL-C	NA	0	0	0.00	NIL
						P Basmati, Shatabdi,Bhogwati,RS-1113,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,FL

SN	CH	States	N	FN	F%	Genotypes
		Straw	1	16	16.84	478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,S MAHSURI,IRRI 104,IRRI 192
		Gold	2	3	3.16	RP Bio 197,IRRI 123,Sonsali
		Red	3	8	8.42	P Sugandha-3,P Sugandha-4,P Samruddhi,Sugandha,KJT 1,MTU1010,MILYANG 63,ARC 10550
		Purple	4	6	6.32	Kothambir Sal, Bhadasbhog,NDR6315,Ambemohar,Ajaya,IRRI 193
		White	5	62	65.26	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,S Basmati ,Chinoor,P Sugandha-1,P Sugandha-5,CR2713-180,Kalanamak,Indrayani,Dhanesal,RP-BIO-226,BG 367-2,IRRI 190,TN-1
		Total		95	100.00	NIL
50	TW	NA	0	0	0.00	NIL
		Very low (<15 g)	1	5	5.26	Kothambir Sal,Chinoor, Bhadasbhog,RS-1113,S MAHSURI
		Low (15-20 g)	3	26	27.37	MO-8,MO-13,PR-114,RTN 11-2-1-3,BL-184AR,DRR-50-12,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,HRTMS-61,CR-3993-2-24-45-2,CR2713-180,NDR6315,P Samruddhi,Indrayani,Dhanesal,Ambemohar,K Shatabdi,RP Bio 197,Ajaya,MUT NS 1,IRRI 190,IRRI 193,ARC 10550 ,IRRI 192
		Medium (21-25 g)	5	46	48.42	MO-6,MO-17,MO-19,Munga,Mahsad,Waksal-207,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Lal Patani,KJT-2R,KJT-3R,KJT-4R,PR-118,DRR-215,RTN-69-1-1,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,RTN-27-1-1-2,VDN-9-10-1,P Basmati,S Basmati, P Sugandha-1,P Sugandha-3,P Sugandha-4,Kalanamak,Bhogwati,Sugandha,RP-BIO-226,KJT 1,KJT 2,IR-64,MILYANG 46, MTU1010,MILYANG 63,FL 478,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 123,IRRI 104,Sonsali ,TN-1
		High (26-30)	7	18	18.95	Khara Rata,Mayekar Bhat,Barmil,Jyoti,Kochari,Dodak,Karhad,Ratnagiri 7,Bela ,Valai, KJT-1R,NAUR-1,Gurjari,Sahyadri 5 R,P Sugandha-5,MUDGO ,PTB 33,BG 367-2
		Very high (>30g)	9	0	0.00	NIL
		Total		95	100.00	NIL

SN	CH	States	N	FN	F%	Genotypes
51	G-L	NA	0	0	0.00	NIL
		V. Short (<6.0mm)	1	1	1.05	Kothambir Sal
		Short (6.1-8.5 mm)	3	13	13.68	MO-6,MO-17,Mayekar Bhat,Munga,Jyoti,Patani-6,Bhadas-79,DRR-363-5,Ambemohar,K Shatabdi,RS-1113,Ajaya,S MAHSURI
		Med. (8.6-10.5 mm)	5	70	73.68	MO-8,MO-13,MO-19,Khara Rata,Mahsad,Waksal-207,Barmil,Pandy,Dular,Try-1, Kochari, Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-50-13,DRR-50-10,DRR-86-8,RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Chinoor,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, Kalanamak, NDR6315, Indrayani,Dhanesal,RP Bio 197,RP-BIO-226,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367- 2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193, ARC 10550 , IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1, TN-1
		L. (10.6-12.5 mm)	7	10	10.53	KJT-2R,KJT-3R,PR-114,RTN 11-2-1-3,PR-118,IR-63879-195-2-2-3-2,P Sugandha-1,P Samruddhi, Bhogwati, KJT- 2R,KJT-3R, KJT-4RP R-114,RTN 11-2-1-3,PR-118,IR-63879-195-2-2-3-2,P Sugandha-1,P Samruddhi,Bhogwati,Sugandha
		V. Long (>12.5mm)	9	1	1.05	Sugandha
		Total		95	100.00	NIL
52	G-W	NA	0	0	0.00	NIL
		V. Narrow (<2.0 mm)	1	0	0.00	NIL
		Narrow (2.1- 2.5 mm)	3	6	6.32	DRR-215,Chinoor,Bhogwati,Sugandha,RS-1113,Ajaya
		Med. (2.6-3.0 mm)	5	57	60.00	MO-8,MO-13,MO-19,Bhadas-79,Lal Patani,Dodak,KJT-1R,KJT-2R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,RTN-69-1-1,NAUR-1,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,HRTMS-61,P Basmati,S Basmati ,P Sugandha-1,P Sugandha-3,P Sugandha-4,Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,RP Bio 197,RP-BIO-226,KJT 1,KJT 2,IR-64,MUDGO , MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,SINNA SIVAPPU ,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123, IRRI 104,IRRI 192

SN	CH	States	N	FN	F%	Genotypes
		Broad (3.1-3.5mm)	7	28	29.47	MO-6,MO-17,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Pandy,Dular,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-3R,BL-184AR,Gurjari,Sahyadri 5 R,CR-3993-2-24-45-2,Kothambir Sal,P Sugandha-5,K Shatabdi,MUT NS 1,RATHU HEENATI ,IRRI 190,Sonsali
		V. broad (>3.5mm)	9	4	4.21	Try-1,Kochari,FL 478,TN-1
		Total		95	100.00	NIL
53	G-PRL	NA	0	0	0.00	NIL
		Absent	1	23	24.21	Mahsad,Waksal-207,Barmil,Pandy,Dular,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-13,DRR-50-10,HRTMS-61,CR-3993-2-24-45- 2, Bhadasbhog,CR2713-180, Kalanamak, Dhanesal, MILYANG 46,PTB 33,MTU1010,MUT NS 1,RATHU HEENATI ,S MAHSURI,IRRI 123
		Present	9	72	75.79	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Jyoti,Patani-6,Bhadas-79,Try-1,Kochari,LalPatani,Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR- 215,Gurjari,DRR-50-12,DRR-363-5,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha- 5,NDR6315,P Samruddhi, Indrayani, Ambemohar, K Shatabdi,Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,BG 367-2,MILYANG 63,FL 478, SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , IRRI 104, IRRI 192, Sonsali , TN-1
		Total		95	100.00	NIL
54	G-PRL	NA	0	0	0.00	NIL
		Short	1	15	15.79	MO-6,MO-17, Patani-6, Bhadas-79, Kochari,Ratnagiri 7, HRTMS-61,Kothambir Sal, Kalanamak, NDR6315, Ambemohar,K Shatabdi,RS-1113,KJT 1,TN-1
		Medium	3	4	4.21	BL-184AR,VDN-9-10-1,Ajaya,S MAHSURI
		Long	5	63	66.32	MO-8,MO-13,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207, Barmil, Jyoti,Pandy, Dular, Try-1,Lal Patani,Dodak,Karhad,Bela ,Valai , KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,Gurjari,DRR-50-12, DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,CR-3993-2-24-45-2, Dhanesal, RP Bio 197,RP-BIO-226,KJT 2,IR-64,MUDGO,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550 ,IRRI 123,IRRI 104,IRRI 192,Sonsali ,Sonsali

SN	CH	States	N	FN	F%	Genotypes
		Long* (Longfor Basmati type)	7	11	11.57	Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,P Samruddhi,Indrayani,Bhogwati,Sugandha
		Extra Long	9	2	2.11	P Basmati and S Basmati
		Total		95	100.00	NIL
55	DG-W	NA	0	0	0.00	NIL
		Narrow<2.0mm)	3	4	4.21	HRTMS-61,Bhogwati,RS-1113,S MAHSURI
		Med. (2.0-2.5 mm)	5	59	62.11	MO-8,MO-13,MO-19,Kochari,Lal Patani,Dodak,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1, NAUR-1,BL-184AR,DRR-50-12,DRR-50-13,DRR-50-10,DRR-86-8, IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,P Basmati,S Basmati ,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,K Shatabdi,Sugandha,RP Bio197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2,SINNA SIVAPPU ,IRRI193,ARC 10550 ,IRRI 123,IRRI 192,Sonsali
		Broad (>2.5mm)	7	32	33.68	MO-6,MO-17,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79,Pandy,Dular,Try-1,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,Gurjari,DRR-363-5,Sahyadri 5 R,CR-3993-2-24-45-2,Kothambir Sal,P Sugandha- 4,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,IRRI 190,IRRI 104,TN-1
		Total		95	100.00	NIL
56	DG-S	NA	0	0	0.00	NIL
		Short Slender (KL < 6.0 mm; LB ratio >3.0 mm)	1	2	2.11	HRTMS-61, RS-1113
		Short Bold (KL<6.0mm; LB ratio < 2.5mm)	2	13	13.68	MO-6,MO-17,Patani-6,Bhadas-79,Kochari,Ratnagiri 7, Kothambir Sal, Kalanamak, NDR6315, Ambemohar, K Shatabdi, KJT 1,TN-1
		Medium Slender (KL< 6.0 mm; LB ratio = 2.5 -3.0 mm)	3	4	4.21	BL-184AR,VDN-9-10-1,Ajaya,S MAHSURI
		Long BoldKL > 6.0mm;				MO-8,MO-13,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207, Barmil, Jyoti,

SN	CH	States	N	FN	F%	Genotypes
		LB ratio < 3.0mm)	4	31	32.63	Pandy,Dular,Try-1,Karhad,Bela ,Valai ,KJT-1R,Gurjari,DRR-50-12,DRR-363-5,DRR-50-10,Sahyadri 5 R,CR-3993-2-24-45-2,Dhanesal,RP-BIO-226,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,IRRI 190,IRRI 104
		Long Slender (KL > 6.0 mm; LB ratio > 3.0mm)	5	32	3.68	Lal Patani,Dodak,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,DRR-50-13,DRR-86-8, IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,RP Bio 197,KJT 2,IR-64,MUDGO ,MILYANG46,PTB 33,MTU1010,BG 367 2,SINNA SIVAPPU ,IRRI 193,ARC 10550 ,IRRI 123,IRRI 192,Sonsali
		Long Slender (Basmati type) (KL >6.61 mm; LBratio > 3.0mm)	6	11	11.57	,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,P Samruddhi,Indrayani,Bhogwati,Sugandha
		Extra-long Slender (KL> 7.5 mm; LB ratio >3.0 mm)	7	2	2.11	P Basmati and S Basmati
		Total		95	100.00	NIL
57	DG-C	NA	0	0	0.00	NIL
		White	1	72	75.79	Bhogwati, Dular,Try-1,Kochari,Dodak,Karhad,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713- 180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2, MUT NS 1,SINNA SIVAPPU ,IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali
		Light brown	2	0	0.00	NIL
		Variegated brown	3	0	0.00	NIL
		Dark brown	4	0	0.00	NIL
		Light red	5	5	5.26	Khara Rata,MILYANG 63,FL 478,RATHU HEENATI ,TN-1

SN	CH	States	N	FN	F%	Genotypes
		Red	6	18	18.95	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat,Munga,Mahsad,Waksal-207, Barmil, Jyoti, Patani-6,Bhadas-79,Pandy,L Patani,Ratnagiri7,Bela, Valai
		Variegated purple	7	0	0.00	NIL
		Purple	8	0	0.00	NIL
		Dark Purple	9	0	0.00	NIL
		Total		95	100.00	NIL
58	E-PA	NA	0	0	0.00	NIL
		Absent	1	0	0.00	NIL
		Present	9	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13, DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1, VDN-10-18, RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Total		95	100.00	NIL
59	E-CA	NA	0	0	0.00	NIL
		Very low (<10%)	1	0	0.00	NIL
		Low (10-19%)	3	19	20.00	Try-1,PR-118,NAUR-1,NDR6315,P Samruddhi,Indrayani,K Shatabdi,Sugandha,RS-1113, KJT 2,MUDGO, MILYANG 46,BG 367- IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,Sonsali
		Medium				MO-6,MO-13,Khara Rata,Barmil,Patani-6,Bhadas-79,Pandy,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-3R,KJT-4R,PR-114, RTN 11-2-1-3,DRR-215,RTN-69-1-1,BL-184AR, Gurjari,

SN	CH	States	N	FN	F%	Genotypes
		(20-25 %)	5	48	50.53	DRR-50-12,DRR-50-10,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2, P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, Dhanesal, Ambemohar, Bhogwati, KJT 1,IR-64,PTB 33,MTU1010,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 192,TN-1
		High (26 -30%)	7	26	27.37	MO-8,MO-17,MO-19,Mayekar Bhat,Munga,Mahsad,Waksal-207,Jyoti,Dular,Kochari,Lal Patani,Dodak,KJT-2R,DRR-363-5,DRR- 50-13,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,Kalanamak,RP Bio 197,RP-BIO-226,FL 478,MUT NS 1
		Very high(>30%)	9	2	2.11	Ajaya, MILYANG 63
		Total		95	100.00	NIL
60	E-CAWC	NA	0	0	0.00	NIL
		Absent orvery small	1	95	100.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12, DRR-363-5, DRR-50-13,DRR-50-10,DRR-868,IR-63879-195-2-2-3-2,RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315, P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Small	3	0	0.00	NIL
		Medium	5	0	0.00	NIL
		Large	7	0	0.00	NIL
		Fully chalky	9	0	0.00	NIL
		Total		95	100.00	NIL
61	GT-ASV	NA	0	0	0.00	NIL
		Low	1	1	1.05	KJT-3R
		Medium	3	33	34.74	Mayekar Bhat,Jyoti,Try-1,Dodak,Karhad,KJT-4R,PR-114,RTN 11-2-1-3,RTN-69-1-1,NAUR-1,BL-184AR,RTN-27-1-1-2,P Sugandha-3, P Sugandha-5, Bhadasbhog,P Samruddhi,

SN	CH	States	N	FN	F%	Genotypes
						Dhanesal, Ambemohar,K Shatabdi, Bhogwati, Sugandha,RS- 1113,KJT 1,MUDGO, MILYANG 46,MTU1010,FL 478,MUT NS 1,IRRI 190,IRRI 193,IRRI 123,IRRI 104,TN-1
		High medium	5	61	64.21	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Munga,Mahsad,Waksal-207,Barmil,Patani-6,Bhadas-79,Pandy,Dular,Kochari, Lal Patani,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,PR-118,DRR-215,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61, CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-4,CR2713-180,Kalanamak,NDR6315,Indrayani,RP Bio 197,RP-BIO-226,Ajaya,KJT 2,IR-64,PTB 33,BG 367-2,MILYANG 63,RATHU HEENATI ,SINNA SIVAPPU ,ARC 10550 ,S MAHSURI,IRRI 192,Sonsali
		High	7	0	0.00	NIL
		Total		95	100.00	NIL
62	DG-A	NA	0	0	0.00	NIL
		Absent	1	76	80.00	MO-6,MO-8,MO-13,MO-17,MO-19,Khara Rata,Mayekar Bhat,Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas- 79,Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN11-2-1-3, PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8, IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO,MILYANG 46,PTB 33,MTU1010,BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1
		Present	9	19	20.00	P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Kalanamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,K Shatabdi,Bhogwati,Sugandha
		Total		95	100.00	NIL

Table 4.23 Notes observed for 62 DUS descriptors on 95 rice genotypes.

SN	SN	1+	2*	3+	4+	5+	6+	7+	8*	9*	10*	11+	12+	13+
	Genotype/Character	CC	BL-SC	L-IGC	L-AC	L-DAC	LS-AC	LS-IAC	L-PBS	L-A	L-ACA	L-C	L-ACC	L-L
1	MO-6	Colourless	Green	Medium	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
2	MO-8	Colourless	Green	Light	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
3	MO-13	Colourless	Green	Light	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
4	MO-17	Colourless	Green	Medium	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
5	MO-19	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
6	Khara Rata	Colourless	Green	Light	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
7	Mayekar Bhat	Colourless	Green	Light	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
8	Munga	Colourless	Green	Light	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
9	Mahsad	Purple	Purple Lines	Light	Present	Uniform	Present	Medium	Weak	Present	Colourless	Present	Absent	Present
10	Waksal-207	Purple	Light Purple	Light	Present	On Margins Only	Present	Weak	Medium	Present	Colourless	Present	Absent	Present
11	Barmil	Purple	Light Purple	Light	Present	Uniform	Present	Very weak	Strong	Present	Purple	Present	Present	Present
12	Jyoti	Colourless	Green	Light	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
13	Patani-6	Purple	Light Purple	Light	Absent	NA	Present	Weak	Medium	Present	Purple	Present	Present	Present
14	Bhadas-79	Colourless	Light Purple	Light	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
15	Pandy	colourless	Light Purple	Dark	Absent	NA	Present	Very weak	Medium	Present	Purple	Present	Present	Present
16	Dular	Colourless	Green	Medium	Absent	NA	Present	Weak	Weak	Present	Colourless	Present	Absent	Present
17	Try-1	colourless	Uniform purple	Medium	Absent	NA	Present	Very Strong	Medium	Present	Colourless	Present	Absent	Present
18	Kochari	Purple	Light Purple	Light	Absent	NA	Present	Medium	Weak	Present	Colourless	Present	Absent	Present
19	Lal Patani	Colourless	Green	Light	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
20	Dodak	Colourless	Green	Light	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
21	Karhad	Green	Green	Light	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
22	Ratnagiri 7	Colourless	Green	Light	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
23	Bela	Purple	Uniform purple	Light	Absent	NA	Present	Very Strong	Medium	Present	Colourless	Present	Absent	Present
24	Valai	Purple	Light Purple	Light	Absent	NA	Present	Very weak	Weak	Present	Purple	Present	Absent	Present
25	KJT-1R	Colourless	Green	Light	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
26	KJT-2R	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
27	KJT-3R	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
28	KJT-4R	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
29	PR-114	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
30	RTN 11-2-1-3	Colourless	Green	Light	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
31	PR-118	Colourless	Green	Dark	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
32	DRR-215	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
33	RTN-69-1-1	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
34	NAUR-1	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
35	BL-184AR	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
36	Gurjari	Purple	Light Purple	Dark	Absent	NA	Present	Weak	Weak	Present	Purple	Present	Present	Present
37	DRR-50-12	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
38	DRR-363-5	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present</

SN	SN	1+	2*	3+	4+	5+	6+	7+	8*	9*	10*	11+	12+	13+
	Genotype/Character	CC	BL-SC	L-IGC	L-AC	L-DAC	LS-AC	LS-IAC	L-PBS	L-A	L-ACA	L-C	L-ACC	L-L
49	HRTMS-61	Colourless	Green	Dark	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
50	CR-3993-2-24-45-2	Colourless	Green	Medium	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
51	P Basmati	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
52	S Basmati	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
53	Kothambir Sal	Colourless	Green	Light	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
54	Chinoor	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
55	P Sugandha-1	Colourless	Green	Dark	Absent	NA	Absent	NA	Very strong	Present	Colourless	Present	Absent	Present
56	P Sugandha-3	Colourless	Green	Dark	Absent	NA	Absent	NA	Very strong	Present	Colourless	Present	Absent	Present
57	P Sugandha-4	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
58	P Sugandha-5	Colourless	Green	Dark	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
59	Bhadasbhog	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
60	CR2713-180	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
61	Kalanamak	Colourless	Green	Medium	Absent	NA	Absent	NA	Very strong	Present	Colourless	Present	Absent	Present
62	NDR6315	Colourless	Green	Light	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
63	P Samruddhi	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
64	Indrayani	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
65	Dhanesal	Colourless	Uniform purple	Light	Absent	NA	Present	Strong	Medium	Present	Colourless	Present	Absent	Present
66	Ambemohar	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
67	K Shatabdi	Colourless	Green	Medium	Absent	NA	Absent	NA	Weak	Present	Colourless	Present	Absent	Present
68	Bhogwati	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
69	Sugandha	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
70	RS-1113	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
71	RP Bio 197	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
72	RP-BIO-226	Colourless	Light Purple	Light	Absent	NA	Present	Very weak	Strong	Present	Colourless	Present	Absent	Present
73	Ajaya	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
74	KJT 1	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
75	KJT 2	Colourless	Green	Medium	Absent	NA	Absent	NA	Very strong	Present	Colourless	Present	Absent	Present
76	IR-64	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
77	MUDGO	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
78	MILYANG 46	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Light purple	Present	Absent	Present
79	PTB 33	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Purple	Present	Absent	Present
80	MTU1010	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
81	BG 367-2	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
82	MILYANG 63	Colourless	Green	Dark	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
83	FL 478	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
84	MUT NS 1	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
85	RATHU HEENATI	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
86	SINNA SIVAPPU	Colourless	Green	Light	Absent	NA	Absent	NA	Very strong	Present	Colourless	Present	Absent	Present
87	IRRI 190	Purple	Green	Light	Absent	NA	Present	Strong	Very strong	Present	Purple	Present	Present	Present
88	IRRI 193	Colourless	Green	Medium	Absent	NA	Absent	NA	Weak	Present	Light purple	Present	Absent	Present
89	ARC 10550	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
90	S MAHSURI	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
91	IRRI 123	Colourless	Green	Medium	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
92	IRRI 104	Colourless	Green	Medium	Absent	NA	Absent	NA	Strong	Present	Colourless	Present	Absent	Present
93	IRRI 192	Colourless	Green	Light	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
94	Sonsali	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
95	TN-1	Colourless	Green	Dark	Absent	NA	Absent	NA	Medium	Present	Colourless	Present	Absent	Present
Type of variation		Polymorphic	Polymorphic	Polymorphic	Dimorphic	Dimorphic	Dimorphic	Polymorphic	Polymorphic	Monorphic	Polymorphic	Monorphic	Monorphic	Monomorphic
SN		1	2	3	4	5	6	7	8	9	10	11	12	13

SN	SN	14*	15*	16+	17+	18+	19+	20*	21*	22*	23+	24+	25*	26+	27*
	otype/Chara	L-SL	L-CL	L-LB	L-WB	C-A (FR)	C-A	TH	FL-AB (EO)	S-DBL	MS	L-ACK	L-ACABA	L-ACA	S-CS
1	MO-6	Split	White	Long	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
2	MO-8	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
3	MO-13	Split	White	Long	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
4	MO-17	Split	White	Long	Narrow	NA	Erect	Early	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
5	MO-19	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
6	Khara Rata	Split	White	Long	Medium	NA	Erect	Medium	Semi-erect	Weak	Absent	Absent/Very Weak	Absent	Very Strong	Purple
7	Mayekar Bhat	Split	White	Long	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
8	Munga	Split	White	Long	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
9	Mahsad	Split	White	Long	Medium	NA	Erect	Early	Erect	Medium	Absent	Absent/Very Weak	Absent	Strong	Purple
10	Waksal-207	Split	White	Long	Medium	NA	Semi-erect	Early	Semi-erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
11	Barmil	Split	White	Long	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Strong	Purple
12	Jyoti	Split	White	Long	Narrow	NA	Semi-erect	Early	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White
13	Patani-6	Split	White	Long	Medium	NA	Semi-erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Strong	Purple
14	Bhadas-79	Split	White	Long	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
15	Pandy	Split	White	Long	Narrow	NA	Semi-erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Strong	Purple
16	Dular	Split	White	Medium	Narrow	NA	Erect	Medium	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White
17	Try-1	Split	White	Long	Medium	NA	Semi-erect	Medium	Semi-erect	Strong	Absent	Strong	Absent	Absent	White
18	Kochari	Split	White	Long	Narrow	NA	Semi-erect	Early	Erect	Very Stong	Absent	Strong	Medium	Strong	Purple
19	Lal Patani	Split	White	Medium	Narrow	NA	Semi-erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
20	Dodak	Split	White	Medium	Narrow	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
21	Karhad	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
22	Ratnagiri 7	Split	White	Medium	Medium	NA	Erect	Early	Semi-erect	Strong	Absent	Absent/Very Weak	Absent	Absent	Purple
23	Bela	Split	White	Medium	Medium	NA	Semi-erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Strong	Purple
24	Valai	Split	White	Medium	Narrow	NA	Semi-erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Strong	Purple
25	KJT-1R	Split	White	Long	Medium	NA	Erect	Medium	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White
26	KJT-2R	Split	White	Medium	Narrow	NA	Erect	Early	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
27	KJT-3R	Split	White	Long	Medium	NA	Erect	Medium	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White
28	KJT-4R	Split	White	Medium	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
29	PR-114	Split	White	Long	Medium	NA	Erect	Early	Semi-erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
30	RTN 11-2-1-3	Split	White	Medium	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
31	PR-118	Split	White	Long	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
32	DRR-215	Split	White	Long	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
33	RTN-69-1-1	Split	White	Long	Medium	NA	Erect	Early	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White
34	NAUR-1	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Strong	Purple
35	BL-184AR	Split	White	Long	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
36	Gurjari	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
37	DRR-50-12	Split	White	Long	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
38	DRR-363-5	Split	White	Long	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
39	DRR-50-13	Split	White	Long	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
40	DRR-50-10	Split	White	Long	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
41	DRR-86-8	Split	White	Long	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
42	3879-195-2-2	Split	White	Medium	Medium	NA	Erect	Medium	Semi-erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
43	RTN-27-1-1-2	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
44	TN-214-1-1-1	Split	White	Medium	Narrow	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
45	VDN-9-10-1	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
46	VDN-10-18	Split	White	Long	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
47	RTN-35-1-1	Split	White	Long	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
48	Sahyadri 5 R	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White

SN	SN	14*	15*	16+	17+	18+	19+	20*	21*	22*	23+	24+	25*	26+	27*
	otype/Chara	L-SL	L-CL	L-LB	L-WB	C-A (FR)	C-A	TH	FL-AB (EO)	S-DBL	MS	L-ACK	L-ACABA	L-ACA	S-CS
49	HRTMS-61	Split	White	Long	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
50	-3993-2-24-4	Split	White	Long	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
51	P Basmati	Split	White	Long	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
52	S Basmati	Split	White	Long	Medium	NA	Erect	Medium	Semi-erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
53	Kothambir Sa	Split	White	Long	Narrow	NA	Erect	Medium	Semi-erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
54	Chinoor	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
55	P Sugandha-1	Split	White	Medium	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
56	P Sugandha-3	Split	White	Medium	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
57	P Sugandha-4	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
58	P Sugandha-5	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
59	Bhadasbhog	Split	White	Long	Medium	NA	Erect	Early	Horizontal	Weak	Absent	Absent/Very Weak	Very Stong	Very Strong	White
60	CR2713-180	Split	White	Long	Medium	NA	Erect	Early	Semi-erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
61	Kalanamak	Split	White	Long	Narrow	NA	Erect	Late	Semi-erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
62	NDR6315	Split	White	Long	Narrow	NA	Erect	Medium	Semi-erect	Medium	Absent	Very Stong	Very Stong	Very Strong	White
63	P Samruddhi	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
64	Indrayani	Split	White	Long	Narrow	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
65	Dhanesal	Split	Light purple	Long	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Very Stong	Very Stong	Very Strong	White
66	Ambemohar	Split	White	Long	Narrow	NA	Erect	Medium	Semi-erect	Weak	Absent	Very Stong	Very Stong	Very Strong	White
67	K Shatabdi	Split	White	Medium	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
68	Bhogwati	Split	White	Medium	Narrow	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
69	Sugandha	Split	White	Long	Medium	NA	Erect	Early	Horizontal	Strong	Absent	Absent/Very Weak	Absent	Absent	White
70	RS-1113	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
71	RP Bio 197	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
72	RP-BIO-226	Split	White	Long	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
73	Ajaya	Split	White	Long	Medium	NA	Erect	Medium	Erect	Weak	Absent	Absent/Very Weak	Absent	Absent	White
74	KJT 1	Split	White	Long	Narrow	NA	Erect	Early	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
75	KJT 2	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
76	IR-64	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
77	MUDGO	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
78	MILYANG 46	Split	White	Medium	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
79	PTB 33	Split	White	Long	Medium	NA	Erect	Early	Erect	Strong	Absent	Absent/Very Weak	Absent	Absent	White
80	MTU1010	Split	White	Medium	Narrow	NA	Erect	Medium	Semi-erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
81	BG 367-2	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
82	MILYANG 63	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
83	FL 478	Split	White	Long	Medium	NA	Semi-erect	Early	Semi-erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
84	MUT NS 1	Split	White	Long	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
85	ATHU HEENA	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
86	INNA SIVAPP	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
87	IRRI 190	Split	White	Medium	Narrow	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Strong	Purple
88	IRRI 193	Split	White	Medium	Narrow	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
89	ARC 10550	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Medium	Absent	Absent/Very Weak	Absent	Absent	White
90	S MAHSURI	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
91	IRRI 123	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
92	IRRI 104	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
93	IRRI 192	Split	White	Medium	Medium	NA	Erect	Early	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
94	Sonsali	Split	White	Medium	Medium	NA	Erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
95	TN-1	Split	White	Long	Medium	NA	Semi-erect	Medium	Erect	Very Stong	Absent	Absent/Very Weak	Absent	Absent	White
Type of variation		Monorphic	Dimorphic	Dimorphic	Dimorphic	Monomorphic	Dimorphic	Polymorphic	Polymorphic	Polymorphic	Monomorphic	Polymorphic	Polymorphic	Polymorphic	Dimorphic
SN		14	15	16	17	18	19	20	21	22	23	24	25	26	27

SN	SN	28+	29*	30*	31+	32+	33*	34*	35*	36+	37*	38+	39*
	otype/Chara	ST	S- L (FR)	S-CAN	S-IACN	S-ACI	P-LMA	FL-AB (LO)	P-CMA	P-NP	S-CTL	LP-C	P-A
1	MO-6	Thick	Very Short	Absent	NA	Absent	Long	Erect	Deflexed	Medium	White	Straw	Absent
2	MO-8	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Deflexed	Few	White	Straw	Absent
3	MO-13	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Absent
4	MO-17	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Deflexed	Few	White	Straw	Absent
5	MO-19	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Deflexed	Medium	Black	Brown (tawny)	Absent
6	Khara Rata	Thick	Medium	Absent	NA	Absent	Long	Semi-erect	Straight	Few	White	Straw	Present
7	Mayekar Bhat	Thick	Medium	Absent	NA	Absent	Medium	Erect	Straight	Medium	White	Purple spots/furrows on straw	Absent
8	Munga	Thick	Medium	Absent	NA	Absent	Medium	Erect	Straight	Medium	Brown	Straw	Absent
9	Mahsad	Thick	Long	Absent	NA	Present	Medium	Erect	Deflexed	Few	White	Brown furrows on straw	Present
10	Waksal-207	Thick	Medium	Absent	NA	Absent	Medium	Semi-erect	Deflexed	Few	Purple	Brown (tawny)	Absent
11	Barmil	Thick	Long	Absent	NA	Absent	Long	Erect	Deflexed	Few	White	Straw	Absent
12	Jyoti	Thick	Short	Absent	NA	Absent	Long	Erect	Deflexed	Few	Purple	Brown (tawny)	Absent
13	Patani-6	Thick	Long	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Absent
14	Bhadas-79	Thick	Medium	Absent	NA	Absent	Long	Erect	Straight	Few	Purple	Brown (tawny)	Absent
15	Pandy	Thick	Long	Absent	NA	Absent	Long	Erect	Straight	Few	Purple	Brown (tawny)	Absent
16	Dular	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Straight	Few	White	Straw	Absent
17	Try-1	Thick	Long	Absent	NA	Absent	Very Long	Semi-erect	Straight	Few	White	Straw	Present
18	Kochari	Thick	Long	Absent	NA	Absent	Very Long	Erect	Deflexed	Few	Brown	Reddish to light purple	Present
19	Lal Patani	Thick	Very Short	Present	Weak	Absent	Long	Erect	Deflexed	Few	Yellowish	Straw	Present
20	Dodak	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Straight	Few	White	Straw	Absent
21	Karhad	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Deflexed	Few	White	Straw	Absent
22	Ratnagiri 7	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Deflexed	Few	White	Straw	Absent
23	Bela	Thick	Medium	Absent	NA	Present	Long	Semi-erect	Straight	Few	Purple	Brown spots on straw	Present
24	Valai	Thick	Long	Absent	NA	Absent	Long	Semi-erect	Straight	Few	Purple	Brown spots on straw	Absent
25	KJT-1R	Thick	Short	Absent	NA	Absent	Very Long	Erect	Semi-straight	Few	White	Straw	Absent
26	KJT-2R	Thick	Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Absent
27	KJT-3R	Thick	Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Present
28	KJT-4R	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Present
29	PR-114	Thick	Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Absent
30	RTN 11-2-1-3	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Absent
31	PR-118	Thick	Short	Absent	NA	Absent	Very Long	Erect	Semi-straight	Medium	White	Straw	Absent
32	DRR-215	Thick	Medium	Absent	NA	Absent	Very Long	Erect	Semi-straight	Medium	White	Straw	Absent
33	RTN-69-1-1	Thick	Medium	Absent	NA	Absent	Long	Erect	Semi-straight	Few	Purple	Straw	Absent
34	NAUR-1	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Present
35	BL-184AR	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Absent
36	Gurjari	Thick	Short	Present	Medium	Absent	Medium	Erect	Semi-straight	Few	White	Straw	Absent
37	DRR-50-12	Thick	Medium	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Absent
38	DRR-363-5	Thick	Medium	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Present
39	DRR-50-13	Thick	Medium	Absent	NA	Absent	Very Long	Erect	Semi-straight	Medium	White	Straw	Absent
40	DRR-50-10	Thick	Medium	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Absent
41	DRR-86-8	Thick	Medium	Present	Weak	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Present
42	3879-195-2-2	Thick	Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	Yellowish	Straw	Absent
43	RTN-27-1-1-2	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	Yellowish	Straw	Present
44	TN-214-1-1-1	Thick	Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	Yellowish	Straw	Absent
45	VDN-9-10-1	Thick	Short	Absent	NA	Absent	Long	Semi-erect	Drooping	Medium	White	Straw	Absent
46	VDN-10-18	Thick	Short	Absent	NA	Absent	Long	Erect	Drooping	Medium	White	Straw	Absent
47	RTN-35-1-1	Thick	Short	Absent	NA	Absent	Medium	Erect	Drooping	Medium	Yellowish	Straw	Absent
48	Sahyadri 5 R	Thick	Short	Absent	NA	Absent	Long	Semi-erect	Drooping	Medium	Yellowish	Straw	Present

SN	SN	28+	29*	30*	31+	32+	33*	34*	35*	36+	37*	38+	39*
	otype/Chara	ST	S- L (FR)	S-CAN	S-IACN	S-ACI	P-LMA	FL-AB (LO)	P-CMA	P-NP	S-CTL	LP-C	P-A
49	HRTMS-61	Thick	Medium	Present	Weak	Absent	Medium	Erect	Drooping	Few	Yellowish	Straw	Present
50	-3993-2-24-4	Thick	Very Short	Absent	NA	Absent	Long	Erect	Deflexed	Few	Yellowish	Brown furrows on straw	Present
51	P Basmati	Thick	Short	Absent	NA	Absent	Long	Horizontal	Semi-straight	Few	White	Straw	Present
52	S Basmati	Thick	Short	Absent	NA	Absent	Medium	Horizontal	Drooping	Medium	Yellowish	Straw	Present
53	Kothambir Sa	Thick	Long	Absent	NA	Absent	Long	Semi-erect	Drooping	Medium	Yellowish	Straw	Present
54	Chinoor	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Deflexed	Few	White	Straw	Absent
55	P Sugandha-1	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Deflexed	Few	White	Straw	Absent
56	P Sugandha-3	Thick	Very Short	Absent	NA	Absent	Long	Horizontal	Deflexed	Medium	White	Straw	Absent
57	P Sugandha-4	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Straight	Few	White	Straw	Absent
58	P Sugandha-5	Thick	Short	Absent	NA	Absent	Long	Horizontal	Straight	Few	White	Straw	Absent
59	Bhadasbhog	Thick	Long	Absent	NA	Absent	Long	Horizontal	Semi-straight	Medium	Black	Straw	Present
60	CR2713-180	Thick	Short	Absent	NA	Absent	Very Long	Semi-erect	Semi-straight	Medium	Yellowish	Straw	Present
61	Kalanamak	Thick	Long	Absent	NA	Absent	Long	Semi-erect	Drooping	Medium	Yellowish	Brown spots on straw	Present
62	NDR6315	Thick	Long	Absent	NA	Absent	Very Long	Deflexed	Semi-straight	Few	Black	Black	Absent
63	P Samruddhi	Thick	Very Short	Absent	NA	Absent	Long	Horizontal	Semi-straight	Medium	White	Straw	Present
64	Indrayani	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Deflexed	Few	White	Straw	Present
65	Dhanesal	Thick	Long	Absent	NA	Absent	Long	Erect	Drooping	Medium	Brown	Reddish to light purple	Present
66	Ambemohar	Thick	Medium	Absent	NA	Absent	Very Long	Semi-erect	Semi-straight	Medium	Black	Purple	Absent
67	K Shatabdi	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Deflexed	Medium	White	Straw	Absent
68	Bhogwati	Thick	Very Short	Absent	NA	Absent	Long	Horizontal	Drooping	Medium	White	Straw	Absent
69	Sugandha	Thick	Very Short	Absent	NA	Absent	Long	Semi-erect	Deflexed	Medium	White	Straw	Present
70	RS-1113	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Absent
71	RP Bio 197	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Brown (tawny)	Present
72	RP-BIO-226	Thick	Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Absent
73	Ajaya	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Absent
74	KJT 1	Thick	Short	Absent	NA	Absent	Long	Erect	Straight	Medium	White	Straw	Absent
75	KJT 2	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Absent
76	IR-64	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Present
77	MUDGO	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Semi-straight	Few	White	Straw	Present
78	MILYANG 46	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Semi-straight	Medium	White	Straw	Absent
79	PTB 33	Thick	Very Short	Absent	NA	Absent	Long	Erect	Deflexed	Medium	White	Straw	Absent
80	MTU1010	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Present
81	BG 367-2	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Medium	White	Straw	Present
82	MILYANG 63	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Absent
83	FL 478	Thick	Long	Absent	NA	Absent	Long	Erect	Deflexed	Few	White	Reddish to light purple	Absent
84	MUT NS 1	Thick	Very Short	Absent	NA	Absent	Very Long	Erect	Deflexed	Medium	White	Straw	Present
85	ATHU HEENA	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Medium	White	Straw	Absent
86	INNA SIVAPPU	Thick	Very Short	Absent	NA	Absent	Long	Erect	Semi-straight	Few	White	Straw	Present
87	IRRI 190	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Medium	White	Straw	Present
88	IRRI 193	Thick	Very Short	Absent	NA	Absent	Long	Erect	Straight	Few	White	Straw	Present
89	ARC 10550	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Straight	Few	White	Straw	Absent
90	S MAHSURI	Thick	Very Short	Absent	NA	Absent	Medium	Semi-erect	Semi-straight	Few	White	Straw	Absent
91	IRRI 123	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Deflexed	Few	White	Straw	Absent
92	IRRI 104	Thick	Very Short	Absent	NA	Absent	Medium	Erect	Straight	Medium	White	Straw	Absent
93	IRRI 192	Thick	Very Short	Absent	NA	Absent	Medium	Semi-erect	Deflexed	Medium	White	Straw	Absent
94	Sonsali	Thick	Medium	Absent	NA	Absent	Long	Erect	Straight	Few	White	Brown furrows on straw	Absent
95	TN-1	Thick	Short	Absent	NA	Absent	Medium	Erect	Straight	Many	White	Straw	Absent
Type of variation		Monomorphic	Polymorphic	Dimorphic	Dimorphic	Dimorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Dimorphic
SN		28	29	30	31	32	33	34	35	36	37	38	39

Note:- * Indicates Essesntial DUS character while, + denotes Additional DUS character. NA is Not Applicable

SN	SN	40*	41+	42*	43+	44+	45*	46*	47+	48+	49*	50+
	otype/Chara	P-CA (LO)	P-LLA	P-DA	P-PSB	P-SB	P-AB	P-E	TM	L-S	SL-C	TW
1	MO-6	NA	NA	NA	Absent	NA	NA	Well exerted	Medium	Early	White	Medium
2	MO-8	NA	NA	NA	Absent	NA	NA	Well exerted	Early	Early	White	Low
3	MO-13	NA	NA	NA	Absent	NA	NA	Well exerted	Medium	Early	White	Low
4	MO-17	NA	NA	NA	Absent	NA	NA	Mostly exerted	Early	Early	White	Medium
5	MO-19	NA	NA	NA	Absent	NA	NA	Well exerted	Early	Early	White	Medium
6	Khara Rata	Light Purple	Very Long	Upper half only	Absent	NA	NA	Mostly exerted	Medium	Early	White	High
7	Mayekar Bhat	NA	NA	Whole length	Absent	NA	NA	Well exerted	Early	Early	White	High
8	Munga	NA	NA	NA	Absent	NA	NA	Well exerted	Medium	Early	White	Medium
9	Mahsad	Red	Short	Tip only	Present	Strong	Semi- erect to spreading	Well exerted	Early	Early	White	Medium
10	Waksal-207	NA	NA	NA	Present	Strong	Spreading	Well exerted	Early	Early	White	Medium
11	Barmil	NA	NA	NA	Present	Weak	Erect to semi- Erect	Well exerted	Medium	Early	White	High
12	Jyoti	NA	NA	NA	Absent	NA	NA	Mostly exerted	Early	Early	White	High
13	Patani-6	NA	NA	NA	Absent	NA	NA	Well exerted	Medium	Early	White	Medium
14	Bhadas-79	NA	NA	NA	Present	Weak	Semi-erect	Well exerted	Medium	Early	White	Medium
15	Pandy	NA	NA	NA	Present	Weak	Erect	Well exerted	Medium	Early	White	Medium
16	Dular	NA	NA	NA	Present	Weak	Erect	Mostly exerted	Medium	Early	White	Medium
17	Try-1	Yellowish White	Short	Upper half only	Absent	NA	NA	Well exerted	Medium	Early	White	Medium
18	Kochari	Yellowish Brown	Medium	Tip only	Present	Weak	Semi- erect to spreading	Well exerted	Early	Early	White	High
19	Lal Patani	Yellowish White	Medium	Upper half only	Present	Weak	Semi- erect to spreading	Well exerted	Early	Early	White	Medium
20	Dodak	NA	NA	NA	Present	Weak	Erect to semi- Erect	Well exerted	Early	Early	White	High
21	Karhad	NA	NA	NA	Present	Weak	Erect to semi- Erect	Well exerted	Early	Early	White	High
22	Ratnagiri 7	NA	NA	NA	Present	Weak	Erect to semi- Erect	Well exerted	Early	Early	White	High
23	Bela	Black	Short	Tip only	Present	Weak	Erect to semi- Erect	Well exerted	Medium	Early	White	High
24	Valai	NA	NA	NA	Present	Weak	Erect to semi- Erect	Well exerted	Medium	Early	White	High
25	KJT-1R	NA	NA	NA	Absent	NA	NA	Mostly exerted	Medium	Medium	White	High
26	KJT-2R	NA	NA	NA	Absent	NA	NA	Well exerted	Early	Medium	White	Medium
27	KJT-3R	Yellowish White	Medium	Whole length	Absent	NA	NA	Well exerted	Medium	Medium	White	Medium
28	KJT-4R	Yellowish White	Short	Tip only	Absent	NA	NA	Well exerted	Early	Early	White	Medium
29	PR-114	NA	NA	NA	Present	Strong	Erect	Well exerted	Early	Early	White	Low
30	RTN 11-2-1-3	NA	NA	NA	Present	Weak	Erect	Well exerted	Medium	Early	White	Low
31	PR-118	NA	NA	NA	Present	Weak	Erect	Well exerted	Medium	Early	White	Medium
32	DRR-215	NA	NA	NA	Present	Strong	Erect	Well exerted	Medium	Early	White	Medium
33	RTN-69-1-1	NA	NA	NA	Present	Weak	Erect to semi- Erect	Well exerted	Early	Early	White	Medium
34	NAUR-1	Light red	Short	Tip only	Absent	NA	NA	Well exerted	Medium	Early	White	High
35	BL-184AR	NA	NA	NA	Present	Strong	Spreading	Well exerted	Early	Early	White	Low
36	Gurjari	NA	NA	NA	Present	Strong	Spreading	Well exerted	Medium	Early	White	High
37	DRR-50-12	NA	NA	NA	Present	Weak	Erect	Well exerted	Medium	Early	White	Low
38	DRR-363-5	Yellowish White	Short	Tip only	Present	Strong	Erect to semi- Erect	Well exerted	Medium	Early	White	Medium
39	DRR-50-13	NA	NA	NA	Present	Strong	Erect	Well exerted	Medium	Early	White	Medium
40	DRR-50-10	NA	NA	NA	Present	Strong	Erect	Well exerted	Medium	Early	White	Medium
41	DRR-86-8	Yellowish White	Short	Tip only	Present	Weak	Erect	Well exerted	Medium	Medium	White	Medium
42	3879-195-2-2	NA	NA	NA	Present	Strong	Erect	Well exerted	Early	Early	White	Low
43	RTN-27-1-1-2	Yellowish White	Short	Tip only	Present	Weak	Semi- erect to spreading	Well exerted	Early	Early	White	Medium</

SN	SN	40*	41+	42*	43+	44+	45*	46*	47+	48+	49*	50+
	otype/Chara	P-CA (LO)	P-LLA	P-DA	P-PSB	P-SB	P-AB	P-E	TM	L-S	SL-C	TW
49	HRTMS-61	Yellowish White	Short	Tip only	Present	Weak	Semi-erect	Well exserted	Medium	Medium	White	Low
50	-3993-2-24-4	Yellowish White	Medium	Whole length	Present	Weak	Semi- erect to spreading	Partly exserted	Medium	Late	White	Low
51	P Basmati	Yellowish White	Very Long	Whole length	Present	Strong	Erect	Well exserted	Medium	Early	Straw	Medium
52	S Basmati	Yellowish White	Short	Tip only	Present	Weak	Erect	Well exserted	Medium	Early	White	Medium
53	Kothambir Sa	Yellowish White	Short	Tip only	Present	Weak	Semi-erect	Well exserted	Medium	Medium	Purple	Very low
54	Chinoor	NA	NA	NA	Present	Strong	Semi-erect	Well exserted	Medium	Early	White	Very low
55	P Sugandha-1	NA	NA	NA	Present	Strong	Semi-erect	Mostly exserted	Early	Early	White	Medium
56	P Sugandha-3	NA	NA	NA	Present	Weak	Semi-erect	Well exserted	Early	Early	Red	Medium
57	P Sugandha-4	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Red	Medium
58	P Sugandha-5	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	White	High
59	Bhadasbhog	Reddish Brown	Medium	Upper half only	Present	Weak	Semi-erect	Well exserted	Early	Medium	Purple	Very low
60	CR2713-180	Light Purple	Short	Tip only	Present	Weak	Semi-erect	Well exserted	Early	Medium	White	Low
61	Kalanamak	Yellowish Brown	Very Long	Whole length	Present	Weak	Erect	Well exserted	Late	Medium	White	Medium
62	NDR6315	NA	NA	NA	Present	Weak	Semi-erect	Well exserted	Medium	Medium	Purple	Low
63	P Samruddhi	Yellowish White	Short	Tip only	Present	Weak	Erect	Well exserted	Medium	Early	Red	Low
64	Indrayani	Yellowish White	Short	Tip only	Present	Strong	Erect	Well exserted	Medium	Early	White	Low
65	Dhanesal	Yellowish White	Medium	Tip only	Present	Weak	Semi-erect	Well exserted	Early	Medium	White	Low
66	Ambemohar	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Late	Purple	Low
67	K Shatabdi	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	Straw	Low
68	Bhogwati	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Straw	Medium
69	Sugandha	Yellowish Brown	Short	Tip only	Present	Weak	Erect	Well exserted	Medium	Early	Red	Medium
70	RS-1113	NA	NA	NA	Present	Strong	Erect to semi- Erect	Well exserted	Early	Early	Straw	Very low
71	RP Bio 197	Yellowish White	Short	Tip only	Present	Strong	Erect	Well exserted	Early	Early	Gold	Low
72	RP-BIO-226	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	White	Medium
73	Ajaya	NA	NA	NA	Present	Strong	Erect	Well exserted	Medium	Early	Purple	Low
74	KJT 1	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	Red	Medium
75	KJT 2	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Straw	Medium
76	IR-64	Yellowish White	Medium	Upper half only	Present	Weak	Erect	Well exserted	Medium	Early	Straw	Medium
77	MUDGO	Yellowish White	Medium	Upper half only	Present	Weak	Semi-erect	Well exserted	Early	Early	Straw	High
78	MILYANG 46	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	Straw	Medium
79	PTB 33	NA	NA	NA	Present	Strong	Erect	Well exserted	Early	Early	Straw	High
80	MTU1010	Yellowish White	Medium	Whole length	Present	Weak	Erect	Well exserted	Medium	Early	Red	Medium
81	BG 367-2	Yellowish White	Medium	Tip only	Present	Weak	Erect	Well exserted	Medium	Early	White	High
82	MILYANG 63	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	Red	Medium
83	FL 478	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	Straw	Medium
84	MUT NS 1	Yellowish White	Medium	Tip only	Present	Weak	Erect	Well exserted	Medium	Early	Straw	Low
85	ATHU HEENA	NA	NA	NA	Present	Strong	Erect	Well exserted	Early	Early	Straw	Medium
86	INNA SIVAPPU	Yellowish White	Short	Tip only	Present	Strong	Semi-erect	Well exserted	Early	Early	Straw	Medium
87	IRRI 190	Light Purple	Short	Tip only	Present	Weak	Erect	Well exserted	Early	Early	White	Low
88	IRRI 193	Yellowish White	Short	Tip only	Present	Weak	Erect	Well exserted	Early	Early	Purple	Low
89	ARC 10550	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Red	Low
90	S MAHSURI	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Straw	Very low
91	IRRI 123	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Gold	Medium
92	IRRI 104	NA	NA	NA	Present	Weak	Erect	Well exserted	Early	Early	Straw	Medium
93	IRRI 192	NA	NA	NA	Present	Strong	Erect	Well exserted	Early	Early	Straw	Low
94	Sonsali	NA	NA	NA	Present	Weak	Erect	Well exserted	Medium	Early	Gold	Medium
95	TN-1	NA	NA	NA	Present	Weak	Spreading	Well exserted	Medium	Early	White	Medium
Type of variation		Polymorphic	Polymorphic	Polymorphic	Dimorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic
SN		40	41	42	43	44	45	46	47	48	49	50

SN	SN	51+	52+	53+	54*	55*	56*	57*	58+	59*	60+	61+	62*
	notype/Charac	G-L	G-W	G-PRL	DG-L	DG-W	DG-S	DG-C	E-PA	E-CA	E-CAWC	GT-ASV	DG-A
1	MO-6	Short	Broad	Present	Short	Broad	SB	Red	Present	Medium	Absent or very small	High-Medium	Absent
2	MO-8	Medium	Medium	Present	Long	Medium	LB	Red	Present	High	Absent or very small	High-Medium	Absent
3	MO-13	Medium	Medium	Present	Long	Medium	LB	Red	Present	Medium	Absent or very small	High-Medium	Absent
4	MO-17	Short	Broad	Present	Short	Broad	SB	Red	Present	High	Absent or very small	High-Medium	Absent
5	MO-19	Medium	Medium	Present	Long	Medium	LB	Red	Present	High	Absent or very small	High-Medium	Absent
6	Khara Rata	Medium	Broad	Present	Long	Broad	LB	Light Red	Present	Medium	Absent or very small	High-Medium	Absent
7	Mayekar Bhat	Short	Broad	Present	Long	Broad	LB	Red	Present	High	Absent or very small	Medium	Absent
8	Munga	Short	Broad	Present	Long	Broad	LB	Red	Present	High	Absent or very small	High-Medium	Absent
9	Mahsad	Medium	Broad	Absent	Long	Broad	LB	Red	Present	High	Absent or very small	High-Medium	Absent
10	Waksal-207	Medium	Broad	Absent	Long	Broad	LB	Red	Present	High	Absent or very small	High-Medium	Absent
11	Barmil	Medium	Broad	Absent	Long	Broad	LB	Red	Present	Medium	Absent or very small	High-Medium	Absent
12	Jyoti	Short	Broad	Present	Long	Broad	LB	Red	Present	High	Absent or very small	Medium	Absent
13	Patani-6	Short	Broad	Present	Short	Broad	SB	Red	Present	Medium	Absent or very small	High-Medium	Absent
14	Bhadas-79	Short	Medium	Present	Short	Broad	SB	Red	Present	Medium	Absent or very small	High-Medium	Absent
15	Pandy	Medium	Broad	Absent	Long	Broad	LB	Red	Present	Medium	Absent or very small	High-Medium	Absent
16	Dular	Medium	Broad	Absent	Long	Broad	LB	Light Brown	Present	High	Absent or very small	High-Medium	Absent
17	Try-1	Medium	Very Broad	Present	Long	Broad	LB	Light Brown	Present	Low	Absent or very small	Medium	Absent
18	Kochari	Medium	Very Broad	Present	Short	Medium	SB	Light Brown	Present	High	Absent or very small	High-Medium	Absent
19	Lal Patani	Medium	Medium	Present	Long	Medium	LS	Red	Present	High	Absent or very small	High-Medium	Absent
20	Dodak	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	Medium	Absent
21	Karhad	Medium	Broad	Present	Long	Broad	LB	Light Brown	Present	Medium	Absent or very small	Medium	Absent
22	Ratnagiri 7	Medium	Broad	Present	Short	Broad	SB	Red	Present	Medium	Absent or very small	High-Medium	Absent
23	Bela	Medium	Broad	Present	Long	Broad	LB	Red	Present	Medium	Absent or very small	High-Medium	Absent
24	Valai	Medium	Broad	Present	Long	Broad	LB	Red	Present	Medium	Absent or very small	High-Medium	Absent
25	KJT-1R	Medium	Medium	Present	Long	Broad	LB	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
26	KJT-2R	Long	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
27	KJT-3R	Long	Broad	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	Low	Absent
28	KJT-4R	Very Long	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	Medium	Absent
29	PR-114	Long	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	Medium	Absent
30	RTN 11-2-1-3	Long	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	Medium	Absent
31	PR-118	Long	Medium	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	High-Medium	Absent
32	DRR-215	Medium	Narrow	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
33	RTN-69-1-1	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	Medium	Absent
34	NAUR-1	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	Medium	Absent
35	BL-184AR	Medium	Broad	Absent	Medium	Medium	MS	Light Brown	Present	Medium	Absent or very small	Medium	Absent
36	Gurjari	Medium	Broad	Present	Long	Broad	LB	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
37	DRR-50-12	Medium	Medium	Present	Long	Medium	LB	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
38	DRR-363-5	Short	Medium	Present	Long	Broad	LB	Light Brown	Present	High	Absent or very small	High-Medium	Absent
39	DRR-50-13	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
40	DRR-50-10	Medium	Medium	Absent	Long	Medium	LB	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
41	DRR-86-8	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
42	63879-195-2-2-	Long	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
43	RTN-27-1-1-2	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	Medium	Absent
44	RTN-214-1-1-1-2	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
45	VDN-9-10-1	Medium	Medium	Present	Medium	Medium	MS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
46	VDN-10-18	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
47	RTN-35-1-1	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
48	Sahyadri 5 R	Medium	Broad	Present	Long	Broad	LB	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent

SN	SN	51+	52+	53+	54*	55*	56*	57*	58+	59*	60+	61+	62*
	otype/Charac	G-L	G-W	G-PRL	DG-L	DG-W	DG-S	DG-C	E-PA	E-CA	E-CAWC	GT-ASV	DG-A
49	HRTMS-61	Medium	Medium	Absent	Short	Narrow	SS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
50	R-3993-2-24-45	Medium	Broad	Absent	Long	Broad	LB	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
51	P Basmati	Medium	Medium	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
52	S Basmati	Medium	Medium	Present	Extra Long	Medium	ELS	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
53	Kothambir Sal	Very Short	Broad	Present	Short	Broad	SB	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
54	Chinoor	Medium	Narrow	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
55	P Sugandha-1	Long	Medium	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
56	P Sugandha-3	Medium	Medium	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	Medium	Present
57	P Sugandha-4	Medium	Medium	Present	Long (B)	Broad	LS (B)	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
58	P Sugandha-5	Medium	Broad	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	Medium	Present
59	Bhadasbhog	Medium	Medium	Absent	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	Medium	Present
60	CR2713-180	Medium	Medium	Absent	Long (B)	Medium	LS (B)	Light Brown	Present	Medium	Absent or very small	High-Medium	Present
61	Kalanamak	Medium	Medium	Absent	Short	Medium	SB	Light Brown	Present	High	Absent or very small	High-Medium	Present
62	NDR6315	Medium	Medium	Present	Short	Medium	SB	Light Brown	Present	Low	Absent or very small	High-Medium	Present
63	P Samruddhi	Long	Medium	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Low	Absent or very small	Medium	Present
64	Indrayani	Medium	Medium	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Low	Absent or very small	High-Medium	Present
65	Dhanesal	Medium	Medium	Absent	Long	Medium	LB	Light Brown	Present	Medium	Absent or very small	Medium	Present
66	Ambemohar	Short	Medium	Present	Short	Medium	SB	Light Brown	Present	Medium	Absent or very small	Medium	Present
67	K Shatabdi	Short	Broad	Present	Short	Medium	SB	Light Brown	Present	Low	Absent or very small	Medium	Present
68	Bhogwati	Long	Narrow	Present	Long (B)	Narrow	LS (B)	White	Present	Medium	Absent or very small	Medium	Present
69	Sugandha	Long	Narrow	Present	Long (B)	Medium	LS (B)	Light Brown	Present	Low	Absent or very small	Medium	Present
70	RS-1113	Short	Narrow	Present	Short	Narrow	SS	Light Brown	Present	Low	Absent or very small	Medium	Absent
71	RP Bio 197	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	High	Absent or very small	High-Medium	Absent
72	RP-BIO-226	Medium	Medium	Present	Long	Medium	LB	Light Brown	Present	High	Absent or very small	High-Medium	Absent
73	Ajaya	Short	Narrow	Present	Medium	Medium	MS	Light Brown	Present	Very High	Absent or very small	High-Medium	Absent
74	KJT 1	Medium	Medium	Present	Short	Medium	SB	Light Brown	Present	Medium	Absent or very small	Medium	Absent
75	KJT 2	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	High-Medium	Absent
76	IR-64	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
77	MUDGO	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	Medium	Absent
78	MILYANG 46	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	Medium	Absent
79	PTB 33	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
80	MTU1010	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	Medium	Absent
81	BG 367-2	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	High-Medium	Absent
82	MILYANG 63	Medium	Medium	Present	Long	Broad	LB	Light Red	Present	Very High	Absent or very small	High-Medium	Absent
83	FL 478	Medium	Very Broad	Present	Long	Broad	LB	Light Red	Present	High	Absent or very small	Medium	Absent
84	MUT NS 1	Medium	Broad	Absent	Long	Broad	LB	Light Brown	Present	High	Absent or very small	Medium	Absent
85	PATHU HEENAT	Medium	Broad	Absent	Long	Broad	LB	Light Red	Present	Medium	Absent or very small	High-Medium	Absent
86	SINNA SIVAPPU	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
87	IRRI 190	Medium	Broad	Present	Long	Broad	LB	Light Brown	Present	Medium	Absent or very small	Medium	Absent
88	IRRI 193	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	Medium	Absent
89	ARC 10550	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	High-Medium	Absent
90	S MAHSURI	Short	Medium	Absent	Medium	Narrow	MS	Light Brown	Present	Low	Absent or very small	High-Medium	Absent
91	IRRI 123	Medium	Medium	Absent	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	Medium	Absent
92	IRRI 104	Medium	Medium	Present	Long	Broad	LB	Light Brown	Present	Low	Absent or very small	Medium	Absent
93	IRRI 192	Medium	Medium	Present	Long	Medium	LS	Light Brown	Present	Medium	Absent or very small	High-Medium	Absent
94	Sonsali	Medium	Broad	Present	Long	Medium	LS	Light Brown	Present	Low	Absent or very small	High-Medium	Absent
95	TN-1	Medium	Very Broad	Present	Short	Broad	SB	Light Red	Present	Medium	Absent or very small	Medium	Absent
Type of variation		Polymorphic	Polymorphic	Dimorphic	Polymorphic	Polymorphic	Polymorphic	Polymorphic	Monomorphic	Polymorphic	Monomorphic	Polymorphic	Dimorphic
SN		51	52	53	54	55	56	57	58	59	60	61	62

Table 4.24 : List of monomorphic, dimorphic and polymorphic DUS descriptors observed in the present study

SN	Monomorphic	SN	Dimorphic	SN	Polymorphic
1	Leaf: Auricles	1	Leaf: Anthocyanin colouration	1	Coleoptile: Colour
2	Leaf: Collar	2	Leaf: Distribution of anthocyanin colouration	2	Basal leaf: Sheath colour
3	Leaf: Anthocyanin colouration of collar	3	Leaf Sheath: anthocyanin colouration	3	Leaf: Intensity of green colour
4	Leaf: Ligule	4	Leaf: Colour of ligule	4	Leaf sheath: Intensity of anthocyanin colouration
5	Leaf: Shape of ligule	5	Leaf: Length of blade	5	Leaf: Pubescence of Blade Surface
6	Male sterility	6	Leaf: Width of blade	6	Leaf: Anthocyanin colouration of auricles
7	Stem: Thickness	7	Culm: attitude	7	Time of heading (50% of plants with panicles)
8	Endosperm: Presence of amylose	8	Spikelet: Colour of stigma	8	Flag leaf: Attitude of blade (early observation)
9	Varieties with endosperm of amylose absent only Polished grain: Expression of white core	9	Stem: Anthocyanin colouration of nodes	9	Spikelet: Density of pubescence of lemma
		10	Stem: Intensity of anthocyanin coloration of nodes	10	Lemma: Anthocyanin colouration of keel
		11	Stem: Anthocyanin colouration of internodes	11	Lemma: Anthocyanin colouration of area below apex
		12	Panicle: Awns	12	Lemma: Anthocyanin colouration of apex
		13	Panicle : Presence of secondary branching	13	Stem: Length (excluding panicle;excluding floating rice)
		14	Grain: Phenol reaction of lemma	14	Panicle: Length of main axis
		15	Decorticated grain: Aroma	15	Flag leaf: Attitude of blade (late observation)
				16	Panicle: Curvature of main axis
				17	Panicle: Number per plant
				18	Spikelet: Colour of tip of lemma
				19	Lemma and Palea: Colour
				20	Panicle: Colour of awns (late observation)
				21	Panicle: Length of longest awn
				22	Panicle: Distribution of awns
				23	Panicle: Secondary branching
				24	Panicle: Attitude of branches
				25	Panicle: Exertion
				26	Time maturity(days)
				27	Leaf: Senescence
				28	Sterile lemma: Colour
				29	Grain: Weight of 1000 fully developed grains
				30	Grain: Length
				31	Grain: Width
				32	Decorticated grain:Length
				33	Decorticated grain:Width
				34	Decorticated grain:Shape (in lateral view)
				35	Decorticated grain:Colour
				36	Endosperm: Content of amylose
				37	Gelatinization temperature through alkali spreading value

Table 4.25 : Pair-wise distinctiveness matrix of 95 rice germplasm obtained from COYD analysis

[illegible]

Table 4.26 Combined over year's distinctiveness analysis of 14 measurable characteristics in rice varieties using MJRA

Particulars	Leaf: Length of blade (cm)	Leaf: Width of blade (cm)	Time of heading (50% plants with panicles) (days)	Stem: Thickness (cm)	Stem: Length excluding panicle (cm)	Panicle: Length of main axis (cm)	Panicle: Number per plant
	1	2	3	4	5	6	7
YEAR MS	0.003	0.000	1.639	0.000	0.275	8.751	0.008
VARIETY MS	69.821	0.000	1757.119	0.000	1266.805	97.552	50.651
VAR.YEAR MS	0.248	0.000	3.199	0.000	7.310	2.064	1.251
F1 RATIO	281.941*	0.000	549.196*	0.000	173.303	47.262	40.490
VAR.REP MS	0.307	0.000	4.649	0.000	2.041	3.992	1.185
F2 RATIO	0.807	0.000	0.688*	0.000	3.581	0.517	1.056
BETWEEN SE	0.203	0.000	0.730	0.000	1.104	0.587	0.457
WITHIN SE	0.226	0.000	0.880	0.000	0.583	0.816	0.444
MJRA SLOPE 2020	0.995	0.000	0.992	0.000	1.018	0.972	0.953
MJRA SLOPE 2021	1.005	0.000	1.008	0.000	0.982	1.028	1.047
REG F VAL	0.195	0.000	0.733	0.000	1.220	0.855	2.022
REG PROB	66.323	0.000	40.122	0.000	28.133	36.518	16.910

Table 4.26 contd.....

Particulars	Time maturity (days)	Grain: Weight of 1000 fully developed grains (g)	Grain: Length (mm)	Grain: Width (mm)	Decorticated grain: Length (mm)	Decorticated grain: Width (mm)	Endosperm: Content of amylose
	8	9	10	11	12	13	14
YEAR MS	0.007	0.293	1.734	0.000	43.451	0.000	1.191
VARIETY MS	5.166	411.062	6.238	0.000	152.437	0.000	2.589
VAR.YEAR MS	0.007	0.501	1.382	0.000	4.279	0.000	0.144
F1 RATIO	718.575	821.082	4.514	0.000	35.625	0.000	17.919
VAR.REP MS	0.007	2.202	1.747	0.000	5.354	0.000	0.269
F2 RATIO	1.035	0.227	0.791	0.000	0.779	0.000	0.537
BETWEEN SE	0.035	0.289	0.480	0.000	0.844	0.000	0.155
WITHIN SE	0.034	0.606	0.540	0.000	0.945	0.000	0.150
MJRA SLOPE 2020	0.997	0.980	1.276	0.000	0.949	0.000	0.957
MJRA SLOPE 2021	1.003	1.020	0.696	0.000	1.051	0.000	1.005
REG F VAL	0.171	7.609	7.097	0.000	2.102	0.000	2.012
REG PROB	68.342	1.147	1.417	0.000	16.118	0.000	2.428

Table 4.28 Combined over years uniformity analysis of 14 measurable characters															
	DUS No.	16	17	20	28	29	33	36	47	50	51	52	54	55	58
SN	Character	LL (cm)	LB (cm)	DFE (Nos.)	ST (cm)	SLEP (cm)	PLMA (cm)	PPP (Nos.)	DM (Days)	TW (gm)	GL (mm)	GW (mm)	DGL (mm)	DGB (mm)	AC (%)
	Genotype	1	0	3	4	5	6	7	8	9	10	11	12	13	14
1	MO-6	49	0	91	0	63	28	11	121	21	0	0	0	0	24
2	MO-8	54	0	86	0	54	24	10	116	18	0	0	0	0	26
3	MO-13	58	0	90	0	88	26	10	120	19	0	0	0	0	24
4	MO-17	59	0	85	0	79	24	10	115	25	0	0	0	0	29
5	MO-19	44	0	82	0	64	24	12	112	22	0	0	0	0	29
6	Khara Rata	69	0	92	0	113	29	10	122	27	0	0	0	0	23
7	Mayekar Bhat	55	0	86	0	113	25	11	116	26	0	0	0	0	29
8	Munga	61	0	97	0	118	25	11	127	24	0	0	0	0	26
9	Mahsad	67	0	90	0	136	25	8	120	25	0	0	0	0	27
10	Waksal-207	62+2	0	86	0	116	25	9	116	24	0	0	0	0	29
11	Barmil	59	0	93	0	133	28	9	123	27	0	0	0	0	25
12	Jyoti	48	0	86	0	108 1	26	9	116	27	0	0	0	0	27
13	Patani-6	72	0	93	0	136	27	9	123	23	0	0	0	0	22
14	Bhadas-79	47	0	92	0	118	28	10	122	23	0	0	0	0	21
15	Pandy	49	0	92	0	133	27	9	122	24	0	0	0	0	25
16	Dular	44	0	92	0	74	24	9	122	25	0	0	0	0	27
17	Try-1	63	0	93	0	140	31	9	122+1	24	0	0	0	0	18
18	Kochari	62	0	80	0	135	33	10	110	27	0	0	0	0	27
19	Lal Patani	41	0	77	0	81	26	8	107	25	0	0	0	0	29
20	Dodak	36	0	76	0	66	27	9	106	27	0	0	0	0	27
21	Karhad	45	0	75	0	67	23	10	105	27	0	0	0	0	20
22	Ratnagiri 7	53	0	87	0	81	25	10	117	26	0	0	0	0	21
23	Bela	60	0	94	0	129	27	9	124	29	0	0	0	0	20
24	Valai	58	0	96	0	134	26	10	125-2	26	0	0	0	0	23
25	KJT-1R	48	0	98	0	103	31	11	128	28	0	0	0	0	21
26	KJT-2R	43	0	85	0	104	28	10	115	21	0	0	0	0	27
27	KJT-3R	53	0	97	0	108 2	28	9	127	25	0	0	0	0	25
28	KJT-4R	43	0	86	0	83 2	26	11	116	23	0	0	0	0	25
29	PR-114	46	0	84	0	99	26	12	114	18	0	0	0	0	25
30	RTN 11-2-1-3	41	0	93	0	71	28	11	123	17	0	0	0	0	23
31	PR-118	55	0	99	0	109	32	13	129	21	0	0	0	0	14
32	DRR-215	52	0	96	0	128	32	15	126	22	0	0	0	0	22
33	RTN-69-1-1	60	0	87	0	118	27	11	117	23	0	0	0	0	23
34	NAUR-1	54	0	94	0	87	27	11	124	28	0	0	0	0	19
35	BL-184AR	51	0	90	0	88	28	11	120	15	0	0	0	0	24
36	Gurjari	33	0	96	0	92	22	9	126	27	0	0	0	0	24
37	DRR-50-12	69	0	96	0	114	28	10	126	20	0	0	0	0	23
38	DRR-363-5	66	0	98	0	113	29	9	128	24	0	0	0	0	31
39	DRR-50-13	57	0	98	0	112	30	13	128	22	0	0	0	0	28
40	DRR-50-10	56	0	99	0	109	28	10	129	23	0	0	0	0	25
41	DRR-86-8	52	0	90	0	100	29	11	120	25	0	0	0	0	29
42	IR-63879-195-2-2-3-2	38	0	85	0	85	27	11	115	18	0	0	0	0	29
43	RTN-27-1-1-2	39	0	86	0	98	25	10	116	22	0	0	0	0	29
44	RTN-214-1-1-1-2	30	0	92	0	99	25	10	122	19	0	0	0	0	28
45	VDN-9-10-1	53	0	91	0	105	25	12	121	24	0	0	0	0	28
46	VDN-10-18	67	0	98	0	103	26	11	128	13	0	0	0	0	27
47	RTN-35-1-1	54	0	99	0	102	25	12	129	17	0	0	0	0	25
48	Sahyadri 5 R	33	0	96	0	129	26	11	126	27	0	0	0	0	24
49	HRTMS-61	59	0	100	0	114	26	10	130	16	0	0	0	0	25
50	CR-3993-2-24-45-2	54	0	101	0	75	26	10	131	21	0	0	0	0	23
51	P Basmati	64	0	99	0	101	27	11	129	23	0	0	0	0	21
52	S Basmati	45	0	107	0	104	23	16	137	21	0	0	0	0	22
53	Kothambir Sal	54	0	106	0	135	27	12	136	12	0	0	0	0	21
54	Chinoor	37	0	93	0	69	27	11	123	15	0	0	0	0	20
55	P Sugandha-1	43	0	87	0	71	28	10	117	23	0	0	0	0	23
56	P Sugandha-3	43	0	85	0	80	28	11	115	25	0	0	0	0	20
57	P Sugandha-4	41	0	92	0	67	27	11	122	25	0	0	0	0	20
58	P Sugandha-5	50	0	88	0	100	27	11	118	27	0	0	0	0	22+1
59	Bhadasbhog	61	0	88	0	149	31	15	118	11	0	0	0	0	25
60	CR2713-180	55	0	80	0	99	32	12	110	17	0	0	0	0	19
61	Kalanamak	53	0	112	0	144	29	14	142	21	0	0	0	0	26
62	NDR6315	68	0	96	0	157	36	11	126	15	0	0	0	0	17
63	P Samruddhi	39	0	91	0	87	29	11	121	18	0	0	0	0	19
64	Indrayani	47	0	91	0	79	27	11	121	16	0	0	0	0	16
65	Dhanesal	66	0	83	0	135	29	13	113	14	0	0	0	0	24
66	Ambemohar	52	0	96	0	111	32	13	126	13	0	0	0	0	21
67	K Shatabdi	41	0	89	0	79	26	11	119	14	0	0	0	0	19
68	Bhogwati	38+1	0	92	0	81	27	12	122	22	0	0	0	0	21
69	Sugandha	51	0	87	0	82	26	14	117	24	0	0	0	0	17
70	RS-1113	45	0	81	0	90	27	11	111	14	0	0	0	0	15
71	RP Bio 197	50	0	88	0	87	27	10	118	18	0	0	0	0	29
72	RP-BIO-226	52	0	99	0	103	27	9	129	23	0	0	0	0	30
73	Ajaya	51	0	99	0	86	26	10	129	20	0	0	0	0	35
74	KJT 1	57	0	89	0	93	26	12	119	21	0	0	0	0	21
75	KJT 2	33	0	108	0	67	28	11	137	21	0	0	0	0	18
76	IR-64	36	0	99	0	74	27	11	129	24	0	0	0	0	20
77	MUDGO	49	0	84	0	69	26	11	114	27	0	0	0	0	12
78	MILYANG 46	41	0	85	0	62	26	11	115	25	0	0	0	0	13
79	PTB 33	51	0	86	0	76	28	11	116	28	0	0	0	0	23
80	MTU1010	41	0	91	0	84	28	10	121	23	0	0	0	0	28
81	BG 367-2	44	0	93	0	79	29	11	123	27	0	0	0	0	14
82	MILYANG 63	33	0	81	0	72	26	9	111	22	0	0	0	0	31
83	FL 478	57	0	83	0	142	28	9	113	25	0	0	0	0	29
84	MUT NS 1	50	0	98	0	77	30	11	128	19	0	0	0	0	26
85	R HEENATI	37	0	88	0	80	28	11	118	25	0	0	0	0	24
86	S SIVAPPU	43	0	88	0	72	28	11	118	22	0	0	0	0	25
87	IRRI 190	34	0	87	0	70	28	11	117	20	0	0	0	0	24
88	IRRI 193	41	0	85	0	81	27	9	115	20	0	0	0	0	16
89	ARC 10550	44	0	92	0	86	24	10	122	19	0	0	0	0	16
90	S MAHSURI	40	0	102	0	57+1	24	10	132	12	0	0	0	0	19
91	IRRI 123	39	0	93	0	70	25	9	123	22	0	0	0	0	15
92	IRRI 104	34	0	73	0	63	22	11	103	21	0	0	0	0	12
93	IRRI 192	35	0	90	0	80	25	11	120	20	0	0	0	0	23
94	Sonsali	44	0	93	0	120	26	10	123	23	0	0	0	0	13
95	TN-1	52	0	93	0	94	24	21	123	24	0	0	0	0	21

Table 5.1: Details of 62 DUS descriptors studied on 95 genotypes pertaining to desirable notes only.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
1	CC	Coleoptiles are cylindrical organs that enclose the first leaf and shoot apex in grass seedlings.	Coleoptile functions like a 'snorkel'; the elongated. They help in the emergence of the first leaf (and shoot apex) by protecting it during its passage through the soil. On emergence, the first leaf breaks through the coleoptile tip. (Kordan, 1974).	Variation in colour viz., colourless, green and purple among germplasm, it serves as morphological marker.	Green	1	Karhad	As polymorphic variation was observed, can be considered as morphological marker to distinguish diverse germplasm.
					Purple	9	Mahsad, Waksal-207, Barmil, Patani-6, Kochari, Bela, Valai, Gurjari, IRRI 190	
2	BL-SC	It is an elongated, cylindrical structure that encloses younger parts of the shoot.	Its major function is to protect younger shoots inside of it and to support the whole plant, which explains why there are very few chloroplasts found in the sheath mesophyll. (N Guo <i>et al</i> · 2020)	Variation in colour viz., colourless, green and purple among germplasm, it serves as morphological marker.	Green	82	MO-6, MO-8, MO-13, MO-17, MO-19, Kala Rata, MayekarBhat, Munga,Jyoti, Dular, LalPatani, Dodak, Karhad, Ratnagiri 7, KJT-1R, KJT-2R,KJT-3R ,KJT-4R ,PR-114, RTN 11-2-1-3, PR-118, DRR-215, RTN-69-1-1,NAUR-1 , BL-184AR, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, , HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha- 1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Numbernamak, NDR6315, P Samruddhi, Indrayani, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, Ajaya, KJT 1, KJT 2, IR-64MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190,IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali, TN-1	As polymorphic variation was observed, can be considered as morphological marker to distinguish diverse germplasm.
					Light Purple	9	Waksal-207, Barmil, Patani-6 , Bhadas-79, Pandey, Kochari, Valai, Gurjari, RP-BIO-226	
					Purple Lines	1	Mahsad	
					Uniform Purple	3	Try-1, Bela, Dhanesal	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
3	L-IGC	The leaves grow alternately on the stem, with one leaf per node.	The leaves are the growth engine of the plant, as they capture solar radiation and produce carbohydrates. The plant breathes and perspires through its leaves. Scale of green coloration serves as the index of nitrogen status of the crop (Giha 2021 <i>et. al.</i>)	Intensity of green colouration is directly correlated with nitrogen uptake and photosynthetic efficiency of plant.	Dark	30	Pandy,KJT-3R,KJT-4R,PR-118,NAUR-1,Gurjari, DRR-363-5, VDN-9-10-1, RTN-35-1-1,Sahyadri 5 R,HRTMS-61,S Basmati,Chinoor,P Sugandha-1, P Sugandha-3,P Sugandha-5,CR2713-180, Indrayani, Sugandha, RS-1113,RP Bio 197,KJT 1,MUDGO, MILYANG 46,PTB 33,BG 367-2,MILYANG 63,MUT NS 1,Sonsali ,TN-1	As polymorphic variation was observed, can be considered as morphological marker to distinguish diverse germplasm. Genotypes with dark green colour are of more desirable note (30) as photo-synthetically more efficient than of light and medium note.
4	L-AC	Anthocyanins, a major subclass of flavonoids, are the main <u>secondary metabolites</u> that give color to rice tissues.	Anthocyanin accumulation in plants has diverse functions; including resisting UV radiation, participating in hormone regulation, and responding to biotic and abiotic stress, and are beneficial to human health. (Xia <i>et. al.</i> 2021)	Presence of anthocyanin colouration is desirable as it acts as morphological mechanism (non-preference by insect-pests) of defense against insect-pests attack.	Present	3	Mahsad,Waksal-207,Barmil	Out 95 genotype only 3 exhibited presence of this trait hence these 3 genotypes are desirable to include in crop improvement programe for insect-pest resistance breeding

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
5	L-DAC	-	-	Anthocyanin accumulates in many plant tissues or organs, in rice for example leading to red, purple red and purple phenotypes for protection from damage by biotic and abiotic stresses and for reproduction. Uniformly distributed Purple pigmentation leaves are common in wild rice and landraces and occasionally found in modern cultivars. (Han-shiuan <i>et. al.</i>2020)	Uniform	01	Waksal-207	
6	LS-AC	Leaf sheath is an elongated, cylindrical structure that encloses younger parts of the shoot.	Its major function is to protect younger shoots inside of it and to support the whole plant. (Davis <i>et. al.</i> , 2020)	Accumulation of anthocyanin pigmentation on basal leaf sheath in rice highlights the phenotypic defense mechanism against biotic stresses. (E Mackon <i>et. al.</i> 2021)	Present	14	Mahsad,Waksal-207,Barmil,Patani-6,Pandy, Dular, Try-1, Kochari, Bela, Valai, Gurjari, Dhanesal,RP-BIO-226,IRRI 190	Out 95 genotype only 14 exhibited presence of this trait. Hence these 14 genotypes are desirable to include in crop improvement for biotic resistance breeding programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
7	LS-IAC	-	-	Darker intensity of anthocyanin pigmentation on leaf sheath indicates more the phenotype is repellent against pests attack (Yamuangmorn <i>et.al</i> 2021)	Strong	2	Dhanesal,IRRI 190	Out 95 genotype only 2 exhibited strong intensity of anthocyanin colouration and other 2 showed very strong intensity, hence these 4 genotypes desirable to include in crop improvement for pests resistance breeding programe.
					Very Strong	2	Try-1, Bela	
8	L-PBS	Pubescence is characterized by trichomes gathering on the plant surface, consisting of unicellular or multicellular exogenous substances on leaves, stems, and root surfaces.	Pubescence may be related to the development of glandular cells and thus are called glandular hairs. Glandular hairs can accumulate and secrete alkaloids such as nicotine and terpenoids as well as some chemical substances against injurious insect. The hairy surface serves as morphological barrier against sucking pests. (Zeng <i>et.al</i> 2019.) Many plants have pubescence designed to provide a tiny bit of shade to reduce the temperature of the leaves and stems and protect the leaves from losing too much water from transpiration (Hamaoka <i>et.al</i> .2017)	Stronger the pubescence, more the phenotype is non- preferred by sucking pests. As well as stronger pubescence prevent water loss from leaves during transpiration.	Strong	27	Barmil,Jyoti,Dodak,Karhad,KJT-1R,KJT-3R,PR-114, DRR-215,IR-63879-195-2-2-3-2,RTN-27-1-1-2, Sahyadri 5 R,S Basmati, Chinoor, P Sugandha-4, Bhadasbhog, Sugandha,RS-1113,RP-BIO-226, Ajaya, KJT1, IR-64, MILYANG 46,PTB 33,MILYANG630, FL 478,S MAHSURI, IRRI 104	Out 95 genotypes 27 exhibited strong pubescence and other 6 showed very strong note. Hence these 33 genotypes should be included in crop improvement for biotic and abiotic stress breeding as a donor parents.
					Very Strong	6	P Sugandha-1,P Sugandha-3,Numbernamak,KJT 2,SINNA SIVAPPU ,IRRI 190	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
9	L-A	Auricles are pair of hairy, sickle-shaped appendages located in the junction of the collar and the sheath The auricles are located at the lower end of the leaf-blade, where it meets the leaf-sheath. They may be extended as a pair of claw-like projections.	It keeps the leaf sheath and culm together. (Lee <i>et. al</i> , 2022)	Presence of auricle is desirable which serves as binding agent for leaf sheath and culm.	Present	95	MO-6, MO-8, MO-13, MO-17, MO-19, KalaRata, Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6, Bhadas 79, Pandey, Dular, Try-1, Kochari, LalPatani, Dodak, Karhad, Ratnagiri 7, Bela, Valai, KJT-1R, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN 11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Numbernamak, NDR6315, P Samruddhi, Indrayani, Dhanelal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali, TN-1	All 95 genotypes showed presence of auricles and can be included in crop improvement programme or can directly be used for commercial cultivation.
10	L-ACA	-	Anthocyanins are a group of polyphenolic pigments that are ubiquitously found in the leaf of rice. In rice, anthocyanins play a role not only in reproduction, by attracting pollinators and seed dispersers, but also in protection against various abiotic and biotic stresses. (Ying <i>et. al</i> 2018)	Dark colouration such as purple is of desirable note as it works as shield against various biotic stresses.	Purple	7	Barmil, Patani-6, Pandey, Valai, Gurjari, PTB 33, IRRI 190	Out of 95 genotypes studied, 7 showed purple anthocyanin colouration on the leaves, thus these 7 germplasm can be included in development of insect-pests resistant lines as a donor parent.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
11	L-C	It is a white band at the junction of the blade and the sheath.	-	Presence of leaf color serves as morphological marker.	Present	95	MO-6, MO-8, MO-13, MO-17, MO-19, KalaRata, Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandya, Dular, Try-1, Kochari, Lal Patani, Dodak, Karhad, Ratnagiri 7, Bela, Valai, KJT-1R, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN 11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Numbernarnak, NDR6315, P Samruddhi, Indrayani, Dhaneal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali, TN-1	All the genotypes can be included in crop ideotype breeding.
12	L-ACC	-	-	Presence of this trait is of desirable note as it works as shield against various biotic stresses.	Present	5	Barmil, Patani-6, Pandya, Gurjari, IRRI 190,	Out of 95 genotypes studied, only 5 showed presence of anthocyanin colouration on the leaf collar, thus these 5 germplasm can be included development of insect-pests resistant lines as a donor parent.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
13	L-L	It is a triangular, papery scale located inside the blade it looks like a continuation of the sheath	It protects the culm and leaves that it encloses from the entry of water, dust and harmful spores (Davis <i>et. al.</i> , 2020)	Presence of this trait is of desirable note as it works as filter to avoid the entry of water, dust and harmful spores in culm..	Present	95	MO-6,MO-8,MO-13,MO-17,MO-19,KalaRata,Mayekar Bhat, Munga, Mahsad,Waksal-207,Barmil,Jyoti,Patani-6,Bhadas-79, Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114, RTN 11- 2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10, DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,KothambirSal, Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4, P Sugandha-5, Bhadasbhog,CR2713-180,Numbernamak,NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	All the 95 genotypes exhibited presence of ligule. Hence all the genotypes found to be desirable and can be included in resistance breeding against biotic stresses
14	L-SL	-	-	Different shapes serves as morphological markers.	Split	95	MO-6,MO-8,MO-13,MO-17,MO-19,Kala Rata,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti,Patani-6,Bhadas- 79,Pandy, Dular,Try-1,Kochari, Lal Patani, Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118, DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati , Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Numbernamak, NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	Though all the 95 genotypes found to have split shape of ligule, shape of ligule can be used to distinguish diverse germplasm and serves as morphological marker.

[illegible]

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
19	C-A	The jointed stem of rice, called a culm, is made up of a series of nodes and internodes. The node (nodal region) bears a leaf and a bud.	The main role of culm is to support rice plant and helps to transport minerals and water absorbed by roots to upper parts. (Davis <i>et al.</i> , 2020)	Culm attitude is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for culm attitude.	Erect	84	MO-6,MO-8,MO-13,MO-17,MO-19,KalaRata, Mayekar Bhat, Munga,Mahsad,Barmil,Bhadas-79, Dular, Dodak, Karhad, Ratnagiri 7, KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari, DRR-50- 12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-2, VDN-9-10-1,VDN-10- 18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, Kothambir Sal,Chinoor,P Sugandha-1, P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180, Numbernamak, NDR6315, P Samruddhi, Indrayani, Dhaneasal,Ambemohar,K Shatabdi, Bhogwati, Sugandha, RS-1113,RP Bio 197,RP-BIO-226,Ajaya, KJT 1, KJT 2, IR-64, UDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali	Out of 95 only 84 genotype showed erect culm attitude while 11 had semi-erect culm attitude. Thus these genotype can be used as donor parent in crop ideotype breeding programme.
					Semi-erect	11	Waksal-207,Jyoti,Patani-6,Pandy,Try-1,Kochari,Lal Patani, Bela, Valai, FL 478,TN-1,	
20	TH	Days to 50% flowering was determined by recording the number of days following transplanting (DAT) until 50% of plants in a plot had at least one open flower.	-	Time for heading to 50% flowering indicates the duration of the genotype for maturity and adaptability for different ecosystems. (Anputhas <i>et al.</i> 2021)	Early (71-90)	42	MO-8,MO-17,MO-19,Mayekar Bhat,Mahsad,Waksal-207, Jyoti, Kochari,Lal Patani,Dodak,Karhad,Ratnagiri 7,KJT-2R,KJT-4R,PR-114, RTN-69-1-1,NAUR-1,BL-184AR,RTN-214-1-1-2,VDN-9-10-1,P Sugandha-1,P Sugandha-3,P Sugandha-5, Bhadasbhog,CR2713-180, Dhaneasal,K Shatabdi,Sugandha,RS-1113,RP Bio 197, KJT 1,MUDGO ,MILYANG 46,PTB 33,MILYANG 63,FL 478, RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,IRRI 104,IRRI 192	Out of 95 genotypes 42 were early indicated their adaptability for upland ecosystem, while 52 showed mid-late duration which are adaptable for midland and rest 1 found be of late duration which is adaptable for lowland.
					Medium (91-110)	52	MO-13,Kala Rata,Munga,Barmil,Patani-6,Bhadas-79, Pandy, Dular, Try-1,Bela ,Valai , KJT-1R,KJT-3R,RTN 11-2-1-3,PR-118, DRR-215, Gurjari,DRR-50-12,DRR-363-5,DRR-50-13, DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-4,NDR6315,P Samruddhi,Indrayani, Ambemohar, Bhogwati,RP-BIO-226,Ajaya,KJT 2,IR-64,MTU1010,BG 367-2,MUT NS 1,ARC 10550 ,S MAHSURI,IRRI 123,Sonsali ,TN-1,	
					Late (111-130)	1	Numbernamak	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
21	FL-AB (EO)	The flag leaf is the top leaf on a rice stem, closest to the grain-producing panicle	Flag leaves have a major role in providing energy to the developing grain, and any impact on photosynthesis in the flag leaf can have a dramatic effect on grain productivity.(Davis <i>et. al.</i> , 2020)	It is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for flag leaf attitude.	Erect	79	MO-6,MO-8,MO-13,MO-17,MO-19,Mayekar Bhat, Munga, Mahsad, Barmil,Jyoti,Patani-6,Bhadas-79, Pandy, Dular, Kochari, Lal Patani, Dodak, Karhad,Bela ,alai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN- 10-18,RTN-35-1-1, Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,P Samruddhi, Indrayani, Dhanesal, K Shatabdi, Bhogwati,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46, PTB 33, BG 367-2, MILYANG 63, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	Out of 95 only 79 genotype showed erect attitude while 14 had semi-erect attitude and rest 1showed horizontal attitude. Thus these genotype can be used as donor parent in crop ideotype breeding programme.
					Semi-erect	14	Kala Rata,Waksal-207,Try-1,Ratnagiri 7,PR-114,IR-63879-195-2-2-3-2, S Basmati, Kothambir Sal, CR2713-180,Numbernamak,NDR6315,Ambemohar, MTU1010,FL 478	
					Horizontal	2	Bhadasbhog, Sugandha	
22	S-DBL	Spikelets are the basic inflorescence units in rice and typically consist of a flower of interlocked lemma and palea forming a husk, two lodicules, six stamens, and one pistil.	In rice, the spikelet meristem develops a pair of rudimentary glumes and then produces two lateral floral meristems and one terminal floral meristem. The two lateral floral meristems form one pair of sterile lemmas (degraded lateral florets), and the terminal floral meristem develops one fertile terminal floret (Fu <i>et. al.</i> , 2019).	Pubescence plays an important role in insect resistance, drought tolerance, and other stresses.	Very Strong	37	MO-19,Mayekar Bhat, Waksal-207, Patani-6, Kochari, Lal Patani, Dodak, Karhad, Valai, PR-114,BL-184AR,Gurjari,DRR-86-8,IR-63879-195-2-2-3-2, RTN-35-1-1,Chinoor,P Sugandha-4, Numbernamak, P Samruddhi, Indrayani, Dhanesal, RS-1113, MTU1010,BG 367-2,MILYANG 63, FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU, IRRI 190,IRRI 193,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali,TN-1,	Out of 95 genotypes studies 37 had shown very strong pubescent lemma. Thus these genotypes can be included in biotic stress resistance breeding programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
23	MS	Male sterility is defined as the failure of plants to produce functional anthers, pollen, or male gametes.	The use of male sterility reduces the cost of hybrid seed production for several reasons. It avoids hand emasculation and pollination, accelerating the hybrid breeding programs and allowing the large-scale production of hybrid seeds and the commercial exploitation of hybrid vigo (Laura <i>et. al.</i> , 2020)	For commercial cultivation, absence of male sterility is desirable.	Absent	95	MO-6,MO-8,MO-13,MO-17,MO-19,KalaRata,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6,Bhadas- 79,Pandy, Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7, Bela, Valai, KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118, DRR-215,RTN-69-1-1,NAUR-1, BL-184AR, Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2,P Basmati,S Basmati, Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4, P Sugandha-5, Bhadasbhog,CR2713-180,Numbernamak, NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	All 95 genotypes showed absence of male sterile. Thus all are desirable for commercial cultivation and can be included in crop improvement programme.
24	L-ACK	The lemma has a constricted structure at its end called the keel.	-	Presence of this trait is of desirable note as it works as shield against various biotic stresses.	Very Strong	3	NDR6315, Dhanesal and Ambemohar	Out of 95 genotypes studied, 3 showed very strong anthocyanin colouration on the keel, thus these 3 germplasm can be included development of insect-pests resistant lines as a donor parent.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
25	L-ACABA	-	-	The anthocyanin biosynthesis attracts strong interest due to the potential antioxidant value and as an important morphological marker.(Khan <i>et. al.</i> 2020)	Very Strong	4	Bhadasbhog, NDR6315, Dhanesal, Ambemohar	Out of 95 genotypes studied, 4 showed very strong anthocyanin colouration area below apex. Thus these 4 germplasm can be included development of insect-pests resistant lines as a donor parent. As well as this trait can be used morphological marker to distinguish the germplasm.
26	L-ACA	-	-	The anthocyanin biosynthesis attracts strong interest due to the potential antioxidant value and as an important morphological marker.(Khan <i>et. al.</i> 2020)	Very Strong	5	Kala Rata, Bhadasbhog, NDR6315,Dhanesal and Ambemohar	Out of 95 genotypes studied, 4 showed very strong anthocyanin colouration area below apex. Thus these 4 germplasm can be included development of insect-pests resistant lines as a donor parent. As well as this trait can be used morphological marker to distinguish the germplasm.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
27	S-CS	In rice, the pistil is the female reproductive organ, and it consists of two stigmas and an ovary.	The stigma is capable of receiving pollen grains and guiding pollen tube growth	Furthermore, the stigma color is often regarded as an important trait in variety identification in some crop plants such as rice (Han <i>et. al.</i> , 2018)	Purple	11	Kala Rata,Mahsad,Barmil,Patani-6, Pandy, Kochari, Ratnagiri 7, Bela ,Valai ,NAUR 1,IRRI 190,	Out of 95, 84 genotypes showed white stigma while rest 11 had purple stigma. Thus this trait can be used as morphological marker to distinguish the germplasm
28	ST	The stem of rice popularly known as the haulm or the culm, is generally erect, cylindrical, hollow at the internodes and solid at the nodes. The number and length of internodes vary with the different varieties.	The stem's main function is to transport water and nutrients and to bring air to the roots. (Davis <i>et. al.</i> , 2020).	Thicker stems are preferred as such stems gives support to plants while lodging.	Thick	95	MO-6,MO-8,MO-13,MO-17,MO-19,KalaRata,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6, Bhadas- 79,Pandy, Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad, Ratnagiri 7, Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118, DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2,P Basmati,S Basmati, Kothambir Sal,Chinoor, P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180, Numbernamak, NDR6315, P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	All 95 genotype showed thick stem habit. Thus all genotype can be used as donor parent in crop ideotype breeding programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
29	S- L (FR)	The lower internodes are shorter than the upper ones. The shorter the lower internodes, the more resistant the plant will be to lodging.	Each node has one leaf and one bud that can develop into a tiller.(Rice hub portal, 2020)	Shorter stem length viz., dwarf and semi-dwarf stature of plant is preferred as these are climate smart structure as they have lodging resistance and are responsive to fertilizers.	V. Short (<91 cm)	46	MO-6,MO-8,MO-13,MO-17,MO-19,Dular,LalPatani, Dodak, Karhad, Ratnagiri 7, KJT-4R, RTN 11-2-1-3, NAUR-1,BL-184AR, RTN-27-1-1-2,CR-3993-2-24-45-2,Chinoor, P Sugandha-1, PSugandha-3, PSugandha-4,P Samruddhi, Indrayani, KShatabdi, Bhogwati, Sugandha,RS-1113,RP Bio 197, Ajaya,KJT 2,IR-64,UDGO ,MILYANG 46,PTB 33,MTU1010,BG 367- 2,MILYANG 63,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI104,IRRI 192	Stem length in the range of 70-110 cm s considered to be of dwarf to semi-dwarf stature. Out of 95, 46 genotypes were very short and 20 showed short plant type thus these genotypes can be used as donor parent in crop ideotype breeding programme.
					Short (91-110 cm)	20	Jyoti,KJT-1R,KJT-2R,KJT-3R,PR-114,PR-118, Gurjari, IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1, VDN-10-18,RTN-35-1-1,Sahyadri 5 R,P Basmati,S Basmati,P Sugandha-5,CR2713-180,RP-BIO-226,KJT 1,TN-1	
30	S-CAN	-	-	Accumulation of anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (E Mackon et. al.2021)	Present	4	Lal Patani,Gurjari,DRR-86-8,HRTMS-61	Out of 95, only 4 genotypes showed presence of anthocyanin colouration of nodes. Thus these genotypes can be included in biotic stress resistance breeding programme.
31	S-IACN	-	-	Stronger the presence anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (E Mackon et. al.2021)	Medium	1	Gurjari	Out of 95, only1 genotypes showed medium scale intensity of anthocyanin colouration of nodes. Thus this genotype can be included in biotic stress resistance breeding as donor parent.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
32	S-ACI	-	-	Accumulation of anthocyanin pigmentation on nodes and inter nodes of stem in rice highlights the phenotypic defense mechanism against biotic stresses. (E Mackon <i>et. al.</i> 2021)	Present	2	Mahsad, Bela	Out of 95, only 2 genotypes showed presence of anthocyanin colouration of inter nodes. Thus this genotype can be included in biotic stress resistance breeding programme.
33	P-LMA	Panicles form the rice inflorescence. It is the top part of the rice plant, carried on the last inter-node. Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets.	Schematic representation of a rice panicle comprising a main central axis named rachis, to which primary branches are attached; the primary branches bear secondary branches, which in turn bear tertiary branches. Spikelets are attached to the branches by a peduncle. (Antonio <i>et. al.</i> 2021)	Longer panicles indicated more number of grains and thus length of main axis is directly correlated to the yield.	Long (26-30 cm)	63	MO-6,MO-13, Kala Rata,Barmil,Jyoti,Patani-6,Bhadas-79, Pandy, Lal Patani,Dodak,Bela ,Valai ,KJT-2R,KJT-3R,KJT-4R,PR- 114,RTN 11-2-1-3,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-12,DRR-363-5,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18, Sahyadri 5 R,CR-3993-2-24-45-2,P Basmati,Kothambir Sal,Chinoor,PSugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, Numbernamak, P Samruddhi, Indrayani, Dhanesal, KShatabdi, Bhogwati,Sugandha,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,PTB 33,MTU1010,BG 367- 2,MILYANG 63,FL 478,RATHU HEENATI, SINNA SIVAPPU ,IRRI 190,IRRI 193,Sonsali	Out of 95, 63 genotypes showed long panicles and other 10 had very long panicle. Thus these genotypes can be directly released for commercial cultivation or can be used in crop improvement as donor parent.
					V. Long (>30cm)	10	Try-1,Kochari,KJT-1R,PR-118,DRR-215,DRR-50-13,CR2713-180,NDR6315,Ambemohar,MUT NS 1	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
34	FL-AB (LO)	The flag leaf is the top leaf on a rice stem, closest to the grain-producing panicle	Flag leaves have a major role in providing energy to the developing grain, and any impact on photosynthesis in the flag leaf can have a dramatic effect on grain productivity.(Davis <i>et. al.</i> , 2020)	It is an indicator of the growth habit of a particular species. During the current study valuable variation was observed among the accessions for flag leaf attitude.	Erect	67	MO-6,MO-8,MO-13,MO-17,MO-19, Mayekar Bhat, Munga, Mahsad, Barmil, Jyoti,Patani-6,Bhadas-79, Pandy, Dular, Kochari, Lal Patani,Karhad,Ratnagiri 7,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,HRTMS-61,CR-3993-2-24-45-2,Dhanesal,RS-1113,RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550 ,IRRI 123, IRRI 104, Sonsali , TN-1	Out of 95 only 67 genotype showed erect attitude while 20 had semi-erect attitude and 7 had horizontal attitude rest 1 showed deflexed attitude. Thus these genotypes can be used as donor parent in crop ideotype breeding progrmme
					Semi-erect	20	Kala Rata,Waksal-207,Try-1,Dodak,Bela ,Valai ,VDN-9-10-1,Sahyadri 5 R,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-4,CR2713-180, Numbernamak, Indrayani, Ambemohar, K Shatabdi,Sugandha, S MAHSURI,IRRI 192	
					Horizontal	7	P Basmati,S Basmati ,P Sugandha-3,P Sugandha-5, Bhadasbhog,P Samruddhi,Bhogwati	
					Deflexed	1	NDR6315	
35	P-CMA	-	-	Over the past 30 years, super rice played an important role in boosting rice yield. The phenotype of erect panicle (EP) architecture controlled by dense and erect panicle 1 (dep1) is the typical characteristic of super rice, and the phenotype has been used in rice breeding for nearly a century (Sibo <i>et. al.</i> 2022)	Straight	28	Kala Rata,Mayekar Bhat,Munga,Patani-6, Bhadas-79, Pandy, Dular, Try-1, Dodak, Bela, Valai ,P Sugandha-4,P Sugandha-5,RS-1113, RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,MTU1010,BG 367-2,MILYANG 63,IRRI 190,IRRI 193,ARC 10550 ,IRRI104,Sonsali ,TN-1	Bending-type lodging is caused by increases in panicle weight during maturation and occurs over the entire internode of rice during strong wind, thus these 28 straight type genotypes are suitable to include in crop improvement programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
36	P-NP	Panicles form the rice inflorescence. It is the top part of the rice plant, carried on the last inter-node. Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets.	-	Panicle number is directly correlated with yield.	Medium (11-20)	39	MO-6,MO-19,Mayekar Bhat,Munga,PR-114,RTN 11-2-1-3,PR-118,DRR-215,NAUR-1,BL-184AR,DRR-50-13,DRR-86-8,IR-63879-195-2-2-3-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1, Sahyadri 5 R, S Basmati, Kothambir Sal, P Sugandha-3,Bhadasbhog, CR2713-180, Numbernamak, P Samruddhi, Dhaneasal, Ambemohar, K Shatabdi, Bhogwati,Sugandha,KJT 1,IR-64,MILYANG 46,PTB 33,BG 367-2,MUT NS 1, RATHU HEENATI ,IRRI 190,IRRI 104,IRRI 192	Out of 95, 39 genotypes had medium number of panicles and only 1 showed many number of panicles. Thus these genotypes are suitable to include in crop improvement programme.
					Many (>20)	1	TN-1	
37	S-CTL	-	-	More variation in colour for this trait serves morphological marker.	Yellowish	2	Lal Patani, IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2, RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,S Basmati , Kothambir Sal,CR2713-180,Numbernamak	This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm.
					Brown	3	Munga,Kochari,Dhaneasal	
					Purple	5	Waksal-207,Jyoti,Bhadas-79,Pandy,Bela ,Valai ,RTN-69-1-1	
					Black	6	MO-19, Bhadasbhog,NDR6315,Ambemohar	
38	LP:C	Lemma is specialized bracts or bracteate. Example- Rice, in rice the palea is in bended form and facing towards the lemma. Palea is one of the chaffy scales on the receptacle of many composite plants. : the upper bract that with the lemma encloses the flower in rice.	The other scales, the lemma and the palea, occur in pairs. Generally the lemma is larger than the palea, which is hidden between the lemma and the spikelet axis. The lemma and palea surround and protect the flower, and all three of these structures form the floret. (Lombardo <i>et. al.</i> , 2022)	More variation in colour for this trait serves morphological marker	Straw	7	MO-6,MO-8,MO-13,MO-17,Kala Rata, Munga,Barmil, Patani-6,Dular,Try-1,Lal Patani, Dodak, Karhad, Ratnagiri 7,KJT-1R,KJT- 2R,KJT-3R,JT-4R,PR-114,RTN 11-2-1-3, PR-118, DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, Gurjari,DRR-50-12,DRR-363-5,DRR-50-13, DRR-50-10, DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1, VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,P Basmati,S Basmati, Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4, P Sugandha-5, Bhadasbhog,CR2713-180,P Samruddhi, Indrayani, K Shatabdi, Bhogwati, Sugandha,RS-1113,RP-BIO-226, Ajaya,KJT 1,KJT 2,IR- 64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367-2, MILYANG 63, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, TN-1	This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm.
					Brown spots on straw	3	Bela,Valai, Numbernamak	
					Brown furrows on straw	3	Mahsad,CR-3993-2-24-45-2,Sonsali	
					Brown (tawny)	6	MO-19,Waksal-207,Jyoti,Bhadas-79,Pandy,RP Bio 197	
					Reddish to light purple	3	Kochari, Dhaneasal, FL 478	
					Purple spots/ furrows on straw	1	Mayekar Bhat	
					Purple	1	Ambemohar	
					Black	1	NDR6315	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
39	P-A	The filiform extension of the keel of the lemma is known as awn having bristles or hair like structure	They contribute to grain dispersal and burial and fend off animal predators.	But not preferred for modern cultivars as it is inconvenient for mechanical threshing.	Absent	61	MO-6,MO-8, MO-13, MO-17, MO-19, MayekarBhat, Munga, Waksal207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandy, Dular, Dodak, Karhad, Ratnagiri 7, Valai, KJT-1R, KJT-2R, PR-114,RTN11-2-1-3,PR-118,DRR-215,RTN-69-1-1, BL184AR, Gurjari, DRR-50-12, DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1, VDN-10-18,RTN-35-1-1,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,NDR6315,Ambemohar,K Shatabdi,Bhogwati, RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,MILYANG 46,PTB 33,MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550, S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali ,TN-1	Out of 95, 61 genotypes were awnless. Thus these genotypes should be included in crop improvement.
40	P-CA (LO)	-	-	More variation in colour for this trait serves morphological marker	Yellowish White	24	Try-1,Lal Patani,KJT-3R,KJT-4R,DRR-363-5,DRR-86-8,RTN-27-1-1-2,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, Kothambir Sal, P Samruddhi, Indrayani, Dhanelal, RP Bio 197,IR-64,MUDGO ,MTU1010,BG 367-2,MUT NS 1,SINNA SIVAPPU ,IRRI 193	This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm
					Yellowish brown	3	Kochari,Numbernarnamak,Sugandha	
					Reddish Brown	1	Bhadasbhog	
					Light red	1	NAUR-1	
					Light Purple	3	Kala Rata,CR2713-180,IRRI 190	
					Black	1	Bela	
41	P-LLA	-	-	Not preferable character for presence of all its notes except absent.	NA	61	MO-6,MO-8,MO-13,MO-17,MO-19, MayekarBhat, Munga, Waksal207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandy, Dular, Dodak, Karhad,Ratnagiri 7,Valai ,KJT-1R,KJT-2R, PR-114, RTN 11-2-1-3,PR-118, DRR-215,RTN-69-1-1,BL-184AR, Gurjari, DRR-50-12, DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1, Chinoor, P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,NDR6315,Ambemohar,K Shatabdi,Bhogwati,RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,MILYANG 46,PTB 33, MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550, S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali,TN-1	Out of 95, these 61 awnless genotypes are desirable and can be included in breeding programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
42	P-DA	-	-	Not preferable character for presence of all its notes except absent.	NA	61	MO-6,MO-8,MO-13,MO-17,MO-19, MayekarBhat, Munga, Waksal207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandya, Dular, Dodak, Karhad,Ratnagiri 7,Valai ,KJT-1R, KJT-2R, PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR,Gurjari,DRR-50-12, DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Chinoor, P Sugandha-1, P Sugandha-3,P Sugandha-4,P Sugandha-5,NDR6315,Ambemohar,K Shatabdi,Bhogwati,RS-1113,RP-BIO-226,Ajaya,KJT 1,KJT 2,MILYANG 46,PTB 33, MILYANG 63,FL 478,RATHU HEENATI ,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali ,TN-1	Out of 95, these 61 awnless genotypes are desirable and can be included in breeding programme.
43	P-PSB	Panicles are composed of primary ramifications (small branches) that carry secondary branches themselves carrying the pedicels which carry the spikelets.	The acquisition of greater secondary branching potential plays an important role in increasing grain yield in cultivated rice.(Huang <i>et al.</i> , 2021)	It is directly correlated with yield.	Present	79	Mahsad,Waksal-207,Barmil,Bhadas-79, Pandya, Dular, Kochari, Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,PR-114,RTN 11-2- 1-3,PR-118,DRR-215,RTN-69-1-1,BL-184AR, Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Numbernarnak,NDR6315,P Samruddhi, Indrayani, Dhaneal, Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113,RP Bio 197,RP- BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	Out of 95, 79 shown presence of secondary branching. Thus these genotypes are desirable and can be included in breeding programme
44	P-SB	-	-	Stronger note is desirable for this trait	Strong	21	Mahsad,Waksal-207,PR-114,DRR-215,BL-184AR,Gurjari,DRR-363-5,DRR-50-13,DRR-50-10,IR-63879-195-2-2-3-2,P Basmati, Chinoor,P Sugandha-1,Indrayani,RS-1113,RP Bio 197,Ajaya,PTB 33,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 192	Out of 95, 21 shown presence of strong secondary branching. Thus these genotypes are desirable and can be included in breeding programme

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
45	P-AB	-	-	Erect attitude is desirable as it indicates bending resistance	Erect	47	Pandy,Dular,PR-114,RTN 11-2-1-3,PR-118,DRR-215,DRR-50-12,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,P Basmati, S Basmati, P Sugandha-4, P Sugandha-5, Numbernamak, P Samruddhi, Indrayani, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RP Bio 197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,IRRI 190,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123,IRRI 104,IRRI 192,Sonsali	Out of 95, 47 genotypes shown presence of erect attitude of branching. Thus these genotypes are desirable and can be included in ideotype breeding programme
46	P-E	Panicle exertion, the distance between the leaf cushion of flag and the neck-panicle node, is an important morphological trait, which has significant impact on hybrid seed production of rice.(Yang <i>et. al.</i> , 2020)	-	Well exerted panicles are meant to be exposed for full sunlight and hence all the grains are fully developed in such genotypes.	Well exerted	88	MO-6,MO-8,MO-13,MO-19,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Patani-6, Bhadas-79, Pandy, Try-1, Kochari, Lal Patani,Dodak,Karhad,Ratnagiri 7,Bela, Valai, KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215, RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18, RTN-35-1-1,Sahyadri 5 R,HRTMS-61,P Basmati,S Basmati, Kothambir Sal,Chinoor,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,Numbernamak,NDR6315,P Samruddhi, Indrayani, Dhanesal,Ambemohar,K Shatabdi, Bhogwati,Sugandha,RS-1113,RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI , SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550 , S MAHSURI, IRRI 123,	Out of 95, 88 genotypes shown presence of well exerted panicles. Thus these genotypes are desirable and can be included in ideotype breeding programme

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
							IRRI 104, IRRI 192, Sonsali , TN-1	
47	TM	The biological cycle of rice (days from seedling to harvest)		All notes are preferable for this trait. As early genotypes are suitable for upland ecosystem, mid-late cultures are adaptable for midland ecosystem whereas late lines are good for lowland ecosystem.(Sandhu <i>et. al.</i> 2019) (Anputhas <i>et al.</i> 2021)	Early (101-120)	40	MO-8,MO-17,MO-19,MayekarBhat,Mahsad,Waksal-207, Jyoti, Kochari,Lal Patani,Dodak,Karhad,Ratnagiri 7,KJT-2R,KJT-4R,PR- 114,RTN-69-1-1,BL-184AR,IR-63879-195-2-2-3-2, RTN-27-1-1-2,P Sugandha-1,P Sugandha-3,P Sugandha-5, Bhadasbhog,CR2713-180,Dhanesal,K Shatabdi,RS-1113,RP Bio 197,KJT 1,MUDGO ,MILYANG 46,PTB 33,MILYANG 63,FL478,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,IRRI 104,IRRI 192	Out of 95 genotypes 40 were early indicated their adaptability for upland ecosystem, while 54 showed mid-late duration which are adaptable for midland and rest 1 found be of late duration which is adaptable for lowland.
					Medium (121-140)	54	MO-6,MO-13,Kala Rata, Munga, Barmil, Patani-6, Bhadas-79, Pandya, Dular, Try-1, Bela ,Valai ,KJT-1R,KJT-3R,RTN 11-2-1-3,PR-118,DRR-215,NAUR-1,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati ,Kothambir Sal, Chinoor, P Sugandha 4,NDR6315,P Samruddhi, Indrayani, Ambemohar, Bhogwati, Sugandha, RP-BIO-226, Ajaya,KJT 2,IR-64, MTU1010, BG 367-2,MUTNS 1,ARC 10550 ,S MAHSURI,IRRI 123,Sonsali ,TN-1	
					Late (141 -160)	01	Numbernamak	
48	L-S	Leaf senescence, which is the last developmental phase of plant growth, is controlled by multiple genetic and environmental factors. Leaf yellowing is a visual indicator of senescence due to the loss of the green pigment chlorophyll	Leaf senescence constitutes the final stage of leaf development and is critical for plants' fitness as nutrient relocation from leaves to reproducing seeds is achieved through this process. (Schippers <i>et .al</i> 2022).	Late senescence of leaf is desirable as underdeveloped grain sin panicle will get nutritional support even after maturity to get complete development.	Late	03	VDN-10-18,CR-3993-2-24-45-2,Ambemohar	Late leaf senescence is shown by 3 genotypes out of 95. Thus genotypes can be utilized in crop improvement programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
49	SL-C	Sterile lemmas are produced between the fertile floret and the rudimentary glumes (Lombardo <i>et. al.</i> , 2022)	-	More variation in colour for this trait serves morphological marker	Straw	16	P Basmati, Shatabdi,Bhogwati,RS-1113,KJT 2,IR-64,MUDGO , MILYANG 46,PTB 33,FL 478,MUT NS 1,RATHU HEENATI, SINNA SIVAPPU, S MAHSURI,IRRI 104,IRRI 192	This trait exhibited polymorphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm.
					Gold	3	RP Bio 197,IRRI 123,Sonsali	
					Red	8	P Sugandha-3,P Sugandha-4,P Samruddhi,Sugandha, KJT 1, MTU1010,MILYANG 63,ARC 10550	
					Purple	6	Kothambir Sal, Bhadasbhog,NDR6315,Ambemohar,Ajaya,IRRI 193	
					White	62	MO-6,MO-8,MO-13,MO-17,MO-19,Kala Rata,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti,Patani-6,Bhadas- 79, Pandy, Dular, Try-1, Kochari, Lal Patani, Dodak, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2,S Basmati, Chinoor,P Sugandha-1, P Sugandha-5,CR2713-180, Numbernamak, Indrayani,Dhanesal,RP-BIO- 226,BG 367-2,IRRI 190,TN-1	
50	TW	The 1,000 kernel (1,000 K) weight is a measure of seed size.	Thousand kernel weight (TKW) is an important parameter for the evaluation of variety breeding. TKW is not only directly related to the grain yield and milling quality of grain, but also has an impact on the seedling vigor and growth indirectly affecting the yield (Wu <i>et. al.</i> . 2021)	Test weight below 14 g indicates superfine grains, whereas more the test weight, grains will be coarse and bold.	Very low (<15 g)	5	P Basmati,S Basmati, P Sugandha-1,P Sugandha-3,P Sugandha-4	Out of 95 genotypes 5 showed very low an 26 had low test weight below 15 g. thus these grains are super fine and can be used for table purpose.while ream rest showed high and very high test weight. Thus these genotypes will be considered for flour making, roti making and beaten rice manufacturing.
					Low (15-20 g)	26	MO-8,MO-13,PR-114,RTN 11-2-1-3,BL-184AR,DRR-50-12,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,HRTMS-61,CR-3993-2-24-45-2,CR2713-180,NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar,K Shatabdi,RP Bio 197,Ajaya,MUT NS 1,IRRI 190,IRRI 193,ARC 10550 ,IRRI 192	
					Medium (21-25 g)	46	MO-6, MO-17,MO-19,Munga,Mahsad,Waksal-207,Patani-6, Bhadas-79, Pandy, Dular, Try-1,Lal Patani, KJT-2R, KJT-3R, KJT-4R, PR-118,DRR-215,RTN-69-1-1,DRR-363-5,DRR-50-13,DRR-50-10, DRR-86-8, RTN-27-1-1-2,VDN-9-10-1 Chinoor, Bhadasbhog,RS-1113,S MAHSURI, Numbernamak, Bhogwati, Sugandha, RP-BIO-226,KJT 1,KJT 2,IR-64,MILYANG 46,MTU1010,MILYANG 63,FL 478,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 123,IRRI 104,Sonsali, TN-1	
					High (26-30)	18	Kala Rata,Mayekar Bhat, Barmil, Jyoti, Kochari, Dodak, Karhad, Ratnagiri 7, Bela ,Valai ,KJT-1R, NAUR-1, Gurjari, Sahyadri 5 R, P Sugandha-5, MUDGO ,PTB 33,BG 367-2	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
51	G-L	Grain length and width determine rice grain size.	Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021).	Extra long grain and short slender , medium slender size Basmati is preferred for table purpose. While long and medium bold grain s are desirable for roti making and other industrial purposes.	V.Short (<6.0mm)	1	Kothambir Sal	All variations for this trait are desirable as per its utility and can be included in crop improvement programme.
					Short (6.1-8.5 mm)	13	MO-6,MO-17,Mayekar Bhat,Munga,Jyoti,Patani-6,Bhadas-79,DRR-363-5,Ambemohar,K Shatabdi,RS-1113,Ajaya,S MAHSURI	
					Med. (8.6-10.5 mm)	70	MO-8,MO-13,MO-19,Kala Rata,Mahsad,Waksal-207, Barmil, Pandy, Dular,Try-1,Kochari,Lal Patani, Dodak, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, Gurjari,DRR-50-12,DRR-50-13, DRR-50-10, DRR-86-8, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, Chinoor,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180, Numbernamak, NDR6315, Indrayani, Dhanelal,RP Bio 197,RP-BIO-226,KJT 1,KJT 2,IR-64,MUDGO ,MILYANG 46,PTB 33,MTU1010,BG 367- 2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193, ARC 10550 , IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1, TN-1	
					L. (10.6-12.5 mm)	10	KJT-2R,KJT-3R,KJT-4R, PR-114,RTN 11-2-1-3,PR-118,IR-63879-195-2-2-3-2, P Sugandha-1,P Samruddhi, Bhogwati, Sugandha KJT- 2R,KJT-3R,PR-114,RTN 11-2-1-3,PR-118,IR-63879-195-2-2-3-2,P Sugandha-1, P Samruddhi, Bhogwati, Sugandha	
52	G-W	Grain length and width determine rice grain size.	Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021).	-	V. Long (>12.5mm)	1	Sugandha	All variations for this trait are desirable as per its utility and can be included in crop improvement programme.
					V. Narrow (<2.0 mm)	6	DRR-215, Chinoor, Bhogwati, Sugandha, RS-1113, Ajaya	
					Narrow (2.1- 2.5 mm)	57	MO-8,MO-13,MO-19,Bhadas-79,Lal Patani,Dodak,KJT-1R,KJT-2R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,RTN-69-1-1,NAUR-1, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,HRTMS-61,P Basmati, S Basmati ,P Sugandha-1,P Sugandha-3,P Sugandha-4, Bhadasbhog, CR2713-180, Numbernamak, NDR6315,P Samruddhi, Indrayani, Dhanelal, Ambemohar, RP Bio 197,RP-BIO-226,KJT 1,KJT 2,IR-64,MUDGO , MILYANG 46,PTB 33,MTU1010,BG 367-2,MILYANG 63,SINNA SIVAPPU ,IRRI 193,ARC 10550 ,S MAHSURI,IRRI 123, IRRI 104,IRRI 192	
					Med. (2.6-3.0 mm)	28	MO-6,MO-17,Kala Rata,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil,Jyoti,Patani-6,Pandy, Dular, Karhad, Ratnagiri 7,Bela ,Valai ,KJT-3R,BL-184AR,Gurjari,Sahyadri 5 R,CR-3993-2-24-45-2,Kothambir Sal,P Sugandha-5,K Shatabdi,MUT NS 1,RATHU HEENATI ,IRRI 190,Sonsali	
					Broad (3.1- 3.5 mm)	4	Try-1,Kochari,FL 478,TN-1	
					V. broad (>3.5mm)		Try-1,Kochari,FL 478,TN-1	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
53	G-PRL	-	Phenol colour reaction on grains and glumes is used for characterization of rice varieties for distinctiveness, uniformity and stability (DUS) testing in plant variety protection. According to DUS test guidelines, rice varieties are classified into two groups based on presence and absence of phenol colour reaction on the grains (Sahil <i>et. al.</i> , 2021)	Variation for this trait is used to distinguish germplasm.	Absent	23	Mahsad,Waksal-207,Barmil,Pandy,Dular,RTN-69-1-1,NAUR-1,BL-184AR,DRR-50-13,DRR-50-10,HRTMS-61,CR-3993-2-24-45- 2, Bhadasbhog,CR2713-180, Numbernamak, Dhanesal, MILYANG 46,PTB 33,MTU1010, MUT NS 1,RATHU HEENATI ,S MAHSURI,IRRI 123	This trait exhibited di-morphic variation for color. Thus this trait can be used as morphological marker to distinguish diverse germplasm.
					Present	72	MO-6,MO-8,MO-13,MO-17,MO-19,Kala Rata,Mayekar Bhat, Munga, Jyoti, Patani-6, Bhadas-79, Try-1, Kochari, LalPatani, Dodak,Karhad, Ratnagiri 7, Bela,Valai, KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114, RTN 11-2-1-3,PR-118, DRR- 215, Gurjari, DRR-50-12,DRR-363-5,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18, RTN-35-1-1,Sahyadri 5 R,P Basmati,S Basmati, Kothambir Sal,Chinoor, P Sugandha-1, P Sugandha-3,P Sugandha-4,P Sugandha- 5,NDR6315, P Samruddhi,Indrayani,Ambemohar, K Shatabdi, Bhogwati, Sugandha,RS-1113,RP Bio 197,RP-BIO-226, Ajaya, KJT 1,KJT 2,IR-64,MUDGO ,BG 367-2,MILYANG 63,FL 478, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550 , IRRI 104, IRRI 192, Sonsali, TN-1	
54	DG-L	Decorticated grain length (After dehulling, before milling) Decorticated grain length was measured in mm and a digital caliper was used for clear visualization	Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021).	Extra long grain and short slender , medium slender size Basmati is preferred for table purpose. While long and medium bold grain s are desirable for roti making and other industrial purposes.	Short	15	MO-6,MO-17,Patani-6,Bhadas-79,Kochari,Ratnagiri 7,HRTMS-61,Kothambir Sal, Numbernamak, NDR6315, Ambemohar, K Shatabdi,RS-1113,KJT 1,TN-1	All variations for this trait are desirable as per its utility and can be included in crop improvement programme.
					Medium	4	BL-184AR,VDN-9-10-1,Ajaya,S MAHSURI	
					Long	63	MO-8,MO-13,MO-19,Kala Rata,Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Pandy, Dular, Try-1, Lal Patani,Dodak,Karhad,Bela ,Valai,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2, VDN-10-18,RTN-35-1-1,Sahyadri 5 R,CR-3993-2-24-45-2, Dhanesal, RP Bio 197,RP-BIO-226,KJT 2, IR-64, MUDGO, MILYANG 46, PTB 33,MTU1010,BG 367-2,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 193,ARC 10550, IRRI 123,IRRI 104,IRRI 192,Sonsali, Sonsali	
					Long* (Long for Basmati type)	11	Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180,P Samruddhi, Indrayani, Bhogwati,Sugandha	
					Extra Long	2	P. Basmati and S Basmati	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
55	DG-W	Decorticated grain width (After dehulling, before milling) Decorticated grain width was measured in mm and a digital caliper was used for clear visualization	Therefore affect yield and appearance, thus representing two of the most agronomically important traits in rice breeding (Li and Li, 2021).	-	Narrow<2.0mm)	4	HRTMS-61,Bhogwati,RS-1113,S MAHSURI	All variations for this trait are desirable as per its utility and can be included in crop improvement programme.
					Med. (2.0-2.5 mm)	59	MO-8,MO-13,MO-19,Kochari,Lal Patani,Dodak,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1, NAUR-1,BL-184AR,DRR-50-12,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2, VDN-9-10-1,VDN-10-18,RTN-35-1-1,P Basmati,S Basmati ,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-5, Bhadasbhog,CR2713-180,Numbernamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,K Shatabdi,Sugandha,RP Bio197,RP-BIO-226,Ajaya,KJT 1,KJT 2,IR-64,MUDGO, MILYANG 46,PTB 33,MTU1010,BG 367-2,SINNA SIVAPPU, IRRI193,ARC 10550 ,IRRI 123,IRRI 192,Sonsali	
					Broad (>2.5mm)	32	MO-6,MO-17,Kala Rata,Mayekar Bhat,Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandy, Dular, Try-1, Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,Gurjari,DRR-363-5,Sahyadri 5 R,CR-3993-2-24-45-2,Kothambir Sal,P Sugandha- 4,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,IRRI 190,IRRI 104,TN-1	
56	DG-S	-Common variety which gives raise short bold and long bold rice -Fine variety which gives raise to medium slender rice -Super fine variety which gives raise to long slender and short slender rice.	-Short bold and long bold genotypes are utilized for flour roti making. -Medium slender varieties are used for various chinese, Italian dishes. -Short slender and long slender germplasm can be used for table purpose (Hori <i>et. al.</i> , 2022)	Long grain rice tends to cook up light, fluffy and separate when cooked rather than clumping together.-table purpose. Biryani etc Medium grain rice tends to cook up moist and tender. Chinese, Spanish and Italian cuisine etc. while short grain rice tends to clump together when cooked and forms what is called glutinous rice.flour <i>atta</i> roti making.	Short Slender	2	HRTMS-61, RS-1113	All variations for this trait are desirable as per its utility and can be included in crop improvement programme.
					Short Bold	13	MO-6,MO-17,Patani-6,Bhadas-79,Kochari,Ratnagiri 7,Kothambir Sal,Numbernamak,NDR6315,Ambemohar,K Shatabdi,KJT 1,TN-1	
					Medium Slender	4	BL-184AR,VDN-9-10-1,Ajaya,S MAHSURI	
					Long Bold	31	MO-8,MO-13,MO-19,Kala Rata,Mayekar Bhat,Munga, Mahsad, Waksal-207, Barmil,Jyoti, Pandy, Dular,Try-1,Karhad,Bela ,Valai ,KJT-1R,Gurjari,DRR-50-12,DRR-363-5,DRR-50-10,Sahyadri 5 R,CR-3993-2-24-45-2,Dhanesal,RP-BIO-226,MILYANG 63,FL 478,MUT NS 1,RATHU HEENATI ,IRRI 190,IRRI 104	
					Long Slender	32	Lal Patani,Dodak,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,DRR-50-13,DRR-86-8, IR-63879-195-2-2-3-2,RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-10-18,RTN-35-1-1,RP Bio 197, KJT 2, IR-64,MUDGO, MILYANG46,PTB 33, MTU1010, BG 367 2,SINNA SIVAPPU ,IRRI 193,ARC 10550 ,IRRI 123,IRRI 192,Sonsali	
					Long Slender (Basmati)	11	Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog,CR2713-180,P Samruddhi, Indrayani,Bhogwati,Sugandha	
					Extra-long Slender	2	S Basmati and P Basmati,	

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
57	DG-C	It's true that most rice (<i>Oryza sativa</i> L.) is white, but some varieties offer phytochemicals (mainly polyphenols and anthocyanins) in the outer bran layer, which not only imbues them with hues of a different color but also boosts their nutrient content. (Webb, 2021)	-	Research shows that black rice has the highest antioxidant activity of all the varieties, making it a nutritious choice, followed by brown and then red rice. (Kubala, 2019)	White	72	Dular, Try-1, Kochari, Dodak, Karhad, KJT-1R, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Numbernamak, NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MUT NS 1, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali	All variations for this trait are desirable as per its utility and can be included in crop improvement programme.
					Light red	5	Kala Rata, MILYANG 63, FL 478, RATHU HEENATI, TN-1	
					Red	18	MO-6, MO-8, MO-13, MO-17, MO-19, Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandey, L Patani, Ratnagiri7, Bela, Valai	
58	E-PA	Amylose is a polysaccharide made of α -D-glucose units, bonded to each other through $\alpha(1\rightarrow4)$ glycosidic bonds. It is one of the two components of starch.	Starch is the abundant component in rice endosperm, and its microstructure determines the quality and functional properties of rice grain. (X fan <i>et. al.</i> , 2019)	Presence of amylose is desirable in medium scale for commercial table purpose use.	Present	95	MO-8, MO-13, MO-17, MO-19, Kala Rata, Mayekar Bhat, Munga, Mahsad, Waksal-207, Barmil, Jyoti, Patani-6, Bhadas-79, Pandey, Dular, Try-1, Kochari, Lal Patani, Dodak, Karhad, Ratnagiri 7, Bela, Valai, KJT-1R, KJT-2R, KJT-3R, KJT-4R, PR-114, RTN 11-2-1-3, PR-118, DRR-215, RTN-69-1-1, NAUR-1, BL-184AR, Gurjari, DRR-50-12, DRR-363-5, DRR-50-13, DRR-50-10, DRR-86-8, IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2, VDN-9-10-1, VDN-10-18, RTN-35-1-1, Sahyadri 5 R, HRTMS-61, CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1, P Sugandha-3, P Sugandha-4, P Sugandha-5, Bhadasbhog, CR2713-180, Numbernamak, NDR6315, P Samruddhi, Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO, MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU, IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali, TN-1	All 95 genotypes showed presence of amylose. Thus all these genotypes can be included in crop improvement programme.

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
59	E-CA		After cooking, the high-amylose and intermediate-amylose rices are firm and fluffy; while the low-amylose and waxy rices are soft, moist, and sticky in texture.(Chen, 2020)	Medium range of amylose content is preferable Low amylose varieties can be used for Chinese cuisine. Medium amylose varieties are directly used table purpose. While high amylose varieties are used for beaten rice, puffed rice. (<i>poha and murmura</i>)	Low (10-19%)	19	Try-1,PR-118,NAUR-1, NDR6315, P Samruddhi, Indrayani, K Shatabdi,Sugandha,RS-1113,KJT 2, MUDGO , MILYANG 46,BG 367- IRRI 193,ARC 10550, S MAHSURI,IRRI 123,IRRI 104,Sonsali	Out of 95 genotypes 48 exhibited medium scale of amylose, which is highly and widely preferred by consumers for table purpose. Thus these genotypes are good donors for crop improvement.
					Medium (20-25 %)	48	MO-6,MO-13,Kala Rata,Barmil,Patani-6,Bhadas-79, Pandy, Karhad, Ratnagiri 7, Bela ,Valai ,KJT-1R,KJT-3R,KJT-4R,PR-114, RTN 11-2-1-3,DRR-215,RTN-69-1-1,BL-184AR, Gurjari, DRR-50-12,DRR-50-10,RTN-35-1-1,Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2, P Basmati, S Basmati, Kothambir Sal, Chinoor, P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180, Dhanesal, Ambemohar, Bhogwati, KJT 1, IR-64,PTB 33,MTU1010,RATHU HEENATI ,SINNA SIVAPPU ,IRRI 190,IRRI 192,TN-1	
					High (26 -30%)	26	MO-8, MO-17, MO-19, Mayekar Bhat, Munga, Mahsad, Waksal-207, Jyoti, Dular, Kochari, Lal Patani, Dodak, KJT-2R, DRR-363-5, DRR-50-13, DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2, RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18, Numbernamak,RP Bio 197, RP-BIO-226,FL 478,MUT NS 1	
					Very high (>30%)	2	Ajaya, MILYANG 63	
60	E-CAWC	Grain chalkiness reduces the quality of rice (<i>Oryza sativa</i>) and is a highly undesirable trait for breeding and marketing. (Wu et. al., 2022)	-	Absence of chalkiness is desirable for this trait. As well variation for this trait serves as morphological marker.	Absent or very small	95	MO-6,MO-8,MO-13,MO-17,MO-19,KalaRata,Mayekar Bhat, Munga,Mahsad,Waksal-207,Barmil,Jyoti,Patani-6, Bhadas- 79, Pandy,Dular,Try-1,Kochari,Lal Patani, Dodak,Karhad,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,KJT-3R,KJT-4R,PR-114,RTN 11-2-1-3,PR-118,DRR-215,RTN-69-1-1,NAUR-1,BL-184AR, Gurjari, DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2, RTN-27-1-1-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1,Sahyadri 5 R, HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati , Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5,Bhadasbhog,CR2713-180,Numbernamak, NDR6315,P Samruddhi,Indrayani, Dhanesal, Ambemohar, K Shatabdi, Bhogwati, Sugandha, RS-1113, RP Bio 197, RP-BIO-226, Ajaya, KJT 1, KJT 2, IR-64, MUDGO , MILYANG 46, PTB 33, MTU1010, BG 367-2, MILYANG 63, FL 478, MUT NS 1, RATHU HEENATI, SINNA SIVAPPU , IRRI 190, IRRI 193, ARC 10550, S MAHSURI, IRRI 123, IRRI 104, IRRI 192, Sonsali , TN-1	This trait exhibited monomorphic variation for color. Thus this trait can't be used as morphological marker to distinguish diverse germplasm

SN	CH	Structure	Function	Desirable note	N	F	Genotypes	Remarks
61	GT-ASV	Alkali spreading value of whole kernel milled rice is the measure of volume expansion in contact with dilute alkali and also a measure of gelatinization temperature. Again gelatinization temperature is partly associated with the amylose content of the starch. (Akuli <i>et al.</i> , 2019)	It determines the cooking time and energy required for the rice.	High-medium note is desirable as requires less cooking time and low energy. ASV is inversely proportional to the GT.	Low	1	KJT-3R	Out of 95, 61 genotypes had high medium ASV. Thus these genotypes can be included in crop improvement programme.
					Medium	33	Mayekar Bhat,Jyoti,Try-1,Dodak,Karhad,KJT-4R,PR-114,RTN 11-2-1-3, RTN-69-1-1, NAUR-1,BL-184AR,RTN-27-1-1-2,P Sugandha-3,P Sugandha-5, Bhadasbhog, P Samruddhi, Dhanesal, Ambemohar,K Shatabdi, Bhogwati, Sugandha,RS- 1113,KJT 1,MUDGO , MILYANG 46,MTU1010,FL 478,MUT NS 1,IRRI 190,IRRI 193,IRRI 123,IRRI 104,TN-1	
					High medium	61	MO-6,MO-8,MO-13,MO-17,MO-19,Kala Rata, Munga, Mahsad, Waksal-207, Barmil, Patani-6, Bhadas-79,Pandy,Dular,Kochari, Lal Patani,Ratnagiri 7,Bela ,Valai ,KJT-1R,KJT-2R,PR-118,DRR-215,Gurjari,DRR-50-12,DRR-363-5,DRR-50-13,DRR-50-10,DRR-86-8,IR-63879-195-2-2-3-2,RTN-214-1-1-1-2,VDN-9-10-1,VDN-10-18,RTN-35-1-1, Sahyadri 5 R,HRTMS-61,CR-3993-2-24-45-2,P Basmati,S Basmati, Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-4,CR2713-180,Numbernamak,NDR6315,Indrayani,RP Bio 197,RP-BIO-226,Ajaya,KJT 2,IR-64,PTB 33,BG 367-2,MILYANG 63,RATHU HEENATI, SINNA SIVAPPU ,ARC 10550, S MAHSURI,IRRI 192,Sonsali	
62	DG-A	Aroma in scented and basmati rice is due to 2-acetyl-1-pyrroline. (Bharati <i>et al.</i> , 2020)	Makes rice varieties of special value and have wide consumer preference.	Presence is desirable.	Present	19	P Basmati,S Basmati ,Kothambir Sal,Chinoor,P Sugandha-1,P Sugandha-3,P Sugandha-4,P Sugandha-5, Bhadasbhog, CR2713-180,Numbernamak,NDR6315,P Samruddhi, Indrayani, Dhanesal, Ambemohar,K Shatabdi,Bhogwati,Sugandha	Out of 95, 19 germplasm found to be aromatic and thus can be used in crop improvement programme.

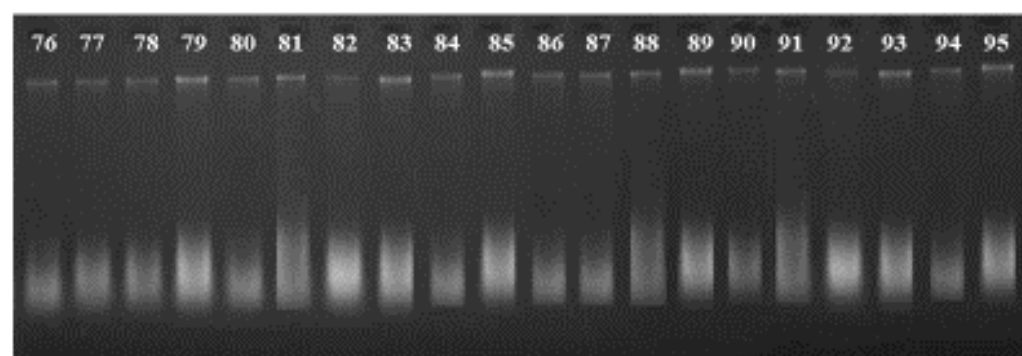
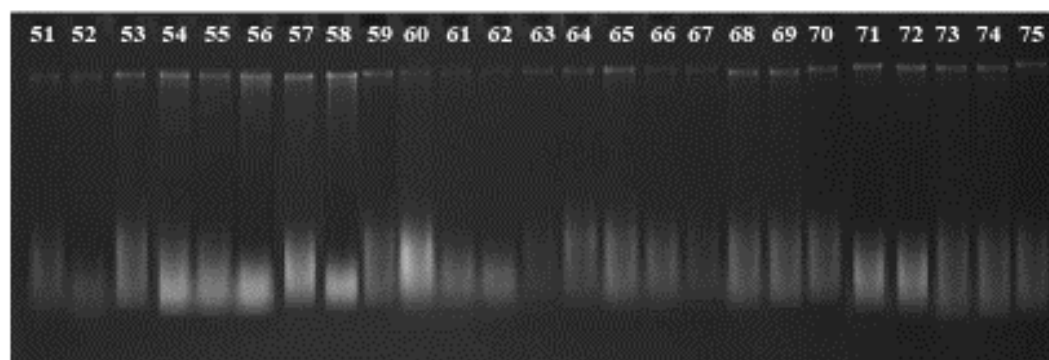
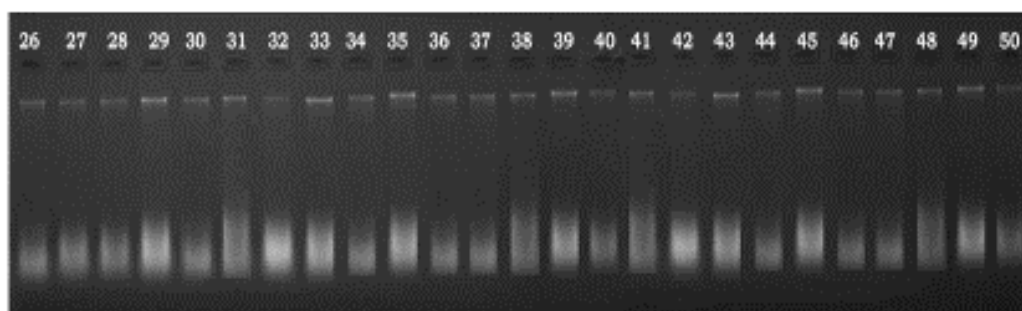
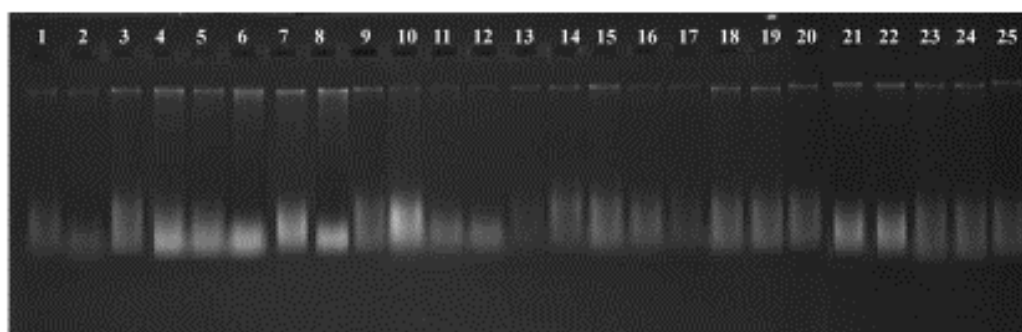


Plate No. 1: Gel photograph of DNA isolated from 95 rice genotypes.

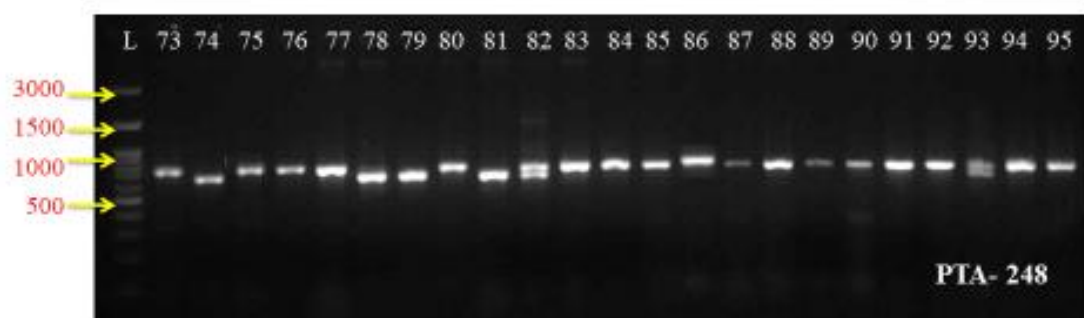
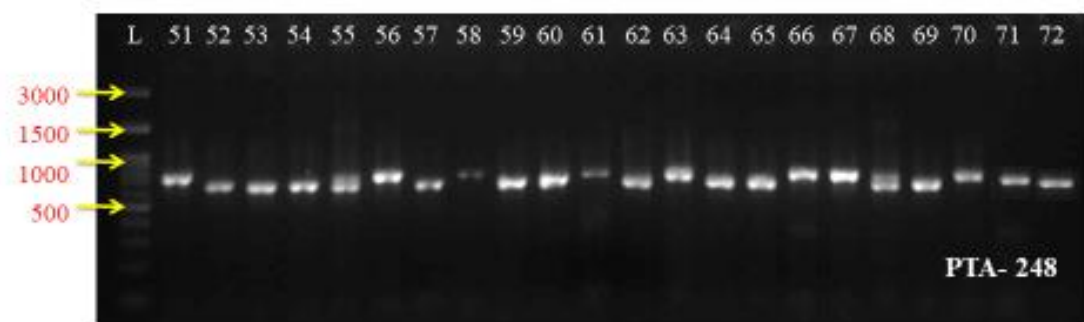
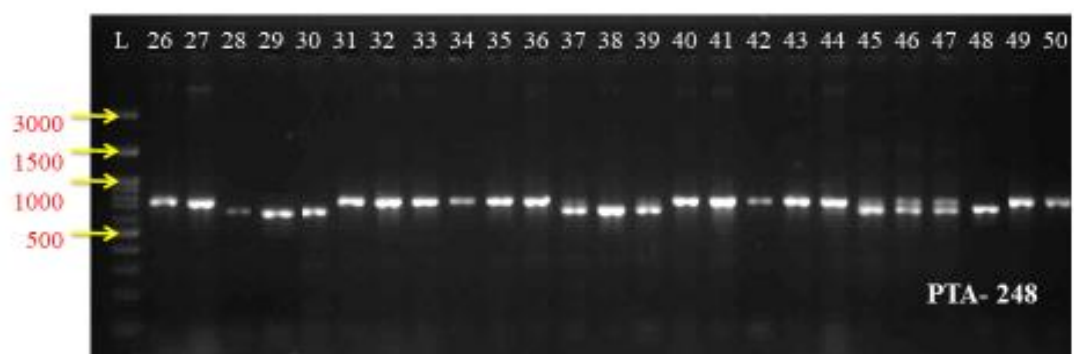
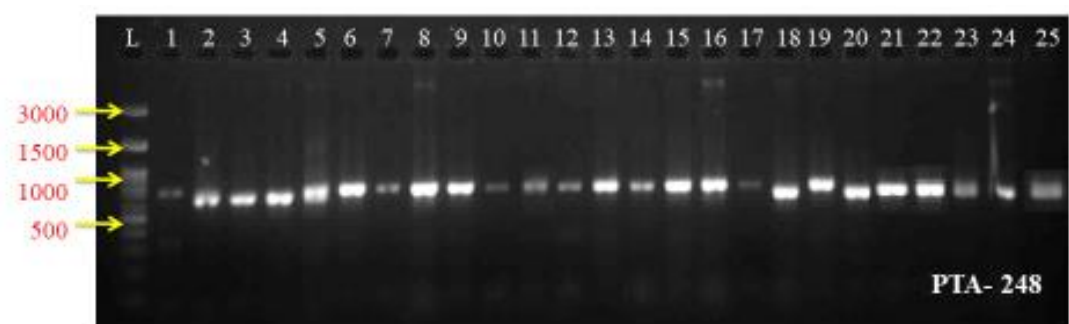


Plate No. 2: DNA bands amplified from 95 rice genotypes using microsatellite pta 248 marker linked to Bacterial blight and electrophoresed in a 1.8% agarose gel. L= 100bp ladder.

All showed absence of the resistance linked allele

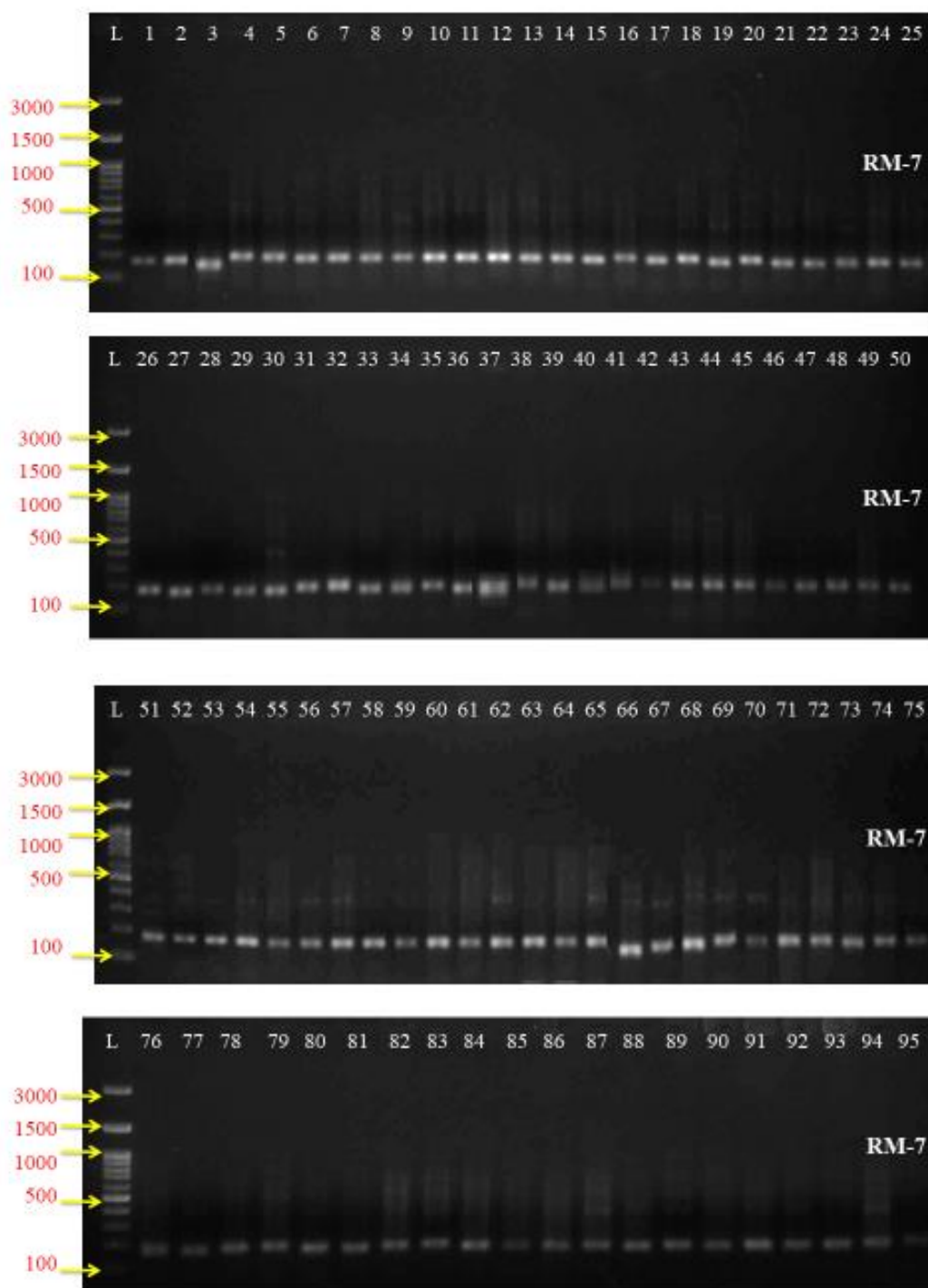


Plate No. 3: DNA bands amplified from 95 rice genotypes using microsatellite RM 7 marker linked to grain weight and electrophoresed in a 1.8% agarose gel. L= 100bp ladder.

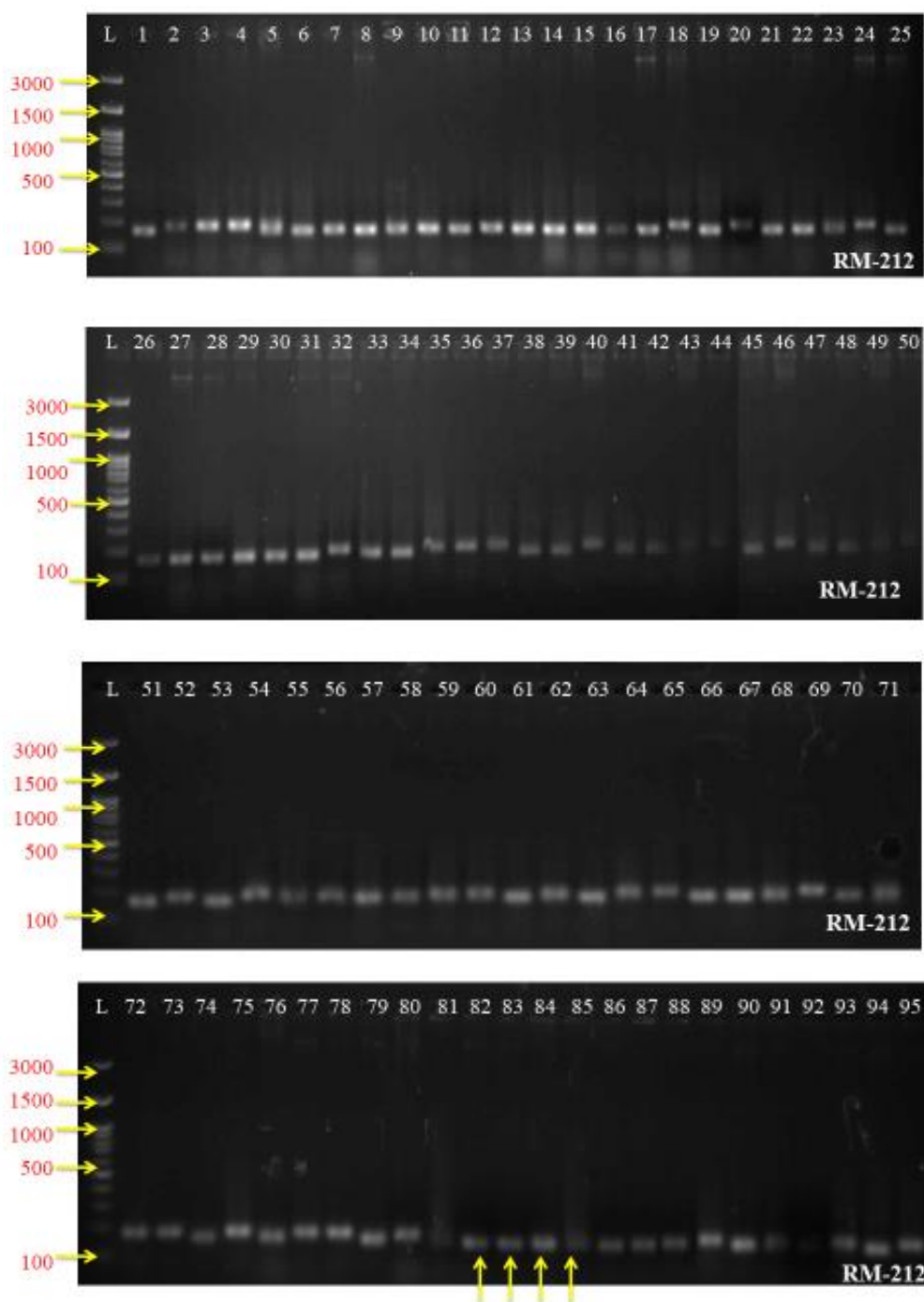


Plate No. 4: DNA bands amplified from 96 rice genotypes using microsatellite RM-212 marker linked to Drought and electrophoresed in a 1.8% agarose gel. L= 100bp ladder. (Arrow indicates presence of the resistance linked allele)

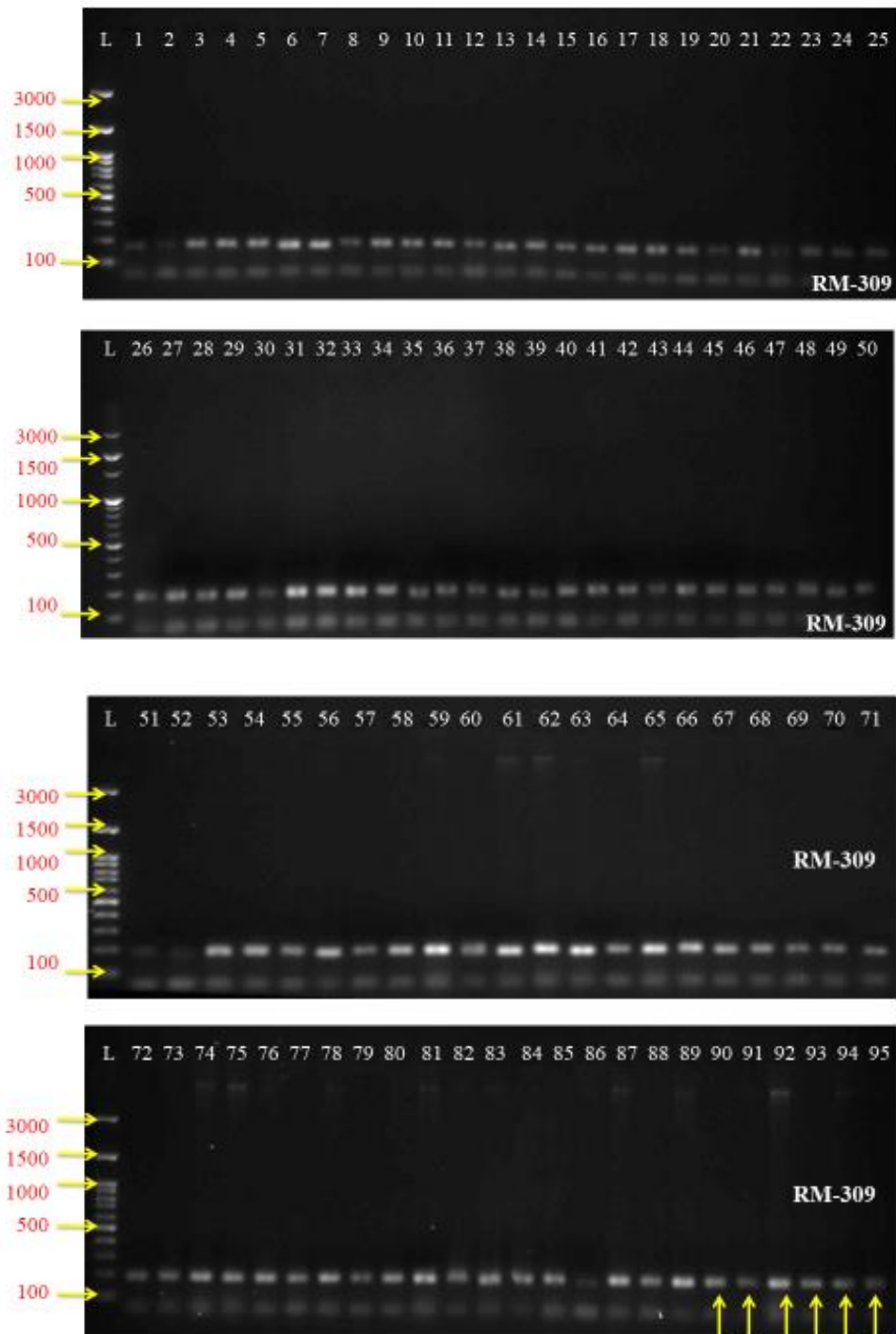


Plate No. 5: DNA bands amplified from 96 rice genotypes using microsatellite RM-309 marker linked to Brown Plant Hopper and electrophoresed in a 1.8% agarose gel. L= 100bp ladder. (Arrow indicates presence of the resistance linked allele)

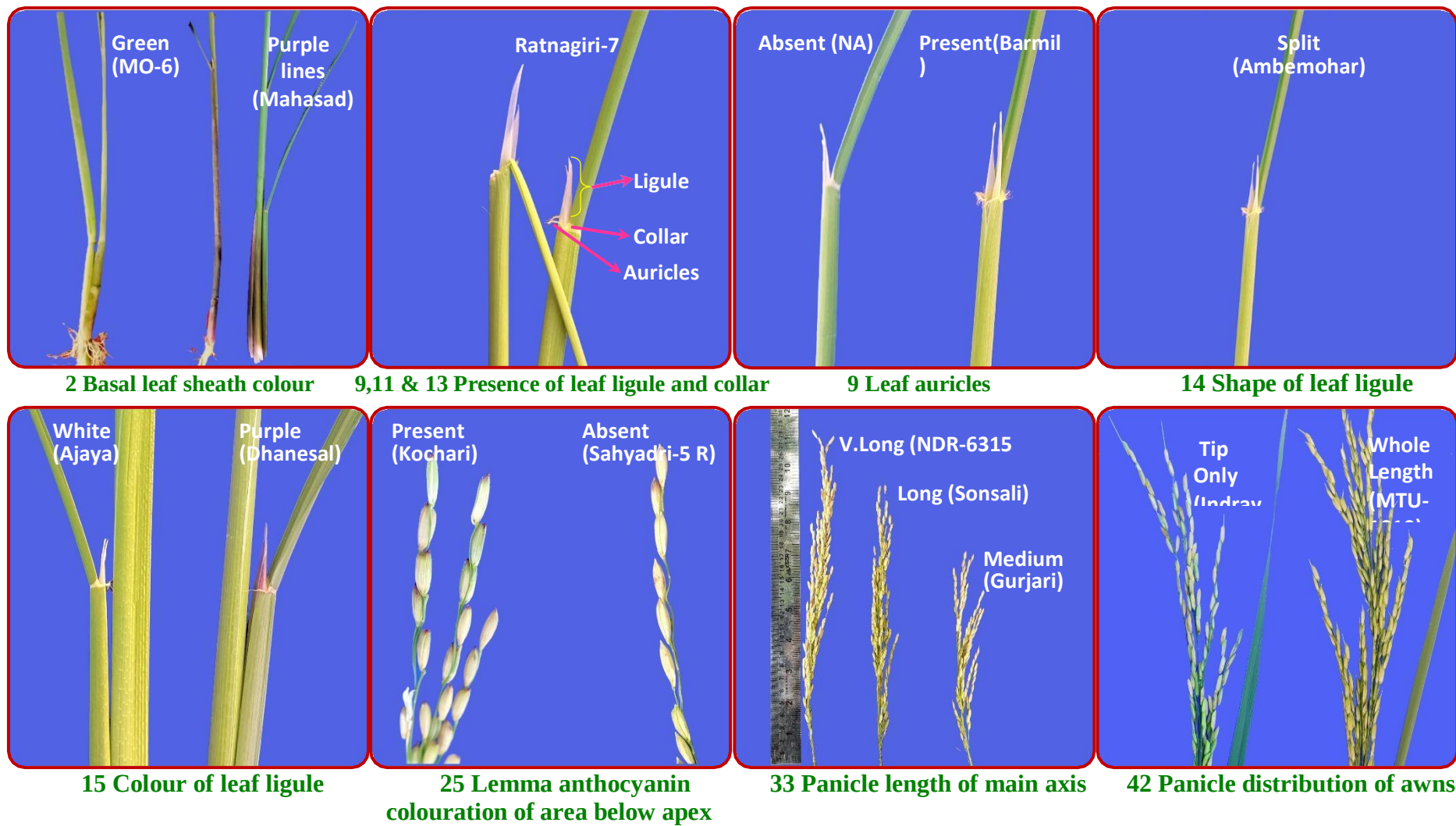


Plate VI : DUS descriptors related to leaf and panicle



51 Grain length



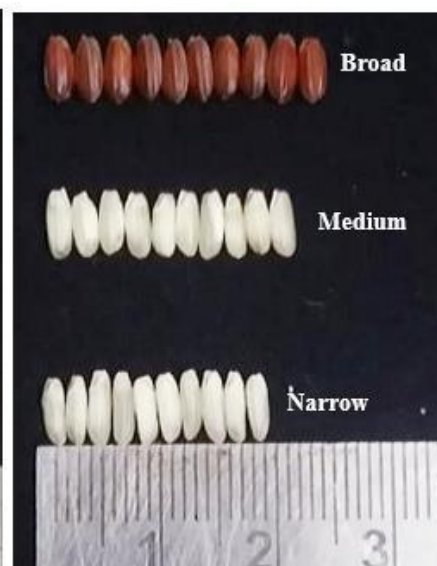
54 Decorticated grain length

Bela

Kala Namak



52 Grain width



55 Decorticated grain width

Kala rata

Indrayani

Bhogawati

Plate VII : DUS descriptors related to grain and decorticated grain



Absent
(Dular)

Present
(Barmil)

4 Anthocyanin colouration



Short
(NA)

Medium
(Dodak)

Long
(S. Basmati)

16 Length of Leaf Blade



Broad
(NA)

Medium
(MO-8)

Narrow
(Valai)

17 Width of Leaf Blade

Plate IX Characterization of morphological traits related to leaf



Present
(NDR6315)

Absent
(Bhadas-79)

**24 Lemma: Anthocyanin
colouration of Keel**



Present
(P. Basmati)

Absent
(Mayekar Bhat)

39 Awns



Semi erect
(PR-114)

Erect
(TN-1)

21 Attitude of blade

Plate VIII Characterization of morphological traits related to panicle



Whole length

(MTU-1010)



Short

Medium

Long

Very long

(NA)

(IRRI-104)

(FL-478)

(NDR-6315)

42 Panicle: Distribution of awns

33 Length of main axis



Green

Purple

(Patni-6)

(Tri-1)

2Basal leaf: Sheath colour

Plate X Characterization of morphological traits related to panicle and stem



White (Munga)



Purple (Ratnagiri-7)

Plate XI : Photograph representing various in spikelet colouration of stigma



Short
(Kothimbir Sal)

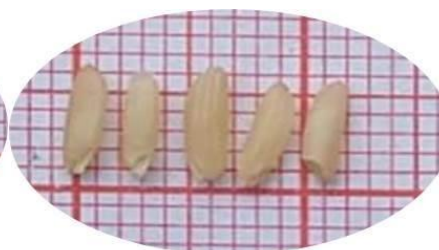


Medium
(BL-184 AR)

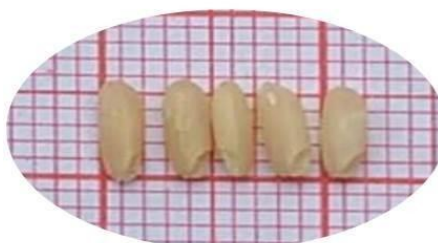
54 Decorticated grain: length



Short bold (Kothimbir Sal)



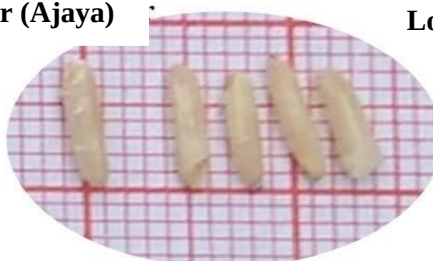
Short slender (RS-1113)



Medium slender (Ajaya)



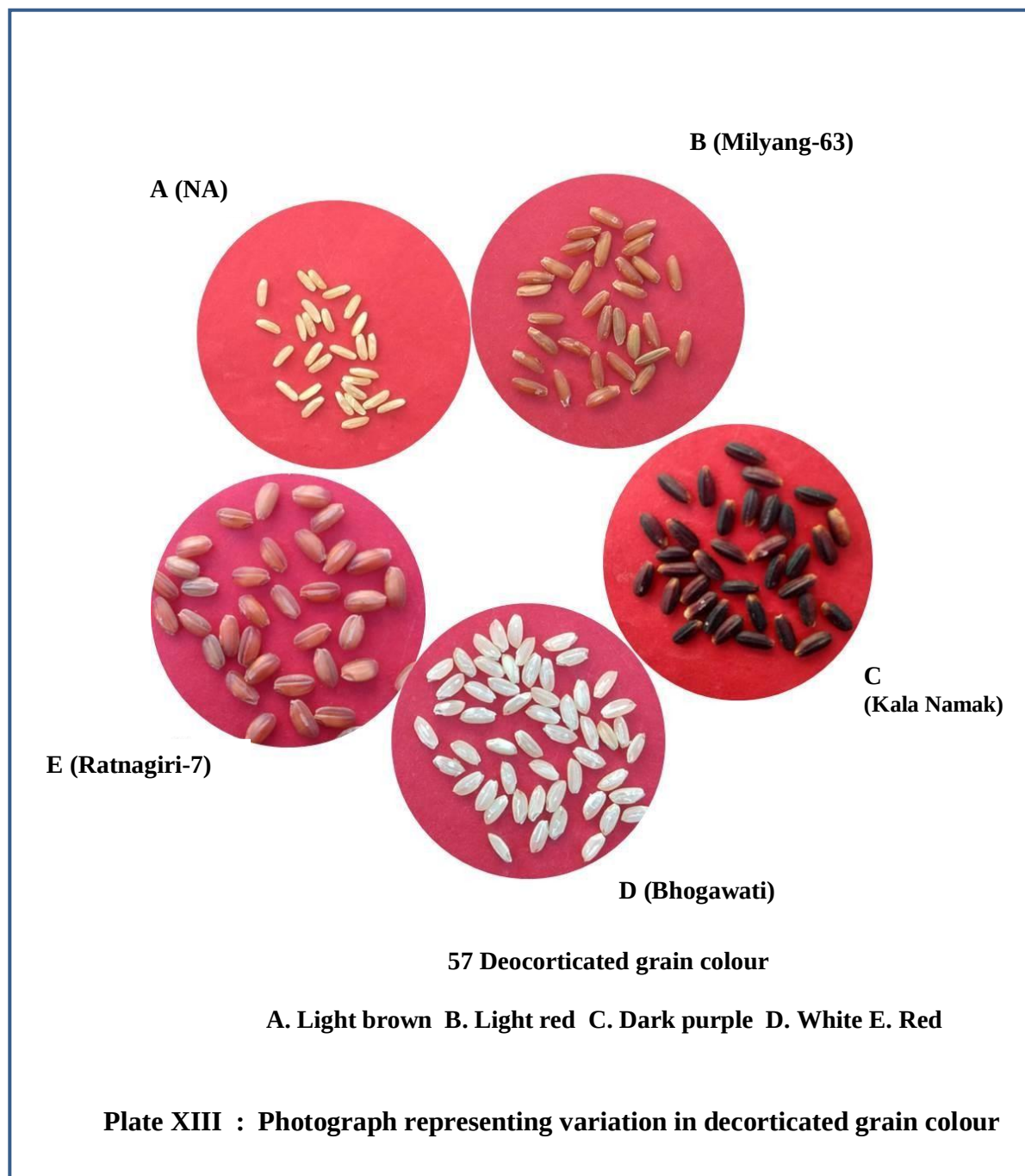
Long bold (R.Heenati)



Long slender (P. Basmati)

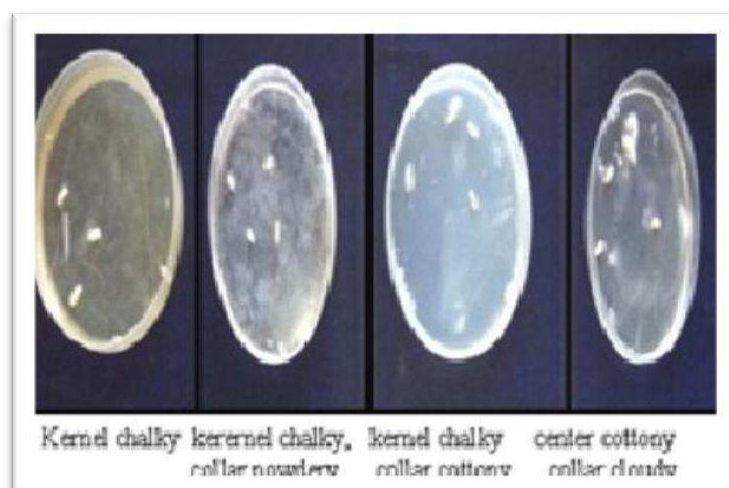
56 Decorticated grain: shape

Plate XII Characterization of grain quality parameters in rice





Grain: Phenol reaction of lemma



Alkali spreading test

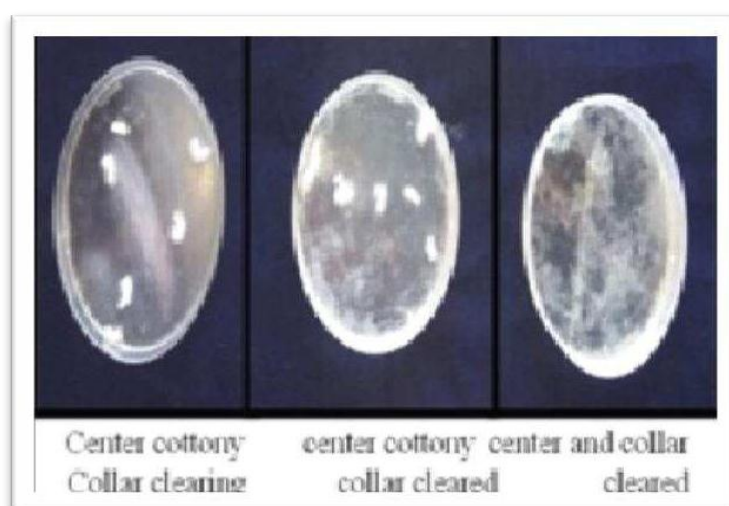


Plate XIV : Alkali spreading test



Green
(MO-6)



Purple lines
(Mahsad)



Light purple
(Barmil)



Purple
(Try-1)

2 Basal leaf sheath colour



Green
(Absent)

(Chinoor)



Purple magin
(On margins
only)

(Waksal-207)



Purple tip
(On tips only)

(NA)

Plate XV : Leaf distribution of anthocyanin colour

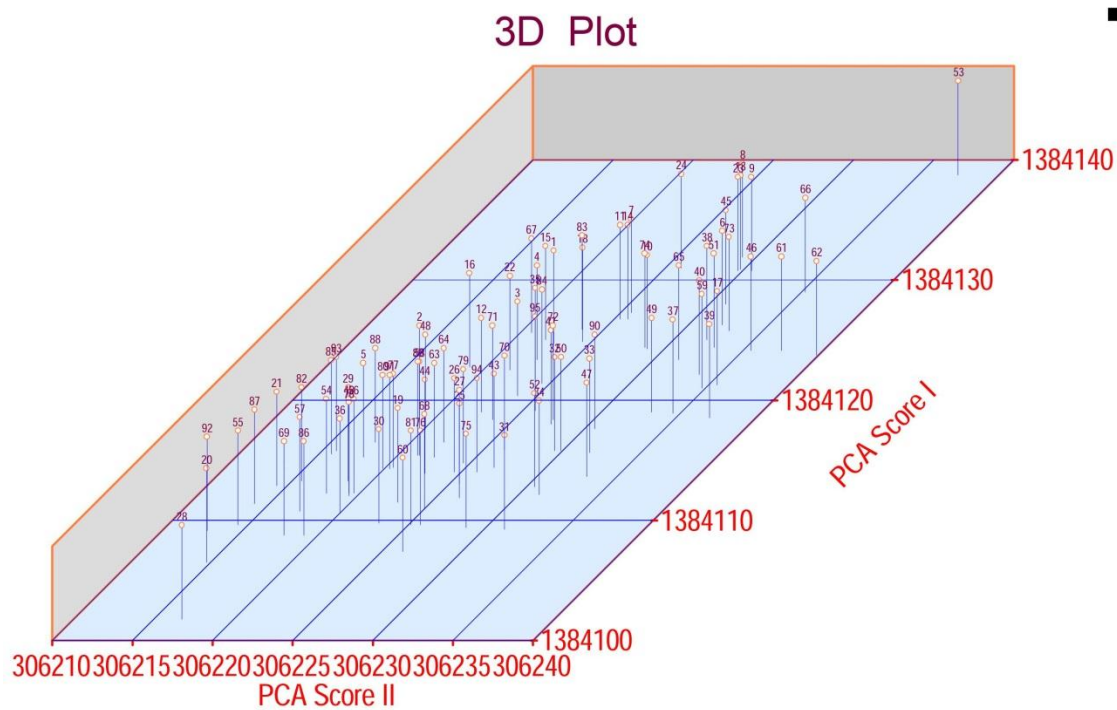


Fig. 1 : 3D plot of location ARS, Shirgaon

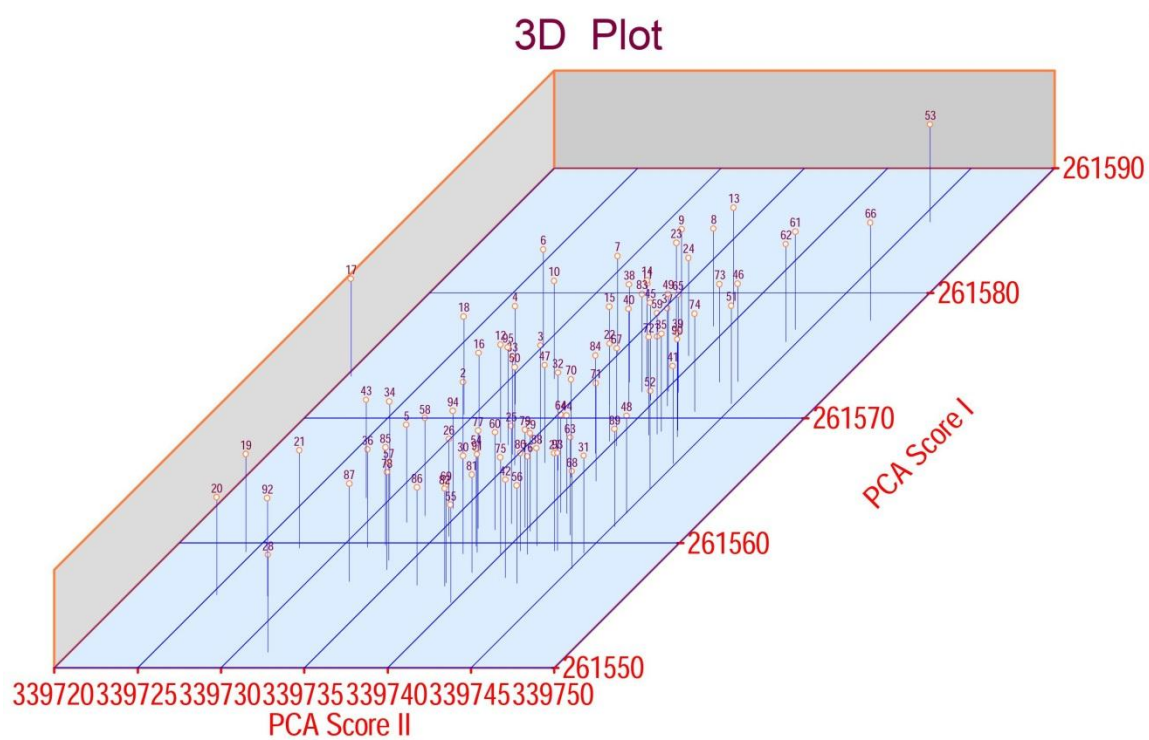


Fig. 2 : 3D plot of location RARS, Karjat

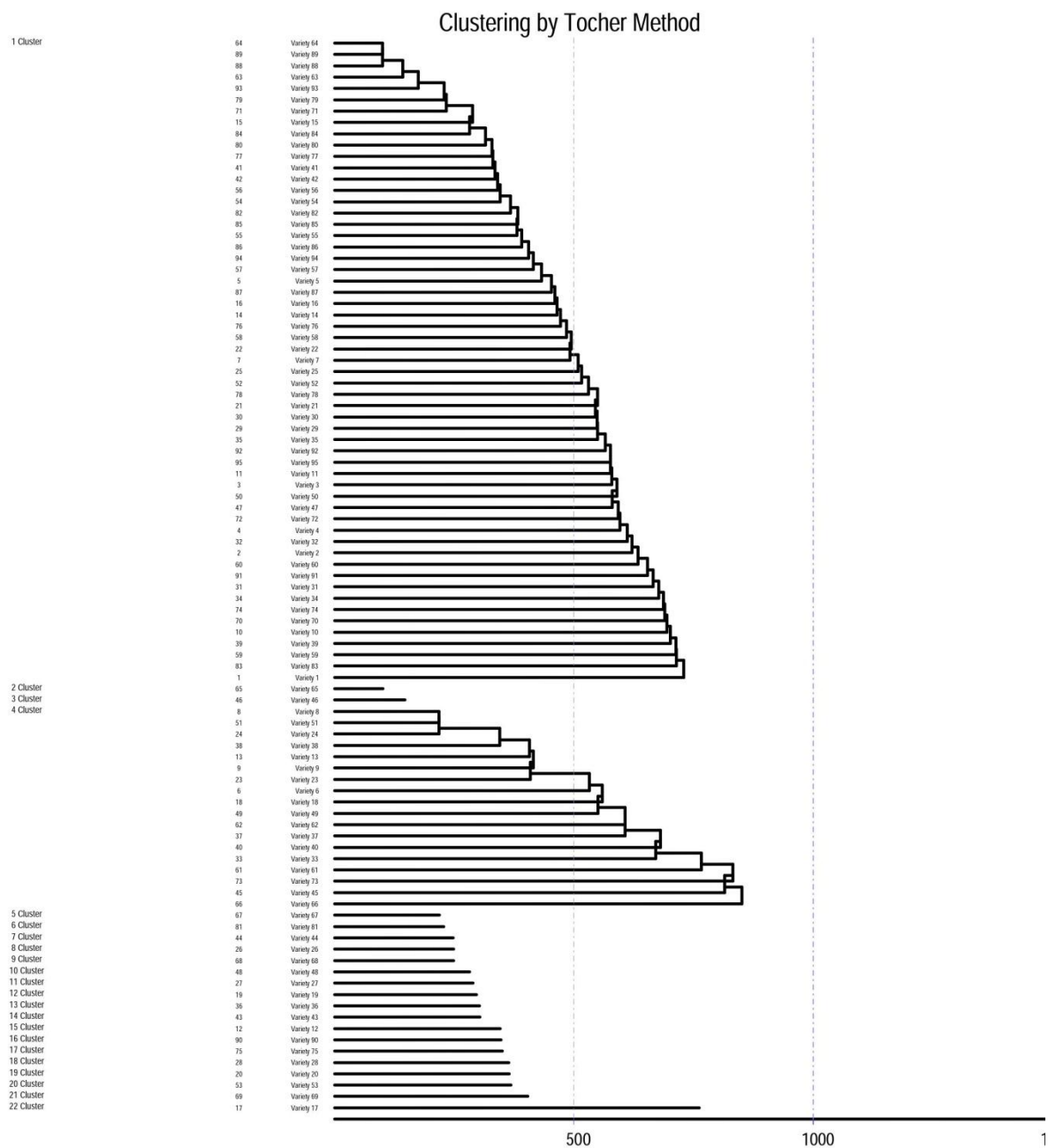


Fig. 3 : Dendrogram (Tochers method) location ARS, Shirgaon

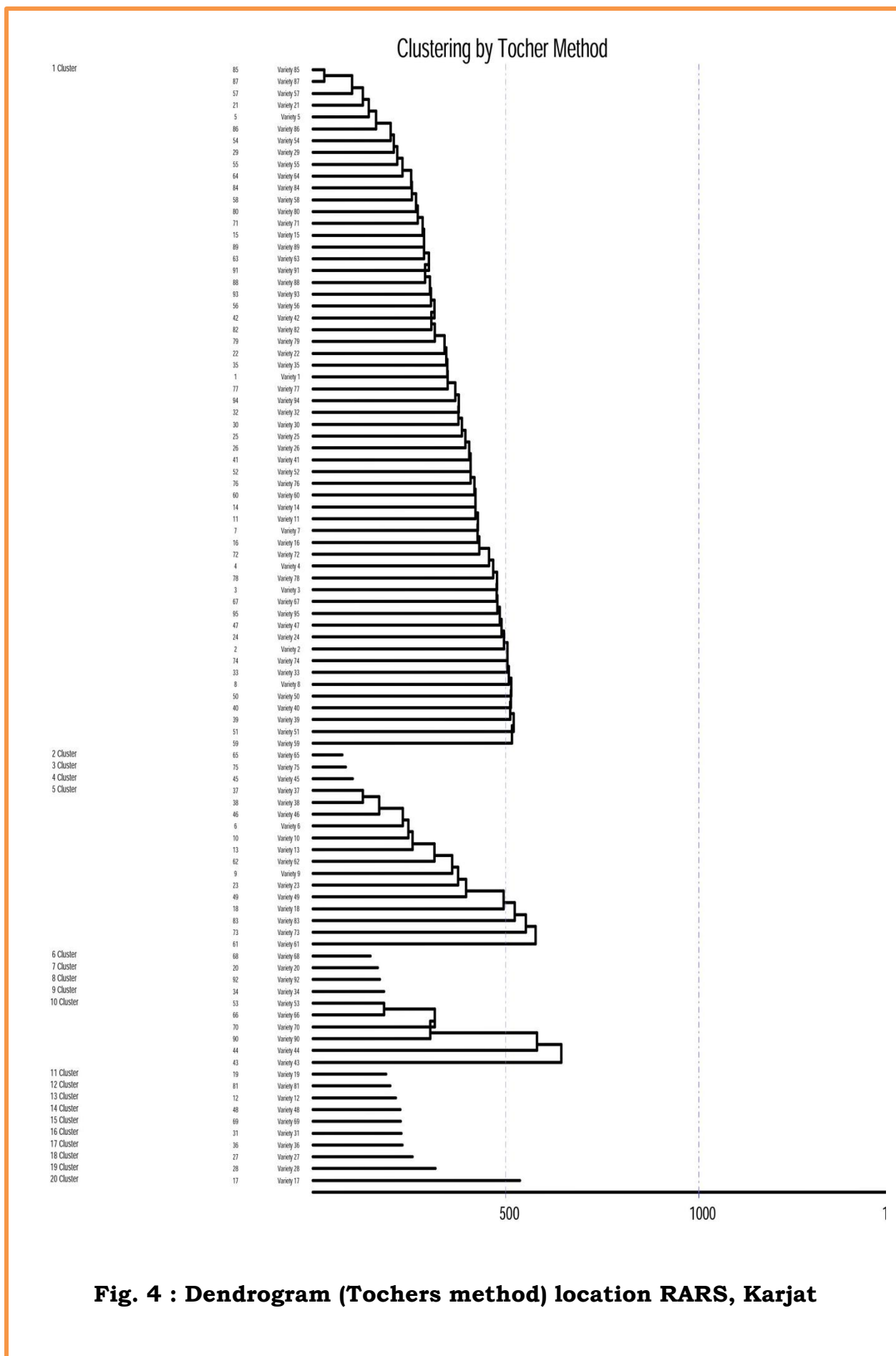


Fig. 4 : Dendrogram (Tochers method) location RARS, Karjat

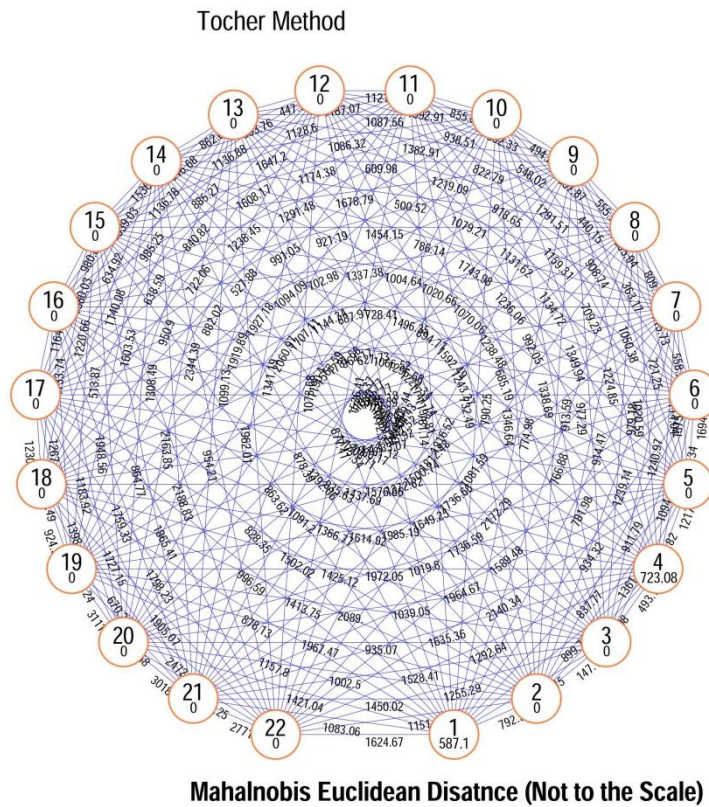


Fig. 5 : Mahalanobis Euclidean Distance (Not to the scale) location ARS Shirgaon.

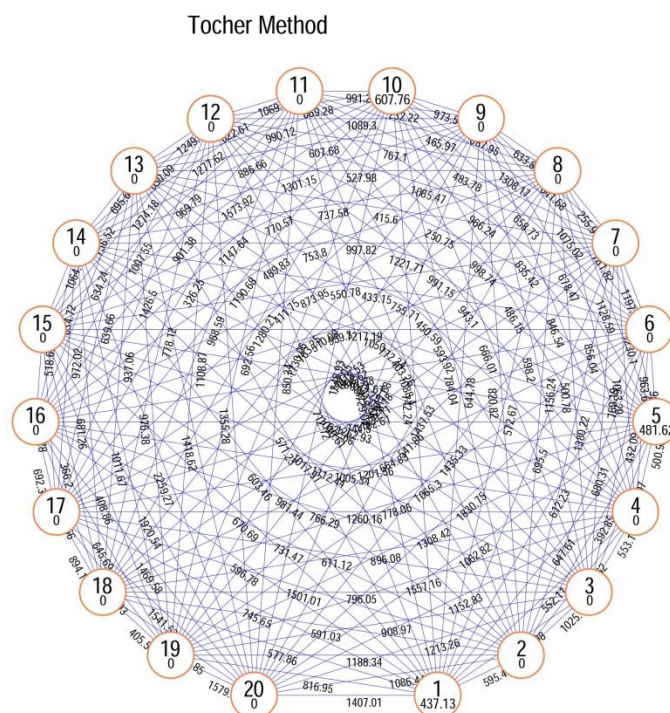
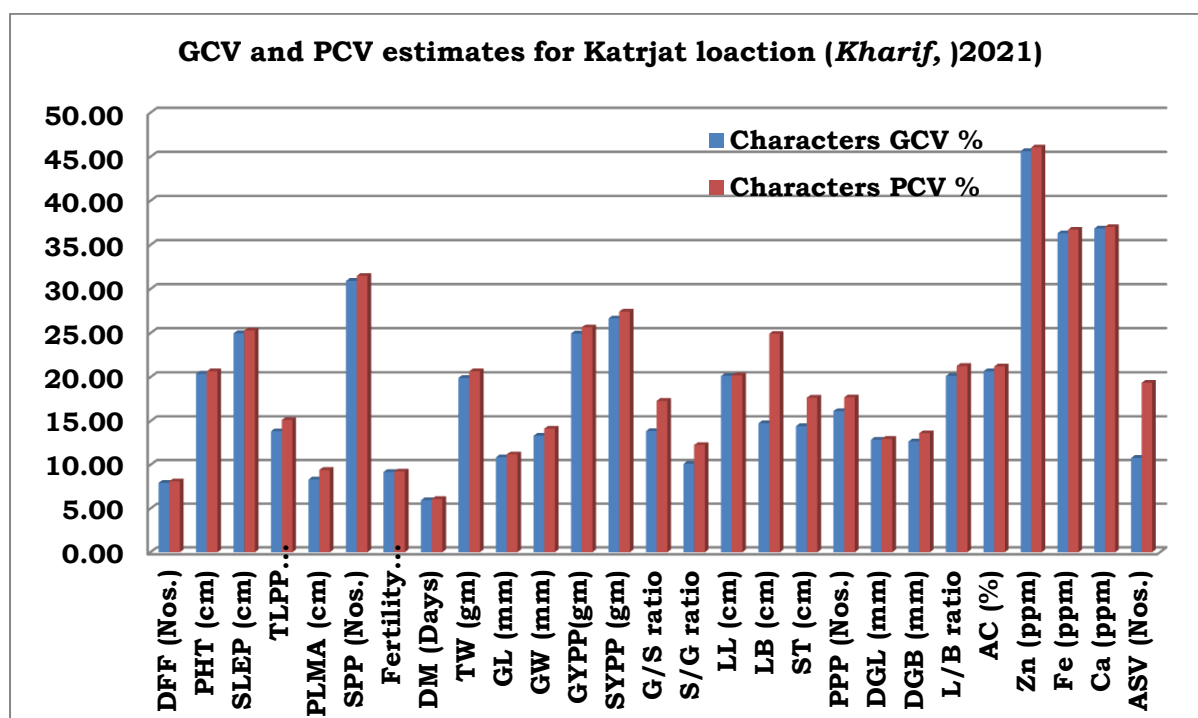
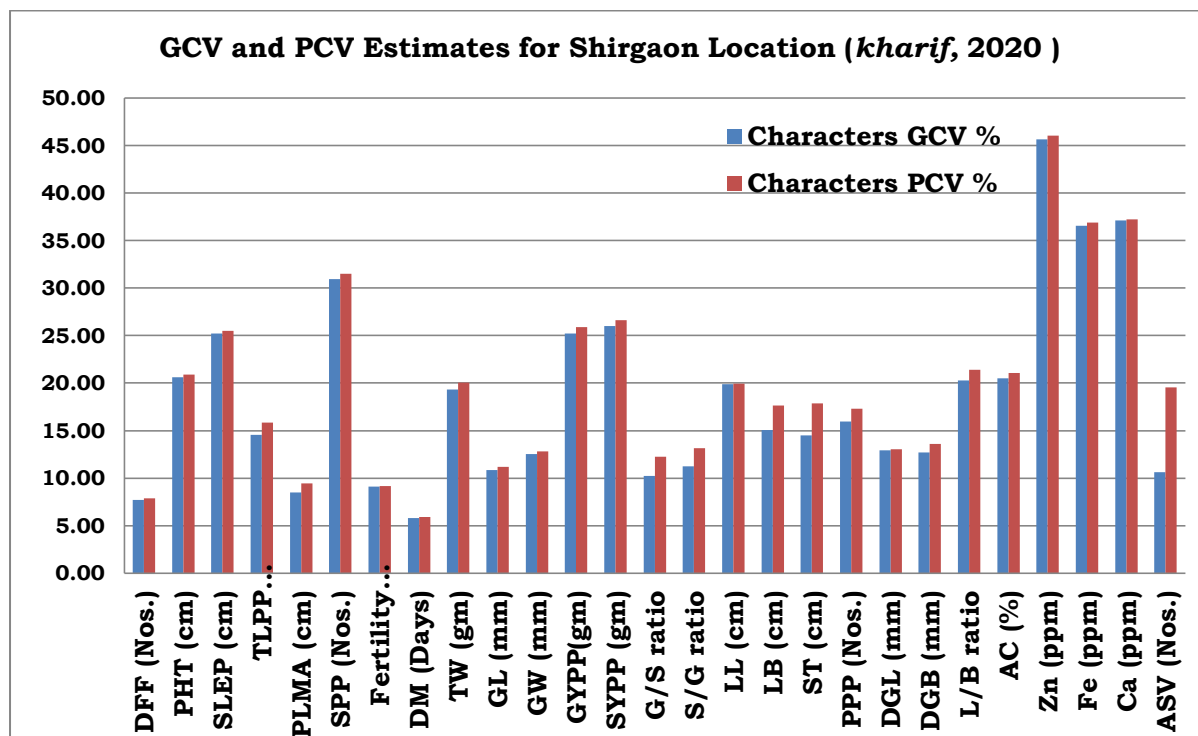
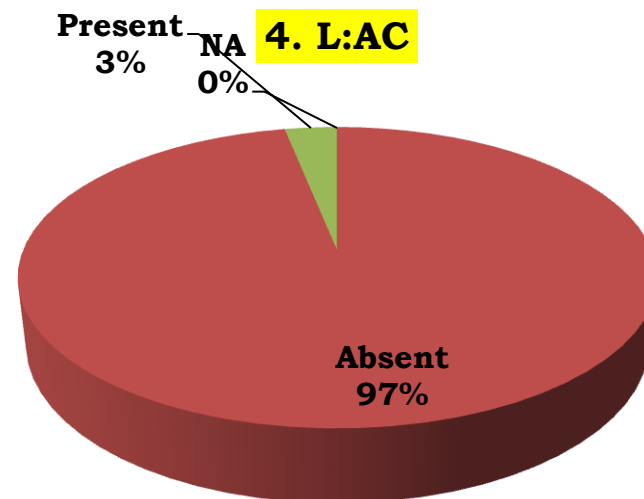
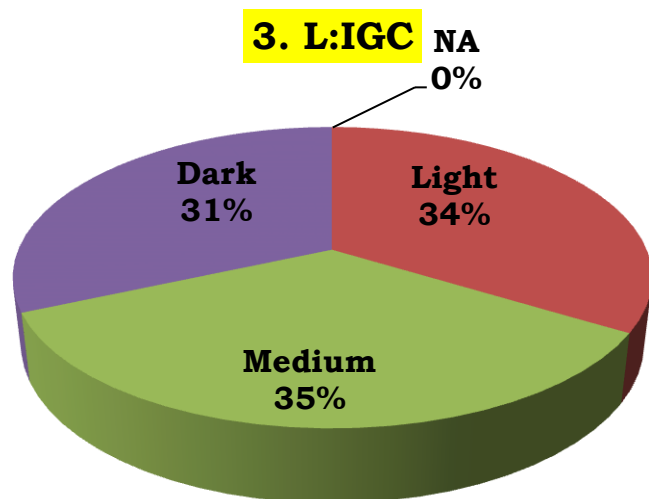
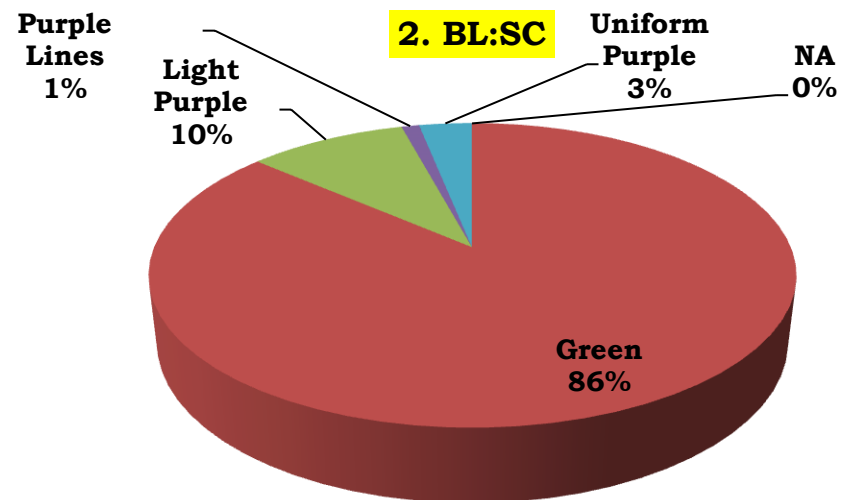
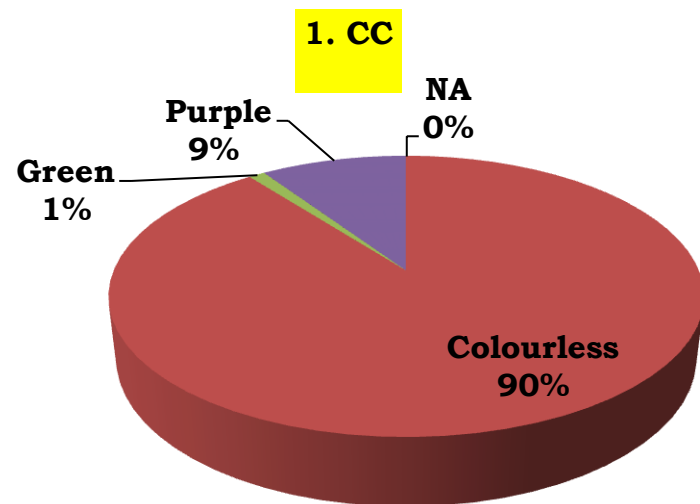


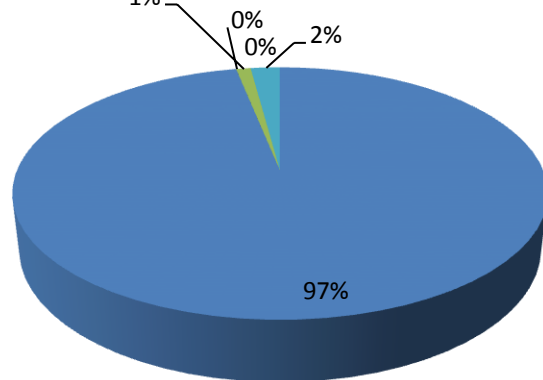
Fig. 6 : Mahalanobis Euclidean Distance (Not to the scale) location RARS Karjat.



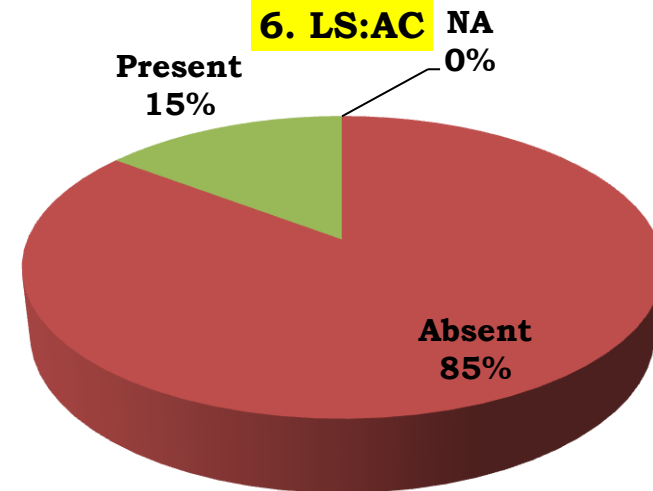


5. L:DAC

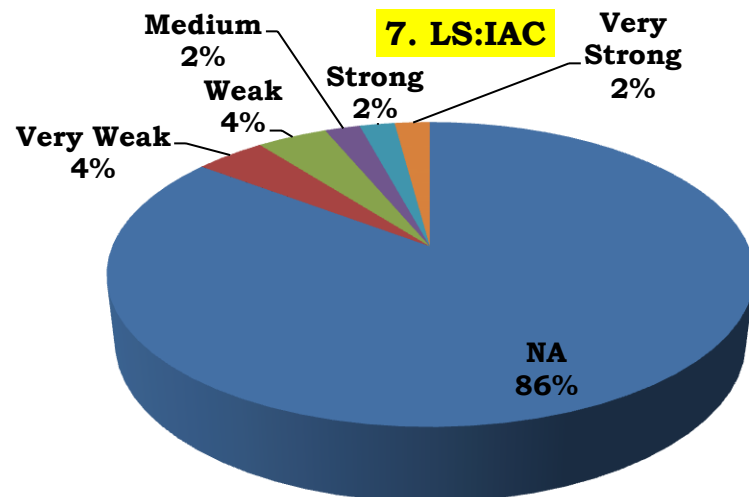
■ NA ■ On tips only ■ On margins only ■ In blotches only ■ Uniform



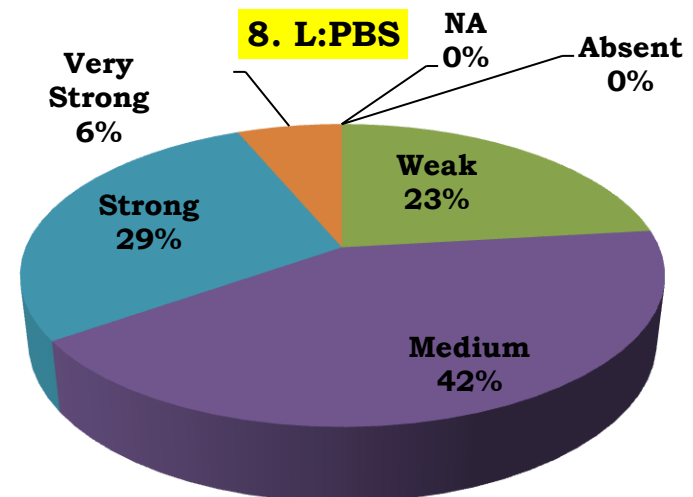
6. LS:AC

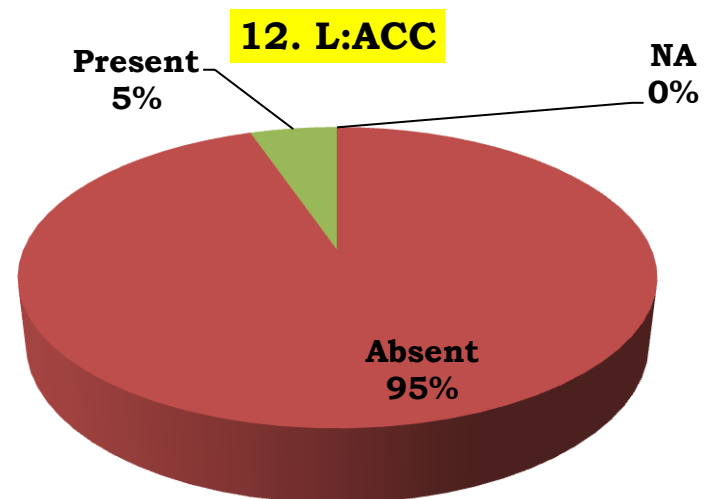
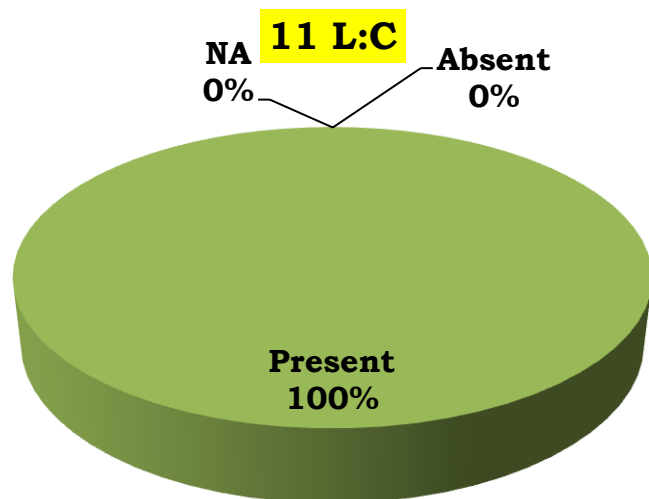
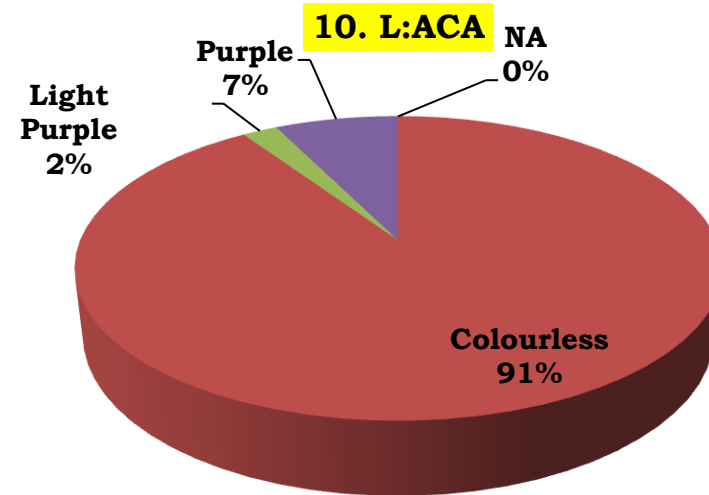
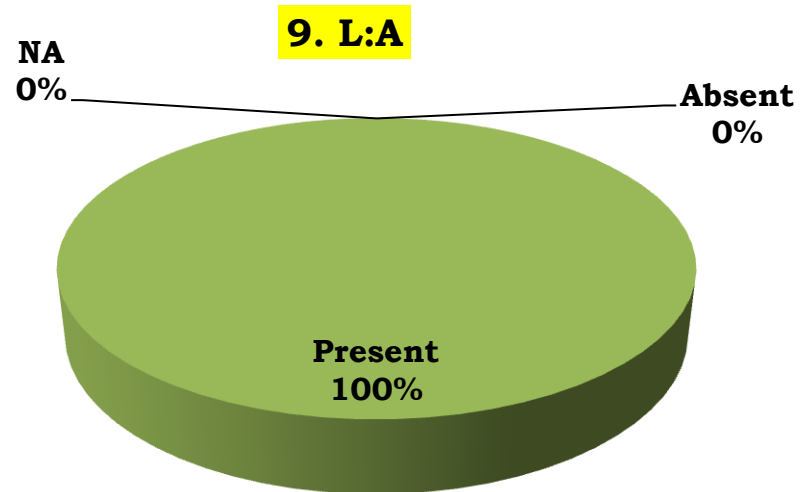


7. LS:IAC

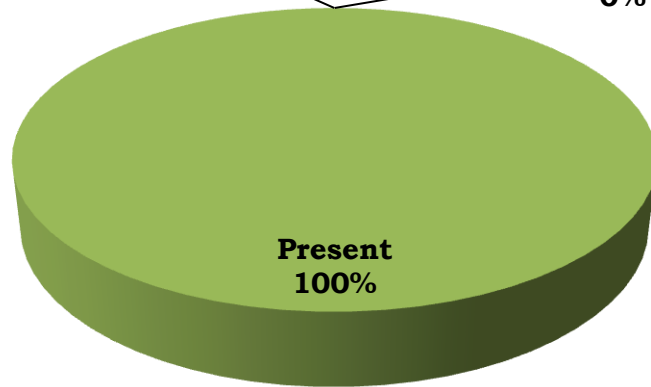


8. L:PBS

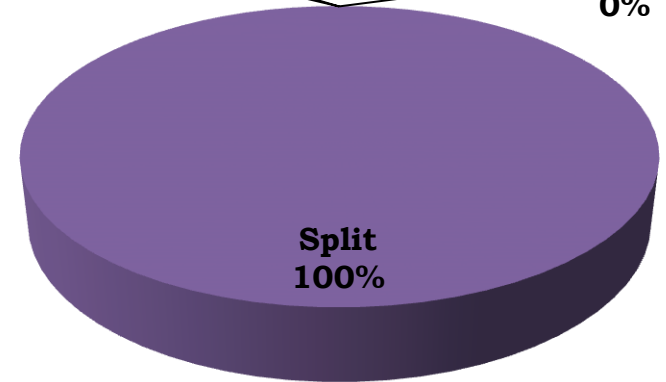




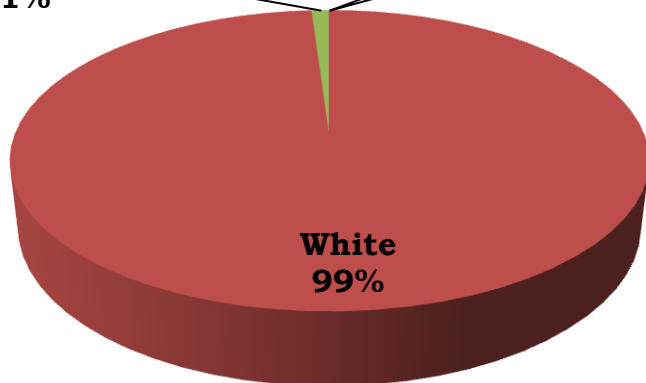
13. L:L
NA 0% Absent 0%



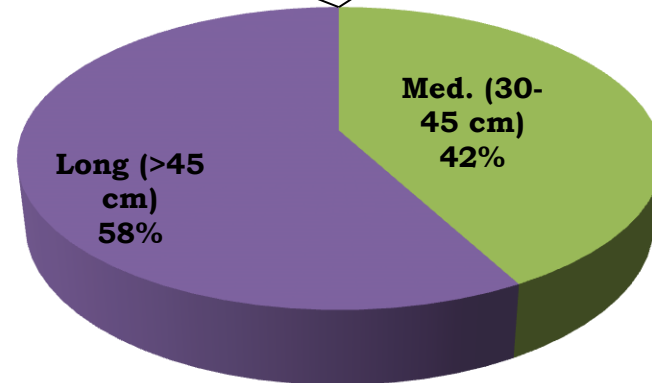
14. L:SL
Truncate 0% NA 0% Acute 0%

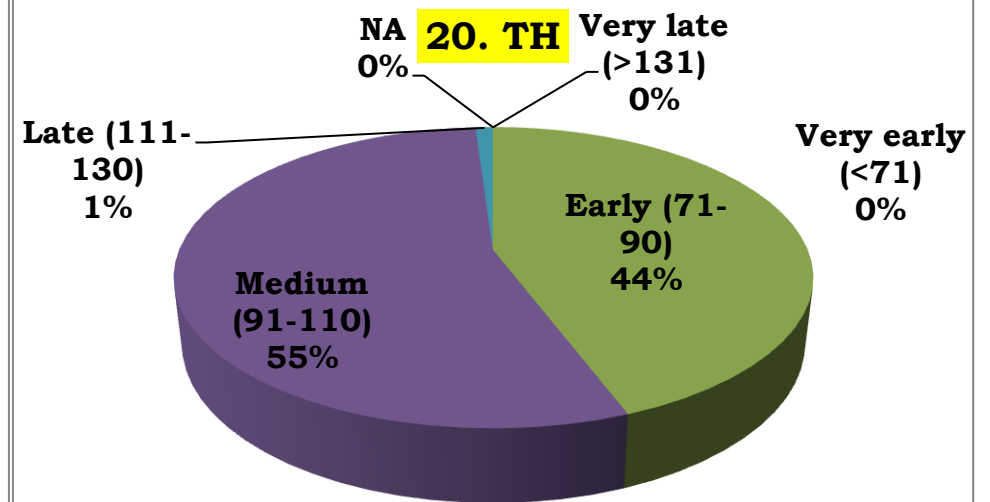
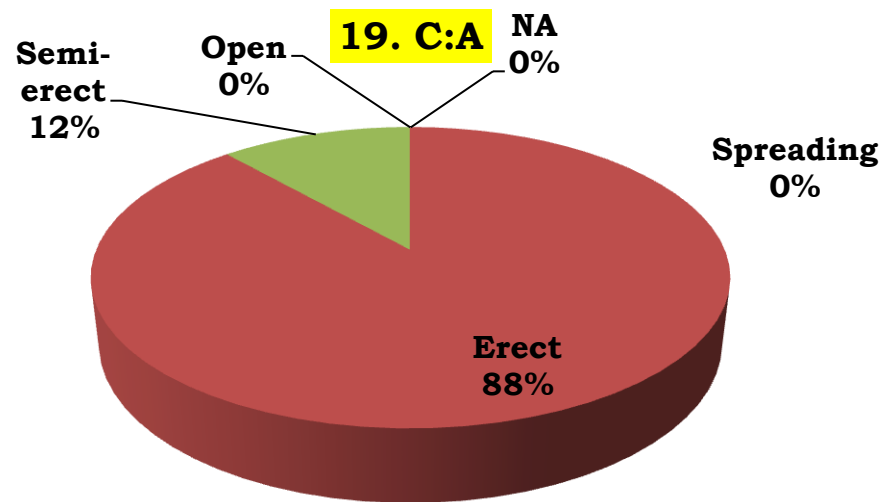
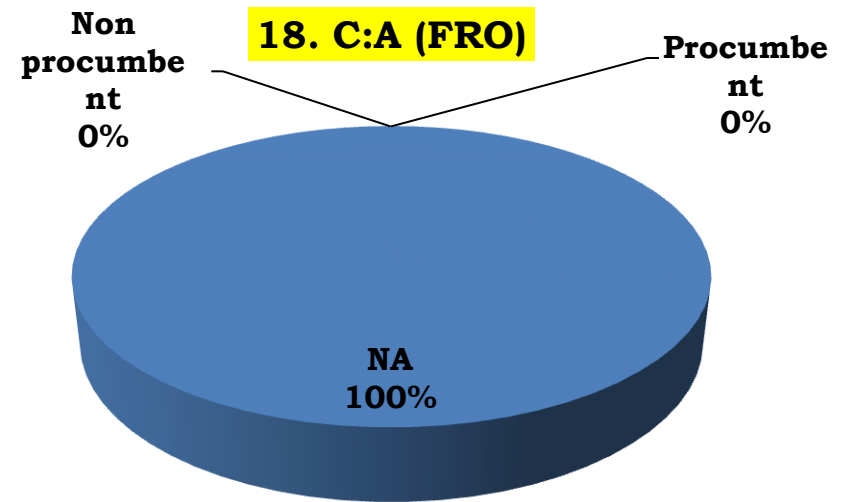
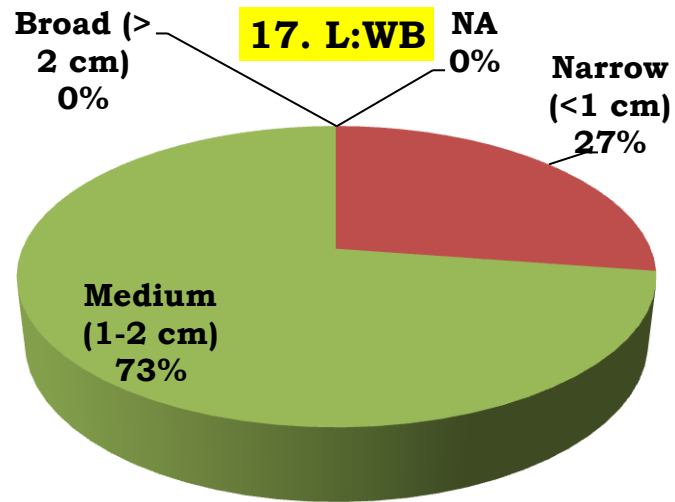


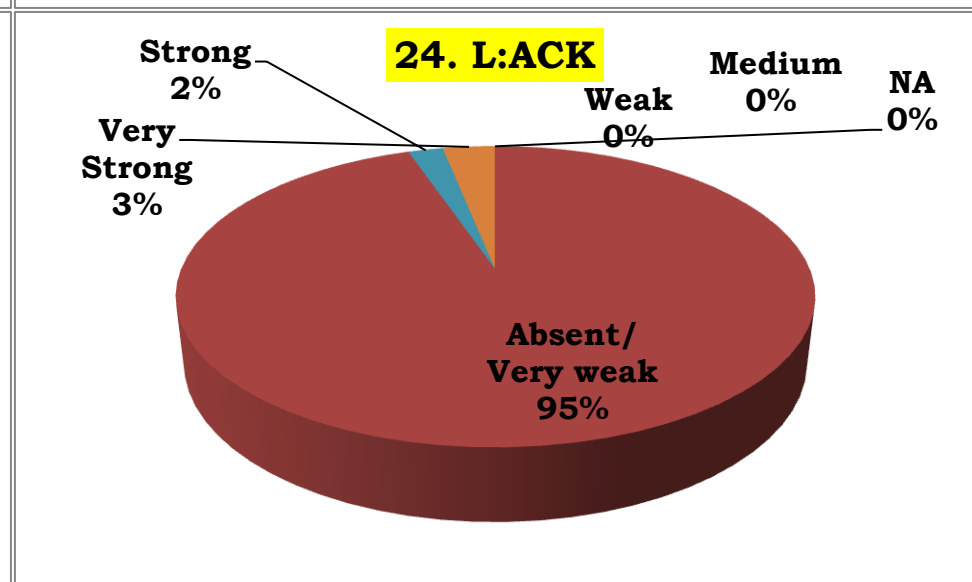
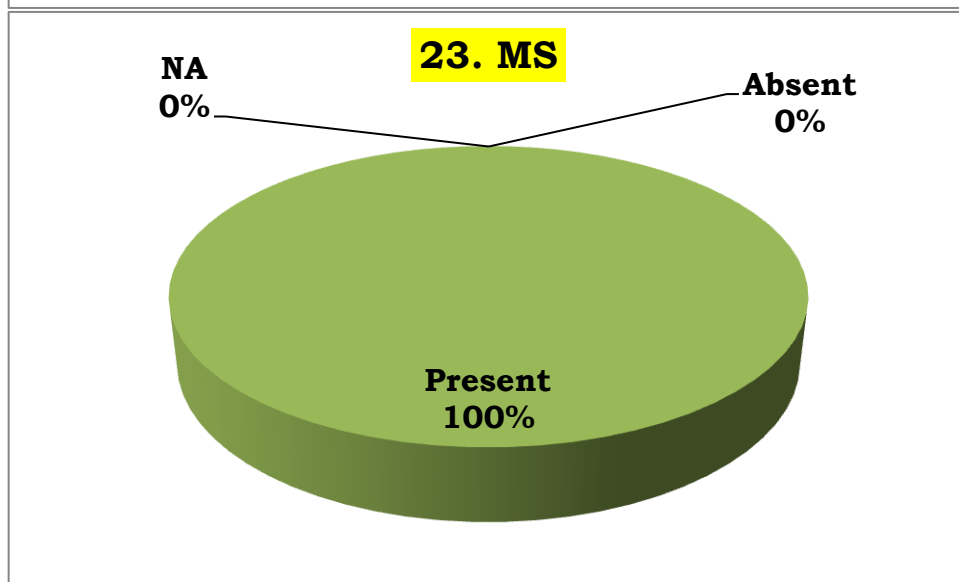
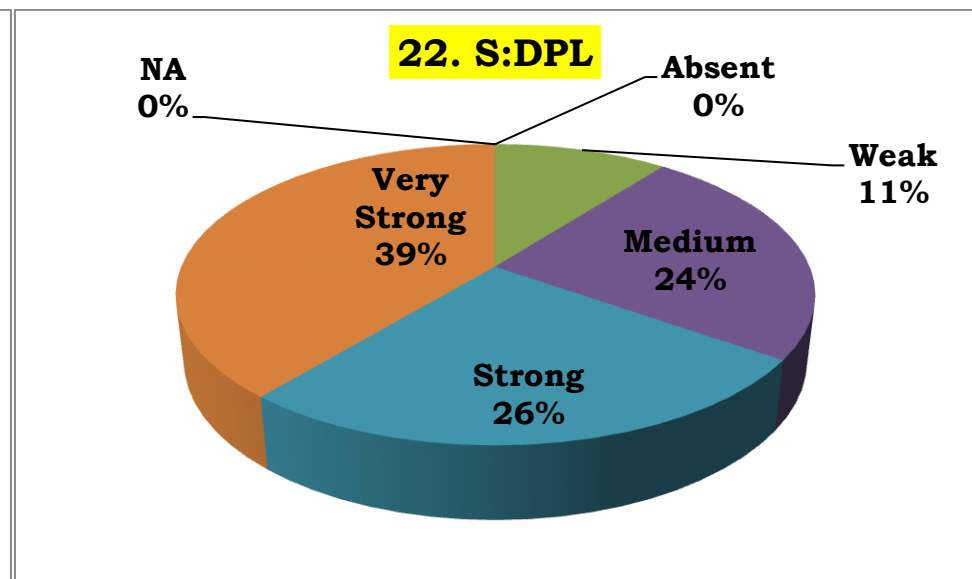
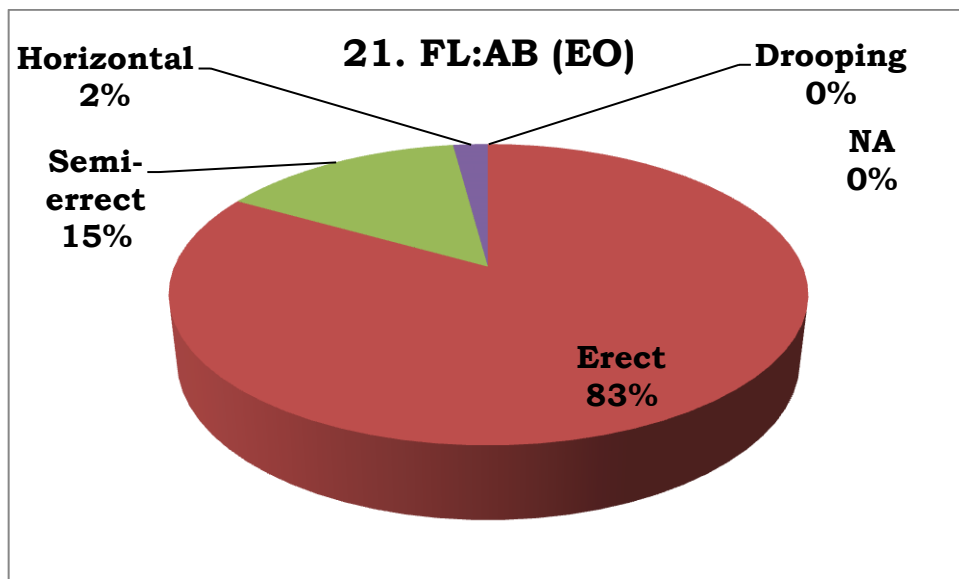
15. L:CL
Light Purple 1% NA 0% Purple 0%

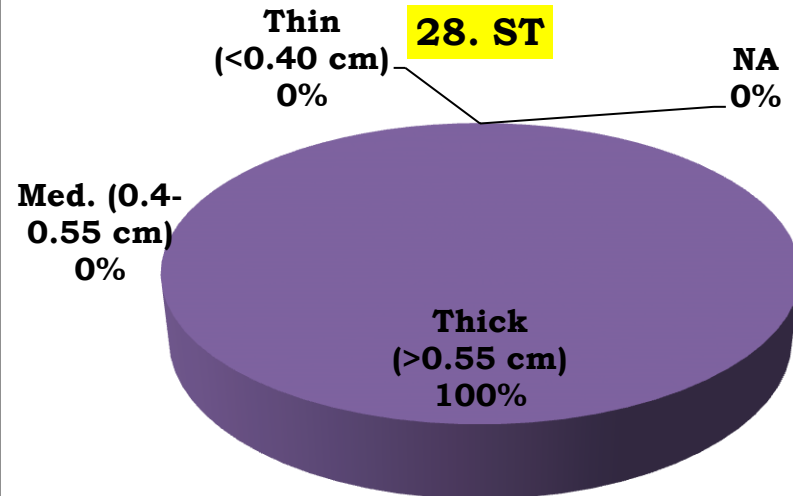
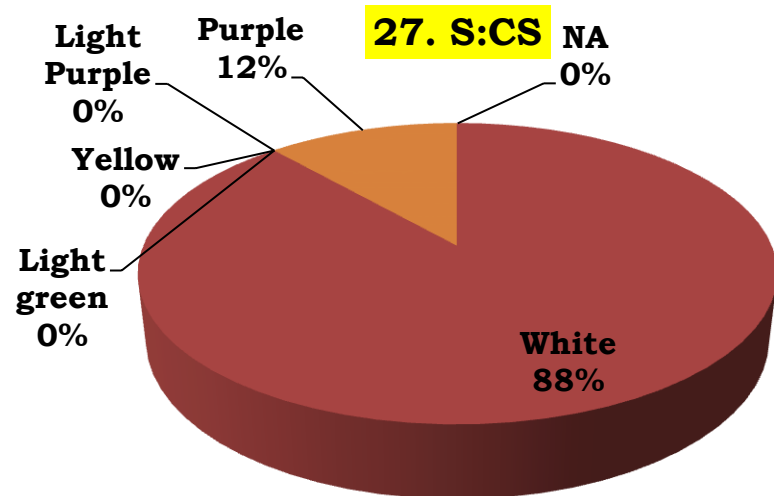
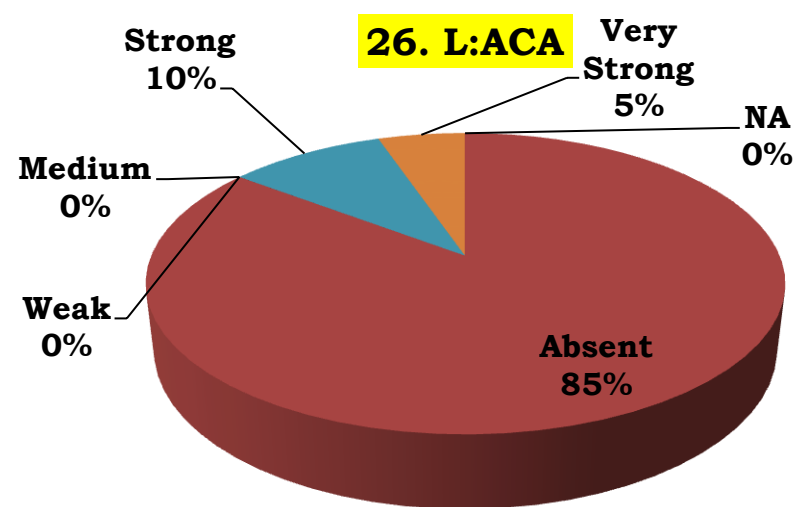
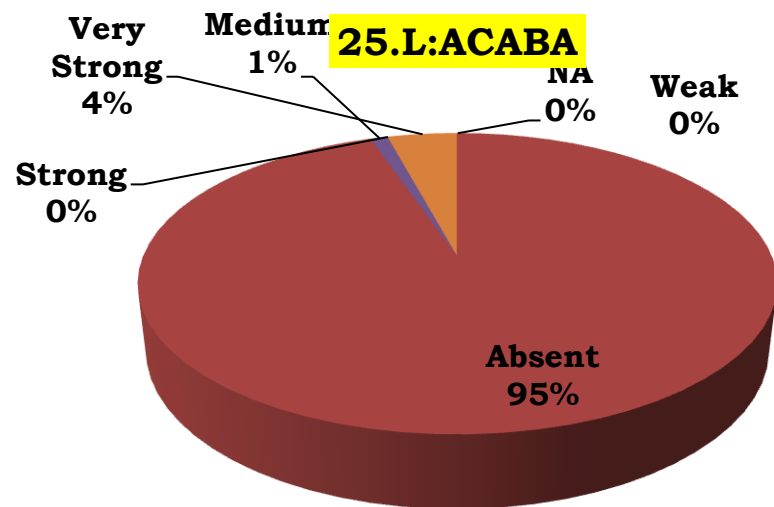


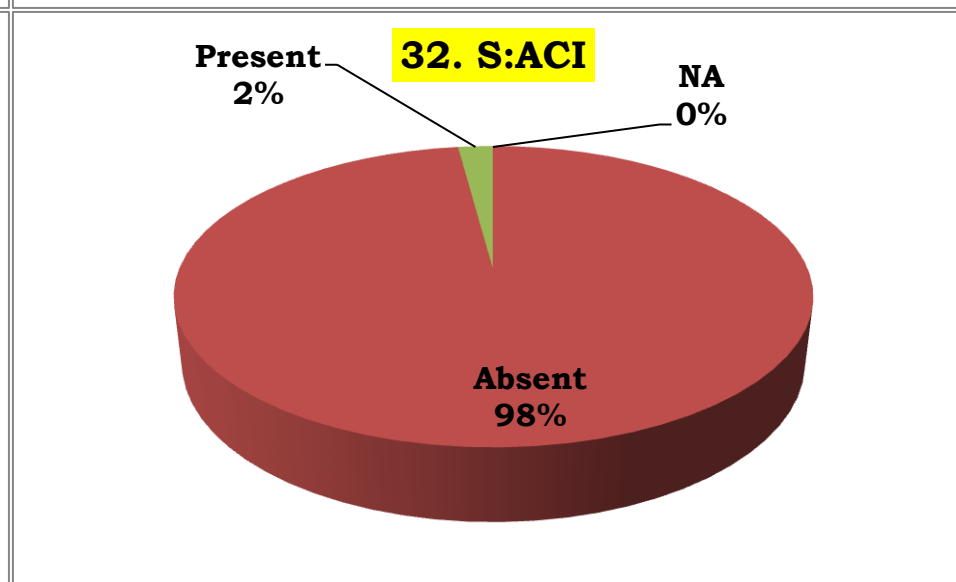
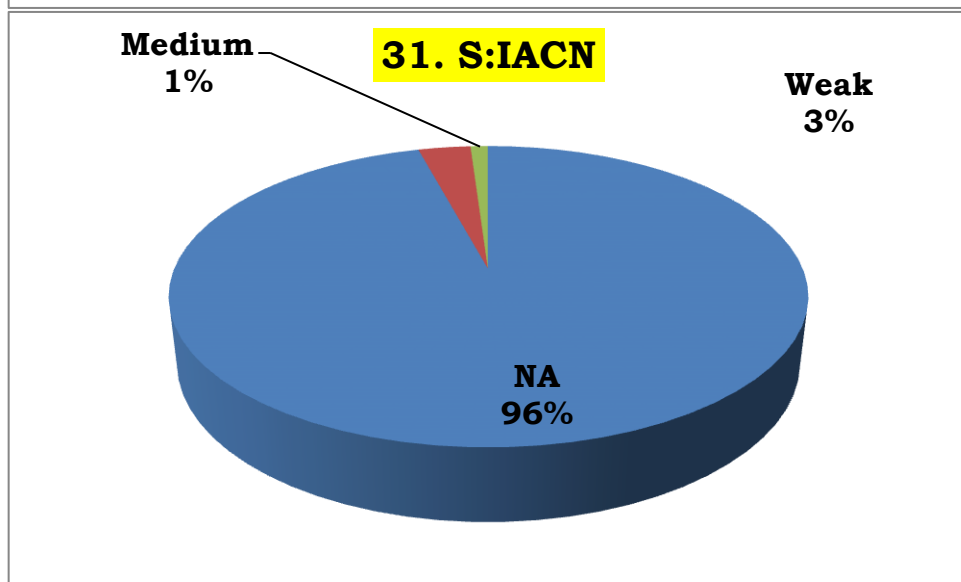
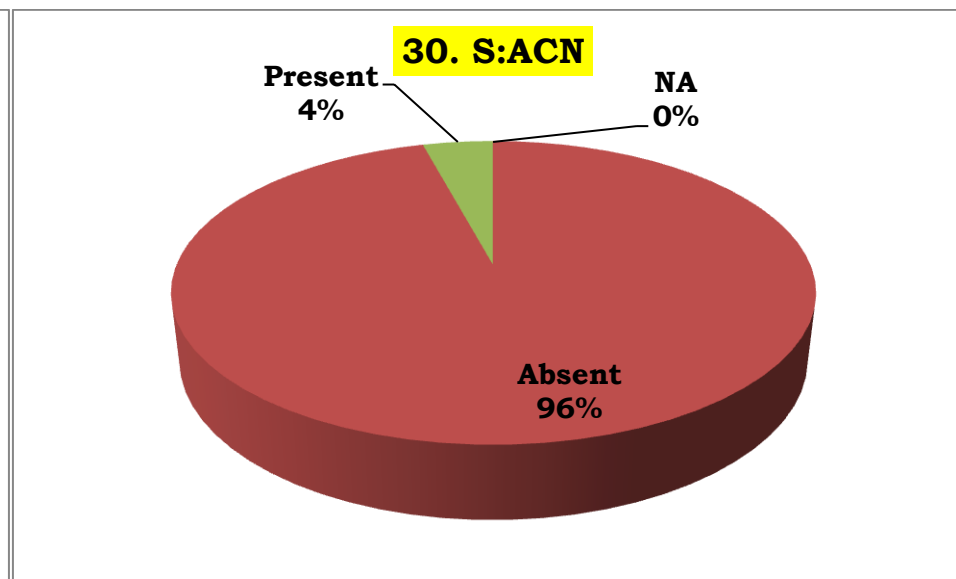
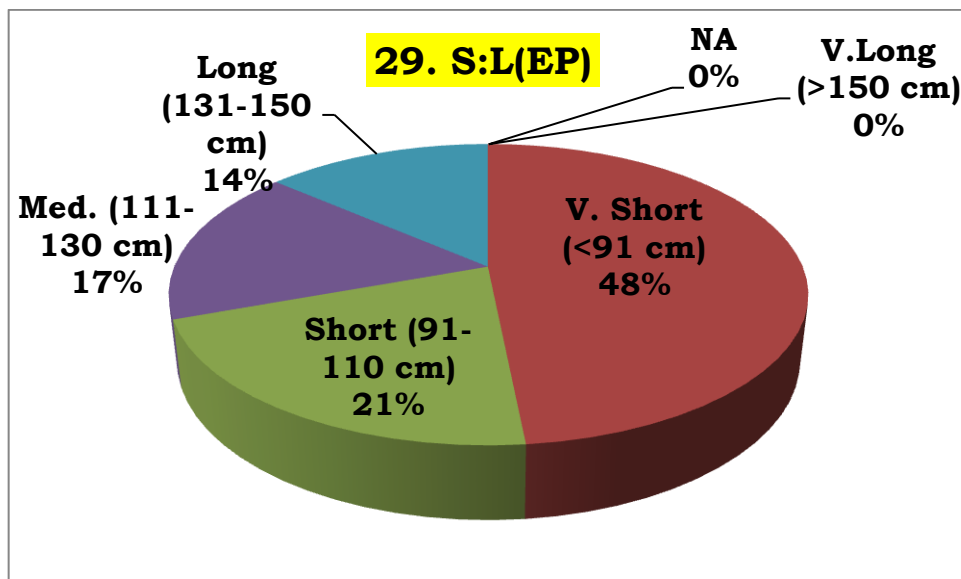
16. L:LB
NA 0% Short (<30 cm) 0%

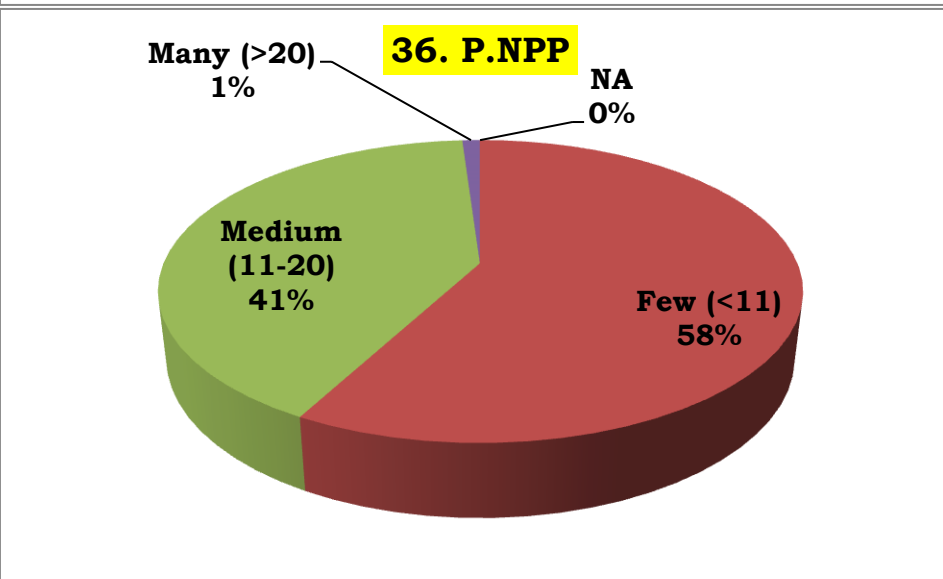
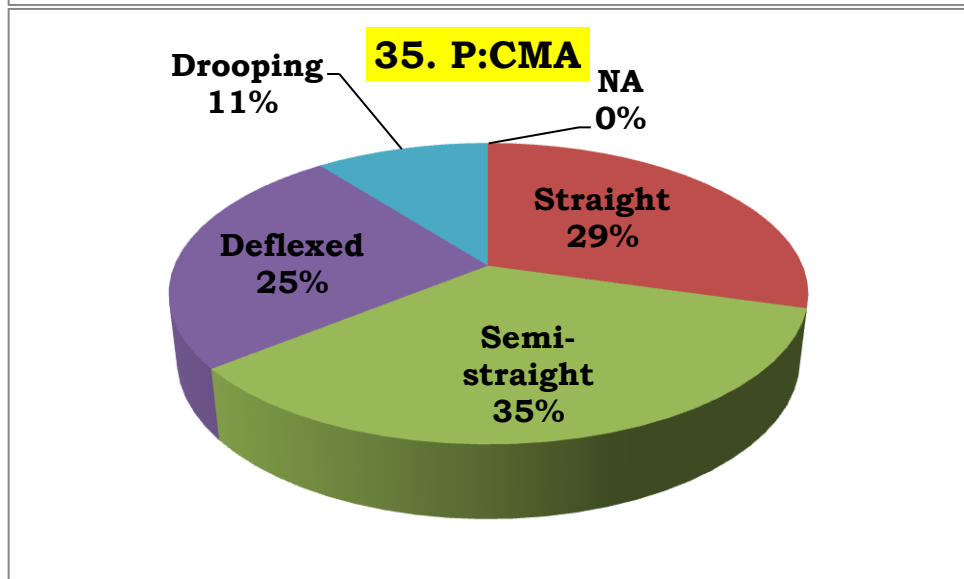
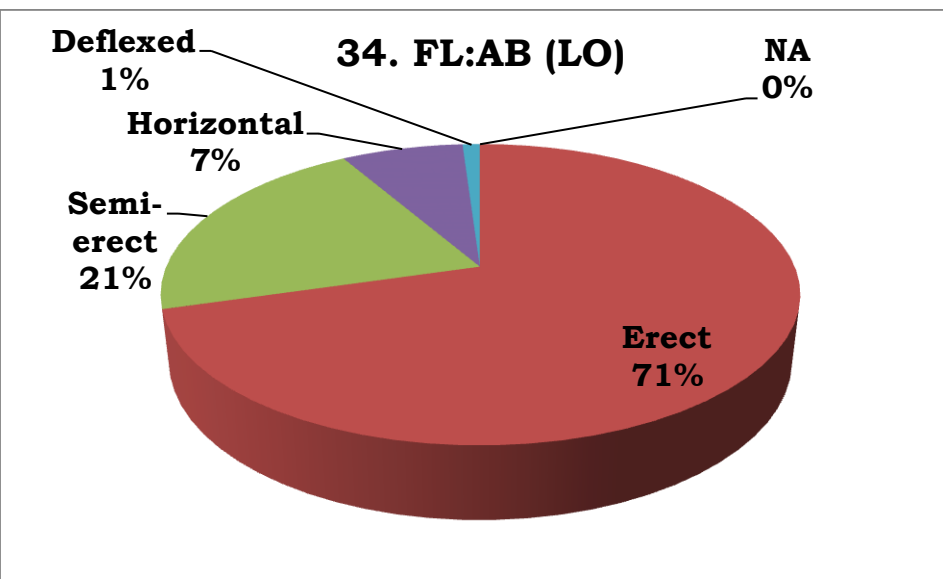
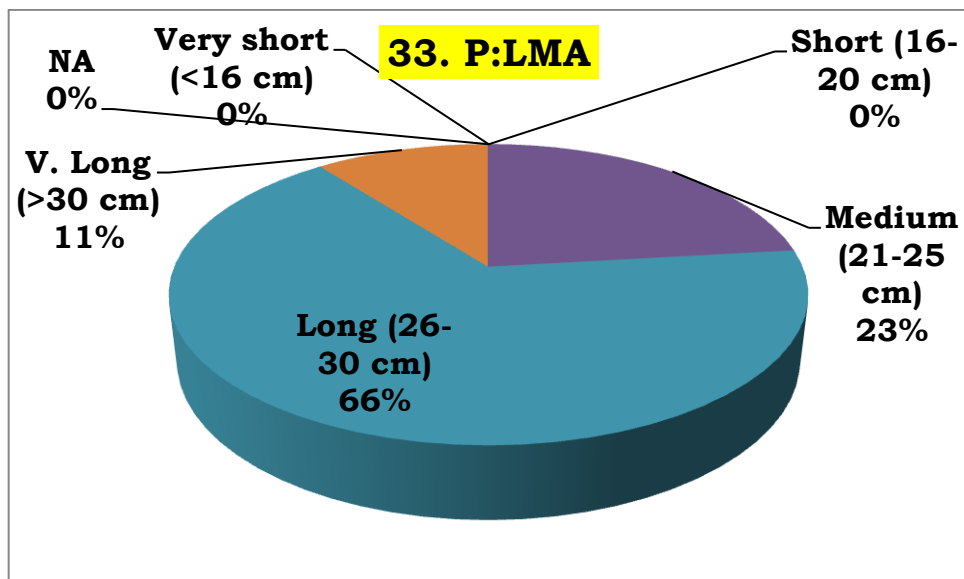


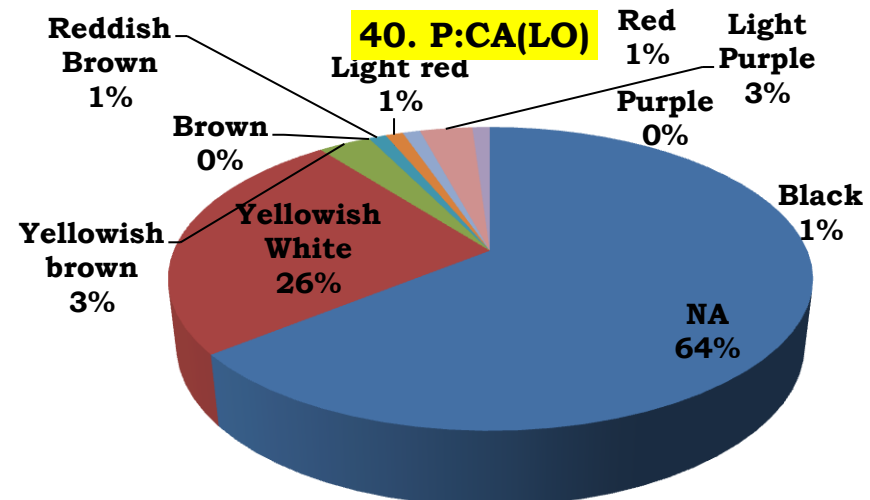
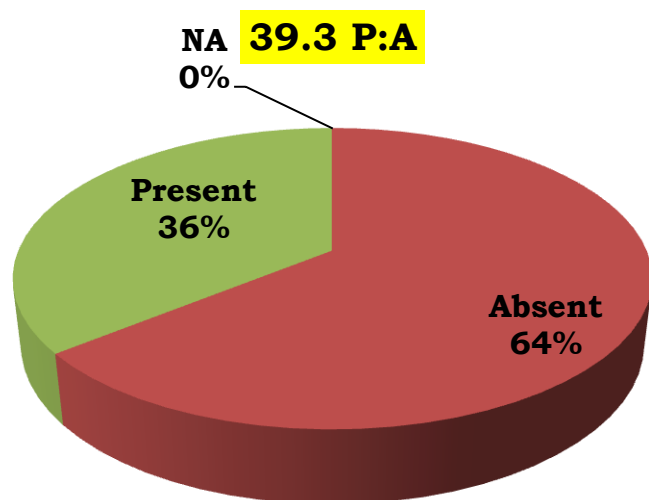
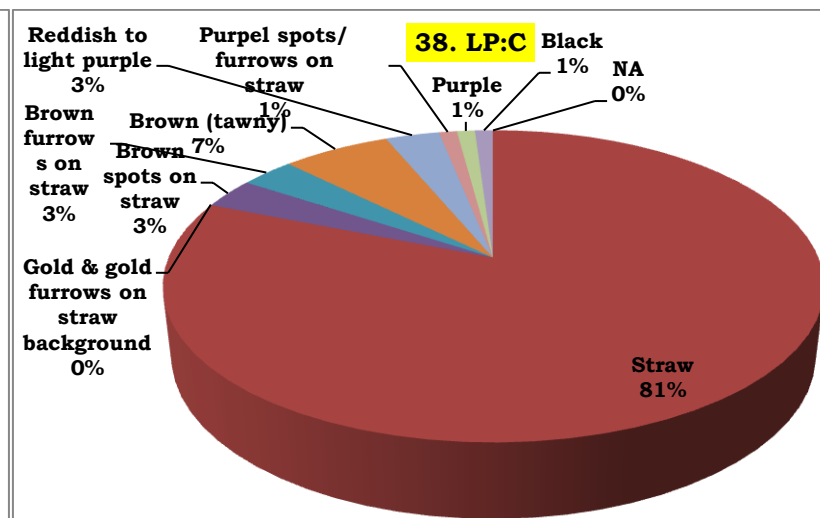
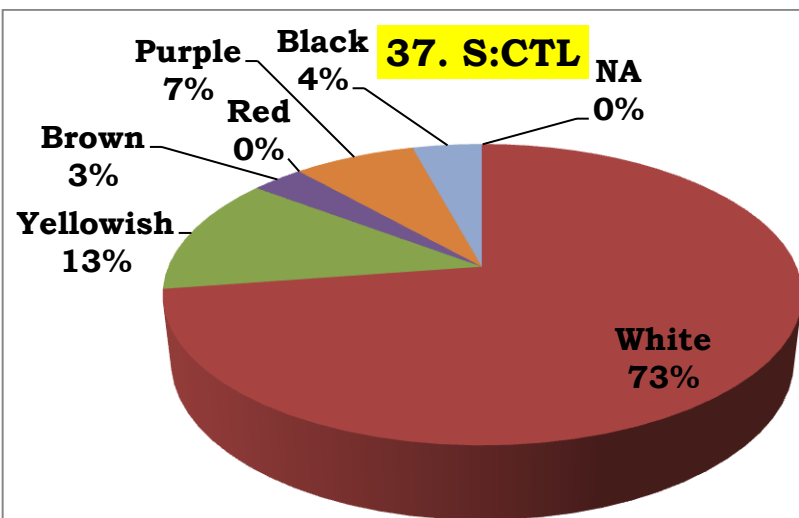


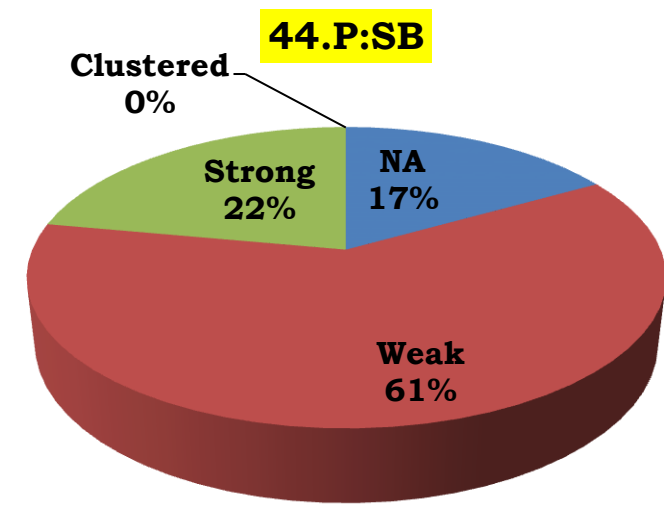
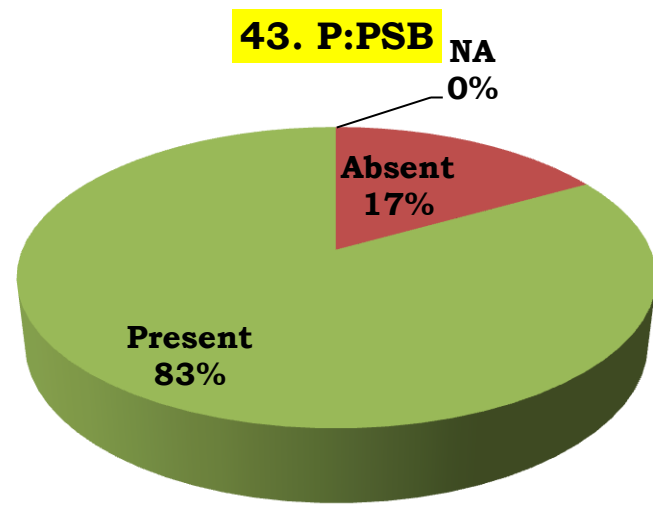
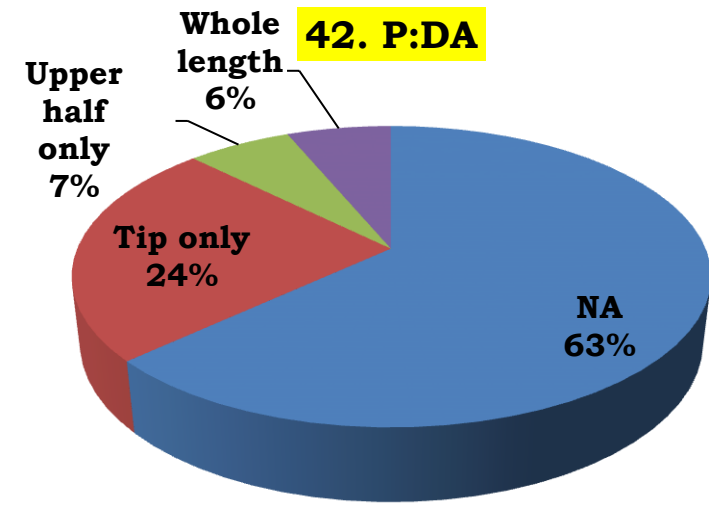
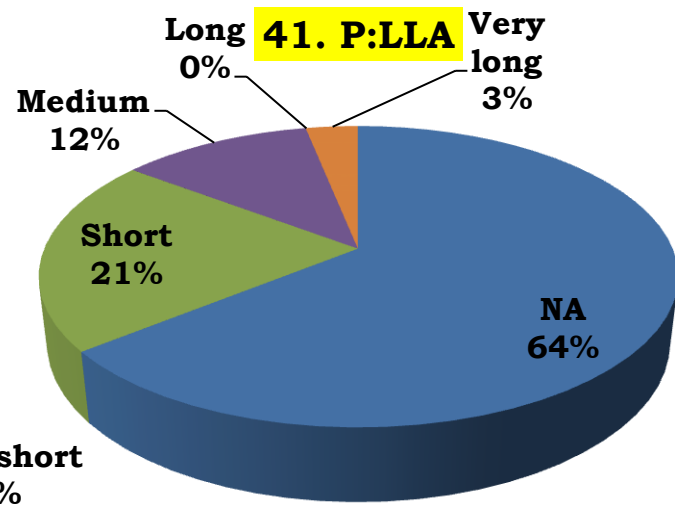


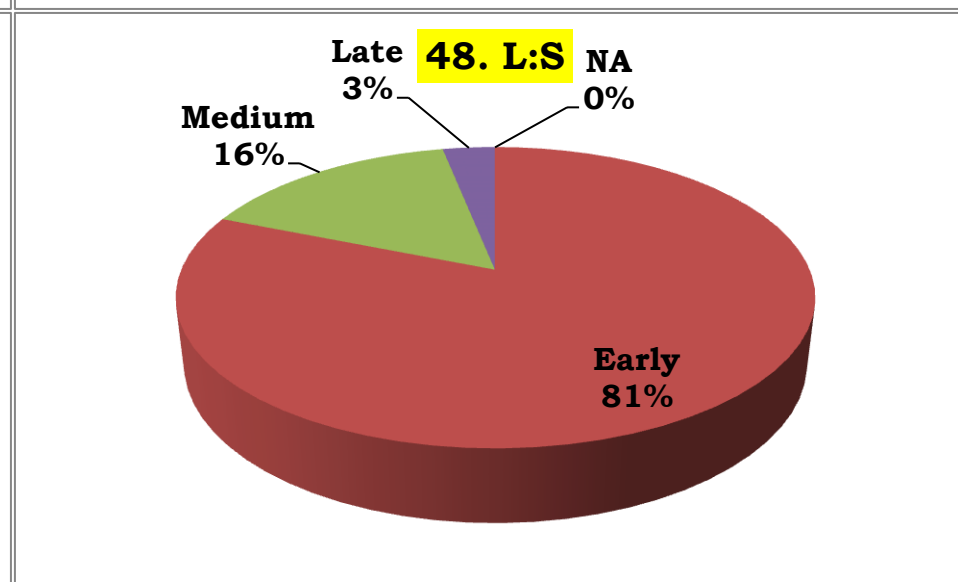
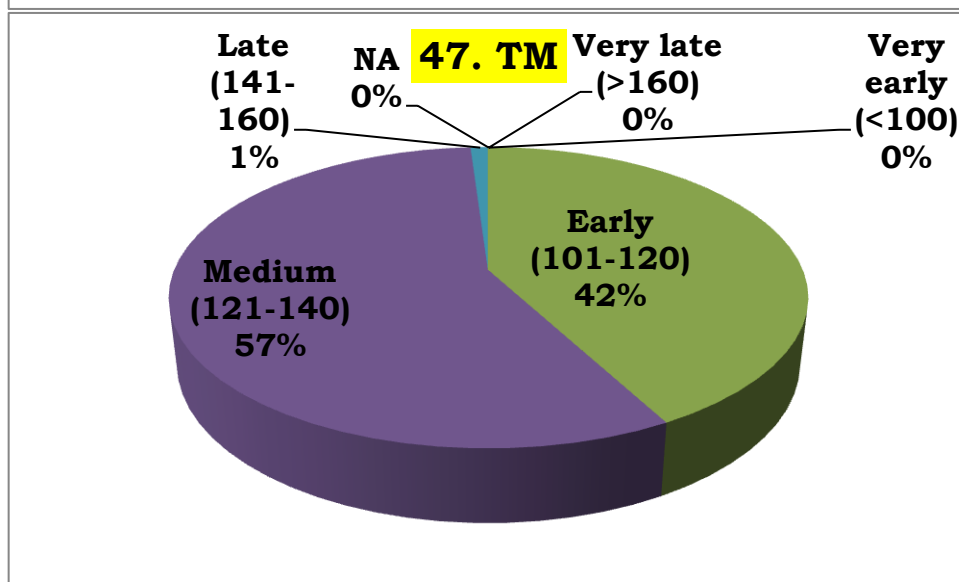
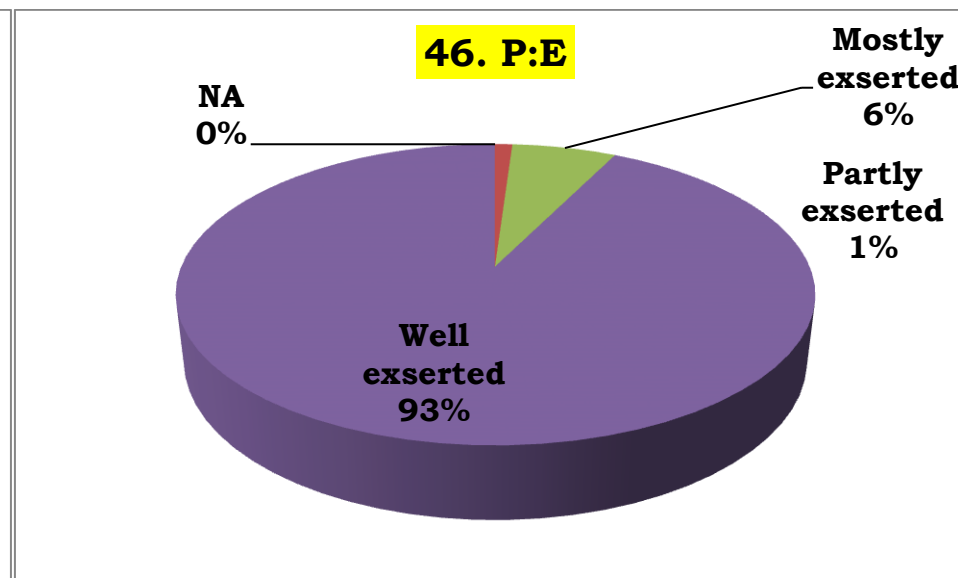
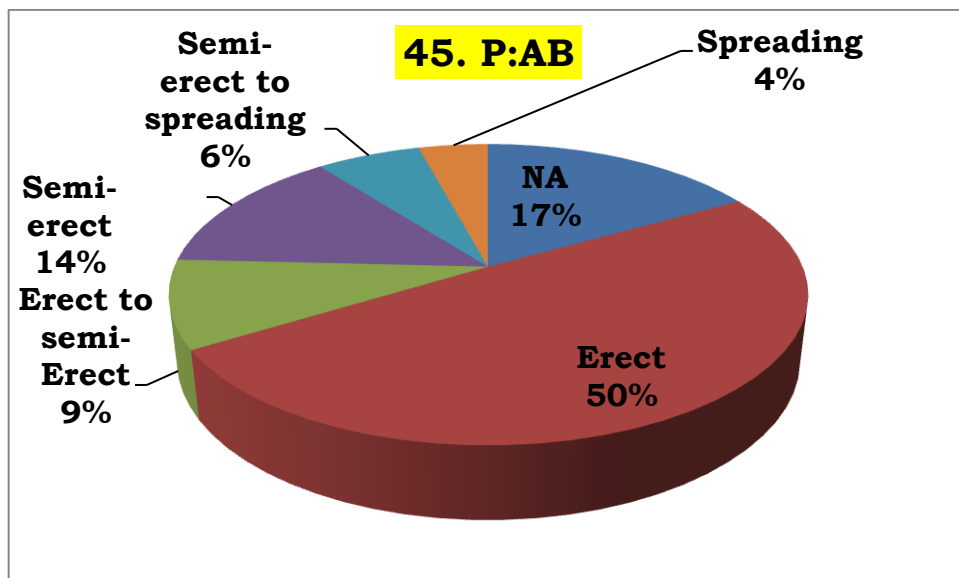




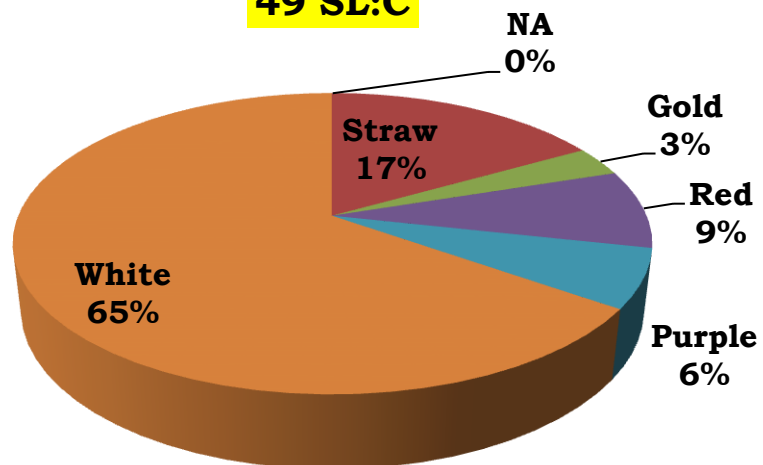




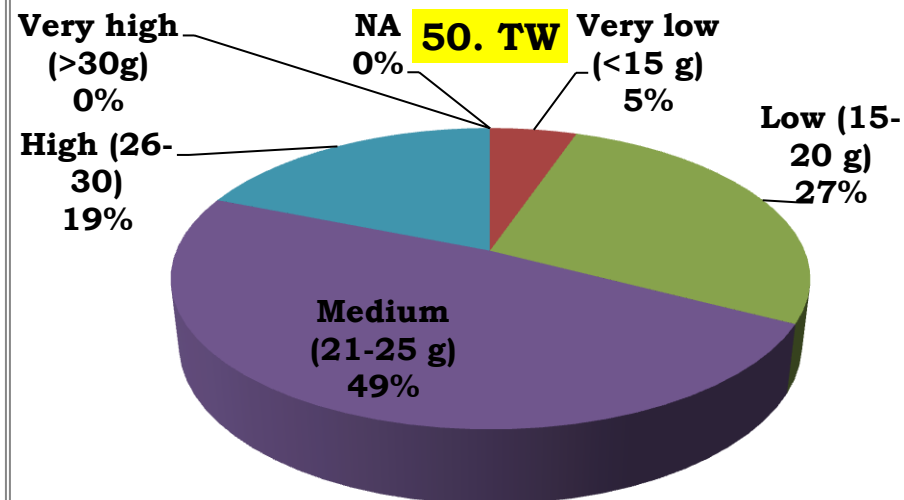




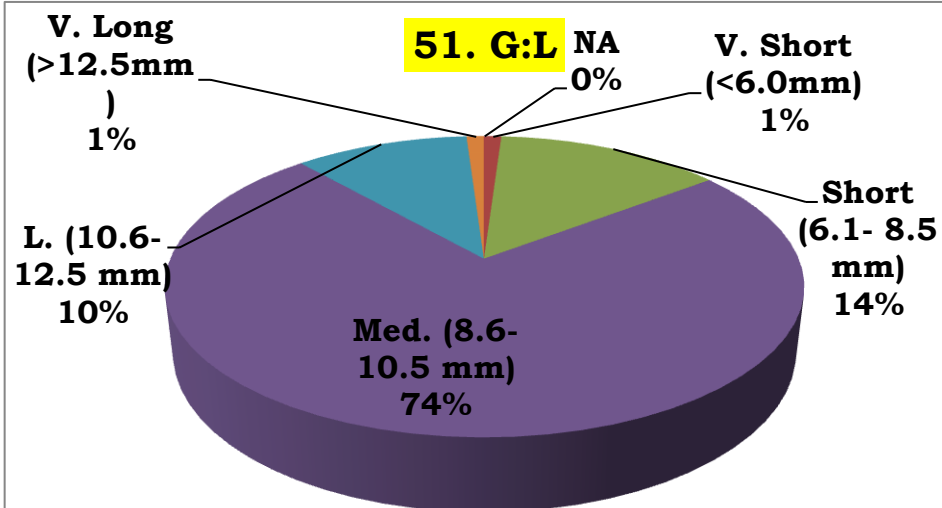
49 SL:C



50. TW



51. G:L



52. G:W

