DIVERSITY ANALYSIS IN LANDRACES OF RICE (*Oryza sativa* L.) IN WAYANAD THROUGH MORPHOLOGICAL AND MOLECULAR POLYMORPHISM STUDY

by

MANJUNATHA, G. A.

(2015-21 -029)

THESIS

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DEDICATION

I dedicate this thesis to my beloved parents

RATHNAMMA

and

AMARANARAYANASWAMY

DECLARATION

I, hereby declare that this thesis entitled **"DIVERSITY ANALYSIS IN LANDRACES OF RICE (*Oryza sativa* L.) IN WAYANAD THROUGH MORPHOLOGICAL AND MOLECULAR POLYMORPHISM STUDY"** is a bonafide record of research work done by me during the course of research and that this thesis has not been previously formed the basis for the award to me of any degree, diploma, fellowship or other similar title of any other University or Society.

Place: Vellanikkara

Date: 05/11/2018

Manjunatha, G. A.

(2015-21-029)

CERTIFICATE

Certified that this thesis entitled **"DIVERSITY ANALYSIS IN LANDRACES OF RICE (*Oryza sativa* L.) IN WAYANAD THROUGH MORPHOLOGICAL AND MOLECULAR POLYMORPHISM STUDY"** is a record of research work done independently by Mr. Manjunatha, G. A., under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to him.

Place: Vellanikkara

Date: 05/11/2018

Dr. C. R. Elsy
(Major Advisor)
Professor (Dept. of Plant Breeding and Genetics)and
Co-ordinator, IPR Cell-KAU
Agricultural Research Station,
Mannuthy

CERTIFICATE

We, the undersigned members of advisory committee of **Mr. Manjunatha, G. A.**, a candidate for the degree of **Doctor of Philosophy in Agriculture** with major in **Plant Breeding and Genetics**, agree that the thesis entitled **"DIVERSITY ANALYSIS IN LANDRACES OF RICE (*Oryza sativa* L.) IN WAYANAD THROUGH MORPHOLOGICAL AND MOLECULAR POLYMORPHISM STUDY"** may be submitted by **Mr. Manjunatha, G. A.**, in partial fulfilment of the requirement for the degree.

Dr. C. R. Elsy
(Major Advisor)
Professor (Dept. of Plant Breeding and Genetics) and
Co-ordinator, IPR Cell-KAU
Agricultural Research Station, Mannuthy

Dr. Jiji Joseph
(Member)
Professor and Head
Dept. of Plant Breeding and Genetics
College of Horticulture
Vellanikkara

Dr. P. Rajendran
(Member)
Associate Director of Research
Regional Agricultural Research Station,
Ambalavayal

Dr. Rose Mary Francies
(Member)
Professor and Head
Dept. of Seed Science and Technology
College of Horticulture
Vellanikkara

S. K 3/11/18

Dr. S. Krishnan
(Member)
Professor and Head
Dept. of Agricultural Statistics
College of Horticulture,
Vellanikkara

R. Ravi 3/11/18

EXTERNAL EXAMINER

K. LAKSHMANAN
Prof & Head
Dept. of Millets TNAU

5

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Manjunatha, G. A.

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

INTRODUCTION

1. INTRODUCTION

'Rice is life', the theme of International Year of Rice-2004, denoted the importance of rice in food, commerce and culture worldwide. Devoting an International Year to a single crop was the first of its kind in the world's history. In the global scenario, rice occupies an area of 160.8 million ha, with a total production of 738.8 million tonnes and productivity of 4.6 tonnes/ha (FAO, 2016) and it is the staple food for nearly 3.5 billion people.

In rice growing countries, India stands first in area (43.39 million ha) and second in production (104.32 metric tonnes) next to China and the productivity is about 2400 kg/ha (GOI, 2017). In India, it is one of the most diversified crop species, with wide variety of cultivars, landraces, wild types and weedy relatives. It plays a vital role in the food security of our country.

Rice is a major cereal and staple food in the state of Kerala. It occupied an area of 7.53 lakh ha with a production of 10.68 lakh tonnes and productivity of 1371 kg/ha, respectively, during 1960's. Owing to conversion of paddy fields for non-agricultural use and urbanization, the area under paddy has declined to 1.71 lakh ha with a production of 4.36 lakh tonnes during 2017 (GOK, 2017).

'Rices of India' a famous book by Indian rice researchers Richharia and Govindasamy (1990), explores the Vedic and the present day literature to reveal the diversity of rice in India. Richharia identified more than 20,000 rice genotypes from parts of Chhattisgarh and Maharashtra. In Kerala, NBPGR Regional Station, Thrissur, collected 855 accessions of rice including 710 accessions of cultivated and 145 of wild rice (Latha *et al.*, 2013).

Wayanad is a part of Western Ghats and is considered as a 'hot-spot' of biodiversity. This district has the maximum tribal population in Kerala. As a part of their rituals, the tribal people conserve many rice landraces. It has been reported that, in Wayanad there were 106 traditional rice varieties, including scented (Jeerakasala and Gandhakasala) and medicinal varieties (Latha *et al.*, 2013). In recent years due to change in varietal spectrum and use of paddy fields for non-

agricultural purposes, valuable rice germplasm of this region is disappearing fast (Latha *et al.*, 2013). Hence, there is an urgent need for characterization and conservation of the traditional landraces of Wayanad.

Government of India has introduced the Protection of Plant Varieties and Farmers' Rights (PPV&FR) Act in 2001, for the protection of crop varieties including the farmers' rights over the traditional varieties. Protection of IP rights over varieties can be accomplished by their registration under this Act. Morphological characterization based on DUS (Distinctness, Uniformity and Stability) is the requisite for registering varieties under PPV&FR Act. Hence, the present programme was undertaken for DUS characterization and diversity analysis of landraces of Wayanad. The DUS characterization will support their registration under PPV&FR Act. This will also support benefit sharing mechanism and protection of traditional knowledge over these varieties.

In the evolution of rice and its genetic differentiation into distinct varietal groups, consumer quality preferences have played a significant role besides agroecological factors. One such varietal group, comprising the aromatic rices of the India, are highly priced rices in domestic as well as international markets. Wayanad Jeerakasala rice and Wayanad Gandhakasala rice are the two unique aromatic rices of Wayanad registered as Geographical Indications (GI) from Kerala (Elsy, 2012).

Characterization of these aromatic genotypes at molecular level is necessary for establishing their genetic identity. Characterization of these cultivars based on phenotype has limitations since most of the morphological characters are greatly influenced by environmental factors and developmental stage of the plant. In contrast to morphological characters, molecular markers can reveal abundant difference among genotypes at DNA level, providing a more direct, reliable and efficient tool for varietal characterization (Prabakaran *et al.*, 2010). Thus, molecular characterization can reveal the cultivar identity of these rices registered as Geographical Indications in India. Characterization of aromatic genotypes at

molecular level is more important for the commercial identification of their genuine goods.

Assessment of genetic diversity is very important in rice breeding from the standpoint of selection and conservation of different landraces for further utilization in crop improvement programmes (Patra, 2000). The landraces are valuable as they possess a huge treasure of genetic material which may prove important in future varietal development programmes.

The success of plant breeding depends on the extent of variability present in any crop. Knowledge on the nature and magnitude of genetic variation in quantitative characters like yield and its component traits is very essential for genetic improvement. A critical analysis of genetic variability present in the germplasm of any crop and its analysis is a pre-requisite for initiating any crop breeding programme adopting appropriate breeding techniques.

In the above background the present investigation was undertaken with the following objectives:

1. Collection and DUS characterization of rice landraces of Wayanad at morphological level.
2. Characterization of popular aromatic genotypes of Wayanad at molecular level.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

In recent years increased dependence on high yielding varieties and support system of govt. agencies, has posed a great threat to cultivation of traditional rice varieties and landraces which may have immense potential for different desirable traits. In order to prevent any further gene erosion, characterization and assessment of genetic diversity is very important from the standpoint of selection and conservation of different landraces for further utilization in varietal improvement programmes. These landraces are valuable as they are the treasure of genetic material which may prove important in future variety development programmes.

The present study, "Diversity analysis in landraces of rice (*Oryza sativa* L.) in Wayanad through morphological and molecular polymorphism study" was undertaken with the main objective of characterization of rice landraces of Wayanad at morphological level and the characterization of popular aromatic genotypes of the area at molecular level.

The available comprehensive literature on morphological characterization, genetic variability, character association, genetic divergence and molecular characterization in rice are presented in the following chapter.

2.1. Morphological characterization
2.2. Genetic parameters
2.3. Character association
2.4. Genetic divergence
2.5. Molecular characterization

2.1. Morphological characterization

Morphological characterization of germplasm is fundamental in order to provide information for varietal development programmes (Das and Ghosh, 2010; Nascimento *et al.*, 2011). Morphological characterization is a system of recording and storing useful data that can be made readily available to others and help in planning of breeding programmes (Umarani *et al.*, 2017). Sinha and Mishra (2013)

reported that morphological traits were useful for preliminary evaluation for varietal development program and can be used for genetic diversity analysis among rice landraces.

Government of India has introduced its *Sui generis* system, as Protection of Plant Varieties and Farmers' Right Act (PPV&FRA) in 2001 for the protection of crop varieties including farmer varieties based on Distinctiveness, Uniformity, Stability (DUS) and Novelty. Therefore, morphological characterization of a variety based on DUS is the prerequisite for registering varieties under PPV and FR Act, 2001. This DUS characterization will also support to identify uniqueness of a variety from existing varieties and also support benefit sharing mechanism and protection of traditional knowledge over these varieties.

Patra *et al.* (2010) characterized 18 basmati rice varieties for 46 morphological descriptors following DUS guidelines of PPV & FR Authority and subsequently examined their DUS characters. The study revealed that, out of 46 visually observed characters, 26 characters were monomorphic, 11 characters were dimorphic and seven characters were polymorphic indicating their potential for varietal characterization and distinctiveness.

Mathure *et al.* (2011) conducted an experiment to characterize 88 aromatic cultivars collected from Maharashtra state and Belgaum Dist., Karnataka. They studied kernel characters such as kernel size, kernel shape, test weight and aroma of kernels and grain morphology such as awning, lemma and palea characters, pubescence, colour of sterile lemma and apiculus colour. The results showed that, 36 cultivars were reported to have one or more superior traits such as dwarf stature, early flowering, long panicles, higher number of filled grains per panicle, higher number of productive tillers per plant and strong aroma.

Nascimento *et al.* (2011) conducted an experiment at Pernambuco, Brazil to characterize 146 accessions of upland rice for 14 qualitative and 14 quantitative descriptors following Descriptors for Rice, IRRI and reported that polymorphism was observed for 12 out of 14 qualitative characters and also for 11 out of 14

quantitative traits studied. This data could be useful for identification of cultivars with distinct morphological traits for varietal development programmes.

Rajanna *et al.* (2011) evaluated two Indian rice hybrids such as KRH-2 and DRRH-2 and their parents *viz.*, IR-58025B, KMR-3R, IR-68897B, IR58025A, IR-68897A and DR-714-1-2R for 38 qualitative and quantitative morphological traits as per the DUS test guidelines and reported that out of 38 traits studied, 13 traits *viz.*, flag leaf attitude, flag leaf length and width, days to 50 per cent flowering, leaf senescence, days to maturity and seed traits such as 1000 grain weight, grain length, grain width and shape of grain were found to be more helpful for grouping of genotypes. More variation was observed among parents and hybrids for six parameters *viz.*, leaf length, days to 50 per cent flowering, panicle secondary branching, 1000 grains weight, decorticated grain shape, and days to maturity.

Chakravorty and Ghosh (2012b) evaluated 51 rice landraces for 46 agro-morphological traits following DUS test. The results revealed that, out of 51 rice landraces studied, 27 landraces were found to be distinctive on the basis of 22 essential and 24 additional characters.

Chakrabarty *et al.* (2012b) evaluated 91 farmer varieties for 55 morphological characters following DUS Test Guidelines on Rice and reported that out of 55 traits studied, maximum variability was recorded for pubescence of lemma, colour of tip of lemma and palea, anthocyanin colour of keel in lemma, attitude of branches of panicle and curvature of main axis of panicle. Based on the results it was reported that, the varieties with distinguishable characteristics and economic values could be registered under the PPV&FR Act, 2001 and also the prominent characters were helpful in the commercial production of genetically pure seeds of such varieties.

Parikh *et al.* (2012) carried out an experiment to characterize 71 aromatic rice germplasm and recorded twelve morphological characters following Rice Descriptors, IRRI and observed wide variability among these landraces and reported that, on the basis of mean performance, two landraces each for fertile

spikelets per panicle and spikelet density, three landraces each for low spikelet sterility percentage and hundred seed weight were selected as parents for future varietal development programmes.

Sarawgi *et al.* (2013) carried out a characterization study, to evaluate 782 rice germplasm accessions for 29 morphological and eight agronomical traits following DUS test. The results revealed that, out of 29 morphological traits studied, most of the morphological characters showed variation in different accessions. Based on the results, promising ten accessions were identified for the yield related traits and also reported that these traits could be used to identify phenotypically divergent sources for traits of interest in varietal development programmes.

Sinha and Mishra (2013) characterized 20 landraces of rice at Bankura district of West Bengal following DUS test and reported that out of the 20 landraces studied, 11 landraces were distinctive according to the five essential and 18 additional characters proposed by the DUS guideline.

Rao *et al.* (2013) characterized 65 rice landraces for 43 morphological traits including both qualitative and quantitative traits and reported that, out of 65 landraces studied, 32 landraces were found to be distinctive on the basis of 22 essential and 24 additional characters.

Chouhan *et al.* (2014) conducted an experiment to evaluate and characterize 35 wild rice germplasm for 26 morphological traits, including 14 quantitative and 12 qualitative traits. The results reported a significant variability for all the traits studied. Based on the results, the genotypes namely NKSWR-64, NKSWR-48 and NKSWR-75 were identified and selected as most promising genotypes for fertile spikelet per panicle, panicle length, test weight, spikelet fertility percentage and grain yield per plant, indicating that these accessions could be utilized for improving yield and yield traits in future breeding programmes.

Gupta *et al.* (2014) conducted an experiment to characterize 53 traditional rice germplasm of Chhattisgarh based on 14 qualitative characters and 17

quantitative characters following DUS descriptor. Based on the results, the genotypes S: 663, K: 1514, and J: 311 were identified as promising and selected for agronomical characteristics, indicating that these identified genotypes could be used in rice hybridization programme to achieve higher yield.

Rabara *et al.* (2014) characterized 307 traditional rice varieties for 39 qualitative and 18 quantitative morphological characters at Philippine Rice Research Institute, Philippines. The analysis of results revealed a significant diversity in major traits assessed in farmers' rice varieties. Based on the results of plant height and maturity, 11 accessions were selected as potential donor parents for future breeding programmes.

Roy and Sharma (2014) collected 84 rice landraces from various agroecological regions of West Bengal and characterized for 16 important morphological characters and eight quality characters along with zinc (Zn) and iron (Fe) content following standard method of DUS test and all the descriptors evaluated in this study showed that there is wide genetic diversity among landraces and many genotypes were identified as promising donors for different characters studied, which will be more useful for the breeders to choose the right parent for varietal development programmes.

Samal *et al.* (2014) evaluated 78 aromatic rice germplasm including international check varieties and traditional Basumati types for morphological and biochemical parameters following DUS guidelines (PPV and FRA, 2007) and reported that, traditional aromatic and evolved Basumati varieties had good morpho-physical and biochemical characteristics. Based on the results, the indigenous aromatic rice genotypes *viz.*, Nuakalajeera, Bishnubhog, Thakurbhog, Pimpudibasa-1, Kalajauvan, Kaminibhog-1, Jalaka, Kalajerra, Basnaparijat, Dubraj and Badsahbhog were identified as promising parental genotypes for high grain fertility and abiotic stress tolerance.

Sarawgi *et al.* (2014) characterized 408 rice germplasm accessions of dwarf (< 110 cm) and medium duration (110-130 days) group with six popular standard

checks *viz.*, IR 64, Annada, Swarna, NDR 97, Pusa Basmati and Jaya on the basis of 18 morphological and seven agronomical traits. Based on the results of the means of the checks, IC 491282 for 100-seed weight, IC 292977 for highest number of effective tillers per plant, IC491367 for high grain yield per plant along with high 100 seed weight and IC132899 for grain yield per plant along with number of effective tillers were identified and selected for future breeding programmes.

Kioko *et al.* (2015) evaluated aromatic and non-aromatic rice collected from Kenya and Tanzania. The results revealed that, there is an enormous diversity among all the varieties for all the traits studied. Based on the results, the wide distinct morphological characters *viz.,* grain length, kernel length, grain weight and kernel L:B ratio were identified to use in future breeding programmes.

Solis *et al.* (2015) evaluated 13 traditional rice cultivars collected from Pinardel rio province of Spain, for 15 qualitative and 10 quantitative parameters following Standard Assessments System for Rice and reported high range of variation among the cultivars. Based on the results, the unique characters identified among the genotypes (*i.e.*, Bluebonnet, Andres, Estrella Roja and Caracol) were plant erection, earliness, panicle length, high tillering capacity, compact and well emerged panicles and slow senescence.

Ahmed *et al.* (2016) characterized 27 *Jesso-Balam* rice accessions of Bangladesh for 21 qualitative agro-morphological characters and reported wide range of variability among all the varieties for 19 traits out of 21 traits studied, except for presence and shape of penultimate leaf ligule among these accessions. Based on the variability, the qualitative traits like strong pubescence on the surface of the leaf blade, dark green colour leaf and purple margin leaf blade etc. were selected as donors, to use in improving rice varieties with tolerance to leaf surface related insects and diseases.

Ahmed *et al.* (2016) conducted an experiment to evaluate ten similar or duplicate rice germplasm named *Dhaliboro,* of Bangladesh for 21 qualitative morphological characters following DUS tests for rice hybrid and reported that all

the studied *Dhaliboro* germplasm showed wide range of variability and unique prominent qualitative features of rice and also stated that these identified unique characters could be helpful for developing new varieties with unique DUS characters.

Kumar *et al.* (2016) carried out an investigation to study the distinctness among 64 aromatic rice germplasm for 35 agro-morphological and quality traits following DUS test guidelines of PPV & FR Act, 2001. The results revealed that, all 64 aromatic landraces were found to be distinct for 31 morphological and quality characters studied. Based on the results, the genotypes with short stem length, very long panicle length, extra-long slender grain and more number of panicles per plant could be used as potential donor parents in hybridization programmes. It is also reported that, this data would be helpful for breeders and farmers to identify and conserve the beneficial genes for future breeding programmes.

Sanyal and Joshi (2016) characterized 61 extant varieties of rice belonging to non-basmati and basmati group for 55 morphological descriptors including 44 qualitative characters and 11 quantitative characters following DUS guidelines and the results revealed that, out of 55 morphological traits studied, six traits were found monomorphic, nine were dimorphic and rest 40 traits were found polymorphic in state of expression.

Agro-morphological characterization of 45 aromatic short grain rices for 21 morphological characters was done at Faizabad, Utter Pradesh. The results showed that, all the germplasm studied were distinct and had unique morphological traits. Based on the results, it was concluded that this characterization data would be useful in identification and conservation of these germplasm (Giri and Pandey, 2017).

Giri *et al.* (2017) carried out an investigation at Faizabad, Utter Pradesh for DUS characterization of high yielding rice variety Narendra Lahar for 64 characters following DUS test. The results showed that, Narendra Lahar is medium maturing, with good tillering ability, semi tall rice variety and also reported that this data would be helpful for the identification and to maintain genetic purity of this variety.

Kalyan *et al.* (2017a) conducted an experiment to characterize 35 landraces of rice at DRR farm, ICRISAT campus for 29 morphological traits following DUS test and reported that out of 35 landraces studied, 22 landraces were found to be distinctive on the basis of 29 essential characters. It was also reported that, this data would be useful for breeders, researchers and farmers to identify and conserve beneficial genes for crop improvement and also to seek protection under PPV and FR Act, 2001.

Pachauri *et al.* (2017) characterized 124 rice germplasm accessions of NBPGR, New Delhi on the basis of 19 morphological and 11 agronomical traits following DUS guideline and identified unique accessions with distinct features for different morphological traits like basal leaf sheath colour, shape of ligule, spikelet colour of stigma, lemma and palea colour and decorticated grain colour. Out of 124 accessions studied, top ten accessions were selected for yield and yield contributing traits as donors for future varietal development programmes.

Umarani *et al.* (2017) conducted an experiment at DRR farm, Hyderabad to characterize 70 landraces of rice for 14 characters including both qualitative and quantitative traits following DUS guideline. The results revealed that, out of 14 characters studied, stem anthocyanin colouration of node was dimorphic. Three traits *viz.*, stem length, panicle exsertion and spikelet colour of stigma were trimorphic. Six traits *viz.*, time of heading, basal leaf sheath colour, panicle length, flag leaf attitude, decorticated grain length and shape were tetramorphic and two traits *viz.*, lemma anthocyanin colouration of apex and amylose content showed five states of expression and six states of expression for decorticated grain colour. **2.2. Genetic parameters (*Genetic variability, Heritability and Genetic advance*)**

The term 'variability' refer to the presence of differences among individuals for a particular trait and it may results partly due to genotypic (heritable) and partly due to environmental (non-heritable) factors. The success of any breeding program depends on the amount of genetic variability among the individuals of population and the degree to which the desirable characters are heritable. Genetic variability is

31

the base material of any plant breeding programme on which selection acts to evolve superior parents (Singh *et al.*, 1980; Tripathi *et al.*, 2018).

Vanaja and Babu (2006) evaluated 56 high yielding diverse rice genotypes to study variability, heritability and genetic advance of 10 quality parameters. The analysis of variance revealed that, significant and wide variability was observed for alkali spreading value and moderate variability for milling percentage, L:B ratio of grain, water uptake, amylose content and volume expansion. Heritability analysis revealed that, all quality characters exhibited high broad sense heritability. High heritability along with high genetic advance were noted for L:B ratio of grain, alkali spreading value, amylose content, milling percentage, volume expansion ratio and water uptake, indicating the potential of these characters to be used in rice breeding programmes.

Genetic variability, heritability and genetic advance were studied for 150 rice genotypes for 11 characters. The analysis of variance revealed that, there is highly significant variation among all the genotypes for all the characters studied, except for leaf width and 100 seed weight. High GCV and PCV were recorded for all the characters except for panicle length and days to 50 per cent flowering. High heritability along with high genetic advance were recorded for all the characters except for days to 50 per cent flowering and panicle length. This indicated the involvement of additive gene action in controlling these characters (Padmaja *et al.*, 2008).

Bisne *et al.* (2009) studied genetic variability, heritability and genetic advance by evaluating four CMS lines, eight testers and 32 hybrids for 13 yield and yield contributing traits. The analysis of variance revealed a significant difference between all the traits among all the genotypes studied. High GCV and PCV values was reported for number of grains per panicle, harvest index, spikelet fertility per cent and 100 grain weight. High heritability along with high genetic advance was reported for total number of chaffy spikelets per panicle, harvest index, number of grains per panicle, grain yield per plant and spikelet fertility per cent which

indicated that direct selection might be effective for improvement of these characters.

Genetic analysis of yield and yield component traits were analysed by evaluating 21 upland rice genotypes grown under acid soils and reported high genetic variability among the genotypes for all the traits studied. High GCV was reported for plant height, flag leaf area, number of tillers per plant, number of ear bearing tillers, number of filled grains per panicle, root length, panicle weight, straw weight and grain yield. The broad sense heritability along with high genetic advance indicated that grain yield per plant and panicle weight were the two most important yield contributing traits and these traits could be used in selection criteria in upland rice grown under acid soils (Fukrei *et al.,* 2011).

Singh *et al.* (2011) evaluated 81 rice genotypes for 13 quantitative traits to study the genetic variability, heritability and genetic advance. The analysis of variance revealed that, there is a significant and wide variation among all genotypes for all the characters except for width of flag leaf. High GCV and PCV were exhibited for number of spikelets per panicle followed by harvest index, grain yield per plant and number of productive tillers per plant. Highest broad sense heritability was reported for biological yield per plant. High heritability along with high genetic advance was recorded for number of spikelets per panicle.

The extent of genetic variability, heritability and genetic advance among 48 hybrids and 16 parents for 34 characters revealed high GCV and PCV for total number of productive tillers per plant, harvest index and alkali spreading value in parents and characters like number of grains per panicle, total number of productive tillers per plant, alkali spreading value and amylose content in hybrids. High heritability along with high genetic advance were recorded for alkali spreading value, harvest index, number of grains per panicle, total number of productive tillers per plant, kernel length, kernel L:B ratio and grain yield in case of parents and alkali spreading value, amylose content, number of grains per panicle, total number of productive tillers per plant and harvest index in case of hybrids (Subbaiah *et al.*, 2011).

Yadav *et al.* (2011) evaluated 40 rice genotypes to study the genetic variability, heritability and genetic advance and reported high PCV and GCV values for harvest index, seed yield, number of spikelets per panicle, biological yield, plant height, flag leaf length and number of tillers per plant. High heritability along with high genetic advance was registered for harvest index, seed yield, biological yield, number of spikelets per panicle and flag leaf length.

Babu *et al.* (2012) studied genetic variability in 21 rice hybrids for yield, yield contributing, quality and nutritional characters. The analysis of variance revealed that, there was significant variation among all the hybrids for all the characters under study. The characters *viz.,* number of grains per panicle, number of chaffy grains per panicle and Fe content exhibited high GCV than PCV. This indicated less influence of environmental factors on these characters.

Subudhi *et al.* (2012) collected 55 rice germplasm accessions from the tribal dominated districts of Orissa and Cuttack and evaluated to analyse variability for 16 quantitative characters according to IRRI descriptor for rice and reported a very significant variability for the characters. In this study, leaf length varied from 30.7 cm to 73.6 cm, culm height varied from 90.5 cm to 184.4 cm, culm number varied from 8.9 to 20.0 and panicle length varied from 22.2 cm to

32.06 cm. Based on the results, the genotypes like Chhotbasmati, Lajkuri, Pimpudibas, Kanika, Jaigundi and Bishnubhog were selected as superior parents based on yield for rice breeding programmes.

Dhanwani *et al.* (2013) studied genetic variability, heritability and genetic advance for 13 quantitative and 19 quality traits in rice. The analysis of variance revealed that, there was significant and wide variability for all the traits under study. High GCV and PCV were reported for grain yield per plant, number of grains per panicle, gel consistency, alkali spreading value, water uptake. High heritability was reported for length of kernel, length of brown rice, L/B ratio of brown rice, paddy length, alkali spreading value, plant height, days to 50 per cent flowering, spikelet sterility percentage and grain yield per plant. The genetic advance was highest for

biological yield followed by grain yield per plant, alkali spreading value and gel consistency.

Sanghera *et al.* (2013) evaluated 14 red rice ecotypes from temperate region of Kashmir to study the genetic variability of grain yield and yield contributing traits. The analysis of variance revealed that, there was a significant difference among all the ecotypes for all the traits studied and revealed a wide range of variability. High GCV and PCV were reported for grain yield per plant, panicle weight and secondary branches per panicle. High heritability along with high to moderate genetic advance was reported for days to 50 per cent flowering, panicle density, number of grains per panicle and plant height, indicating the expression of these characters by additive gene action.

Soni *et al.* (2013) evaluated 45 rice lines including 30 derived hybrid lines obtained from ten tropical *Japonica*, three *Indica* and two national checks *viz.*, Pusa Basmati 1121 and Sarjoo-52 to study the genetic variability, heritability and genetic advance. The analysis of variance revealed that, there is a significant difference among all the genotypes for 18 characters studied. High PCV and GCV were recorded for flag leaf area, panicle bearing tillers per plant, grains per panicle, grain yield per plant, biological yield per plant, spikelets per panicle, panicle weight, flag leaf width and flag leaf length. The highest estimates heritability along with high genetic advance was recorded for plant height, spikelets per panicle followed by spikelets per panicle, L:B ratio, biological yield per plant, grains per panicle, days to 50 per cent flowering, flag leaf area and plant height, indicating that these traits would be reliable for the effective selection of individuals.

Alam *et al.* (2014) evaluated 76 rice genotypes with an objective to study variability, heritability and genetic advance of yield and its components. The results revealed that, there is significant and wide range of variability among all the genotypes for all the characters. For all the characters under study, PCV was higher than GCV, indicating that to some extent they all interacted with the environmental factors. High heritability was reported for all the characters ranging from 78.4 to 99.1 per cent. High heritability along with high genetic advance was recorded for

the traits like number of unfilled grains per panicle and number of grains per panicle.

Fifteen CMS and ten restorer lines were evaluated to study the genetic variability, heritability and genetic advance and reported high PCV and GCV for effective tillers per plant followed by grain yield per plant, angle of floret and plant height. High heritability along with high genetic advance were reported for traits like 1,000 grain weight, anther breadth, plant height, anther length, effective tillers per plant and angle of floret opening. Based on the results, CMS lines *viz.*, IR 69622A, APMS 6A, IR 70369A, IR 62829A and IR 68886A were identified as superior female lines with respect to floral, yield and its contributing traits, whereas, among the restorer lines NPT-13-01, NPT-10, R-710 and Sugandh-3 were identified as putative lines (Bornare *et al.*, 2014).

Venkanna *et al.* (2014) evaluated F2 population of 36 crosses to estimate the genetic variability, heritability and genetic advance. The analysis of variance revealed that, the GCV and PCV were low to moderate for all the characters studied. Moderate heritability along with moderate genetic advance were reported for grain quality characters *viz.*, kernel breadth, kernel length and kernel L:B ratio. Low heritability along with low genetic advance was reported for harvest index, which indicated that the character was highly influenced by non-additive gene action and selection for this character was ineffective.

Islam *et al.* (2015) conducted a field experiment using 23 rice genotypes with an objective to study genetic variability, heritability and genetic advance (GA) for yield and yield contributing traits in rice. The variability study revealed a significant variance for all traits studied and wide range of variation was observed among 23 rice genotypes for plant height, number of grains per panicle, days to 50 per cent flowering, 1000- grain weight, grain width and grain yield. This study concluded that, number of grains per panicle, days to 50 per cent flowering and days to maturity were the important yield traits and these could be used for selection in rice breeding programmes.

Variability study on physio-chemical and cooking quality characters among 65 rice genotypes, including landraces of Kerala were evaluated under organic management following IRRI Rice Descriptor and reported highly significant variation among the genotypes for kernel length, kernel breadth, L/B ratio of kernel, kernel elongation ratio, hulling per cent and volume expansion, alkali spreading value and sensory evaluation (Manjunatha *et al.*, 2015b).

Kumar *et al.* (2016) conducted an experiment to characterize 120 landraces of rice genotypes of north Bihar for nine morphological characteristics. The analysis of variance revealed that, there was a wide range of variation for number of primary branches, panicle length, number of grains per panicle, L/B ratio, 1000 grain weight, grain elongation and grain yield per plant. And also stated that these morphological characteristics would be helpful in formulating breeding programme of lowland rice.

Manjunatha *et al.* (2016a) studied genetic variability among 65 rice genotypes, including traditional landraces, with the aim of identifying donor parents having organic varietal characters suited for development of organic varieties through hybridization. The results revealed that, there was a significant and wide range of variability for all the characters studied. Based on the results, number of productive tillers per plant, straw yield per plant, number of grains per panicle, number of tillers per plant at harvest, sensory evaluation, volume expansion ratio, and pest and disease incidence were identified and selected as organic varietal traits.

Babu *et al.* (2017) evaluated 200 progenies of four crosses of rice to study the genetic variability, heritability and genetic advance in segregating generations for yield and bran oil content. The analysis of variance revealed significant and wide variations for 14 characters among the progenies. High heritability was reported for plant height and high genetic advance reported for number of filled grains per panicle. High heritability along with low genetic advance was reported for panicle length, number of productive tillers per plant, 1000 grain weight, kernel length and bran oil content, which indicated the predominance of nonadditive gene action in controlling the traits. Hence, improvement of these traits is not possible through

simple selection and requires heterosis breeding or recurrent selection for improvement.

Bhinda *et al.* (2017) evaluated 42 rice genotypes (*Oryza sativa* L.) with an objective to study genetic variability, heritability and genetic advance for yield, yield contributors and quality traits. The analysis of variance revealed a significant and wide differences among all the genotypes for all the 15 traits studied. Highest GCV and PCV was exhibited for alkali spreading value followed by number of grains per panicle. Highest broad sense heritability was recorded for gel-consistency followed by alkali spreading value, whereas, highest value of genetic advance was exhibited for filled grains per panicle and number of spikelets per panicle. High heritability along with high genetic advance was recorded for gel consistency, number of grains per panicle, plant height, number of spikelets per panicle and days to 50 per cent flowering.

Gour *et al.* (2017) carried out analysis of variance for seed yield and its component characters among 83 rice genotypes. The variability analysis revealed that, there was a significant and wide range of variation for all the characters studied. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were observed for grain yield per plant, biological yield per plant, panicle weight, number of grains per panicle, harvest index, 1000 grain weight and number of tillers per plant. In this study, the GCV for all the characters were lower than the PCV, which indicated the small effect of environment factors on these traits. Hence, phenotypic selection for these traits would be effective.

Genetic variability, heritability and genetic advance for nine characters among 70 genotypes of rice were studied and reported significant and wide differences among the genotypes for all the characters. High GCV and PCV was reported for all the characters except for days to maturity and days to 50 per cent flowering. High heritability along with high genetic advance was reported for days to maturity and days to 50 per cent flowering. The results confirmed the involvement of additive and non-additive type of gene action in controlling the above characters (Kalyan *et al.*, 2017b).

For assessing variability, heritability and genetic advance of ten yield and its component traits, 64 rice landraces were evaluated. Analysis of variance revealed that, there was a significant variation among the genotypes for all the characters under study. High PCV and GCV were reported for grain yield per plant, followed by number of productive tillers per plant. Lowest PCV and GCV were recorded for days to 50 per cent flowering and days to maturity. High heritability along with high genetic advance were reported for plant height, number of spikelet per panicle, test weight, spikelet fertility and grain yield per plant (Kumar *et al.*, 2017).

Limbani *et al.* (2017) evaluated 72 genotypes of upland rice to study the magnitude of genetic variability for yield and component traits. High estimates of GCV and PCV were reported for number of unfilled grains per panicle, number of non-effective tillers per plot, grain yield per plot, harvest index and number of productive tillers per plot. High heritability along with high genetic advance was recorded for number of productive tillers per plot, number of grains per panicle, harvest index and grains yield per plot, indicating that these could be used in selection criteria in the segregating generations for genetic improvement of upland rice.

Prasad *et al.* (2017) evaluated 50 *Boro* rice genotypes to estimate genetic variability, heritability and genetic advance in yield and yield contributing traits. The analysis of variance revealed that, there was significant genotypic differences among all the genotypes for all the characters. High GCV and PCV values were reported for number of unfilled grains per panicle, number of filled grains per panicle and grain yield per plant. High heritability along with high genetic advance was observed for number of tillers per plant, plant height, number of filled grains per panicle, number of productive tillers per plant, 1000 grain weight, number of unfilled grains per panicle and grain yield per plant. This indicated that, these traits were controlled by additive gene action.

An experiment was conducted to study the genetic variability of ten rice genotypes. The analysis of variance revealed that, yield and yield contributing traits showed significant differences among the genotypes for all the characters studied.

Higher values of PCV and GCV were reported for number of unfilled grains per panicle, number of grains per panicle and plant height, indicating the chances of improvement of these traits through direct selection. While, days to maturity, days to 50 per cent flowering, number of effective tillers per plant, panicle length, 1000 seed weight, fertility per cent and grain yield per panicle reported low PCV and GCV, indicating the creation of variability by hybridization followed by selection or mutation followed by selection. High heritability along with high genetic advance was reported for all the traits studied, indicating prevalence of additive gene action (Rashid *et al.,* 2017).

Srujana *et al.* (2017) evaluated 29 rice genotypes to study genetic variability, heritability and genetic advance for 13 quantitative characters. The analysis of variance revealed that, there was significant variability among the genotypes for all the characters studied. High to moderate values of GCV and PCV were reported for harvest index, number of grains per panicle, yield per hill, tillers per hill, number of spikelets per panicle, number of panicles per hill and flag leaf length. High heritability was reported for days to maturity, spikelets per panicle, grain yield per hill, biological yield, number of tillers per hill and panicles per hill. High heritability along with moderate to low genetic advance was reported for seed yield per plant, number of spikelets per panicle, number of panicles per plant, number of tillers per plant and biological yield per hill.

Sumanth *et al.* (2017) conducted an experiment to study variability, heritability and genetic advance among 23 rice genotypes for 13 quantitative characters. Analysis of variance revealed significant amount of variation among 23 genotypes for all characters studied. Highest GCV and PCV were recorded for grain yield per plant followed by number of spikelets per panicle, flag leaf length, panicles per plant and biological yield per plant. High heritability was reported for flag leaf length, plant height, spikelets per panicle, biological yield per plant and panicles per plant. High genetic advance was reported for number of plant height and number of spikelets per panicle, indicating possibilities of effective selection of these traits for the improvement of these characters.

40

Mamata *et al.* (2018) evaluated two F_2 populations of rice *viz.*, 'Rathnachoodi × BR-2655' and 'Rajamudi × BR-2655' with 500 single plants to study the genetic variability, heritability and genetic advance. High PCV and GCV values were reported for grain yield per plant and low PCV and GCV were reported for 1000 grain weight and panicle length. High heritability along with high genetic advance was reported for traits like spikelet fertility, plant height, grain yield per plant and harvest index. This indicated that, these characters were controlled by additive gene action, hence improvement of these characters could be achieved through direct selection.

Singh *et al.* (2018) evaluated 20 diverse rice genotypes to assess genetic variability, heritability and genetic advance. The results of the study revealed that, high estimates of GCV and PCV were observed for characters like number of sterile spikelets per panicle followed by grain yield per plant and per plot. High heritability along with high genetic advance was reported for the traits like grain yield per plant, panicle weight, kernel L:B ratio, kernel breadth, proline content, followed by days to first flowering, days to 50 per cent flowering, 1000 grain weight, kernel length and panicle length.

Tripathi *et al.* (2018) carried out an experiment under salt affected soil with the objective to estimate genetic variability for yield and yield contributing traits among 80 genotypes. The analysis of variance revealed that, there was a significant variation among all the genotypes for majority of yield and its contributing traits. High heritability along with high genetic advance was reported for panicle bearing tillers per plant, flag leaf area, grains per panicle, spikelets per panicle, L:B ratio, biological yield per plant and grain yield per plant, indicating the presence of additive gene action and these traits could be used to enhance the grain yield in salt affected soil.

2.3. Character association (*Correlation analysis* and *Path analysis)*

Knowledge of character association between yield and its contributing characteristics are pre-requisite and foremost endeavour to find out guidelines for

41

plant selection in any plant breeding programme. Direct and indirect effects of correlation and path coefficient analysis helps the plant selection more effective (Priya and Joel, 2009). According to Karpagam *et al.* (2014) complete knowledge on interrelationship of plant traits is important to the rice breeders for making improvement in complex characters like grain yield for which direct selection is not much effective.

Association among yield and its component characters along with the nature of direct and indirect effects of yield contributing characters on yield in aromatic rice genotypes through correlation and path coefficient analysis was studied and reported that, grain yield per plant showed significant and positive correlation with panicle length, panicle number per plant, plant height, total number of grain per panicle and total number of spikelets per panicle at both genotypic and phenotypic levels (Nayak *et al.*, 2001).

Experiment on correlation and path analysis of grain yield and sixteen yield related traits were studied using 25 rice genotypes at Chaparsar Rice Research Institute, Iran (Agahi *et al.*, 2007). The results revealed that, grain yield was positively correlated with days to heading, number of tillers per plant, number of productive tillers, days to maturity, number of grains per panicle, flag leaf length, flag leaf width and plant height. Path coefficient analysis revealed that the number of productive tillers per plant had the highest positive and direct effect on grain yield. According to the results, grain yield could be improved by selecting the parental lines for higher number of productive tillers per plant and higher number of grains per panicle, followed by flag leaf width, 100 grain weight, grain length and width.

Kole *et al.* (2008) evaluated 18 induced mutants of aromatic non-Basmati rice of West Bengal to study variability, correlation and path coefficients for 12 morphological characters and reported high genotypic and phenotypic coefficients of variation for panicle number per plant, flag leaf angle; moderate values for number of grains per panicle, harvest index, straw weight and grain yield per plant and low values for plant height, days to flower, spikelet number, panicle length,

spikelet fertility (per cent) and test weight. Correlation coefficient analysis revealed that, grain yield was positively and significantly correlated with panicle number per plant, plant height, harvest index and straw weight at both genotypic and phenotypic levels. Path coefficient analysis revealed that, panicle number per plant had the highest positive direct effect followed by plant height, grain number, test weight, straw weight and days to flower. Hence, selection for these traits would help to achieve higher grain yield.

Chandra *et al.* (2009) studied correlation and path analysis for yield and yield attributes using 49 diverse rice genotypes. Correlation analysis revealed significant and positive association of grain yield per plant with 1000-grain weight, number of productive tillers per plant, number of grains per panicle and panicle length. Path analysis revealed that days to 50 per cent flowering, number of grains per panicle, number of productive tillers per plant and 1000 grain weight had high positive and direct effect on grain yield. For most of the characters studied, genotypic correlation coefficients were greater than phenotypic correlation coefficients, indicating less influence of environmental factors on these characters.

Sabu *et al.* (2009) conducted an experiment with an objective to study genetic variability and character association for agronomically important traits in *Oryza sativa* x *O. rufipogon* crosses and reported a considerable amount of genetic variation among these crosses. Character association for yield and its contributing traits revealed that, grain yield was significantly correlated with number of panicles per plant, number of tillers per plant and number of grains per panicle.

Akhtar *et al.* (2011) conducted a study to find the association between yield and yield contributing characters using ten fine grain rice genotypes. The results revealed that, grain yield had strong correlation and direct effect with days to maturity, number of grains per panicle and 1000 grain weight. Based on the results, number of grains per panicle, 1000 grain weight and days to maturity should be considered while planning for breeding program for higher yields.

Bagheri *et al.* (2011) evaluated 26 rice genotypes to study the relationship between grain yield and yield components in rice (*Oryza sativa* L.). The results revealed that, panicle length, total number of spikelets per panicle, number of grains per panicle and number of panicles per plant showed positive and significant association with grain yield. Path analysis resulted that, panicle length had the highest positive and direct effect on grain yield. Hence, selection for these traits could result in increased the grain yield in rice.

Babu *et al.* (2012a) evaluated 21 popular hybrids of rice (*Oryza sativa* L.) with an objective to study correlation and path analysis. Character association among yield and yield contributing traits revealed a significant and positive association of grain yield per plant with number of productive tillers per plant. Path coefficient analysis revealed that, number of productive tillers per plant possessed high direct effects and positive association with yield. Selection for number of productive tillers per plant in varietal development programme could improve yield.

Kumar and Senapati (2013) studied character association for important quantitative traits in advanced lines of Samba mahsuri derivatives along with parents for 19 characters. The character association study revealed that, grain yield was significantly correlated with panicle weight, number of panicle per plant, number of secondary branches per panicle and also reported that kernel length followed by grain L/B ratio, grain breadth and fertility per cent imparted the highest positive direct effect on grain yield.

Nagaraju *et al.* (2013) studied correlation and path analysis in rice genotypes using six parents and 15 F_1 crosses for 11 traits including grain yield. The results revealed that, total number of productive tillers per plant, number of grains per panicle, kernel L/B ratio, harvest index, panicle length and milling per cent showed highly significant and positive association with grain yield per plant. In the path coefficient analysis, total number of productive tillers per plant and number of grains per panicle showed the highest positive and direct effect on grain yield. Based on the finding of this study, total number of productive tillers per plant and number

of grains per panicle could be effective in selection to improve genetic yield potential of rice.

Dhurai *et al.* (2014) studied 32 rice genotypes to understand the character association among grain yield, yield contributing traits and grain quality traits under organic fertilizer management. The results revealed that, grain yield showed significant and positive association with number of grains per panicle, harvest index, and days to maturity. Path coefficient analysis revealed that, plant height, kernel length, kernel breadth, kernel L/B ratio, kernel elongation ratio, harvest index, panicle length and days to maturity had positive and direct effect on grain yield.

The nature and extent of association among grain yield and various traits under drought stress condition was studied in 60 hybrids and 16 parental lines. The results revealed that, grain yield per plant had significant and positive association with number of productive tillers per plant, root volume and root length. Panicle length was positively correlated with biomass yield, 1000 grain weight, root volume and root length. Among root traits, dry root weight recorded high positive and significant association with root length, root and shoot ratio, root volume and root thickness (Karpagam *et al.*, 2014).

Ketan and Sarkar (2014) studied variability and character association in 26 indigenous *aman* rice cultivars. A wide range of variability was observed for 19 quantitative characters studied and five superior cultivars *viz.,* Kamini, Sabita, Sadakamisoru, Kumorogor and Narkelchari for grain yield were identified and selected for grain yield. Character association study revealed that, grain yield per plant was significantly correlated with number of secondary branches per panicle, florets number per panicle, panicle weight, fertility per cent and number of grains per panicle at genotypic and phenotypic level and also reported that, florets number per panicle had highest positive direct effect on grain yield per plant.

Character association of grain yield and its component traits was studied using 30 aerobic rice genotypes. The results revealed that, relative water content,

chlorophyll content, root length, panicle per plant, 1000 grain weight, grains per panicle, spikelet fertility and root volume showed significant and positive association with grain yield per plant. Path analysis revealed that, tillers per plant, panicles per plant, chlorophyll content, grains per panicle, root volume and 1000 grain weight were the major contributor of grain yield per plant with positive and direct effect on grain yield per plant (Kumar and Nilanjaya, 2014).

Lakshmi *et al.* (2014) evaluated 70 genetically diverse genotypes of rice to study the nature of correlation among yield and yield contributing characters. The results revealed that, the traits like plant height, number of productive tillers per plant, days to maturity and kernel length were positively and significantly associated with grain yield per plant and hence indicated the importance of these traits in deciding selection criteria in varietal improvement programmes for yield.

Twenty genotypes of rice (*Oryza sativa* L.) were evaluated for character association by correlation and path-analysis by Naseem *et al.* (2014). The results revealed that, number of productive tillers per plant, flag leaf area, number of grains per panicle, number of spikelets per panicle and 1000 grain weight had a high positive significant genotypic correlation with grain yield per plant. The path analysis revealed that, number of spikelets per panicle, number of productive tillers per plant, days to maturity and number of grains per panicle had positive direct effect on grain yield per plant. Based on these results, characters like number of spikelets per panicle and number of productive tillers per plant could be used as direct selection criteria for higher grain yield.

Ranawake and Amarasinghe (2014) evaluated 100 rice cultivars to study the charter association between yield and yield parameters by Pearson's correlation coefficient. The results revealed that, grain yield was significantly and highly correlated with number of grains per panicle, number of spikelets per panicle, panicle weight, number of fertile tillers per plant, filled grain percentage, number of tillers per plant, 100 grain weight and plant height. Based on the results, the above traits could be considered as selection criteria to achieve the higher grain yield in rice.

Allam *et al.* (2015) evaluated 23 genotypes of Basmati rice to study correlation and path analysis among grain yield, yield contributing traits and grain quality traits. The results revealed that, days to maturity, effective panicles, spikelets per panicle and amylose content had highly significant and positive association with grain yield per plant. L/B of kernel ratio showed positive and significant association with kernel length after cooking and showed negative association with kernel elongation ratio. Based on the results, the traits like effective panicles, days to maturity, spikelet fertility, spikelets per panicle, kernel length, test weight, kernel L/B ratio, kernel length after cooking, kernel elongation ratio could be used as selection criteria to develop high yielding and quality varieties in Basmati rice types.

Chandra *et al.* (2015) evaluated 25 genotypes of rice under aerobic and normal conditions to study the correlation and path analysis based on 15 morphophysiological traits. Correlation study revealed that, plant height, panicle length, number of tillers per plant, number of spikelets per panicle, relative water content, maximum root length, flag leaf area, harvest index, chlorophyll content and 1000 grain weight exhibited significant and positive association with grain yield per plot. Path analysis revealed that, traits like days to fifty per cent flowering, number of spikelets per panicle, number of tillers per plant, relative water content in flag leaf and maximum root length had highest positive and direct effect on grain yield. Hence, these important traits should be considered to achieve higher yield in rice under aerobic condition.

Character association by correlation and path analysis was made to identify organic varietal traits among 65 rice genotypes, including landraces of Kerala. The association study among yield and yield contributing characters revealed that, number of productive tillers per plant, number of tillers per plant, number of grains per panicle, number of spikelets per panicle, straw yield per plant and seed setting percentage resulted significant and positive correlation and also reported highest positive direct effect of these characters on grain yield (Manjunatha *et al.*, 2015).

A character association study was conducted with 58 rice germplasm, including 13 hybrids, 20 *indica* genotypes, 25 tropical *japonica* genotypes for eleven characters including grain yield. The results revealed that, number of panicles per plant, panicle weight, panicle length, total dry matter production, number of spikelets per panicle, number of grains per panicle, seed setting percentage and harvest index showed significant and positive association with grain yield per plant. Path-coefficient analysis revealed that, panicle weight, seed setting percentage, total dry matter at flowering, total dry matter at harvesting stage, harvest index and number of grains per panicle, recorded positive and direct effect on grain yield. Based on the results of the study, the above parameters could be used in effective selection criteria for yield improvement in rice breeding programmes (Guru *et al.*, 2016).

Tejaswini *et al.* (2016) evaluated 42 F_5 segregation lines of rice along with five parents to establish the nature of association between yield and yield components. The correlation and path coefficient analysis revealed that, panicle length had positive significant correlation and positive direct effect with grain yield per plant and hence direct selection for panicle length would be effective for improving yield.

To determine the degree and nature of association between yield and yield contributing traits in aerobic rice, 22 aerobic rice genotypes were evaluated. The results revealed that, plant height, fertility percentage, number of grains per panicle and 100 grain weight showed significant and positive association with grain yield per plant. The path analysis resulted that, fertility percentage followed by 100 grain weight exhibited highest indirect effect on grain yield. Thus, these traits could be considered as selection criteria for achieving higher yield under aerobic conditions (Behera *et al.*, 2017).

Gour *et al.* (2017) studied correlations and path coefficients from data collected from 83 rice genotypes. The results from correlation study revealed that, panicle weight, biological yield per plant, number of tillers per plant and harvest index showed positive association with grain yield per plant. The biological yield

per plant had maximum direct effect on grain yield per plant followed by panicle length, harvest index, filled grains per panicle, panicle length and days to maturity. Based on the observed results, the above traits could be considered as key traits for achieving higher yield in rice.

Fifty rice genotypes were evaluated to study path coefficient analysis with direct and indirect effect for nine quantitative traits. The results revealed that, number of grains per panicle had highest positive and direct effect on grain yield followed by 1000 grain weight, number of productive tillers per plant, number of tillers per plant, plant height and days to 50 per cent flowering. Based on the results, a plant with medium height, higher number of filled grains per panicle, sturdy culm with increased panicle length and more number of productive tillers per plant would be more desirable for selection to improve higher yield (Kalyan *et al.*, 2017c).

Sixty four rice landraces were evaluated with an objective to study character association of ten yield and its component traits under controlled and drought conditions. The analysis of correlation revealed that, grain yield per plant had significant and positive association with number of tillers per plant, test weight, number of spikelets per panicle, number of productive tillers per plant and spikelet fertility both under control and low-moisture stress conditions at both phenotypic and genotypic level. Hence, selection for these characters could achieve high grain yield under drought conditions (Kumar *et al.*, 2017).

Limbani *et al.* (2017) evaluated 72 genotypes of upland rice to study the character association for yield and component traits. The results showed that, grain yield per plant showed significant and positive association with number of effective tillers per plot, harvest index, number of filled grains per panicle, milling percentage and plant height. Highly significant but negative correlation was reported with days to 50 per cent flowering and number of non-effective tillers per plot at genotypic and phenotypic levels. Hence, priority has to be given to these traits in selection process to achieve higher yields.

Madhukar *et al.* (2017) studied association by correlation and path analysis of yield and its components in aerobic rice involving 47 genotypes (32 hybrids, 12 parents and 3 check varieties). The analysis for both character association and path analysis revealed that, among several yield traits in rice, number of grains per panicle played a key role for higher yields under aerobic situation. The significant correlation was noticed between panicle length and grains per panicle and also between panicle length and plant height. Based on the results, medium stature plant with sturdy culms, long panicles and more number of grains per panicle would be highly advantageous for higher yield in aerobic rice.

Manjunatha *et al.* (2017) studied character association and path analysis in 65 rice genotypes under organic management. The results revealed that, among the correlation of 13 growth characteristics with grain yield per plant, three characters *viz.*, number of tillers per plant at 30DAT, chlorophyll content of third leaf and flag leaf resulted higher genotypic correlation coefficients than phenotypic correlation coefficients, indicating the less influence of environmental factors on these characters. However, number of tillers per plant at 60DAT, 90DAT and at harvest resulted in high phenotypic correlation coefficients than genotypic correlation coefficients, which indicated the influence of environmental factors on these characters. Path coefficient study revealed that, number of tillers at harvest and 60DAT had both positive and direct association with grain yield. Hence, selection for these characters could bring improvement in yield especially for organic rice.

Rathod *et al.* (2017) studied correlation and path analysis using 56 high Fe and Zn genotypes of rice. Character association among yield and other traits revealed that, number of productive tillers per plant, number of grains per panicle, panicle length and grain Fe concentration showed significant and positive association with grain yield per plant. Path coefficient analysis revealed that, the traits like, plant height, number of productive tillers per plant, 1000 grains weight, numbers of grains per panicle, days to 50 per cent flowering, grain Fe concentration and Zn concentration, showed positive and direct effect on grain yield per plant.

Hence, these characters could be considered as important yield contributors and selection for these traits could improve yield.

Yadav and Suresh (2018) evaluated 16 rice genotypes procured from IRRI, Phillipines, to determine the relationship between yield and yield contributing components. The results showed that, harvest index, biological yield per plant, flag leaf width, tillers per plant, number of panicles per plant and number of spikelets per panicle correlated positively and significantly with grain yield. Path coefficient analysis revealed that, harvest index reported to have highest positive direct effect (1.02) on grain yield. Therefore, these traits could be used in the selection criteria for improvement of yield.

2.4. Genetic divergence (*Mehalanobis D^2 Statistics*)

Study of genetic diversity between different genotypes in the crop of interest is the pre-requisite and foremost process in any plant breeding programme for efficient choice of parents for hybridization (Rai *et al.*, 2014). The D^2 statistical technique developed by Mahalanobis (1928 and 1936) is a powerful tool for the assessment of degree of divergence between biological populations at genetic level. Several researchers studied genetic diversity previously.

Chuahan and Chauhan (1994) evaluated 44 breeding lines of rainfed upland rice to study the genetic divergence among them by Mahalanobis D^2 analysis. Based on D^2 analysis all the 44 breeding lines were grouped into twelve clusters. Out of eleven characters studied, four characters *viz.,* 1000 grain weight followed by days to 50 per cent flowering, weight of panicles and number of spikelets per panicle were reported to have maximum contribution towards genetic diversity.

Bose and Pradhan (2005) evaluated 35 deep water rice genotypes to assess the nature and the magnitude of genetic divergence among them using Mahalonobis D^2 statistics. The D^2 analysis grouped all the 35 deep water rice genotypes into 10 clusters and revealed a significant genetic divergence among the studied genotypes. Among the 10 clusters formed, cluster IV reported maximum intra cluster divergence. Inter-cluster distances was maximum between clusters IX and X. Days

to 50 per cent flowering, yield per plant and plant height were reported as major contributors to genetic diversity.

Fifty aromatic rice genotypes including improved aromatic varieties *viz.*, Taraori Basmati, Pusa Basmati, Dubraj, Indira 9 and Madhuri 11 were evaluated to study the nature and magnitude of genetic diversity by Mahalanobis D^2 analysis. In the study, 50 aromatic genotypes were grouped under seven clusters, indicating a significant amount of genetic diversity among the genotypes studied. Out of seven clusters formed, highest inter-cluster distance was recorded between cluster III and cluster IV. While, the least distance was reported between cluster I and cluster V. Based on the results, 12 genotypes *viz.*, Jaigundhi, Taraori Basmati, Samunderphool, Krishnabhog, AmtmaShital, Sansari, Ghodapunchi, Bhataphool, Dumerphool, Tulsimala, Elaychi and Loktimachii were identified as potential donors in future breeding programmes to develop scented rice variety (Naik *et al.*, 2006).

Genetic divergence analysis was done among 32 traditional *Aman* rice genotypes through Mahalanobis D^2 statistic and principal component analysis (PCA). As per the diversity analysis, all the 32 traditional *Aman* rice genotypes were grouped into five distinct clusters. Out of five clusters formed, the highest number of genotypes were reported in cluster II. Days to flowering, plant height, tillers per hill, days to maturity, primary branches per panicle, panicles per hill, 1000 grain weight and filled grains per plant were reported to be the maximum contributors towards genetic diversity. Hatisail, Doirgura, BRRI dhan34 and BRRI dhan38 were selected as promising parents for future breeding programmes (Nath *et al.*, 2008).

To study the genetic divergence among aromatic rice genotypes for grain quality and nutritional characters, 40 aromatic rice genotypes were evaluated. Based on D^2 analysis all the 40 aromatic genotypes were grouped into six clusters. Out of six clusters formed, cluster I reported maximum number of genotypes. Kernel length, kernel weight and L/B ratio reported to have highest contribution to the total diversity in cluster I. Thus, these varieties could be used in breeding programme for improvement of germplasms in cluster I (Shahidullah *et al.*, 2009).

Banumathy *et al.* (2010) evaluated fifty three rice genotypes for eight yield and yield attributing characters using D^2 analysis to identify diverse genotypes for hybridization. The D^2 analysis grouped the 53 genotypes into 11 clusters. Out of 11 clusters, more number of genotypes were reported in cluster XI

and I. Among the eight yield and yield contributing traits studied, nearly 86.62 per cent contribution was reported from grain yield followed by days to 50 per cent flowering, total grains per panicle and plant height. Hence, these traits had to be given importance during rice breeding programmes.

Hosan *et al.* (2010) collected and evaluated twenty rice landraces to study the nature and magnitude of genetic diversity. The results revealed that, the 20 rice genotypes were grouped into five clusters based on 12 characters studied. In this study, inter-cluster distances were reported higher than the intra cluster distances, which indicated wider genetic diversity among the genotypes studied. Number of grains per panicle, number of panicles per plant, biomass index and grain yield per plant were reported to have highest contribution towards total genetic diversity.

Genetic diversity was studied among 29 rice landraces for eight quantitative traits using Mahalanobis D^2 statistics. Based on the resulted genetic distances, the 29 landraces were grouped into five clusters. Two characters *viz.,* grain yield per plant and days to first flowering were reported to be maximum contributors towards genetic diversity. The highest inter-cluster distance was reported between cluster IV and cluster V. Based on the results, the genotypes Vattan and Vellai Chitraikar and Thulasi Manjari were selected as potential donors for future breeding programmes (Rajesh *et al.*, 2010).

Genetic divergence among 38 traditional local rice genotypes were studied at hilly areas, through Mahalanobis D^2 analysis for yield and yield contributing traits. The D^2 analysis grouped all 38 traditional local rice genotypes into five clusters. The inter-cluster distances were reported to be higher than intra-cluster distances, indicating wider genetic diversity among the clusters. Out of five clusters formed, cluster V reported to have highest number of genotypes. The characters

viz., flag leaf width, flag leaf length, days to maturity, days to 50 per cent flowering, grain length, unfilled grain per panicle and grain L:B ratio were reported to be maximum contributors towards the genetic diversity (Siddique *et al.*, 2011).

Ali *et al.* (2012) studied genetic diversity among 66 local aromatic rice genotypes to identify the distantly related parental genotypes through Mahalanobis D^2 statistics. Based on D^2 analysis all the 66 genotypes were grouped into ten clusters. Out of ten clusters formed, clusters III and VII had maximum number of genotypes. Grain yield per plant had highest contribution to total diversity followed by days to maturity, grain breadth and others. Highest inter cluster distance was between clusters I and V. Among the 66 local aromatic rice genotypes studied, ten genotypes *viz.,* Sakkorkhora, Oval Tapl, Dubsail, Black, Badshahbhog-8, Rajbhog-2, Elai, Guamori, BRRI dhan-38 and Kataribhog were selected for different characters from different clusters for future breeding program.

Biswas *et al.* (2012) assessed genetic divergence among 30 rice (*Oryza sativa* L.) cultivars for 12 agro-morphological characters through principal component analysis and Mahalonobis D^2 statistics and all these cultivars were grouped into seven clusters. Highest inter-cluster distance was reported between clusters III with Chiconsarna, Malshira, Radhunipagal, Lalchicon, Lalfota, Nazirshail and Sumonsarna and clusters VI with BR34 and Darkashail and hence parents were selected from these clusters to obtain desirable segregants in the F_2 generation. Out of 12 agro-morphological characters studied, number of spikelets per panicle reported as maximum contributors on the total genetic diversity.

Chakravorty and Ghosh (2012a) studied 51 rice landraces for 18 morphological traits to assess the genetic divergence following Mahalanobis D^2 statistics. The D^2 analysis revealed that, the 51 rice genotypes were grouped into 11 clusters. Out of 11 clusters formed, cluster II reported to have more number of genotypes. Among the 18 morphological traits studied, maximum contribution towards genetic diversity was reported from the characters like culm diameter, culm length and grain length. These traits could be given importance during hybridization program.

Ovung *et al.* (2012) assessed the nature and magnitude of genetic diversity among 70 rice genotypes for 13 quantitative characters using Mahalanobis D^2 statistics. The D^2 analysis revealed significant amount of diversity among the genotypes studied and these were grouped into nine clusters. Out of nine clusters formed, cluster I and cluster III included maximum number of genotypes (12 each). Maximum inter cluster distance was reported between cluster VI and VII, suggesting that the genotypes reported in these clusters might be used for exploitation of hybrid vigour in breeding programmes. Out of 13 quantitative characters studied, plant height, spikelets per panicle and biological yield were reported as major contributors towards genetic diversity.

Genetic diversity among 96 rice genotypes was assessed by Mahalanobis D^2 statistics which grouped all these genotypes into nine distinct clusters. Among the nine clusters formed, cluster VII reported to have maximum genotypes (20) and cluster V had minimum genotypes (6). The highest inter cluster distance was reported between cluster IV and VIII, where the genotypes reported in these clusters were highly divergent from each other. Maximum intra-cluster distance was reported in cluster III followed by cluster V, cluster I and cluster II, indicating wide genetic diversity among the constituent genotypes (Ekka *et al.*, 2013).

Genetic divergence among 40 traditional *Boro* rice genotypes was assessed through Mahalanobis D^2 statistics for yield and yield contributing traits.

The diversity analysis grouped all the 40 traditional genotypes into five clusters. The inter-cluster distances were reported higher than intra-cluster distances, indicating wider genetic diversity among the clusters. Based on the results, number panicle per hill was reported to be the maximum contributor towards genetic diversity (Siddique *et al.*, 2013).

Haque *et al.* (2014) evaluated 76 rice genotypes to assess the genetic diversity using Mahalanobis D^2 analysis. The D^2 analysis revealed the grouping of 76 genotypes into eight clusters. Out of eight distinct clusters, cluster I was reported to have maximum number of genotypes. Among the 11 quantitative traits studied,

plot yield reported as maximum contributor (56.49 per cent), followed by 1000 grain weight (22.28 per cent). Six traits *viz.,* sterility per cent, harvest index, kernel length, plot yield, 1000 grain weight and kernel breadth contributed nearly 88.78 per cent towards total divergence. Hence, these characters could be used in hybridization programme to develop drought tolerant varieties.

Rai *et al.* (2014) evaluated 40 rice genotypes to identify diverse genotypes using Mahalanobis D^2 statistics. The D^2 analysis revealed a significant amount of diversity among the genotypes and all the 40 rice genotypes were grouped into seven clusters. Out of seven clusters formed, cluster III reported for more number of genotypes. The highest inter cluster distance was observed between cluster IV and VII, hence the genotypes in these clusters could be utilized for exploitation of hybrid vigour in further hybridization programmes. Out of thirteen traits studied, number of spikelets per panicle followed by grain yield, plant height and flag leaf length were reported as maximum contributors towards genetic diversity. Hence, these traits should be given importance during breeding programme.

Genetic diversity among 18 rice varieties cultivated in Bihar, India was assessed by Shamim and Sharma (2014), based on 14 qualitative traits. The results revealed that, all the 18 varieties were grouped into seven distinct clusters, indicating sufficient amount of variability among the studied genotypes. Out of 18 rice varieties, Richharia with Rajshree and Gautam with Rajendra Mahsuri were identified as suitable parents for quality improvement.

Devi *et al.* (2015) studied genetic divergence for grain quality among 92 rice cultivars using Mahalanobis D^2 statistics. The D^2 analysis grouped 92 rice cultivars into 10 clusters. Out of 10 clusters formed, clusters VII and IX were reported as largest clusters consisting of 16 genotypes each. Cluster V was reported as smallest with only a single genotype. Volume expansion ratio, kernel breadth and elongation ratio failed to contribute to genetic diversity. Whereas, gel consistency, amylose content, head rice recovery and 1000 grain weight were reported to be the highest contributing traits towards genetic diversity. This indicated that, these traits should be selected for breeding programme aiming for grain quality.

Genetic diversity among 40 elite rice (*Oryza sativa* L.) genotypes was assessed for 13 quantitative characters using Mahalanobis D^2 statistics, to select divergent genotypes. The D^2 analysis revealed that, the 40 rice genotypes were grouped into seven clusters. Out of seven clusters, maximum number of genotypes were reported in cluster IV. Out of 13 quantitative characters studied, flag leaf length, plant height, spikelets per panicle, days to 50 per cent flowering, test weight and harvest index contributed maximum towards genetic diversity. Hence these characters should be considered in selection criteria for further crop improvement programme (Kumar *et al.*, 2015).

Rajkumar *et al.* (2015) studied genetic divergence among 118 rice genotypes for 11 quantitative characters using Mahalanobis D^2 statistics. The D^2 analysis revealed a significant amount of diversity among genotypes and these genotypes were grouped into twelve clusters. Cluster III was reported to have highest number of genotypes. The characters like number of filled grains per panicle, yield per plot and plant height were reported as major contributors towards genetic diversity.

Chandramohan *et al.* (2016) evaluated 44 rice genotypes to study the genetic divergence among them by Mahalanobis D^2 analysis. The D^2 analysis grouped the 44 rice genotypes into 11 clusters. Out of 11 clusters formed, Cluster III reported for highest number of genotypes followed by clusters II, I, IV, VIII and X, while the remaining clusters were comprised of single genotype each. Two characters *viz.*, 1000 grain weight and days to 50 per cent flowering reported to have highest contribution towards total divergence. Hence, these traits are to be given due importance in crop improvement programmes.

Garg *et al.* (2016) studied genetic diversity among 33 rice genotypes for 17 different quantitative and qualitative traits under stress and non-stress condition using Mahalanobis D^2 statistics. Based on the D^2 values, all the 33 rice genotypes were grouped into six clusters. The maximum inter cluster distance was reported between cluster III and VI, hence the genotypes in these clusters might be utilized to get high yielding recombinants if the crosses are made among the genotypes. Among 17 characters studied, chlorophyll content reported as maximum contributor

57

towards genetic diversity followed by plant height, number of grains per panicle, 1000 grain weight and harvest index under stress conditions.

Panigrah *et al.* (2016) evaluated 100 local rice landraces from Bastar plateau of Chhattisgarh state to study genetic diversity among the landraces on the basis of 19 quantitative characters. The analysis grouped the 100 genotypes into ten distinct clusters. Out of ten distinct clusters formed, cluster III comprised of maximum genotypes (46 no's) and cluster I, II and X included only one genotype each. Grain yield per plant showed highest contribution to the total divergence, followed by number of grains per panicle, harvest index, number of grains per panicle and lowest contribution was reported for spikelet fertility per cent.

Genetic divergence among 46 landraces of *Aus* rice was assessed through Mahalanobis D^2 statistics for yield and yield contributing characters. The D^2 analysis grouped the 46 landraces into seven clusters and revealed high degree of diversity among *Aus* landraces. Intra-cluster distances was reported to be low for all the clusters ranging from 0.64 (cluster IV) to 1.17 (cluster I). The highest intercluster distance was 11.45 (between III and V) and the lowest inter-cluster was 4.36 (between VI and VII). Based on the results from genetic distance, the genotypes Rang mahal, Begun bitchi, Katar, Laxmijhota, Manikmendal, Chiknal and Baismugur were selected as donors for further breeding programs (Siddique *et al.*, 2016).

Babu and Sreelakshmi (2017) evaluated fifty rice genotypes to study the genetic divergence among them using D^2 statistics. Based on D^2 analysis all the 50 genotypes were grouped into six clusters. Out of six clusters formed, cluster I reported to have maximum number of genotypes followed by cluster II. Three characters *viz.*, gelatinization temperature, days to 50 per cent flowering and water uptake together contributed nearly 72 per cent to the total diversity.

Assessment of diversity among 53 aromatic rice genotypes revealed significant amount of genetic diversity. Diversity analysis, grouped all the 53 aromatic rice genotypes into six clusters with cluster I with highest number of

genotypes. The inter-cluster distances were reported higher than intra-cluster distances, indicating wider genetic diversity among the clusters. Out of many traits studied, days to 50 per cent flowering, grain yield per hill and seed length reported as maximum contributors towards genetic diversity (Islam *et al.,* 2017).

Kumar *et al.* (2017) assessed the nature and magnitude of genetic diversity among 25 rice germplasm lines using Mahalanobis D^2 statistics. Based on D^2 values, all the 25 germplasm lines were grouped into six clusters. Out of six clusters formed, cluster IV reported to have more number of genotypes followed by cluster V and cluster VI. Inter-cluster distances were reported higher than intra-cluster distances indicating the wide diversity among the germplasm under study. Number of productive tillers per plant reported as maximum contributor towards genetic diversity followed by days to 50 per cent flowering and grain yield.

Burman *et al.* (2018) studied genetic diversity among 100 rice genotypes for 12 quantitative traits and all these rice genotypes were grouped into eight distinctive clusters, revealing the significant amount of genetic divergence for traits among genotypes. Out of eight clusters formed, cluster V included maximum genotypes, followed by cluster I and cluster III. Based on the results, two genotypes Banspor and Chingi were identified as potential donors for future breeding programmes to achieve quality and higher yields.

Mishra *et al.* (2018) evaluated 36 advance rice lines to study genetic diversity through Mahalanobis D^2 statistics, for 21 traits including yield and quality traits. Based on the D^2 statistics analysis, the 36 genotypes were grouped into six distinct clusters. Inter-cluster distances were reported higher than the intra cluster distances, indicating the wider genetic diversity among the genotypes studied. Out of 21 traits studied, kernel elongation ratio followed by biological yield per plant, amylase content and 1000 grain weight were reported as maximum contributors towards genetic diversity. Hence, these characters should be given importance during hybridization program.

Srinivas *et al.* (2018) evaluated 76 rice genotypes to assess the genetic divergence through Mahalanobis D^2 analysis. The D^2 analysis grouped all the 76 rice genotypes into nine clusters. The maximum inter cluster distance was reported between cluster VI and cluster IX and lowest inter cluster distance between cluster I and cluster II. Out of ten characters studied, days to 50 per cent flowering was reported to be the maximum contributor for genetic diversity followed by number of spikelets per panicle and filled grains per panicle.

2.5. Molecular characterization

Characterization based on morphological traits, including both qualitative and quantitative traits, isozymes and storage proteins were employed for genetic diversity analysis. However, morphological characterization alone is less reliable due to stage specific expression of characters and influence of environment over genotypes. Moreover, morphological differences are usually determined by a few genes and may not represent entire genome for genetic divergence analysis (Singh *et al.,* 1999; Guedira *et al.,* 2000). Molecular markers offer a number of advantages over morphological markers in varietal identification and demonstrating distinctness among the germplasm at early stages of growth. Many protocols of DNA analysis are available worldwide to solve the problem of characterization and variety identification. Bostein *et al. (*1980) and Tanksley *et al. (*1989) reported that, marker differences in DNA sequence between individuals generally detect more polymorphism than morphological markers. Hence utilization of molecular markers for varietal identification directly overcome the limitations associated with morphological identification methods. Hence, molecular marker technology is supposed to be the most effective genetic tool for the analysis of genetic diversity.

Molecular polymorphism technique is the best way to study genetic diversity, varietal identification and utilization of plant genetic resources (Gautheir *et al.,* 2002; Ghebru *et al.,* 2002). Molecular analysis is the effective tool for effective selection of desirable characters since they are purely based on plant genotype and are independent of environmental fluctuations. In contrast to morphological characters, molecular markers can reveal abundant difference among

genotypes at DNA level, providing a more direct, reliable and efficient tool for varietal characterization (Prabakaran *et al.*, 2010).

Terzi *et al.* (2005) reported various DNA based methods for identification and quantification of mixtures of small grain cereals by recently developed molecular markers for varietal fingerprinting. Varietal identification using molecular markers is the current tool being investigated in almost every varietal development programmes using different molecular markers *viz.,* RAPD, RFLP, AFLP, SSR, ISSR etc.

Among various PCR based molecular markers, SSR markers are more popular in rice because they are highly polymorphic, mono locus, co-dominant, cost effective and can be easily analysed (Chambers and Avoy, 2000) and microsatellite markers cover the whole genome of rice with at least one microsatellite for every 16 to 20 cm (Chen *et al.*, 1997). In rice, microsatellites could be utilized for gene tagging and marker assisted selection (McCouch *et al.,* 1997) and are highly polymorphic between the rice varieties (Akagi *et al.*, 1997; Chen *et al.*, 1997; Yang *et al.*, 1994) and within the rice varieties (Olufowote *et al.*, 1997). Hence, out of several DNA markers available, microsatellites or SSRs were considered as most ideal genetic markers in rice.

Molecular marker technology is a powerful tool for determining genetic variation in rice varieties (Xu *et al.*, 1974). Molecular markers of DNA base were ubiquitous, repeatable, stable and highly reliable (Virk *et al.*, 2000; Song *et al.,* 2003). Among the several DNA markers available, microsatellite or simple sequence repeat (SSR) markers were considered as most suitable due to their multi-allelic nature, codominant inheritance, high reproducibility, abundance and extensive genome coverage (Gracia *et al.*, 2004). A large number of SSR Rice Markers (RM) had been developed and mapped in rice (Temnykh *et al.*, 2000; McCouch *et al.*, 2002). Hence an ideal set of SSR markers covering whole genome will facilitate an unbiased assessment of genetic diversity which in turn will provide a robust, unambiguous molecular description of rice varieties.

SSR's or microsatellites are useful in distinguishing indigenous non-Basmati aromatic rice genotypes from Basmati aromatic rice and this could help in genetic conservation, management and support for intellectual property protection (Joshi and Behera, 2006).

Garland *et al.* (1999) conducted an experiment for microsatellite screening of 43 cultivars of rice including 27 Australian breeding lines and Australian commercial cultivars. The results revealed that Polymorphism-InformationContent (PIC) values ranged from 0.62 to 0.92 and concluded that the SSR or microsatellite markers were highly helpful in the identification of varieties and assessment of genetic relationship.

Jain *et al.* (2004) studied genetic relationships in aromatic and quality rice germplasm of India, using 30 fluorescently labelled rice microsatellite markers. Sixty nine rice genotypes, including 52 Basmati types and other scented/quality rice varieties from different parts of India where evaluated. A total of 235 alleles were detected for 30 simple sequence repeat (SSR) loci and out of which, 62 (26.4 per cent) alleles were present only in Basmati and non-Basmathi germplasm accessions. The results concluded that, RM252 was a powerful marker to distinguish among closely related Basmati types.

Microsatellite (SSR) marker analysis was carried out to study the diversity among 24 rice genotypes, including three traditional Basmati types, nine crossbred Basmati types, one local aromatic selection, eight *indica* and three *japonica* rice genotypes, using 50 SSR primer pairs. A total of 229 alleles were detected for 50 SSR loci and the size difference between the smallest and largest allele varied from 1 (RM333) to 82 (RM206). PIC values ranged from 0.0 (RM167) to 0.78 (RM170), with an average of 0.62 per marker. Based on the results, seven SSR markers (RM1, RM38, RM21, RM210, RM170, RM229 and RM226) were reported to distinguish the Basmati rice varieties from non-Basmati rice varieties and eight SSR markers (RM207, RM215, RM222, RM44, RM2, RM22, RM60 and RM3) were reported to distinguish the closely related traditional Basmati rice varieties, such as Taraori Basmati from Basmati 370 (Siwach *et al.*, 2004).

Hossain *et al.* (2007) conducted a study for characterization and discrimination of 21 aromatic rice genotypes, including 18 genotypes of aromatic landraces and three basmati types using 30 microsatellite molecular markers and reported that SSR (RM) markers like RM243, RM180, RM207, RM163, RM510, RM256, RM566, RM590, RM224, and RM338 were highly suitable for assessment of genetic diversity in aromatic rice landraces.

Pervaiz *et al.* (2009) used 32 simple sequence repeat (SSR) markers to determine the genetic diversity of 35 Asian rice cultivars of rice, including 19 aromatic, 13 non-aromatic and 3 *japonica* type cultivars. A total of 144 alleles were detected at the 32 SSR loci, of which 141 (98 per cent) were polymorphic and showed a clear division of cultivars into aromatic and non-aromatic groups. The study revealed that, microsatellite analysis could be efficiently utilized to study the diversity and differentiation of aromatic and non-aromatic rice genotypes. In addition, molecular characterization and differentiation of Basmati rices could be helpful to maintain high quality rice varieties such as basmati and aromatic varieties, to benefit both farmers and consumers communities.

Rabbani *et al.* (2010) conducted a study to evaluate genetic variability and diversity among 41 cultivars, including traditional and improved rice cultivars of Pakistan and to study the variation between Basmati and non-Basmati types using 30 microsatellite markers (SSR) distributed over the whole genome of rice. A total of 104 alleles were detected by 30 markers and all of them (100 per cent) were polymorphic. The PIC values varied from 0.259 to 0.782 with an average of 0.571 and reported a wide range of genetic diversity between Basmati and non-Basmati types. These results suggested that SSR markers could be utilized efficiently for diversity analysis, and differentiation of Basmati from non-Basmati rice cultivars. Marker-based identification of traditional basmati rice will be more helpful in maintaining the integrity of this good quality product and it will benefit to both farmers and consumers.

Ashfaq and Khan (2012) studied genetic diversity of 20 rice genotypes, including 15 *indica* Basmati advanced lines and five Basmati improved varieties by

28 SSR markers, covering all the 12 chromosomes of rice genomes. The results showed that, the dendrogram based on cluster analysis using SSR polymorphism grouped the 20 genotypes of rice into five clusters based on their genetic similarity.

Behera *et al.* (2012) studied 38 high yielding rice varieties, released by CRRI (Central Rice Research Institute), Cuttack, suitable for different ecosystems, for assessment of fingerprinting and genetic diversity, using a set of 31 rice microsatellite markers (SSR). A total of 136 alleles were amplified, of which 135 were polymorphic. The PIC value ranged from 0 to 0.976. This study indicated the high level of genetic diversity among high yielding rice varieties.

The diversity and relationship among 12 aromatic rice cultivars were determined using 24 microsatellite markers. Out of 24 SSR markers studied, 10 were polymorphic for different chromosome numbers. The PIC values ranged from 0.239 to 0.765 with an average of 0.508. The RM180 recorded the highest PIC value (0.765), followed by RM207 (0.746), RM224 (0.680), RM163 (0.593), and RM566 (0.505). Considering the high PIC value, RM180 was reported to be the best marker, followed by RM207, RM224, RM163 and RM566 for characterizing aromatic rice genotypes (Hossain *et al.*, 2012).

Kumar *et al.* (2012) studied genetic diversity of 64 rice genotypes with 20 SSR markers on chromosome number 7-12 and the results revealed that out of 20 markers studied, eight markers showed distinct polymorphism. Average number of alleles per locus was 8.49, indicating a greater magnitude of diversity among the genotypes under this investigation. The cluster analysis showed higher level of genetic variation among the genotypes. Similarly PIC values ranged from 0.40

to 0.96. The dendrogram revealed eight major distinct clusters. The information obtained from DNA fingerprinting studies helped to distinctly identify and characterize the various genotypes.

Myint *et al.* (2012) assessed the genetic diversity of 147 rice varieties, including aromatic and non-aromatic varieties originating from different geographical regions in Myanmar, using 19 SSR Rice Markers and differentiated

aromatic from non-aromatic varieties and also Myanmar aromatic rice varieties from non-Myanmar varieties. Among the Myanmar accessions, a very high proportion (44 per cent) of aromatic varieties was reported.

Rahman *et al.* (2012) studied genetic diversity and molecular characterization among elite rice genotypes, including aromatic rice genotypes of Bangladesh using 34 microsatellite markers. The number of alleles per locus resulted from 2 to 11, with an average of 4.18 alleles across 34 loci and the PIC values ranged from 0.157 to 0.838, with an average of 0.488, which indicated the wide variation among the studied varieties. Based on high PIC values generated, RM401 was reported to be the best marker for identification and diversity estimation of rice genotypes, followed by RM3428, RM566, RM8094 and RM463 markers.

Sajib *et al.* (2012) used 12 elite aromatic rice cultivars (*viz.*, Jamaisohagi, Sugandha, Darsail, Chinikani, Bhogganijia, Dolargura, Depa, Patnai-23, Opchaya, Holdijorun, Jingasail and Basmati PNR 346) in Bangladesh for their characterization and discrimination by using 24 SSR markers. Out of 24 markers studied, nine microsatellite markers showed polymorphism and number of alleles per locus ranged from 2 alleles (RM277, RM510 and RM244) to 6 alleles (RM 163). The PIC value ranged from 0.14 (RM510) to 0.71 (RM163) and these values indicated the capability of these primers in distinguishing genotypes. Based on the results, RM163, RM247 and RM493 were reported as best markers for the identification of aromatic genotypes.

The microsatellite (SSR) markers were used to determine diversity and relationship among 48 traditional indigenous aromatic rice genotypes of Eastern part of India, using 30 SSR markers. Out of 30 primers studied, 12 primers showed polymorphism among 48 aromatic rice genotypes. The results indicated wide range of genetic variation in the germplasm. A total of 28 different reproducible bands were amplified, which were ranging in size from 100bp to 220bp. Out of the total 28 bands generated, RM44 and RM154 were monomorphic, whereas 25 SSR bands were polymorphic (Meti *et al.*, 2013).

Shah *et al.* (2013) evaluated 40 rice accessions to study the genetic diversity and differences in the patterns of diversity within the aromatic and nonaromatic rice varieties using 24 microsatellite markers (SSR) distributed over the whole rice genome. The PIC values ranged from 0.0476 (RM315) to 0.5993 (RM252), with an average of 0.3785 per marker. The dendrogram based on the cluster analysis by SSR polymorphism, grouped 40 rice accessions into three groups by differentiating Basmati genotypes from non-basmati cultivars. These results would be helpful in monitoring genetic purity, identification and protection of plant varieties.

Vhora *et al.* (2013) evaluated 20 rice cultivars, including aromatic and non-aromatic cultivars to analyze the genetic diversity among aromatic and nonaromatic rice genotypes using 25 microsatellite markers (SSR). These markers resulted in a high level of polymorphism and generated 356 polymorphic reproducible bands with 164 loci. The cluster analysis using these SSR markers distinguished these cultivars for aroma and quality traits.

Molecular and morphological characterization of 26 rice landraces and four high yielding rice varieties were studied using 27 SSR markers by Nadia *et al.* (2014). A wide range of morphological diversity was found among the rice genotypes studied and these landraces were grouped into four clusters based on morphological markers. The PIC values varied from 0.68 to 0.94 with an average of 0.84, indicating the presence of high genetic diversity among the rice germplasm studied. Based on the results, the SSR markers RM474, RM171 RM564, RM17, RM1026, RM205 and RM152 were reported as best markers for diversity analysis and varietal identification.

Microsatellite (SSR) analysis was carried out to assess the genetic polymorphism in 38 aromatic landraces of rice (*Oryza sativa* L.) using 19 SSR primers. Out of 19 primers studied, 10 SSR markers *viz.,* RM 9, RM 251, RM 247, RM 410, RM 335, RM 433, RM 411, RM 444, RM 484 and RM 535 were reported to be polymorphic and three SSR markers *viz.,* RM 288, RM 215 and RM 506 were reported as monomorphic (Patel *et al.*, 2015).

Salgotra *et al.* (2015) collected 141 Basmati rice accessions, including landraces, elite cultivars and advanced breeding lines from Basmati growing geographic regions of North Western Himalaya regions of India and characterized using 40 microsatellite markers. Out of 40 markers studied, two markers (RM130 and RM571) were reported as monomorphic and 95 per cent markers were found to be polymorphic. Maximum PIC value (0.63) was reported for RM206 and minimum polymorphic information (0.17) was reported for RM213.

Sharma *et al.* (2015) studied genetic polymorphism in 25 Basmati rice genotypes, including locally adapted and improved Basmati rice genotypes, using 22 microsatellite (SSRs) markers. A total of 63 alleles (3 monomorphic and 60 polymorphic) were detected. Out of 22 SSR primers studied, 3 primers *viz.*, RM 60, RM 159 and RM 308 were reported as monomorphic and the rest 19 primers were reported to be polymorphic. The PIC value ranged from 0.07 (RM60) to 0.55 (RM173) with an average of 0.33. Clustering analysis grouped the genotypes into two main clusters which were further divided into sub clusters in dendogram and thereby, indicating it to be very useful for diversity analysis of rice germplasm.

Venkatesan and Bhat (2015) conducted an experiment to evaluate the genetic diversity and relationship among 40 aromatic germplasm of Odisha, including 34 small and medium-grained aromatic rice genotypes along with six long-grained Basmati rice using 24 microsatellite (SSR) primer pairs, of which 22 primers (91.6 per cent) were found polymorphic. The results revealed a wide range of genetic diversity in 40 aromatic rice genotypes at molecular level and the SSR markers such as RM249, RM216, RM228 and RM223 were reported to be useful to distinguish different aromatic rice genotypes and RM104 was capable of distinguishing basmati from non-basmati aromatic types.

To study the genetic diversity among 16 pigmented and aromatic rice genotypes found in Western Himalayas of Kashmir and Himachal Pradesh, a set of 24 SSR markers were used. Through the use of 24 SSR markers, a total of 68 alleles were detected across the 16 genotypes and the number of alleles per locus resulted from 2 (RM 452, RM 338, RM 171) to 6 (RM 249, RM 585, RM 162, RM 481).

PIC values ranged from 0.36 (RM 1) to 0.86 (RM 249) with an average of 0.62. Based on high PIC values generated, RM 249, RM 585, RM 162 and RM 481 were reported to be useful in determining the genetic diversity among the rice genotypes of the Western Himalayas of Kashmir and Himachal Pradesh (Ashraf *et al.*, 2016).

An experiment was carried out to study the genetic diversity of 12 Bangladeshi local *Boro* rice (*Oryza sativa* L.) germplasm using eight SSR markers and the PIC values ranged from 0.67 (RM1) to 0.86 (RM314) with an average of 0.76. The marker RM314 recorded highest PIC value (0.86) and maximum alleles. Hence, based on PIC value, RM314 was reported as the best marker for diversity analysis and varietal identification (Halder *et al.*, 2016).

Mishra *et al.* (2016) conducted a study to investigate the genetic diversity among the nine Basmati rice genotypes (*viz.*, Basmati 370, Tarori Basmati, Pusasugandha 1, Type 3, Basmati 386, Pusa Basmati 1, Vallabh Basmati 22, Pusasugandha 5 and Vallabh Basmati 24) for molecular analysis with 11 SSR markers. Molecular analysis with 11 SSR markers resulted in 125 bands, out of which 82 bands were polymorphic and remaining 43 bands were monomorphic. The highest PIC of these markers was 0.74. for RM4469 and RM1067. Based on PIC values, RM4469 and RM1067 were reported as best markers to study Basmati type rice.

Twenty four rice genotypes including 19 aromatic genotypes were evaluated to identify the desirable genotypes for future breeding programme and out of 159 alleles reported, primer RM 6959 reported highest number of alleles (8) and RM 5499 exhibited lowest number of alleles (2). PIC values ranged from 0.150 to 0.758 with an average of 0.53. The highest PIC value (0.7548) was reported for RM 242 followed by RM 215 and RM 6959. Based on the PIC values revealed, primer RM 242 was reported as best marker for assessing the genetic constitutions of rice genotypes (Bashar *et al.*, 2017).

Becerra *et al.* (2017) assessed the level of polymorphism of 249 genotypes by 30 polymorphic microsatellites and reported an overall mean gene diversity of

0.52 and mean PIC value of 0.47 across 30 SSR markers studied.

Krupa *et al.* (2017) studied genetic diversity of five rice genotypes using 20 SSR markers and reported that PIC value ranged from 0.215 to 0.791, where the highest PIC value of 0.791 was obtained for RM260 followed by RM219 (0.74), and RM72 (0.70). Based on the results, RM260 marker was reported as best marker to test the genotypes in study.

Aljumaili *et al.* (2018) studied genetic diversity analysis among 50 aromatic rice germplasm from three regions (Peninsular Malaysia, Sabah, and Sarawak) using 32 SSR markers, with an objective to quantify the genetic divergence of aromatic rice germplasm and to identify the potential genotypes for introgression into the existing varietal development breeding program. The results revealed that, there existed wide genetic variation among 50 aromatic rice genotypes. Out of 50 genotypes, seven accessions (Acc9993, Acc6893, Acc6288, Acc6288, Acc6009, Acc6288, Acc11816 and Acc9956) were identified and selected for future aromatic rice varietal development programme.

MATERIALS AND METHODS

3. MATERIALS AND METHODS

The present investigation on "Diversity analysis in landraces of rice (*Oryza sativa* L.) in Wayanad through morphological and molecular polymorphism study" was conducted in two experiments as detailed below.

Experiment 1: Diversity analysis in landraces of Wayanad based on DUS characters

Experiment 2: Molecular characterization of aromatic cultivars of Wayanad with following sub experiments

2a: Molecular characterization with SSR markers of different linkage groups

2b: Molecular characterization with aroma specific markers

3.1. Experiment 1

3.1.1. Experimental site

The field experiment was carried out at the Regional Agricultural Research Station (RARS), Ambalavayal, Wayanad, during *Nancha* season (first crop) of 2016, situated at 11° 61' N latitude, 76° 21' E longitude and altitude of 938m above mean sea level (Plates 1 to 10).

3.1.2. Experimental material

The experimental material for diversity analysis comprised of 60 landraces of rice collected from different parts of Wayanad district, including three check varieties namely, Kanchana, Uma and Aathira. The details of genotypes used in the study are given in Table 1.

3.1.3. Experimental methods

Seeds of the genotypes were sown separately in raised bed nursery. Thirty days old seedlings were transplanted along with three check varieties (Kanchana, Uma and Aathira) in Augmented Block Design with 6 blocks (10 entries with 3 check varieties in each block). The layout of the field experiment is shown in Fig.1. Each entry was planted in three rows of 20 plants each, at a spacing of

Table 1. Details of rice genotypes used in the study

Sl. No.	Genotype	Source	Sl. No.	Genotype	Source
1	Kalladi Aryan (AMB 12)	RARS, Ambalavayal	33	Palthondi (AMB 22)	RARS, Ambalavayal
2	Thondi-1 (AMB 14)	RARS, Ambalavayal	34	Vaalicha (AMB 33)	RARS, Ambalavayal
3	Ambalavayal-1 (AMB 3)	RARS, Ambalavayal	35	Veliya thondi (AMB 13)	RARS, Ambalavayal
4	Ayirankana (AMB 15)	RARS, Ambalavayal	36	Edavaka (AMB 45)	RARS, Ambalavayal
5	Palveliyan (AMB 6)	RARS, Ambalavayal	37	Velumpala (AMB 34)	RARS, Ambalavayal
6	Kannali (AMB 35)	RARS, Ambalavayal	38	Kumbali	Cheruvayal Raman
7	Chomala (AMB 37)	RARS, Ambalavayal	39	Adukkan (AMB 28)	RARS, Ambalavayal
8	Keervana (AMB 20)	RARS, Ambalavayal	40	AMBalavayal-2 (AMB 7)	RARS, Ambalavayal
9	Kothandon (AMB 26)	RARS, Ambalavayal	41	Uruni kayama	Cheruvayal Raman
10	Kanni kayama (AMB 16)	RARS, Ambalavayal	42	Gandhakasala (ABL 3)	RARS, Ambalavayal
11	Addy (AMB 18)	RARS, Ambalavayal	43	Kothandan (AMB 26)	RARS, Ambalavayal
12	Kodu veliyan (AMB 5)	RARS, Ambalavayal	44	Thavalakannan	Cheruvayal Raman
13	Thondi-2 (AMB 9)	RARS, Ambalavayal	45	Kunam kulumban	Cheruvayal Raman
14	Chenthondi (AMB 43)	RARS, Ambalavayal	46	Chomala-2	Cheruvayal Raman
15	Mangalapuram puncha	RARS, Ambalavayal	47	Jeerakasala (ABL 7)	RARS, Ambalavayal

	(AMB 30)				
16	Chennellu (AMB 19)	RARS, Ambalavayal	48	Kutti veliyan (AMB 36)	RARS, Ambalavayal
17	Punnadan thondi (AMB 4)	RARS, Ambalavayal	49	Thonnooran thondi (AMB 31)	RARS, Ambalavayal
18	Putta batta (AMB 23)	RARS, Ambalavayal	50	Chomala-1	Cheruvayal Raman
19	Rajameni (AMB 47)	RARS, Ambalavayal	51	Rasagatham	RARS, Ambalavayal
20	Chettu veliyan (AMB 10)	RARS, Ambalavayal	52	Njavara (AMB 1)	RARS, Ambalavayal
21	Kuruva (AMB 44)	RARS, Ambalavayal	53	Sugandhamathi	RARS, Ambalavayal
22	Mulla kuruva (AMB 17)	RARS, Ambalavayal	54	Palthondi matta	Cheruvayal Raman
23	Mannu veliyan (AMB 21)	RARS, Ambalavayal	55	Vellimuthu	Cheruvayal Raman
24	Njavara black (AMB 39)	RARS, Ambalavayal	56	Mara thondi	Cheruvayal Raman
25	Veliyan (AMB 24)	RARS, Ambalavayal	57	Kayama	Cheruvayal Raman
26	Mahi kuruva (AMB 29)	RARS, Ambalavayal	58	Onamottan (AMB 11)	RARS, Ambalavayal
27	Valichoori (AMB 48)	RARS, Ambalavayal	59	Karimpalan	Cheruvayal Raman
28	Urulan kayama (AMB 8)	RARS, Ambalavayal	60	Gandhakasala dwarf (ABL 6)	RARS, Ambalavayal
29	Thondi-3 (AMB 32)	RARS, Ambalavayal	**Check varieties**		
30	Mullan puncha (AMB 27)	RARS, Ambalavayal	1	Kanchana (Ptb 50)	Kerala Agril. University
31	Chenthadi (AMB 38)	RARS, Ambalavayal	2	Uma (Mo 16)	Kerala Agril. University
32	Peruvaya (AMB 2)	RARS, Ambalavayal	3	Aathira (Ptb 51)	Kerala Agril. University

Block- 1	Block- 2	Block- 3
Kanchana	Addy	Kanchana
Uma	Kodu veliyan	Uma
Aathira	Thondi-2	Aathira
Kalladi aryan	Chenthondi	Kuruva
Thondi-1	Mangalapuram puncha	Mulla kuruva
Ambalavayal-1	Chennellu	Mannu veliyan
Ayirankana	Punnadan thondi	Njavara black
Palveliyan	Putta batta	Veliyan
Kannali	Rajameni	Mahi kuruva
Chomala	Chettu veliyan	Valichoori
Keervana	Kanchana	Urulan kayama
Kothandon	Uma	Thondi-3
Kanni kayama	Aathira	Mullan puncha

Block- 4	Block- 5	Block- 6
Chenthadi	Kanchana	Rasagatham
Peruvaya	Uma	Njavara
Palthondi	Aathira	Sugandhamathi
Vaalicha	Uruni kayama	Palthondi matta
Veliya thondi	Gandhakasala	Vellimuthu
Edavaka	Kothandan	Mara thondi
Velumpala	Thavalakannan	Kayama
Kumbali	Kunam kulumban	Onamottan
Adukkan	Chomala-2	Karimpalan
Ambalavayal-2	Jeerakasala	Gandhakasala (dwarf)
Kanchana	Kutti veliyan	Kanchana
Uma	Thonnooran thondi	Uma
Aathira	Chomala-1	Aathira

Fig. 1. Layout of the experimental plot

10 cm between rows and 20 cm between plants, and 1 m distance between two entries. All the cultural practices were followed according to Package of Practices Recommendations: Crops (KAU, 2011).

3.1.4. Morphological characterization

In this experiment, observations on 38 qualitative characters and 20 quantitative characters were recorded to fulfil the objectives of this study. Observations were recorded on 10 randomly selected plants of each genotype for majority of the traits under study, at different growth stages with appropriate procedures as per the "Guidelines for the Conduct of Test for DUS on Rice" (PPV & FRA, 2007).

Some traits were recorded as per the 'Standard Evaluation System for Rice' (IRRI, 1996). The details of DUS descriptor followed in the study is given in Table 4.

3.1.4.1. Coleoptile: Colour

The coleoptile colour was recorded by visual observation of seedlings at emergence of first leaf through coleoptile. The genotypes were grouped into colourless, green and purple with respect to coleoptile colour.

3.1.4.2. Basal leaf: Sheath colour

The colour of the basal leaf sheath, which is wrapped around the culm above the basal node, was visually recorded at booting stage in individual plants. The genotypes were grouped into green, light purple, purple lines and purple based on basal leaf sheath colour.

3.1.4.3. Leaf: Intensity of green colour

The intensity of green colour of leaves was visually recorded by observation of group of plants, at booting stage. The genotypes were grouped into light, medium and dark green colour.

3.1.4.4. Leaf: Anthocyanin colouration

The presence or absence of anthocyanin colouration of leaf was recorded at booting stage in a group of plants.

3.1.4.5. Leaf: Distribution of anthocyanin colouration

Distribution of anthocyanin colouration on leaf was recorded by visual assessment of group of plants, at booting stage. The genotypes were grouped into on tips only, on margins only, in blotches only and uniform.

3.1.4.6. Leaf sheath: Anthocyanin colouration

The presence or absence of anthocyanin colouration of leaf sheath was recorded at booting stage by visual assessment of group of plants.

3.1.4.7. Leaf: Pubescence of blade surface

The pubescence of leaf blade surface was recorded at booting stage by touch and feel method of leaf individually. The genotypes were grouped into very weak, weak, medium, strong and very strong.

3.1.4.8. Leaf: Auricles

Auricles are the small paired hairy appendages of a leaf on either side of the base of the blade. These auricles were visually assessed for its presence or absence at booting stage by individual plant observation.

3.1.4.9. Leaf: Anthocyanin colouration of auricles

The anthocyanin colouration of leaf auricles was recorded at booting stage by visual assessment of individual plants. The genotypes were grouped into colourless, light purple and purple according to colour of auricles.

3.1.4.10. Leaf: Collar

Leaf collar is the structure between leaf blade and leaf sheath. Observations were recorded for its presence or absence, at booting stage by visual assessment of individual plants.

3.1.4.11. Leaf: Anthocyanin colouration of collar

The anthocyanin colouration of the collar was recorded for its presence or absence at booting stage by visual assessment of individual plants.

3.1.4.12. Leaf: Ligule

Leaf ligule is the papery structure at the juncture between the leaf blade and leaf sheath. Its presence or absence was recorded at booting stage by visual observation of individual plants.

3.1.4.13. Leaf: Shape of ligule

The shape of the leaf ligule was recorded at booting stage by visual observation of individual plants. Based on the shape of ligule, the genotypes were grouped into truncate, acute and split (Fig. 2).

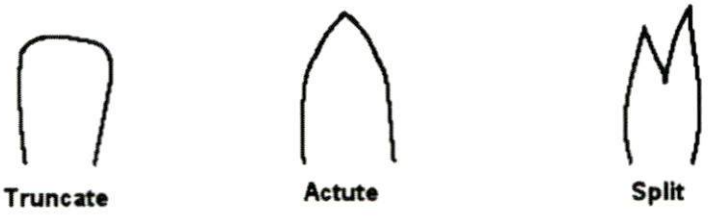


Fig. 2. Shape of ligule.

3.1.4.14. Leaf: Colour of the ligule

The colour of the leaf ligule was recorded at booting stage by visual observation of individual plants. Based on the colour of ligule, the genotypes were grouped into green, light purple and purple.

3.1.4.15. Culm: Attitude

The culm attitude was recorded at booting stage by visual assessment and the genotypes were grouped into erect, semi-erect, open and spreading types (Fig. 3).

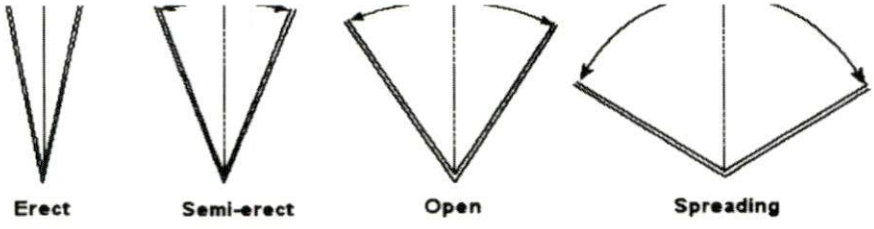


Fig. 3. Attitude of culm

3.1.4.16. Stem: Anthocyanin colouration of nodes

The anthocyanin colouration of nodes was recorded for its presence or absence at milk development stage by visual observation of individual plant nodes.

3.1.4.17. Flag leaf: Attitude of blade

The attitude of flag leaf was recorded at anthesis half way by visual observation of flag leaf of individual plant and the genotypes were grouped into erect, semi-erect, horizontal and deflexed types (Fig. 4).

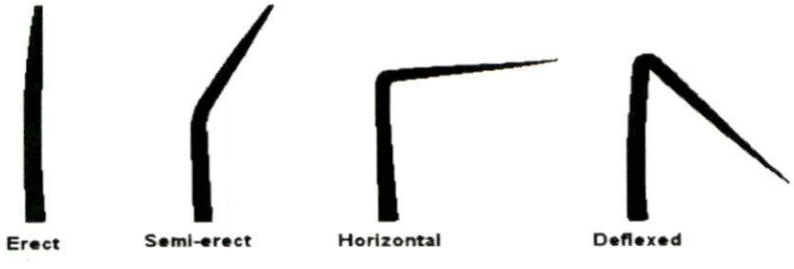


Fig. 4. Attitude of flag leaf blade

3.1.4.18. Leaf: Senescence

Leaf senescence was recorded at maturity stage by visual observation of group of plants. The genotypes were grouped into early, medium and late classes.

3.1.4.19. Leaf: Length of blade

The length of the leaf blade was measured in centimetre at booting stage and the genotypes were grouped into short, medium and long leaves.

3.1.4.20. Leaf: Width of the blade

The width of blade was measured in centimetre at booting stage and the genotypes were grouped into narrow, medium and broad.

3.1.4.21. Stem: Thickness

The plant stem thickness was recorded in centimetre at milk development stage and the genotypes were grouped into thin, medium and thick stem classes.

3.1.4.22. Stem: Length (excluding panicle)

The length of stem was measured in centimetre at the stage of milk development from ground level to the tip of the longest leaf, excluding panicle. The genotypes were grouped into very short, short, medium, long and very long.

3.1.4.23. Time for heading

Number of days was recorded from sowing to the days when panicles emerge in 50 per cent of plants.

3.1.4.24. Spikelet: Colour of stigma

The colour of the stigma was assessed at the stage of flowering by visual observation using stereomicroscope and the genotypes were grouped into white, light green and purple stigma.

3.1.4.25. Lemma: Anthocyanin colouration of keel

The anthocyanin colouration on keel of lemma was recorded at anthesis by visual observation of lemma and genotypes were grouped into absent or very weak, weak, medium, strong and very strong.

3.1.4.26. Lemma: Anthocyanin colouration of apex

The anthocyanin colouration of apex of lemma was assessed by visual observation of lemma and genotypes were grouped into absent, weak, medium, strong and very strong.

3.1.4.27. Lemma: Anthocyanin colouration of area below apex

The anthocyanin colouration of area below apex of lemma was assessed by visual observation of lemma and genotypes were grouped into absent, weak, medium, strong and very strong.

3.1.4.28. Spikelet: Density of pubescence of lemma

The density of pubescence of lemma of spikelet was recorded at dough development to maturity stage by visual assessment using stereomicroscope and grouped into absent, medium and strong categories.

3.1.4.29. Panicle: Curvature of main axis

The panicle curvature of main axis was recorded at maturity stage by visual observation of group of plants and grouped into straight, semi-straight, drooping and deflexed (Fig. 5).

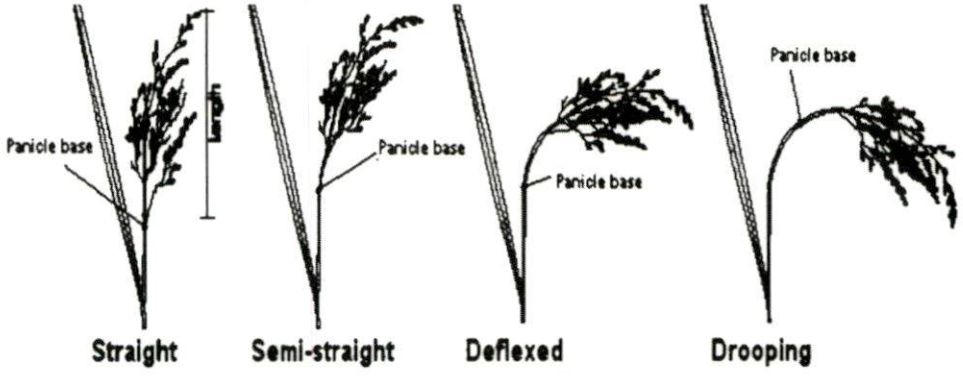


Fig. 5. Curvature of panicle main axis

3.1.4.30. Panicle: Awns

Spikelets were recorded for the presence or absence of awns at ripening stage by visual assessment of a group of plants.

3.1.4.31. Panicle: Colour of awns

The colour of awns was recorded by visual assessment of individual plants at ripening stage and genotypes were grouped into yellowish white, yellowish brown, brown, reddish brown, light red, red, light purple, purple and black.

3.1.4.32. Panicle: Distribution of awns

The distribution of awns in the panicle was recorded by visual assessment of individual plants at ripening stage and genotypes were grouped into awns present at tip only, upper half only and whole length.

3.1.4.33. Panicle: Presence of secondary branching

The presence or absence for panicle secondary branching was assessed by visual observation of group of individual panicles (Fig. 6).

Fig. 6. Presence of secondary branching in panicles

3.1.4.34. Panicle: Secondary branching

The secondary branching of panicle was recorded at prior to harvesting by visual observation of group of panicles and grouped the genotypes into weak, strong and clustered (Fig. 7).

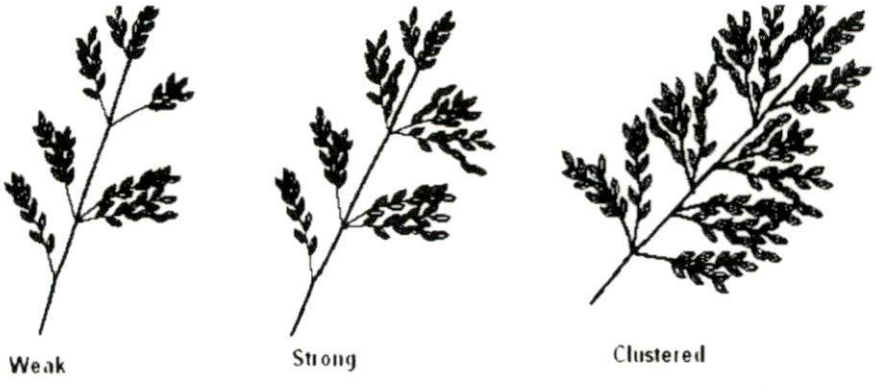


Fig. 7. Secondary branching in panicles

3.1.4.35. Panicle: Attitude of branches

The attitude of branches in panicle was observed at prior to harvesting by visual observation of a group of panicles and the genotypes were grouped into erect, erect to semi-erect, semi-erect, semi-erect to spreading and spreading (Fig. 8).

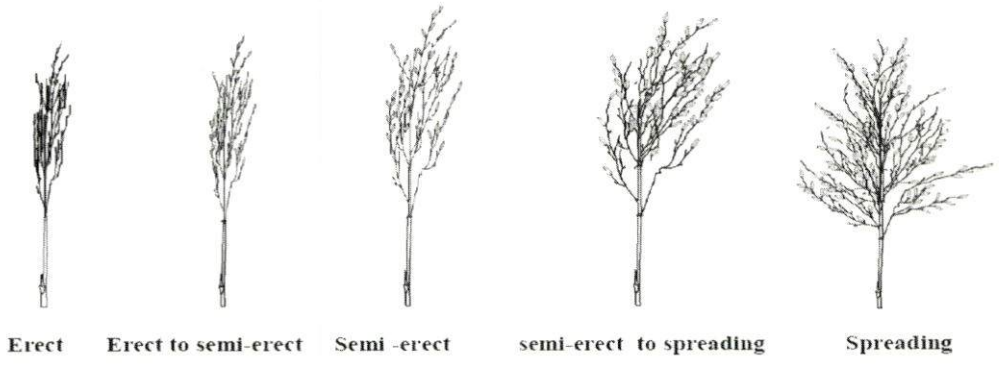


Fig. 8. Attitude of branches in panicles

3.1.4.36. Panicle: Exsertion

Exsertion of the panicle from flag leaf was assessed by visual observation of group of plants at maturity stage and the genotypes were grouped into partly exserted, mostly exserted and well exserted classes (Fig. 9).

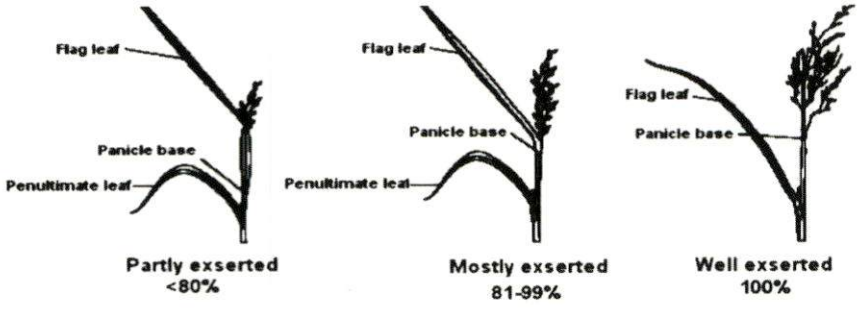


Fig. 9. Exsertion of panicles

3.1.4.37. Panicle: Length of main axis

The length of panicle was measured in centimetre at the time of prior to harvesting from base of panicle to the tip of last spikelet. The genotypes were grouped into very short, short, medium, long and very long.

3.1.4.38. Panicle: Number per plant

The number of panicles per plant was counted prior to harvesting from ten randomly selected plants. The genotypes were grouped into few, medium and many.

3.1.4.39. Time of maturity

The maturity was recorded in days from sowing to the ripening and genotypes were grouped into very early, early, medium, late and very late duration.

3.1.4.40. Lodging nature

The lodging or non-lodging nature was assessed by visual observation of group of plants at maturity stage.

3.1.4.41. Sterile lemma: Colour

The sterile lemma colour was recorded by visual assessment of individual panicle at maturity stage when caryopsis get hard and genotypes were grouped into straw, gold, red and purple sterile lemma classes.

3.1.4.42. Lemma and palea: Colour

The colour of lemma and palea was recorded at ripening stage by visual observation of group of plants and genotypes were grouped into straw, gold and gold furrows on straw background, brown spots on straw, brown furrows on straw, brown (tawny), reddish to light purple, purple spots on straw, purple furrows on straw and purple black.

3.1.4.43. Grain: Length (mm)

Grain length was measured in randomly selected ten fully filled grains in terms of millimetre at maturity stage and the genotypes were grouped into very short, short, medium, long and very long classes.

3.1.4.44. Grain: Width (mm)

Ten randomly selected grains were measured for their average width in terms of millimetre at maturity stage and the genotypes were grouped into very narrow, narrow, medium, broad and very broad classes.

3.1.4.45. Grain: Length/ Breadth (L/B) ratio

This was calculated by the following formula:

$$\text{Grain L /B ratio} = \frac{\text{Length of grain}}{\text{Breadth of grain}}$$

3.1.4.46. Spikelet: Number per panicle

The number of spikelets per panicle was counted after harvesting in ten randomly selected panicles from each genotype and mean was worked out.

3.1.4.47. Grain: Number per panicle

The number of grains per panicle was counted after harvesting in ten randomly selected panicles from each genotype and mean was worked out.

3.1.4.48. Seed setting per cent

Seed setting per cent was worked out in ten randomly selected panicles from each genotype and calculated using the formula given below and mean was worked out.

$$\text{Seed setting per cent} = \frac{\text{Number of grains}}{\text{Total number of spikelets}} \times 100$$

3.1.4.49. Decorticated grain: Length (mm)

Average decorticated grain length was measured in ten randomly selected kernels in millimetre and the genotypes were grouped into short, medium, long and extra-long classes.

3.1.4.50. Decorticated grain: Width (mm)

The randomly selected ten hulled kernels were measured for their average width in millimetre and the genotypes were grouped into narrow, medium and broad classes.

3.1.4.51. Decorticated grain: Length/ Breadth (L/B) ratio

This was calculated by the following formula:

$$\text{Decorticated grain L /B ratio} = \frac{\text{Length of kernel}}{\text{Breadth of kernel}}$$

3.1.4.52. Decorticated grain: Colour

The grain colour of hulled kernels were recorded by visual observation of group of kernels and the genotypes were grouped into white, light brown, variegated brown, dark brown, light red, red, variegated purple, purple and dark purple classes.

3.1.4.53. Decorticated grain: Shape

The shape of the kernel was recorded by measuring the length and breadth of ten full grains and average of length and breadth was calculated in millimetres and length/breadth (L:B) ratio was calculated and based on L:B ratio the genotypes were grouped into short slender, short bold, medium slender, medium bold, long slender, long bold and extra-long slender classes.

3.1.4.54. Decorticated grain: Aroma

The presence or absence of aroma of cooked rice was assessed in the following way. 15 ml of water was added to 5 g of rice samples in a test tube, and soaked for ten minutes. Then the samples were cooked in the water bath for 15 minutes. The cooked rice was transferred to a petri dish and allowed for cooling. After cooling, the petri plates were kept in refrigerator for 20 minutes. Then the petri plates were opened and aroma was assessed to classify as 'aroma absent' of 'aroma present'.

3.1.4.55. Grain: Weight of 1000 fully developed grains (g)

The grain weight of 1000 fully developed seeds were taken randomly and weighed in grams and the genotypes were grouped into very low, low, medium, high and very high classes.

3.1.4.56. Grain: Yield per plant (g)

The average grain yield per plant was measured by weighing the grain yield from ten randomly selected plants and the average was calculated.

3.1.4.57. Gelatinization temperature through alkali spreading value

Alkali spreading value was determined as per the following procedure described by Jennings *et al.* (1979)

1) Six milled rice kernels without cracks were selected of each landrace and space placed in a petri plate
2) 10 ml of 1.7 per cent Potassium Hydroxide (KOH) solution was added to each petri plate
3) These petri plates were covered and kept at 30^0 C for 23 hours
4) The spreading of endosperm was visually rated as per following 7-point scale (Table 2)
5) The gelatinization temperature was scored based on alkali spreading values (Table 3)

Table 2. Numerical scale for scoring alkali spreading value

Score	Spreading value
1	Kernel not affected
2	Kernel swollen
3	Kernel swollen, collar incomplete and narrow
4	Kernel swollen, collar complete and wide
5	Kernel split or segmented, collar complete
6	Kernel dispersed, merging with collar
7	All kernel dispersed and intermingled

Table 3. Numerical scale for estimation of gelatinization temperature through alkali spreading value

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

Table 4. DUS descriptor for morphological characterization

Sl. No.	Characteristics	States	Note	Stage of observation
1	Coleoptile: Colour	Colourless	1	Emergence of first leaf through coleoptile
		Green	2	
		Purple	3	
2	Basal leaf: Sheath colour	Green	1	Booting
		Light purple	2	
		Purple lines	3	
		Uniform purple	4	
3	Leaf: Intensity of green colour	Light	3	Booting
		Medium	5	
		Dark	7	
4	Leaf: Anthocyanin colouration	Absent	1	Booting
		Present	9	
5	Leaf: Distribution of anthocyanin colouration	Absent	1	Booting
		On tips only	2	
		On margins only	3	
		In blotches only	4	

		Uniform	5	
6	Leaf Sheath: Anthocyanin colouration	Absent	1	Booting
		Present	9	
7	Leaf: Pubescence of blade surface	Absent	1	Booting
		Weak	3	
		Medium	5	
		Strong	7	
		Very strong	9	
8	Leaf: Auricles	Absent	1	Booting
		Present	9	
9	Leaf: Anthocyanin colouration of auricles	Absent	1	Booting
		Colourless	2	
		Light purple	3	
		Purple	4	
10	Leaf: Collar	Absent	1	Booting
		Present	9	
11	Leaf: Anthocyanin colouration of collar	Absent	1	Booting
		Present	9	
12	Leaf: Ligule	Absent	1	Booting
		Present	9	
13	Leaf: Shape of ligule	Truncate	1	Booting
		Acute	2	
		Split	3	
14	Leaf: Colour of ligule	White	1	Booting
		Light purple	2	
		Purple	3	
15	Culm: Attitude	Erect	1	Booting
		Semi-erect	3	

		Open	5	
		Spreading	7	
16	Stem: Anthocyanin colouration of nodes	Absent	1	Booting
		Present	9	
17	Flag leaf: Attitude of blade	Erect	1	Anthesis half way
		Semi-erect	3	
		Horizontal	5	
		Deflexed	7	
18	Leaf: Senescence	Early	3	Caryopsis hard
		Medium	5	
		Late	7	
19	Leaf: Length of blade	Short (< 30 cm)	3	Booting
		Medium (30-45 cm)	5	
		Long (> 45 cm)	7	
20	Leaf: Width of blade	Narrow (< 1 cm)	3	Booting
		Medium (1-2 cm)	5	
		Broad (> 2 cm)	7	
21	Stem: Thickness	Thin (< 0.40 cm)	3	Milk development
		Medium (0.40-0.55 cm)	5	
		Thick (> 0.55 cm)	7	
22	Stem: Length (excluding panicle)	Very short (< 91 cm)	1	Milk development
		Short (91-110 cm)	3	
		Medium (111-130 cm)	5	
		Long (131-150 cm)	7	
		Very long (>150 cm)	9	
23	Time of heading (50per cent of plants with panicles)	Very early (< 71 days)	1	50 per cent of plants with panicles
		Early (71-90 days)	3	
		Medium (91-110 days)	5	

		Late (111-130 days)	7	
		Very late (> 131 days)	9	
24	Spikelet: Colour of stigma	White	1	Flowering
		Light green	2	
		Yellow	3	
		Light purple	4	
		Purple	5	
25	Lemma: Anthocyanin colouration of keel	Absent or very weak	1	Anthesis
		Weak	3	
		Medium	5	
		Strong	7	
		Very strong	9	
26	Lemma: Anthocyanin colouration of apex	Absent	1	Anthesis
		Weak	3	
		Medium	5	
		Strong	7	
		Very strong	9	
27	Lemma: Anthocyanin colouration of area below apex	Absent	1	Anthesis
		Weak	3	
		Medium	5	
		Strong	7	
		Very strong	9	
28	Spikelet: Density of pubescence of lemma	Absent	1	Dough development to maturity
		Weak	3	
		Medium	5	
		Strong	7	
		Very strong	9	
29	Panicle: Curvature of	Straight	1	Maturity

	main axis	Semi-straight	3	
		Deflexed	5	
		Dropping	7	
30	Panicle: Awns	Absent	1	Ripening
		Present	9	
31	Panicle: Colour of awns	Absent	1	Ripening
		Yellowish White	2	
		Yellowish brown	3	
		Brown	4	
		Reddish brown	5	
		Light red	6	
		Red	7	
		Light purple	8	
		Purple	9	
		Black	10	
32	Panicle: Distribution of awns	Absent	1	Ripening
		Tip only	3	
		Upper half only	5	
		Whole length	7	
33	Panicle : Presence of secondary branching	Absent	1	Prior to harvesting
		Present	9	
34	Panicle: Secondary branching	Weak	1	
		Strong	2	
		Clustered	3	
35	Panicle: Attitude of branches	Erect	1	Prior to harvesting
		Erect to semi-erect	3	
		Semi-erect	5	
		Semi-erect to spreading	7	

		Spreading	9	
36	Panicle: Exertion	Partly exerted	3	Prior to harvesting
		Mostly exerted	5	
		Well exerted	7	
37	Panicle: Length of main axis	Very short (< 16 cm)	1	Ripening
		Short (16-20 cm)	3	
		Medium (21-25 cm)	5	
		Long (26-30 cm)	7	
		Very long (> 30 cm)	9	
38	Panicle: Number per plant	Few (< 11)	3	Ripening
		Medium (11-20)	5	
		Many (> 20)	7	
39	Time maturity (days)	Very early (< 100)	1	Ripening
		Early (101-120)	3	
		Medium (121-140)	5	
		Late (141-160)	7	
		Very late (> 160)	9	
40	Sterile lemma: Colour	Straw	1	Ripening
		Gold	2	
		Red	3	
		Purple	4	
41	Lemma and Palea: Colour	Straw	1	Ripening
		Gold and gold furrows on straw background	2	
		Brown spots on straw	3	
		Brown furrows on straw	4	
		Brown (tawny)	5	
		Reddish to light purple	6	

		Purple spots / furrows on straw	7	
		Purple/ Black	8	
42	Grain: Length	Very short (< 6.0 mm)	1	Caryopsis hard
		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	
43	Grain: Width	Very narrow (<2.0 mm)	1	Caryopsis hard
		Narrow (2.1-2.5 mm)	3	
		Medium (2.6-3.0 mm)	5	
		Broad (3.1-3.5 mm)	7	
		Very broad (> 3.5mm)	9	
44	Decorticated grain: Length	Short (< 6 mm)	1	Caryopsis hard
		Medium (6.1-8.0 mm)	3	
		Long (8.1-10.0 mm)	5	
		Extra-long (> 10 mm)	7	
45	Decorticated grain: Width	Narrow (< 2.0 mm)	3	Caryopsis hard
		Medium (2.0-2.5 mm)	5	
		Broad (> 2.5 mm)	7	
46	Decorticated grain: Colour	White	1	Caryopsis hard
		Light brown	2	
		Variegated brown	3	
		Dark brown	4	
		Light red	5	
		Red	6	
		Variegated purple	7	
		Purple	8	

		Dark purple	9	
47	Decorticated grain: Shape	Short slender	1	Caryopsis hard
		Short bold	2	
		Medium slender	3	
		Medium bold	4	
		Long slender	5	
		Long bold	6	
		Extra-long slender	7	
48	Decorticated grain: Aroma	Absent	1	Caryopsis hard
		Present	9	
49	Grain: Weight of 1000 fully developed grains	Very low (< 15 g)	1	Caryopsis hard
		Low (15-20 g)	3	
		Medium (21-25 g)	5	
		High (26-30)	7	
		Very high (> 30 g)	9	
50	Gelatinization temperature through alkali spreading value	Low	1	Caryopsis hard
		Medium	3	
		High medium	5	
		High	7	

3.2. Experiment 2

3.2.1. Experimental site

Molecular characterization was performed at Molecular Lab, Department of Seed Science and Technology, College of Horticulture, Kerala Agricultural University, Thrissur.

3.2.2. Experimental material

The experimental material comprised of 18 genotypes of rice, including the 12 Gandhakasala types, three Jeerakasala types collected from different parts of Wayanad district and 3 check varieties, including one aromatic variety (Basmati) and two non-aromatic varieties (Uma and Aathira). The details of genotypes used in the study are given in Table 5.

Table 5. List of rice genotypes used for molecular characterization

Sl. No.	Genotype	Sl. No.	Genotype
1	Gandhakasala-1	10	Gandhakasala-10
2	Gandhakasala-2	11	Gandhakasala-11
3	Gandhakasala-3	12	Gandhakasala-12
4	Gandhakasala-4	13	Jeerakasala-1
5	Gandhakasala-5	14	Jeerakasala-2
6	Gandhakasala-6	15	Jeerakasala-3
7	Gandhakasala-7	16	Basmati (aromatic check variety)
8	Gandhakasala-8	17	Uma (non-aromatic check variety)
9	Gandhakasala-9	18	Aathira (non-aromatic check variety)

3.2.3. Isolation of DNA

All the landraces were grown in pots and 20-25 days older seedlings were used in order to get sufficient leaf material for isolation of genomic DNA by

following the protocol described for CTAB method (Dellaporta *et al.*, 1983). The steps for DNA isolation is given below.

1. Tender and healthy leaf samples were collected from 20-25 days older seedlings and 200 mg of leaves weighed.
2. The weighed leaf samples were cut into 0.5 cm long segments and placed in a pre-chilled mortar and pestle.
3. The weighed leaf tissues was ground by adding 30 µl of β-mercapto ethanol, pinch of Poly vinyl pyrolidine (PVP) along with liquid nitrogen and ground into fine powder.
4. The ground material was transferred to the sterile 2 ml eppendorf tube and added 1ml of pre-warmed CTAB (2 per cent) buffer and mixed by inverting the tube for several times.
5. This mixture was incubated in hot water bath at 65° C for 15 min and in between inverted the tube occasionally.
6. After incubation, 1ml of pre-chilled chloroform: isoamyl alcohol (24:1) added to the tube and mixed by inversion several times and centrifuged at 12,000 rpm for 10 minutes at 4° C.
7. The aqueous phase was transferred to 2 ml eppendorf tube and added equal volume chloroform: isoamyl alcohol (24:1) and centrifuged at 12,000 rpm for 10 minutes at 4° C.
8. After centrifugation the supernatant was collected and added 2 µl of RNase and incubated in hot water bath at 37° C for 15 min.
9. After incubation, added equal volume of chloroform: isoamyl alcohol (24:1) and centrifuged at 12,000 rpm for 10 minutes at 4° C.
10. After centrifugation the supernatant was transferred to 1.5 ml tube and added equal volume of 0.6 ml of pre chilled isopropanol and incubated at 4° C overnight.
11. Later the tube was centrifuged at 12,000 rpm for 10 minutes and the supernatant poured out gently by inverting tube.

12. Then the pellet was washed by adding 200 µl of 70 per cent ethanol and centrifuged at 10000 rpm for 5min.
13. The supernatant was removed and pellet was air dried at room temperature.
14. After drying, the DNA pellet was dissolved in the 60 µl sterile double distilled water and stored at -20° C for long storage.

3.2.4. Determination of quantity and quality of isolated DNA

The genomic DNA extracted from the plant samples was quantified using Genova Nano (Micro volume life science UV-visible spectrophotometer) both at 260 nm and 280 nm. The ratio of absorbance at 260 nm and 280 nm was used as DNA purity indicator. The ratio of 1.8 to 2.0 indicate pure DNA. Protein contamination was evident if the ratio was less than 1.8 and for values greater than 2, RNA contamination was inferred. The good quality DNA stock samples were used to dilute the DNA samples to working concentration of 25 ng/µl. The quantity of DNA obtained was calculated based on the relation that optical density (OD) for a DNA sample with a concentration of 50µg/ml (double stranded) at 260 nm equals one.

1 OD 260 = 50 µg/ml (ds)

Quantity of DNA (µg/ml) = Absorbance at OD 260 x 50

The quantity of DNA in the samples were calculated based on Beer-Lambert's law. OD 260 = 1 is equivalent to 50 µg of double stranded DNA. The quantity of DNA (µg/ml) in the sample is therefore calculated by formula OD 260 x 50.

3.2.5. Normalization of concentration DNA for PCR

Normalization of DNA was done to bring down the DNA concentrations to a relatively equal level (25 ng/µl) by appropriate dilutions as per the formula *i.e.*, $N_1V_1=N_2V_2$. Dilutions were done with autoclaved double distilled water.

Where,

N_1= Initial known concentration of DNA

V_1= Initial known volume of solution

N_2= Final unknown concentration of DNA V_2=

Final unknown volume of solution

3.2.6. Selection of primers for SSR profiling

A total of 86 SSR (RM) markers, including 64 hypervariable SSR markers available at www.gramene.org. (Table 6) and 22 aroma specific SSR markers were used for SSR profiling (Table 7). SRL Proxio 100 bp DNA Ladder plus was used as molecular size marker.

3.2.7. Polymerase Chain Reaction (PCR)

Master reaction mix for PCR was prepared in 0.2 ml flat cap PCR tubes by mixing the following components together to prepare the reaction volume of 13 µl for each reaction (Table 8).

Table 8. List of components of PCR mixture

Sl. No.	Components	Quantity
1	Template DNA (25 ng/µl)	3 µl
2	Forward primer	1 µl
3	Reverse primer	1 µl
3	PCR master mix	8 µl
	Total	**13 µl**

3.2.8. PCR amplification

Amplification of DNA with specific markers was carried out as detailed in Table 9 and Fig. 10.

Table 6. List of hypervariable SSR (RM) markers used for molecular characterization

SSR Primer	Chromosome number	Primer sequences	
		Forward sequence	Reverse sequence
RM1	1	GCGAAAACACAATGCAAAAA	GCGTTGGTTGGACCTGAC
RM490	1	ATCTGCACACTGCAAACACC	AGCAAGCAGTGCTTTCAGAG
RM11069	1	GGTACAATGAAGCTTGGCAACG	CGGTGGAGTAGAACCACGAAGC
RM11313	1	TGAGGCTGATAGAAAGCAGAATGC	CCCGTTTCTTCCATATCATGTCG
RM233	1	CCAAATGAACCTACATGTTG	GCATTGCAGACAGCTATTGA
RM250	2	GTTCAAACCAAGCTGATCACAAGC	GGCGTCAGAGTCAGAGATGAAGG
RM482	2	TCTGAAAGCCTGACTCATCG	GTCAATTGCAGTGCCCTTTC
RM12941	2	TTATGCCATGTGGTCCAATCAGC	ATTTGAACCATTTGGGCCTTGG
RM13599	2	GTTCATGGCACTCCTCTCCTAGC	GAGGAATGAACAGTGCCTACACG
RM13910	2	GAGCGAGCTATACCACCGTGACC	ATCGCGTCCAAGAAAGGTGTCG
RM16	3	GTGCGCCAGGAGTAGTTGTCTCC	GACGTGTACACATAGCCAAATCATCC
RM60	3	CAAGTTCACCCGCCTTCTCG	TTTCCATCATTAGCAGGCAGTAGC
RM85	3	CCAAAGATGAAACCTGGATTG	GCACAAGGTGAGCAGTCC
RM251	3	GAATGGCAATGGCGCTAG	ATGCGGTTCAAGATTCGATC
RM411	3	ACACCAACTCTTGCCTGCAT	TGAAGCAAAAACATGGCTAGG

RM14723	3	GCAAAGTCCTTTGGACAGGTAGC	CGTCCCAGATCAAAGTACACTCTTCC
RM307	4	GTACTACCGACCTACCGTTCAC	CTGCTATGCATGAACTGCTC
RM5586	4	AGATGGCTGGCCAACAGACTGG	ACAATGCCCATCCACTGCTTCC
RM13	5	TCCAACATGGCAAGAGAGAG	GGTGGCATTCGATTCCAG
RM110	5	TCGAAGCCATCCACCAACGAAG	TCCGTACGCCGACGAGGTCGAG
RM163	5	ATCCATGTGCGCCTTTATGAGGA	CGCTACCTCCTTCACTTACTAGT
RM18622	5	GGCATGCATGTGTCTAACATTCG	AAGCAGAATTTGGCCGTGTTAGC
RM18941	5	GTGAAGTGCAGCCGAAGAGC	ATCGATCTCTCATCACGATCAACC
RM217	6	ATCGCAGCAATGCCTCGT	GGGTGTGAACAAAGACAC
RM238	6	GATGGAAAGCACGTGCACTA	ACAGGCAATCCGTAGACTCG
RM253	6	TCCTTCAAGAGTGCAAAACC	GCATTGTCATGTCGAAGCC
RM340	6	GGTAAATGGACAATCCTATGGC	GACAAATATAAGGGCAGTGTGC
RM402	6	GAGCCATGGAAAGATGCATG	TCAGCTGGCCTATGACAATG
RM541	6	TATAACCGACCTCAGTGCCC	CCTTACTCCCATGCCATGAG
RM18	7	TTCCCTCTCATGAGCTCCAT	GAGTGCCTGGCGCTGTAC
RM214	7	CTGATGATAGAAACCTCTTCTC	AAGAACAGCTGACTTCACAA
RM248	7	TCCTTGTGAAATCTGGTCCC	GTAGCCTAGCATGGTGCATG
RM295	7	CGAGACGAGCATCGGATAAG	GATCTGGTGGAGGGGAGG

RM25	8	GGAAAGAATGATCTTTTCATGG	CTACCATCAAAACCAATGTTC
RM72	8	CCGGCGATAAAACAATGAG	GCATCGGTCCTAACTAAGGG
RM223	8	GAGTGAGCTTGGGCTGAAAC	GAAGGCAAGTCTTGGCACTG
RM264	8	GTTGCGTCCTACTGCTACTTC	GATCCGTGTCGATGATTAGC
RM5556	8	GTAAGCCATTTGCACGGACAAGG	GAGCTCAGGATCATCCCTACATGC
RM23087	8	GATATTAGCTAGACATGGCACTCTGC	GTACATCCGCATGAATAGAGTGG
RM205	9	CTGGTTCTGTATGGGAGCAG	CTGGCCCTTCACGTTTCAGTG
RM266	9	GATGGTAAAGGAAGAACGTGTGC	CACTCATAGACGCATCACATAGCC
RM257	9	CAGTTCCGAGCAAGAGTACTC	GGATCGGACGTGGCATATG
RM524	9	ATCATAGCCCAGACCAAGAATGC	AGATGAAGAGCAGGAACCGTAGG
RM23998	9	CTGCACGTACGGTCAAGTCTACC	GCATTGCAAGGGTTGAAGTGG
RM216	10	GATGGTAAAGGAAGAACGTGTGC	CACTCATAGACGCATCACATAGCC
RM222	10	CTTAAATGGGCCACATGCG	CAAAGCTTCCGGCCAAAAG
RM271	10	TCAGATCTACAATTCCATCC	TCGGTGAGACCTAGAGAGCC
RM304	10	TCAAACCGGCACATATAAGAC	GATAGGGAGCTGAAGGAGATG
RM333	10	GTACGACTACGAGTGTCACCAA	GTCTTCGCGATCACTCGC
RM24866	10	CCCTTTCATTTGCGCTTTATGG	GGGTTATTTCAGTCCGTGATTGC
RM25066	10	GTTGTTAGGTGTAGCCGTGTAGG	GTACACCAATAACTGTGGAAGAGC

RM21	11	ACAGTATTCCGTAGGCACGG	GCTCCATGAGGGTGGTAGAG
RM202	11	TGGAACACCCATAGACAAACAGC	TGGCAAGTGGTATTCTTCCTTCC
RM224	11	ATCGATCGATCTTCACGAGG	TGCTATAAAAGGCATTCGGG
RM254	11	AGCCCCGAATAAATCCACCT	CTGGAGGAGCATTTGGTAGC
RM332	11	GAAGGCGAAGGTGAAGAAGAAGC	CCTCCCTTGCATGATACCTTGG
RM26213	11	GCCACAGGAGACAGCAAGAACC	CGATCCAATTCCAGCCTAGATAGC
RM17	12	TGCCCTGTTATTTTCTTCTCTC	GGTGATCCTTTCCCATTTCA
RM19	12	CAAAAACAGAGCAGATGAC	CTCAAGATGGACGCCAAGA
RM20	12	ATCTTGTCCCTGCAGGTCAT	GAAACAGAGGCACATTTCATTG
RM247	12	TAGTGCCGATCGATGTAACG	CATATGGTTTTGACAAAGCG
RM260	12	ACTCCACTATGACCCAGAG	GAACAATCCCTTCTACGATCG
RM27841	12	TAAATACCCGACAATGCCCTAGC	GGAAATCCCATCAATCACAAGAGC
RM28277	12	TGCACCACCTATTTCAATCCACTCC	CCTTCCTCAAGGGAAATCACAGAAGC

Source: www.gramene.org.

Table 7. List of aroma specific SSR (RM) markers used for molecular characterization

SSR Primer	Primer sequences	
	Forward sequence	**Reverse sequence**
RM9	GGTGCCATTGTCGTCCTC	ACGGCCCTCATCACCTTC
RM180	CTACATCGGCTTAGGTGTAGCAACACG	ACTTGCTCTACTTGTGGTGAGGGACTG
RM215	CAAAATGGAGCAGCAAGAGC	TGAGCACCTCCTTCTCTGTAG
RM228	CTGGCCATTAGTCCTTGG	GCTTGCGGCTCTGCTTAC
RM243	GATCTGCAGACTGCAGTTGC	AGCTGCAACGATGTTGTCC
RM245	ATGCCGCCAGTGAATAGC	CTGAGAATCCAATTATCTGGGG
RM249	GGCGTAAAGGTTTTGCATGT	ATGATGCCATGAAGGTCAGC
RM256	GACAGGGAGTGATTGAAGGC	GTTGATTTCGCCAAGGGC
RM288	CCGGTCAGTTCAAGCTCTG	ACGTACGGACGTGACGAC
RM302	TCATGTCATCTACCATCACAC	ATGGAGAAGATGGAATACTTGC
RM323	CAACGAGCAAATCAGGTCAG	GTTTTGATCCTAAGGCTGCTG
RM335	GTACACACCCACATCGAGAAG	GCTCTATGCGAGTATCCATGG
RM338	CACAGGAGCAGGAGAAGAGC	GGCAAACCGATCACTCAGTC
RM410	GCTCAACGTTTCGTTCCTG	GAAGATGCGTAAAGTGAACGG
RM433	TGCGCTGAACTAAACACAGC	AGACAAACCTGGCCATTCAC
RM444	GCTCCACCTGCTTAAGCATC	TGAAGACCATGTTCTGCAGG
RM484	TCTCCCTCCTCACCATTGTC	TGCTGCCCTCTCTCTCTCTC
RM493	TAGCTCCAACAGGATCGACC	GTACGTAAACGCGGAAGGTG
RM510	AACCGGATTAGTTTCTCGCC	TGAGGACGACGAGCAGATTC
RM535	ACTACATACACGGCCCTTGC	CTACGTGGACACCGTCACAC
RM566	ACCCAACTACGATCAGCTCG	CTCCAGGAACACGCTCTTTC
RM590	CATCTCCGCTCTCCATGC	GGAGTTGGGGTCTTGTTCG

Table 9. Steps followed during PCR amplification

Sl. No.	Steps	Temperature	Time
1	Initial denaturation	94^0c	5 min
2	Denaturation	94^0c	1 min
3	Primer annealing	55^0 - 62^0c	45 sec
4	Extension	72^0c	1 min
5	Final extension	72^0c	10 min
6	Cooling	4^0c	∞

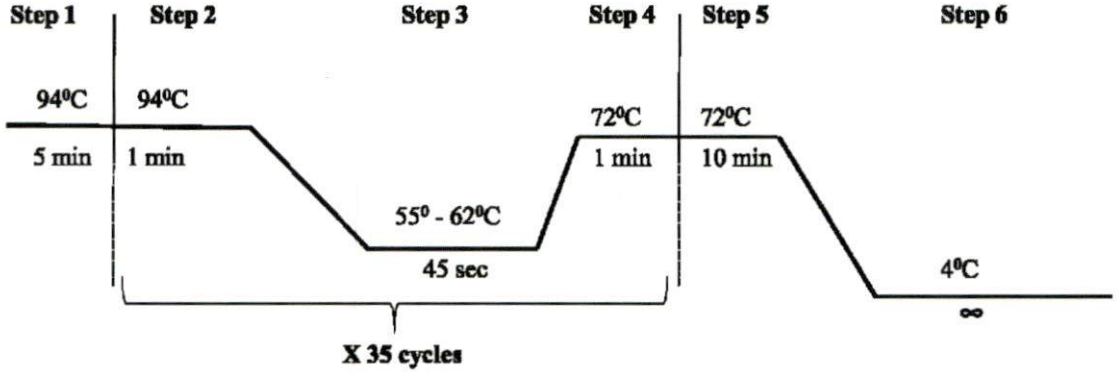


Fig. 10. Temperature profile of PCR amplification

3.2.9. Preparation of agarose gel for electrophoresis

1. Agarose gel (1.5 per cent) was prepared by weighing out 1.5 g agarose and transferred it to a conical flask containing 100 ml of 1X TAE buffer and mixed well. The components for preparing 250 ml of 50X TAE buffer are detailed in Table 10.
2. The contents were than boiled in a microwave oven with intermittent mixing, until complete melting of agarose was achieved and the solution became crystal clear.
3. The boiled agarose was cooled down substantially and 5 ml of Ethidium bromide was added to the melted agarose and mixed thoroughly.

4. The melted agarose was poured in to a gel casting tray, which was prewashed (with distilled water and wiped with 70 per cent ethanol) and the ends sealed. Care was taken to avoid air bubbles
5. The comb was placed in gel tray approx. 1 to 2 mm above the surface of the tray and agarose allowed to solidify at room temperature for 25 min.
6. The comb was subsequently removed after the gel solidified.

3.2.10. Separation of amplified products by agarose gel electrophoresis

1. The agarose gel, in the gel casting tray was placed in horizontal electrophoresis chamber containing 1X TAE buffer.
2. The 13 µl PCR amplified products were mixed well and loaded into the wells carefully.
3. Electrophoresis was carried out at 60 volts and 300 amp until the dye migrated two third of the gel (approx. 80 min).
4. Before electrophoresis, 1 kb ladder was also added to help determine the size of bands.

Table 10. Components for preparing 250 ml of 50X TAE buffer

Sl. No.	Chemical	Quantity
1	Tris Base	60.50 g
2	Glacial acetic acid	14.275 ml
3	EDTA	4.653 g
4	Distilled water	250 ml

3.2.11. Gel documentation

On completion of the electrophoresis, the gel was placed in documentation unit (gel doc) and banding pattern was visualized by exposing it to UV light and banding pattern recorded. Documentation was done using Uvitech Fire Reader 1D Software.

3.3. Statistical analysis

3.3.1. Experiment 1: Diversity analysis based on DUS characters

Analysis of variance, estimation of genetic parameters, character association by correlation and path analysis, cluster analysis by NTSYS, diversity analysis by Mahalanobis D^2 statistics were done using software Windostat 9.2 from Indostat Services, Hyderabad, India.

3.3.1.1. Analysis of variance

The mean values were worked out for all traits for each landrace and these mean data were utilized to analyse the variation. The format of analysis of variance is given below:

Source of variation	Degrees of freedom	Sum of squares	F ratio
Block (ignoring Treatments)	(b-1)	SSB	SSB/SSE
Treatment (eliminating Blocks)	(t-1)	SST	SST/SSE
Varieties	(v-1)	SSV	SSV/SSE
Checks	(c-1)	SSC	SSC/SSE
Checks Vs variety	1	SSCV	SSCV/SSE
Error	(b-1) (c-1)	SSE	

t = number of treatments; v = number of varieties/genotypes; b = number of blocks

3.3.1.2. Coefficient of variation

The coefficient of variation for different traits was calculated by the formula given below.

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

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

The magnitude of PCV and GCV was categorized as high (> 20 per cent), moderate (20-10 per cent) and low (< 10 per cent).

3.3.1.3. Heritability in broad sense (h^2)

Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance (total variance). It is calculated in a broad sense by adopting the formula as suggested by Hanson *et al.* (1956).

$$\text{Heritability in broad sense } (h^2) = \frac{\text{Genotypic variance}}{\text{Phenotypic variance}} \times 100$$

The heritability estimates were categorized as high (> 60per cent), Medium (60-30 per cent) and low (< 30 per cent) as suggested by Johnson *et al.* (1955).

3.3.1.4. Genetic Advance (GA)

Genetic advance refers to improvement in the mean genotypic value of selected plants over the parental population. It was estimated by the formula suggested by Johnson *et al.* (1955).

$GA = h^2 \times \sigma p \times K$

Where,

h^2 = Heritability estimate in broad sense

σp = Phenotypic standard deviation of the trait

K = Standard selection differential (constant) having the value of 2.06 at 5 per cent level of selection intensity.

Genetic advance was categorized as high (> 20per cent), moderate (20-10 per cent) and low (< 10 per cent) as suggested by Johnson *et al.* (1955).

3.3.1.5. Genetic advance as per cent of mean (Genetic gain)

The genetic gain was calculated by the formula given below

$$\text{Genetic gain} = \frac{\text{Genetic advance}}{\text{Grand mean}} \times 100$$

Genetic advance as per cent of mean (Genetic gain) was categorised as high (>20 per cent), moderate (20-10 per cent) and low (< 10 per cent) as suggested by Johnson *et al.* (1955).

3.3.1.6. Character association analysis

Character association study was done by correlation coefficients analysis and path coefficients analysis.

3.3.1.6.1. Correlation coefficients analysis

Correlation coefficients analysis estimates degree of association of characters with yield. Correlation coefficients between characters were determined by the following formulas given below.

$$r = \frac{N\sum xy - (\sum x)(\sum y)}{\sqrt{[N\sum x^2 - (\sum x)^2][N\sum y^2 - (\sum y)^2]}}$$

Where,

N = number of pairs of scores

Σxy = sum of the products of paired scores

Σx = sum of x scores

Σy = sum of y scores

Σx^2 = sum of squared x scores

Σy^2 = sum of squared y scores

3.3.1.6.2. Path coefficients analysis

Path coefficient analysis was first developed by Wright (1923) and this was first used for plant selection by Dewey and Lu (1959). It estimates the direct and indirect contribution of independent variables on dependent variable. The path

coefficient analysis results were interpreted as negligible (0.00 to 0.09), Low (0.10 to 0.19), Moderate (0.20 to 0.29), High (0.30 to 0.99) and very high (> 1.00) as suggested by Lenka and Mishra (1973).

3.3.1.7. Cluster analysis

Cluster analysis was carried out using qualitative characters of 60 landraces and three check varieties. The genetic association among the genotypes were estimated by Jaccard's similarity coefficients (Jaccard, 1908) using NTSYS (Numerical Taxonomy and Multivariate Analysis System) software version 2.1 (Rohlf, 2000). Dendrogram was constructed using UPGMA clustering method based on similarity coefficients.

3.3.1.8. Genetic divergence analysis

The D^2 statistics was developed in 1928 by P.C. Mahalanobis. But, application of this technique for the genetic divergence study between the populations was done by Rao (1952). It measures the forces of differentiation at inter and intra cluster levels and also determine the relative contribution of each component trait to the total divergence.

The landraces were grouped into a number of clusters as per the standard procedure Mahalanobis D^2 Statistics using Tocher's method.

3.3.2. Experiment 2: Molecular characterization of aromatic cultivars of Wayanad

Molecular characterization was carried out for twelve genotypes of Gandhakasala and three genotypes of Jeerakasala, including three check varieties *i.e.,* Basmati (aromatic variety), Uma and Aathira (non-aromatic varieties) by using Simple Sequence Repeats (SSR).

3.3.2.1. Molecular characterization

The banding pattern generated on electrophoresis of amplified DNA were scored based on the molecular weight using the molecular weight analysis option of Uvitech Fire Reader 1D Software.

3.3.2.2. Scoring of bands and data analysis

Clear DNA bands of various molecular weights were scored manually for the presence of band in a particular base pair position and scored as '1' (one) and absence of band at that particular base pair position was scored as '0' (zero) respectively. Each marker was individually scored and binary matrix was prepared using Excel sheet. This data matrix was subjected to analysis using NTSYS (Numerical Taxonomy and Multivariate Analysis System) version 2.1 (Rohlf, 2000).

Polymorphic Information Content (PIC) of each SSR (RM) marker was calculated (Anderson *et al.*, 1993). Marker Index (MI) along with PIC value were used for measuring the performance of markers (Powell *et al.*, 1996). PIC values represents the ability of a marker to detect the polymorphism within a population and markers can be classified as informative when PIC was ≥ 0.5. Marker Index values helps to understand the capacity of primer to detect polymorphic loci among varieties and Both PIC and MI confirm the suitability of the primer.

$$PIC = 1 - \sum_{j=1}^{n} (Pij)^2$$

Where,

n - Number of marker alleles for marker i

P*ij* - Frequency of the j^{th} allele for marker i

Marker Index (MI) = PIC × No. of polymorphic band

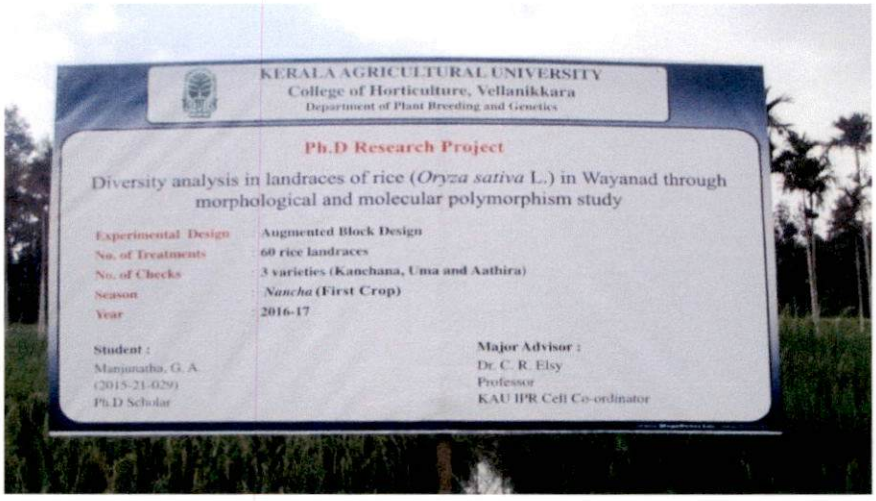


Plate 1. Experimental plot

Plate 2. Experimental plot before transplanting

Plate 3. Nursery plot

Plate 4. Transplanting of experimental plot

Plate 5. Experimental plot at seedling stage

Plate 6. Experimental plot at tillering stage

Plate 7. Experimental plot at 120 days after transplanting

Plate 8. Experimental plot at maturity stage

Plate 9. Harvesting of experimental plot

RESULTS

4. RESULTS

"Diversity analysis in landraces of rice (*Oryza sativa* L.) in Wayanad through morphological and molecular polymorphism study" was conducted and the results are presented in this chapter.

Experiment 1: Diversity analysis in landraces of Wayanad, based on DUS characters

4.1. Morphological characterization

Observations were recorded on 38 qualitative and 13 quantitative characters and presented in Table 11 to 39.

4.1.1. Qualitative characters

4.1.1.1. Coleoptile: Colour

The coleoptile colour of 60 landraces and three check varieties are presented in Table 11. Among the 60 genotypes studied, 42 genotypes exhibited purple coleoptile and 18 genotypes and all check varieties exhibited colourless coleoptile.

Table 11. Grouping of genotypes based on coleoptiles colour

State	Genotypes
Colourless	**Landraces:** Kalladi aryan, Chomala, Addy, Mangalapuram puncha, Mulla kuruva, Njavara black, Mahi kuruva, Valichoori, Gandhakasala, Kothandan, Kunam kulumban, Jeerakasala, Chomala-1, Rasagatham, Njavara, Sugandhamathi, Kayama, Gandhakasala (dwarf) **Check varieties**: Kanchana, Uma, Aathira
Purple	**Landraces:** Thondi-1, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Keervana, Kothandon, Thondi-3, Chomala-2, Kanni kayama, Kodu veliyan, Thondi-2, Chenthondi, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mannu veliyan, Veliyan, Urulan kayama, Mullan puncha,

	Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Thavalakannan, Kutti veliyan, Thonnooran thondi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan, Karimpalan

4.1.1.2. Basal leaf: Sheath colour

The colour of basal leaf sheath of the genotypes are presented in Table 12. Among the 60 landraces studied, 18 genotypes and all the check varieties showed green basal leaf sheath colour, 25 genotypes showed light purple colour for basal leaf sheath, ten genotypes showed purple lines and seven genotypes exhibited purple colour (Plate 10). Genotypes with light purple colour formed the biggest group.

Table 12. Grouping of genotypes based on basal leaf sheath colour

State	Genotypes
Green	**Landraces:** Kalladi aryan, Chomala, Addy, Mangalapuram puncha, Mulla kuruva, Njavara black, Mahi kuruva, Valichoori, Gandhakasala, Kothandan, Kunam kulumban, Jeerakasala, Chomala-1, Rasagatham, Njavara, Sugandhamathi, Kayama, Gandhakasala (dwarf) **Check varieties**: Kanchana, Uma and Aathira
Light purple	**Landraces:** Thondi-1, Ayirankana, Kannali, Chomala-2, Kothandon, Kanni kayama, Thondi-2, Chennellu, Punnadan thondi, Rajameni, Chettu veliyan, Mannu veliyan, Urulan kayama, Peruvaya, Palthondi, Vaalicha, Edavaka, Velumpala, Uruni kayama, Kutti veliyan, Thonnooran thondi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan
Purple lines	**Landraces:** Palveliyan, Ambalavayal-1, Chenthondi, Mullan puncha, Chenthadi, Veliya thondi, Adukkan, Ambalavayal-2, Karimpalan, Thondi-3

Uniform purple	**Landraces:** Keervana, Kodu veliyan, Putta batta, Kuruva, Veliyan, Kumbali, Thavalakannan

4.1.1.3. Leaf: Intensity of green colour

The intensity of green colour of leaf of 60 landraces and three check varieties are presented in Table 13. Forty-eight out of 60 genotypes and all check varieties possessed dark green colour for leaves and 12 genotypes exhibited medium green colour for leaves.

Table 13. Grouping of genotypes based on intensity of green colour of leaf

State	Genotypes
Medium	**Landraces:** Kalladi aryan, Addy, Thondi-2, Kuruva, Mulla kuruva, Mahi kuruva, Urulan kayama, Thondi-3, Edavaka, Jeerakasala, Rasagatham, Kayama
Dark	**Landraces:** Thondi-1, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Kanni kayama, Kodu veliyan, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta ,Rajameni, Chettu veliyan, Mannu veliyan, Njavara black, Veliyan, Valichoori, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Gandhakasala, Kothandan, Thavalakannan, Kunam kulumban, Chomala-2, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Sugandhamathi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan, Karimpalan, Gandhakasala (dwarf) **Check varieties**: Kanchana, Uma and Aathira

4.1.1.4. Leaf: Anthocyanin colouration and distribution

The genotype Thavalakannan exhibited leaf anthocyanin colouration as blotches on leaf and remaining 59 genotypes and all check varieties showed no anthocyanin colouration on leaf.

4.1.1.5. Leaf sheath: Anthocyanin colouration

The anthocyanin colouration of leaf sheath of 60 landraces and three check varieties are presented in Table 14. Out of 60 genotypes, majority (42) genotypes exhibited leaf sheath anthocyanin colouration and 18 genotypes and all check varieties exhibited no anthocyanin colouration on leaf sheath (Plate 11).

Table 14. Grouping of genotypes based on anthocyanin colouration of leaf sheath

State	Genotypes
Absent	**Landraces:** Kalladi aryan, Chomala, Addy, Mangalapuram puncha, Mulla kuruva, Njavara black, Mahi kuruva, Valichoori, Gandhakasala, Kothandan, Kunam kulumban, Jeerakasala, Chomala-1, Rasagatham, Njavara, Sugandhamathi, Kayama, Gandhakasala (dwarf) **Check varieties**: Kanchana, Uma and Aathira
Present	**Landraces:** Gandhakasala (dwarf), Thondi-1, Ayirankana, Palveliyan, Kannali, Keervana, Ambalavayal-1, Adukkan, Kothandon, Kanni kayama, Kodu veliyan, Thondi-2, Chenthondi, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mannu veliyan, Veliyan, Urulan kayama, Thondi-3, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Ambalavayal-2, Uruni kayama, Thavalakannan, Chomala-2, Kutti veliyan, Thonnooran thondi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan, Karimpalan

4.1.1.6. Leaf: Pubescence of blade surface

The pubescence of leaf blade surface of 60 landraces and three check varieties are presented in Table 15. Ten genotypes and Aathira (check) possessed medium pubescence of blade surface of leaf and remaining 50 genotypes exhibited strong pubescence of leaf blade surface, along with check varieties Kanchana and Uma.

Table 15. Grouping of genotypes based on pubescence of leaf blade surface

State	Genotypes
Medium	**Landraces:** Kalladi aryan, Kanni kayama, Ayirankana, Kodu veliyan, Njavara black, Mahi kuruva, Edavaka, Rasagatham, Gandhakasala (dwarf), Kayama **Check variety**: Aathira
Strong	**Landraces:** Thondi-1, Ambalavayal-1, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Addy, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Veliyan, Valichoori, Urulan kayama, Thondi-3, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Gandhakasala, Kothandan, Thavalakannan, Kunam kulumban, Chomala-2, Jeerakasala, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Sugandhamathi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan, Karimpalan **Check variety:** Kanchana, Uma

4.1.1.7. Leaf: Auricles

Fifty-nine out of 60 genotypes and all check varieties exhibited leaf auricles, whereas auricles were not present in Mullan puncha (Plate 12).

4.1.1.8. Leaf: Anthocyanin colouration of auricles

Fifty-eight out of 59 genotypes (one genotype did not possess auricles) and all check varieties possessed colourless auricles. Only one genotype (Thavalakannan) recorded purple colour for auricles (Plate 12).

4.1.1.9. Leaf: Collar

All the 60 genotypes and check varieties exhibited leaf collar.

4.1.1.10. Leaf: Anthocyanin colouration of collar

Out of 60 genotypes and check varieties, none of the genotypes including check varieties exhibited anthocyanin colouration of leaf collar.

4.1.1.11. Leaf: Ligule

All genotypes and check varieties exhibited leaf ligule.

4.1.1.12. Leaf: Shape of ligule

All the genotypes and check varieties, exhibited split type of leaf ligule (Plate 13).

4.1.1.13. Leaf: Colour of ligule

Fifty-nine out of 60 genotypes and all check varieties exhibited white colour for ligule and Thavalakannan exhibited purple colour for ligule (Plate 13).

4.1.1.14. Culm: Attitude

The attitude of the culm of 60 landraces and three check varieties are presented in Table 16. Erect culm type was present in 12 genotypes and in all check varieties, semi-erect type of culm in 37 genotypes and open type of culm in ten genotypes. It was interesting to note spreading culm attitude in one genotype (Kalladi aryan).

Plate 10. Uniform purple colour of basal leaf sheath

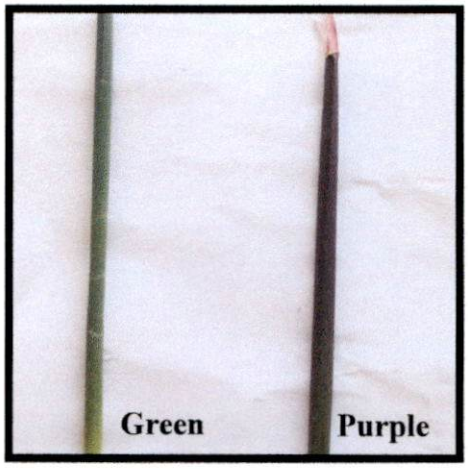
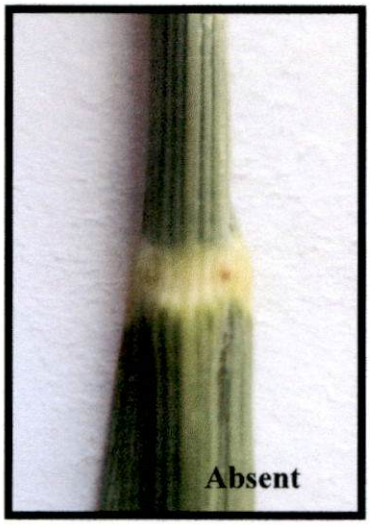
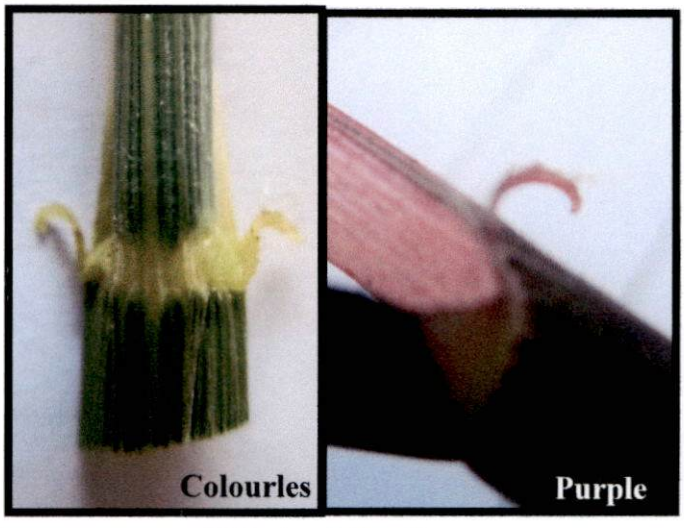


Plate 11. Anthocyanin colouration of leaf sheath



12A. Absence of auricle



12B. Auricle colour

Plate 12. State and colour of auricles

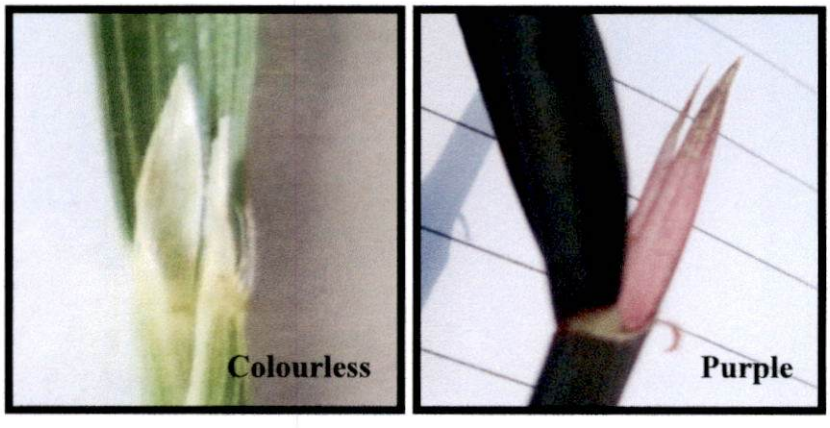


Plate 13. Colour and shape of ligule

Table 16. Grouping of genotypes based on culm attitude

State	Genotypes
Erect	**Landraces:** Kannali, Addy, Chenthondi, Mangalapuram puncha, Putta batta, Njavara black, Mahi kuruva, Valichoori, Adukkan, Kunam kulumban, Rasagatham, Sugandhamathi **Check varieties:** Kanchana, Uma and Aathira
Semi-erect	**Landraces:** Ambalavayal-1, Ayirankana, Palveliyan, Chomala, Keervana, Kothandon, Kanni kayama, Thondi-2, Chennellu, Punnadan thondi, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Veliyan, Urulan kayama, Thondi-3, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Ambalavayal-2, Uruni kayama, Kothandan, Thavalakannan, Chomala-2, Jeerakasala, Njavara, Vellimuthu, Mara thondi, Kayama, Gandhakasala (dwarf)
Open	**Landraces:** Thondi-1, Kodu veliyan, Mullan puncha, Gandhakasala, Kutti veliyan, Thonnooran thondi, Chomala-1, Palthondi matta, Onamottan, Karimpalan
Spreading	**Landrace:** Kalladi aryan

4.1.1.15. Spikelet: Density of pubescence of lemma

The density of pubescence of lemma in 60 landraces and three check varieties are presented in Table 17. Out of 60 genotypes, six genotypes possessed weak pubescence, 16 genotypes exhibited medium pubescence along with check varieties Kanchana and Uma, 37 genotypes showed strong pubescence along with Aathira and Mullan puncha alone exhibited very strong type of pubescence of lemma.

Table 17. Grouping of genotypes based on density of pubescence of lemma

State	Genotypes
Weak	**Landraces:** Kannali, Kuruva, Njavara black, Thondi-3, Thavalakannan, Sugandhamathi
Medium	**Landraces:** Ambalavayal-1, Putta batta, Mannu veliyan, Valichoori, Urulan kayama, Mangalapuram puncha, Vaalicha, Veliya thondi, Velumpala, Ambalavayal-2, Jeerakasala, Rasagatham, Njavara, Palthondi matta, Mara thondi, Onamottan **Check varieties:** Kanchana and Uma
Strong	**Landraces:** Kalladi aryan, Thondi-1, Ayirankana, Palveliyan, Chomala, Keervana, Kothandon, Kanni kayama, Addy, Kodu veliyan, Thondi-2, Chenthondi, Chennellu, Punnadan thondi, Rajameni, Chettu veliyan, Mulla kuruva, Veliyan, Mahi kuruva, Chenthadi, Peruvaya, Palthondi, Edavaka, Kumbali, Adukkan, Uruni kayama, Gandhakasala, Kothandan, Kunam kulumban, Chomala-2, Kutti veliyan, Thonnooran thondi, Chomala-1, Vellimuthu, Kayama, Karimpalan, Gandhakasala (dwarf) **Check varieties:** Aathira
Very strong	**Landrace:** Mullan puncha

4.1.1.16. Lemma: Anthocyanin colouration of keel

None of the genotypes including check varieties exhibited anthocyanin colouration of keel.

4.1.1.17. Lemma: Anthocyanin colouration of lemma apex

The anthocyanin colouration of apex of 60 landraces and three check varieties are presented in Table 18. Strong anthocyanin colouration of apex was present in 12 genotypes, very strong anthocyanin colouration in 27 genotypes and

remaining 21 genotypes and all check varieties did not showed anthocyanin colouration of apex (Plate 14).

Table 18. Grouping of genotypes based on anthocyanin colouration of lemma apex

State	Genotypes
Absent	**Landraces:** Kalladi aryan, Ambalavayal-1, Chomala, Addy, Mangalapuram puncha, Mulla kuruva, Njavara black, Mahi kuruva, Valichoori, Thondi-3, Mullan puncha, Gandhakasala, Kunam kulumban, Chomala-2, Jeerakasala, Chomala-1, Rasagatham, Njavara, Sugandhamathi, Kayama, Gandhakasala (dwarf) **Check varieties:** Kanchana, Uma and Aathira
Strong	**Landraces:** Kodu veliyan, Punnadan thondi, Putta batta, Adukkan, Kothandan, Kutti veliyan, Thonnooran thondi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan, Karimpalan
Very strong	**Landraces:** Thondi-1, Ayirankana, Palveliyan, Kannali, Keervana, Kothandon, Kanni kayama, Thondi-2, Chenthondi, Chennellu, Rajameni, Chettu veliyan, Kuruva, Mannu veliyan, Veliyan, Urulan kayama, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Ambalavayal-2, Uruni kayama, Thavalakannan

4.1.1.18. Lemma: Anthocyanin colour of area below lemma apex

None, out of the genotypes studied exhibited anthocyanin colouration of area below apex of lemma and also the check varieties.

4.1.1.19. Spikelet: Colour of stigma

The colour of stigma of 60 landraces and three check varieties are presented in Table 19. Twenty-one out of 60 genotypes and all check varieties possessed

white stigma, whereas Gandhakasala and Gandhakasala (dwarf) possessed light green stigma and 37 genotypes exhibited purple stigma (Plate 15).

Table 19. Grouping of genotypes based on stigma colour

State	Genotypes
White	**Landraces:** Kalladi aryan, Ambalavayal-1, Chomala, Addy, Mangalapuram puncha, Chennellu, Punnadan thondi, Rajameni, Mulla kuruva, Njavara black, Mahi kuruva, Valichoori, Mullan puncha, Kunam kulumban, Chomala-2, Jeerakasala, Chomala-1, Rasagatham, Njavara, Sugandhamathi, Kayama **Check varieties:** Kanchana, Uma and Aathira
Light green	**Landraces:** Gandhakasala, Gandhakasala (dwarf)
Purple	**Landraces:** Thondi-1, Ayirankana, Palveliyan, Kannali, Keervana, Kothandon, Kanni kayama, Kodu veliyan, Thondi-2, Chenthondi, Putta batta, Chettu veliyan, Kuruva, Mannu veliyan, Veliyan, Urulan kayama, Thondi-3, Uruni kayama, Kothandan, Thavalakannan, Kutti veliyan, Thonnooran thondi, Palthondi matta, Vellimuthu, Mara thondi, Onamottan, Karimpalan, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2

4.1.1.20. Stem: Anthocyanin colouration of nodes

Out of 60 landraces and three check varieties, none of the genotypes, including check varieties exhibited anthocyanin colouration of nodes (Plate 16).

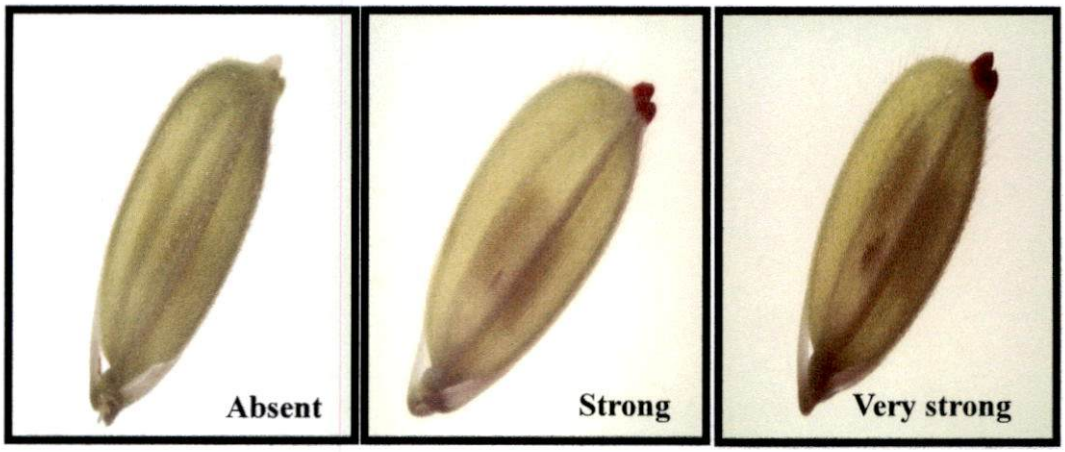


Plate 14. Anthocyanin colouration of lemma apex (Magnification- 35X)

Plate 15. Colour of stigma (Magnification- 35X)

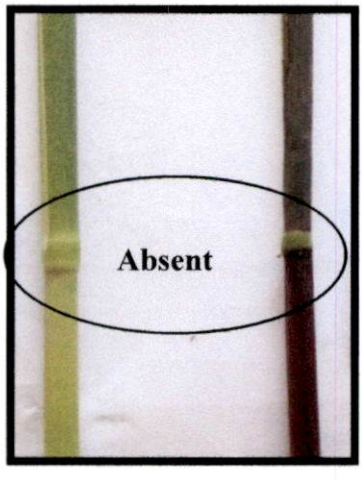


Plate 16. Anthocyanin colouration of stem nodes

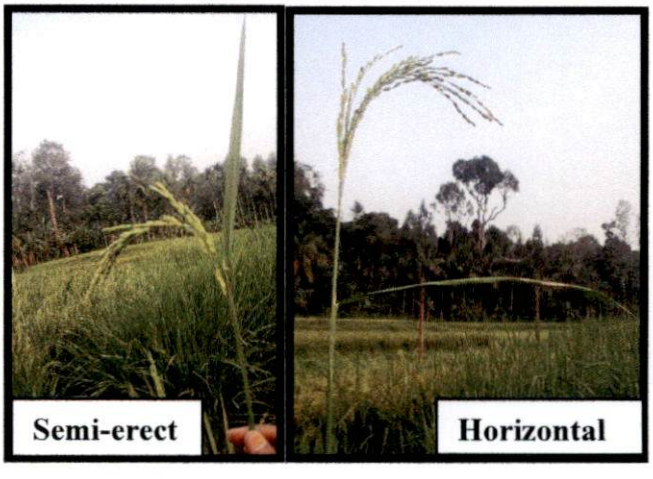


Plate 17. Attitude of flag leaf blade

4.1.1.21. Flag leaf: Attitude of blade

Fifty-two out of 60 genotypes and all check varieties exhibited semi-erect type of blade and eight genotypes namely Thondi-1, Addy, Kodu veliyan, Rajameni, Chettu veliyan, Kutti veliyan, Palthondi matta and Onamottan exhibited horizontal type of blade (Plate 17).

4.1.1.22. Panicle: Curvature of main axis

Out of 60 genotypes, seven genotypes namely Mulla kuruva, Mannu veliyan, Njavara black, Mahi kuruva, Valichoori, Veliya thondi and Rasagatham exhibited deflexed type of curvature of main axis. Drooping type of curvature was exhibited in 53 genotypes and in all the check varieties.

4.1.1.23. Lemma and palea: Colour

Lemma and palea colour of 60 landraces and three check varieties are presented in Table 20. Out of 60 genotypes, ten genotypes exhibited straw colour for lemma and palea, two genotypes exhibited gold and gold furrows on straw background, nine genotypes exhibited brown spots on straw, 18 genotypes exhibited brown furrows on straw, 13 genotypes exhibited brown colour and eight genotypes exhibited black colour for lemma and palea (Plate 18 and Plate 21).

Table 20. Grouping of genotypes based on lemma and palea colour

State	Genotypes
Straw	**Landraces:** Kanni kayama, Urulan kayama, Palthondi, Vaalicha, Velumpala, Jeerakasala, Kutti veliyan, Sugandhamathi, Kayama, Onamottan
Gold and gold furrows on straw background	**Landraces:** Chomala, Ambalavayal-2 **Check variety:** Aathira

Brown spots on straw	**Landraces:** Ayirankana, Palveliyan, Addy, Chettu veliyan, Kuruva, Edavaka, Uruni kayama, Gandhakasala, Gandhakasala (dwarf) **Check variety:** Uma
Brown furrows on straw	**Landraces:** Thondi-1, Kodu veliyan, Thondi-2, Mangalapuram puncha, Punnadan thondi, Putta batta, Rajameni, Mulla kuruva, Valichoori, Peruvaya, Veliya thondi, Kumbali, Adukkan, Chomala-2, Chomala-1, Palthondi matta, Vellimuthu, Mara thondi **Check variety:** Kanchana
Brown	**Landraces:** Kalladi aryan, Ambalavayal-1, Chennellu, Mannu veliyan, Veliyan, Mahi kuruva, Thondi-3, Kothandan, Thavalakannan, Kunam kulumban, Thonnooran thondi, Rasagatham, Njavara
Black	**Landraces:**Kannali, Keervana, Kothandon, Chenthondi, Njavara black, Mullan puncha, Chenthadi, Karimpalan

4.1.1.24. Panicle: Presence of awns and colouration

Out of 60 genotypes, six genotypes namely Kothandon, Mullan puncha, Chomala-2, Jeerakasala, Sugandhamathi and Kayama exhibited presence of awns and awnlessness was exhibited by 54 genotypes and all the check varieties. Among of six genotypes with awns, three genotypes namely Chomala-2, Jeerakasala and Sugandhamathi exhibited yellowish brown awns, Kothandon exhibited brown awns, Kayama exhibited purple awns. Presence of long black awns in a panicle was observed in 'Mullan puncha' (Plate 19, 20 and 22).

4.1.1.25. Panicle: Distribution of awns

Out of six genotypes with awns, distribution of awns was seen in tip of the panicle of Kothandon, Chomala-2 and Sugandhamathi, in the upper half of the panicles in Jeerakasala and in the whole length of panicles in Mullan puncha and Kayama.

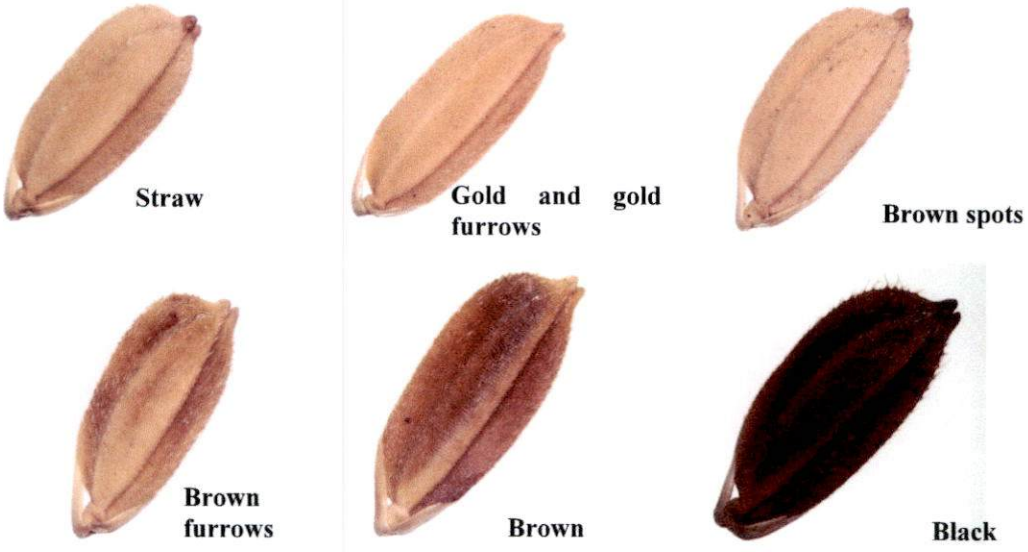


Plate 18. Lemma and palea colour (Magnification- 35X)

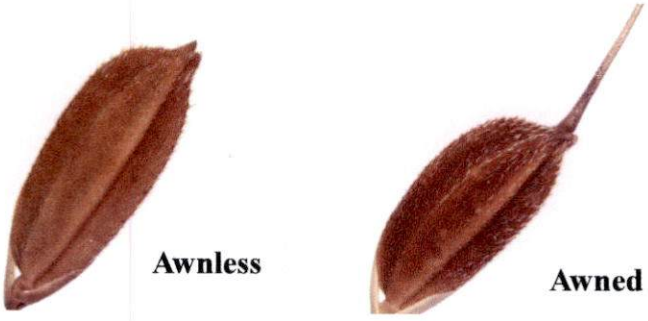


Plate 19. State of awns (Magnification- 35X)

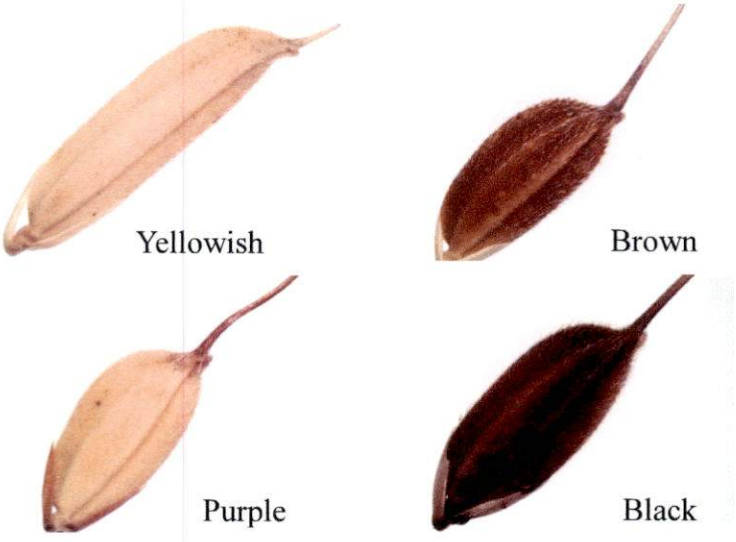


Plate 20. Colour of awns (Magnification- 35X)

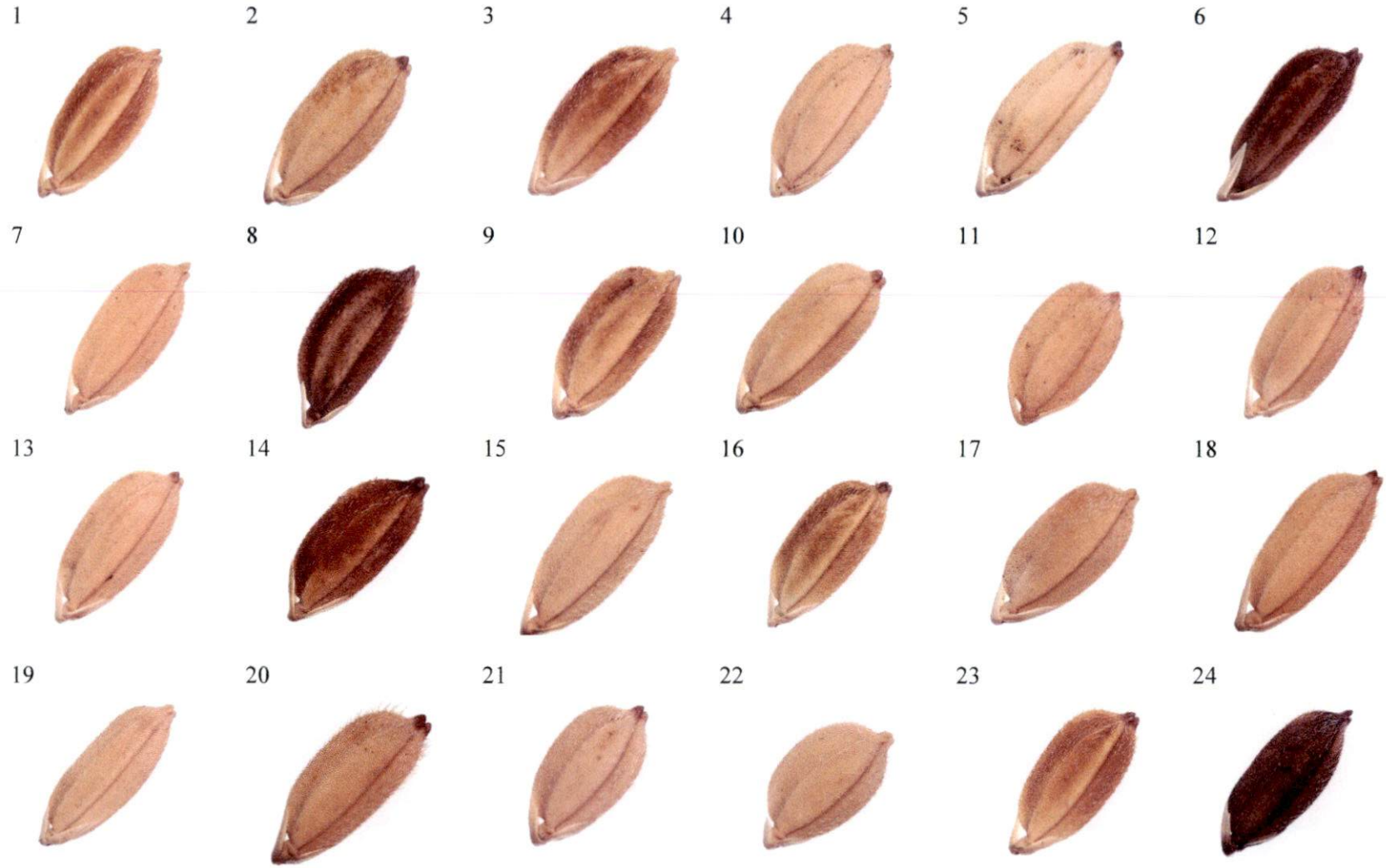


Plate 21. Stereomicroscopic images of grains of Wayanad rice landraces (Magnification- 35X)

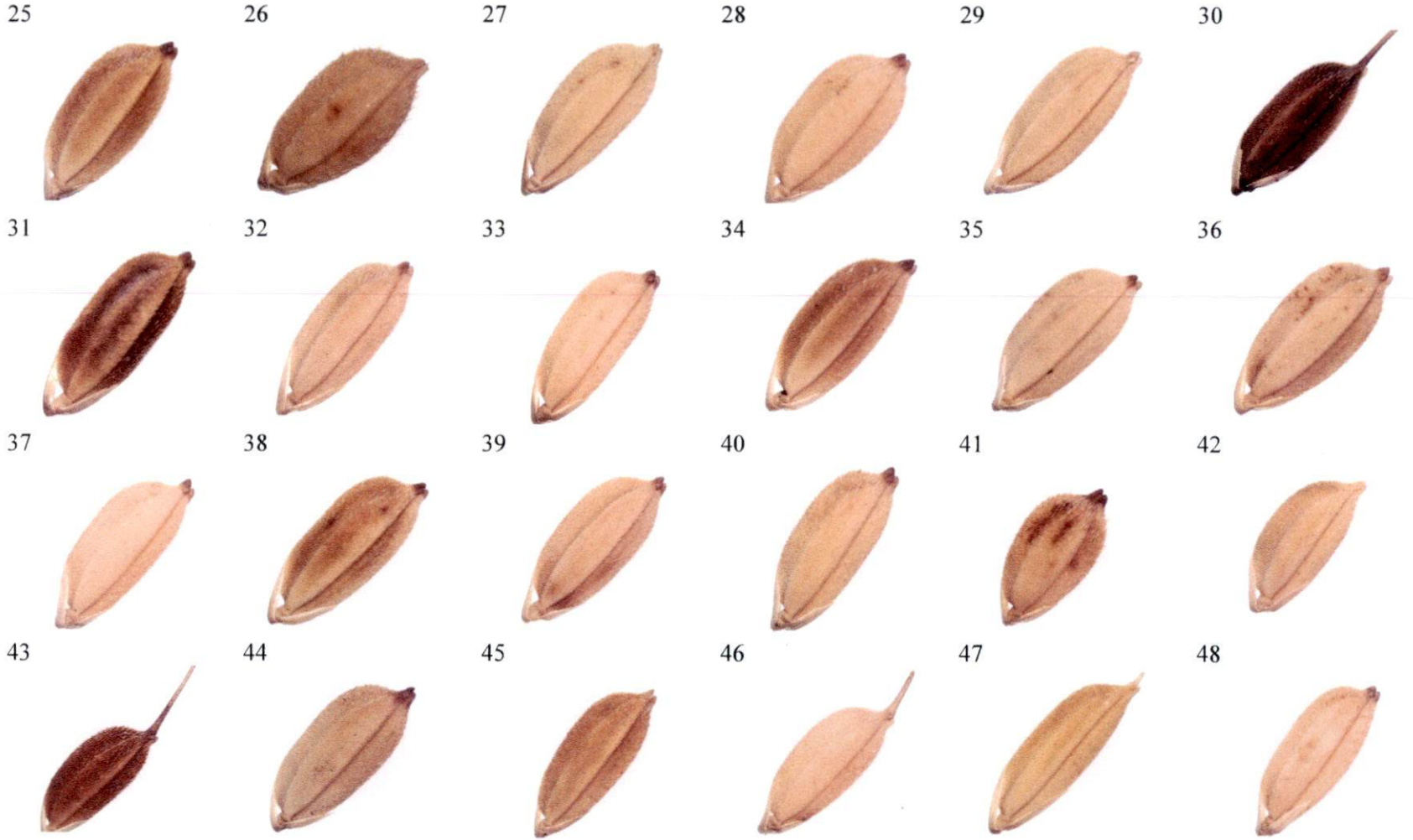


Plate 21. Stereomicroscopic images of grains of Wayanad rice landraces (Continued….)

Plate 21. Stereomicroscopic images of grains of Wayanad rice landraces

(1) Kalladi aryan, **(2)** Thondi-1, **(3)** Ambalavayal-1, **(4)** Ayirankana, **(5)** Palveliyan, **(6)** Kannali, **(7)** Chomala, **(8)** Keervana, **(9)** Kothandon, **(10)** Kanni kayama, **(11)** Addy, **(12)** Kodu veliyan, **(13)** Thondi-2, **(14)** Chenthondi, **(15)** Mangalapuram puncha, **(16)** Chennellu, **(17)** Punnadan thondi, **(18)** Putta batta, **(19)** Rajameni, **(20)** Chettu veliyan, **(21)** Kuruva, **(22)** Mulla kuruva, **(23)** Mannu veliyan, **(24)** Njavara black, **(25)** Veliyan, **(26)** Mahi kuruva, **(27)** Valichoori, **(28)** Urulan kayama, **(29)** Thondi-3, **(30)** Mullan puncha, **(31)** Chenthadi, **(32)** Peruvaya, **(33)** Palthondi, **(34)** Vaalicha, **(35)** Veliya thondi, **(36)** Edavaka, **(37)** Velumpala, **(38)** Kumbali, **(39)** Adukkan, **(40)** Ambalavayal-2, **(41)** Uruni kayama, **(42)** Gandhakasala, **(43)** Kothandan, **(44)** Thavalakannan, **(45)** Kunam kulumban, **(46)** Chomala-2, **(47)** Jeerakasala, **(48)** Kutti veliyan, **(49)** Thonnooran thondi, **(50)** Chomala-1, **(51)** Rasagatham, **(52)** Njavara, **(53)** Sugandhamathi, **(54)** Palthondi matta, **(55)** Vellimuthu, **(56)** Mara thondi, **(57)** Kayama, **(58)** Onamottan, **(59)** Karimpalan, **(60)** Gandhakasala (dwarf).

4.1.1.26. Panicle: Presence of secondary branching

All the genotypes, including check varieties exhibited presence of secondary branching in panicles.

4.1.1.27. Panicle: Secondary branching

Fifty-two out of 60 genotypes and Aathira (check) recorded clustered type of branching, seven genotypes namely Addy, Kodu veliyan, Njavara black, Thonnooran thondi, Rasagatham, Sugandhamathi, Onamottan and two check varieties (Kanchana and Uma) showed strong branching character. Only one genotype (Mullan puncha) exhibited weak type of branching (Plate 23).

4.1.1.28. Panicle: Attitude of branches

Attitude of branches in panicles of all the genotypes studied are presented in Table 21. Out of 60 genotypes, erect to semi-erect type of branches were seen in six genotypes, semi-erect branching in four genotypes, semi-erect to spreading branching in 16 genotypes, along with check varieties Kanchana and Uma. Remaining 34 genotypes and Aathira (check) exhibited spreading type of branching (Plate 24).

Table 21. Grouping of genotypes based on attitude of branches in panicle

State	Genotypes
Erect to semi-erect	**Landraces:** Addy, Mulla kuruva, Njavara black, Mahi kuruva, Thavalakannan, Rasagatham
Semi-erect	**Landraces:** Ayirankana, Kuruva, Thonnooran thondi, Njavara
Semi-erect to spreading	**Landraces:** Kalladi aryan, Kannali, Kanni kayama, Kodu veliyan, Thondi-2, Mangalapuram puncha, Chennellu, Punnadan thondi, Rajameni, Veliyan, Valichoori, Thondi-3, Mullan puncha, Sugandhamathi, Vellimuthu, Karimpalan **Check varieties:** Kanchana and Uma

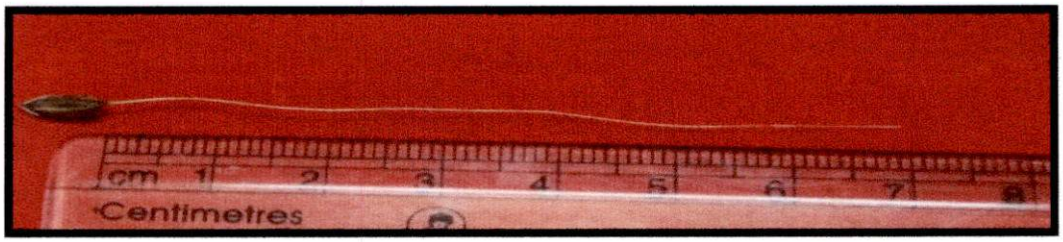


Plate 22. Mullan puncha grain with longest awns

Plate 23. Secondary branching in panicles

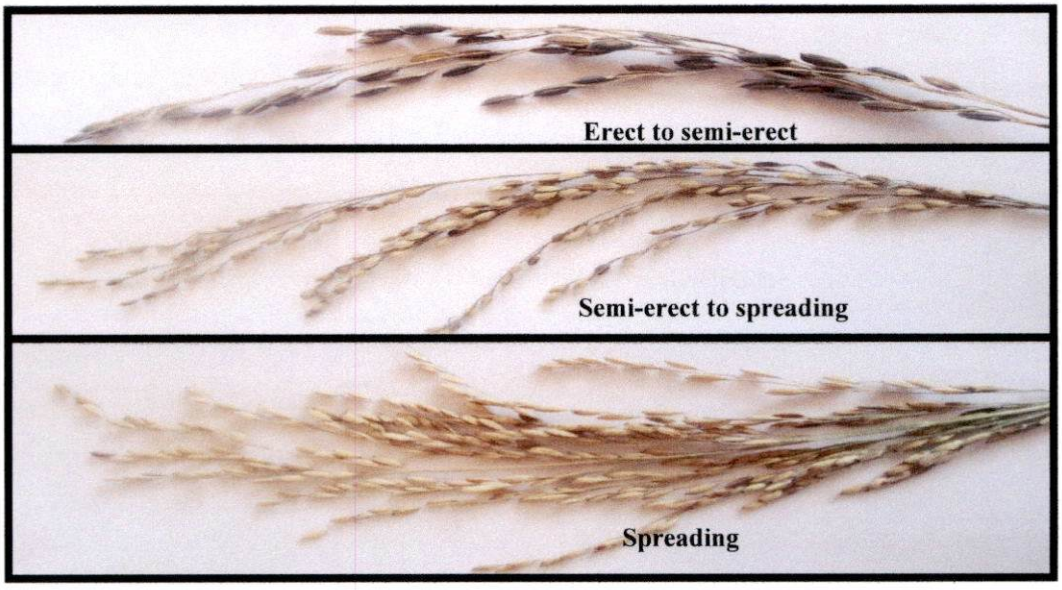


Plate 24. Attitude of branches in panicles

Spreading	**Landraces:** Thondi-1, Ambalavayal-1, Palveliyan, Chomala, Keervana, Kothandon, Chenthondi, Putta batta, Chettu veliyan, Mannu veliyan, Urulan kayama, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Gandhakasala, Kothandan, Kunam kulumban, Chomala-2, Jeerakasala, Kutti veliyan, Chomala-1, Palthondi matta, Mara thondi, Kayama, Onamottan, Gandhakasala (dwarf) **Check variety:** Aathira

4.1.1.29. Panicle: Exsertion

Well exserted panicles were recorded in 55 genotypes and also in all the check varieties. Mostly exserted type of panicles were seen in five genotypes namely, Ayirankana, Valichoori, Kothandan, Thonnooran thondi and Palthondi matta (Plate 25).

4.1.1.30. Leaf: Senescence

The senescence of leaf in 60 landraces and three check varieties are presented in Table 22. Out of 60 genotypes, eight genotypes showed early senescence, 27 genotypes and all check varieties showed medium senescence, whereas 25 genotypes exhibited late senescence.

Table 22. Grouping of genotypes based on leaf senescence

State	Genotypes
Early	**Landraces:** Kothandon, Addy, Putta batta, Urulan kayama, Thavalakannan, Rasagatham, Sugandhamathi, Kayama
Medium	**Landraces:** Kalladi aryan, Thondi-1, Ambalavayal-1, Kannali, Keervana, Kanni kayama, Kodu veliyan,, Mangalapuram puncha, Chennellu, Punnadan thondi, Kuruva, Mannu veliyan, Mahi kuruva,

	Thondi-3, Chenthadi, Veliya thondi, Edavaka, Adukkan, Uruni kayama, Gandhakasala, Kothandan, Kunam kulumban, Thonnooran thondi, Njavara, Palthondi matta, Onamottan, Gandhakasala (dwarf) **Check varieties:** Kanchana, Uma and Aathira
Late	**Landraces:** Ayirankana, Palveliyan, Chomala, Thondi-2, Chenthondi, Rajameni, Chettu veliyan, Mulla kuruva, Njavara black, Veliyan, Valichoori, Mullan puncha, Peruvaya, Palthondi, Vaalicha, Velumpala, Kumbali, Ambalavayal-2, Chomala-2, Jeerakasala, Kutti veliyan, Chomala-1, Vellimuthu, Mara thondi, Karimpalan

4.1.1.31. Sterile lemma: Colour

All the landraces and check varieties exhibited straw colour for sterile lemma, except for Kayama, which exhibited purple colour for the sterile lemma (Plate 26).

4.1.1.32. Decorticated grain: Shape

The shape of decorticated grain of 60 landraces and three check varieties are presented in Table 23. Out of 60 landraces, three genotypes exhibited short slender kernel, five genotypes exhibited short bold kernel, two genotypes exhibited medium slender kernel and remaining 49 genotypes and all check varieties exhibited medium bold kernel. Only one genotype (Sugandhamathi) exhibited long slender kernel (Plate 27).

Table 23. Grouping of genotypes based on decorticated grain shape

State	Genotypes
Short slender	**Landraces:** Gandhakasala, Rasagatham, Gandhakasala (dwarf)

Short bold	**Landraces:** Addy, Kuruva, Mulla kuruva, Mahi kuruva, Uruni kayama
Medium slender	**Landraces:** Kunam kulumban, Jeerakasala **Check varieties:** Kanchana, Uma and Aathira
Medium bold	**Landraces:** Kalladi aryan, Thondi-1, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Kanni kayama, Kodu veliyan, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Mannu veliyan, Njavara black, Veliyan, Valichoori, Urulan kayama, Thondi-3, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Kothandan, Thavalakannan, Chomala-2, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Palthondi matta, Vellimuthu, Mara thondi, Kayama, Onamottan, Karimpalan
Long slender	**Landrace:** Sugandhamathi

4.1.1.33. Decorticated grain (kernel): Colour

The colour of kernel in 60 landraces and three check varieties are presented in Table 24. Out of 60 genotypes, white type of kernel was seen in 17 genotypes, light red kernel was present in 14 genotypes and red kernel present in 29 genotypes and all the check varieties (Plate 28 and Plate 29).

Table 24. Grouping of genotypes based on kernel colour

State	Genotypes
White	**Landraces:** Palveliyan, Addy, Putta batta, Chettu veliyan, Mahi kuruva, Urulan kayama, Palthondi, Velumpala, Ambalavayal-2, Uruni

	kayama, Gandhakasala, Jeerakasala, Kutti veliyan, Rasagatham, Sugandhamathi, Kayama, Gandhakasala (dwarf)
Light red	**Landraces:** Kannali, Chomala, Keervana, Kothandon, Chenthondi, Chennellu, Rajameni, Mullan puncha, Chenthadi, Edavaka, Kumbali, Kunam kulumban, Karimpalan, Chomala-2
Red	**Landraces:** Kalladi aryan, Thondi-1, Ambalavayal-1, Ayirankana, Kanni kayama, Kodu veliyan, Thondi-2, Mangalapuram puncha, Punnadan thondi, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Valichoori, Thondi-3, Peruvaya, Vaalicha, Veliya thondi, Adukkan, Kothandan, Thavalakannan, Thonnooran thondi, Chomala-1, Njavara, Palthondi matta, Vellimuthu, Mara thondi, Onamottan **Check varieties:** Kanchana, Uma and Aathira

4.1.1.34. Decorticated grain (kernel): Aroma

Out of 60 genotypes, four genotypes namely Gandhakasala, Jeerakasala, Sugandhamathi and Gandhakasala (dwarf) were the aromatic type. Remaining 56 genotypes and all the check varieties were non-aromatic type.

4.1.1.35. Gelatinization temperature through alkali spreading value

Majority of genotypes and all check varieties exhibited high gelatinization temperature and two genotypes namely Addy and Sugandhamathi showed medium gelatinization temperature.

4.1.1.36. Lodging nature

Out of 60 genotypes, lodging was seen in seven genotypes namely Thondi-1, Ambalavayal-1, Chenthadi, Veliya thondi, Kumbali, Chomala-2 and Chomala-1. Remaining 53 and all the check varieties exhibited non-lodging nature.

Characterization of all the genotypes based on above described qualitative characters is presented in Table 25.

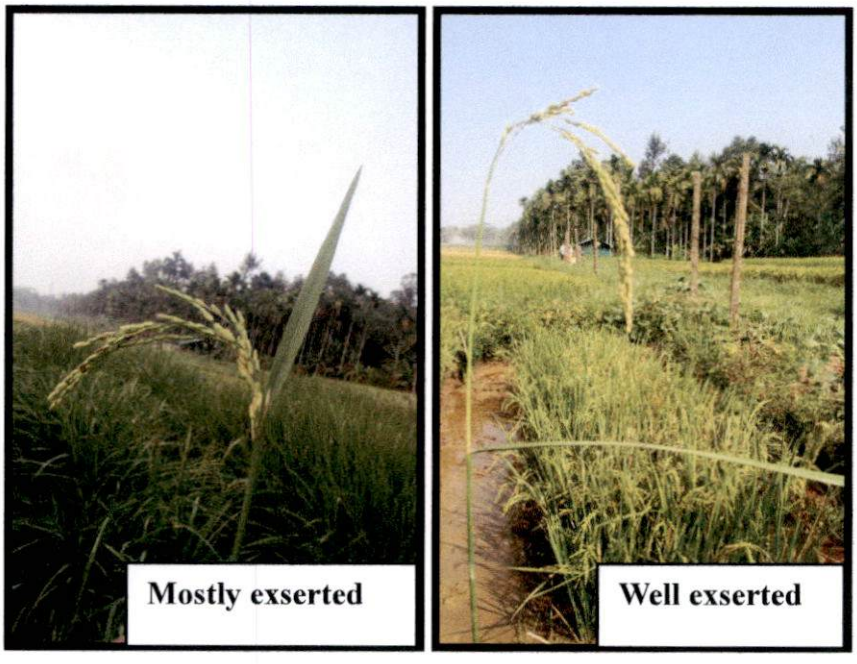


Plate 25. Panicle exsertion

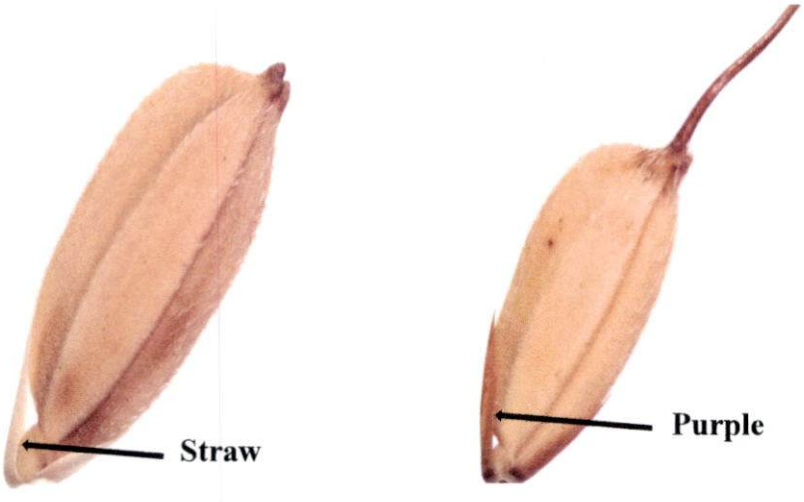


Plate 26. Sterile lemma colour (Magnification- 35X)

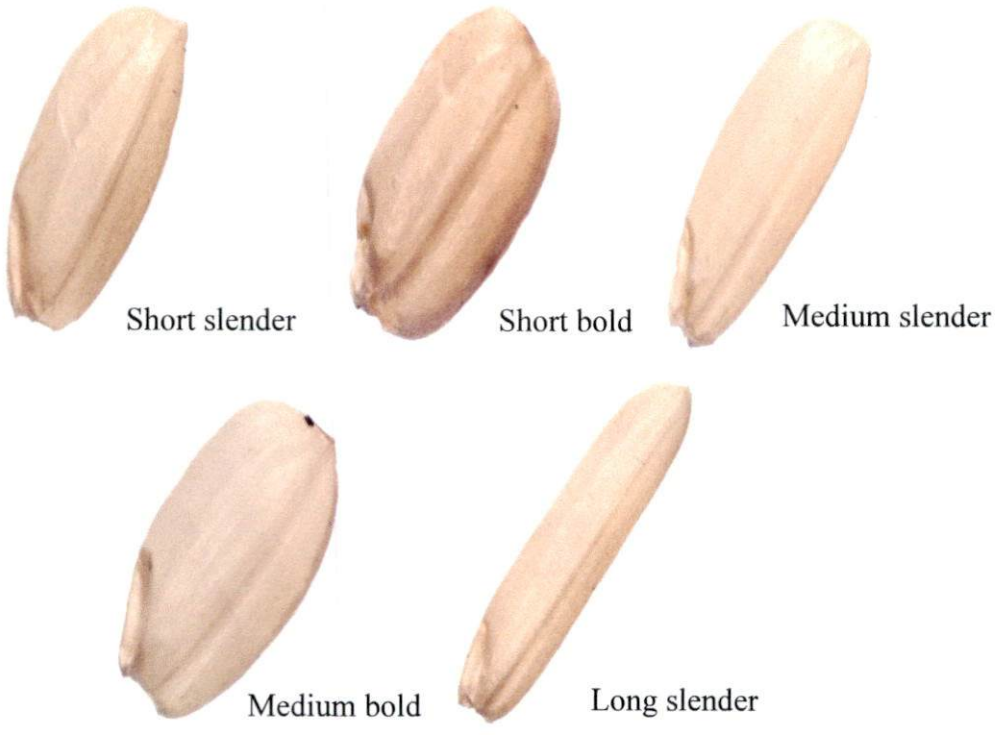


Plate 27. Decorticated grain shape (Magnification- 35X)

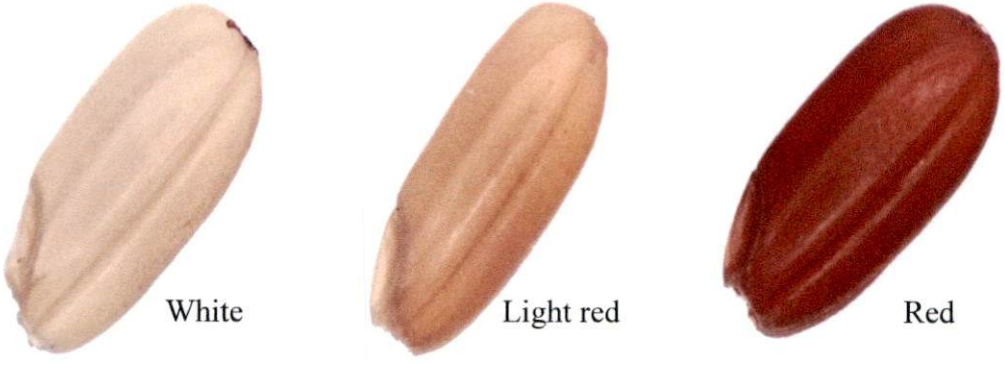


Plate 28. Decorticated grain colour (Magnification- 35X)

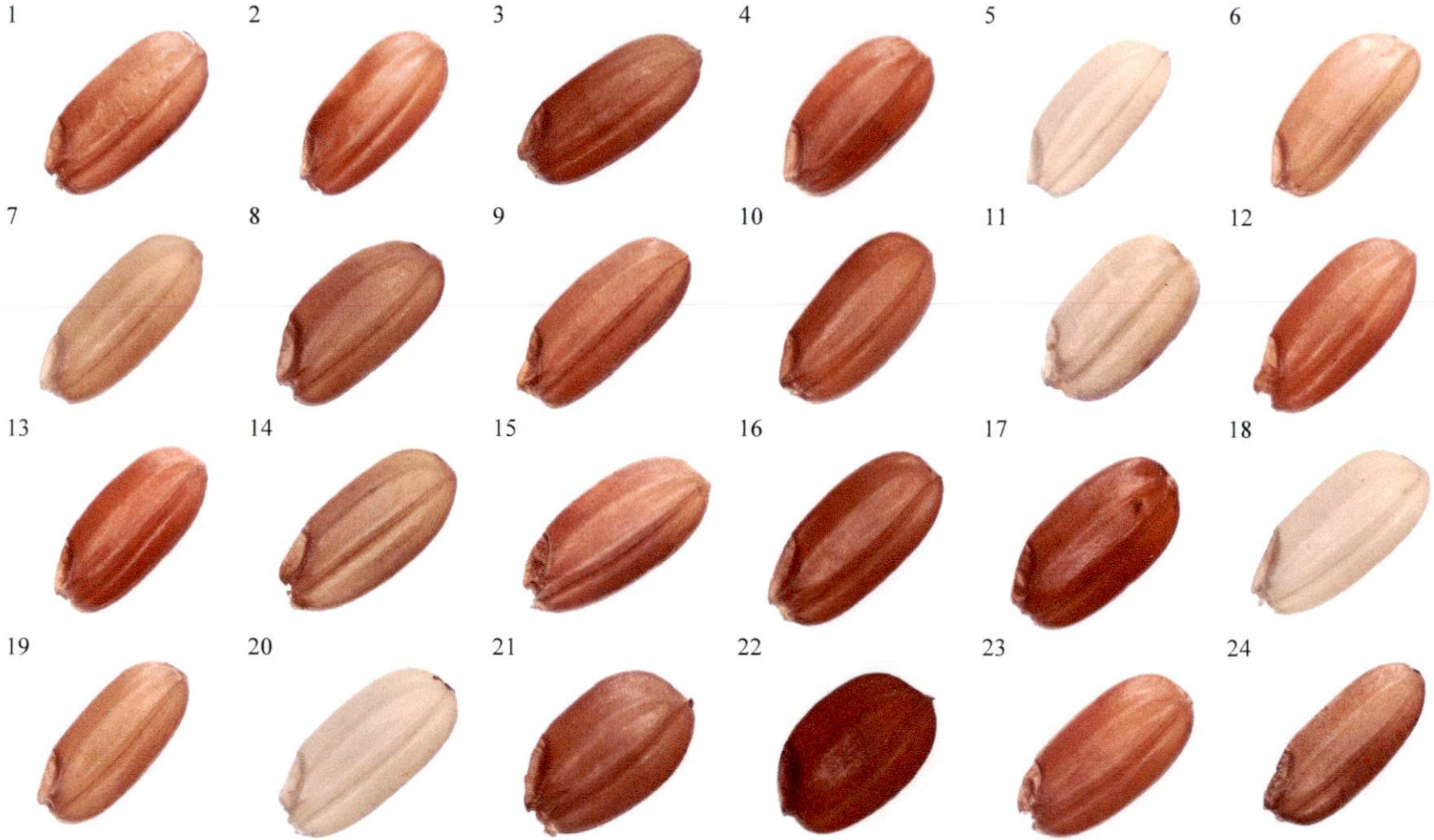


Plate 29. Stereomicroscopic images of kernels of Wayanad rice landraces (Magnification- 35X)

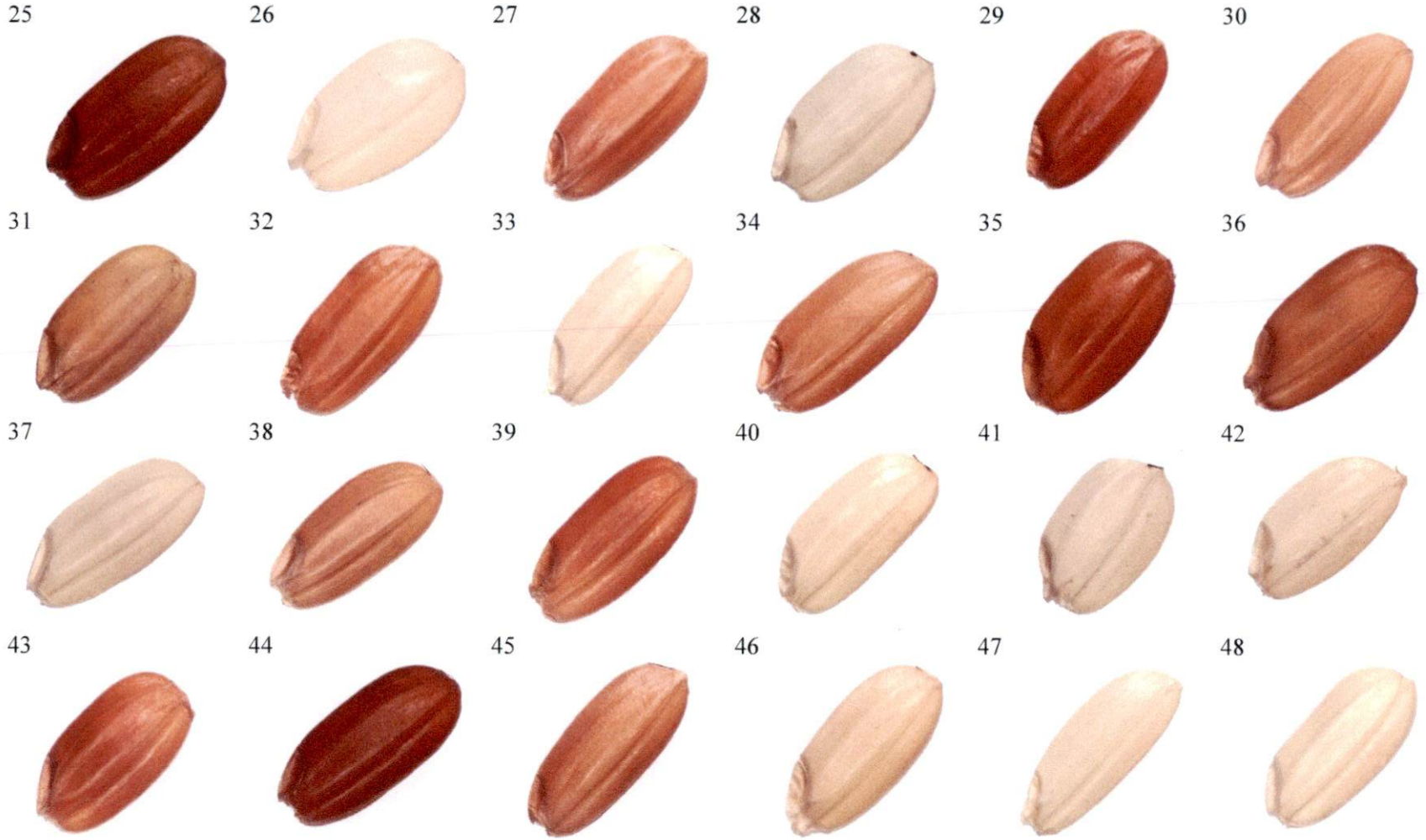


Plate 29. Stereomicroscopic images of kernels of Wayanad rice landraces (Continued…)

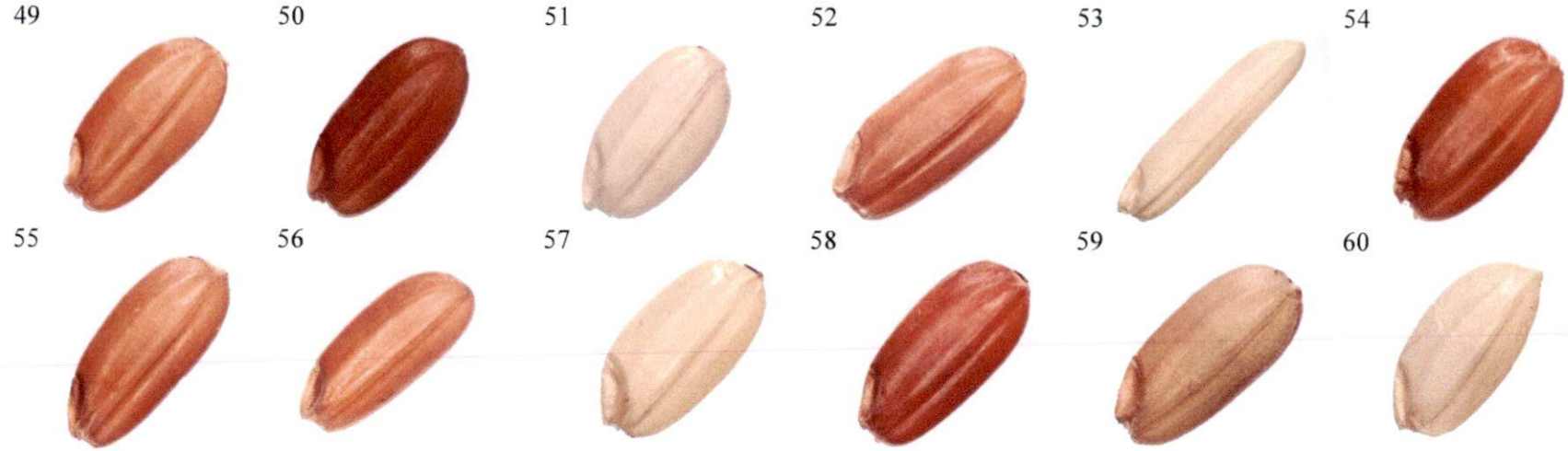


Plate 29. Stereomicroscopic images of kernels of Wayanad rice landraces

(1) Kalladi aryan, **(2)** Thondi-1, **(3)** Ambalavayal-1, **(4)** Ayirankana, **(5)** Palveliyan, **(6)** Kannali, **(7)** Chomala, **(8)** Keervana, **(9)** Kothandon, **(10)** Kanni kayama, **(11)** Addy, **(12)** Kodu veliyan, **(13)** Thondi-2, **(14)** Chenthondi, **(15)** Mangalapuram puncha, **(16)** Chennellu, **(17)** Punnadan thondi, **(18)** Putta batta, **(19)** Rajameni, **(20)** Chettu veliyan, **(21)** Kuruva, **(22)** Mulla kuruva, **(23)** Mannu veliyan, **(24)** Njavara black, **(25)** Veliyan, **(26)** Mahi kuruva, **(27)** Valichoori, **(28)** Urulan kayama, **(29)** Thondi-3, **(30)** Mullan puncha, **(31)** Chenthadi, **(32)** Peruvaya, **(33)** Palthondi, **(34)** Vaalicha, **(35)** Veliya thondi, **(36)** Edavaka, **(37)** Velumpala, **(38)** Kumbali, **(39)** Adukkan, **(40)** Ambalavayal-2, **(41)** Uruni kayama, **(42)** Gandhakasala, **(43)** Kothandan, **(44)** Thavalakannan, **(45)** Kunam kulumban, **(46)** Chomala-2, **(47)** Jeerakasala, **(48)** Kutti veliyan, **(49)** Thonnooran thondi, **(50)** Chomala-1, **(51)** Rasagatham, **(52)** Njavara, **(53)** Sugandhamathi, **(54)** Palthondi matta, **(55)** Vellimuthu, **(56)** Mara thondi, **(57)** Kayama, **(58)** Onamottan, **(59)** Karimpalan, **(60)** Gandhakasala (dwarf) .

Table 25. Characterization of 60 genotypes based on qualitative parameters

Sl. No.	Genotype	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	Kalladi aryan	1	1	5	1	1	1	5	9	2	9	1	9	3	1	7	7	1	1	1
2	Thondi-1	3	2	7	1	1	9	7	9	2	9	1	9	3	1	5	7	1	9	1
3	Ambalavayal-1	3	3	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	1	1
4	Ayirankana	3	2	7	1	1	9	5	9	2	9	1	9	3	1	3	7	1	9	1
5	Palveliyan	3	3	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
6	Kannali	3	2	7	1	1	9	7	9	2	9	1	9	3	1	1	3	1	9	1
7	Chomala	1	1	7	1	1	1	7	9	2	9	1	9	3	1	3	7	1	1	1
8	Keervana	3	4	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
9	Kothandon	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
10	Kanni kayama	3	2	7	1	1	9	5	9	2	9	1	9	3	1	3	7	1	9	1
11	Addy	1	1	5	1	1	1	7	9	2	9	1	9	3	1	1	7	1	1	1
12	Kodu veliyan	3	4	7	1	1	9	5	9	2	9	1	9	3	1	5	7	1	7	1
13	Thondi-2	3	2	5	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
14	Chenthondi	3	3	7	1	1	9	7	9	2	9	1	9	3	1	1	7	1	9	1
15	Mangalapuram puncha	1	1	7	1	1	1	7	9	2	9	1	9	3	1	1	7	1	1	1
16	Chennellu	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
17	Punnadan thondi	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	7	1
18	Putta batta	3	4	7	1	1	9	7	9	2	9	1	9	3	1	1	5	1	7	1
19	Rajameni	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
20	Chettu veliyan	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
21	Kuruva	3	4	5	1	1	9	7	9	2	9	1	9	3	1	3	3	1	9	1

Continued...

22	Mulla kuruva	1	1	5	1	1	1	7	9	2	9	1	9	3	1	3	7	1	1	1
23	Mannu veliyan	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	9	1
24	Njavara black	1	1	7	1	1	1	5	9	2	9	1	9	3	1	1	3	1	1	1
25	Veliyan	3	4	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
26	Mahi kuruva	1	1	5	1	1	1	5	9	2	9	1	9	3	1	1	7	1	1	1
27	Valichoori	1	1	7	1	1	1	7	9	2	9	1	9	3	1	1	5	1	1	1
28	Urulan kayama	3	2	5	1	1	9	7	9	2	9	1	9	3	1	3	5	1	9	1
29	Thondi-3	3	3	5	1	1	9	7	9	2	9	1	9	3	1	3	3	1	1	1
30	Mullan puncha	3	3	7	1	1	9	7	1	1	9	1	9	3	1	5	9	1	1	1
31	Chenthadi	3	3	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
32	Peruvaya	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
33	Palthondi	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
34	Vaalicha	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	9	1
35	Veliya thondi	3	3	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	9	1
36	Edavaka	3	2	5	1	1	9	5	9	2	9	1	9	3	1	3	7	1	9	1
37	Velumpala	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	9	1
38	Kumbali	3	4	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
39	Adukkan	3	3	7	1	1	9	7	9	2	9	1	9	3	1	1	7	1	7	1
40	Ambalavayal-2	3	3	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	9	1
41	Uruni kayama	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	9	1
42	Gandhakasala	1	1	7	1	1	1	7	9	2	9	1	9	3	1	5	7	1	1	1
43	Kothandan	1	1	7	1	1	1	7	9	2	9	1	9	3	1	3	7	1	7	1
44	Thavalakannan	3	4	7	9	4	9	7	9	4	9	1	9	3	3	3	3	1	9	1
45	Kunam kulumban	1	1	7	1	1	1	7	9	2	9	1	9	3	1	1	7	1	1	1

Continued...

46	Chomala-2	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	1	1
47	Jeerakasala	1	1	5	1	1	1	7	9	2	9	1	9	3	1	3	5	1	1	1
48	Kutti veliyan	3	2	7	1	1	9	7	9	2	9	1	9	3	1	5	7	1	7	1
49	Thonnooran thondi	3	2	7	1	1	9	7	9	2	9	1	9	3	1	5	7	1	7	1
50	Chomala-1	1	1	7	1	1	1	7	9	2	9	1	9	3	1	5	7	1	1	1
51	Rasagatham	1	1	5	1	1	1	5	9	2	9	1	9	3	1	1	5	1	1	1
52	Njavara	1	1	7	1	1	1	7	9	2	9	1	9	3	1	3	5	1	1	1
53	Sugandhamathi	1	1	7	1	1	1	7	9	2	9	1	9	3	1	1	3	1	1	1
54	Palthondi matta	3	2	7	1	1	9	7	9	2	9	1	9	3	1	5	5	1	7	1
55	Vellimuthu	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	7	1	7	1
56	Mara thondi	3	2	7	1	1	9	7	9	2	9	1	9	3	1	3	5	1	7	1
57	Kayama	1	1	5	1	1	1	5	9	2	9	1	9	3	1	3	7	1	1	1
58	Onamottan	3	2	7	1	1	9	7	9	2	9	1	9	3	1	5	5	1	7	1
59	Karimpalan	3	3	7	1	1	9	7	9	2	9	1	9	3	1	5	7	1	7	1
60	Gandhakasala (dwarf)	1	1	7	1	1	1	5	9	2	9	1	9	3	1	3	7	1	1	1
Check varieties																				
61	Kanchana	1	1	7	1	1	1	7	9	2	9	1	9	3	1	1	5	1	1	1
62	Uma	1	1	7	1	1	1	7	9	2	9	1	9	3	1	1	5	1	1	1
63	Aathira	1	1	7	1	1	1	5	9	2	9	1	9	3	1	1	7	1	1	1

(**A-** Coleoptile colour; **B-** Basal leaf sheath colour; **C-** Intensity of green colour for leaf; **D-** Anthocyanin colouration of leaf; **E-** Distribution of anthocyanin colouration on leaf; **F-** Leaf sheath anthocyanin colouration; **G-** Pubescence of leaf blade surface; **H-** Presence of leaf auricles; **I-** Anthocyanin colouration of auricles; **J-** Presence of leaf collar; **K-** Anthocyanin colouration of collar; **L-** Presence of leaf ligule; **M-** Shape of ligule; **N-** Colour of ligule; **O-** Culm attitude; **P-** Density of pubescence of lemma; **Q-** Anthocyanin colouration of keel; **R-** Anthocyanin colouration of apex; **S-** Anthocyanin colour of area below apex)

Continued...

Table 25 continued...

Sl. No.	Genotype	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL
1	Kalladi aryan	1	1	3	7	5	1	1	1	9	3	7	7	2	1	4	6	1	7	1
2	Thondi-1	5	1	5	7	4	1	1	1	9	3	9	7	2	1	4	6	1	7	9
3	Ambalavayal-1	1	1	3	7	5	1	1	1	9	3	9	7	2	1	4	6	1	7	9
4	Ayirankana	5	1	3	7	3	1	1	1	9	3	5	5	3	1	4	6	1	7	1
5	Palveliyan	5	1	3	7	3	1	1	1	9	3	9	7	3	1	4	1	1	7	1
6	Kannali	5	1	3	7	8	1	1	1	9	3	7	7	2	1	4	5	1	7	1
7	Chomala	1	1	3	7	2	1	1	1	9	3	9	7	3	1	4	5	1	7	1
8	Keervana	5	1	3	7	8	1	1	1	9	3	9	7	2	1	4	5	1	7	1
9	Kothandon	5	1	3	7	8	9	4	3	9	3	9	7	1	1	4	5	1	7	1
10	Kanni kayama	5	1	3	7	1	1	1	1	9	3	7	7	2	1	4	6	1	7	1
11	Addy	1	1	5	7	3	1	1	1	9	2	3	7	1	1	2	1	1	3	1
12	Kodu veliyan	5	1	5	7	4	1	1	1	9	2	7	7	2	1	4	6	1	7	1
13	Thondi-2	5	1	3	7	4	1	1	1	9	3	7	7	3	1	4	6	1	7	1
14	Chenthondi	5	1	3	7	8	1	1	1	9	3	9	7	3	1	4	5	1	7	1
15	Mangalapuram puncha	1	1	3	7	4	1	1	1	9	3	7	7	2	1	4	6	1	7	1
16	Chennellu	1	1	3	7	5	1	1	1	9	3	7	7	2	1	4	5	1	7	1
17	Punnadan thondi	1	1	3	7	4	1	1	1	9	3	7	7	2	1	4	6	1	7	1
18	Putta batta	5	1	3	7	4	1	1	1	9	3	9	7	1	1	4	1	1	7	1
19	Rajameni	5	1	5	7	4	1	1	1	9	3	7	7	3	1	4	5	1	7	1
20	Chettu veliyan	5	1	5	7	3	1	1	1	9	3	9	7	3	1	4	1	1	7	1
21	Kuruva	5	1	3	7	3	1	1	1	9	3	5	7	2	1	2	6	1	7	1

Continued...

22	Mulla kuruva	1	1	3	5	4	1	1	1	9	3	3	7	3	1	2	6	1	7	1
23	Mannu veliyan	5	1	3	5	5	1	1	1	9	3	9	7	2	1	4	6	1	7	1
24	Njavara black	1	1	3	5	8	1	1	1	9	2	3	7	3	1	4	6	1	7	1
25	Veliyan	5	1	3	7	5	1	1	1	9	3	7	7	3	1	4	6	1	7	1
26	Mahi kuruva	1	1	3	5	5	1	1	1	9	3	3	7	2	1	2	1	1	7	1
27	Valichoori	1	1	3	5	4	1	1	1	9	3	7	5	3	1	4	6	1	7	1
28	Urulan kayama	5	1	3	7	1	1	1	1	9	3	9	7	1	1	4	1	1	7	1
29	Thondi-3	1	1	3	7	5	1	1	1	9	3	7	7	2	1	4	6	1	7	1
30	Mullan puncha	1	1	3	7	8	9	10	7	9	1	7	7	3	1	4	5	1	7	1
31	Chenthadi	5	1	3	7	8	1	1	1	9	3	9	7	2	1	4	5	1	7	9
32	Peruvaya	5	1	3	7	4	1	1	1	9	3	9	7	3	1	4	6	1	7	1
33	Palthondi	5	1	3	7	1	1	1	1	9	3	9	7	3	1	4	1	1	7	1
34	Vaalicha	5	1	3	7	1	1	1	1	9	3	9	7	3	1	4	6	1	7	1
35	Veliya thondi	5	1	3	5	4	1	1	1	9	3	9	7	2	1	4	6	1	7	9
36	Edavaka	5	1	3	7	3	1	1	1	9	3	9	7	2	1	4	5	1	7	1
37	Velumpala	5	1	3	7	1	1	1	1	9	3	9	7	3	1	4	1	1	7	1
38	Kumbali	5	1	3	7	4	1	1	1	9	3	9	7	3	1	4	5	1	7	9
39	Adukkan	5	1	3	7	4	1	1	1	9	3	9	7	2	1	4	6	1	7	1
40	Ambalavayal-2	5	1	3	7	2	1	1	1	9	3	9	7	3	1	4	1	1	7	1
41	Uruni kayama	5	1	3	7	3	1	1	1	9	3	9	7	2	1	2	1	1	7	1
42	Gandhakasala	2	1	3	7	3	1	1	1	9	3	9	7	2	1	1	1	9	7	1
43	Kothandan	5	1	3	7	5	1	1	1	9	3	9	5	2	1	4	6	1	7	1
44	Thavalakannan	5	1	3	7	5	1	1	1	9	3	3	7	1	1	4	6	1	7	1
45	Kunam kulumban	1	1	3	7	5	1	1	1	9	3	9	7	2	1	3	5	1	7	1

Continued...

46	Chomala-2	1	1	3	7	4	9	2	3	9	3	9	7	3	1	4	5	1	7	9
47	Jeerakasala	1	1	3	7	1	9	2	5	9	3	9	7	3	1	3	1	9	7	1
48	Kutti veliyan	5	1	5	7	1	1	1	1	9	3	9	7	3	1	4	1	1	7	1
49	Thonnooran thondi	5	1	3	7	5	1	1	1	9	2	5	5	2	1	4	6	1	7	1
50	Chomala-1	1	1	3	7	4	1	1	1	9	3	9	7	3	1	4	6	1	7	9
51	Rasagatham	1	1	3	5	5	1	1	1	9	2	3	7	1	1	1	1	1	7	1
52	Njavara	1	1	3	7	5	1	1	1	9	3	5	7	2	1	4	6	1	7	1
53	Sugandhamathi	1	1	3	7	1	9	2	3	9	2	7	7	1	1	5	1	9	3	1
54	Palthondi matta	5	1	5	7	4	1	1	1	9	3	9	5	2	1	4	6	1	7	1
55	Vellimuthu	5	1	3	7	4	1	1	1	9	3	7	7	3	1	4	6	1	7	1
56	Mara thondi	5	1	3	7	4	1	1	1	9	3	9	7	3	1	4	6	1	7	1
57	Kayama	1	1	3	7	1	9	9	7	9	3	9	7	1	3	4	1	1	7	1
58	Onamottan	5	1	5	7	1	1	1	1	9	2	9	7	2	1	4	6	1	7	1
59	Karimpalan	5	1	3	7	8	1	1	1	9	3	7	7	3	1	4	5	1	7	1
60	Gandhakasala (dwarf)	2	1	3	7	3	1	1	1	9	3	9	7	2	1	1	1	9	7	1
Check varieties																				
61	Kanchana	1	1	3	7	4	1	1	1	9	2	7	7	2	1	4	6	1	7	1
62	Uma	1	1	3	7	3	1	1	1	9	2	7	7	2	1	4	6	1	7	1
63	Aathira	1	1	3	7	2	1	1	1	9	3	9	7	2	1	4	6	1	7	1

(**T**- Colour of stigma; **U**- Anthocyanin colouration of stem nodes, **V**- Attitude of flag leaf blade; **W**- Curvature of panicle main axis; **X**- Lemma and palea colour; **Y**- Presence of awns; **Z**- Colour of awns; **AA**- Distribution of awns in panicle; **AB**- Presence of secondary branching in panicle; **AC**- Type of secondary branching in panicle; **AD**- Attitude of branches in panicle; **AE**- Panicle exertion; **AF**- Leaf senescence; **AG**- Sterile lemma colour; **AH**- Decorticated grain shape; **AI**- Decorticated grain colour; **AJ**- Aroma of decorticated grain; **AK**- Gelatinization temperature; **AL**- Lodging nature).

4.1.2. Quantitative characters

4.1.2.1. Leaf: Length of blade

Length of leaf blade of 60 landraces and three check varieties are presented in Table 26. Out of 60 genotypes, medium leaf length (30-45 cm) was exhibited by 22 genotypes and Aathira (check), whereas long leaf length (> 45 cm) was present in 38 genotypes. The check varieties Kanchana and Uma recorded short leaf length (< 30 cm).

Table 26. Grouping of genotypes based on length of leaf blade

State	Genotypes
Short (< 30 cm)	**Check varieties:** Kanchana, Uma
Medium (30-45 cm)	**Landraces:** Ayirankana, Addy, Chennellu, Punnadan thondi, Putta batta, Rajameni, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Mahi kuruva, Valichoori, Urulan kayama, Thondi-3, Mullan puncha, Edavaka, Adukkan, Thavalakannan, Thonnooran thondi, Rasagatham, Sugandhamathi **Check variety:** Aathira
Long (> 45 cm)	**Landraces:** Kalladi aryan, Thondi-1, Ambalavayal-1, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Kanni kayama, Kodu veliyan, Thondi-2, Chenthondi, Mangalapuram puncha, Chettu veliyan, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Velumpala, Kumbali, Ambalavayal-2, Uruni kayama, Gandhakasala, Kothandan, Kunam kulumban, Chomala-2, Jeerakasala, Kutti veliyan, Chomala-1, Njavara, Palthondi matta, Vellimuthu, Mara thondi, Kayama, Onamottan, Karimpalan, Gandhakasala (dwarf)

4.1.2.2. Leaf: Width of blade

Width of the leaf blade of 60 landraces and three check varieties are presented in Table 27. Narrow leaf width (< 1 cm) was exhibited in 46 genotypes and check varieties Kanchana and Uma, whereas medium leaf length (1-2 cm) was exhibited in 14 genotypes and also in Aathira (check).

Table 27. Grouping of genotypes based on width of leaf blade

State	Genotypes
Narrow (<1 cm)	**Landraces:** Keervana, Kalladi aryan, Thondi-1, Ayirankana, Chomala, Kanni kayama, Addy, Kodu veliyan, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Mahi kuruva, Valichoori, Urulan kayama, Thondi-3, Mullan puncha, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Jeerakasala, Kutti veliyan, Thonnooran thondi, Rasagatham, Njavara, Palthondi matta, Kayama, Onamottan, Karimpalan, Gandhakasala (dwarf), Mullan puncha **Check varieties:** Kanchana, Uma
Medium (1-2 cm)	**Landraces:** Ambalavayal-1, Palveliyan, Kannali, Kothandon, Chenthadi, Gandhakasala, Kothandan, Kunam kulumban, Chomala-2, Thavalakannan, Chomala-1, Sugandhamathi, Vellimuthu, Mara thondi **Check variety:** Aathira

4.1.2.3. Stem: Thickness

The thickness of stem of 60 landraces and three check varieties are presented in Table 28. Thin stem (< 0.40 cm) was exhibited by 13 genotypes and Kanchana

(check variety), medium stem thickness (0.40-0.55 cm) was exhibited by 39 genotypes and two check varieties (Uma and Aathira) and thick stem (> 0.55 cm) recorded eight genotypes.

Table 28. Grouping of genotypes based on stem thickness

State	Genotypes
Thin (< 0.40 cm)	**Landraces:** Kanchana, Kothandon, Addy, Kodu veliyan, Mulla kuruva, Njavara black, Mahi kuruva, Mullan puncha, Adukkan, Uruni kayama, Thonnooran thondi, Njavara, Vellimuthu, Onamottan **Check variety:** Kanchana
Medium (0.40-0.55 cm)	**Landraces:** Kalladi aryan, Thondi-1, Ambalavayal-1, Ayirankana, Kannali, Keervana, Kanni kayama, Thondi-2, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Palveliyan, Chomala, Kuruva, Mannu veliyan, Veliyan, Valichoori, Urulan kayama, Thondi-3, Palthondi, Edavak, Velumpala, Veliya thondi, Kothandan, Thavalakannan, Kunam kulumban, Chomala-2, Kutti veliyan, Chomala-1, Rasagatham, Sugandhamathi, Palthondi matta, Mara thondi, Kayama, Karimpalan, Gandhakasala (dwarf) **Check varieties:** Uma, Aathira
Thick (> 0.55 cm)	**Landraces:** Chenthondi, Chenthadi, Peruvaya, Vaalicha, Kumbali, Ambalavayal-2, Gandhakasala, Jeerakasala

4.1.2.4. Stem: Length

The stem length in 60 landraces and three check varieties are presented in Table 29. Out of 60 genotypes, very short (<91 cm) stem was present in three genotypes and two check varieties (Kanchana and Uma), short (91-110 cm) stem

was present in seven genotypes and Aathira (check), medium (111-130 cm) stem was present in 13 genotypes, long (131-150 cm)stem in 17 genotypes and very long (> 150 cm) stem in 20 genotypes.

Table 29. Grouping of genotypes based on stem length

State	Genotypes
Very short (< 91 cm)	**Landraces:** Valichoori, Thavalakannan, Sugandhamathi **Check varieties:** Kanchana, Uma
Short (91-110 cm)	**Landraces:** Ayirankana, Addy, Mulla kuruva, Mahi kuruva, Urulan kayama, Rasagatham, Njavara black **Check variety:** Aathira
Medium (111-130 cm)	**Landraces:** Kalladi aryan, Kodu veliyan, Chennellu, Punnadan thondi, Rajameni, Kuruva, Veliyan, Mullan puncha, Edavaka, Gandhakasala, Kunam kulumban, Njavara, Gandhakasala (dwarf)
Long (131-150 cm)	**Landraces:** Kanni kayama, Thondi-2, Mangalapuram puncha, Putta batta, Mannu veliyan, Thondi-3, Adukkan, Uruni kayama, Kothandan, Jeerakasala, Kutti veliyan, Thonnooran thondi, Palthondi matta, Vellimuthu, Kayama, Onamottan, Karimpalan
Very long (> 150 cm)	**Landraces:** Thondi-1, Ambalavayal-1, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Chenthondi, Chettu veliyan, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Velumpala, Kumbali, Ambalavayal-2, Chomala-2, Chomala-1, Mara thondi

4.1.2.5. Time for heading

Days to heading of 60 landraces and three check varieties are presented in Table 30. Out of 60 genotypes, very late (> 131 days) heading was exhibited by 50 genotypes and all check varieties. Ten genotypes were late (111-130 days) in heading.

Table 30. Grouping of genotypes based on number of days for heading

State	Genotypes
Late (111-130 days)	**Landraces:** Kalladi aryan, Kanni kayama, Addy, Kodu veliyan, Kothandan, Onamottan, Palthondi matta, Mara thondi, Thonnooran thondi, Njavara
Very late (> 131 days)	**Landraces:** Keervana, Thavalakannan, Thondi-1, Vellimuthu, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Chomala, Kothandon, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Mahi kuruva, Valichoori, Urulan kayama, Thondi-3, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Gandhakasala, Kunam kulumban, Chomala-2, Jeerakasala, Kutti veliyan, Chomala-1, Rasagatham, Sugandhamathi, Kayama, Karimpalan, Gandhakasala (dwarf), Mullan puncha **Check varieties:** Kanchana, Uma, Aathira

4.1.2.6. Panicle: Number per plant

Number of panicles per plant in 60 landraces and three check varieties are presented in Table 31. Fifty-three genotypes and Aathira (check) exhibited few

panicles (< 11) per plant, whereas medium number of panicles (11-20) were recorded in seven genotypes and also in Kanchana and Uma.

Table 31. Grouping of genotypes based on number of panicles per plant

State	Genotypes
Few (< 11)	**Landraces:** Keervana, Thavalakannan, Thondi-1, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Chomala, Kothandon, Addy, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Mahi kuruva, Valichoori, Thondi-3, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Gandhakasala, Kunam kulumban, Chomala-2, Jeerakasala, Kutti veliyan, Chomala-1, Rasagatham, Njavara, Sugandhamathi, Palthondi matta, Vellimuthu, Kayama, Karimpalan, Gandhakasala (dwarf), Mullan puncha **Check variety:** Aathira
Medium (11-20)	**Landraces:** Kalladi aryan, Kanni kayama, Urulan kayama, Thonnooran thondi, Onamottan, Kothandan, Kodu veliyan **Check varieties:** Kanchana, Uma

4.1.2.7. Panicle: Length of main axis

Length of the main axis of the panicle of 60 landraces and three check varieties are presented in Table 32. Out of 60 genotypes, main axis of panicles exhibited medium length (21-25 cm) in 19 genotypes and Uma (check), long panicle axis (26-30 cm) in 36 genotypes and Aathira (check) and very long panicle (> 30 cm) axis was recorded in five genotypes. The check variety Kanchana exhibited short panicle axis.

Table 32. Grouping of genotypes based on length of panicle main axis

State	Genotypes
Short (< 20 cm)	**Check variety:** Kanchana
Medium (21-25 cm)	**Landraces:** Mulla kuruva, Njavara black, Mahi kuruva, Valichoori, Urulan kayama, Edavaka, Adukkan, Thavalakannan, Rasagatham, Ayirankana, Kanni kayama, Kodu veliyan, Thondi-3, Sugandhamathi, Vellimuthu, Addy, Chennellu, Punnadan thondi, Karimpalan **Check variety:** Uma
Long (26-30 cm)	**Landraces:** Kalladi aryan, Thondi-1, Ambalavayal-1, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Thondi-2, Chenthondi, Mangalapuram puncha, Rajameni, Chettu veliyan, Kuruva, Mannu veliyan, Veliyan, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Velumpala, Kumbali, Ambalavayal-2, Uruni kayama, Kothandan, Kunam kulumban, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Palthondi matta, Mara thondi, Onamottan, Putta batta **Check variety:** Aathira
Very long (> 30 cm)	**Landraces:** Gandhakasala, Chomala-2, Jeerakasala, Kayama, Gandhakasala (dwarf)

4.1.2.8. Grain: Weight of 1000 fully developed grains

The weight of 1000 fully developed grains of genotypes are presented in Table 33. Out of 60 genotypes, Rasagatham exhibited very low (< 15 g) weight of 1000 fully developed grains, five genotypes exhibited low (15-20 g), 11 genotypes exhibited medium (21-25 g), 17 genotypes and two check varieties (Uma and

Aathira) exhibited high (26-30 g) and 26 genotypes and Kanchana (check) exhibited very high (> 30 g) weight of 1000 grains.

Table 33. Grouping of genotypes based on weight of 1000 grains

State	Genotypes
Very low (< 15 g)	**Landrace:** Rasagatham
Low (15-20 g)	**Landraces:** Addy, Mahi kuruva, Uruni kayama, Gandhakasala, Gandhakasala (dwarf)
Medium (21-25 g)	**Landraces:** Rajameni, Kuruva, Mulla kuruva, Njavara black, Urulan kayama, Palthondi, Thavalakannan, Kunam kulumban, Chomala-2, Jeerakasala, Kayama
High (26-30 g)	**Landraces:** Ambalavayal-1, Chomala, Keervana, Kothandon, Kodu veliyan, Chenthondi, Chennellu, Mannu veliyan, Veliyan, Mullan puncha, Chenthadi, Edavaka, Velumpala, Ambalavayal-2, Chomala-1, Sugandhamathi, Mara thondi **Check varieties:** Uma, Aathira
Very high (> 30 g)	**Landraces:** Kalladi aryan, Thondi-1, Ayirankana, Palveliyan, Kannali, Kanni kayama, Thondi-2, Mangalapuram puncha, Punnadan thondi, Putta batta, Chettu veliyan, Valichoori, Thondi-3, Peruvaya, Vaalicha, Veliya thondi, Kumbali, Adukkan, Kothandan, Kutti veliyan, Thonnooran thondi, Njavara, Palthondi matta, Vellimuthu, Onamottan, Karimpalan **Check variety:** Kanchana

4.1.2.9. Grain: Length

Length of the grain of 60 landraces and three check varieties are presented in Table 34. Very short (< 6 mm) grain was exhibited by four genotypes, short (6.1-

8.5 mm) grain was exhibited by 45 genotypes and all the check varieties, medium (8.6-10.5 mm) grain was exhibited by 10 genotypes, whereas only one genotype (Sugandhamathi) exhibited long (10.6-12.5 mm) grain.

Table 34. Grouping of genotypes based on grain length

State	Genotypes
Very short (< 6 mm)	**Landraces:** Addy, Uruni kayama, Rasagatham, Mahi kuruva
Short (6.1-8.5 mm)	**Landraces:** Keervana, Thavalakannan, Kalladi aryan, Thondi-1, Ambalavayal-1, Palveliyan, Chomala, Kothandon, Kanni kayama, Kodu veliyan, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Chenthadi, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Gandhakasala, Kothandan, Chomala-2, Jeerakasala, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Palthondi matta, Kayama, Karimpalan, Gandhakasala (dwarf), Mullan puncha **Check varieties:** Kanchana, Uma, Aathira
Medium (8.6-10.5 mm)	**Landraces:** Ayirankana, Kannali, Valichoori, Thondi-3, Mullan puncha, Peruvaya, Kunam kulumban, Vellimuthu, Mara thondi, Onamottan
Long (10.6-12.5 mm)	**Landrace:** Sugandhamathi

4.1.2.10. Grain: Width

The grain width of 60 landraces and three check varieties are presented in Table 35. Out of 60 genotypes, Sugandhamathi exhibited narrow (2.1-2.5 mm) grain, six genotypes exhibited medium (2.6-3.0 mm) grain, 40 genotypes and all check varieties exhibited broad (3.1-3.5 mm) grain, whereas 13 genotypes exhibited very broad (> 3.5 mm) grain.

Table 35. Grouping of genotypes based on grain width

State	Genotypes
Narrow (2.1-2.5 mm)	**Landrace:** Sugandhamathi
Medium (2.6-3.0 mm)	**Landraces:** Gandhakasala, Jeerakasala, Rasagatham
Broad (3.1-3.5 mm)	**Landraces:** Keervana, Thavalakannan, Thondi-1, Ambalavayal-1, Palveliyan, Chomala, Kothandon, Kanni kayama, Kodu veliyan, Thondi-2, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Veliyan, Urulan kayama, Mullan puncha, Chenthadi, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Ambalavayal-2, Uruni kayama, Kunam kulumban, Chomala-2, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Vellimuthu, Kayama, Karimpalan, Gandhakasala (dwarf), Mullan puncha, Addy, Njavara black, Mahi kuruva **Check varieties:** Kanchana, Uma, Aathira
Very broad (> 3.5 mm)	**Landraces:** Kalladi aryan, Ayirankana, Kannali, Chenthondi, Mangalapuram puncha, Valichoori, Thondi-3, Peruvaya, Kumbali, Adukkan, Kothandan, Palthondi matta, Onamottan

4.1.2.11. Decorticated grain (kernel): Length

The kernel length in 60 landraces and three check varieties are presented in Table 36. Thirty-eight genotypes and Uma (check) exhibited short (< 6 mm) kernel, 21 genotypes and two check varieties (Kanchana and Aathira) exhibited medium (6-8 mm) kernel, whereas only one genotype (Sugandhamathi) exhibited long (8-10 mm) kernel. This genotype was reported to have narrow grain width.

Table 36. Grouping of genotypes based on decorticated grain length

State	Genotypes
Short (< 6 mm)	**Landraces:** Ambalavayal-1, Palveliyan, Chomala, Keervana, Veliya thondi, Adukkan, Kanni kayama, Addy, Kodu veliyan, Chennellu, Punnadan thondi, Rajameni, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Mahi kuruva, Urulan kayama, Mullan puncha, Chenthadi, Palthondi, Vaalicha, Edavaka, Ambalavayal-2, Uruni kayama, Gandhakasala, Kothandan, Thavalakannan, Kunam kulumban, Chomala-2, Kutti veliyan, Chomala-1, Rasagatham, Palthondi matta, Kayama, Gandhakasala (dwarf) **Check variety:** Uma
Medium (6-8 mm)	**Landraces:** Kalladi aryan, Thondi-1, Ayirankana, Kannali, Kothandon, Thondi-2, Chenthondi, Mangalapuram puncha, Putta batta, Valichoori, Thondi-3, Peruvaya, Velumpala, Kumbali, Jeerakasala, Thonnooran thondi, Njavara, Vellimuthu, Mara thondi, Onamottan, Karimpalan **Check variety:** Kanchana, Aathira
Long (8-10 mm)	**Landrace:** Sugandhamathi

4.1.2.12. Decorticated grain width

The kernel width in 60 landraces and three check varieties are presented in Table 37. Out of 60 genotypes, medium (2-2.5 mm) kernel width was exhibited by nine genotypes and broad (> 2.5 cm) kernel width was exhibited by 51 genotypes and all the check varieties.

Table 37. Grouping of genotypes based on decorticated grain width

State	Genotypes
Medium (2-2.5 mm)	**Landraces:** Rajameni, Njavara black, Mahi kuruva, Gandhakasala, Kunam kulumban, Jeerakasala, Rasagatham, Sugandhamathi, Gandhakasala (dwarf)
Broad (> 2.5 cm)	**Landraces:** Keervana, Thavalakannan, Kalladi aryan, Thondi-1, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Chomala, Kothandon, Kanni kayama, Addy, Kodu veliyan, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Chettu veliyan, Kuruva, Mulla kuruva, Mannu veliyan, Veliyan, Valichoori, Urulan kayama, Thondi-3, Mullan puncha, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Kothandan, Chomala-2, Kutti veliyan, Thonnooran thondi, Chomala-1, Njavara, Palthondi matta, Vellimuthu, Kayama, Onamottan, Karimpalan, Mullan puncha **Check varieties:** Kanchana, Uma, Aathira

4.1.2.13. Time for maturity

Days for maturity of 60 landraces and three check varieties are presented in Table 38. Nine out of 60 genotypes came to late (141-160 days) maturity group, whereas 51 genotypes and all check varieties exhibited very late (> 160 days) maturity.

Table 38. Grouping of genotypes based on number of days for maturity

State	Genotypes
Late (141-160 days)	**Landraces:** Kanni kayama, Addy, Kodu veliyan, Kothandan, Thonnooran thondi, Njavara, Palthondi matta, Mara thondi, Onamottan,
Very late (> 160 days)	**Landraces:** Kalladi aryan, Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Chomala, Keervana, Kothandon, Thondi-2, Chenthondi, Mangalapuram puncha, Chennellu, Putta batta, Rajameni, Chettu veliyan, Mulla kuruva, Mannu veliyan, Njavara black, Veliyan, Valichoori, Urulan kayama, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Velumpala, Kumbali, Ambalavayal-2, Uruni kayama, Kunam kulumban, Chomala-2, Jeerakasala, Kutti veliyan, Chomala-1, Rasagatham, Sugandhamathi, Kayama, Karimpalan, Punnadan thondi, Kuruva, Mahi kuruva, Thondi-3, Mullan puncha, Edavaka, Adukkan, Gandhakasala, Thavalakannan, Vellimuthu, Urulan kayama, Gandhakasala (dwarf) **Check varieties:** Kanchana, Uma, Aathira

Table 39. Characterization of 60 genotypes based on quantitative parameters

Sl. No.	Genotype	AM	AN	AO	AP	AQ	AR	AS	AT	AU	AV	AW	AX	AY
1	Kalladi aryan	3	3	3	1	3	5	9	3	7	3	7	9	9
2	Thondi-1	3	3	5	1	5	5	7	3	7	1	7	9	9
3	Ambalavayal-1	5	5	5	3	7	3	7	3	7	3	7	9	9
4	Ayirankana	7	3	5	5	7	5	9	3	9	3	7	7	9
5	Palveliyan	7	3	5	9	7	3	9	3	7	3	7	9	9
6	Kannali	7	5	5	9	7	3	7	3	7	1	7	9	9
7	Chomala	5	3	5	3	5	3	9	5	9	3	7	9	9
8	Keervana	7	5	5	9	7	3	9	3	7	1	7	9	9
9	Kothandon	7	5	5	9	7	3	9	5	9	3	7	9	9
10	Kanni kayama	7	3	5	9	7	3	7	3	7	1	7	9	9
11	Addy	7	3	5	9	7	3	7	3	7	1	7	9	9
12	Kodu veliyan	7	5	3	9	7	3	7	3	7	3	7	9	9
13	Thondi-2	7	3	5	7	5	5	9	3	7	1	7	7	7
14	Chenthondi	5	3	3	3	5	3	3	1	7	1	7	7	7
15	Mangalapuram puncha	7	3	3	5	5	5	7	3	7	1	7	7	7
16	Chennellu	7	3	5	7	7	3	9	3	7	3	7	9	9
17	Punnadan thondi	7	3	7	9	7	3	7	3	9	3	7	9	9
18	Putta batta	7	3	5	7	7	3	9	3	9	3	7	9	9
19	Rajameni	5	3	5	5	5	3	7	3	7	1	7	9	9
20	Chettu veliyan	3	3	5	5	5	3	9	3	7	1	7	9	9
21	Kuruva	5	3	5	7	7	3	9	3	7	3	7	9	9

Continued...

22	Mulla kuruva	5	3	5	5	7	3	5	3	7	1	5	9	9
23	Mannu veliyan	7	3	5	9	7	3	9	3	7	1	7	9	9
24	Njavara black	5	3	5	5	7	3	5	3	7	1	7	9	9
25	Veliyan	5	3	3	3	5	3	5	3	7	1	7	9	9
26	Mahi kuruva	5	3	5	7	7	3	7	3	7	1	7	9	9
27	Valichoori	5	3	3	3	5	3	5	3	7	1	5	9	9
28	Urulan kayama	5	3	5	5	7	3	7	3	7	1	7	9	9
29	Thondi-3	5	3	3	3	5	3	3	1	7	1	5	9	9
30	Mullan puncha	5	3	5	1	5	3	9	5	9	3	7	9	9
31	Chenthadi	5	3	5	3	5	5	5	3	7	1	7	9	9
32	Peruvaya	7	3	5	7	5	3	9	5	9	3	7	9	9
33	Palthondi	5	3	3	5	7	3	7	5	7	1	7	9	9
34	Vaalicha	7	5	7	9	7	3	7	3	7	1	7	9	9
35	Veliya thondi	7	3	7	9	7	3	9	5	9	3	7	9	9
36	Edavaka	5	3	5	9	7	3	5	3	7	1	7	9	9
37	Velumpala	5	3	7	9	7	3	9	3	7	1	7	9	9
38	Kumbali	5	3	5	9	7	3	9	3	7	1	7	9	9
39	Adukkan	3	3	5	5	5	3	7	3	7	1	7	9	9
40	Ambalavayal-2	7	3	5	9	7	3	7	3	7	3	7	9	9
41	Uruni kayama	7	3	7	9	7	3	9	3	9	3	7	9	9
42	Gandhakasala	5	3	3	7	5	3	9	3	9	1	7	9	9
43	Kothandan	7	3	7	9	7	3	7	3	7	1	7	9	9
44	Thavalakannan	7	3	3	7	7	3	3	1	7	1	7	9	9
45	Kunam kulumban	7	5	7	5	9	3	3	3	5	1	5	9	9

Continued...

46	Chomala-2	7	5	5	7	7	5	9	3	9	1	7	7	7
47	Jeerakasala	5	5	5	1	5	3	5	3	7	1	7	9	9
48	Kutti veliyan	7	5	5	5	7	3	5	5	7	1	5	9	9
49	Thonnooran thondi	7	5	5	9	9	3	5	3	7	1	7	9	9
50	Chomala-1	7	3	7	7	9	3	5	3	5	3	5	9	9
51	Rasagatham	7	3	5	7	7	3	9	3	7	1	7	9	9
52	Njavara	5	3	3	7	7	5	9	3	7	3	7	7	7
53	Sugandhamathi	7	5	5	9	7	3	7	3	7	1	7	9	9
54	Palthondi matta	5	3	5	3	5	3	1	1	5	1	5	9	9
55	Vellimuthu	7	3	3	5	7	3	9	3	7	3	7	7	7
56	Mara thondi	5	5	5	1	5	3	7	7	3	5	7	9	9
57	Kayama	7	3	5	7	7	3	9	3	9	1	5	7	7
58	Onamottan	7	5	3	7	5	3	9	5	7	3	7	9	9
59	Karimpalan	7	5	5	9	7	3	7	5	7	3	7	7	7
60	Gandhakasala (dwarf)	7	3	5	7	9	3	5	3	7	1	7	9	9
Check varieties														
61	Kanchana	7	3	3	7	7	5	9	5	9	3	7	7	7
62	Uma	7	3	5	7	5	3	9	3	7	3	7	9	9
63	Aathira	7	3	5	5	9	3	3	3	7	1	5	9	9

(**AM-** Length of leaf blade; **AN-** Width of leaf blade; **AO-** Stem thickness; **AP-** Stem length; **AQ-** Length of panicle main axis; **AR-** Number of panicles per plant, **AS-** Weight of 1000 grains; **AT-** Grain length; **AU-** Grain width; **AV-** Decorticated grain length; **AW-** Decorticated grain width; **AX-** Time for heading; **AY-** Time for maturity).

4.1.3. Analysis of variance

Observations were recorded on 20 quantitative characters and the mean values and analysis of variance are presented in Table 40 and Table 41.

4.1.3.1. Leaf: Length of blade

Length of leaf blade of 60 landraces and three check varieties varied from 30.20 cm in Chennellu to 66.28 cm in Mara thondi with an overall mean of 48.04 cm. The maximum leaf blade length was recorded in Mara thondi and was on par with Gandhakasala, Kothandon and Chenthondi. Among the check varieties, Aathira recorded highest mean leaf blade length (34.53 cm) followed by Uma (29.65 cm) and Kanchana (25.86 cm)

4.1.3.2. Leaf: Width of blade

Minimum width of leaf blade was exhibited in Njavara black (0.54 cm) and maximum width of leaf blade was exhibited in Thavalakannan (1.33 cm) and an overall mean of 0.88 cm. Among the check varieties, Aathira recorded a mean leaf blade width of 1.11 cm followed by Kanchana (0.83 cm).

4.1.3.3. Stem: Thickness

The stem thickness of 60 landraces and three check varieties varied from 0.28 cm in Njavara black to 0.63 cm in Peruvaya with an overall mean of 0.47 cm. The stem thickness recorded in Peruvaya was on par with Chenthadi, Ambalavayal-2 and Chenthondi. Among the check varieties, Aathira recorded the maximum stem thickness (0.46 cm) followed by Uma (0.44 cm).

4.1.3.4. Stem: Length

Minimum stem length was recorded in Valichoori (72.12 cm) and maximum stem length was recorded in Peruvaya (177.83 cm) with an overall mean of 135.93cm. Among the check varieties, Aathira recorded the maximum stem length (105.91 cm) followed by Uma (75.42 cm).

4.1.3.5. Number of tillers per plant

Number of tillers per plant of 60 landraces and three check varieties varied from 8.25 in Kannali to 16.61 in Urulan kayama with an overall mean of 11.33. The maximum number of tillers per plant was recorded in Urulan kayama and was on par with Kothandan, Valichoori and Kanni kayama. Among the check varieties, Kanchana recorded the maximum number of tillers per plant (17.31) followed by Uma (14.24).

4.1.3.6. Time of heading

Among 60 genotypes, Njavara exhibited the minimum number of days for heading (117 days) and Urulan kayama recorded maximum number of days for heading (162 days) and an overall mean of 141.43 days. Among the check varieties, Aathira recorded the maximum number of days for heading (142 days) followed by Uma (140 days).

4.1.3.7. Panicle: Number per plant

Number of panicles per plant of 60 landraces and three check varieties varied from 1.33 in Mulla kuruva to 14.95 in Urulan kayama, with an overall mean of 8.13. The maximum number of panicles per plant was recorded in Urulan kayama and it was on par with Onamottan. Among the check varieties, Kanchana recorded the maximum number of panicles per plant (13.22) followed by Uma (11.75).

4.1.3.8. Panicle: Length of main axis

The minimum and maximum length of main axis of panicle was exhibited by Njavara black (20.56 cm) and Kayama (39.42 cm) respectively and the overall mean was 27.46 cm. Among the check varieties, Aathira recorded the maximum length of the main axis of panicle (26.34 cm) followed by Uma (23.46 cm).

4.1.3.9. Number of spikelets per panicle

Number of spikelets per panicle in 60 landraces and three check varied from 68.55 spikelets per panicle in Njavara black to 298.42 spikelets per panicle in Chenthondi, with an overall mean of 179.24 spikelets per panicle. Chenthondi, Ambalavayal-2, Chomala-2, Chenthadi, Ambalavayal-1 and Chomala-1 recorded significantly superior number of spikelets per panicle. Among the check varieties, Aathira recorded the maximum number of spikelets per panicle (196.23) followed by Uma (159.52).

4.1.3.10. Number of grains per panicle

Njavara black exhibited the minimum number of grains per panicle (63.24) and Ambalavayal-2 recorded the maximum number of grains per panicle (272.06), with an overall mean of 146.88 grains. Among the check varieties, Aathira recorded the maximum number of grains per panicle (169.41) followed by Uma (137.67).

4.1.3.11. Seed setting (per cent)

The ratio of number of grains to the number of spikelets per panicle of 60 landraces and three check varieties varied from 50.81 per cent in Ayirankana to 96.9 per cent in Vaalicha and an overall mean of 82.67 per cent. The highest seed setting per cent was recorded in Vaalicha and was on par with Jeerakasala, Kuruva, Addy, Mullan puncha, Ambalavayal-2, Keervana, Velumpala, Palthondi, Adukkan, Njavara black and Edavaka. Among the check varieties, Aathira recorded the maximum seed setting per cent (86.22 per cent) followed by Uma (86.12 per cent).

4.1.3.12. Grain: Weight of 1000 fully developed grains

Minimum value for 1000 grain weight was exhibited by Rasagatham (12.43 g) and maximum by Onamottan (36.57 g), with an overall mean of 28.27 g. Significantly, high 1000 grain weight was recorded in Onamottan, Ayirankana, Peruvaya and Vellimuthu. Among the check varieties, Kanchana recorded the maximum 1000 grains weight (31.16 g).

4.1.3.13. Grain: Length

The length of the grain of 60 landraces and three check varied from 5.2 mm in Addy to 11.20 mm in Sugandhamathi with an overall mean of 7.96 mm. Among the check varieties, Kanchana recorded the maximum length of the grain (8.4 mm) followed by Aathira (8.1 mm).

4.1.3.14. Grain: Width

Sugandhamathi recorded the minimum grain width (2.50 mm) and Ayirankana exhibited maximum gain width (3.90), with an overall mean of 3.37 mm. Among the check varieties, Uma recorded the maximum grain width (3.4 mm) followed by Kanchana and Aathira (3.3 mm).

4.1.3.15. Grain: L/B ratio

Grain length and breadth ratio of 60 landraces and three check varieties varied from 1.73 in Addy to 4.48 in Sugandhamathi with an overall mean of 2.37. Among the check varieties, Kanchana recorded the maximum grain L/B ratio (2.55) followed by Aathira (2.45).

4.1.3.16. Decorticated grain (kernel): Length

Rasagatham exhibited the minimum kernel length (4.10 mm) and Sugandhamathi exhibited the maximum kernel length (8.60 mm), with an overall mean of 5.85 mm. Among the check varieties, Kanchana recorded the maximum length of the kernel (6.4 mm) followed by Aathira (6.2 mm).

4.1.3.17. Decorticated grain (kernel): Width

The width of the kernel of 60 landraces and three check varieties varied from 2.10 mm in Rasagatham to 3.80 mm in Thondi-1 with an overall mean of 2.81 mm. Among the check varieties, Uma recorded the maximum width of the kernel (2.8 mm) followed by Kanchana and Aathira (2.7 mm).

4.1.3.18. Decorticated grain (kernel): L/B ratio

Out of 60 genotypes, Mulla kuruva exhibited the minimum kernel L/B ratio (1.57) and Sugandhamathi exhibited the maximum L/B ratio (4.10), with an overall mean of 2.10. Among the check varieties, Kanchana recorded maximum kernel L/B ratio (2.37) followed by Aathira (2.30).

4.1.3.19. Time for maturity

The number of days for maturity of 60 landraces and three check varieties varied from 147 days in Njavara to 191 days in Urulan kayama and Ambalavayal-1, with an overall mean of 176.37 days. Among the check varieties, Aathira recorded the maximum number of days for maturity (185 days) followed by Uma (180 days).

4.1.3.20. Grain yield per plant (g)

Njavara black recorded the minimum grain yield per plant (10.35 g) and Kanni kayama recorded the maximum grain yield per plant (36.45 g), with an overall mean of 23.67 g. Significantly, superior grain yield per plant was recorded in Kanni kayama, Ambalavayal-1, Kothandan, Onamottan, Thondi-2, Chenthadi, Kannali and Thondi-1 (Plate 30). Among the check varieties, Uma recorded maximum grain yield per plant (35.20 g) followed by Aathira (29.14 g).

A) Kanni kayama B) Ambalavayal-1

C) Kothandan D) Onamotton

Plate 30. Panicles of better yielding landraces (continued…)

E) Thondi-2 F) Chenthadi

G) Kannali H) Thondi-1

Plate 30. Panicles of better yielding landraces

Table 40. Mean performance of 60 landraces of rice based on quantitative characters

Sl. No.	Genotype	LLB (cm)	WLB (cm)	ST (cm)	SL (cm)	NTP (no.)	TH (days)	NPP (no.)	LPA (cm)	NSP (no.)	NGP (no.)
1	Kalladi aryan	47.41	0.82	0.44	121.22	14.32	125	12.85	28.32	99.53	91.37
2	Thondi-1	55.13	0.93	0.49	165.51	10.71	140	8.02	29.31	171.24	156.41
3	Ambalavayal-1	56.34	1.12	0.52	163.24	13.10	157	10.34	26.12	261.46*	195.24
4	Ayirankana	41.47	0.90	0.51	96.37	13.44	144	8.47	25.54	124.55	63.52
5	Palveliyan	56.76	1.01	0.55	162.35	9.32	148	6.75	28.51	171.74	154.73
6	Kannali	56.69	1.02	0.54	162.51	8.25	145	7.26	29.32	188.47	152.60
7	Chomala	49.97	0.91	0.55	155.33	9.57	141	6.18	29.83	221.52	169.12
8	Keervana	56.75	0.73	0.41	154.84	10.14	148	6.42	27.50	136.21	128.24
9	Kothandon	62.54*	1.12	0.39	152.17	8.61	149	7.53	28.62	213.14	154.37
10	Kanni kayama	45.48	0.81	0.41	147.81	15.22*	125	12.24	25.14	114.44	101.51
11	Addy	40.84	0.73	0.33	97.42	9.03	130	9.95	21.35	101.23	96.03
12	Kodu veliyan	50.48	0.94	0.38	114.51	14.15	127	12.02	25.47	111.21	97.45
13	Thondi-2	47.8	0.92	0.46	149.94	11.37	147	7.71	27.48	221.10	174.71
14	Chenthondi	62.04*	0.93	0.61	160.61	8.74	151	6.34	28.22	298.42*	153.10
15	Mangalapuram puncha	50.42	0.81	0.44	148.52	12.11	135	9.17	27.85	198.55	139.23

Continued...

16	Chennellu	30.2	0.74	0.46	126.33	10.72	146	8.61	22.77	175.60	158.34
17	Punnadan thondi	40.01	0.92	0.47	113.74	14.43	140	7.82	23.99	174.35	130.51
18	Putta batta	37.13	0.93	0.49	138.71	9.35	147	7.45	30.12	140.25	113.70
19	Rajameni	34.36	0.71	0.44	117.32	9.04	150	5.34	29.85	204.73	136.42
20	Chettu veliyan	54.67	0.94	0.52	168.91	8.41	150	6.76	29.44	212.85	177.15
21	Kuruva	35.78	0.72	0.49	117.65	9.52	138	7.88	28.21	169.28	162.08
22	Mulla kuruva	36.36	0.63	0.38	105.52	14.24	138	1.32	22.32	135.16	124.26
23	Mannu veliyan	40.64	0.71	0.46	133.21	12.37	143	6.81	28.83	234.42	158.37
24	Njavara black	30.41	0.54	0.28	93.74	15.11	142	8.94	20.56	68.55	63.24
25	Veliyan	41.17	0.92	0.43	130.05	11.75	142	6.67	26.74	183.65	149.11
26	Mahi kuruva	37.74	0.63	0.38	102.86	12.28	140	6.13	23.38	144.33	117.40
27	Valichoori	38.4	0.71	0.43	72.12	16.19*	143	8.43	23.87	125.02	88.73
28	Urulan kayama	42.08	0.74	0.41	102.61	16.61*	162*	14.95*	24.21	231.15	176.16
29	Thondi-3	36.86	0.82	0.46	132.84	9.82	140	6.44	25.30	172.26	139.59
30	Mullan puncha	34.63	0.63	0.38	113.25	9.54	137	6.37	29.12	108.42	102.61
31	Chenthadi	59.33	1.01	0.62*	168.92	8.30	155	6.71	29.73	261.74*	178.82
32	Peruvaya	61.32	0.93	0.63*	177.83*	10.12	137	7.42	27.35	193.13	172.20
33	Palthondi	45.29	0.84	0.52	160.42	8.61	157	6.94	27.17	225.05	211.03

Continued...

34	Vaalicha	48.94	0.81	0.57	164.81	8.43	155	6.81	28.31	226.24	219.15
35	Veliya thondi	47.41	0.92	0.55	170.34	9.34	154	7.52	29.11	204.41	177.34
36	Edavaka	41.19	0.84	0.41	120.37	12.57	137	9.93	23.42	217.82	201.47
37	Velumpala	51.95	0.81	0.49	166.45	9.31	152	7.85	27.60	219.03	206.51
38	Kumbali	53.5	0.92	0.57	162.62	10.10	152	8.57	28.33	172.34	141.60
39	Adukkan	42.08	0.73	0.38	140.73	14.32	140	10.64	24.86	125.57	116.25
40	Ambalavayal-2	48.81	0.91	0.61*	158.36	10.76	154	7.11	28.58	289.81*	272.06*
41	Uruni kayama	55.15	0.76	0.39	146.35	10.28	149	8.52	28.87	187.72	164.37
42	Gandhakasala	62.52*	1.04	0.57	124.54	9.57	138	5.93	32.01	228.13	192.14
43	Kothandan	56.22	1.16	0.46	145.61	16.11*	126	11.10	29.10	123.54	113.41
44	Thavalakannan	42.28	1.33*	0.44	85.22	9.30	137	6.45	24.22	133.61	100.72
45	Kunam kulumban	46.86	1.12	0.47	118.55	10.22	142	5.84	29.21	252.02	196.50
46	Chomala-2	55.61	1.15	0.52	163.27	9.83	142	5.91	31.34	271.25*	219.23
47	Jeerakasala	54.12	0.96	0.57	144.84	9.41	141	4.92	33.33	175.54	169.32
48	Kutti veliyan	49.28	0.81	0.54	137.61	10.11	142	7.24	28.60	173.41	155.64
49	Thonnooran thondi	38.8	0.72	0.36	138.82	12.32	127	12.24	26.01	99.33	91.17
50	Chomala-1	52.01	1.03	0.54	159.83	9.10	146	7.01	28.14	256.82*	221.01
51	Rasagatham	37.17	0.73	0.41	103.65	12.23	145	9.92	24.37	189.24	142.22

Continued...

52	Njavara	53.75	0.94	0.39	113.81	10.45	117	9.75	26.42	166.22	127.33
53	Sugandhamathi	36.54	1.01	0.47	82.42	9.44	137	6.93	25.85	149.45	116.10
54	Palthondi matta	47.44	0.92	0.41	133.43	15.11	117	9.35	28.26	109.24	83.25
55	Vellimuthu	53.42	1.03	0.36	141.10	14.02	137	9.04	25.68	126.53	100.24
56	Mara thondi	66.28*	1.04	0.46	155.60	13.34	124	9.27	28.21	196.20	142.16
57	Kayama	49.87	0.75	0.43	138.82	9.78	150	6.28	39.42*	191.24	174.40
58	Onamottan	55.78	0.92	0.38	142.61	14.52	122	13.79*	28.63	125.33	96.73
59	Karimpalan	58.87	0.81	0.54	145.54	13.31	144	8.11	25.44	132.26	101.12
60	Gandhakasala (dwarf)	59.72	0.94	0.49	122.37	11.91	140	9.40	32.45	219.17	184.21
											Check varieties
61	Kanchana	25.86	0.83	0.35	63.61	17.31	132	13.22*	19.84	119.45	98.34
62	Uma	29.65	0.82	0.44	75.42	14.24	140	11.75	23.46	159.52	137.67
63	Aathira	34.53	1.11	0.46	105.91	12.46	142	8.54	26.34	196.23	169.41
	Mean	48.04	0.88	0.47	135.93	11.33	141.43	8.13	27.46	179.24	146.88
	Minimum	30.20	0.54	0.28	72.12	8.25	117	1.33	20.56	68.55	63.24
	Maximum	66.28	1.33	0.63	177.83	16.61	162	14.95	39.42	298.42	272.06
	CD (Ci - Vi)	2.615	0.088	0.225	3.907	1.462	0.006	1.74	1.942	29.083	22.723

('*' - Significant and superior; **LLB-** Length of leaf blade; **WLB-** Width of leaf blade; **ST-** Stem thickness; **SL-** Stem length; **NTP-** Number of tillers per plant; **TH-** Time for heading; **NPP-** Number of panicles per plant; **LPA-** Length of panicle main axis; **NSP-** Number of spikelets per panicle; **NGP-** Number of grains per panicle)

Table 40. Continued...

Sl. No.	Genotype	SSP (%)	TGW (g)	GL (mm)	GW (mm)	GLBR	DGL (mm)	DGW (mm)	DGLBR	TM (days)	GYP (g)
1	Kalladi aryan	91.92	33.01	8.3	3.7*	2.24	6.3	3.1	2.03	168	25.13
2	Thondi-1	91.23	32.22	8.3	3.5*	2.37	6.2	3.8*	1.63	168	29.01*
3	Ambalavayal-1	74.71	26.40	7.7	3.3	2.33	6.0	2.7	2.22	191*	33.74*
4	Ayirankana	50.81	36.23*	8.6	3.9*	2.21	6.3	3.4	1.85	182	19.02
5	Palveliyan	90.06	31.58	8.0	3.4*	2.35	6.0	2.7	2.22	183	25.91
6	Kannali	80.85	34.16	8.7	3.6*	2.42	6.2	3.0	2.07	182	29.24*
7	Chomala	76.47	26.25	8.2	3.1	2.65	5.8	2.6	2.23	181	23.40
8	Keervana	94.12*	29.85	8.1	3.4*	2.38	5.9	2.9	2.03	183	21.12
9	Kothandon	72.30	29.42	8.2	3.5*	2.34	6.2	2.8	2.21	181	23.03
10	Kanni kayama	88.60	30.93	8.0	3.3	2.42	5.9	2.8	2.11	155	36.45*
11	Addy	95.05*	18.86	5.2	3.0	1.73	4.5	2.6	1.73	159	17.44
12	Kodu veliyan	87.39	29.32	8.3	3.5*	2.37	6.0	2.9	2.07	158	24.41
13	Thondi-2	78.73	33.13	8.4	3.5*	2.40	6.1	2.8	2.18	183	32.62*
14	Chenthondi	51.34	29.22	8.3	3.6*	2.31	6.1	3.0	2.03	182	22.80
15	Mangalapuram puncha	70.20	33.98	8.3	3.7*	2.24	6.2	3.0	2.07	168	26.93

Continued...

16	Chennellu	90.29	27.91	8.2	3.4*	2.41	5.8	2.8	2.07	183	25.37
17	Punnadan thondi	74.71	30.04	7.7	3.5*	2.20	5.5	2.9	1.90	183	23.02
18	Putta batta	80.71	30.56	8.4	3.5*	2.40	6.2	2.9	2.14	181	23.93
19	Rajameni	66.67	23.11	7.9	3.1	2.55	5.7	2.5	2.28	184	13.81
20	Chettu veliyan	83.49	30.22	8.0	3.4*	2.35	5.8	2.8	2.07	181	18.24
21	Kuruva	95.86*	22.12	6.4	3.5*	1.83	4.7	2.8	1.68	183	18.40
22	Mulla kuruva	91.85	21.69	6.3	3.4*	1.85	4.4	2.8	1.57	168	22.52
23	Mannu veliyan	67.52	28.25	7.9	3.5*	2.26	5.8	2.7	2.15	182	20.83
24	Njavara black	92.65*	23.06	8.0	3.0	2.67	5.9	2.4	2.46	182	10.35
25	Veliyan	81.42	27.06	7.7	3.3*	2.33	5.6	2.7	2.07	183	19.86
26	Mahi kuruva	81.25	17.22	5.8	3.0	1.93	4.2	2.4	1.75	168	12.77
27	Valichoori	70.40	33.57	8.9	3.6*	2.47	6.7	3.1	2.16	183	20.64
28	Urulan kayama	76.19	25.51	6.8	3.3*	2.06	5.1	2.9	1.76	191*	21.41
29	Thondi-3	80.81	30.98	8.6	3.7*	2.32	6.4	3.4	1.88	184	18.10
30	Mullan puncha	94.44*	28.51	8.8	3.3*	2.67	6.0	2.7	2.22	182	11.92
31	Chenthadi	68.20	26.28	7.9	3.5*	2.26	5.9	2.9	2.03	188	30.80*
32	Peruvaya	89.12	35.56*	8.9	3.8*	2.34	7.0	3.2	2.19	168	25.91
33	Palthondi	93.78*	25.71	7.9	3.2	2.47	5.9	2.7	2.19	187	27.63

Continued...

34	Vaalicha	96.90*	30.61	8.1	3.3	2.45	5.7	2.7	2.11	188	19.62
35	Veliya thondi	86.76	30.63	8.0	3.4*	2.35	6.0	2.9	2.07	189	23.24
36	Edavaka	92.63*	27.95	8.0	3.5*	2.29	5.7	2.8	2.04	169	23.75
37	Velumpala	94.06*	29.91	7.9	3.5*	2.26	6.2	2.9	2.14	188	27.01
38	Kumbali	81.98	33.67	8.3	3.6*	2.31	6.3	3.0	2.10	188	25.52
39	Adukkan	92.80*	32.91	8.4	3.8*	2.21	6.0	2.9	2.07	169	25.20
40	Ambalavayal-2	94.12*	28.54	8.1	3.3	2.45	5.7	2.7	2.11	185	23.13
41	Uruni kayama	87.70	19.81	5.9	3.1	1.90	4.4	2.6	1.69	183	17.62
42	Gandhakasala	84.21	15.47	6.1	2.8	2.18	4.6	2.4	1.92	181	17.11
43	Kothandan	91.87	32.54	8.2	3.6*	2.28	5.6	3.1	1.81	156	33.64*
44	Thavalakannan	75.19	25.97	8.0	3.4*	2.35	5.8	2.7	2.15	168	11.81
45	Kunam kulumban	77.78	24.69	8.6	3.1	2.77	6.0	2.5	2.40	182	19.32
46	Chomala-2	80.81	25.86	8.3	3.2	2.59	5.6	2.7	2.07	183	19.20
47	Jeerakasala	96.57*	24.31	8.4	2.7	3.11	6.6	2.5	2.64	183	15.53
48	Kutti veliyan	89.60	30.78	7.8	3.4*	2.29	5.9	2.8	2.11	181	24.22
49	Thonnooran thondi	91.92	31.12	8.5	3.5*	2.43	6.1	3.0	2.03	157	24.41
50	Chomala-1	86.33	29.11	8.1	3.5*	2.31	5.7	2.7	2.11	181	14.44
51	Rasagatham	75.13	12.43	5.7	2.7	2.11	4.1	2.1	1.95	181	12.51

Continued...

52	Njavara	76.51	33.84	8.5	3.5*	2.43	6.8	3.1	2.19	147	27.10
53	Sugandhamathi	77.85	29.28	11.2*	2.5	4.48*	8.6*	2.1	4.10*	169	14.43
54	Palthondi matta	76.15	34.05	8.4	3.7*	2.27	5.8	3.0	1.93	149	21.72
55	Vellimuthu	79.37	35.01*	8.6	3.4*	2.53	6.5	2.9	2.24	169	18.71
56	Mara thondi	72.45	27.42	8.8	3.2	2.75	6.3	2.6	2.42	156	28.32
57	Kayama	91.10	23.90	7.7	3.5*	2.20	5.3	2.8	1.89	181	17.63
58	Onamottan	76.80	36.57*	8.9	3.7*	2.41	6.3	3.0	2.11	151	32.85*
59	Karimpalan	76.52	31.03	8.2	3.4*	2.41	6.1	2.9	2.10	181	14.34
60	Gandhakasala (dwarf)	84.02	16.59	6.4	3.0	2.13	4.9	2.4	2.04	182	21.31
											Check varieties
61	Kanchana	82.35	31.16	8.4	3.3*	2.55	6.4	2.7	2.37	176	26.42
62	Uma	86.16	26.09	7.5	3.4*	2.21	5.8	2.8	2.07	180	35.20*
63	Aathira	86.22	29.72	8.1	3.3*	2.45	6.2	2.7	2.30	185	29.14*
	Mean	82.67	28.27	7.96	3.37	2.37	5.85	2.81	2.10	176.37	23.67
	Minimum	50.81	12.43	5.2	2.5	1.73	4.1	2.1	1.57	147	10.35
	Maximum	96.90	36.57	11.2	3.9	4.48	8.6	3.8	4.10	191	36.45
	CD (Ci - Vi)	3.785	1.674	0.358	0.447	0.301	0.264	0.141	0.11	0.085	6.81

('*' - Significant and on par) **(SSP-** Seed setting per cent; **TGW-** 1000 grains weight; **GL-** Grain length; **GW-** Grain width; **GLBR-** Grain L/B ratio; **DGL-** Decorticated grain length; **DGW-** Decorticated grain width; **DGLBR-** Decorticated grain L/B ratio; **TM-** Time for maturity; **GYP-** Grain yield per plant)

Table 41. Analysis of variance for quantitative characters in 60 landraces of rice

Source	Df	LLB	WLB	ST	SL	NTP	TH	NPP	LPA	NSP	NGP
Block (ignoring Treatments)	5	273.47**	0.08**	0.61**	2160.80**	9.64 **	209.90**	3.08**	15.64**	3439.99**	4597.50**
Treatment (eliminating Blocks)	62	130.43**	0.02**	0.23**	1182.94**	7.51**	86.04**	8.76**	14.61**	2742.68**	1692.42**
Genotypes	59	81.40**	0.02**	0.24**	650.77**	5.61**	99.74**	5.34**	9.56**	2794.23**	1883.91**
Checks	2	109.08**	0.15**	0.92**	2690.78**	30.57**	168.00**	36.17**	74.29**	8477.39**	7620.39**
Checks vs. Genotypes	1	4431.49**	0.01**	1.11**	40355.45**	112.29**	163.22**	170.59**	268.47**	5304.07**	1424.90**
Error	10	0.89	0.001	0.01	1.98	0.28	0.00	0.39	0.49	109.52	66.86

(*- significant at 5 per cent level; **- significant at 1 per cent level; **LLB**- Length of leaf blade; **WLB**- Width of leaf blade; **ST**- Stem thickness; **SL**- Stem length; **NTP**- Number of tillers per plant; **TH**- Time for heading; **NPP**- Number of panicles per plant; **LPA**- Length of panicle main axis; **NSP**- Number of spikelets per panicle; **NGP**- Number of grains per panicle)

Table 41. Continued...

Source	Df	SSP	TGW	GL	GW	GLBR	DGL	DGW	DGLBR	TM	GYP
Block (ignoring Treatments)	5	140.77**	32.88**	0.57**	0.08	0.08**	0.52**	0.09**	0.08**	224.27**	103.03**
Treatment (eliminating Blocks)	62	92.62 **	25.53**	0.86**	0.07*	0.12**	0.49**	0.07**	0.11**	112.72**	52.28**
Genotypes	59	106.05**	28.09**	0.91**	0.08*	0.13**	0.52**	0.08**	0.11**	129.63**	35.87**
Checks	2	43.71**	32.92**	1.22**	0.001	0.1**	0.62**	0.03**	0.18**	122**	147.99**
Checks vs. Genotypes	1	93.68**	20.32**	0.01	0.05	0.03	1.00**	0.13**	0.37**	217.86**	1224.89**
Error	10	1.85	0.36	0.02	0.03	0.01	0.01	0.003	0.002	-0.001	5.99

(*- significant at 5 per cent level; **- significant at 1 per cent level; **SSP**- Seed setting per cent; **TGW**- 1000 grains weight; **GL**- Grain length; **GW**- Grain width; **GLBR**- Grain L/B ratio; **DGL**- Decorticated grain length; **DGW**- Decorticated grain width; **DGLBR**- Decorticated grain L/B ratio; **TM**- Time for maturity; **GYP**- Grain yield per plant)

4.1.4. Genetic parameters

Genetic parameters including Phenotypic Coefficient of Cariation (PCV), Genotypic Coefficient of Variation (GCV), heritability (h^2), Genetic Advance (GA) and Genetic Gain (GG) were estimated for 20 quantitative characters and presented in Table 42.

4.1.4.1. Leaf: Length of blade

The phenotypic and genotypic coefficients of variation (PCV and GCV) values recorded for length of leaf blade were moderate *i.e.,* 17.04 per cent and 16.93 per cent respectively. The heritability for this character was high (98.68 per cent) with high genetic advance (32.91 per cent) and high genetic gain (34.64 per cent).

4.1.4.2. Leaf: Width of blade

Both PCV and GCV values were moderate (16.20 per cent and 15.77 per cent) for width of leaf blade. This character exhibited high heritability (94.79 per cent), low genetic advance (0.27 per cent) and high genetic gain (31.63 per cent).

4.1.4.3. Stem: Thickness

Thickness of the stem exhibited moderate PCV and GCV values (15.07 per cent and 14.82 per cent) high heritability (96.69 per cent), low genetic advance (0.89 per cent) and high genetic gain (30.01 per cent).

4.1.4.4. Stem: Length

Both PCV and GCV values were moderate (17.00 per cent and 16.97 per cent) for stem length. This character recorded high heritability (99.63 per cent), high genetic advance (47.41 per cent) and high genetic gain (34.89 per cent).

4.1.4.5. Tillers: Number per plant

The PCV and GCV values for number of tillers per plant were moderate i.e., 19.08 per cent and 18.51 per cent respectively. The heritability for this character

was high (94.04 per cent) with low genetic advance (4.18 per cent) and high genetic gain (36.97 per cent).

4.1.4.6. Time of heading

Both PCV and GCV values were low (6.39 per cent and 6.39 per cent) for time of heading. This character exhibited high heritability (100 per cent), moderate genetic advance (18.62 per cent) and moderate genetic gain (13.17 per cent).

4.1.4.7. Panicle: Number per plant

Number of panicles per plant recorded high PCV and GCV values (26.06 per cent and 24.89 per cent), high heritability (91.22 per cent), low genetic advance (3.96 per cent) and high genetic gain (48.96 per cent).

4.1.4.8. Panicle: Length of main axis

The PCV and GCV values were moderate (10.26 per cent) and low (9.94 per cent) respectively for length of main axis of panicle. This character recorded high heritability (93.83 per cent), low genetic advance (5.44 per cent) and moderate genetic gain (19.84 per cent).

4.1.4.9. Spikelets: Number per panicle

Number of spikelets per panicle exhibited high PCV and GCV values (26.87 per cent and 26.23 per cent), high heritability (95.26 per cent), high genetic advance (94.30 per cent) and high genetic gain (52.73 per cent).

4.1.4.10. Grains: Number per panicle

Both PCV and GCV values were high (26.92 per cent and 26.33 per cent) for number of grains per panicle. This character exhibited high heritability (95.70 per cent), high genetic advance (77.76 per cent) and high genetic gain (53.07 per cent).

4.1.4.11. Seed setting (per cent)

The PCV and GCV values for seed setting (per cent) were medium *i.e.,* 11.30 per cent and 11.18 per cent respectively. The heritability for this character was high (97.87 per cent) with moderate genetic advance (18.83 per cent) and high genetic gain (22.78 per cent).

4.1.4.12. Grain: Weight of 1000 grains

Weight of 1000 grains exhibited medium PCV and GCV values (17.00 per cent and 16.86 per cent), high heritability (98.43 per cent), low genetic advance (9.74 per cent) and high genetic gain (34.47 per cent).

4.1.4.13. Grain: Length

Both PCV and GCV values were medium (10.88 per cent and 10.76 per cent) for grain length. This character exhibited high heritability (97.80 per cent), low genetic advance (1.75 per cent) and high genetic gain (21.92 per cent).

4.1.4.14. Grain: Width

The PCV and GCV values for grain width were low *i.e.,* 7.82 per cent and 6.19 per cent respectively. The heritability for this character was high (62.71 per cent) with low genetic advance (0.34 per cent) and moderate genetic gain (10.09 per cent).

4.1.4.15. Grain: L/B ratio

Grain L/B ratio exhibited moderate PCV and GCV values (13.82 per cent and 13.05 per cent), high heritability (89.10 per cent), low genetic advance (0.60 per cent) and high genetic gain (25.37 per cent).

4.1.4.16. Decorticated grain: Length

Both PCV and GCV values were moderate (11.22 per cent and 11.10 per cent) for decorticated grain length. This character exhibited high heritability (97.91 per cent), low genetic advance (1.32 per cent) and low genetic gain (2.62 per cent).

4.1.4.17. Decorticated grain: Width

The PCV and GCV values for decorticated grain width were low *i.e.,* 9.21 per cent and 9.04 per cent respectively. The heritability for this character was high (96.18 per cent) with low genetic advance (0.51 per cent) and moderate genetic gain (18.25 per cent).

4.1.4.18. Decorticated grain: L/B ratio

Decorticated grain L/B ratio recorded moderate PCV and GCV values (14.25 per cent and 14.12 per cent), high heritability (98.25 per cent), low genetic advance (0.60 per cent) and high genetic gain (28.84 per cent).

4.1.4.19. Time for maturity

Both PCV and GCV values for time for maturity were low (5.84 per cent). This character exhibited high heritability (100 per cent), high genetic advance (21.23 per cent) and moderate genetic gain (12.04 per cent).

4.1.4.20. Grain: Yield per plant

The PCV and GCV values for grain yield per plant were high *i.e.,* 24.94 per cent and 22.35 per cent respectively. The heritability for this character was high (80.31 per cent) with low genetic advance (9.13 per cent) and high genetic gain (41.26 per cent).

Table 42. Genetic parameters of quantitative characters of 60 landraces of rice

Characters	PCV (per cent)	GCV (per cent)	h^2 (per cent)	GA (per cent)	GG (per cent)
LLB	17.04	16.93	98.68	16.62	34.64
WLB	16.20	15.77	94.79	0.27	31.63
ST	15.07	14.82	96.69	0.89	30.01
SL	17.00	16.97	99.63	47.41	34.89
NTP	19.08	18.51	94.04	4.18	36.97
TH	6.39	6.39	100.0	18.62	13.17
NPP	26.06	24.89	91.22	3.96	48.96
LPA	10.26	9.94	93.83	5.44	19.84
NSP	26.87	26.23	95.26	94.30	52.73
NGP	26.92	26.33	95.70	77.76	53.07
SSP	11.30	11.18	97.87	18.83	22.78
TGW	17.00	16.86	98.43	9.74	34.47
GL	10.88	10.76	97.80	1.75	21.92
GW	7.82	6.19	62.71	0.34	10.09
GLBR	13.82	13.05	89.10	0.60	25.37
DGL	11.22	11.10	97.91	1.32	2.62
DGB	9.21	9.04	96.18	0.51	18.25
DGLBR	14.25	14.12	98.25	0.60	28.84
TM	5.84	5.84	100.0	21.23	12.04
GYP	24.94	22.35	80.31	9.13	41.26

(**PCV**- Phenotypic Coefficient of Variation; **GCV**- Genotypic Coefficient of Variation; **h^2**- Heritability; **GA**- Genetic Advance; **GG**- Genetic Gain)

(**LLB**- Length of leaf blade; **WLB**- Width of leaf blade; **ST**- Stem thickness; **SL**- Stem length; **NTP**- Number of tillers per plant; **TH**- Time for heading; **NPP**- Number of panicles per plant; **LPA**- Length of panicle main axis; **NSP**- Number of spikelets per panicle; **NGP**- Number of grains per panicle; **SSP**- Seed setting per cent; **TGW**- 1000 grains weight; **GL**- Grain length; **GW**- Grain width; **GLBR**- Grain L/B ratio; **DGL**- Decorticated grain length; **DGW**- Decorticated grain width; **DGLBR**- Decorticated grain L/B ratio; **TM**- Time for maturity; **GYP**- Grain yield per plant).

4.1.5. Character association studies

4.1.5.1. Correlation

Correlation coefficients were worked out for 20 quantitative characters including growth and yield characters and are presented in Table 43 and Fig. 11.

4.1.5.1.1. Grain yield per plant

Grain yield per plant exhibited significant positive association at 1 per cent level with the characters namely, length of leaf blade (0.389), stem length (0.505), panicle number per plant (0.389), 1000 grains weight (0.488), grain width (0.463), decorticated grain width (0.461). Positive association of grain yield per plant at 5 per cent level of significance was recorded for width of leaf blade (0.267).

4.1.5.1.2. Leaf characters

Among the leaf characters, length of leaf blade showed significant positive association at 1 per cent level with width of leaf blade (0.564), stem thickness (0.472), stem length (0.658), length of main axis of panicle (0.504), number of spikelets per panicle (0.389) and grain yield per plant (0.389). Significant positive association at 5 per cent level was exhibited by length of leaf blade with number of grains per panicle (0.326). Width of leaf blade showed significant positive association at 1 per cent level with stem thickness (0.442), number of spikelets per panicle (0.344), grain length (0.343) and decorticated grain length (0.335). Significant positive association of width of leaf blade at 5 per cent level was showed by stem length (0.301), length of main axis of panicle (0.291), grain L/B ratio (0.275) and grain yield per plant (0.267).

4.1.5.1.3. Stem characters

Among the stem characters, stem thickness showed significant positive association at 1 per cent level with stem length (0.579), time of heading (0.445), length of main axis of panicle (0.468), number of spikelets per panicle (0.635), number of grains per panicle (0.599), time for maturity (0.473) and significant

negative association of stem thickness at 1 per cent level was exhibited with number of tillers per plant (-0.493) and panicle number per plant (-376). Stem length showed significant positive association at 1 per cent level with length of main axis of panicle (0.480), number of spikelets per panicle (0.484), number of grains per panicle (0.536) and grain yield per plant (0.505). Stem thickness exhibited significant positive association at 5 per cent level with time of heading (0.294), weight of 1000 grains (0.323), grain width (0.274) and decorticated grain width (0.269). At the same time stem length exhibited negative significant association at 1 per cent level with number of tillers per plant (-0.384). Number of tillers per plant showed significant positive association at 1 per cent level with number of panicles per plant (0.594). At the same time number of tillers per plant exhibited significant negative association at 1 per cent level with time of heading (-0.413), length of main axis of panicle (-0.434), number of spikelets per panicle (-0.466), number of grains per panicle (-0.500) and time for maturity (0.408).

4.1.5.1.4. Time for heading

Time for heading showed significant positive association at 1 per cent level with number of spikelets per panicle (0.593), number of grains per panicle (0.570) and time for maturity (0.906). At the same time, days for heading exhibited significant negative association (-0.356) at 1 per cent level with panicle number per plant.

4.1.5.1.5. Panicle characters

Among the panicle characters, number of panicles per plant showed significant positive association (0.389) at 1 per cent level with grain yield per plant. At the same time, number of panicles per plant exhibited significant negative association at 1 per cent level with time for maturity (-0.424) and also showed significant negative association at 5 per cent level with panicle length of main axis (-0.258), number of spikelets per panicle (-0.318) and number of grains per panicle (-0.314). Length of main axis of panicle showed significant positive association at

1 per cent level with number of spikelets per panicle (0.398) and number of grains per panicle (0.417).

4.1.5.1.6. Number of spikelets and filled grains per panicle

Number of spikelets per panicle showed significant positive association at 1 per cent level with number of grains per panicle (0.887) and time for maturity (0.540). Number of grains per panicle showed significant positive association at 1 per cent level with time for maturity (0.523).

4.1.5.1.7. Grain characters

Weight of 1000 grains showed significant positive association at 1 per cent level with grain length (0.754), grain width (0.741), decorticated grain length (0.728), decorticated grain width (0.710) and grain yield per plant (0.488). Grain length showed significant positive association at 1 per cent level with grain L/B ratio (0.756), decorticated grain length (0.941), and decorticated grain L/B ratio (0.662). Significant positive association at 5 per cent level was showed for grain width (0.286) and decorticated grain width (0.298). Grain width showed significant positive association at 1 per cent level with decorticated grain width (0.833) and grain yield per plant (0.463). However, grain width exhibited significant negative association at 1 per cent level with grain L/B ratio (-0.399) and decorticated grain L/B ratio (-0.431). Grain L/B ratio showed significant positive association at 1 per cent level with decorticated grain length (0.751) and decorticated grain L/B ratio (0.941). Grain L/B ratio exhibited significant negative association at 5 per cent level with decorticated grain width (-0.279).

4.1.5.1.8. Decorticated grain characters

Decorticated grain length showed significant positive association at 1 per cent level with decorticated grain L/B ratio (0.715) and also showed significant positive association at 5 per cent level with decorticated grain width (0.301). Decorticated grain width showed significant positive association at 1 per cent level with grain yield per plant (0.461). Decorticated grain width exhibited

Table 43. Correlation coefficient for grain yield and quantitative traits of 60 rice landraces

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
A	1	0.564**	0.472**	0.658**	-0.191^{NS}	0.014^{NS}	0.024^{NS}	0.504**	0.389**	0.326*	-0.120^{NS}	0.177^{NS}	0.080^{NS}	0.115^{NS}	-0.030^{NS}	0.133^{NS}	0.166^{NS}	-0.037^{NS}	-0.056^{NS}	0.389**
B	0.564**	1	0.442**	0.301*	-0.220^{NS}	-0.043^{NS}	-0.053^{NS}	0.291*	0.344**	0.242^{NS}	-0.292*	0.242^{NS}	0.343**	0.053^{NS}	0.275*	0.335**	0.067^{NS}	0.254^{NS}	-0.059^{NS}	0.267*
C	0.472**	0.442**	1	0.579**	-0.493**	0.445**	-0.376**	0.468**	0.635**	0.599**	-0.130^{NS}	0.142^{NS}	0.194^{NS}	0.056^{NS}	0.143^{NS}	0.211^{NS}	0.099^{NS}	0.112^{NS}	0.473**	0.179^{NS}
D	0.658**	0.301*	0.579**	1	-0.384**	0.294*	-0.102^{NS}	0.480**	0.484**	0.536**	0.147^{NS}	0.323*	0.163^{NS}	0.274*	-0.065^{NS}	0.141^{NS}	0.269*	-0.109^{NS}	0.190^{NS}	0.505**
E	-0.191^{NS}	-0.220^{NS}	-0.493**	-0.384**	1	-0.413**	0.594**	-0.434**	-0.466**	-0.500**	-0.095^{NS}	0.172^{NS}	-0.006^{NS}	0.212^{NS}	-0.142^{NS}	-0.057^{NS}	0.171^{NS}	-0.169^{NS}	-0.408**	0.198^{NS}
F	0.014^{NS}	-0.043^{NS}	0.445**	0.294*	-0.413**	1	-0.356**	0.152^{NS}	0.593**	0.570**	-0.068^{NS}	-0.194^{NS}	-0.149^{NS}	-0.119^{NS}	-0.065^{NS}	-0.131^{NS}	-0.141^{NS}	-0.025^{NS}	0.906**	-0.136^{NS}
G	0.024^{NS}	-0.053^{NS}	-0.376**	-0.102^{NS}	0.594**	-0.356**	1	-0.258*	-0.318*	-0.314*	0.020^{NS}	0.250^{NS}	0.028^{NS}	0.233^{NS}	-0.133^{NS}	0.067^{NS}	0.216^{NS}	-0.102^{NS}	-0.424**	0.389**
H	0.504**	0.291*	0.468**	0.480**	-0.434**	0.152^{NS}	-0.258*	1	0.398**	0.417**	0.030^{NS}	-0.022^{NS}	0.110^{NS}	-0.029^{NS}	0.111^{NS}	0.049^{NS}	-0.009^{NS}	0.039^{NS}	0.211^{NS}	0.076^{NS}
I	0.389**	0.344**	0.635**	0.484**	-0.466**	0.593**	-0.318*	0.398**	1	0.887**	-0.247^{NS}	-0.201^{NS}	-0.078^{NS}	-0.123^{NS}	-0.007^{NS}	-0.096^{NS}	-0.171^{NS}	0.015^{NS}	0.540**	0.125^{NS}
J	0.326*	0.242^{NS}	0.599**	0.536**	-0.500**	0.570**	-0.314*	0.417**	0.887**	1	0.201^{NS}	-0.235^{NS}	-0.141^{NS}	-0.184^{NS}	-0.026^{NS}	-0.161^{NS}	-0.200^{NS}	-0.021^{NS}	0.523**	0.117^{NS}
K	-0.120^{NS}	-0.292*	-0.130^{NS}	0.147^{NS}	-0.095^{NS}	-0.068^{NS}	0.020^{NS}	0.030^{NS}	-0.247^{NS}	0.201^{NS}	1	-0.135^{NS}	-0.180^{NS}	-0.158^{NS}	-0.066^{NS}	-0.178^{NS}	-0.089^{NS}	-0.092^{NS}	-0.060^{NS}	0.007^{NS}
L	0.177^{NS}	0.242^{NS}	0.142^{NS}	0.323*	0.172^{NS}	-0.194^{NS}	0.250^{NS}	-0.022^{NS}	-0.201^{NS}	-0.235^{NS}	-0.135^{NS}	1	0.754**	0.741**	0.214^{NS}	0.728**	0.710**	0.141^{NS}	-0.238^{NS}	0.488**
M	0.080^{NS}	0.343**	0.194^{NS}	0.163^{NS}	-0.006^{NS}	-0.149^{NS}	0.028^{NS}	0.110^{NS}	-0.078^{NS}	-0.141^{NS}	-0.180^{NS}	0.754**	1	0.286*	0.756**	0.941**	0.298*	0.662**	-0.136^{NS}	0.217^{NS}
N	0.115^{NS}	0.053^{NS}	0.056^{NS}	0.274*	0.212^{NS}	-0.119^{NS}	0.233^{NS}	-0.029^{NS}	-0.123^{NS}	-0.184^{NS}	-0.158^{NS}	0.741**	0.286*	1	-0.399**	0.224^{NS}	0.833**	-0.431**	-0.163^{NS}	0.463**
O	-0.030^{NS}	0.275*	0.143^{NS}	-0.065^{NS}	-0.142^{NS}	-0.065^{NS}	-0.133^{NS}	0.111^{NS}	-0.007^{NS}	-0.026^{NS}	-0.066^{NS}	0.214^{NS}	0.756**	-0.399**	1	0.751**	-0.279*	0.941**	-0.027^{NS}	-0.114^{NS}
P	0.133^{NS}	0.335**	0.211^{NS}	0.141^{NS}	-0.057^{NS}	-0.131^{NS}	0.067^{NS}	0.049^{NS}	-0.096^{NS}	-0.161^{NS}	-0.178^{NS}	0.728**	0.941**	0.224^{NS}	0.751**	1	0.301*	0.715**	-0.128^{NS}	0.232^{NS}
Q	0.166^{NS}	0.067^{NS}	0.099^{NS}	0.269*	0.171^{NS}	-0.141^{NS}	0.216^{NS}	-0.009^{NS}	-0.171^{NS}	-0.200^{NS}	-0.089^{NS}	0.710**	0.298*	0.833**	-0.279*	0.301*	1	-0.434**	-0.187^{NS}	0.461**
R	-0.037^{NS}	0.254^{NS}	0.112^{NS}	-0.109^{NS}	-0.169^{NS}	-0.025^{NS}	-0.102^{NS}	0.039^{NS}	0.015^{NS}	-0.021^{NS}	-0.092^{NS}	0.141^{NS}	0.662**	-0.431**	0.941**	0.715**	-0.434**	1	0.004^{NS}	-0.138^{NS}
S	-0.056^{NS}	-0.059^{NS}	0.473**	0.190^{NS}	-0.408**	0.906**	-0.424**	0.211^{NS}	0.540**	0.523**	-0.060^{NS}	-0.238^{NS}	-0.136^{NS}	-0.163^{NS}	-0.027^{NS}	-0.128^{NS}	-0.187^{NS}	0.004^{NS}	1	-0.251^{NS}
T	0.389**	0.267*	0.179^{NS}	0.505**	0.198^{NS}	-0.136^{NS}	0.389**	0.076^{NS}	0.125^{NS}	0.117^{NS}	0.007^{NS}	0.488**	0.217^{NS}	0.463**	-0.114^{NS}	0.232^{NS}	0.461**	-0.138^{NS}	-0.251^{NS}	1

(**A-** Length of leaf blade; **B-** Width of leaf blade; **C-** Stem thickness; **D-** Stem length; **E-** Number of tillers per plant; **F-** Time for heading; **G-** Number of panicles per plant; **H-** Length of panicle main axis; **I-** Number of spikelets per panicle; **J-** Number of grains per panicle; **K-** Seed setting per cent; **L-** Weight of 1000 grains; **M-** Grain length; **N-** Grain width; **O-** Grain L/B ratio; **P-** Decorticated grain length; **Q-** Decorticated grain width; **R-** Decorticated grain L/B ratio; **S-** Time for maturity; **T-** Grain yield per plant).

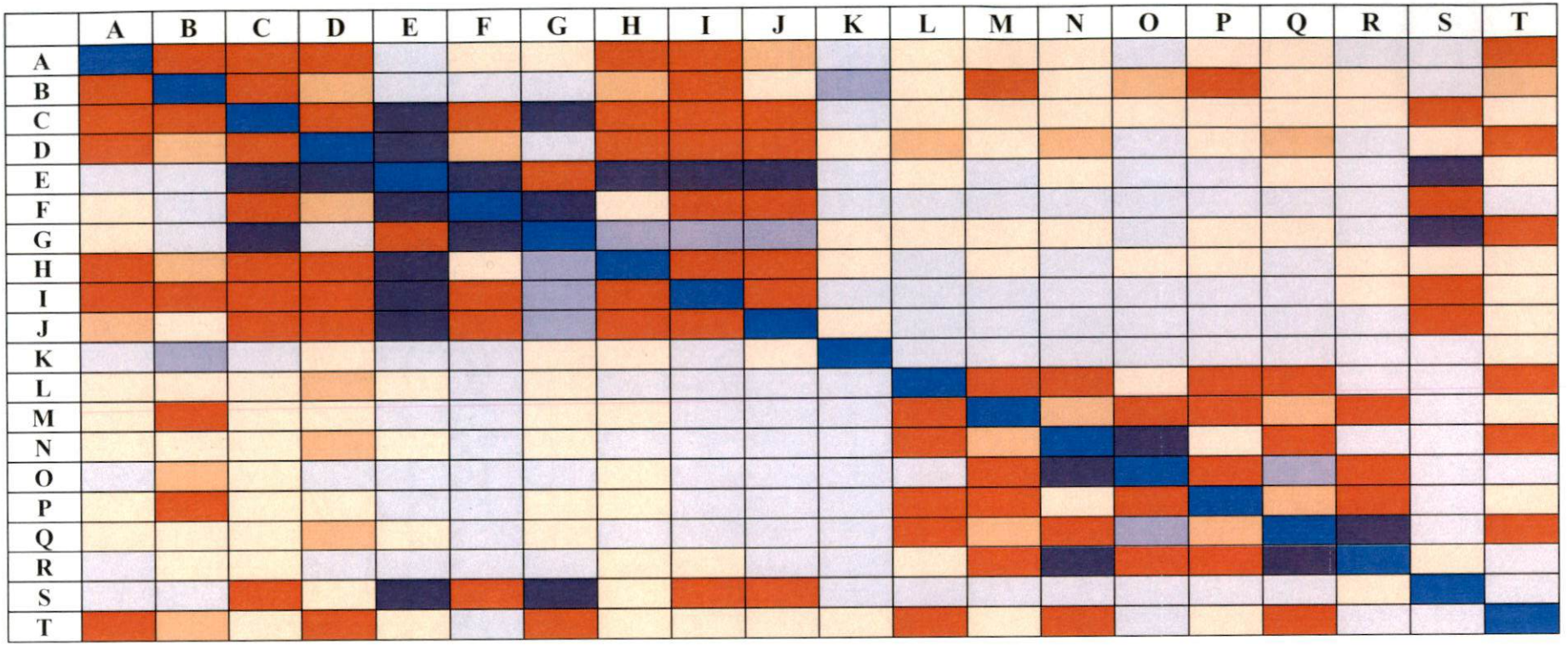


Fig. 11. Shade correlation matrix for grain yield and quantitative traits of 60 rice landraces

(**A-** Length of leaf blade; **B-** Width of leaf blade; **C-** Stem thickness; **D-** Stem length; **E-** Number of tillers per plant; **F-** Time for heading; **G-** Number of panicles per plant; **H-** Length of panicle main axis; **I-** Number of spikelets per panicle; **J-** Number of grains per panicle; **K-** Seed setting per cent; **L-** Weight of 1000 grains; **M-** Grain length; **N-** Grain width; **O-** Grain L/B ratio; **P-** Decorticated grain length; **Q-** Decorticated grain width; **R-** Decorticated grain L/B ratio; **S-** Time for maturity; **T-** Grain yield per plant).

192

significant negative association at 1 per cent level with decorticated grain L/B ratio (-0.434).

4.1.5.2. Path coefficient analysis

The estimate of direct and indirect effects of different growth and yield components on grain yield were estimated using correlation coefficients and are presented in Table 44.

The residual effect of path analysis was found to be 0.605. The characters those exhibited direct positive effect on grain yield per plant were width of leaf blade, stem thickness, stem length, number of tillers per plant, time of heading, panicle number per plant, panicle length of main axis, number of spikelets per panicle, seed setting per cent, grain weight of 1000 grains, decorticated grain width and decorticated grain L/B ratio. Similarly, the characteristics, length of leaf blade number of grains per panicle, grain length, grain width, grain L/B ratio, decorticated grain length and time for maturity shared direct negative effect on grain yield per plant.

Out of 20 characters studied, number of spikelets per panicle had the highest positive direct effect (0.981) on grain yield per plant, followed by decorticated grain L/B ratio (0.833), decorticated grain width (0.528), stem length (0.502), seed setting per cent (0.401), number of tillers per plant (0.372), weight of 1000 grains (0.207), width of leaf blade (0.203), panicle number per plant (0.137), length of main panicle axis (0.083), stem thickness (0.061) and time of heading (0.043). However, grain L/B ratio had the highest negative direct effect (-0.755) on grain yield per plant, followed by number of grains per panicle (-0.690), time for maturity (-0.306), length of leaf blade (-0.259), grain width (-0.253), grain length (-0.100) and decorticated grain length (-0.045).

The highest positive indirect effect with grain yield per plant was exhibited by number of grains per panicle *via.* number of spikelets per panicle (0.870), followed by

number of grains per panicle (0.269). Grain L/B ratio exhibited positive indirect effect with grain yield per plant *via.* decorticated grain L/B ratio (0.784), followed by grain width (0.101). Stem thickness exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.623), followed by stem length (0.291). Decorticated grain length exhibited positive indirect effect with grain yield per plant *via.* decorticated grain L/B ratio (0.596), followed by decorticated grain width (0.159), weight of 1000 grains (0.151) and number of grains per panicle (0.111). Time of heading exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.581), followed by stem length (0.148). Grain length exhibited positive indirect effect with grain yield per plant *via.* decorticated grain L/B ratio (0.552), followed by decorticated grain width (0.157) and weight of 1000 grains (0.156). Time for maturity exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.530). Stem length exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.474), followed by decorticated grain width (0.142). Grain width exhibited positive indirect effect with grain yield per plant *via.* decorticated grain width (0.440), followed by grain L/B ratio (0.301), weight of 1000 grains (0.153), stem length (0.137) and number of grains per panicle (0.127). Panicle length of main axis exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.391), followed by stem length (0.241). Length of leaf blade exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.382), followed by stem length (0.330) and width of leaf blade (0.115). Weight of 1000 grains exhibited positive indirect effect with grain yield per plant *via.* decorticated grain width (0.375), followed by stem length (0.162), number of grains per panicle (0.162) and decorticated grain L/B ratio (0.118). Number of tillers per plant exhibited positive indirect effect with grain yield per plant *via.* number of grains per panicle (0.345), followed by time for maturity (0.125) and grain L/B ratio (0.107). Width of leaf blade exhibited positive indirect effect with grain yield per plant *via.* number of spikelets per panicle (0.338), decorticated grain L/B ratio (0.211), stem length (0.151). Number of spikelets per panicle exhibited positive

indirect effect with grain yield per plant *via.* stem length (0.243). Panicle number per plant exhibited positive indirect effect with grain yield per plant *via.* number of tillers per plant (0.221), followed by number of grains per panicle (0.217), time for maturity (0.130), decorticated grain width (0.114) and grain L/B ratio (0.101). Decorticated grain width exhibited positive indirect effect with grain yield per plant *via.* grain L/B ratio (0.211), followed by weight of 1000 grains (0.147), number of grains per panicle (0.138) and stem length (0.135).

The highest negative indirect effect with grain yield per plant was exhibited by decorticated grain L/B ratio *via* grain L/B ratio (-0.710), followed by decorticated grain width (-0.229). Number of spikelets per panicle exhibited negative indirect effect with grain yield per plant *via.* number of grains per panicle (-0.613), followed by number of tillers per plant (-0.173), time for maturity (-0.165) and leaf length of blade (-0.101). Grain length exhibited negative indirect effect with grain yield per plant *via.* grain L/B ratio (-0.571). Decorticated grain length exhibited negative indirect effect with grain yield per plant *via.* grain L/B ratio (-0.567). Number of tillers per plant exhibited negative indirect effect with grain yield per plant *via.* number of spikelets per panicle (-0.457), followed by number of tillers per plant (-0.193) and decorticated grain L/B ratio (-0.141). Stem thickness exhibited negative indirect effect with grain yield per plant *via.* number of grains per panicle (-0.413), followed by number of tillers per plant (-0.183), time for maturity (-0.145), length of leaf blade (-0.122) and grain L/B ratio (-0.108). Time of heading exhibited negative indirect effect with grain yield per plant *via.* number of grains per panicle (-0.394), followed by time for maturity (-0.277) and number of tillers per plant (-0.153). Stem length exhibited negative indirect effect with grain yield per plant *via.* number of grains per panicle (-0.370), followed by number of tillers per plant (-0.143) and length of leaf blade (-0.170). Decorticated grain width exhibited negative indirect effect with grain yield per plant *via.* decorticated grain L/B ratio (-0.361), followed by grain width (-0.211) and number of spikelets per panicle (-0.168). Time for maturity exhibited negative indirect effect with grain yield per plant

via. number of grains per panicle (-0.361), followed by number of tillers per plant (-0.152). Grain width exhibited negative indirect effect with grain yield per plant *via.* decorticated grain L/B ratio (-0.359), followed by number of spikelets per panicle (-0121). Panicle number per plant exhibited negative indirect effect with grain yield per plant *via.* number of spikelets per panicle (-0.312). Panicle length of main axis exhibited negative indirect effect with grain yield per plant *via.* number of grains per panicle (-0.288), followed by number of tillers per plant (-0.161) and leaf length of blade (-0.131). Seed setting (per cent) exhibited negative indirect effect with grain yield per plant *via.* number of spikelets per panicle (-0.243), followed by number of grains per panicle (-0.139). Length of leaf blade exhibited negative indirect effect with grain yield per plant *via.* number of grains per panicle (-0.225). Width of leaf blade exhibited negative indirect effect with grain yield per plant *via.* grain L/B ratio (-0.208), followed by number of grains per panicle (-0.167), leaf length of blade (-0.146) and seed setting per cent (-0.117). Weight of 1000 grains exhibited negative indirect effect with grain yield per plant *via.* number of spikelets per panicle (-0.197), followed by grain width (-0.187) and grain L/B ratio (-0.162). Number of grains per panicle exhibited negative indirect effect with grain yield per plant *via.* number of tillers per plant (-0.186), followed by time for maturity (-0.160) and decorticated grain width (-0.106). Grain L/B ratio exhibited negative indirect effect with grain yield per plant *via.* decorticated grain width (-0.148).

Table 44. Path matrix of direct and indirect effects for quantitative traits of 60 rice landraces

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
A	**-0.259**	0.115	0.029	0.330	-0.071	0.001	0.003	0.042	0.382	-0.225	-0.048	0.037	-0.008	-0.029	0.023	-0.006	0.088	-0.030	0.017
B	-0.146	**0.203**	0.027	0.151	-0.082	-0.002	-0.007	0.024	0.338	-0.167	-0.117	0.050	-0.034	-0.013	-0.208	-0.015	0.036	0.211	0.018
C	-0.122	0.090	**0.061**	0.291	-0.183	0.019	-0.051	0.039	0.623	-0.413	-0.052	0.029	-0.019	-0.014	-0.108	-0.010	0.052	0.093	-0.145
D	-0.170	0.061	0.035	**0.502**	-0.143	0.013	-0.014	0.040	0.474	-0.370	0.059	0.067	-0.016	-0.069	0.049	-0.006	0.142	-0.091	-0.058
E	0.050	-0.045	-0.030	-0.193	**0.372**	-0.018	0.081	-0.036	-0.457	0.345	-0.038	0.036	0.001	-0.054	0.107	0.003	0.091	-0.141	0.125
F	-0.004	-0.009	0.027	0.148	-0.153	**0.043**	-0.049	0.013	0.581	-0.394	-0.027	-0.040	0.015	0.030	0.049	0.006	-0.075	-0.021	-0.277
G	-0.006	-0.011	-0.023	-0.051	0.221	-0.015	**0.137**	-0.021	-0.312	0.217	0.008	0.052	-0.003	-0.059	0.101	-0.003	0.114	-0.085	0.130
H	-0.131	0.059	0.029	0.241	-0.161	0.007	-0.035	**0.083**	0.391	-0.288	0.012	-0.004	-0.011	0.007	-0.083	-0.002	-0.005	0.033	-0.064
I	-0.101	0.070	0.039	0.243	-0.173	0.026	-0.043	0.033	**0.981**	-0.613	-0.099	-0.042	0.008	0.031	0.005	0.004	-0.091	0.012	-0.165
J	-0.084	0.049	0.037	0.269	-0.186	0.025	-0.043	0.035	0.870	**-0.690**	0.080	-0.049	0.014	0.047	0.020	0.007	-0.106	-0.017	-0.160
K	0.031	-0.059	-0.008	0.074	-0.035	-0.003	0.003	0.002	-0.243	-0.139	**0.401**	-0.028	0.018	0.040	0.050	0.008	-0.047	-0.076	0.018
L	-0.046	0.049	0.009	0.162	0.064	-0.008	0.034	-0.002	-0.197	0.162	-0.054	**0.207**	-0.075	-0.187	-0.162	-0.033	0.375	0.118	0.073
M	-0.021	0.070	0.012	0.082	-0.002	-0.006	0.004	0.009	-0.076	0.097	-0.072	0.156	**-0.100**	-0.072	-0.571	-0.043	0.157	0.552	0.042
N	-0.030	0.011	0.003	0.137	0.079	-0.005	0.032	-0.002	-0.121	0.127	-0.063	0.153	-0.029	**-0.253**	0.301	-0.010	0.440	-0.359	0.050
O	0.008	0.056	0.009	-0.033	-0.053	-0.003	-0.018	0.009	-0.007	0.018	-0.026	0.044	-0.075	0.101	**-0.755**	-0.034	-0.148	0.784	0.008
P	-0.034	0.068	0.013	0.071	-0.021	-0.006	0.009	0.004	-0.094	0.111	-0.072	0.151	-0.094	-0.057	-0.567	**-0.045**	0.159	0.596	0.039
Q	-0.043	0.014	0.006	0.135	0.064	-0.006	0.030	-0.001	-0.168	0.138	-0.036	0.147	-0.030	-0.211	0.211	-0.014	**0.528**	-0.361	0.057
R	0.009	0.052	0.007	-0.055	-0.063	-0.001	-0.014	0.003	0.014	0.014	-0.037	0.029	-0.066	0.109	-0.710	-0.032	-0.229	**0.833**	-0.001
S	0.015	-0.012	0.029	0.095	-0.152	0.039	-0.058	0.018	0.530	-0.361	-0.024	-0.049	0.014	0.041	0.020	0.006	-0.099	0.003	**-0.306**
T	0.389	0.267	0.179	0.505	0.198	-0.136	0.389	0.076	0.125	0.118	0.007	0.488	0.217	0.463	-0.114	0.232	0.461	-0.138	-0.252

(**Residual effect** = 0.605, **Bold values**- direct effects, **Normal values**- indirect effects)

(**A**- Length of leaf blade; **B**- Width of leaf blade; **C**- Stem thickness; **D**- Stem length; **E**- Number of tillers per plant; **F**- Time for heading; **G**- Number of panicles per plant; **H**- Length of panicle main axis; **I**- Number of spikelets per panicle; **J**- Number of grains per panicle; **K**- Seed setting per cent; **L**- Weight of 1000 grains; **M**- Grain length; **N**- Grain width; **O**- Grain L/B ratio; **P**- Decorticated grain length; **Q**- Decorticated grain width; **R**- Decorticated grain L/B ratio; **S**- Time for maturity; **T**- Grain yield per plant).

4.1.6. Cluster analysis based on qualitative characters

Cluster analysis was carried out using 30 qualitative characters of 60 landraces and three check varieties. The genetic association among the genotypes were estimated by Jaccard's similarity coefficients (Jaccard, 1908) using NTSYS (Numerical Taxonomy and Multivariate Analysis System) software version 2.1 (Rohlf, 2000). Dendrogram was constructed using UPGA clustering method based on similarity coefficients (Fig. 12).

Cluster analysis based on UPGA categorized 60 landraces and three check varieties into 11 clusters at 74 per cent similarity level. Among the 11 clusters formed, cluster VI was the largest one comprising of 33 genotypes, followed by cluster I with 11 genotypes (*i.e.,* Kalladi aryan, Chomala, Mangalapuram puncha, Valichoori, Kothandan, Kunam kulumban, Chomala-1, Njavara, Kanchana, Uma and Aathira) including three check varieties, Cluster V with five genotypes (*i.e.,* Thondi-1, Kodu veliyan, Thonnooran thondi, Palthondi matta and Onamottan), Cluster IV with four genotypes (*i.e.,* Mulla kuruva, Njavara black, Mahi kuruva and Rasagatham), Cluster II, Cluster VII and Cluster X with two genotypes each, Cluster III, Cluster VIII, Cluster IX and Cluster XI with single genotype each namely Addy, Thavalakannan, Mullan puncha and Sugandhamathi respectively (Table 45).

Table 45. Clustering of rice genotypes based on qualitative characters

Cluster No.	No. of genotypes	Genotype
Cluster I	**11**	Kalladi aryan, Chomala, Mangalapuram puncha, Valichoori, Kothandan, Kunam kulumban, Chomala-1, Njavara, Kanchana, Uma, Aathira
Cluster II	**2**	Gandhakasala, Gandhakasala (dwarf)
Cluster III	**1**	Addy

Cluster IV	**4**	Mulla kuruva, Njavara black, Mahi kuruva, Rasagatham
Cluster V	**5**	Thondi-1, Kodu veliyan, Thonnooran thondi, Palthondi matta, Onamottan
Cluster VI	**33**	Ambalavayal-1, Ayirankana, Palveliyan, Kannali, Keervana, Kanni kayama, Thondi-2, Chenthondi, Chennellu, Punnadan thondi, Putta batta, Rajameni, Chettu veliyan, Kuruva, Mannu veliyan, Veliyan, Urulan kayama, Thondi-3, Chenthadi, Peruvaya, Palthondi, Vaalicha, Veliya thondi, Edavaka, Velumpala, Kumbali, Adukkan, Ambalavayal-2, Uruni kayama, Kutti veliyan, Vellimuthu, Mara thondi, Karimpalan
Cluster VII	**2**	Kothandon, Chomala-2
Cluster VIII	**1**	Thavalakannan
Cluster IX	**1**	Mullan puncha
Cluster X	**2**	Jeerakasala, Kayama
Cluster XI	**1**	Sugandhamathi

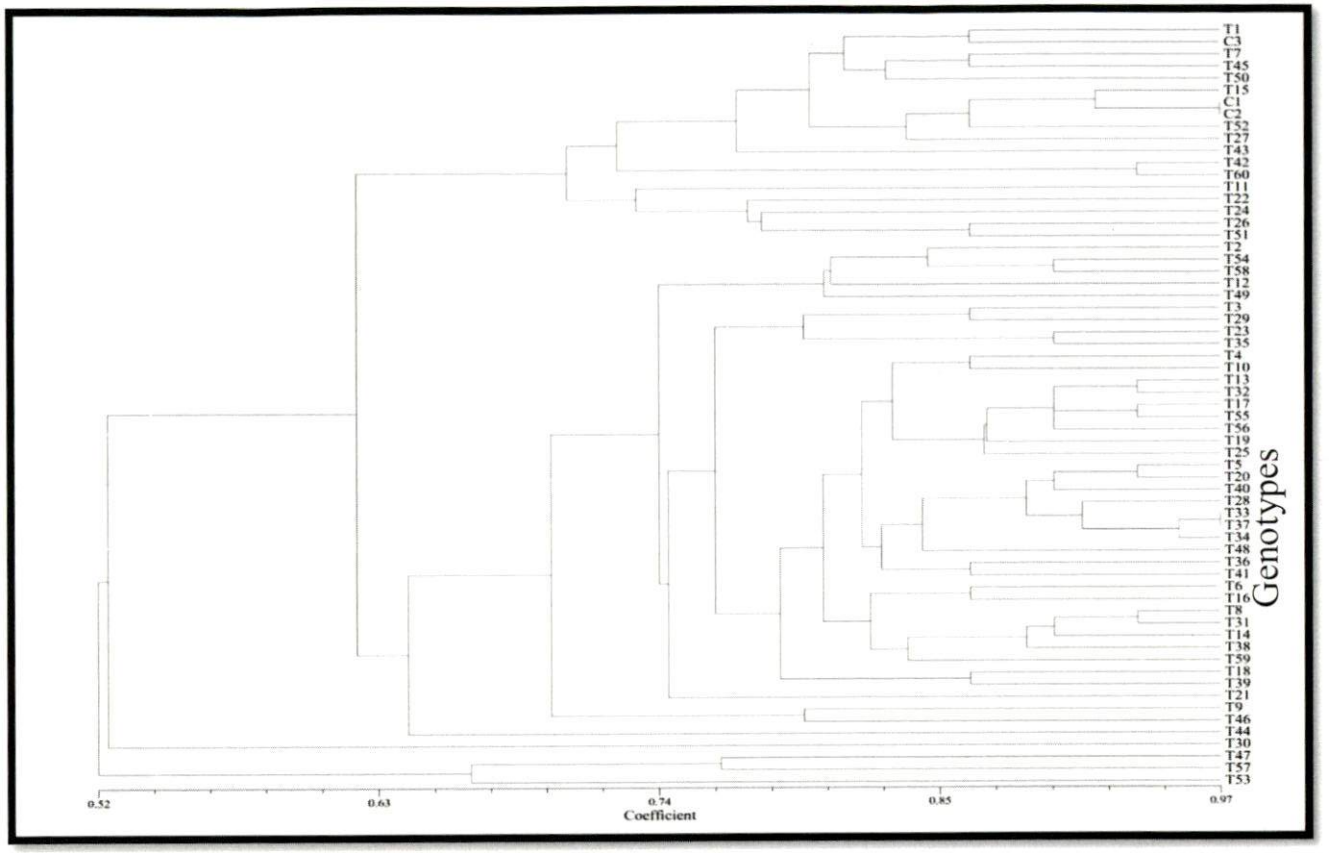


Fig. 12. Dendrogram based on similarity coefficients in 63 rice genotypes

(**T1**- Kalladi aryan, **T2**- Thondi-1, **T3**- Ambalavayal-1, **T4**- Ayirankana, **T5**- Palveliyan, **T6**- Kannali, **T7**- Chomala, **T8**- Keervana, **T9**- Kothandon, **T10**- Kanni kayama, **T11**- Addy, **T12**- Kodu veliyan, **T13**- Thondi-2, **T14**- Chenthondi, **T15**- Mangalapuram puncha, **T16**- Chennellu, **T17**- Punnadan thondi, **T18**- Putta batta, **T19**- Rajameni, **T20**- Chettu veliyan, **T21**- Kuruva, **T22**- Mulla kuruva, **T23**- Mannu veliyan, **T24**- Njavara black, **T25**- Veliyan, **T26**- Mahi kuruva, **T27**- Valichoori, **T28**- Urulan kayama, **T29**- Thondi-3, **T30**- Mullan puncha, **T31**- Chenthadi, **T32**- Peruvaya, **T33**- Pal thondi, **T34**- Vaalicha, **T35**- Veliya thondi, **T36**- Edavaka, **T37**- Velumpala, **T38**- Kumbali, **T39**- Adukkan, **T40**- Ambalavayal-2, **T41**- Uruni kayama, **T42**- Gandhakasala, **T43**- Kothandan, **T44**- Thavalakannan, **T45**- Kunam kulumban, **T46**- Chomala-2, **T47**- Jeerakasala, **T48**- Kutti veliyan, **T49**- Thonnooran thondi, **T50**- Chomala-1, **T51**- Rasagatham, **T52**- Njavara, **T53**- Sugandhamathi, **T54**- Palthondi matta, **T55**- Vellimuthu, **T56**- Mara thondi, **T57**- Kayama, **T58**- Onamottan, **T59**- Karimpalan, **T60**- Gandhakasala (dwarf), **C1**- Kanchana, **C2**- Uma, **C3**- Aathira).

4.1.7. Diversity analysis (Mahalanobis D^2 statistics)

To assess the genetic diversity among 60 rice genotypes, Mahalanobis D^2 statistics was done following the procedure given by Rao (1952), using software Windostat 9.2 from Indostat Services, using 20 quantitative characters recorded.

4.1.7.1. Group constellation

The 60 rice genotypes were grouped into seven clusters using Tocher's method (Rao, 1952) and the distribution of genotypes into various clusters is presented in Table 46 and Fig. 13.

Table 46. Clustering of rice genotypes based on quantitative characters

Cluster No.	No. of genotypes	Genotype
Cluster I	**17**	Palthondi, Vaalicha, Velumpala, Chomala-1, Ambalavayal-1, Chenthadi, Chomala-2, Chomala, Thondi-2, Chettu veliyan, Veliya thondi, Gandhakasala, Gandhakasala (dwarf), Kothandon, Mannu veliyan, Edavaka, Kunam kulumban
Cluster II	**20**	Thondi-1, Palveliyan, Kannali, Keervana, Mangalapuram puncha, Chennellu, Punnadan thondi, Putta batta, Rajameni, Kuruva, Veliyan, Thondi-3, Peruvaya, Kumbali, Uruni kayama, Jeerakasala, Kutti veliyan, Rasagatham, Mara thondi, Kayama
Cluster III	**19**	Kalladi aryan, Ayirankana, Kanni kayama, Addy, Kodu veliyan, Mulla kuruva, Mahi kuruva, Valichoori, Mullan puncha, Adukkan, Kothandan, Thavalakannan, Thonnooran thondi, Njavara, Sugandhamathi, Palthondi matta, Vellimuthu, Onamottan, Karimpalan

Cluster IV	1	Urulan kayama
Cluster V	1	Chenthondi
Cluster VI	1	Njavara black
Cluster VII	1	Ambalavayal-2

Among the seven clusters formed, cluster II was the largest comprising of 20 genotypes, followed by cluster III with 19 genotypes, cluster I with 17 genotypes and Clusters IV, V, VI, VII were represented by single genotype namely Urulan kayama, Chenthondi, Njavara black and Ambalavayal-2 respectively.

4.1.7.2. Mean inter and intra cluster distances

The average intra and inter cluster D^2 values are presented in Table 47 and Fig. 14. Intra cluster D^2 values ranged from 0.00 (cluster IV, V, VI and VII) to 3258.32 (Cluster III). Maximum intra cluster distance was observed in cluster III (3258.32), followed by cluster I (2953.33) and Cluster II (2621.65). The intra D^2 values of cluster IV, V, VI and VII were zero, because these clusters were comprising of single genotype.

The mean inter cluster D^2 values ranged from 4438.64 to 97473.91. The lowest inter cluster distance was recorded between cluster I and IV and maximum was recorded between cluster VI and VII. It was observed that cluster I had the lowest distance with cluster IV (4438.64) and maximum distance with cluster VI (48482.33). Cluster II exhibited the lowest distance with cluster IV (7068.36) and maximum distance with cluster VII (29320.04). Cluster III recorded the lowest distance with cluster VI (7584.89) and maximum distance with cluster VII (60764.42). Cluster IV exhibited lowest distance with cluster V (9774.58) and maximum distance with cluster VI (40488.82). The nearest clusters recorded for cluster V was cluster VII (16275.35) and cluster VI (68568.22) respectively.

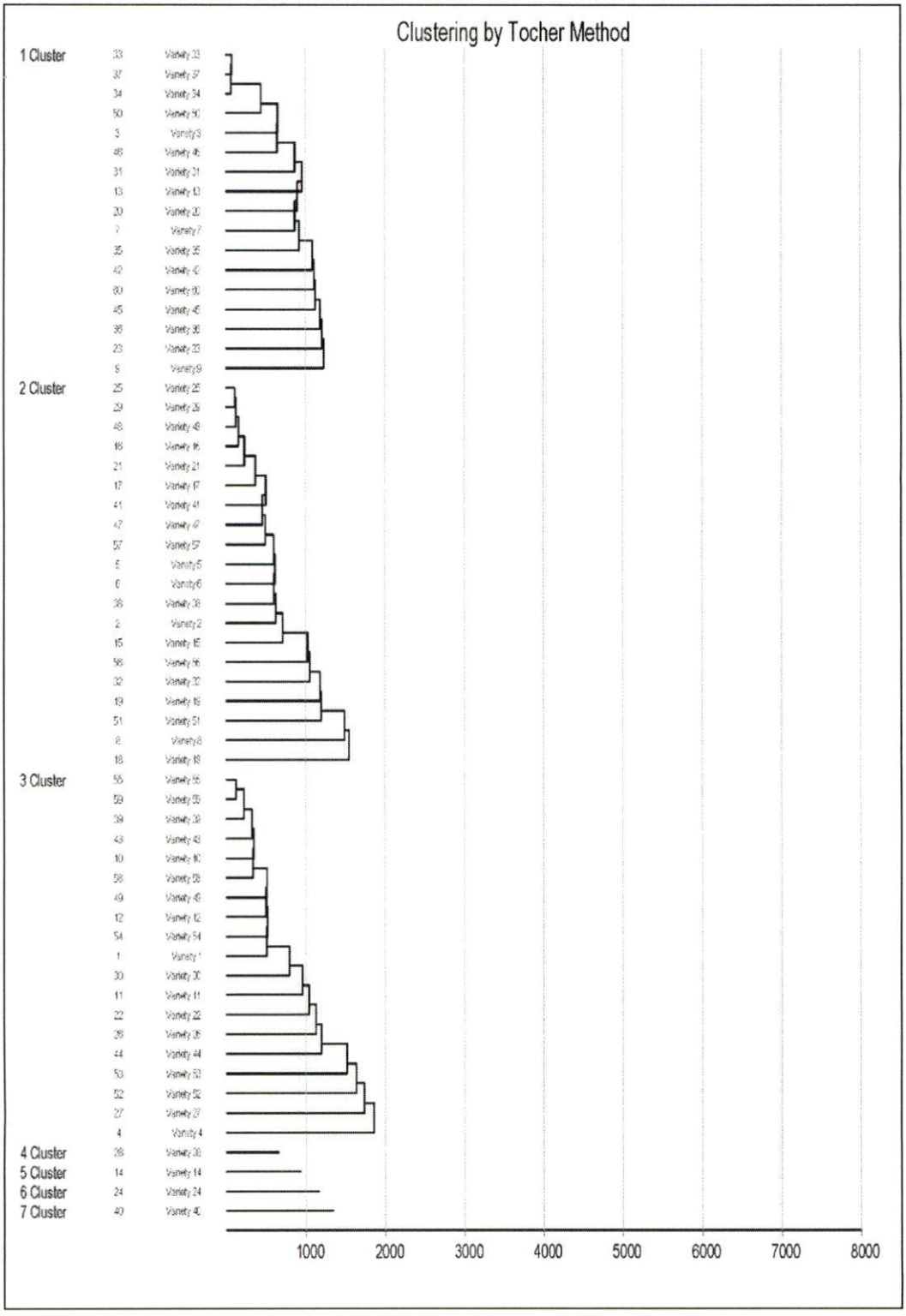


Fig. 13. Clustering of 60 rice landraces by Tocher's method

202

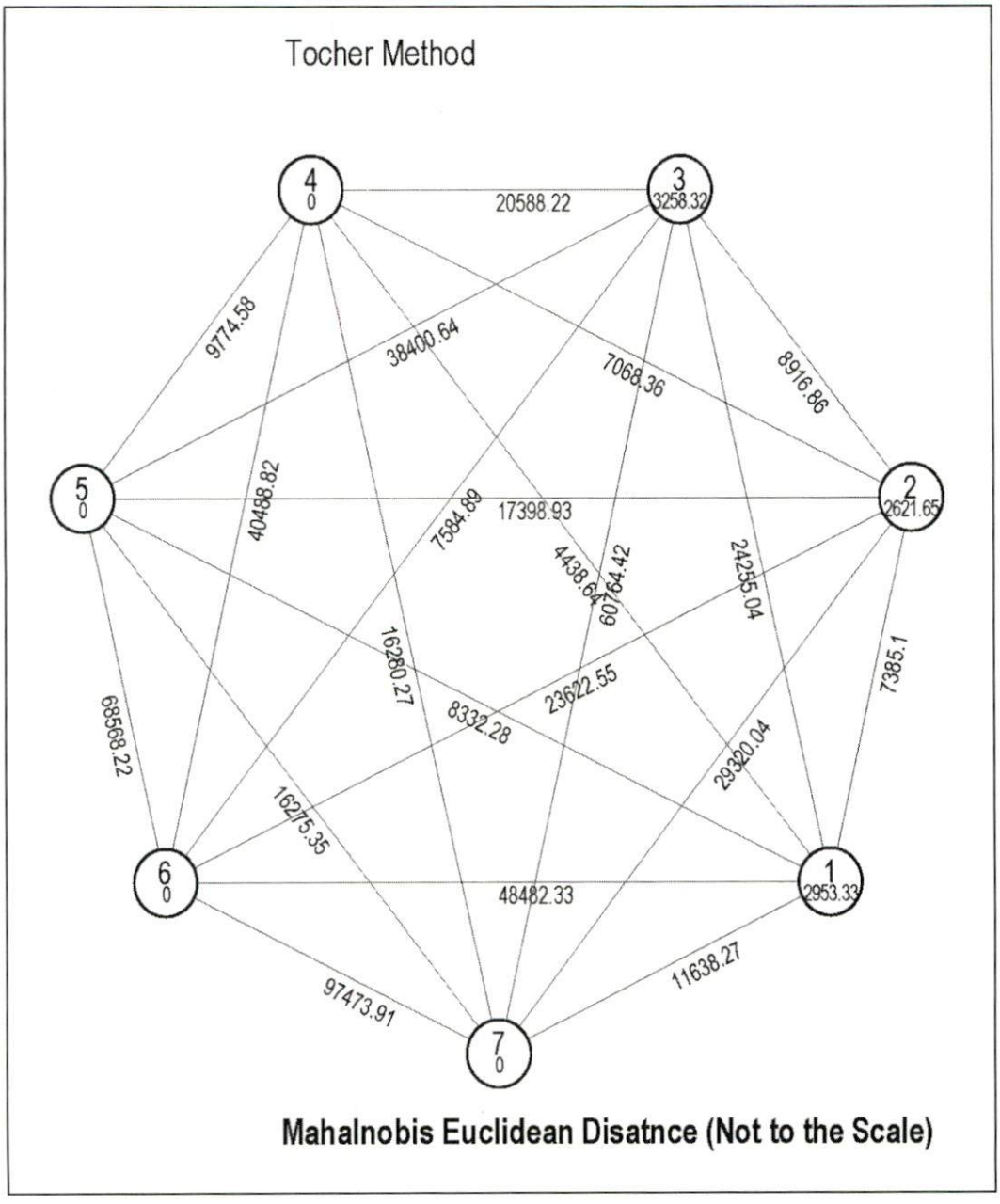


Fig. 14. Intra and inter cluster distances of various clusters

Table 47. Mean intra (bold values) and inter cluster distances estimated using twenty quantitative characters in 60 rice genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**2953.33**	7385.1	24255.04	4438.64	8332.28	48482.33	11638.27
Cluster II		**2621.65**	8916.86	7068.36	17398.93	23622.55	29320.04
Cluster III			**3258.32**	20588.22	38400.64	7584.89	60764.42
Cluster IV				**0**	9774.58	40488.82	16280.27
Cluster V					**0**	68568.22	16275.35
Cluster VI						**0**	97473.91
Cluster VII							**0**

4.1.7.3. Cluster means of the characters

The cluster means for each of 20 characters were analyzed and are presented in Table 48.

4.1.7.3.1. Leaf characters

Mean value for length of leaf blade ranged from 30.4 cm in cluster VI to 62.0 cm in cluster V. The highest cluster mean for width of leaf blade was exhibited by cluster I (0.92 cm) and the lowest cluster mean was observed in cluster VI (0.5).

4.1.7.3.2. Stem characters

Mean value for stem thickness ranged from 1.8 cm (cluster VI) to 3.8 cm (cluster VII). The highest cluster mean for stem length was exhibited by cluster V (160.6 cm) and lowest cluster mean was observed for cluster VI (93.7 cm)

4.1.7.3.3. Number of tillers per plant

Mean value for number of tillers per plant ranged from 8.7 to 16.6. The highest cluster mean was exhibited by cluster IV (16.6), followed by cluster VI (15.1). The lowest cluster mean was observed in cluster V (8.7).

4.1.7.3.4. Panicle characters

Mean value for panicle number per plant ranged from 6.3 (cluster V) to 14.9 (cluster IV). The highest cluster mean for panicle length of main axis was exhibited by cluster VII (28.5) and the lowest cluster mean was observed in cluster VI (20.5). Mean value for number of spikelets per panicle ranged from 68 (cluster VI) to 298 (cluster V). The highest cluster mean for number of grains per panicle was exhibited by cluster VII (272) and the lowest cluster mean was observed for the cluster VI (63). Mean value for seed setting per cent ranged from 51.34 (cluster V) to 94.12 (cluster VII).

4.1.7.3.5. Grain characters

The highest cluster mean for weight of 1000 grains was exhibited by cluster III (30.09 g) and the lowest cluster mean was observed for the cluster IV (23.06). Mean value for grain length ranged from 6.8 mm (cluster IV) to 8.3 mm (cluster V). The highest cluster mean for grain width was recorded by cluster V (3.6 mm) and the lowest cluster mean was observed for the cluster VI (3.0 mm). Mean value for grain L/B ratio ranged from 2.06 (cluster IV) to 2.67 (cluster VI).

4.1.7.3.6. Decorticated grain characters

The highest cluster mean for decorticated grain length was exhibited by cluster V (6.1 mm) and the lowest cluster mean was observed in cluster IV (5.1 mm). Mean value for decorticated grain width ranged from 2.4 mm (cluster VI) to 3.0 mm (cluster V). The highest cluster mean for decorticated grain L/B ratio was recorded for cluster VI (2.46) and the lowest cluster mean was observed for the cluster IV (1.76).

4.1.7.3.7. Time of heading and maturity

The highest cluster mean for time of heading was exhibited by cluster IV (162 days) and the lowest cluster mean was observed for cluster III (132.26 days). Mean value for time for maturity ranged from 165.21 days in cluster III to 191 days in cluster IV.

4.1.7.3.8. Grain yield per plant

The highest cluster mean for grain yield per plant was exhibited by cluster VII (23.1 g), followed by cluster V (22.8 g). The lowest cluster mean was observed for cluster III (10.3 g), followed by cluster IV (21.4 g).

Table 48. Cluster means for quantitative characters in 60 rice landraces

Cluster No.	LLB (cm)	WLB (cm)	ST (cm)	SL (cm)	NTP (no.)	TH (days)	NPP (no.)	LPA (cm)	NSP (no.)	NGP (no.)	SSP (%)	TGW (gm)	GL (mm)	GW (mm)	GLBR	DGL (mm)	DGW (mm)	DGLBR	TM (days)	GYP (g)
I	51.72	0.92	3.19	148.92	10.00	147.18	7.29	28.40	226.47	187.65	83.08	26.20	7.74	3.28	2.36	5.66	2.69	2.10	182.53	22.75
II	47.85	0.83	3.06	141.86	10.50	142.95	7.46	28.37	177.85	148.75	84.03	28.07	7.89	3.38	2.34	5.82	2.85	2.05	179.30	22.08
III	45.11	0.84	2.60	117.89	12.98	132.26	9.18	25.69	123.58	101.16	82.46	30.09	8.16	3.43	2.41	5.99	2.87	2.12	165.21	21.79
IV	42.0	0.7	2.6	102.6	16.6	162	14.9	24.2	231	176	76.19	25.51	6.8	3.3	2.06	5.1	2.9	1.76	191	21.4
V	62.0	0.9	3.8	160.6	8.7	151	6.3	28.2	298	153	51.34	29.22	8.3	3.6	2.31	6.1	3.0	2.03	182	22.8
VI	30.4	0.5	1.8	93.7	15.1	142	8.9	20.5	68	63	92.65	23.06	8.0	3.0	2.67	5.9	2.4	2.46	182	10.3
VII	48.8	0.9	3.8	158.3	10.7	154	7.1	28.5	289	272	94.12	28.54	8.1	3.3	2.45	5.7	2.7	2.11	185	23.1

(**LLB-** Length of leaf blade; **WLB-** Width of leaf blade; **ST-** Stem thickness; **SL-** Stem length; **NTP-** Number of tillers per plant; **TH-** Time for heading; **NPP-** Number of panicles per plant; **LPA-** Length of panicle main axis; **NSP-** Number of spikelets per panicle; **NGP-** Number of grains per panicle; **SSP-** Seed setting per cent; **TGW-** 1000 grains weight; **GL-** Grain length; **GW-** Grain width; **GLBR-** Grain L/B ratio; **DGL-** Decorticated grain length; **DGW-** Decorticated grain width; **DGLBR-** Decorticated grain L/B ratio; **TM-** Time for maturity; **GYP-** Grain yield per plant).

Experiment 2: Molecular characterization of aromatic cultivars of Wayanad

4.2. Molecular characterization of aromatic genotypes using SSR (RM) markers

Fifteen landraces of rice from Wayanad including 12 morphotypes of Gandhakasala and three morphotypes of Jeerakasala were characterized and compared with a aromatic check variety (Basmati) and two non-aromatic check varieties *viz.*, Uma and Aathira. Polymorphism at molecular level was studied using 86 rice microsatellite (RM) markers listed in Table 6 & 7 under Section 3.2.6 of Chapter 3. The 86 SSR markers selected for polymorphism study, included 64 hypervariable rice SSR markers available at www.gramene.org., covering the 12 linkage groups in rice and 22 were aroma specific markers. The quality and quantity of DNA extracted from the genotypes used in the study are presented in Table 49. The nature of amplification is enumerated in the Table 50.

Table 49. Quantity and quality of genomic DNA of 18 genotypes used in molecular characterization

Sl. No.	Genotype	Quantity (ng/µl)	Quality (A260/A280)
1	Gandhakasala-1	1630.55	1.86
2	Gandhakasala-2	939.88	1.89
3	Gandhakasala-3	1208.50	1.83
4	Gandhakasala-4	873.12	1.90
5	Gandhakasala-5	1134.72	1.87
6	Gandhakasala-6	1641.26	1.84
7	Gandhakasala-7	708.40	1.93
8	Gandhakasala-8	634.15	1.96
9	Gandhakasala-9	962.36	1.88
10	Gandhakasala-10	1068.91	1.86

11	Gandhakasala-11	1246.10	1.81
12	Gandhakasala-12	836.43	1.87
13	Jeerakasala-1	1063.67	1.91
14	Jeerakasala-2	748.34	1.86
15	Jeerakasala-3	681.82	1.95
16	Basmati (aromatic check variety)	1450.60	1.91
17	Uma (non- aromatic check variety)	1458.50	1.93
18	Aathira (non- aromatic check variety)	1263.61	1.83

The number of amplicons produced ranged from 1.00 to 5.00 (Table 50). Marker RM247 exhibited maximum number of amplicons (5 nos), followed by RM85, RM251, RM248 and RM493 with four amplicons each. Among the monomorphic bands, amplicons of size 86 bp (RM271 and RM260) to 347 bp (RM110) were produced. In case of polymorphic bands, size of amplicons ranged from 63 bp (RM248) to 518 bp (RM18941). The Polymorphism Information Content (PIC) value ranged from 0.10 (RM541, RM18, RM18941 and RM28277) to 0.90 in RM247, followed by RM85, RM251 and RM493 with 0.88 PIC value each.

Table 50. Details of amplified products of 86 SSR (RM) markers used for molecular characterization

Sl. No.	SSR Primer	Nature of amplification	Number of amplicons	Size of amplicon (bp)		PIC value
				Monomorphic band	Polymorphic bands	
Hypervariable SSR markers						
1	RM1	Polymorphic	2	-	225.95, 240.83	0.60
2	RM490	Polymorphic	2	-	255.71, 319.03	0.64
3	RM11069	Polymorphic	2	-	207.64, 249.50	0.55
4	RM11313	Polymorphic	2	-	332.13, 377.09	0.64
5	RM233	Monomorphic	1	139.77	-	-
6	RM250	Monomorphic	1	140.5	-	-
7	RM482	Monomorphic	1	192.13	-	-
8	RM12941	Polymorphic	3	-	175.48, 200.00, 218.24	0.76
9	RM13599	Monomorphic	1	139.16	-	-
10	RM13910	Monomorphic	1	193.55	-	-
11	RM16	Monomorphic	1	186.21	-	-
12	RM60	Monomorphic	1	192.26	-	-

Continued...

13	RM85	Polymorphic	4	-	93.75, 118.38. 136.84, 149.23	0.88
14	RM251	Polymorphic	4	-	103.90, 124.17, 133.08, 147.87	0.88
15	RM411	Monomorphic	1	105.76	-	-
16	RM14723	Polymorphic	3	-	141.63, 187.71, 211.90	0.76
17	RM307	Polymorphic	2	-	133.13, 166.42	0.55
18	RM5586	Polymorphic	2	-	116.67, 133.80	0.60
19	RM110	Monomorphic	2	347.02	-	-
20	RM13	Monomorphic	1	153.90	-	-
21	RM163	Monomorphic	1	182.71	-	-
22	RM18622	Monomorphic	1	320.55	-	-
23	RM18941	Polymorphic	2	-	152.26, 518.68	0.10
24	RM217	Polymorphic	2	-	135.79, 164.38	0.60
25	RM238	Monomorphic	1	100.00	-	-
26	RM253	Monomorphic	1	137.57	-	-
27	RM340	Monomorphic	2	161.75	-	-
28	RM402	Polymorphic	3	-	135.22, 146.31, 152.13	0.46
29	RM541	Polymorphic	2	-	169.12, 333.01	0.10

Continued...

30	RM18	Polymorphic	2	-	161.83, 412.51	0.10
31	RM214	Polymorphic	3	-	112.02, 124.19, 136.64	0.76
32	RM248	Polymorphic	4	-	62.50, 100.00, 500.00	0.82
33	RM295	Monomorphic	1	143.20	-	-
34	RM25	Monomorphic	1	109.49	-	-
35	RM72	Monomorphic	1	154.29	-	-
36	RM223	Polymorphic	2	-	160.37, 325.86	0.49
37	RM264	Monomorphic	1	160.02	-	-
38	RM5556	Polymorphic	2	-	143.03, 272.63	0.49
39	RM23087	Monomorphic	1	184.24	-	-
40	RM205	Polymorphic	3	-	123.20, 146.36, 177.10	0.73
41	RM216	Monomorphic	1	134.95	-	-
42	RM257	Polymorphic	2	-	119.82, 168.30	0.64
43	RM524	Monomorphic	1	176.43	-	-
44	RM23998	Monomorphic	1	221.73	-	-
45	RM216	Polymorphic	3	-	134.78, 152.31, 187.91	0.76
46	RM222	Polymorphic	2	-	206.53, 219.87	0.60

Continued...

47	RM271	Monomorphic	1	85.71	-	-
48	RM304	Monomorphic	1	162.25	-	-
49	RM333	Monomorphic	1	170.74	-	-
50	RM24866	Polymorphic	2	-	191.88, 318.83	0.49
51	RM25066	Polymorphic	2	-	116.32, 222.80	0.49
52	RM21	Polymorphic	3	-	130.92, 146.36, 161.75	0.73
53	RM202	Monomorphic	1	177.36	-	-
54	RM224	Polymorphic	2	-	143.84, 179.41	0.67
55	RM254	Polymorphic	2	-	130.67, 168.01	0.55
56	RM332	Monomorphic	1	187.80	-	-
57	RM26213	Polymorphic	3	-	161.40, 180.03, 253.64	0.55
58	RM17	Polymorphic	2	-	170.87, 178.09	0.60
59	RM19	Monomorphic	1	200.00	-	-
60	RM20	Monomorphic	1	187.13	-	-
61	RM247	Polymorphic	5	-	107.36, 122.13, 152.18, 167.66, 191.71	0.90
62	RM260	Monomorphic	1	85.71	-	-

Continued...

63	RM27841	Polymorphic	2	-	220.33, 251.53	0.55
64	RM28277	Polymorphic	2	-	214.27, 289.48	0.10
Aroma specific SSR markers						
65	RM9	Polymorphic	3	-	128.97, 200.00, 231.85	0.75
66	RM180	Polymorphic	3	-	109.86, 168.30, 193.29	0.73
67	RM215	Monomorphic	1	151.37	-	-
68	RM228	Polymorphic	3	-	106.34, 112.68, 150.54	0.73
69	RM243	Monomorphic	1	119.34	-	-
70	RM245	Monomorphic	1	129.97	-	-
71	RM249	Monomorphic	1	130.20	-	-
72	RM256	Monomorphic	1	159.23	-	-
73	RM288	Monomorphic	1	126.34	-	-
74	RM302	Polymorphic	2	-	125.34, 187.80	0.60
75	RM323	Monomorphic	1	129.15	-	-
76	RM335	Polymorphic	3	-	94.12, 144.38, 291	0.40
77	RM338	Monomorphic	1	172.36	-	-
78	RM410	Monomorphic	1	180.77	-	-

Continued...

79	RM433	Monomorphic	1	224.08	-	-
80	RM444	Polymorphic	2	-	152.39, 213.26	0.60
81	RM484	Polymorphic	3	-	105.86, 166.47, 300.00	0.43
82	RM493	Polymorphic	4	-	211.93, 216.87, 228.22, 240.08	0.88
83	RM510	Polymorphic	2	-	121.93, 348.47	0.49
84	RM535	Polymorphic	2	-	135.21, 253.07	0.60
85	RM566	Polymorphic	2	-	226.85, 241.26	0.60
86	RM590	Monomorphic	1	136.82	-	-

The details of polymorphism exhibited by selected markers are presented in Plate 31.

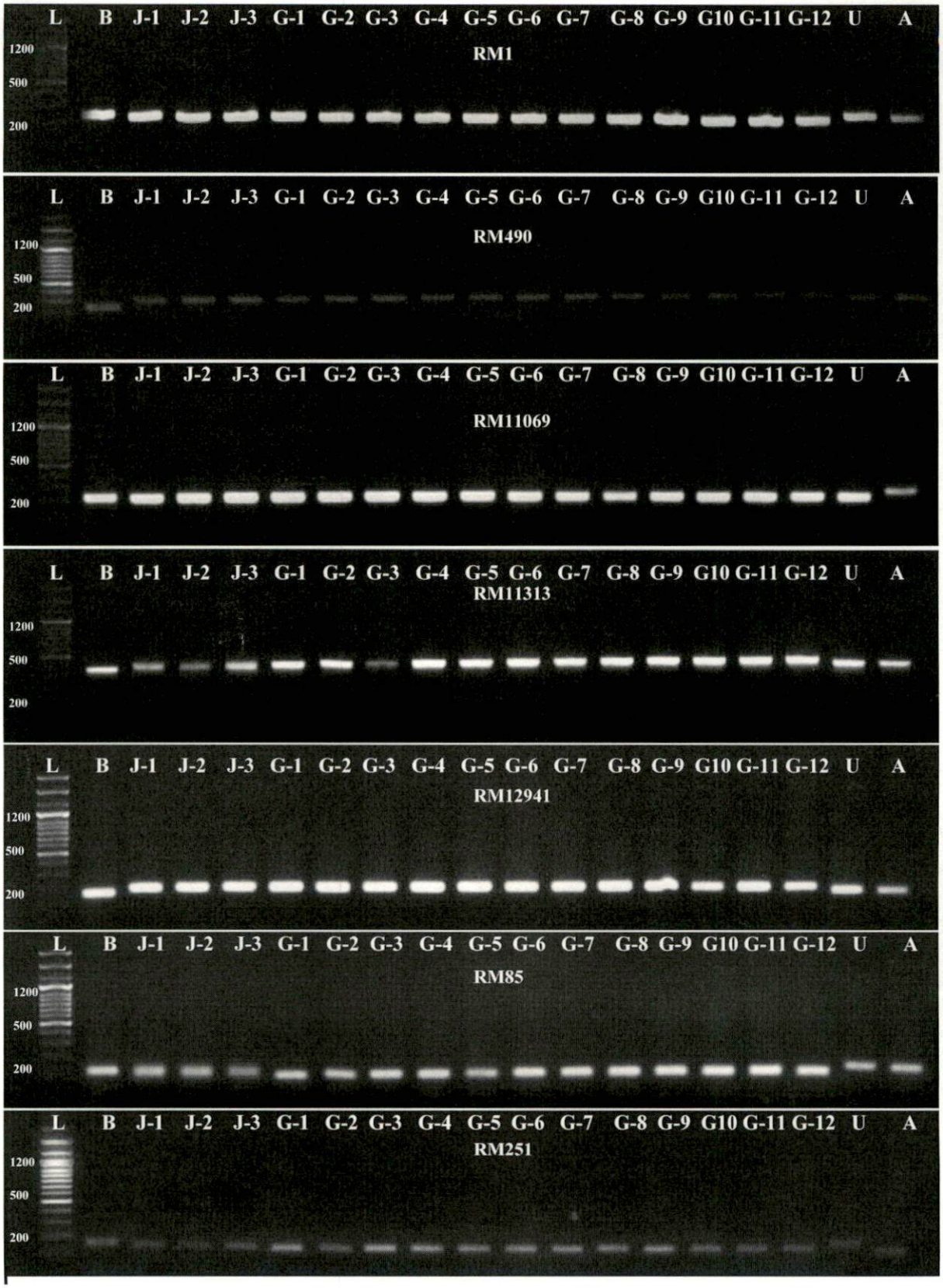


Plate 31. Polymorphic SSR markers identified in molecular characterization (Continued…)

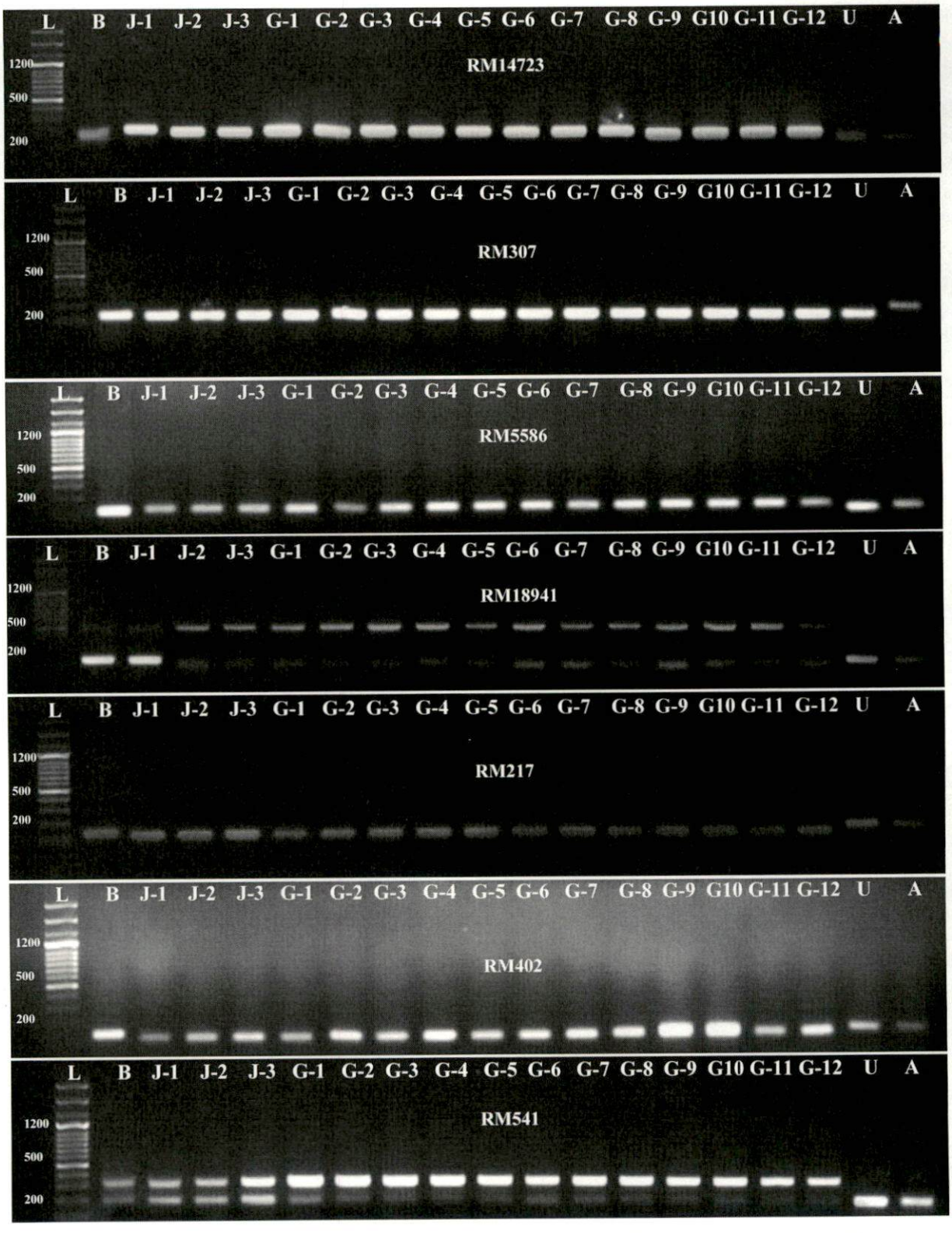


Plate 31. Polymorphic SSR markers identified in molecular characterization (Continued…)

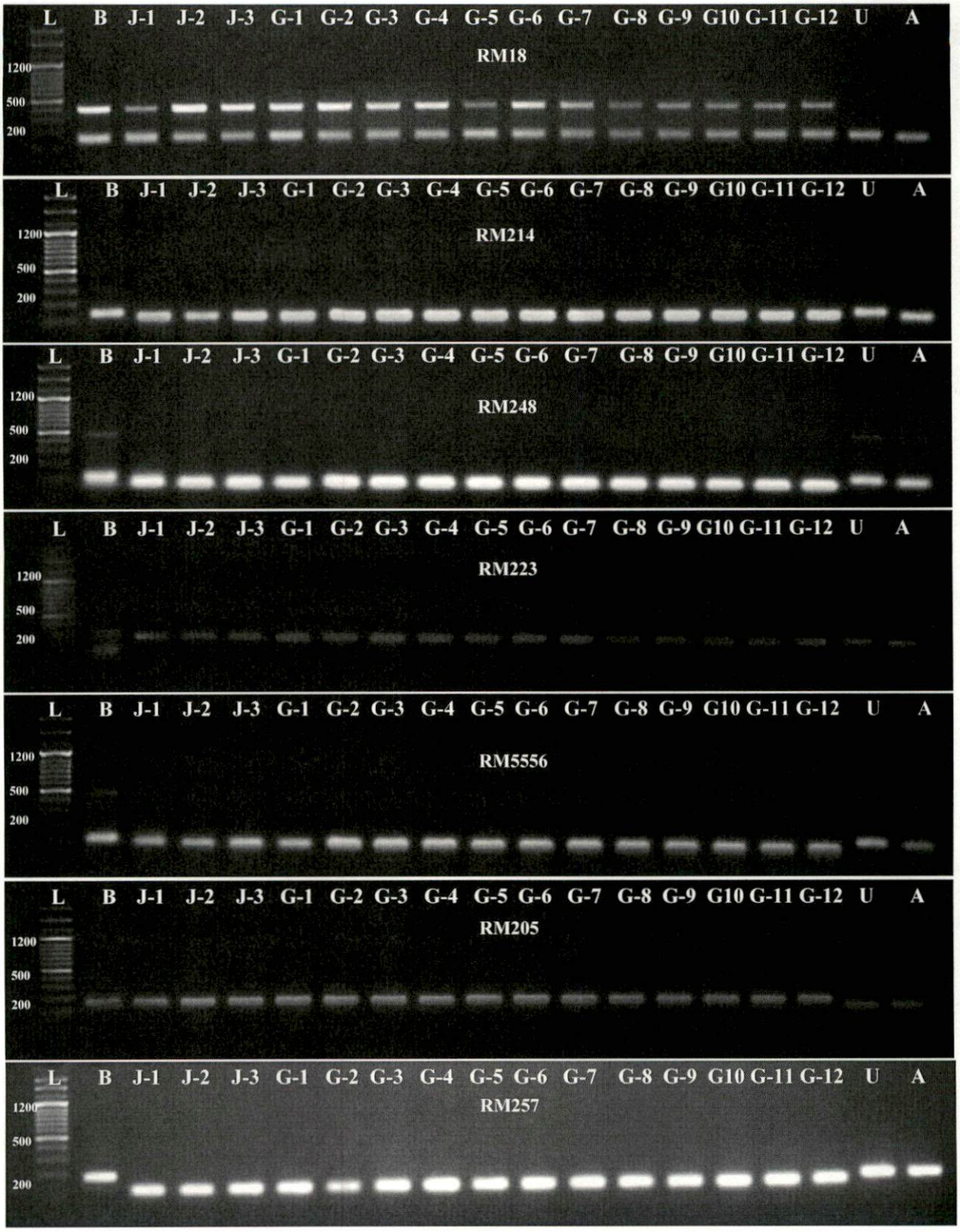


Plate 31. Polymorphic SSR markers identified in molecular characterization (Continued…)

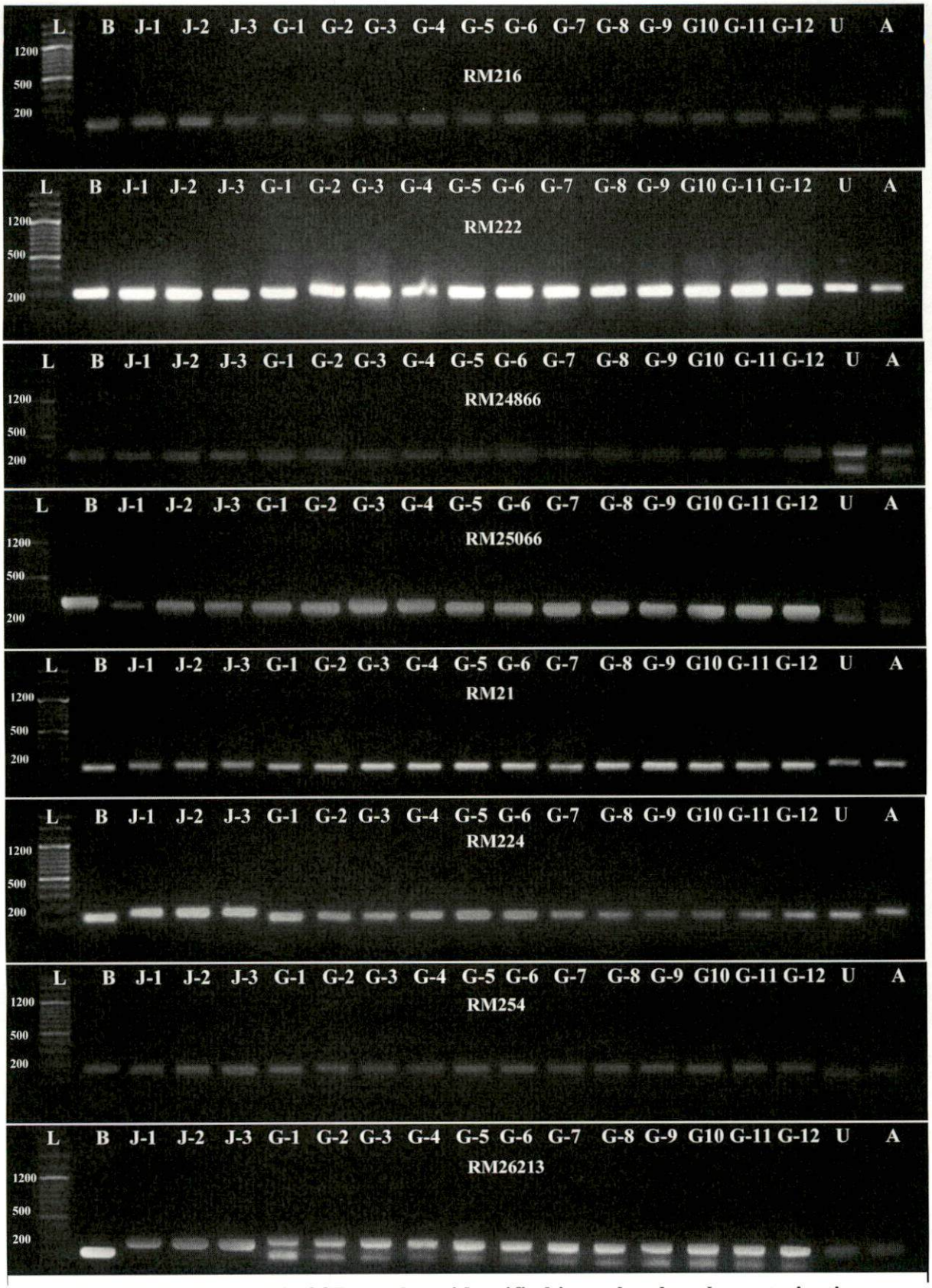


Plate 31. Polymorphic SSR markers identified in molecular characterization (Continued…)

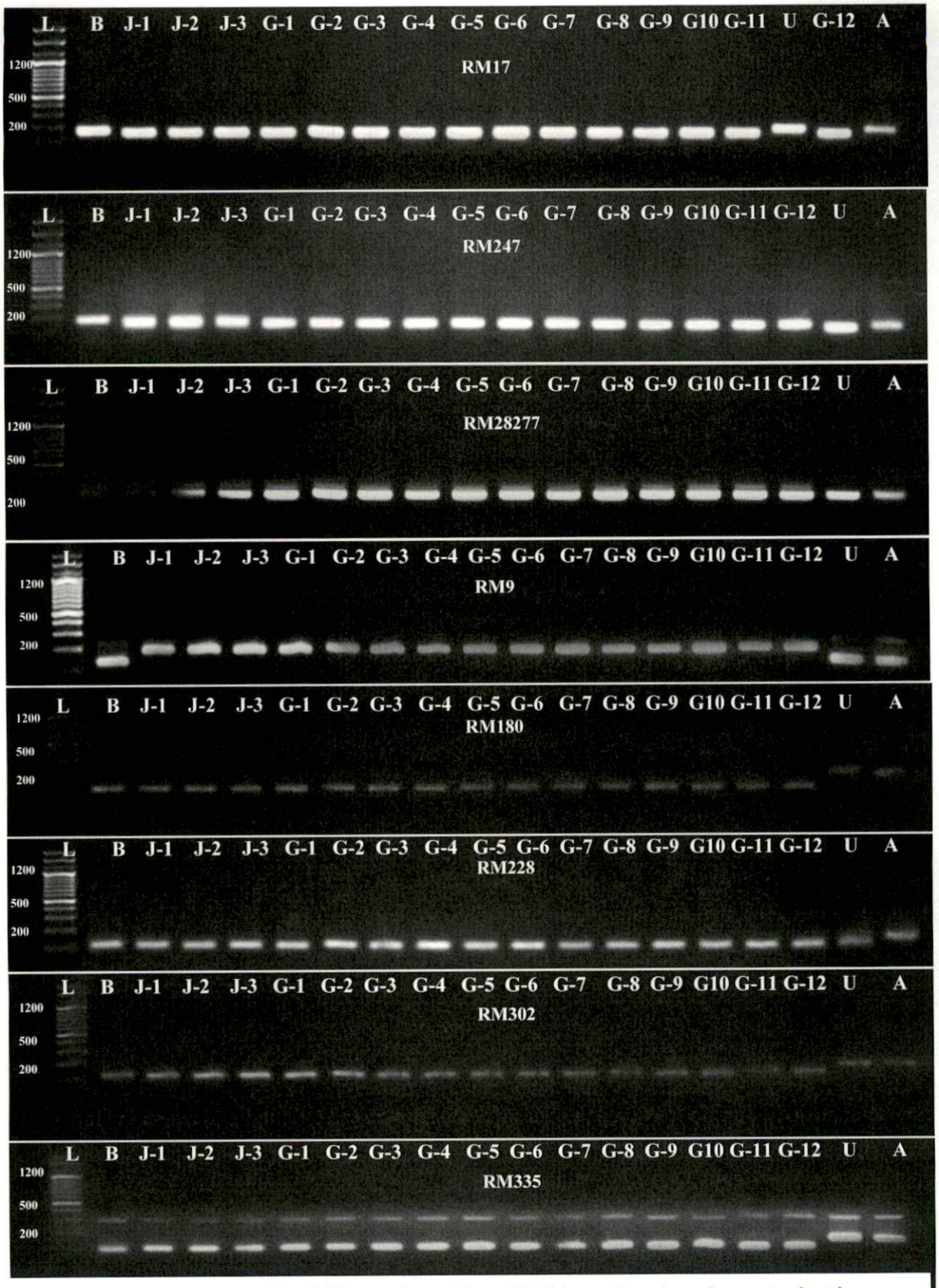
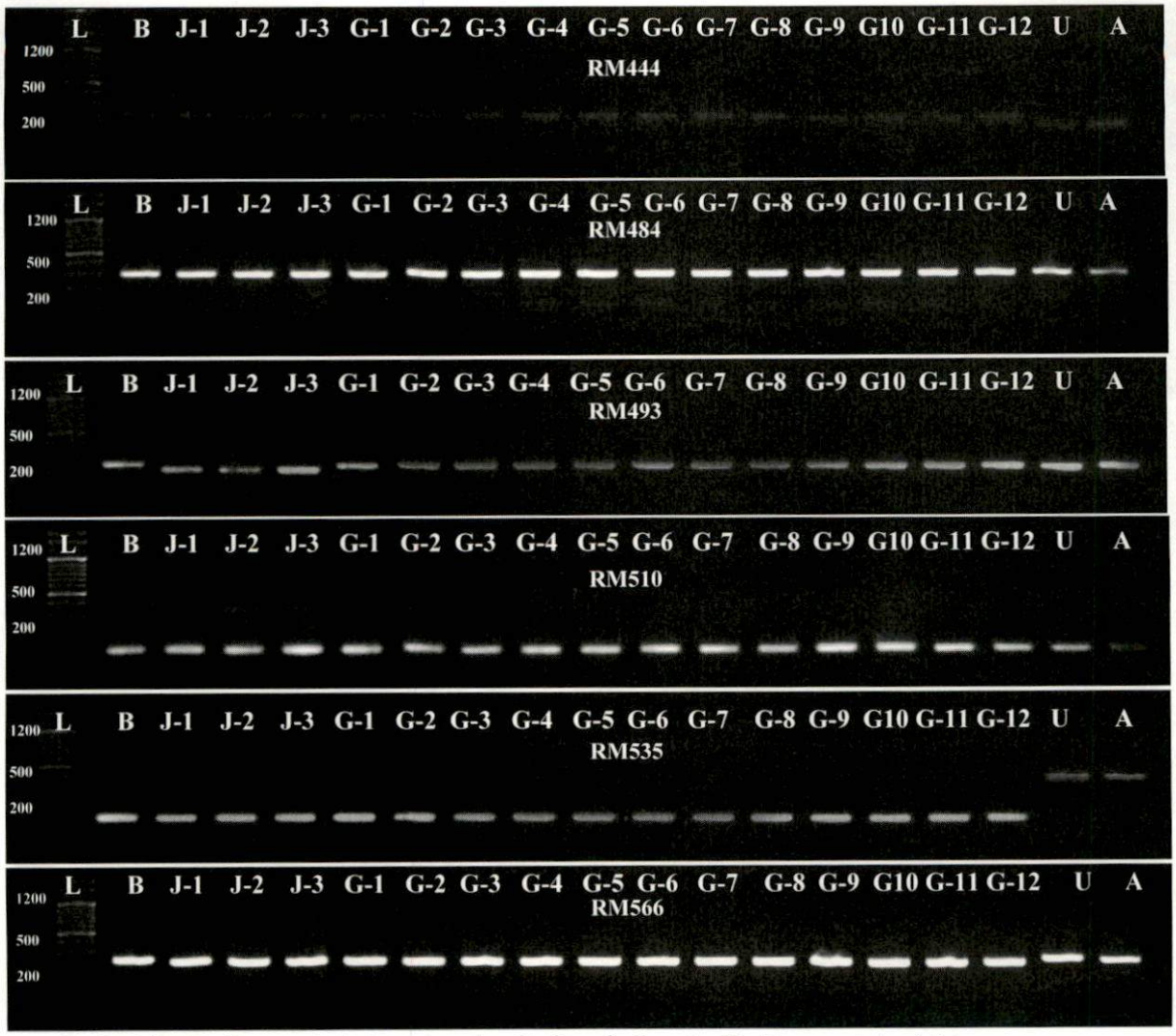


Plate 31. Polymorphic SSR markers identified in molecular characterization (Continued...)



L- Ladder, **B-** Basmati, **J-** Jeerakasala, **G-** Gandhakasala, **U-** Uma and **A-** Athira

Plate 31. Polymorphic SSR markers identified in molecular characterization

4.2.1. Markers showing polymorphism in molecular characterization

Out of 86 SSR (RM) markers used for molecular characterization of aromatic cultivars, 44 markers were recorded as polymorphic and remaining 42 were monomorphic. Among the 44 polymorphic markers, 21 markers showed differential polymorphism in Basmati and non-Basmati aromatic genotypes of Wayanad. The details of these markers are provided in Table 51.

Table 51. Markers showing polymorphism between Basmati and non-Basmati aromatic genotypes

Markers	Amplicon size (bp)		
	Basmati	Jeerakasala	Gandhakasala
RM1	240.83	225.95	225.95
RN490	255.71	319.03	319.03
RM11313	332.13	377.09	377.09
RM12941	175.48	128.24	128.24
RM251	147.87	133.08	214.17
RM14723	187.71	211.90	211.90
RM5586	116.67	133.80	133.80
RM402	146.31	135.22	135.22
RM214	136.64	124.19	124.19
RM248	500/100	75.00	75.00
RM223	325.86/160.37	325.86	325.86
RM5556	272.63/143.03	143.03	143.03
RM257	168.30	119.82	119.80
RM216	134.78	152.31	152.31
RM21	130.92	146.36	146.36
RM26213	108.03	253.64	253.64/161.40
RM247	191.71	167.66	152.18
RM9	231.85/128.97	200.00	200.00
RM484	300	300/105.86	300/105.86

RM493	240.08	211.27	228.22
RM566	241.56	226.85	226.85

Twenty-three markers distinguished Basmati from Jeerakasala. The details are provided in Table 52.

Table 52. Markers showing polymorphism between Basmati and Jeerakasala genotypes

Markers	Amplicon size (bp)	
	Basmati	Jeerakasala
RM1	240.83	225.95
RN490	255.71	319.03
RM11313	332.13	377.09
RM12941	175.48	128.24
RM251	147.87	133.08
RM14723	187.71	211.90
RM5586	116.67	133.80
RM402	146.31	135.22
RM214	136.64	124.19
RM248	500/100	75.00
RM223	325.86/160.37	325.86
RM5556	272.63/143.03	143.03
RM257	168.30	119.82
RM216	134.78	152.31
RM21	130.92	146.36
RM224	143.84	179.41
RM26213	108.03	253.64
RM247	191.71	167.66
RM9	231.85/128.97	200.00
RM484	300.00	300/105.86

RM493	240.08	211.27
RM510	121.93	348.66/21.93
RM566	241.56	226.85

Twenty-two markers distinguished Basmati from Gandhakasala. The details are provided in Table 53.

Table 53. Markers showing polymorphism between Basmati and Gandhakasala genotypes

Markers	Amplicon size (bp)	
	Basmati	Gandhakasala
RM1	240.83	225.95
RN490	255.71	319.03
RM11313	332.13	377.09
RM12941	175.48	128.24
RM85	118.38	93.75
RM251	147.87	214.17
RM14723	187.71	211.90
RM5586	116.67	133.80
RM402	146.31	135.22
RM214	136.64	124.19
RM248	500/100	75.00
RM223	325.86/160.37	325.86
RM5556	272.63/143.03	143.03
RM257	168.30	119.80
RM216	134.78	152.31
RM21	130.92	146.36
RM26213	108.03	253.64/161.40
RM247	191.71	152.18
RM9	231.85/128.97	200.00

RM484	300.00	300/105.86
RM493	240.08	228.22
RM566	241.56	226.85

Seven markers distinguished Gandhakasala from Jeerakasala. The details are provided in Table 54.

Table 54. Markers showing polymorphism between Jeerakasala and Gandhakasala genotypes

Markers	Amplicon size (bp)	
	Jeerakasala	Gandhakasala
RM85	93.75	118.38
RM251	124.17	133.08
RM224	143.84	179.41
RM26213	253.64/161.40	253.64
RM247	152.18	167.66
RM493	228.22	211.27
RM510	121.93	348.66/121.93

Twenty-three markers distinguished aromatic from non-aromatic genotypes. The details are provided in Table 55.

Table 55. Markers showing polymorphism between aromatic and non-aromatic genotypes

Markers	Amplicon size (bp)				
	Basmati	Jeerakasala	Gandhakasala	Uma	Aathira
RM12941	175.48	218.24	218.24	200.00	200.00
RM85	118.38	118.38	93.75	149.23	136.84
RM14723	187.71	211.90	211.90	141.63	141.63
RM18941	518.68/152.26	518.68/152.26	518.68/152.26	152.26	152.26
RN217	135.79	135.79	135.79	164.38	164.38

RM402	146.31	135.22	135.22	152.16	152.16
RM514	333.01/169.12	333.01/169.12	333.01/169.12	169.12	169.12
RM18	412.51/161.83	412.51/161.83	412.51/161.83	161.83	161.83
RM205	117.10	117.10	117.10	123.20	146.36
RM216	134.78	152.31	152.31	187.91	187.91
RM222	206.53	206.53	206.53	219.87	219.87
RM24866	318.83	318.83	318.83	318.83/191.89	318.83/191.89
RM25066	222.80	222.80	222.80	222.80/116.32	222.80/116.32
RM17	170.87	170.87	170.87	178.09	178.09
RM247	191.71	167.66	152.18	107.36	122.13
RM28277	289.48/214.27	289.48/214.27	289.48/214.27	214.27	214.27
RM108	109.87	109.87	109.87	193.29	168.30
RM228	106.34	106.34	106.34	112.68	150.54
RM302	125.34	125.34	125.34	187.80	187.80
RM335	291.47/94.12	291.47/94.12	291.47/94.12	219.47/144.38	129.47/144.38
RM444	213.26	213.26	213.26	252.39	252.39
RM484	300.00	300.00/105.86	300.00/105.86	300/166.47	300/166.47
RM535	135.21	135.21	135.21	353.07	353.07

4.2.2. Cluster analysis

The genetic association among the genotypes were estimated by Jaccard's similarity coefficients (Jaccard, 1908) using NTSYS (Numerical Taxonomy and Multivariate Analysis System) software version 2.1 (Rohlf, 2000). The Jaccard's similarity coefficient values obtained are presented in Table 56. The Dendrogram was constructed by using UPGA clustering method based on Jaccard's similarity coefficient values. Similarity coefficient ranged between 1.00 and 0.46. Maximum similarity coefficient (1.00) was exhibited within all the Jeerakasala morphotypes and all the Gandhakasala morphotypes. Lowest similarity coefficient (0.46) was exhibited between Uma and all other genotypes except Basmati.

Cluster analysis based on UPGA categorized 18 genotypes and three check varieties into five clusters at 60 per cent similarity level (Table 57 and Fig. 15). Out of five clusters formed, cluster III was the largest, comprising 12 Gandhakasala morphotypes namely G-1, G-2, G-3, G-4, G-5, G-6, G-7, G-8, G-9, G-10, G-11, G-12, is followed by cluster IV with J-1, J-2, J-3. Cluster I, Cluster II and Cluster V exhibited one genotype each namely Aathira, Uma and Basmati.

Table 56. Jaccard's similarity coefficient matrix for 18 rice genotypes

	B-1	J-1	J-2	J-3	G-1	G-2	G-3	G-4	G-5	G-6	G-7	G-8	G-9	G-10	G-11	G-12	U	A
B-1	1.00																	
J-1	0.63	1.00																
J-2	0.63	1.00	1.00															
J-3	0.63	1.00	1.00	1.00														
G-1	0.63	0.88	0 88	0.88	1.00													
G-2	0.63	0.88	0.88	0.88	1.00	1.00												
G-3	0.63	0.88	0.88	0.88	1.00	1.00	1.00											
G-4	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00										
G-5	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00									
G-6	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00								
G-7	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00							
G-8	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00						
G-9	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00					
G-10	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00				
G-11	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00			
G-12	0.63	0.88	0.88	0.88	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00		
U	0.60	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	0.46	1.00	
A	0.52	0.50	0.50	0.50	0.49	0.49	0.49	0.49	0.49	0.49	0.49	0.49	0.49	0.49	0.49	0.49	0.69	1.00

B- Basmati, **J-** Jeerakasala, **G-** Gandhakasala, **U-** Uma, **A-** Aathira.

Table 57. Clustering of rice genotypes based on molecular characterization

Cluster No.	No. of genotypes	Genotype
Cluster I	1	Aathira
Cluster II	1	Uma
Cluster III	12	G-1, G-2, G-3, G-4, G-5, G-6, G-7, G-8, G-9, G-10, G-11, G-12
Cluster IV	3	J-1, J-2, J-3
Cluster V	1	Basmati

(G- Gandhakasala, J- Jeerakasala)

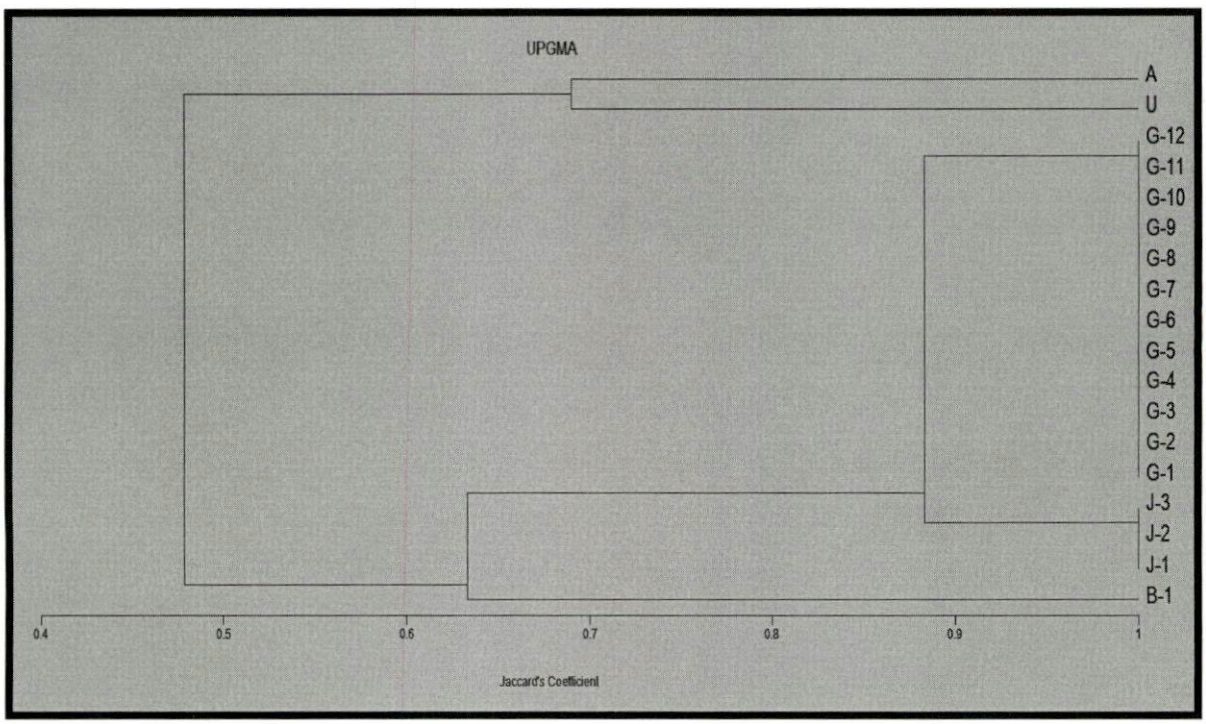


Fig. 15. Dendrogram based on similarity coefficients among 18 rice genotypes

(**A**-Aathira, **U**-Uma, **G**-Gandhakasala, **J**-Jeerakasala, **B**-Basmati).

DISCUSSION

5. Discussion

Assessment of genetic diversity is very important in any crop breeding programme to select the parents in hybridization. Further, conservation of different landraces for utilization in crop improvement programmes (Patra, 2000) and identification of genotypes at molecular level is necessary for their commercial utilization (Prabakaran *et al.*, 2010). Considering the objectives, the experiments were conducted and the results are discussed below.

Experiment 1: Diversity analysis in landraces of Wayanad, based on DUS characters

5.1. Morphological characterization

DUS characterization of 60 rice landraces was done based on 38 qualitative characters and 20 quantitative characters. The landraces showed wide range of variability for most of the characters studied and similar results had been reported by Rao *et al.* (2013) and Umarani *et al.* (2017). Frequency distribution of genotypes for the qualitative characters under study were represented in Table 58.

Table 58. Frequency distribution of landraces for various DUS characters

Sl. No.	Characteristics	States	Number of genotypes	Frequency distribution per cent
1	Coleoptile: Colour	Colourless	18	30.00
		Purple	42	70.00
2	Basal leaf: Sheath colour	Green	18	30.00
		Light purple	25	41.67
		Purple lines	10	16.67
		Uniform purple	7	11.67
3	Leaf: Intensity of green colour	Medium	12	20.00
		Dark	48	80.00
4	Leaf: Anthocyanin	Absent	59	98.33

	colouration	Present	1	1.67
5	Leaf: Distribution of anthocyanin colouration	Absent	59	98.33
		In blotches only	1	1.67
6	Leaf sheath: Anthocyanin colouration	Absent	18	30.00
		Present	42	70.00
7	Leaf: Pubescence of blade surface	Medium	10	16.67
		Strong	50	83.33
8	Leaf: Auricles	Absent	1	1.67
		Present	59	98.33
9	Leaf: Anthocyanin colouration of auricles	Colourless	59	98.33
		Purple	1	1.67
10	Leaf: Collar	Absent	0	0.00
		Present	60	100.00
11	Leaf: Anthocyanin colouration of collar	Absent	60	100.00
12	Leaf: Ligule	Present	60	100.00
13	Leaf: Shape of ligule	Split	60	100.00
14	Leaf: Colour of ligule	White	59	98.33
		Purple	1	1.67
15	Culm: attitude	Erect	12	20.00
		Semi-erect	37	61.67
		Open	10	16.67
		Spreading	1	1.67
16	Spikelet: Density of pubescence of lemma	Weak	6	10.00
		Medium	16	26.67
		Strong	37	61.67
		Very strong	1	1.67
17	Lemma: Anthocyanin colouration of keel	Absent or very weak	60	100.00
18	Lemma: Anthocyanin colouration of apex	Absent	21	35.00
		Strong	12	20.00
		Very strong	27	45.00

19	Lemma: Anthocyanin colouration of area below apex	Absent	60	100.00
20	Spikelet: Colour of stigma	White	21	35.00
		Light green	2	3.33
		Purple	37	61.67
21	Stem: Anthocyanin colouration of nodes	Absent	60	100.00
22	Flag leaf: Attitude of blade	Semi-erect	52	86.67
		Horizontal	8	13.33
23	Panicle: Curvature of main axis	Deflexed	7	11.67
		Dropping	53	88.33
24	Lemma and Palea: Colour	Straw	10	16.67
		Gold and gold furrows on straw background	2	3.33
		Brown spots on straw	9	15.00
		Brown furrows on straw	18	30.00
		Brown (tawny)	13	21.67
		Purple Black	8	13.33
25	Panicle: Awns	Absent	54	90.00
		Present	6	10.00
26	Panicle: Colour of awns	Absent	54	90.00
		Yellowish brown	3	5.00
		Brown	1	1.67
		Purple	1	1.67
		Black	1	1.67
27	Panicle: Distribution of awns	Absent	54	90.00
		Tip only	3	5.00
		Upper half only	1	1.67
		Whole length	2	3.33

28	Panicle : Presence of secondary branching	Present	60	100.00
29	Panicle: Secondary branching	Weak	1	1.67
		Strong	7	11.67
		Clustered	52	86.67
30	Panicle: Attitude of branches	Erect to semi-Erect	6	10.00
		Semi-erect	4	6.67
		Semi-erect to spreading	16	26.67
		Spreading	34	56.67
31	Panicle: Exsertion	Mostly exerted	5	8.33
		Well exerted	55	91.67
32	Leaf: Senescence	Early	8	13.33
		Medium	27	45.00
		Late	25	41.67
33	Sterile lemma: Colour	Straw	59	98.33
		Purple	1	1.67
34	Decorticated grain: Shape	Short slender	3	5.00
		Short bold	5	8.33
		Medium slender	2	3.33
		Medium bold	49	81.67
		Long slender	1	1.67
35	Decorticated grain: Colour	White	17	28.33
		Light red	14	23.33
		Red	29	48.33
36	Decorticated grain: Aroma	Absent	56	93.33
		Present	4	6.67
37	Gelatinization temperature through alkali spreading value	Medium	2	3.33
		high	58	96.67
38	Lodging nature	Present	7	11.67
		Absent	53	88.33

5.1.1. Coleoptile: Colour

Observation on coleoptile colour of genotypes revealed a dimorphic expression *i.e.,* colourless and purple coleoptile. Out of 60 landraces, most of the landraces (70 per cent) exhibited purple colour for coleoptile. Purple colour of coleoptile is not common in high yielding varieties. Pachauri *et al.* (2017) while working with 124 rice germplasm accessions, recorded variation for coleoptile colour.

5.1.2. Leaf and stem characters

Among 19 qualitative characters of leaf and stem studied, absence of variability was observed for five characters namely, presence of leaf collar, anthocyanin colouration of leaf collar, presence of leaf ligule, shape of leaf ligule and anthocyanin colouration of stem nodes. Similar results for leaf collar, anthocyanin colouration of leaf collar, leaf ligule and shape of leaf ligule were reported by Rao *et al.* (2013) while working with 65 landraces and also same findings were reported by Sarawgi *et al.* (2013), while working with 782 rice accessions.

Significant and distinct variation was observed for basal leaf sheath colour, intensity of green colour of leaf, anthocyanin colouration of leaf, distribution of anthocyanin colouration on leaf, anthocyanin colouration of leaf sheath, pubescence of leaf blade surface, leaf auricles, anthocyanin colouration of leaf auricles, colour of ligule, culm attitude, attitude of flag leaf blade, leaf senescence and lodging nature. Parikh *et al.* (2012); Kumar *et al.* (2016); Giri and Pandey (2017) also recorded variation for the above characters in different sets of rice accessions.

Four states (green, light purple, purple lines and uniform purple) of basal leaf sheath colour was exhibited by the genotypes under study. Out of 60 landraces, green basal leaf sheath colour was exhibited in 30 per cent genotypes. The remaining 70 per cent of landraces exhibited purple basal leaf sheath colour

in different sub categories including light purple (41 per cent), purple lines (17 per cent) and uniform purple (12 per cent). Chakrabarty *et al.* (2012) observed variation for basal leaf sheath colour while working with 98 rice genotypes. It was interesting to note that, same trend (genotypes as well as frequency distribution) was observed for purple coleoptile, anthocyanin colouration in basal leaf sheath and also anthocyanin colouration in leaf sheath. In other words, a genotype which exhibited anthocyanin colour for coleoptile also exhibited anthocyanin colouration in basal leaf sheath and anthocyanin colouration in leaf sheath.

Intensity of green colour of leaf indicates the amount of chlorophyll content in leaves, which includes the main pigments of photosynthesis, thereby has an influence on photosynthetic efficiency in plant (Pan and Dong, 1995). It was interesting to note that, majority (80 per cent) of Wayanad landraces under study exhibited dark green in colour. Sarawgi *et al.* (2013) observed variation for intensity of green colour of leaf while working on 782 rice accessions.

Reddy *et al.* (1995) reported that, anthocyanins in rice, belongs to flavonoid class of pigment molecules and important secondary metabolites. Out of 60 landraces, only Thavalakannan exhibited leaf anthocyanin colouration as blotches on leaf. This character can also be considered as morphological marker for identification of Thavalakannan. Chakrabarty *et al.* (2012) and Sarawgi *et al.* (2013) reported variation for leaf anthocyanin colouration in different rice genotypes.

The pubescence of leaf blade surface exhibited dimorphic expression (medium and strong pubescence). Majority of landraces (83 per cent) under study, recorded strong pubescence of leaf blade. Kumar *et al.* (2016) observed 64 rice germplasm for pubescence of leaf blade surface and reported presence of pubescence of leaf blade surface. Ahmed *et al.* (2016) also reported strong pubescence of leaf blade surface, for majority of rice genotypes.

Presence of leaf auricles was recorded in all the genotypes, except Mullan puncha. Absence of auricles is a very rare character in rice and hence, it was

important to note that, absence of auricles on stem can be considered as a distinct morphological character for Mullan puncha. Colour of leaf auricles and ligules showed dimorphic expression (colorless and purple) and among the genotypes studied, only Thavalakannan exhibited purple colour for auricles and ligules. Colouration of auricles and ligules could be considered as a morphological marker character for identification of Thavalakannan in the early stages of plant growth. Gupta *et al.* (2014) worked on 53 rice germplasm and reported colouration of auricles and ligules. Pachauri *et al.* (2017), while working on 124 rice accessions, observed variation in colour of auricles and ligules.

The attitude of flag leaf varied from semi-erect to horizontal in all the landraces studied and most of the landraces (87 per cent) were grouped under semi-erect flag leaf. None of the genotypes showed deflexed flag leaf attitude. Chakravorty and Ghosh (2012), studied flag leaf attitude in 51 rice landraces and reported variation in attitude of flag leaf.

Late leaf senescence is one of the major characters of high yielding varieties, where leaves actively involve in photosynthesis till the maturity of grains and this ultimately contribute to increase in grain yield. Leaf senescence exhibited trimorphic expression from early to late senescence and 45 per cent of landraces were grouped under late leaf senescence. Sarawgi *et al.* (2014) evaluated 408 rice genotypes and reported variation for leaf senescence.

Landraces recorded wide variation for culm attitude with tetramorphic expression (erect, semi-erect, open and spreading). Nearly 60 per cent of landraces showed semi-erect culm attitude and it was interesting to note spreading culm attitude in one genotype (Kalladi aryan). Sinha and Mishra (2013) reported tetramorphic expression for culm attitude in rice landraces.

In crop improvement programmes, selection for lodging resistance is gaining more and more importance for adopting mechanized harvesting. In the present study, 89 per cent of landraces were non-lodging and these results were in

agreement with the finding of Manjunatha *et al.* (2016), who evaluated 65 rice genotypes.

5.1.3. Spikelet characters

Spikelet characters included density of pubescence of lemma, anthocyanin colouration of lemma (keel), anthocyanin colouration of apex of lemma, anthocyanin colour of area below apex of lemma and colour of stigma of spikelet. Out of above five characters studied, absence of variability was recorded for anthocyanin colouration of lemma (keel) and anthocyanin colour of area below apex of lemma. Similar results for anthocyanin colouration of lemma and anthocyanin colour of area below apex were reported by Patra *et al.* (2010).

Among the landraces studied, density of pubescence of lemma exhibited wide variability and showed tetramorphic expression (weak, medium, strong and very strong). Density of pubescence of lemma was strong for 61 per cent of landraces and it was interesting to observe that Mullan puncha, with very rare characters of absence of auricles and presence of long awns recorded very strong density of pubescence of lemma. Kumar *et al.* (2016) recorded variation in density of pubescence of lemma, while working with 64 rice accessions.

Anthocyanin colouration of apex of lemma was a dominating marker character in Wayanad landraces and was recorded in 65 per cent of landraces. Most of the landraces exhibited very strong anthocyanin colouration at lemma apex. Rao *et al.* (2013) evaluated 65 rice germplasm and reported variation for anthocyanin colouration of apex of lemma.

Trimorphic expression was observed for colour of stigma of spikelet namely, white, light green and purple. Purple stigma was the dominating character for stigma colour and was exhibited in 62 per cent of landraces. Gandhakasala and Gandhakasala (dwarf), the two aromatic genotypes recorded light green stigma. Variability for stigma colour was reported by Subudhi *et al.* (2012). He also reported three genotypes with light green stigma among the 55 aromatic landraces evaluated.

5.1.4. Panicle characters

Eight panicle characters *viz.,* curvature of panicle main axis, presence of awns in panicle, colouration of awns, distribution of awns in panicle, presence of secondary branching and mode of secondary branching in panicle, attitude of panicle branches and type of panicle exsertion were studied. All the landraces exhibited secondary branching. Sinha and Mishra (2013) reported all the landraces with secondary branching in a characterization study.

The mode of curvature of panicle main axis depends on length of panicle, number of grains and its weight. Majority of landraces (88 per cent) among the evaluated genotypes exhibited drooping type of panicles and 12 per cent genotypes namely Mulla kuruva, Mannu veliyan, Njavara black, Mahi kuruva, Valichoori, Veliya thondi and Rasagatham exhibited deflexed type of curvature of main axis. The drooping type of panicles in Wayanad landraces might be due to long panicles, bold type grains and grain weight. These results were supported by the findings of Kumar *et al.* (2016).

Awn is the outgrowth of lemma and most of the *indica* varieties are awnless. Farmers prefer awnless varieties because for easy handling in harvesting and post harvesting operations. In the present study, 90 per cent of landraces exhibited awnless panicles and only six genotypes namely Kothandon, Mullan puncha, Chomala-2, Jeerakasala, Sugandhamathi and Kayama exhibited presence of awns. Kothadon, Chomala-2 and Sugandhamati showed awns only at panicle tips where as Jeerakasala and Mullan puncha showed awns in upper half of panicle and Kayama exhibited awns in whole length of panicle. Among these landraces, Chomala-2, Jeerakasala and Sugandhamathi exhibited yellowish brown awns, Kothandon exhibited brown awns, Kayama exhibited purple awns and Mullan puncha exhibited black awns. It was so interesting that, Mullan puncha exhibited longest awns (up to 7.0 cm) and that too with black colour.

About 96 per cent of landraces exhibited strong to clustered secondary branching of panicles and this is the most preferred character in rice as it bears

more number of grains per panicle. Mullan puncha exhibited weak type of branching. The attitude of branching exhibited tetramorphic expression from erect to spreading, where 56 per cent of landraces were grouped under spreading type of attitude of branching. The variation in nature of branching of panicle was reported by Rao *et al.* (2013).

Panicle exsertion varied from mostly exserted to well exserted, where 92 per cent of landraces exhibited well exserted panicles and five genotypes namely Ayirankana, Valichoori, Kothandan, Thonnooran thondi and Palthondi matta recorded mostly exserted panicles. Genotypes with less panicle exsertion are more prone to pest attack as less exserted panicles provide shelter for pests. Umarani *et al.* (2017) evaluated different rice genotypes and observed variation in panicle exsertion.

5.1.5. Grain characters

Among 38 qualitative characters studied, lemma and palea colour exhibited maximum variability and recorded six states of expression. Among the landraces studied, 30 per cent of them exhibited brown furrows on straw background colour for lemma and palea, followed by 22 per cent genotypes with brown colour, 17 per cent with straw colour, 15 per cent with brown furrows on straw, 13 per cent with black colour and only two genotypes (Chomala and Ambalavayal-2) recorded gold and gold furrows on straw background. Variability for lemma and palea colour was also reported by Subudhi *et al.* (2012).

The sterile lemma was exhibited straw colour in 98 per cent of landraces and it was interesting to observe purple colour for sterile lemma in Kayama. Sarawgi *et al.* (2014) and Pachauri *et al.* (2017) reported 97 per cent and 80 per cent genotypes with straw coloured sterile lemma.

5.1.6. Decorticated grain (kernel) characters

Kernel shape, colour and aroma were the three qualitative characters studied. Among these characters, wide variability was exhibited by kernel shape

with five states of expression (short slender, short bold, medium slender, medium bold and long slender). Majority of landraces (82 per cent) exhibited medium bold kernel shape and only one genotype (Sugandhamati) exhibited long slender kernel. Kernel colour was red (including light red and red) in 72 per cent of landraces, and this colour is mostly preferred by people of Kerala. Wayanad Gandhakasala and Jeerakasala (cultivars with GI registration) and Sugandhamathi recorded aromatic grains. Aroma of these landraces might be the reason for higher birds attack at milk development to maturity stage of crop. Rao *et al.* (2013) observed the variation for kernel characters in characterization study and Elsy *et al.* (2010) reported the unique characters of Gandhakasala and Jeerakasala, the aromatic genotypes of Wayanad.

5.1.7. Gelatinization temperature through alkali spreading value

Gelatinization temperature is normally measured by alkali spreading value. It is mainly done to know the time required for cooking. Among the 60 landraces, majority of landraces (97 per cent) exhibited high gelatinization temperature and only Addy and Sugandhamathi showed medium gelatinization temperature. This is an indication that the landraces of Wayanad might require more time for cooking. Samal *et al.* (2014) characterized 78 rice accessions and reported variation of gelatinization temperature in white rice.

The frequency distribution of important qualitative characters presented in Fig. 16.

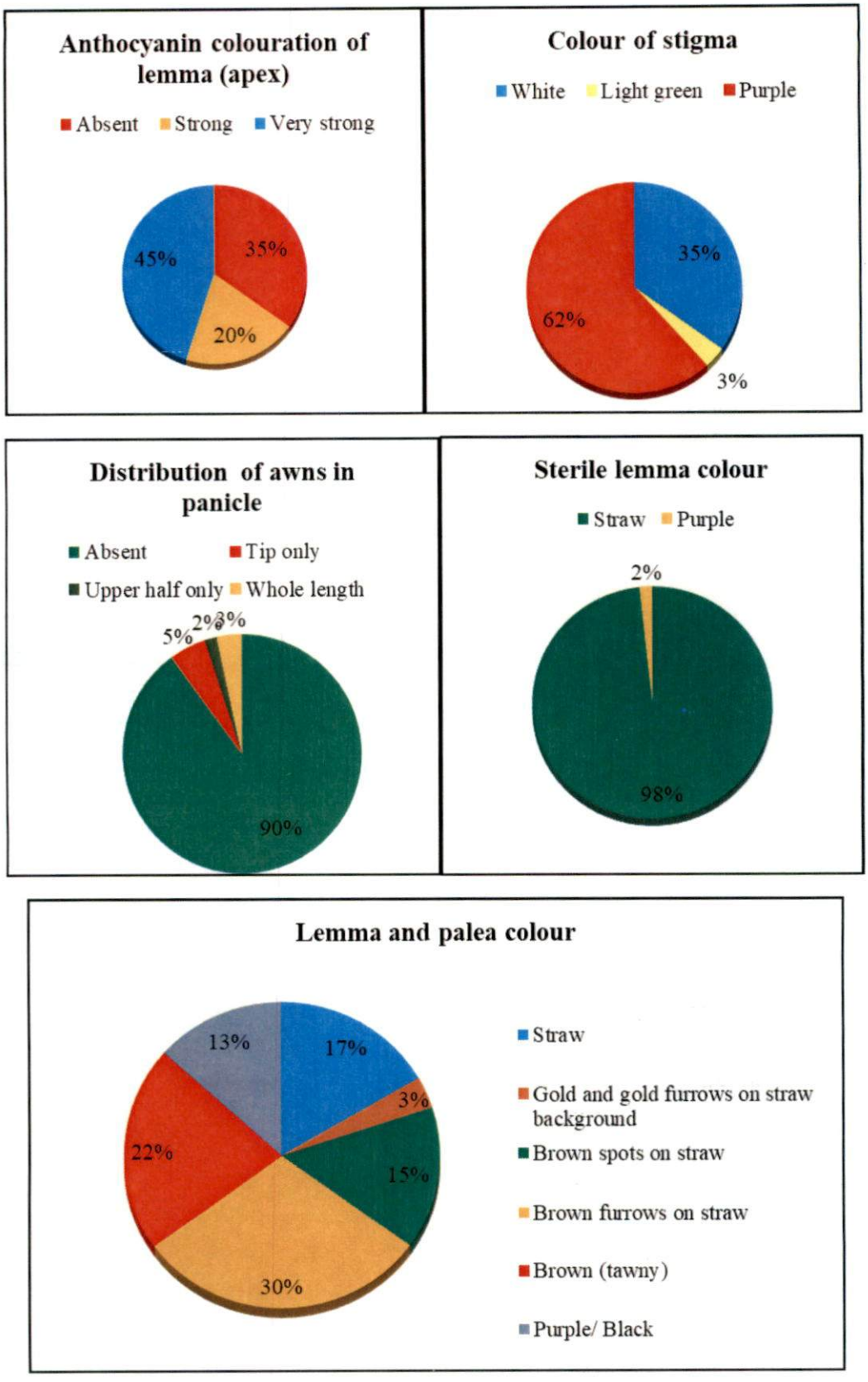
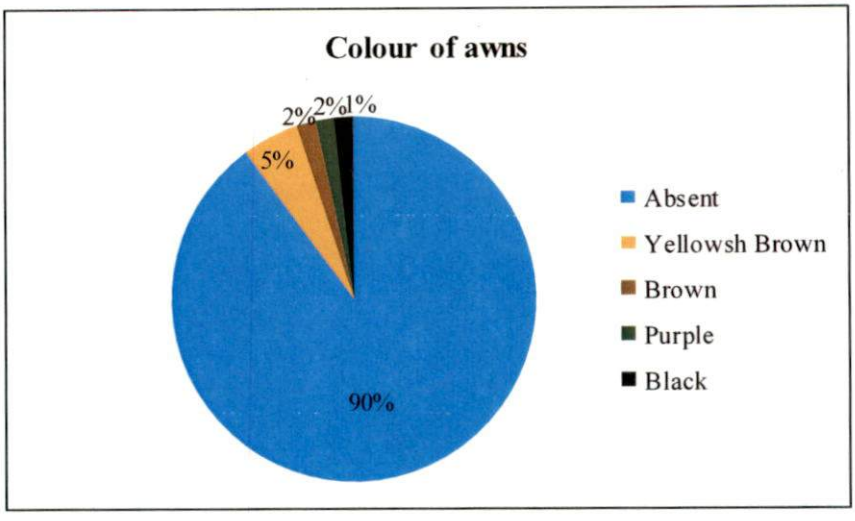
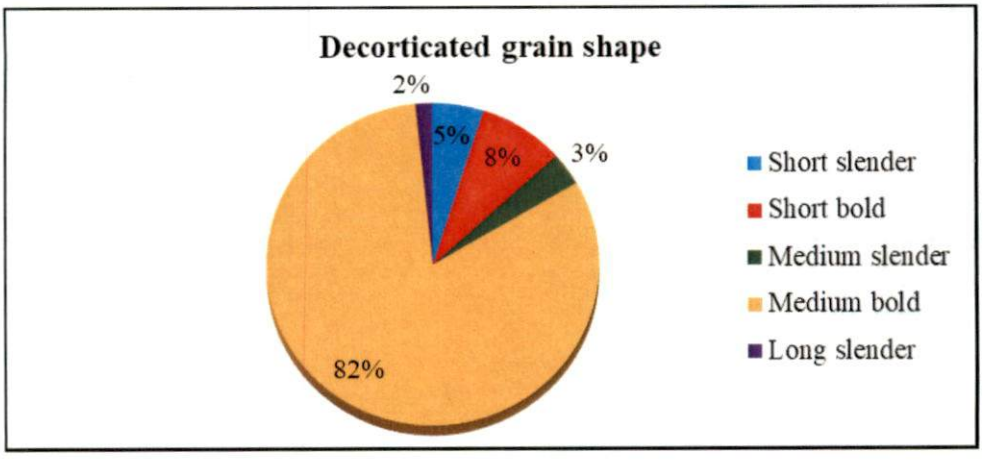


Fig. 16. Frequency distribution of qualitative characters





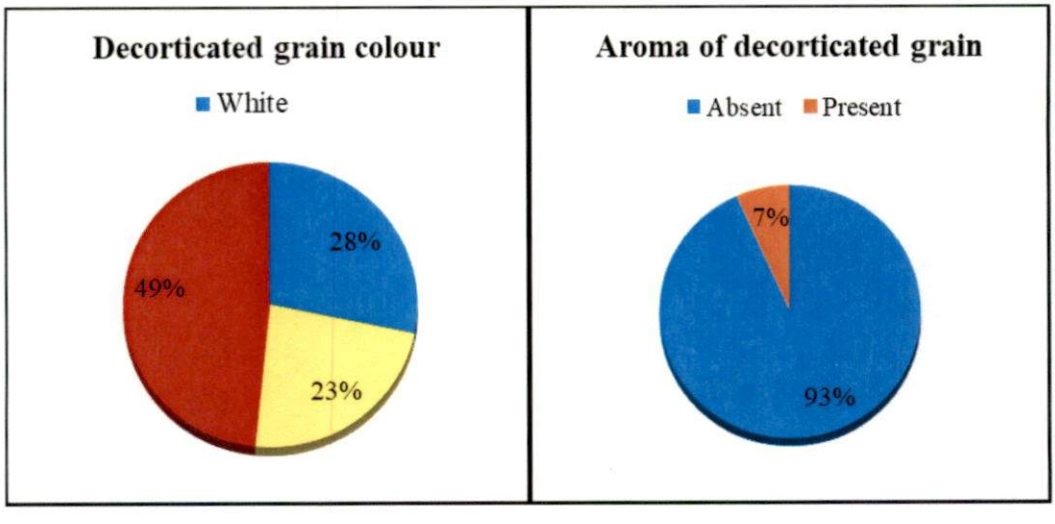


Fig. 16. Frequency distribution of qualitative characters (Continued...)

5.2. Genetic variability

Twenty quantitative characters were studied for variability and the analysis of variance exhibited highly significant differences among the landraces of Wayanad for all the characters, suggesting the presence of broad genetic variability among the landraces. The wide range of variation recorded in all the characters confirmed that the landraces selected were genetically diverse. Variability for different characters among different rice accessions was previously reported by several workers like Padmaja *et al.* (2008), Srujana *et al.* (2017) and Tripathi *et al.* (2018).

5.2.1. Growth characters

Among the 60 landraces studied, analyses of variance showed significant difference at 5 per cent level of significance for all the growth characters studied, namely, length of leaf blade, width of leaf blade, stem length, stem thickness and number of tillers per plant. Among leaf characters, length of leaf blade varied from 30.20 cm to 66.20 cm (Fig. 17). Out of 60 landraces, long leaf blades were present in 32 landraces. Mara thondi, Gandhakasala, Kothandon and Chanthondi recorded maximum length of leaf blade. Width of leaf blade exhibited moderate variability, and it varied from 0.50 cm to 1.30 cm (Fig. 18). Maximum width of leaf blade was recorded in Thavalakannan. Variation for length and width of leaf blade was reported by Sumanth *et al.* (2017) in earlier study.

Stem length in 60 landraces exhibited five states of expression (very short, short, medium, long and very long) and varied from 72.10 cm to 177.80 cm (Fig. 19). Even though Peruvaya showed maximum stem length, it was not exhibiting lodging character may be because of the maximum stem thickness (0.63 cm). Stem thickness is the important character while selecting the variety for non-lodging character. Stem thickness ranged from 0.28 cm to 0.63 cm (Fig. 20). Among the 60 landraces, seven genotypes (Chenthondi, Peruvaya, Vaalicha, Kumbali, Ambalavayal-2, Gandhakasala, Jeerakasala) exhibited significantly high stem thickness. These landraces can be considered as donors to improve the

lodging resistance in rice. In earlier study, Giri *et al.* (2017) reported variation for stem thickness.

Maximum number of tillers per plant leads to increased ground cover and less weeds growth (Bueren *et al.*, 2002). Out of 60 landraces, number tillers per plant varied from 8.20 to 16.60 (Fig. 21). The genotypes Urulan kayama, Kothandan, Valichoori and Kanni kayama recorded maximum number of tillers, and these landraces may have better capacity to suppress the weed growth. It is also one of the major characters contributing for total biomass per plant. Dhanwani *et al.* (2013) also reported similar variation for number tillers per plant.

5.2.2. Panicle characters

Number of panicles per plant and length of panicle main axis recorded significant difference at 5 per cent level of significance. Number of panicles per plant ranged from 1.30 (Mulla kuruva) to 14.90 (Uralan kayama) (Fig. 22) with two classes (few and medium). Maximum number of genotypes (50 out of 60) exhibited few panicles (<11) per plant, indicating shy-tillering nature. The cultivar Urulan kayama even though had recorded maximum panicles per plant, its grain yield was not maximum due to low (76.19) seed setting per cent. Length of panicle main axis varied from 20.50 cm to 39.40 cm (Fig. 23). The landraces Gandhakasala, Chomala-2, Jeerakasala, Kayama and Gandhakasala (dwarf) exhibited very long panicles and among these landraces, maximum length of panicle main axis was recorded in Kayama. Padmaja *et al.* (2008) studied 145 rice genotypes and reported variation in panicle main axis length.

5.2.3. Grain characters

Number of spikelets per panicle is the major yield contributing character, which contribute maximum towards genetic diversity (Sandhya *et al.*, 2014). This character exhibited wide variability, ranging from 68 (Njavara black) to 298 (Chanthondi) (Fig. 24). Even though Chanthondi recorded maximum spikelets per panicle, its grain setting percentage was poor. Njavara black recorded the lowest

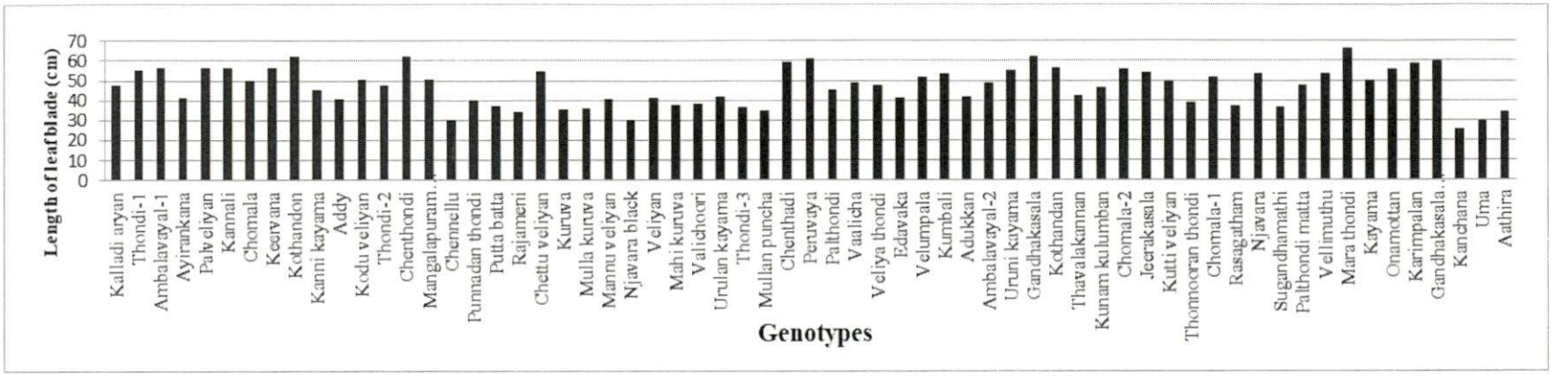


Fig. 17. Variation in length of leaf blade of 60 rice landraces of Wayanad

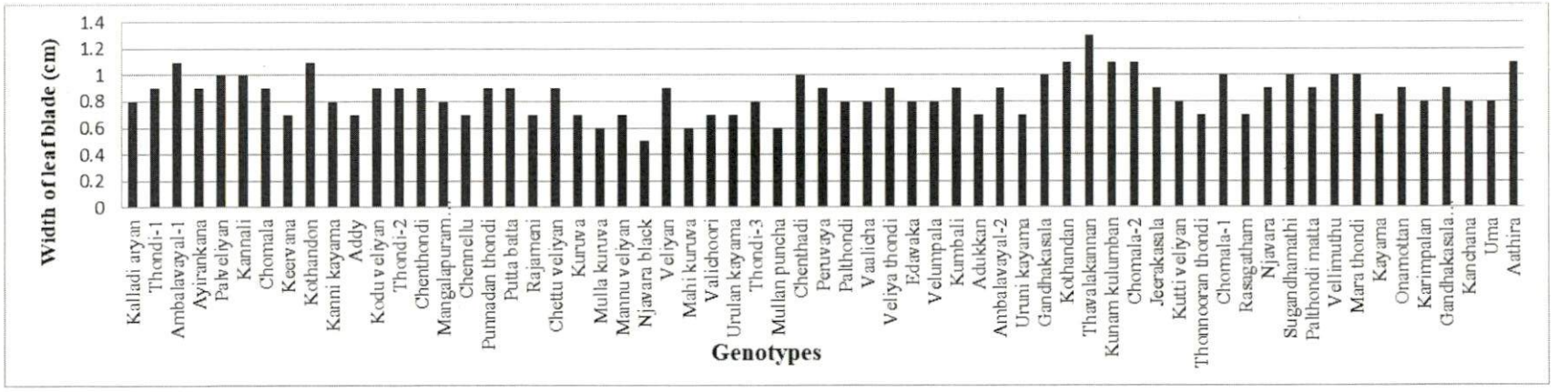


Fig. 18. Variation in width of leaf blade of 60 rice landraces of Wayanad

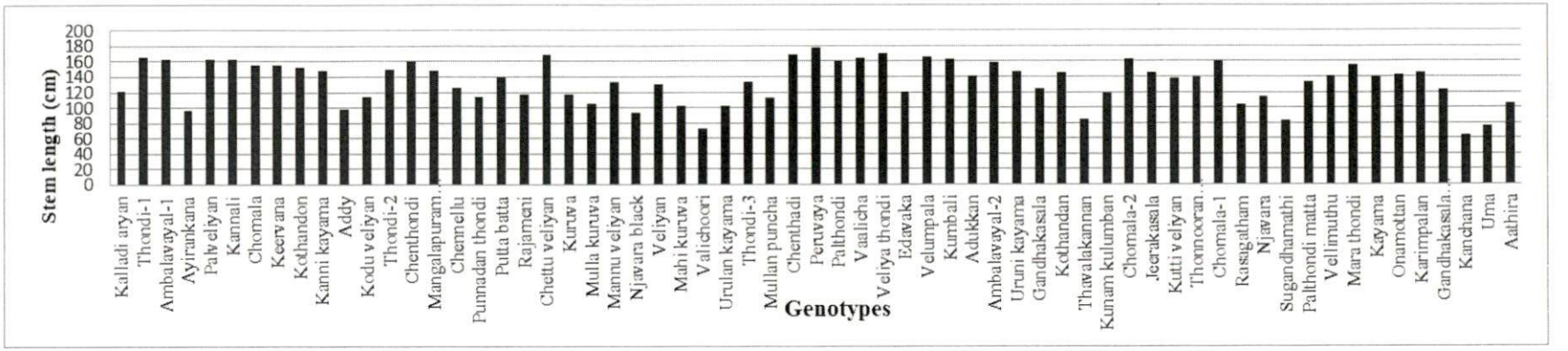


Fig. 19. Variation in stem length of 60 rice landraces of Wayanad

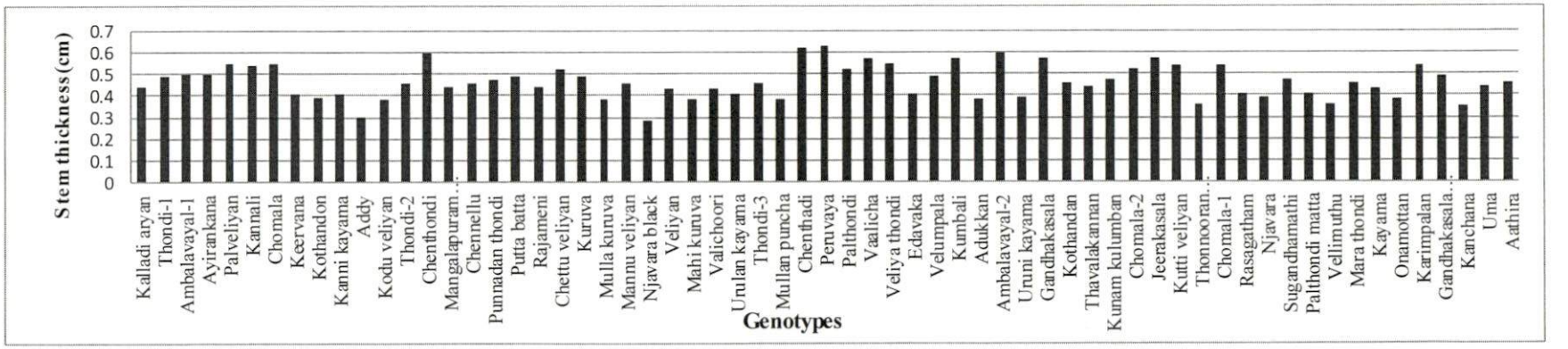


Fig. 20. Variation in stem thickness of 60 rice landraces of Wayanad

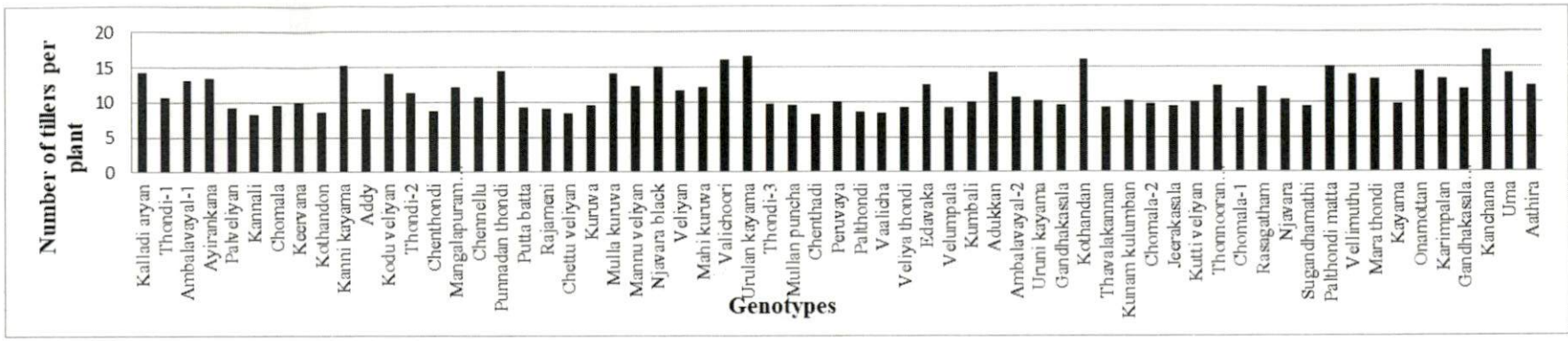


Fig. 21. Variation in number of tillers per plant of 60 rice landraces of Wayanad

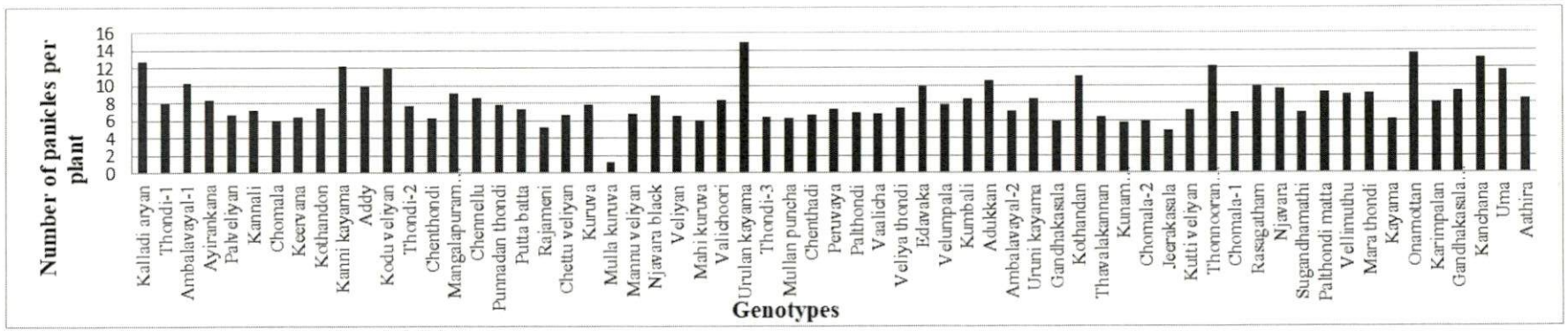


Fig. 22. Variation in number of panicles per plant of 60 rice landraces of Wayanad

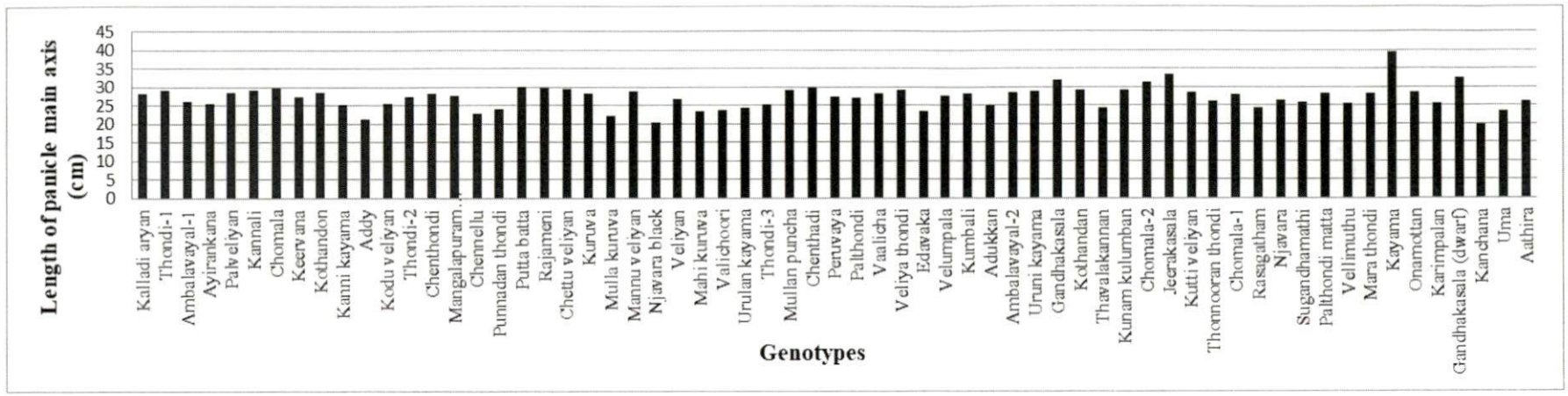


Fig. 23. Variation in length of panicle main axis of 60 rice landraces of Wayanad

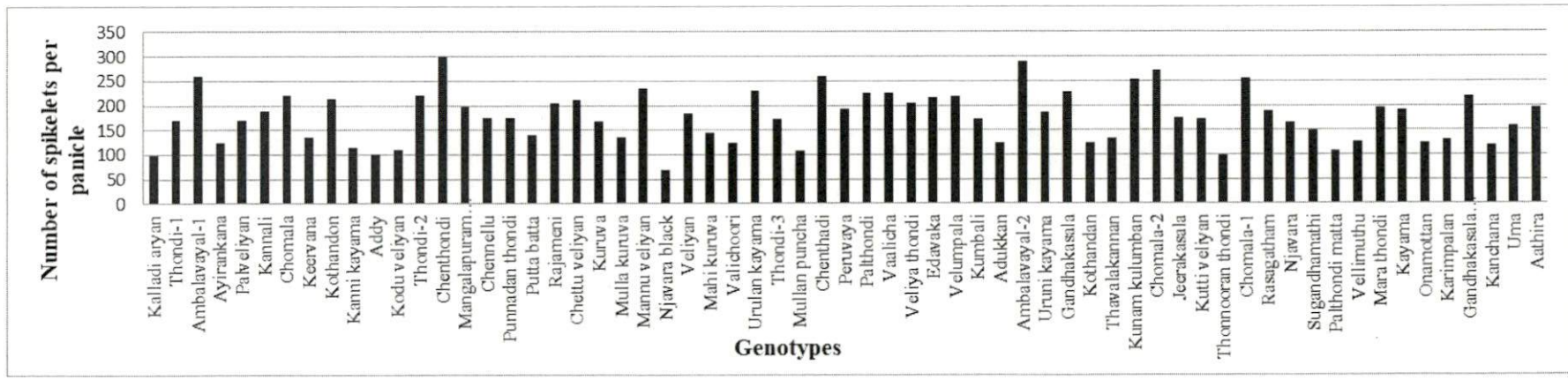


Fig. 24. Variation in number of spikelets per panicle of 60 rice landraces of Wayanad

spikelets per panicle indicating its poor grain yielding ability. Manjunatha *et al.* (2015) evaluated 65 rice landraces and reported variation for number of spikelets per panicle.

Out of 60 landraces, number of grains ranged from 63 to 272 (Fig. 25), which indicates its wide variability in Wayanad landraces. Maximum number of grains per panicle was recorded by Ambalavayal-2 (272), and maximum number of grains per panicle in check varieties was recorded by Aathira (169.40). But the grain number in Ambalavayal-2 was double as that of present in Aathira, the most popular variety of Wayanad district. This indicated that, this landrace could be selected as donor parent in breeding programmes aiming for high yielding varieties in Wayanad. Kalyan *et al.* (2017) studied 70 rice accessions and reported wide variation for number of grains per panicle.

The seed setting (per cent), indicates the number of grains developed out of number of spikelets in a panicle. Among 60 landraces, seed setting (per cent) exhibited wide variability and ranged from 50.81 per cent in Ayirankana to 96.9 per cent in Vaalicha (Fig. 26). Landraces namely, Vaalicha, Jeerakasala, Kuruva, Addy, Mullan puncha, Ambalavayal-2, Keervana, Velumpala, Palthondi, Adukkan, Njavara black and Edavaka exhibited significantly high seed setting per cent. Lowest seed setting per cent was recorded by Ayirankana. In earlier studies Singh *et al.* (2018) reported variation for seed setting per cent in rice germplasm.

Weight of 1000 fully developed grains exhibited significant difference between all the landraces and ranged from 12.43 g to 36.57 g (Fig. 27). Among the 60 landraces, 30 recorded very high 1000 grain weight. Among these Onamottan, Ayirankana, Peruvaya and Vellimuthu recorded significantly high 1000 grain weight. Majority of landraces recorded high to very high weight for 1000 grains and this might be due to medium to bold type of rice. Rasagatham exhibited lowest 1000 grain weight due to short bold type. Babu *et al.* (2012) reported variation among different rice accessions for 1000 grain weight.

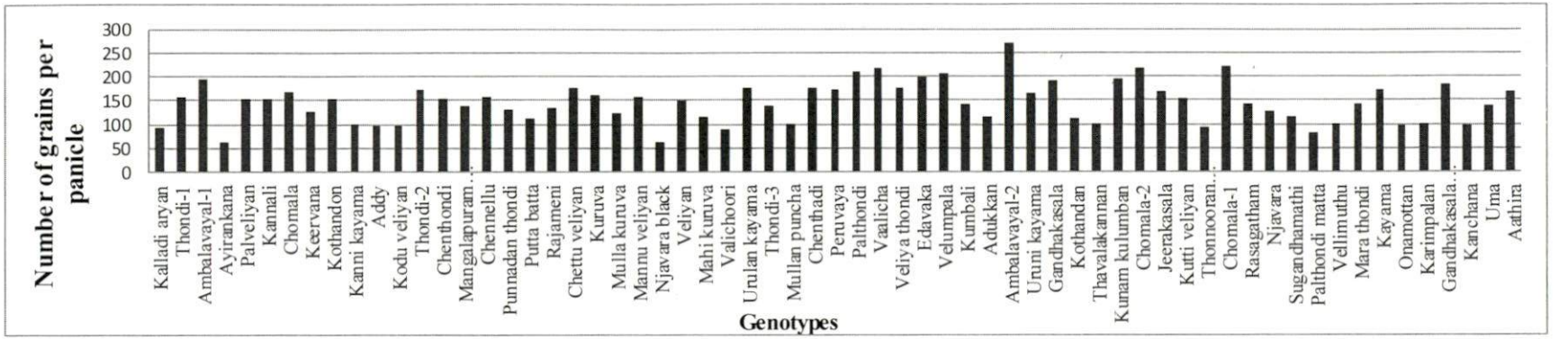


Fig. 25. Variation in number of grains per panicle of 60 rice landraces of Wayanad

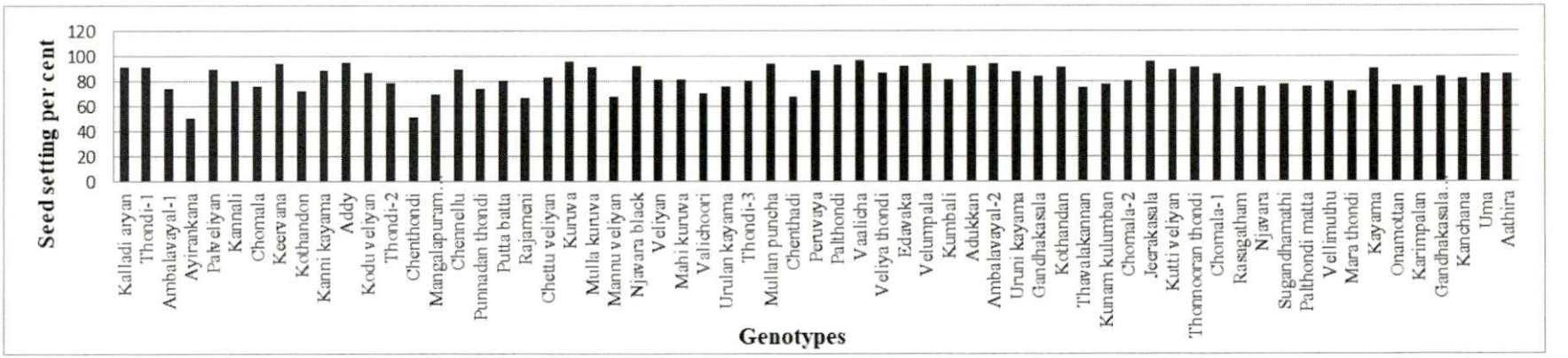


Fig. 26. Variation in seed setting per cent of 60 rice landraces of Wayanad

249

Grain length, width and grain L/B ratio exhibited significant variation among all the landraces studied. Grain length varied from 5.2 mm to 11.20 mm (Fig. 28), grain width varied from 2.5 mm to 3.9 mm (Fig. 29) and grain L/B ratio varied from 1.77 to 4.48 (Fig. 30). Among the 60 landraces, the aromatic landrace Sugandhamathi exhibited significantly high grain length and grain L/B ratio and minimum grain width, giving slender shape to the grain. The bold type rice Ayirankana exhibited maximum grain width. Addy recorded minimum grain length and grain L/B ratio making short and moderate bold grains. Kumar *et al.* (2016) studied 64 rice genotypes and reported variability in grain shape.

5.2.4. Decorticated grain (kernel) characters

Decorticated grain characters including kernel length, width and kernel L/B ratio showed significantly wide variation among the landraces studied (Fig. 31, Fig. 32 and Fig. 33). Maximum kernel length and kernel L/B ratio was exhibited in long slender genotype "Sugandhamathi", whereas Thondi-1 exhibited maximum kernel width. All the landraces of Wayanad were having either short or medium kernel length, whereas the kernel width was either medium or broad. Kumar *et al.* (2016) evaluated rice germplasm and reported variation in kernel characters.

5.2.5. Time for heading and maturity

Days for heading and maturity exhibited significant variation among all the landraces studied and ranged from 117 days to 162 days (Fig. 34) for time of heading and 147 days to 191 days (Fig. 35) for maturity. The medicinal landrace Njavara recorded the minimum number days for both heading (117) and maturity (162), whereas the landrace Uralan kayama recorded the maximum number of days for both heading (162) and maturity (191). Among the 60 landraces, majority of the landraces (51) recorded late heading and maturity. When these landraces are grown at normal altitude area with normal temperature, the duration required for heading and maturity is less. For example, days to maturity of Aathira is 120-130 days under normal altitude area with normal temperature, but it recorded 185

days for maturity in Wayanad. It might be due to high altitude and cool temperature prevailing in Wayanad. Adheena *et al.* (2012) reported wide variation in days to heading and maturity, while working with Wayanad aromatic landraces Gandhakasala and Jeerakalasa at different altitudes of Kerala.

5.2.6. Grain yield per plant

The grain yield per plant is the major aim of any breeding programme. Grain yield exhibited significant variation among all the landraces studied and varied from 10.35 g in Njavara to 36.45 g in Kanni kayama (Fig. 36). The landraces Kanni kayama, Ambalavayal-1, Kothandan, Onamottan, Thondi-2, Chenthadi, Kannali and Thondi-1 exhibited significantly high grain yield per plant and these landraces exhibited on par yield as that of Uma and Aathira (high yielding check varieties), suggesting that, these landraces could be used as donors for improvement of grain yield in rice and also these landraces could be promoted to grow in regions of Wayanad, where the farmers are mainly depending on traditional landraces. In the earlier study, Manjunatha *et al.* (2015) reported wide variation in grain yield per plant while working with 65 rice genotypes.

Among the better yielding landraces identified, Kanni kayama recorded a grain yield of 36.45 g per plant, contributed by 15.22 tillers per plant, 12.24 panicles per plant, 25.14 cm panicle length, 101.51 grains per panicle, 88.60 seed setting per cent and 30.93 g 1000 grain weight. Ambalavayal-1 recorded a grain yield of 33.74 g per plant, along with 13.10 tillers per plant, 10.34 panicles per plant, 26.12 cm panicle length, 195.24 grains per panicle, 74.71 seed setting per cent and 26.40 g 1000 grain weight. Kothandan recorded a grain yield of 33.64 g per plant, due to 16.11 tillers per plant, 11.10 panicles per plant, 29.10 cm panicle length, 113.41 grains per panicle, 91.87 seed setting per cent and 32.54 g 1000 grain weight. Onamottan recorded grain yield of 32.85 g per plant, contributed by 14.52 tillers per plant, 13.79 panicles per plant, 28.63 cm panicle length, 96.73 grains per panicle, 76.82 seed setting per cent and 36.57 g 1000 grain weight.

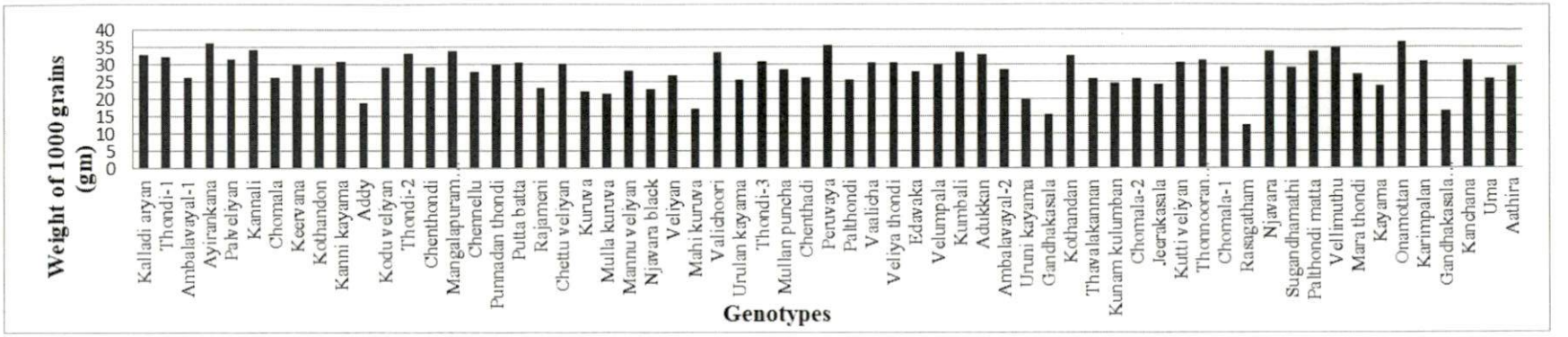


Fig. 27. Variation in weight of 1000 grains of 60 rice landraces of Wayanad

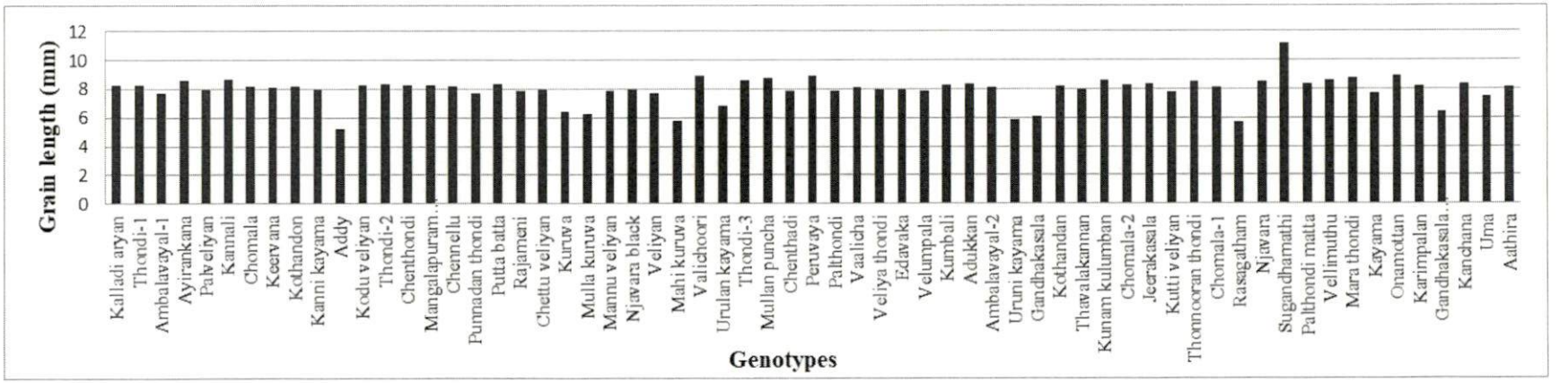


Fig. 28. Variation in grain length of 60 rice landraces of Wayanad

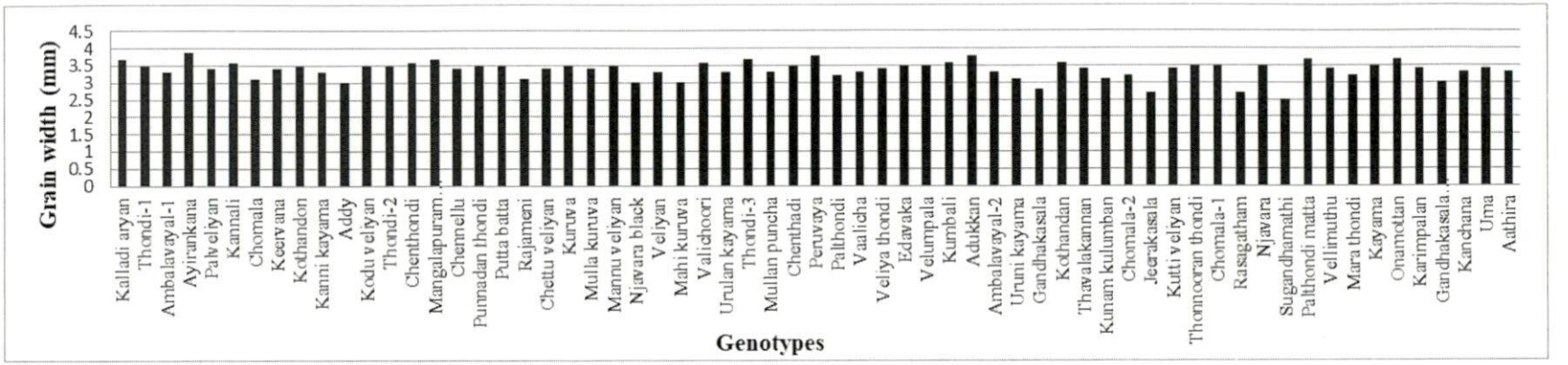


Fig. 29. Variation in grain width of 60 rice landraces of Wayanad

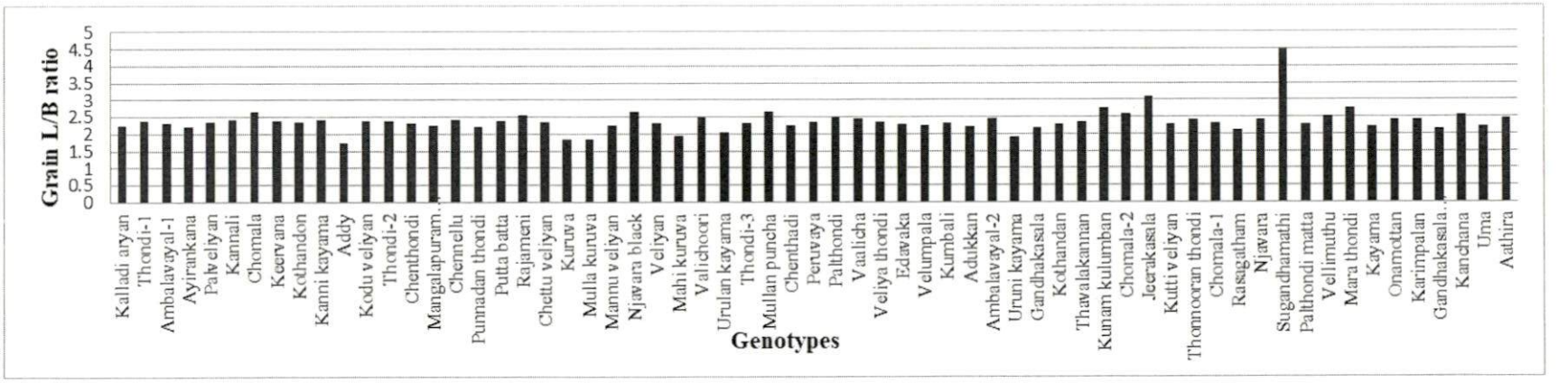


Fig. 30. Variation in grain L/B ratio of 60 rice landraces of Wayanad

253

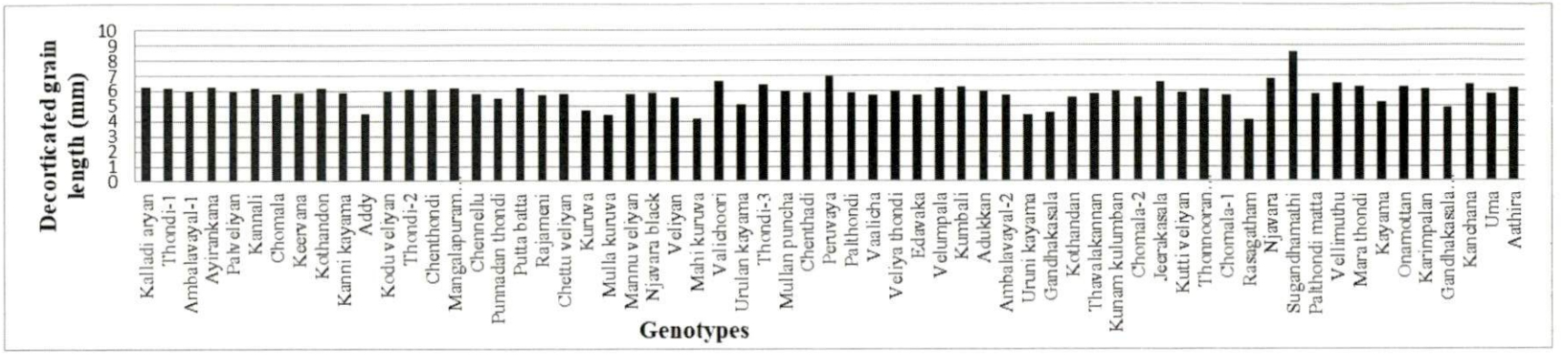


Fig. 31. Variation in decorticated grain length of 60 rice landraces of Wayanad

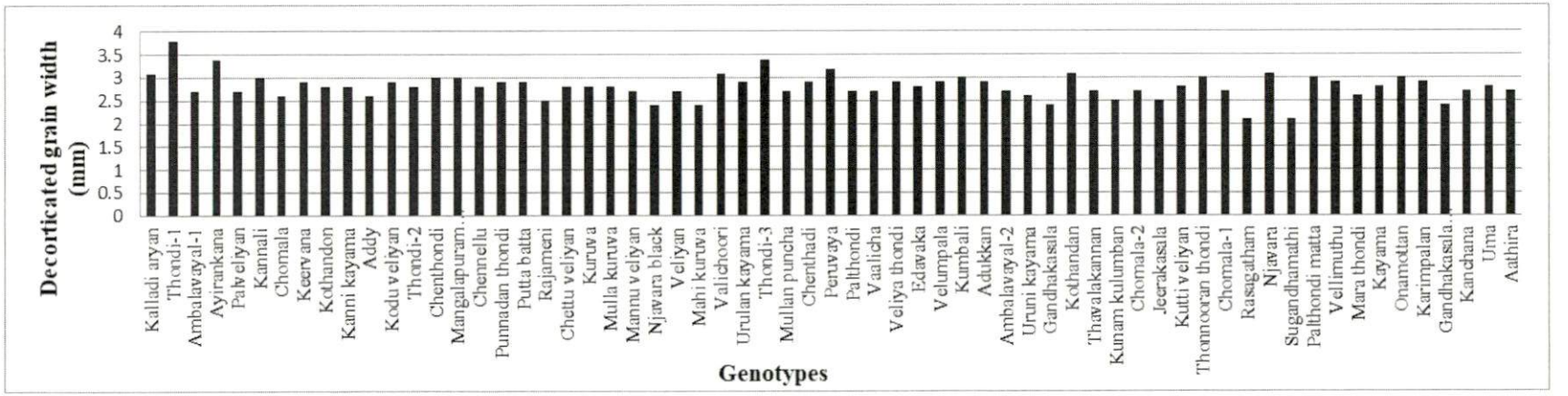


Fig. 32. Variation in decorticated grain width of 60 rice landraces of Wayanad

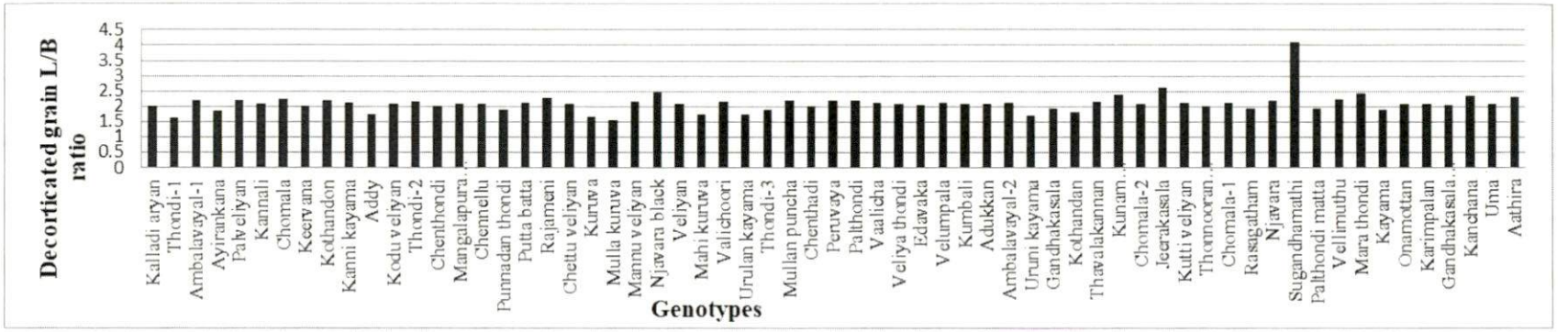


Fig. 33. Variation in decorticated grain L/B ratio of 60 rice landraces of Wayanad

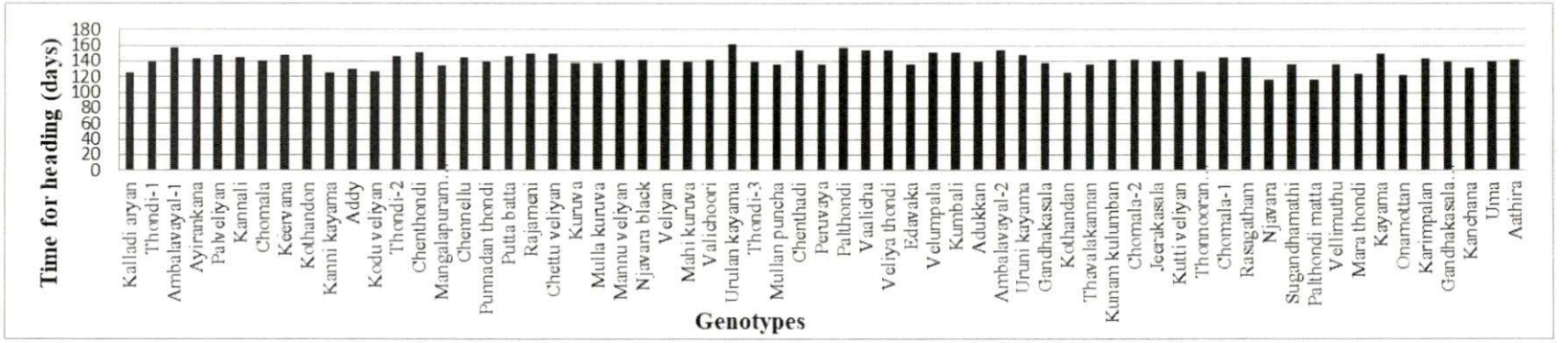


Fig. 34. Variation in time for heading of 60 rice landraces of Wayanad

552

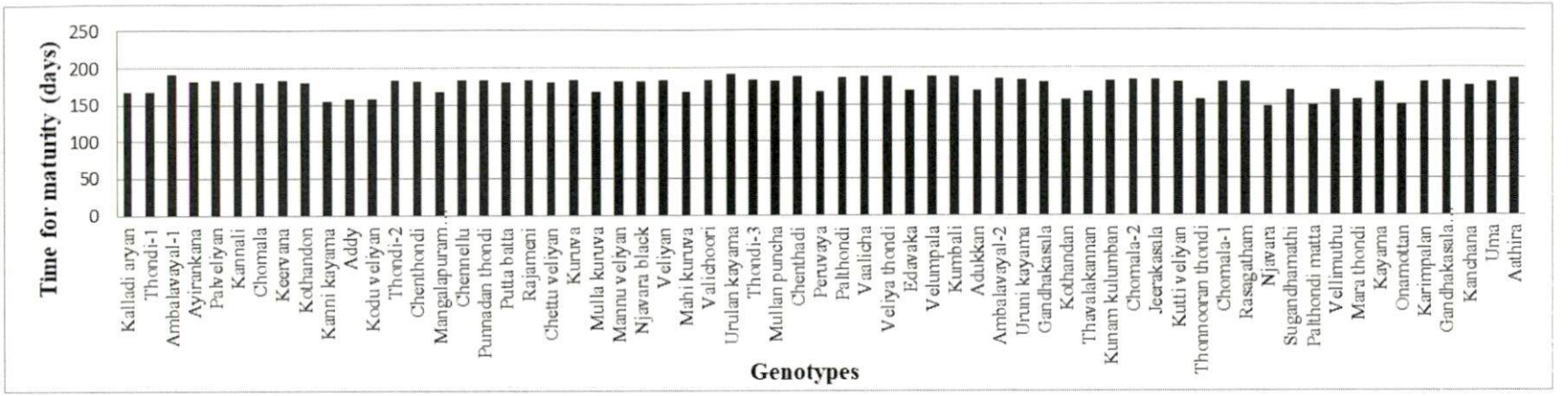


Fig. 35. Variation in time for maturity of 60 rice landraces of Wayanad

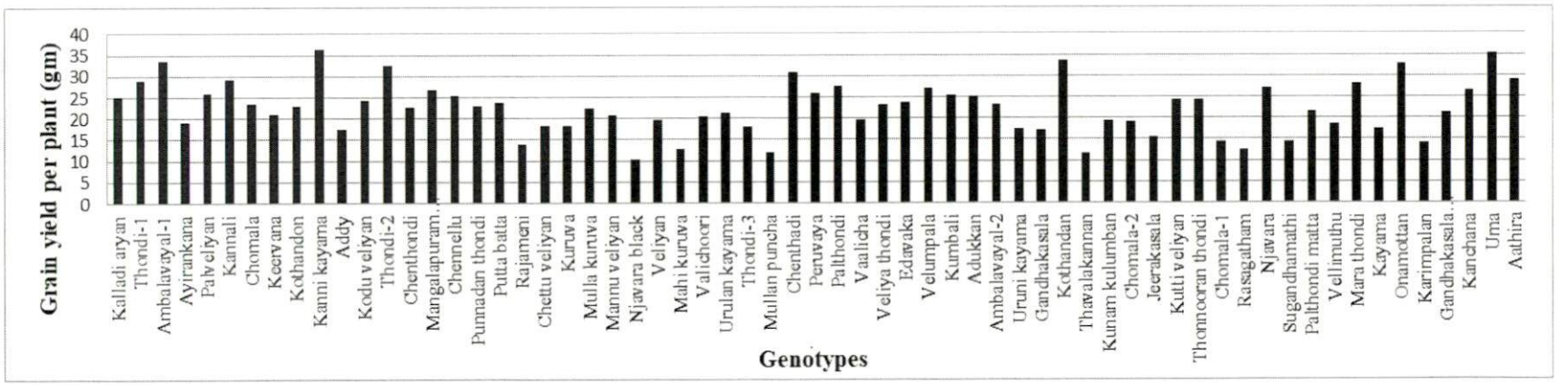


Fig. 36. Variation in grain yield per plant of 60 rice landraces of Wayanad

Thondi-2 recorded grain yield of 32.62 g per plant, along with 11.37 tillers per plant, 7.71 panicles per plant, 27.48 cm panicle length, 174.71 grains per panicle, 78.73 seed setting per cent and 33.13 g 1000 grain weight. Chenthadi recorded grain yield of 30.80 g per plant, due to 8.30 tillers per plant, 6.71 panicles per plant, 29.73 cm panicle length, 178.82 grains per panicle, 68.20 seed setting per cent and 26.28 g 1000 grain weight. Kannali recorded grain yield of 29.24 g per plant, contributed by 8.25 tillers per plant, 7.26 panicles per plant, 29.32 cm panicle length, 152.60 grains per panicle, 80.85 seed setting per cent and 34.16 g 1000 grain weight. Thondi-1 recorded grain yield of 29.01 g per plant, along with 10.71 tillers per plant, 8.02 panicles per plant, 29.31 cm panicle length, 156.41 grains per panicle, 91.23 seed setting per cent and 32.22 g 1000 grain weight.

5.3. Genetic parameters

Genetic parameters (PCV, GCV, heritability and genetic advance) were analyzed for 20 quantitative characters recorded in 60 landraces of Wayanad and the results are discussed below.

5.3.1. Genetic variability

Wide range of variation was exhibited by 60 rice landraces of Wayanad, for 20 quantitative characters. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters under study, indicating the influence of environmental factor on these characters. Similar results were reported by Islam *et al.* (2015) and Tripathi *et al.* (2018).

Among the 20 characters studied, high estimates of PCV and GCV (>20per cent) were exhibited by number of panicles per plant (26.06 per cent and 24.89 per cent respectively), number of spikelets per panicle (26.87 per cent and 26.23 per cent respectively), number of grains per panicle (26.92 per cent and 26.33 per cent respectively) and grain yield per plant (24.94 per cent and 22.35 per cent respectively). High GCV and PCV values for these characters indicated high opportunity of selection for these characters.

The moderate PCV and GCV estimates (10-20per cent) were exhibited by length of leaf blade (17.04 per cent and 16.93 per cent respectively), width of leaf blade (16.20 per cent and 15.77 per cent respectively), stem thickness (15.07 per cent and 14.82 per cent respectively), stem length (17.00 per cent and 16.97 per cent respectively), number of tillers per plant (19.08 per cent and 18.51 per cent respectively), seed setting per cent (11.30 per cent and 11.18 per cent respectively), weight of 1000 fully developed grains (17.00 per cent and 16.86 per cent respectively), grain length (10.88 per cent and 10.76 per cent respectively), grain L/B ratio (13.82 per cent and 13.05 per cent respectively), decorticated grain length (11.22 per cent and 11.10 per cent respectively) and decorticated grain L/B ratio (14.25 per cent and 14.12 per cent respectively). These moderate values indicating little opportunity of selection for these characters. In earlier study, Yadav *et al.* (2011) observed moderate PCV and GCV estimates for plant height and number of tillers per plant, while working with 40 rice genotypes.

Low values of PCV and GCV were exhibited by time for heading (6.39 per cent for both the parameters), length of panicle main axis (10.26 per cent and 9.94 per cent respectively), grain width (7.82 per cent and 6.19 per cent respectively), decorticated grain width (9.21 per cent and 9.04 per cent respectively) and time for maturity (5.84 each). The low PCV and GCV estimates for these characters, indicated that selection directly based on these traits is not much effective. Hence, there is a need for creation of variability in these characters either by hybridization or mutation as suggested by Tripathi *et al.*, 2018. Islam *et al.* (2015) reported low PCV and GCV values for time for heading, time for maturity and grain width, while working with 23 rice genotypes.

5.3.2. Heritability

The heritability is the proportion of genetic variability which is transmitted from parents to offspring. For a plant breeder knowledge of heritability of desirable character is very important, to get information about possibility and extent to which improvement can be done by selection (Tripathi *et al.*, 2018).

All the 20 quantitative characters studied in the present study expressed high heritability estimates ranging from 62.17 per cent to 100 per cent. High heritability was expressed by length of leaf blade (98.68 per cent), width of leaf blade (94.79 per cent), stem thickness (96.69 per cent), stem length (99.63 per cent), number of tillers per plant (94.04 per cent), time of heading (100 per cent), number of panicles per plant (91.22 per cent), length of panicle main axis (93.83 per cent), number of spikelets per panicle (95.26 per cent), number of grains per panicle (95.70 per cent), seed setting percentage (97.87 per cent), weight of 1000 grains (98.43 per cent), grain length (97.40 per cent), grain width (62.71 per cent), grain L/B ratio (89.10 per cent), decorticated grain length (97.91 per cent), decorticated grain width (96.18 per cent), decorticated grain L/B ratio (98.25 per cent), time for maturity (100 per cent) and grain yield per plant (80.31 per cent). It was so interesting to record 100 per cent heritability for two characters *viz.*, time for heading and time for maturity. High heritability estimates for the above characters indicated less influence of environmental factors on these characters and these characters could be selected directly on the basis of phenotypic expression in the individual plant by adopting simple selection methods. Padmaja *et al.* (2008) and Prasad *et al.* (2017) reported high heritability for all the characters studied.

5.3.3. Genetic advance

Genetic advance refers to improvement in mean genotypic value of selected plants over the parental population. Genetic advance was highest for number of spikelets per panicle (94.30), followed by number of grains per panicle (77.76), stem length (47.41) and time for maturity (21.23), and while lowest was recorded by width of leaf blade (0.27). Rashid *et al.* (2017) reported maximum genetic advance for number of grains per panicle, stem length and time for maturity.

Genetic gain (the genetic advance as per cent of mean) can be predicted with the help of information on genetic variation, heritability and genetic advance

(Alam *et al.*, 2014). The genetic gain was highest for number of grains per panicle (53.07 per cent), followed by number of spikelets per panicle (52.73 per cent), number of panicles per plant (48.96 per cent) and grain yield per plant (41.26). Lowest genetic gain was recorded for decorticated grain length. Mamata *et al.* (2018) while working with rice genotypes, observed high genetic gain for number of grains per panicle, number of panicles per plant and grain yield per plant.

Generally the character that exhibited high heritability along with high genetic advance is controlled by additive gene action in the inheritance of these characters, hence these can be directly utilized for improvement of rice (Alam *et al.*, 2014). In this study, high heritability and high genetic gain was exhibited by the characters like length of leaf blade, width of leaf blade, stem thickness, stem length, number of tillers per plant, number of panicles per plant, length of panicle main axis, number of spikelets per panicle, number of grains per panicle, seed setting (per cent), 1000 grain weight, grain length, grain L/B ratio, decorticated grain L/B ratio and grain yield per plant and hence these characters could be used in crop improvement programmes. Those characters with high heritability and moderate to low genetic advance have non-additive gene action and also have the influence of environmental factors to some extent. These characters could be improved by inter-mating superior genotypes of segregating population developed from combination breeding (Kalyan *et al.*, 2017).

Genetic parameters analyzed for 20 quantitative characters recorded in 60 landraces of Wayanad are represented in Fig. 37.

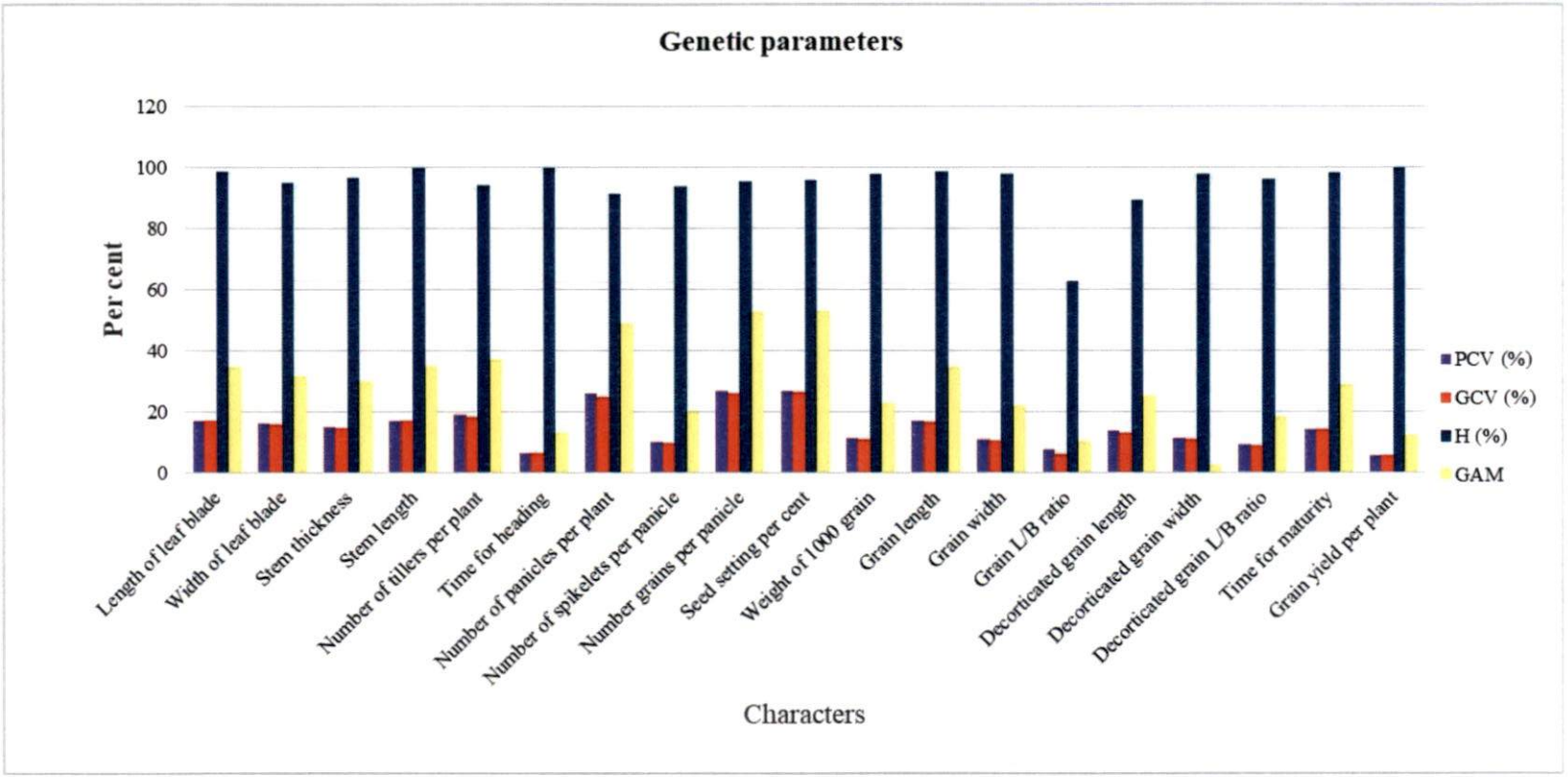


Fig. 37. Genetic parameters for 20 quantitative characters of Wayanad landraces.

5.4. Character association

For a plant breeder, selection of characters based on the knowledge of relationship of quantitative characters with grain yield is very important in rice breeding programme (Babu *et al.*, 2012). Path coefficient analysis is another tool which permits selection of key characters based on estimate of direct and indirect effects of quantitative characters with grain yield using correlation coefficients (Kalyan *et al.*, 2017)

The correlation coefficients and estimates of direct and indirect effects for 20 quantitative characters including growth and yield characters were worked out and the results are discussed below.

5.4.1. Correlation coefficient analysis

Correlation coefficient analysis provide better understanding of yield components which helps the breeder during selection as suggested by Singh and Narayanam (2009).

5.4.1.1. Grain yield per plant

The highest significant positive correlation of grain yield per plant was exhibited by stem length (0.505), followed by weight of 1000 grains (0.488), grain width (0.463), decorticated grain width (0.461), number of panicles per plant (0.389) and length of leaf blade (0.389) at 1 per cent level and also significant positive correlation of grain yield per plant with width of leaf blade (0.267) at 5 per cent level and these results indicated that grain yield per plant in these landraces could be improved by selection of above traits. Thus the indirect improvement in grain yield per plant based on above characters would be reliable. In the earlier studies, Babu *et al.* (2012) and Gour *et al.* (2017) confirmed the positive association of grain yield per plant with stem length, number of panicles per plant and 1000 filled grain weight with grain yield per plant.

The characters including stem thickness, number of tillers per plant, length of panicle main axis, number of spikelets per panicle, number of grains per

panicle, seed setting (per cent), grain length and decorticated grain length exhibited positive non significant association with grain yield per plant. Time for heading, grain L/B ratio, decorticated grain L/B ratio and time for maturity exhibited negative non-significant association with grain yield per plant indicating less influence of these characters on grain yield per plant. Dhurai *et al.* (2014) reported non-significant association of number of tillers per plant, length of panicle main axis, kernel length with grain yield per plant.

5.4.1.2. Leaf characters

Among the leaf characters, length of leaf blade showed positive association (at both 1 per cent and 5 per cent level of significance) with width of leaf blade, stem thickness, stem length, length of main axis of panicle, number of spikelets per panicle and number of grains per panicle. Width of leaf blade showed positive association at 1 per cent and 5 per cent level of significance with stem thickness, number of spikelets per panicle, grain length, decorticated grain length, stem length, length of main axis of panicle and grain L/B ratio.

5.4.1.3. Stem characters

Among the stem characters, stem thickness exhibited positive association at 1 per cent level of significance with stem length, time of heading, length of main axis of panicle, number of spikelets per panicle, number of grains per panicle, time for maturity, whereas stem thickness exhibited negative association at 1 per cent level of significance with number of tillers per plant and panicle number per plant. Lakshmi *et al.* (2014) reported positive association of stem thickness with time of heading and length of main axis of panicle. Stem length showed positive association at 1 per cent level of significance with length of main axis of panicle, number of spikelets per panicle, number of grains per panicle and grain yield per plant. Positive association of stem thickness exhibited significant association at 5 per cent level with time of heading, weight of 1000 grains, grain width and decorticated grain width. At the same time stem length exhibited negative association at 1 per cent level of significance with number of tillers per plant.

Chandra *et al.* (2009) observed positive association of stem length with length of panicle main axis. Number of tillers per plant showed positive association at 1 per cent level of significance with number of panicles per plant. At the same time number of tillers per plant exhibited negative association at 1per cent level of significance with time of heading, length of main axis of panicle, number of spikelets per panicle, number of grains per panicle and time for maturity. Positive correlation between above characters is favorable for breeder because it helps in simultaneous improvement of both the traits. Negative correlation between above characters will hinder the simultaneous expression of both the traits as suggested by Singh and Narayanam (2009).

5.4.1.4. Time for heading

Time of heading exhibited positive association at 1 per cent level of significance with number of spikelets per panicle, number of grains per panicle and time for maturity. At the same time, days for heading exhibited negative association at 1per cent level of significance with panicle number per plant. In earlier studies, Babu *et al.* (2012) observed positive association of time for heading with number of grains per panicle and Naseem *et al.* (2014) reported positive association of time of heading with time for maturity.

5.4.1.5. Panicle characters

Among the panicle characters, number of panicles per plant exhibited negative association with time for maturity, length of panicle main axis, number of spikelets per panicle and number of grains per panicle. Length of panicle main axis exhibited positive association with number of spikelets per panicle along with number of grains per panicle. It indicated that, length of panicle main axis could be improved by selecting more number of spikelets per panicle along with number of grains per panicle. In an earlier study, Babu *et al.* (2012) reported positive association of length of panicle main axis with number of grains per panicle.

5.4.1.6. Number of spikelets and filled grains per panicle

Number of spikelets per panicle could be improved by selecting the positively correlated characters namely more number of grains per panicle and increased time for maturity. Gour *et al.* (2017) and Madhukar *et al.* (2017) reported positive association of number of spikelets per panicle with time for maturity and number of grains per panicle. Number of grains per panicle exhibited positive association at 1 per cent level of significance with time for maturity. Nagaraju *et al.* (2013) observed positive association of number of grains per panicle with time for maturity.

5.4.1.7. Grain characters

Weight of 1000 filled grains could be improved by selecting for increased grain length, grain width, decorticated grain length and decorticated grain width, the characters which exhibited positive association with weight of 1000 filled grains. Allam *et al.* (2015) recorded positive association of weight of 1000 filled grains with decorticated grain length and decorticated grain width. Grain length could be improved by higher grain L/B ratio, decorticated grain length, decorticated grain L/B ratio, grain width and decorticated grain width. Grain width could be improved by selecting positively correlated character namely higher decorticated grain width. High grain L/B ratio could be achieved by selection for decorticated grain length, decorticated grain L/B ratio.

5.4.1.8. Decorticated grain characters

Decorticated grain length could be improved by selecting the positively correlated characters namely decorticated grain L/B ratio and decorticated grain width. In earlier studies, Lakshmi *et al.* (2014) and Allam *et al.* (2015) observed positive association of decorticated grain length with grain L/B ratio. Decorticated grain L/B ratio could be reduced by increasing decorticated grain width, since both characters exhibited negative association. Dhurai *et al.* (2014) reported negative association of decorticated grain width with decorticated grain L/B ratio.

It was evident from correlation analysis that, the yield of Wayanad landraces could be improved by selecting positively correlated characters namely length of leaf blade, width of leaf blade, stem length, number of panicles per plant, weight of 1000 grains, grain width and decorticated grain width. In earlier study, Kumar and Nilanjaya (2014) observed positive association of grain yield per plant with number of panicles per plant and weight of 1000 grains.

5.4.2. Path coefficient analysis

Wright (1923) reported that, though the correlation analysis studies are helpful in measuring the relationship between yield and yield component characters, they do not provide exact picture of the direct and indirect effects of such relationship, which can be analysed through path coefficient analysis. Path coefficient analysis is very useful to pinpoint the important characters in rice breeding programme to select desirable characters.

Out of 20 quantitative characters studied for direct and indirect effects on grain yield, high positive direct effect (0.30 to 0.99) was exhibited by six characters namely stem length (0.502), number of tillers per plant (0.372), number of spikelets per panicle (0.981), seed setting per cent (0.401), decorticated grain width (0.528) and decorticated grain L/B ratio (0.833). These results indicating the importance of above characters while practicing selection for improvement of grain yield of Wayanad landraces. These results were supported by Manjunatha *et al.* (2015), who worked on 65 rice genotypes and reported grain yield can be improved by selection for stem length, number of tillers per plant, number of spikelets per panicle, seed setting per cent and L/B ratio of decorticated grain.

Width of leaf blade and weight of 1000 grains were exhibited moderate positive and direct effect (0.20 to 0.29) on grain yield per plant, whereas, four characters namely, number of panicles per plant, length of panicle main axis, stem thickness and time for heading exhibited low to negligible positive direct effect on grain yield per plant. Hence, these characters should be kept in mind along with characters showed high positive direct effect, in the yield improvement

programme. Chandra *et al.* (2009) evaluated 49 diverse rice genotypes and reported direct positive effect of weight of 1000 grains on grain yield per plant.

While the remaining characters namely, length of leaf blade, number of grains per panicle, grain length, grain width, grain L/B ratio, decorticated grain length and time for maturity exhibited direct negative effect on grain yield per plant. Ketan and Sarkar (2014) observed direct negative effect of number of grains per panicle, grain length decorticated grain length on grain yield per plant, and Kumar and Senapati (2013) reported direct negative effect of time for maturity on grain yield per plant.

Character association studies including correlation and path-analysis conducted in this study revealed that, five characters *viz.,* width of leaf blade, stem length, number of panicles per plant, weight of 1000 grains and decorticated grain width showed both positive correlation and positive direct effect on grain yield per plant. It indicated the true relationship between them and direct selection of above characters will be rewarded for yield improvement in rice breeding programmes as suggested by Singh and Narayanam (2009).

The characters namely, number of spikelets per panicle, seed setting per cent and decorticated L/B ratio recorded high positive direct effect, but the correlation is negligible or negative, indicating the direct selection of above traits should be practiced to reduce the undesirable indirect effect as suggested by Singh and Narayanam (2009).

5.5. Cluster analysis based on qualitative characters

Cluster analysis was carried out for qualitative characters of 60 landraces and three check varieties. The genetic association among the genotypes were estimated by Jaccard's similarity coefficients and dendrogram was constructed using UPGMA clustering method based on similarity coefficients, and the results are discussed below.

Cluster analysis categorized 60 landraces and three check varieties into 11 clusters at 74 per cent similarity level. Out of 60 landraces and three check varieties, cluster I was comprised with 11 genotypes, cluster II with two genotypes, cluster III with one genotype, cluster IV with four genotypes, cluster V with five genotypes, cluster VI with 33 genotypes, cluster VII with two genotypes, cluster VIII with one genotype, cluster IX with one genotype, cluster X with two genotypes and cluster XI with one genotype. Ahmed *et al.* (2016) studied 40 rice genotypes and reported four clusters for 19 qualitative characters. Nascimento *et al.* (2011) reported two clusters while studying 146 rice accessions for 12 qualitative characters.

Among the 11 clusters formed, cluster VI was the largest one comprising of 33 genotypes. These 33 genotypes were grouped under same cluster may be because, all these genotypes exhibited similar expression for 22 characters (*i.e.,* purple coleoptile colour, absence of anthocyanin colouration and its distribution in leaf, presence of anthocyanin colouration in leaf sheath, presence of leaf auricles, absence of anthocyanin colouration in auricles, presence of leaf collar, absence of anthocyanin colouration in leaf collar, presence of leaf ligule, split shape of leaf ligule, colourless leaf ligule, absence of anthocyanin colouration of lemma (keel), absence of anthocyanin colour of area below apex of lemma, absence of anthocyanin colouration of stem nodes, absence of panicle awns, its colour and distribution of awns in panicle, presence of secondary branching in panicle, clustered secondary branching in panicle, straw coloured sterile lemma colour, absence of decorticated grain aroma and high gelatinization temperature) out of 38 characters studied. These common characters could be considered as general morphological characters in Wayanad landraces.

Cluster I was the second largest one comprising of 11 genotypes. All the genotypes in this cluster exhibited similar expression for 23 characters (*i.e.,* coleoptile colour, green basal leaf sheath colour, absence of anthocyanin colouration and its distribution in leaf, absence of anthocyanin colouration in leaf sheath, presence of leaf auricles, absence of anthocyanin colouration in leaf

auricles, presence of leaf collar, absence of anthocyanin colouration in leaf collar, presence of leaf ligule, split shape of leaf ligule, colourless leaf ligule, absence of anthocyanin colouration of lemma (keel), absence of anthocyanin colour of area below apex of lemma, absence of anthocyanin colouration of stem nodes, semi-erect attitude of flag leaf blade, presence of secondary branching in panicle, absence of awns, its colour and distribution of awns, straw colour for sterile lemma, absence of aroma for decorticated grain and high gelatinization temperature) out of 38 characters studied.

Cluster II was comprising of only two genotypes namely Gandhakasala and Gandhakasala (dwarf). Gandhakasala is the famous aromatic rice landrace of Wayanad. The two genotypes in this cluster exhibited similar expression for all the qualitative characters, except for pubescence of leaf blade surface and culm attitude. The distinct characters of these two types were aroma for decorticated grain and light green stigma.

Cluster III was comprising of only one landrace (Addy). Out of all the genotypes, Addy came as a separate cluster, might be due to its uniqueness in expressions of characters like erect to semi-erect attitude of branches in panicle, early leaf senescence, short grain, short kernel, medium-bold grain, medium-bold kernel, white kernel colour and medium gelatinization temperature.

Cluster IV was comprising of four genotypes namely, Mulla kuruva, Njavara black, Mahi kuruva and Rasagatham. These four landraces exhibited similar expression for 29 characters (*i.e.*, coleoptile colour, green basal leaf sheath colour, absence of anthocyanin colouration and its distribution in leaf, absence of anthocyanin colouration in leaf sheath, presence of leaf auricles, absence of anthocyanin colouration of leaf auricles, presence of leaf collar, absence of anthocyanin colouration of leaf collar, presence of leaf ligule, split shape of leaf ligule, colourless leaf ligule, absence of anthocyanin colouration of lemma (keel), absence of anthocyanin colouration of apex of lemma, absence of anthocyanin colour of area below apex of lemma, white colour stigma in spikelet, absence of

anthocyanin colouration of stem nodes, semi-erect attitude of flag leaf blade, deflexed curvature of panicle main axis, absence of awns, its colour and distribution awns in panicle, presence of secondary branching in panicle, well exserted panicles, straw colour sterile lemma, absence of aroma in decorticated grain, high gelatinization temperature and non-lodging nature), indicating the reason for sharing single cluster by these genotypes.

Cluster V was comprising of five genotypes namely Thondi-1, Kodu veliyan, Thonnooran thondi, Palthondimatta and Onamottan. These genotypes exhibited similar expression for 28 characters (*i.e.*, purple coleoptile colour, dark intensity of green colour of leaf, absence of anthocyanin colouration and its distribution in leaf, presence of anthocyanin colouration of leaf sheath, presence of leaf auricles, absence of anthocyanin colouration of leaf auricles, presence of leaf collar, absence of anthocyanin colouration of leaf collar, presence of leaf ligule, split shape of leaf ligule, colourless leaf ligule, open type of culm attitude, absence of anthocyanin colouration of lemma (keel), absence of anthocyanin colour of area below apex of lemma, purple colour stigma, absence of anthocyanin colouration of stem nodes, drooping curvature of panicle main axis, absence of awns, its colour and distribution of awns in panicle, presence of secondary branching in panicle, medium leaf senescence, straw sterile lemma colour, medium bold decorticated grain shape, red decorticated grain colour, absence of decorticated grain aroma and high gelatinization temperature).

Cluster VII was comprising of two genotypes namely Kothandon and Chomala-2. These landraces exhibited similar expression for majority of the characters (32) studied (*i.e.*, purple coleoptile colour, light purple basal leaf sheath colour, dark intensity of green colour of leaf, absence of anthocyanin colouration and its distribution in leaf, presence of anthocyanin colouration of leaf sheath, strong pubescence of leaf blade surface, presence of leaf auricles, absence of anthocyanin colouration of leaf auricles, presence of leaf collar, absence of anthocyanin colouration of leaf collar, presence of leaf ligule, split shape of leaf ligule, colourless leaf ligule, semi-erect culm attitude, strong density of

pubescence of lemma of spikelet, absence of anthocyanin colouration of lemma (keel), absence of anthocyanin colour of area below apex of lemma, absence of anthocyanin colouration of stem nodes, semi-erect attitude of flag leaf blade, drooping curvature of panicle main axis, absence of awns, colour and distribution of awns in panicle, presence of secondary branching in panicle, clustered secondary branching, spreading attitude of branches in panicle, well exserted panicles, straw sterile lemma colour, medium bold decorticated grains, light red colour for decorticated grain, absence of aroma for decorticated grain and high gelatinization temperature), indicating the reason for sharing same cluster by these two genotypes.

Cluster VIII was comprising of only one landrace (Thavalakannan). Out of all the landraces, Thavalakannan shared separate cluster, might be due to its distinct characters like anthocyanin colouration at different plant parts including leaf sheath, basal leaf sheath, leaf blade, auricles and ligules. This anthocyanin colouration could be considered as a morphological marker for Thavalakannan, among the Wayanad landraces.

Cluster IX was comprising of only one landrace (Mullan puncha). This landrace also had unique characters like absence of auricles, presence of long awns (up to 7.0 cm) in panicle and black coloured lemma and palea. It was the only landrace without auricles. Presence of long awns was the peculiar character of this landrace. Hence, these characters can be considered as morphological markers to identify Mullan puncha.

Cluster X was comprising of two genotypes namely Jeerakasala and Kayama. The aromatic landrace (Jeerakasala) and non-aromatic landrace Kayama shared a common cluster might be because, these landraces exhibited similar expression for majority of the characters (31) studied (*i.e.,* colourless coleoptile colour, green basal leaf sheath colour, medium intensity of green colour of leaf, absence of anthocyanin colouration and its distribution in leaf, absence of anthocyanin colouration of leaf sheath, presence of leaf auricles, absence of

anthocyanin colouration of leaf auricles, presence of leaf collar, absence of anthocyanin colouration of leaf collar, presence of leaf ligule, split shape of leaf ligule, colourless leaf ligule, semi-erect culm attitude, absence of anthocyanin colouration of lemma (keel), absence of anthocyanin colouration of leaf auricles, absence of anthocyanin colour of area below apex of lemma, white stigma colour, absence of anthocyanin colouration of stem nodes, semi-erect attitude of flag leaf blade, drooping curvature of main panicle axis, straw lemma and palea colour, absence of awns and its distribution in panicle, presence of secondary branching in panicle, clustered secondary branching in panicle, spreading attitude of branches in panicle, white decorticated grain colour, high gelatinization temperature and non-lodging nature).

Cluster XI was comprising of only one landrace (Sugandhamathi). Out of all the genotypes, Sugandhamathi formed a separate cluster, might be due to its specific characters like aroma of decorticated grain, presence of awns (up to 2.1 cm), long slender shape of grain, medium gelatinization temperature. It showed similar characters as Basmati for aroma, grain shape, kernel shape, kernel colour etc., indicating that, it might be brought from other areas and grown in Wayanad under the denomination 'Sugandhamathi'.

5.6. Diversity analysis (Mahalanobis D^2 statistics)

Genetic diversity was assessed among 60 rice genotypes by Mahalanobis D^2 statistics, following the procedure given by Rao (1952) using 20 quantitative characters and the results are discussed below

Based on D^2 statistical analysis all the 60 Wayanad landraces were grouped in seven clusters with variable number of landraces in each cluster, indicating the wide genetic diversity in the landraces under study. Babu and Sreelakshmi (2017) studied 50 rice genotypes and reported six clusters with wide genetic diversity.

It was observed that cluster II had the maximum number of 20 landraces followed by cluster III with 19 genotypes, cluster I with 17 genotypes. Clusters

IV, V, VI, VII were represented by single genotype namely Urulan kayama, Chenthondi, Njavara black and Ambalavayal-2 respectively. This clustering pattern in 60 rice landraces indicated the rich genetic diversity among the landraces collected from the same geographical region (Wayanad). Chandramohan *et al.* (2016) reported the distribution of genotypes originating from same geographical region into different clusters, indicating the broad genetic base of genotypes in that region.

The mean intra and inter cluster distances (D^2 values) among 60 landraces were recorded, where all the inter-cluster distances were higher than the intra-cluster distance, indicating the wider genetic diversity among landraces of different clusters. Islam *et al.* (2017) evaluated 53 rice genotypes and reported higher inter cluster distances than intra cluster distances in a diversity analysis study.

The intra cluster distances ranged from 0.00 to 3258.32, where highest intra cluster distance was observed in cluster III, followed by cluster I (2953.33) and cluster II (2621.65). Landraces belonging to these clusters (III, I and II) with high intra cluster distances, indicated the wide genetic diversity among landraces of these clusters. Hybridization between genotypes in the highly divergent clusters produces hybrid vigour and more desirable segregating breeding materials for the trait studied (Rajesh *et al.*, 2010).

The maximum inter cluster distance (97473.91) was recorded between cluster VI and VII, followed by cluster V and VI (68568.22), Cluster III and VII (60764.42), cluster I and VI (48482.33), Cluster IV and VI (40488.82), cluster III and V (38400.64), indicating the wide genetic diversity among the landraces between these clusters. The genotypes in clusters separated by high cluster distance can be used in hybridization programme to get wide variation among the segregants for a character (Chandramohan *et al.,* 2016). Minimum inter cluster distance was recorded between cluster I and IV (4438.64), followed by cluster II and IV (7068.36), cluster I and II (7385.10) and cluster III and VI (7584.89),

cluster I and V (8332.28), indicating that, the landraces grouped under these clusters were relatively closer, compared to the landraces grouped in other clusters. Hence crossing among the landraces belonging to these clusters may not produce desirable recombinants for a character. Mishra *et al.* (2018) reported wide variation in intra and inter clusters, while working on 36 advanced rice lines.

Cluster mean analysis exhibited wide range of variation for all the quantitative characters under study, where minimum and maximum cluster means were distributed in widely distanced clusters. Among the seven clusters, cluster V recorded maximum mean values for eight characters namely length of leaf blade (62.0 cm), stems thickness (3.8 cm), stem length (160.6 cm), number of spikelets per panicle (298), grain length (8.3 mm), grain width (3.6 mm), decorticated grain length (6.1 mm) and decorticated grain width (3.0). It indicating that, the landraces in this cluster can be used as donors to develop promising lines with above characters through hybridization and also to create further variability in these characters. Cluster VII recorded maximum mean values for five characters namely stem thickness (3.8 cm), length of panicle main axis (28.5 cm), number of grains per panicle (272), seed setting per cent (94.12) and grain yield per plant (23.1 g). Cluster IV recorded maximum mean values for three characters namely, number of tillers per plant (16.6), time of heading (162 days), number of panicles per plant (14.9) and time for maturity (191 days). Cluster VI recorded maximum mean values for two characters *i.e.,* grain L/B ratio (2.67) and decorticated grain L/B ratio. Cluster I and cluster III recorded maximum mean value for only one character each *viz.*, width of leaf blade (0.92 cm) and weight of 1000 grains (30.09 g). Babu and Sreelakshmi (2017) reported that genotypes of different clusters can be used as donors to develop promising lines through hybridization and also to create further variability in these characters. Chandramohan *et al.* (2016) also reported that, varieties can be developed with desirable characters by hybridization between genotypes of different clusters.

5.7. Molecular characterization of aromatic genotypes using SSR (RM) markers

Characterization of rice genotypes based on phenotype has limitations since most of the morphological characters are greatly influenced by environmental factors and developmental stage of the plant. In contrast to morphological characters, molecular markers can reveal abundant difference among genotypes at DNA level, providing a more direct, reliable and efficient tool for varietal characterization (Prabakaran *et al.*, 2010). Among the various PCR based molecular markers, SSRs are more popular because they are highly informative, mostly monolocus, co-dominant, easily analyzed and cost effective (Gracia *et al.*, 2004). Polymorphism at molecular level was done for 15 aromatic rice morphotypes of Wayanad including 12 morphotypes of Gandhakasala and 3 morphotypes of Jeerakasala and compared with a aromatic check variety (Basmati) and two non-aromatic check varieties (Uma and Aathira) using 86 rice microsatellites (RM) markers.

'Basmati' is long grained fine aromatic rice grown in Indo-Gangetic plains. Agro-climatic conditions of the specific geographical area leads to its superior aroma making it unique among other aromatic rice varieties of the country. Wayanad Jeerakasala and Gandhakasala are two unique aromatic rice cultivars evolved in Wayanad, famous for their aroma and the rices of these cultivars are registered as GIs from Kerala. In this study, morphotypes of Wayanad aromatic cultivars (Jeerakasala and Gandhakasala) were compared with Basmati and two non-aromatic genotypes (Uma and Aathira) by SSR marker profiling. The results of molecular characterization are discussed below.

Characterization of aromatic rice morphotypes of Wayanad by SSR profiling revealed genetic polymorphism between the genotypes studied. The profiling with different markers revealed the presence of amplicons ranging from 63 bp (RM248) to 518 bp (RM18941) in size. Maximum number (5) of amplicons was exhibited by RM247, followed by RM85, RM251, RM248 and RM493

producing 4 amplicons each, indicating the informative nature of these SRR markers in polymorphism study. More number of amplicons in case of a few SSR markers indicated that, the genotypes under study are genetically diverse at the particular marker locus. The various sized amplicons observed relate to the allelic diversity at the gene or marker locus. Sajib *et al.* (2012) studied polymorphism in 12 aromatic rice genotypes and reported similar results for SSR marker RM247. Ashraf *et al.* (2016) studied genetic diversity analysis of 18 aromatic rice genotypes using 24 SSR markers and reported variation in number of amplicons ranging from 2 to 6.

Out of 86 SSR (RM) markers used for molecular characterization of aromatic cultivars, 44 markers were found to be polymorphic. The PIC values of polymorphic markers ranged from 0.10 (RM541, RM18, RM18941 and RM28277) to 0.90 in RM247, followed by RM85, RM251 and RM493 with 0.88 PIC value each (Plate 32).

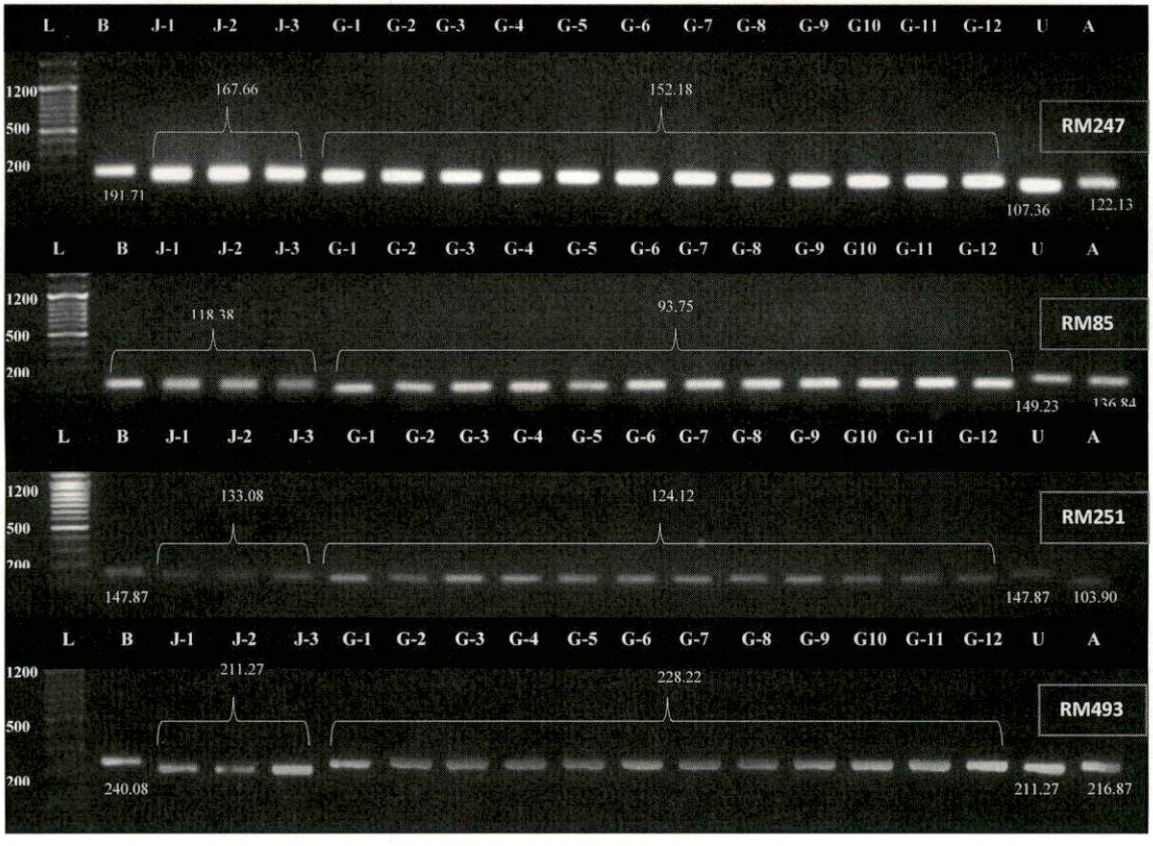


Plate 32. SSR markers exhibiting high PIC value

The PIC value indicated that RM247, followed by RM85, RM251 and RM493 could be considered as the best markers for diversity analysis of these 18 rice genotypes. In earlier study Sajib *et al.* (2012) observed maximum PIC value of 0.64 for SSR marker RM247, while working with 12 aromatic rice genotypes. Hossain *et al.* (2007) and Behera *et al.* (2012) also reported wide range PIC values (0.30 to 0.84 and 0 to 0.976) of SSR marker for aromatic rice genotypes.

a) Markers exhibiting polymorphism between Basmati and traditional aromatic landraces (non-Basmati) of Wayanad

Molecular characterization using SSR markers revealed polymorphism between Basmati and non-Basmati aromatic landraces (Gandhakasala and Jeerakasala) of Wayanad. Diagramatic representation of polymorphism between Basmati and non-Basmati types are given in Fig. 38. Out of 86 SSR (RM) markers, 21 markers (*i.e.,* RM1, RM490, RM11313, RM12941, RM251, RM14723, RM5586, RM402, RM214, RM248, RM223, RM5556, RM257, RM216, RM21, RM26213, RM247, RM9, RM484, RM493 and RM566) distinguished Basmati from Gandhakasala and Jeerakasala. Among the above markers, RM247 exhibited high PIC value (0.90), followed by RM251 (0.88), RM493 (0.88), RM248 (0.82), RM12941 (0.76), RM14723 (0.76), RM402 (0.76), RM214 (0.76), RM216 (0.76), RM9 (0.75), RM21 (0.73) (Table 50). Amplification pattern revealed by three markers *viz.,* RM490, RM12941 and RM5586 are presented in Plate 33. The results indicated that, these polymorphic SSR markers are highly suitable for distinguishing Basmati from aromatic traditional rices of Wayanad. The suitability of RM1 and RM21 to distinguish Basmati from non-Basmati was also earlier reported by Siwach *et al.*, 2004.

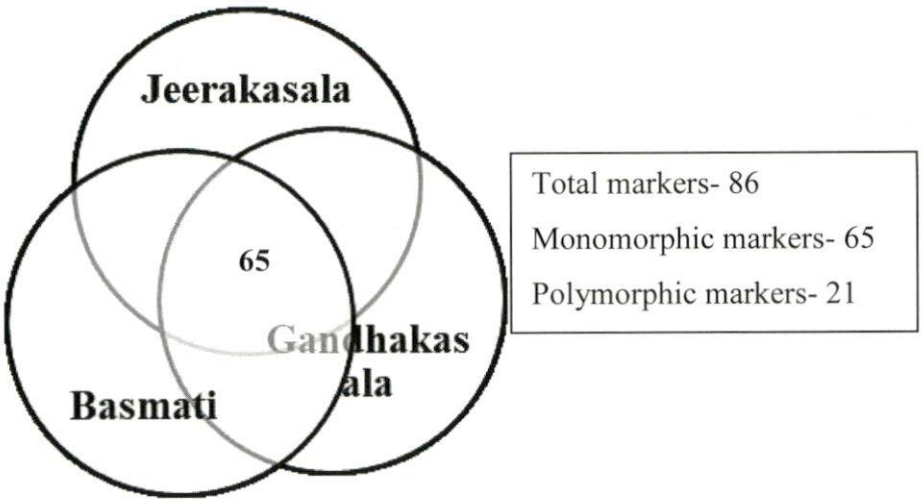


Fig. 38. Diagramatic representation of polymorphism between Basmati and non-Basmati types in SSR profiling

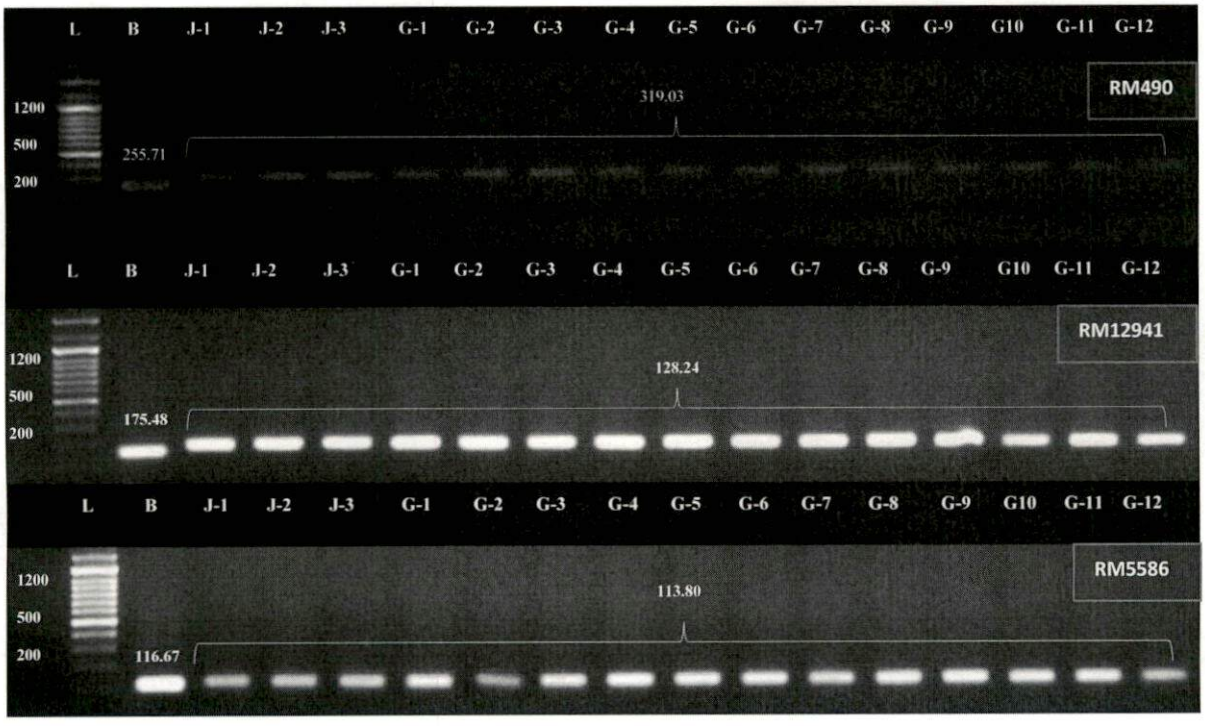


Plate 33. Amplification pattern of SSR markers exhibiting polymorphism between Basmati and traditional aromatic landraces (non-Basmati) of Wayanad

b) Markers exhibiting polymorphism between Jeerakasala and Gandhakasala

Gandhakasala and Jeerakasala, the two famous aromatic cultivars of Wayanad with GI registration. Seventy-nine out of 86 markers showed monomorphic pattern, whereas seven markers were differentiated by seven SSR markers *viz.,* RM85, RM251, RM224, RM26213, RM247, RM493 and RM510 showed polymorphism between these types. Diagramatic representation of polymorphism between Gandhakasala and Jeerakasala are given in Fig. 39. Among these markers, high PIC value (0.90) exhibited by RM 247, followed by RM85 (0.88), RM251 (0.88), RM493 (0.88), RM224 (0.67), RM26213 (0.55) and RM510 (0.49) (Table 50). Hence, these markers could be used to distinguish and differentiate Gandhakasala from Jeerakasala and *vice-versa*. Amplification pattern revealed by three markers *viz.,* RM85, RM224 and RM493 are presented in Plate 34.

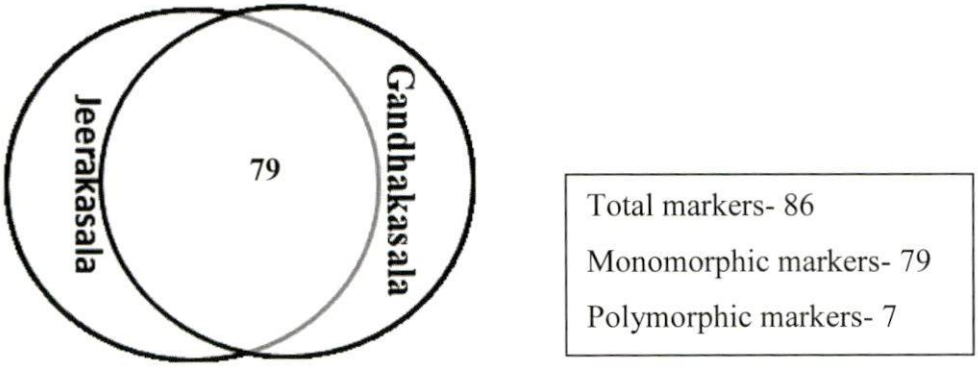


Fig. 39. Diagramatic representation of polymorphism between Jeerakasala and Gandhakasala morphotypes in SSR profiling

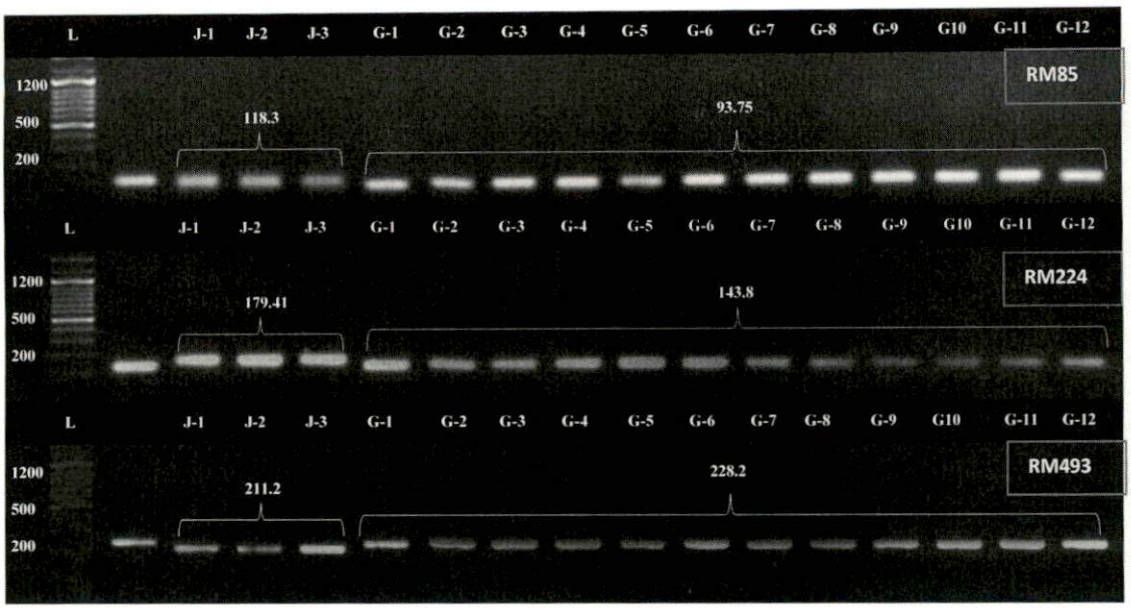


Plate 34. Amplification pattern of SSR markers exhibiting polymorphism between Jeerakasala and Gandhakasala

c) Markers exhibiting polymorphism between Basmati and Jeerakasala

Sixty-three out of 86 markers showed similar amplification pattern between Basmati and Jeerakasala types, whereas 23 markers (RM1, RM490, RM11313, RM12941, RM251, RM14723, RM5586, RM402, RM214, RM248, RM223, RM5556, RM257, RM216, RM21, RM224, RM26213, RM247, RM9, RM484, RM493, RM510 and RM566) showed polymorphism between these types. Diagramatic representation of polymorphism between Basmati and Jeerakasala morphotypes are given in Fig. 40. Among these markers, RM247 exhibited maximum PIC value (0.90), followed by RM251 (0.88), RM493 (0.88), RM248 (0.82), RM12941 (0.76), RM14723 (0.76), RM402 (0.76), RM214 (0.76) (Table 50). Hence, these markers could be used to distinguish and differentiate Basmati and Jeerakasala. Amplification pattern revealed by five markers *viz.*, RM26213, RM490, RM510, RM257 and RM493 are presented in Plate 35.

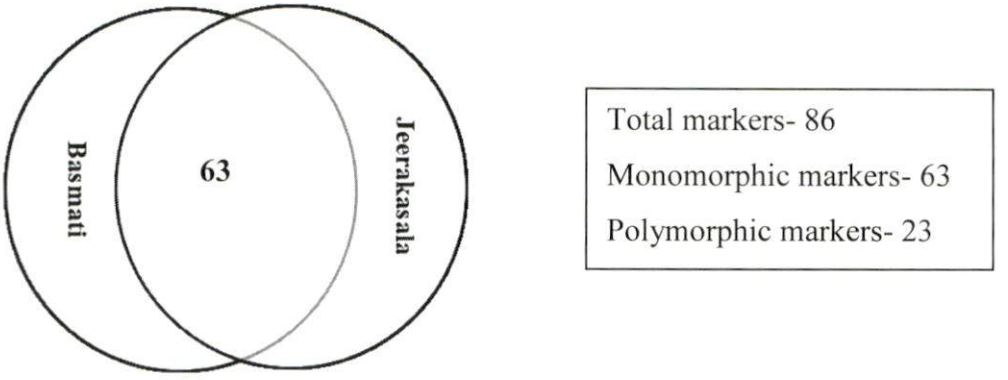


Fig. 40. Diagramatic representation of polymorphism between Basmati and Jeerakasala morphotypes in SSR profiling

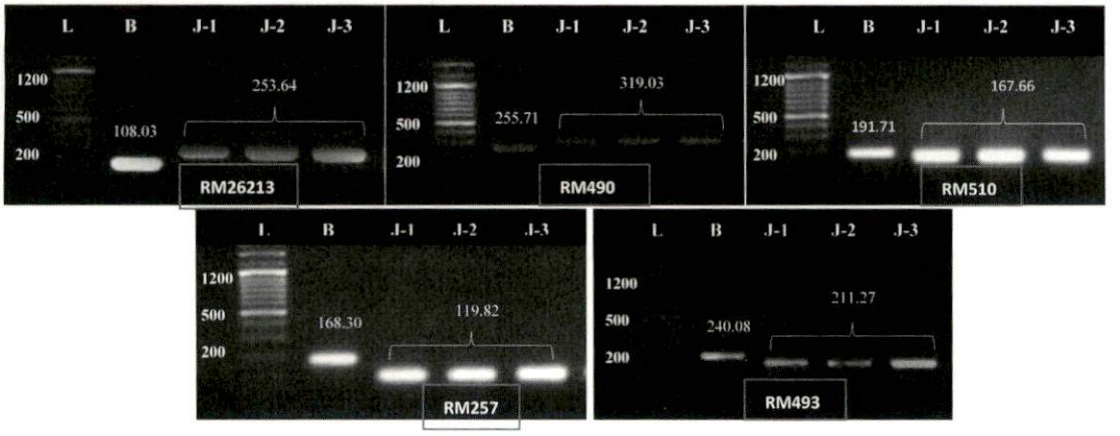


Plate 35. Amplification pattern of SSR markers exhibiting polymorphism between Basmati and Jeerakasala

d) Markers exhibiting polymorphism between Basmati and Gandhakasala

Sixty-four out of 86 markers showed monomorphism between Basmati and Gandhakasala types, whereas 22 markers *viz*., RM1, RM490, RM11313, RM12941, RM85, RM251, RM14723, RM5586, RM402, RM214, RM248, RM223, RM5556, RM257, RM216, RM21, RM26213, RM247, RM9, RM484, RM493 and RM566 showed polymorphism between these types. Diagramatic representation of polymorphism between Basmati and Gandhakasala morphotypes are given in Fig. 41. Among these markers, RM247 exhibited maximum PIC

value (0.90), followed by RM85 (0.88), RM251 (0.88), RM493 (0.88), RM248 (0.82), RM12941 (0.76) (Table 50). These results indicating to use these markers to distinguish and differentiate Basmati and Gandhakasala. Amplification pattern revealed by three markers *viz.,* RM490, RM12941 and RM214 are presented in Plate 36.

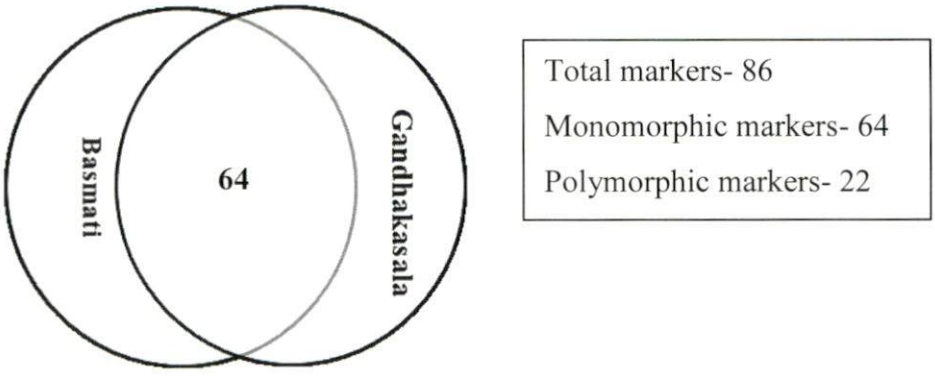


Fig. 41. Diagramatic representation of polymorphism between Basmati and Gandhakasala morphotypes in SSR profiling.

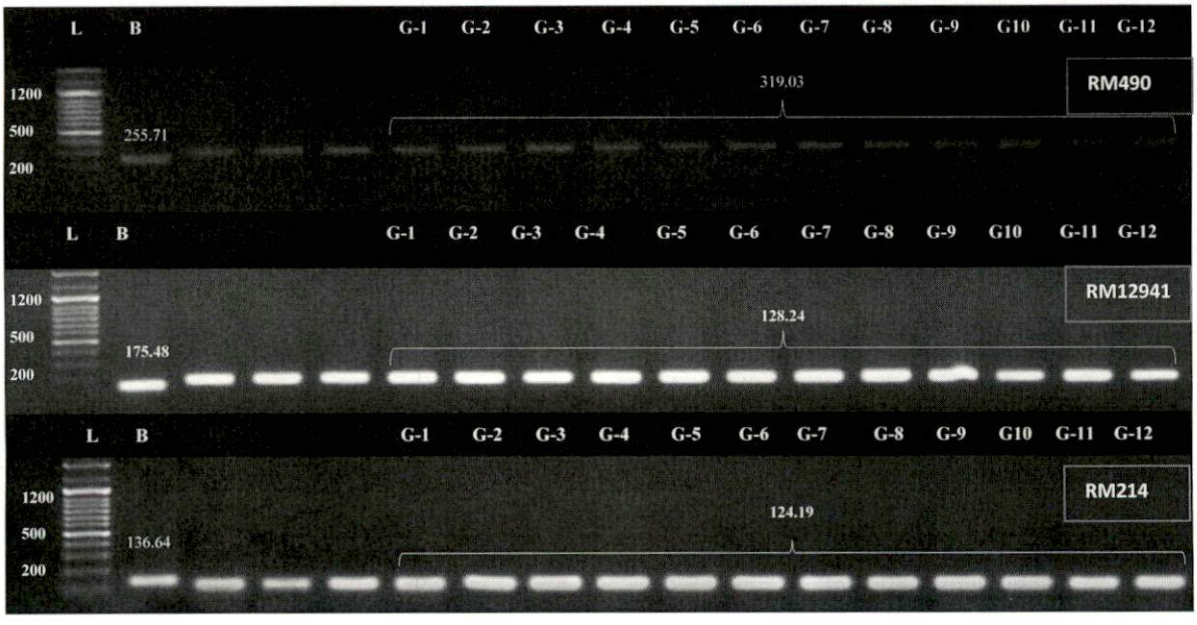


Plate 36. Amplification pattern of SSR markers exhibiting polymorphism between Basmati and Gandhakasala

e) Markers exhibiting polymorphism between aromatic and non-aromatic genotypes

Sixty-three out of 86 markers showed similar amplification pattern between aromatic group comprising Basmati, Jeerakasala and Gandhakasala and non-aromatic group (Uma and Aathira), whereas 23 markers *viz.,* RM12941, RM85, RM14723, RM18941, RM217, RM402, RM541, RM18, RM205, RM216, RM222, RM24866, RM25066, RM17, RM247, RM28277, RM180, RM228, RM302, RM335, RM444, RM484 and RM 535 showed polymorphism between these groups. Diagramatic representation of polymorphism between aromatic group and non-aromatic group are given in Fig. 42. Among these markers, maximum PIC value (0.90) exhibited by RM 247, followed by RM85 (0.88), RM12941 (0.76), RM402 (0.76), RM216 (0.76), RM205 (0.73), RM108 (0.73), RM228 (0.73) (Table 50). Thus these SSR markers could be used to distinguish aromatic genotypes from non-aromatic genotypes. Amplification pattern revealed by three markers *viz.,* RM535, RM444 and RM205 are presented in Plate 37.

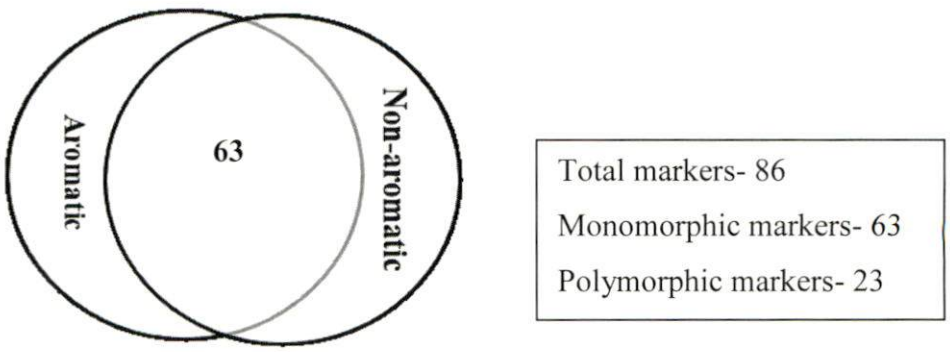


Fig. 42. Diagramatic representation of polymorphism between aromatic group and non-aromatic group in SSR profiling

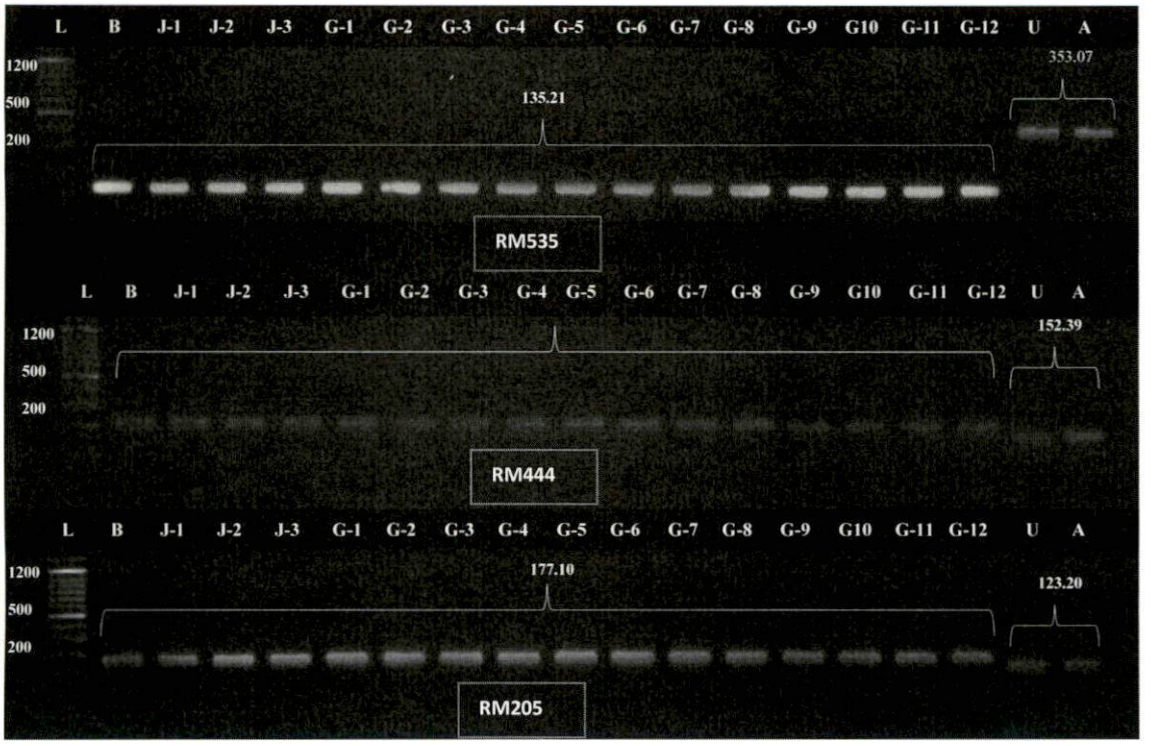


Plate 37. Amplification pattern of SSR markers exhibiting polymorphism between aromatic and non-aromatic groups

The results revealed that, the markers RM18941, RM217, RM541, RM18, RM205, RM222, RM24866, RM25066, RM28277, RM180, RM302, RM335, RM444, RM535, clearly differentiated aromatic and non-aromatic genotypes. These markers should be further studied for confirmation, including more number of genotypes.

The present investigation also revealed that, SSR markers provide adequate power of resolution to distinguish Basmati from traditional aromatic rices of Wayanad (Gandhakasala and Jeerakasala) and it could also serve as a potential tool for the maintenance of purity of these traditional aromatic rices.

Diagramatic representation of polymorphism between 18 rice genotypes in SSR profiling are given in Fig. 43.

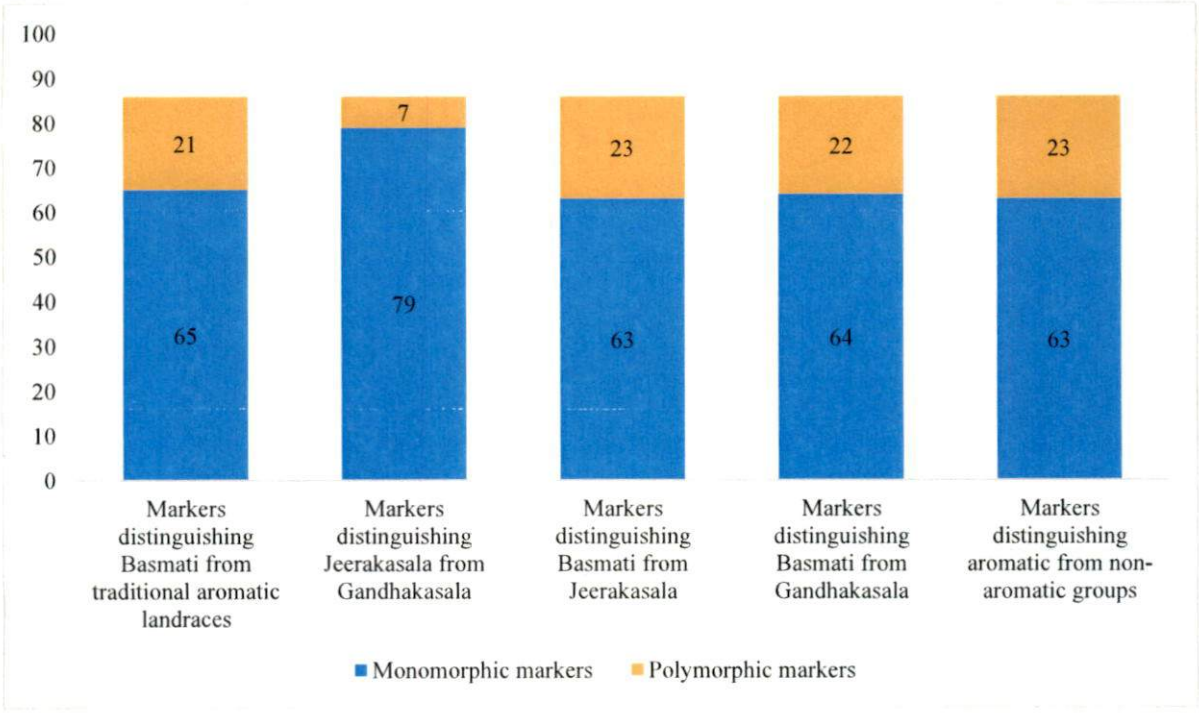


Fig. 43. Diagramatic representation of polymorphism between 18 genotypes in SSR profiling

5.7.1. Cluster analysis

The genetic association among the genotypes were estimated by Jaccard's similarity coefficients (Jaccard, 1908) and Dendrogram was constructed using UPGMA clustering method based on Jaccard's similarity coefficient values and the results are discussed below.

In this study, similarity coefficient ranged between 0.46 to 1.00 (Table 56). Maximum similarity coefficient (1.00) was exhibited within all the Jeerakasala morphotypes and among the Gandhakasala morphotypes. It indicated that, the selected morphotypes of all Gandhakasala were genetically similar and but distinct from the selected morphotypes of Jeerakasala, which in turn were genetically similar among themselves. The lowest similarity coefficient (0.49) was exhibited between Uma and all other genotypes except Basmati.

Among the aromatic genotypes (Basmati, morphotypes of Jeerakasala and morphotypes of Gandhakasala), maximum similarity coefficient (0.88) was recorded between morphotypes of Jeerakasala and morphotypes of Gandhakasala, whereas comparatively lower similarity coefficient (0.63) was recorded between Basmati and non-Basmati traditional landraces (morphotypes of Jeerakasala and morphotypes of Gandhakasala). It clearly indicated that, the traditional aromatic landraces of Wayanad were distinct from Basmati. The comparative proximity of Jeerakasala and Gandhakasala may be due to same geographical origin of Jeerakasala and Gandhakasala. All the aromatic genotypes (Basmati, morphotypes of Jeerakasala and morphotypes of Gandhakasala) were distinct from non-aromatic genotypes (Uma and Aathira). Pervaiz *et al.* (2009) has done diversity analysis in aromatic and non-aromatic genotypes using SSR markers and reported that similarity coefficient ranged between 0.19 to 0.90.

Cluster analysis based on UPGMA categorized 18 genotypes including three check varieties into five clusters at 60 per cent similarity level (Table 57). Among the five clusters, cluster III was the largest comprising 12 Gandhakasala morphotypes namely G-1, G-2, G-3, G-4, G-5, G-6, G-7, G-8, G-9, G-10, G-11 and G-12, followed by cluster IV with three morphotypes of Jeerakasala (J-1, J-2 and J-3) and Cluster I, Cluster II and Cluster V exhibiting one genotype each namely Aathira, Uma and Basmati. Salgotra *et al.* (2015) made cluster analysis in 140 Basmati rice germplasm using SSR markers and reported four clusters.

The results of cluster analysis effectively revealed the uniqueness of Basmati, Jeerakasala, Gandhakasala, Uma and Aathira from each other. Even though the fine grained aromatic variety Basmati exhibited 63 per cent similarity with Gandhakasala and Jeerakasala, it is still different from these traditional aromatic landraces, indicated by forming separate cluster. Hossain *et al.* (2007) studied genetic diversity in aromatic and non-aromatic landraces and reported separate cluster for Basmati type. All the Gandhakasala morphotypes were grouped under same cluster (cluster III); similarly all the Jeerakasala morphotypes were grouped under same cluster (cluster IV), indicating 100 per cent similarity

within them. The non-aromatic genotypes (Uma and Aathira) were separated from all the aromatic genotypes, and grouped under separate clusters individually, indicating less similarity between these non-aromatic genotypes. Genetic diversity in Basmati and non-basmati aromatic rice genotypes using SSR markers revealed higher similarity coefficient in aromatic genotypes as compared to non-aromatic genotypes (Shah *et al.*, 2013).

SUMMARY

6. SUMMARY

The present investigation entitled "Diversity analysis in landraces of rice (*Oryza sativa* L.) in Wayanad through morphological and molecular polymorphism study" was conducted at the Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara, Thrissur and Regional Agricultural Research Station, Ambalavayal, Wayanad during the period 2015- 2018. The study aimed to characterize the rice landraces of Wayanad at morphological level and also to characterize the popular aromatic genotypes of that area at molecular level.

The experimental material comprised of 60 landraces of rice collected from Wayanad and three check varieties namely, Kanchana, Uma and Aathira. The genotypes were raised in Augmented Block Design during *Nancha* season (first crop) of 2016. The experimental material, for molecular characterization using 86 SSR markers, comprised of 18 genotypes, including 12 morphotypes of Gandhakasala, three morphotypes of Jeerakasala and 3 check varieties, including one aromatic variety (Basmati) and two non-aromatic varieties (Uma and Aathira).

The salient findings of the study are:

- Morphological characterization of 38 qualitative characters revealed that all the landraces under study exhibited presence of leaf collar, absence of anthocyanin colouration of leaf collar, presence of leaf ligule, split shape of leaf ligule, absence of anthocyanin colouration for plant parts like lemma (keel), area below apex of lemma, stem nodes and presence of secondary branching in panicle.
- Variation was noticed for majority of the characters namely coleoptile colour, basal leaf sheath colour, intensity of green colour of leaf, anthocyanin colouration of plant parts like leaf, leaf sheath, auricles, ligules, lemma apex, area below apex of lemma, distribution of anthocyanin colouration in leaf, pubescence of leaf blade surface, leaf auricles, culm attitude, density of pubescence of lemma, colour of stigma, attitude of flag leaf blade, curvature of main axis of panicle, lemma and palea colour, presence and colour of awns, distribution of awns in panicle, secondary branching in panicle, attitude of

branches in panicle, panicle exsertion, leaf senescence, sterile lemma colour, shape, colour and aroma of decorticated grain, gelatinization temperature and lodging nature.

- Out of 60 landraces, Thavalakannan was unique, exhibiting very distinct characters like purple blotches on leaf blade, purple auricles and purple ligules. It also exhibited anthocyanin colouration of leaf sheath, basal leaf sheath, lemma apex and stigma.
- Mullan puncha was another distinct landrace with unique characters like absence of auricles, presence of longest awns (up to 7.0 cm) on grains in the whole length of panicles and black colour for lemma and palea, weak secondary branching in panicles and very strong density of pubescence of lemma.
- Morphological characterization of Sugandhamathi revealed that, it is a Basmati type with aroma for decorticated grain, presence of awns on grains (up to 2.1 cm) in the tip of panicles, long slender shape of grain, white kernel colour and medium gelatinization temperature.
- Gandhakasala, Gandhakasala (dwarf), Jeerakasala and Sugandhamathi exhibited aroma for the grains.
- The analysis of variance revealed wide variation for 20 quantitative characters studied namely, length of leaf blade, width of leaf blade, stem thickness, stem length, number of tillers per plant, time for heading, number of panicles per plant, length of main axis of panicle, number of spikelets per panicle, number of grains per panicle, seed setting per cent, weight of 1000 grains, grain length, grain width, grain L/B ratio, decorticated grain length, decorticated grain width, decorticated grain L/B ratio, time for maturity and grain yield per plant.
- Among the 60 landraces, Kanni kayama, Ambalavayal-1, Kothandan, Onamottan, Thondi-2, Chenthadi, Kannali and Thondi-1 exhibited significantly high grain yield per plant, which was on par with that of Uma and Aathira (high yielding check varieties), suggesting that, these landraces could be used as donors for improvement of grain yield. These landraces could also be promoted to grow in regions, where farmers prefer to grow traditional landraces.

- The genetic parameter PCV was higher than GCV for all the characters under study, indicating the influences of environmental factors on these characters. High heritability and high genetic gain was exhibited by the characters like length of leaf blade, width of leaf blade, stem thickness, stem length, number of tillers per plant, number of panicles per plant, length of main axis of panicle, number of spikelets per panicle, number of grains per panicle, seed setting (per cent), 1000 grain weight, grain length, grain L/B ratio, decorticated grain L/B ratio and grain yield per plant, indicating that, these characters are controlled by additive gene action.
- Character association studies including correlation and path-analysis revealed that, five characters *viz.,* width of leaf blade, stem length, number of panicles per plant, weight of 1000 grains and decorticated grain width showed both positive correlation and positive direct effect on grain yield per plant. This indicated that, direct selection of these characters will be rewarding for the improvement of yield in rice breeding programmes.
- Cluster analysis of 38 qualitative characters categorized 60 landraces and three check varieties into 11 clusters at 74 percent similarity level. The genotypes with similar expression for many characters shared a common cluster, whereas the landraces Addy, Thavalakannan, Mullan puncha, Jeerakasala, Kayama and Sugandhamathi shared separate clusters due to difference in expression of their specific characters.
- Genetic diversity analysis by Mahalanobis D^2 statistics categorized 60 landraces in to seven clusters with variable number of landraces in each cluster, indicating the wide genetic diversity in the landraces under study. The inter-cluster distances were higher than the intra-cluster distance, indicating the wider genetic diversity among landraces of different clusters.
- Characterization of aromatic rice landraces by SSR profiling revealed genetic polymorphism between the genotypes studied, with amplicon size ranging from 63 bp to 518.68 bp. Maximum number of amplicons was exhibited by RM247 with five amplicons, followed by RM85, RM251, RM248 and RM493 with 4 amplicons each.

- Out of 86 SSR markers used for molecular characterization, 44 markers were polymorphic and remaining 42 were monomorphic. The PIC values of polymorphic markers varied widely and ranged from 0.10 (RM541, RM18, RM18941 and RM28277) to 0.90 in RM247, followed by RM85, RM251 and RM493 with 0.88 PIC value each. Based on the PIC values, the markers RM247, RM85, RM251 and RM493 were considered as best markers for diversity analysis of these rice genotypes.
- Out of 86 SSR (RM) markers, 21 markers (RM1, RM490, RM11313, RM12941, RM251, RM14723, RM5586, RM402, RM214, RM248, RM223, RM5556, RM257, RM216, RM21, RM26213, RM247, RM9, RM484, RM493 and RM566) distinguished Basmati from traditional aromatic landraces of Wayanad *viz.,* Gandhakasala and Jeerakasala.
- Seven SSR markers (RM85, RM251, RM224, RM26213, RM247, RM493 and RM510) distinguished Gandhakasala from Jeerakasala and *vice-versa.*
- Out of 86, 23 markers (RM1, RM490, RM11313, RM12941, RM251, RM14723, RM5586, RM402, RM214, RM248, RM223, RM5556, RM257, RM216, RM21, RM224, RM26213, RM247, RM9, RM484, RM493, RM510 and RM566) showed polymorphism between Basmati and Jeerakasala.
- Gandhakasala, the aromatic traditional landrace, and Basmati were distinguished by 22 SSR markers (RM1, RM490, RM11313, RM12941, RM85, RM251, RM14723, RM5586, RM402, RM214, RM248, RM223, RM5556, RM257, RM216, RM21, RM26213, RM247, RM9, RM484, RM493 and RM566).
- The aromatic group including Basmati, Jeerakasala and Gandhakasala and non-aromatic group including Uma and Aathira were distinguished by 23 SSR markers (RM12941, RM85, RM14723, RM18941, RM217, RM402, RM541, RM18, RM205, RM216, RM222, RM24866, RM25066, RM17, RM247, RM28277, RM180, RM228, RM302, RM444, RM484 and RM535).
- In molecular characterization study, similarity coefficient ranged between 0.46 to 1.00. Maximum similarity coefficient (1.00) was exhibited within all the Jeerakasala morphotypes and all the Gandhakasala morphotypes, indicating 100 per cent similarity within the selected morphotypes. Within the groups of

traditional aromatic landraces, 88 per cent similarity was exhibited between Gandhakasala and Jeerakasala. Between Basmati and traditional aromatic landraces, 63 per cent similarity was exhibited.

- Cluster analysis based on UPGMA categorized 18 genotypes including three check varieties into five clusters at 60 percent similarity level. Among the five clusters formed, cluster III was the largest one comprising 12 Gandhakasala morphotypes, followed by cluster IV with three Jeerakasala morphotypes and Cluster I, Cluster II and Cluster V with one genotype each namely Aathira, Uma and Basmati. All the Gandhakasala morphotypes were grouped under the same cluster (cluster III). Similarly all the Jeerakasala morphotypes were grouped under same cluster (cluster IV), indicating their genetic distinctness.

SUGGESTED FUTURE LINE OF WORK

- The characterised landraces are to be registered under PPV&FR Act, 2001.
- Milling and cooking quality parameters of Wayanad landraces are to be investigated.
- Yield and yield contributing parameters of the landraces are to be assessed for more number of seasons and better yielding landraces could be promoted for commercial cultivation.
- Confirmation of molecular characterization can be done by including more number of check varieties and also more number of SSR (RM) markers.

REFERENCES

7. REFERENCES

Adheena, R.A., Elsy, C.R., Kumari, K.T.P., Beena, C., Sreelatha, A.K., and Biju, S. 2012. Genotype x environment interaction in aromatic rice (*Oryza sativa* L.) cultivars of Wayanad district of Kerala. M.Sc. (Ag) thesis, Kerala Agricultural University, Thrissur, 164p.

Agahi, K., Fotokian, M.H., and Farshadfar, E. 2007. Correlation and path co-efficient analysis for some yield-related traits in rice genotypes (*Oryza sativa* L.). *Asian J. Plant Sci.* 6: 513-517.

Ahmed, M.S.U., Bashar, M.K., Wazuddin, M., and Shamsuddin, A.K.M. 2016. Agro-morphological qualitative characterization of Jesso-Balam rice (*Oryza sativa* L.) accessions in Bangladesh. *Int. J. Agron. Agril. Res.* 8(1): 50-58.

Ahmed, M.S., Parveen, S., Baktiar, M.H.K., and Siddique, M.A. 2016. Study of qualitative agro-morphological characters of Dhaliboro rice (*Oryza sativa* L.) germplasm of Bangladesh. *Eco-friendly Agril. J.* 8(8): 91-96.

Akagi, H., Yokozeki, Y., AInagaki., and Fujimura, F. 1997. Highly polymorphic micro-satellites of rice consist of AT repeats, and a classification of closely related cultivars with these micro-satellite loci. *Theor. Appl. Genet.* 94: 61-67.

Akhtar, N., Nazir, M.F., Rabnawaz, A., Mahmood, T., Safdar, M.E., Asifand, M., and Rehman, A. 2011. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). *J. Anim. Plant Sci.* 21(4): 660-664.

Alam, M.S., Hassan, L., Islam, M.M., Begum, S.N., and Islam, S.N. 2014. Evaluation of habitual rice (*Oryza sativa* L.) landraces of Bangladesh through different genetic parameters. *Int. J. Innovation Sci. Res.* 11(2): 494-502.

Ali, M., Mian, M. A. K., Rasul, M.G., Miah, M.A.A., Alam, M. Z., and Hossain, M. A. 2012. Genetic diversity in local aromatic rice (*Oryza sativa* L.) genotypes. *Bangladesh J. Plant Breed. Genet.* 25(2): 33-40.

Aljumaili, S.J., Rafii, M.Y., Latif, M.A., Sakimin, S.Z., Arolu, I.W., and Miah, G. 2018. Genetic diversity of aromatic rice germplasm revealed by SSR markers. *Biomed. Res. Int.* 18: 1-11.

Allam, C.R., Jaiswal, H.K., and Qamar, A. 2015. Character association and path analysis studies of yield and quality parameters in Basmati rice (*Oryza sativa* L.). *Bioscan.* 9(4): 1733-1737.

Anderson, J.A., Churchill, G.A., Autrique, J.E., Tanksley, S.D., and Sorrells, M.E. 1993. Optimizing parental selection for genetic linkage maps. *Genome* 36(1): 181-186.

Ashfaq, M. and Khan, A.S. 2012. Genetic diversity in Basmati rice (*Oryza sativa* L.) germplasm as revealed by microsatellite (SSR) markers. *Russian J. Genet.* 48(1): 53-62.

Ashraf, H., Husaini, A.M., Bhat, M.A., Parray, G.A., Khan, S., and Ganai, N.A. 2016. SSR based genetic diversity of pigmented and aromatic rice (*Oryza sativa* L.) genotypes of the Western Himalayan region of India. *Physiol. Mol. Biol. Plants* 22(4): 547-555.

Babu, P.M., Chandramohan, Y., Ravindrababu, V., and Arunakumari, C.H. 2017. Assessment of genetic variability for yield and bran oil content in segregating generations of rice. *Int. J. Curr. Microbiol. Appl. Sci.* 6(11): 117-124.

Babu, R.P. and Sreelakshmi, C.H. 2017. Genetic divergence studies for yield and quality traits in rice (*Oryza sativa* L.). *J. Rice Res.* 10(1): 17-20.

Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G., and Shankar, A.S. 2012a. Correlation and path analysis studies in popular rice hybrids of India. *Int. J. Sci. Res. Publ.* 2(3): 1-5.

Babu, V.R., Shreya, K., Dangi, K.S., Usharani, G., and Nagesh, P. 2012b. Genetic variability studies for qualitative and quantitative traits in popular rice (*Oryza sativa* L.) hybrids of India. *Int. J. Sci. Res. Publ.* 2(6): 1-5.

Bagheri, N., Jelodar, N.B., and Pasha, A. 2011. Path coefficient analysis for yield and yield components in diverse rice (*Oryza sativa* L.) genotypes. *Biharean Biologist* 5(1): 32-35.

Banumathy, S., Manimaran, R., Sheeba, A., Manivannan, N., Ramya, B., Kumar, D., and Ramasubramanian, G.V. 2010. Genetic diversity analysis of rice germplasm lines for yield attributing Traits. *Elect. J. Plant Breed.* 1(4): 500-504.

Bashar, K.K., Ivy, N.A., Mian, M.A.K., Iftekharuddaula, K.M., and Hoque, M.A. 2017. Assessment of genetic diversity among selected aromatic rice genotypes using SSR markers. *Int. J. Biosci.* 11(3): 184-198.

Becerra, V., Paredes, M., Ferreira, M.E., Gutierrez, E., and Diaz, L.M. 2017. Assessment of the genetic diversity and population structure in temperate *japonica* rice germplasm used in breeding in Chile, with SSR markers. *Chilean J. Agric. Res.* 77(1): 15-26.

Behera, L., Sahu, R.K., Datta, S., Nanda, A., Sahu, S.C., Pradhan, S.K., Rao, G.J.N., and Singh, O.N. 2012. DNA fingerprinting and assessment of genetic diversity of high yielding rice varieties using microsatellite markers. *Int. J. Agric. Env. Biotechnol.* 5(2): 89-99.

Behera, M., Monalisa, S.P., Bastia, D.N., and Kulkarni, C.C. 2017. Correlation and path analysis studies in aerobic rice. *Int. J. Curr. Microbiol. Appl. Sci. 6*(8): 2851-2856.

Bhinda, M.S., Karnwal, M.K., and Choudhary, M.K. 2017. Estimates of genetic variability, heritability and genetic advance for yield contributing and quality traits in advance breeding lines of rice (*Oryza sativa* L.). *Int. J. Adv. Biol. Res.* 7(2): 229-233.

Bisne, R., Sarawgi, A.K., and Verulkar, S.B. 2009. Study of heritability, genetic advance and variability for yield contributing characters in rice. *Bangladesh J. Agril. Res.* 34(2): 175-179.

Biswas, B.K., Alam, N., da Silva, J.A.T., Haque, M.M., Azad, M.A.K., and Hossain, M.K. 2012. Existing status and genetic divergence of agro-morphological characters in Bangladeshi fine rice. *Int. J. Plant Breed.* 6(2): 129-134.

Bornare, S.S., Mittra, S.K., and Mehta, A.K. 2014. Genetic variability, correlation and path analysis of floral, yield and its component traits in CMS and restorer lines of rice (*Oryza sativa* L.). *Bangladesh J. Bot.* 43(1): 45-52.

Bose, L.K. and Pradhan, S.K. 2005. Genetic divergence in deep water rice genotypes. *J. Cent. Eur. Agric.* 6(4): 635-640.

Bostein, D., White, R.L., Skolnick, M., and Davis, R.W. 1980. Construction of genetic linkage map in man using restriction fragment length polymorphism (RFLP). *Am. J. Hum. Genet.* 32: 314-331.

Bueren, L.E.T., Struik, P.C., and Jacobsen, E. 2002. Ecological concepts in organic farming and their consequences for an organic crop ideotype. *Neth. J. Agric. Sci.* 50: 1-26.

Burman, M., Nair, S.K., and Sarawgi, A.K. 2018. Genetic diversity in upland rice germplasm accessions (*Oryza sativa* L.) of Chhattisgarh, India. *Int. J. Curr. Microbiol. Appl. Sci.* 7(3): 2113-2117.

Chakrabarty, S.K., Joshi, M.A., Singh, Y., Maity, A., Vashisht, V., and Dadlani, M. 2012. Characterization and evaluation of variability in farmers' varieties of rice from West Bengal. *Indian J. Genet.* 72(2): 136-142.

Chakravorty, A. and Ghosh, P. D. 2012a. Genetic divergence in landraces of rice (*O. sativa* L.) of West Bengal, Indian. *J. Crop Weed.* 8(2): 23-28.

Chakravorty, A. and Ghosh, P.D. 2012b. Characterization of Landraces of rice following DUS guidelines. *Res. Plant Biol.* 2(6): 30-40.

Chambers, M. and Avoy, M. 2000. Comparison of microsatellites and amplified fragment length polymorphism markers for parentage analysis. *Mol. Ecol.* 9: 1037-1048.

Chandra, B.S., Reddy, T.D., Ansari, N.A., and Kumar, S.S. 2009. Correlation and path analysis for yield and yield components in rice (*Oryza sativa* L.). *Agric. Sci. Digest.* 29(1): 45-47.

Chandra, K., Nilanjaya, and Kumar, P. 2015. Study of interrelationship and cause-effect of morpho-physiological characters of rice under normal and aerobic conditions. *Ecoscan* 9(1): 643-651.

Chandramohan, Y., Srinivas, B., Thippeswamy, S., and Padmaja, D. 2016. Diversity and variability analysis for yield parameters in rice (*Oryza sativa* L.) genotypes. *Indian J. Agric. Res.* 50 (6): 609-613.

Chauhan, J.S., Chuahan, V.S., and Lodh, S.B. 1994. Studies on milling quality components of rainfed upland rice. *Oryza* 31: 50-52.

Chen, X., Temnykh, S., Xu, Y., Cho, Y.G., and McCouch, S.R. 1997. Development of a microsatellite framework map providing genome-wide coverage in rice (*Oryza sativa* L.). *Theor. Appl. Genet.* 95: 553-567.

Chouhan, S.K., Singh, A.K., Aparajita, S., Ram, M., Singh. P.K., and Singh, N.K. 2014. Characterization and evaluation of *Oryza nivara* and *Oryza rufipogon. Bioscan* 9(2): 853-858.

Das, S. and Ghosh, A. 2010. Characterization of rice germplasm of West Bengal. *Oryza* 47(3): 201-205.

Dellaporta, S.C., Wood, J., and Hicks, T.B. 1983. A plant DNA mini preparation: Version II. *Plant Mol. Biol. Rep.* 1: 19-21.

Devi, G.N., Babu, V.R., Padmavathi, G., and Sunitha, T. 2015. Genetic diversity in grain quality traits of rice genotypes. *J. Rice Res.* 8(1): 6-14.

Dhanwani, R.K., Sarawgi, A.K., Solanki, A., and Tiwari, J.K. 2013. Genetic variability analysis for various yield attributing and quality traits in rice (*O. sativa* L.). *Bioscan* 8(4): 1403-1407.

Dhurai, S.Y., Reddy, D.M., and Bhati, P.K. 2014. Correlation and path coefficient analysis for yield and quality traits under organic fertilizer management in rice (*Oryza sativa* L.). *Electr. J. Plant Breed.* 5(3): 581-587.

Dewey, J.R. and Lu, K.H. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.* 51: 515-518.

Ekka, R.E., Sarawgi, A.K., and Kanwar, R.R. 2013. Genetic divergence in traditional rice accessions in Chhattisgarh. *Int. J. Plant Sci.* 8(2): 419-422.

Elsy, C.R., Devadas, V.S., Thomas, J., and Sumalatha, T.V. 2010. Intellectual property protection of speciality rices of Kerala as Geographical Indications. In: Yasodharan, E. P. (ed.), *Proceedings of the Twenty Second Kerala Science Congress*. Kerala State Council for Science, Technology and Environment, Government of Kerala, pp. 8-9.

Elsy, C.R. 2012. Geographical Indications - A marketing tool for unique goods from specific environments. The Kerala Environment Congress, Centre for Environment and Development, Thiruvananthapuram, India, pp. 247-254.

FAO (Food and Agriculture Organization), 2016. *FAO rice market monitor*. Trade and markets division, Food and Agriculture Organization of the United Nations, 19(2): 1-34.

Fukrei, K.P., Kumar, A., Tyagi, W., Rai, M., and Pattanayak, A. 2011. Genetic variability in yield and its components in upland rice grown in acid soils of North East India. *J. Rice Res.* 4(1): 4-7.

Garg, H.S., Kumar, R., and Singh, A.K. 2016. Genetic diversity of drought tolerant rice (*Oryza sativa* L.) genotypes under drought stress and non-stress condition. *Ecoscan* 10(1): 277-283.

Garland, S.H., Lewin, L., Abedinia, M., Henry, R., and Blakeney, A. 1999. The use of microsatellite polymorphisms for the identification of Australian breeding lines of rice (*Oryza sativa* L.). *Euphytica* 108: 53-63.

Gauthier, P., Gouesnard, B., Dallard, J., Redaelli, R., Rebourg, C., Charcosset, A., and Boyat, A. 2002. RFLP diversity and relationships among traditional European maize populations. *Theo. Appl. Genet.* 105: 91-99.

Ghebru, B., Schmidt, R.J., and Bennetzen, J.L. 2002. Genetic diversity of Eritrean sorghum landraces assessed with simple sequence repeat (SSR) markers. *Theor. Appl. Genet.* 105: 229-236.

Giri, S.P. and Pandey, A. 2017.Characterization of aromatic short grain rices of eastern Uttar Pradesh for qualitative traits. *J. Pharmacognosy and Phytochem.* 1: 180-183.

Giri, S.P., Pandey, A., Singh, V.N., Verma, D.K., Tripathi, R.M., Singh, A.K., Maurya, M.L., and Singh, R.V. 2017. DUS characterization of Narendra Lahar: a new high yielding rice variety. *Int. J. Curr. Microbiol. Appl. Sci.* *6*(11): 5444-5453.

GOI (Govt. of India). 2017. *Annual report: 2016-17.* Ministry of Agriculture and Farmers Welfare. Government of India, New Delhi, 157p.

GOK (Govt. of Kerala). 2017. *Agricultural statistics: 2016-17.* Department of Economics and Statistics. Government of Kerala, Thiruvananthapuram, 220p.

Gour, L., Koutu, G.K., Singh, S.K., Patel, D.D., Shrivastava, A., and Singh, Y. 2017. Genetic variability, correlation and path analyses for selection in elite breeding materials of rice (*Oryza sativa* L.) genotypes in Madhya Pradesh. *Pharma Innovation J.* 6(11): 693-696.

Gracia, A. A. F., Benchimol, L. L., Antonica, M. M., Geraldi, I. O., and Deuza, A. P. 2004. Comparison of RAPD, RFLP, AFLP and SSR markers for diversity studies in tropical maize inbred lines. *Euphytica* 108: 53-63.

Guedira, B.G.L., Thompson, J.A., Nelson, R.L., and Warburton, M.L. 2000. Evaluation of genetic diversity of soybean introductions and North American ancestors using RAPD and SSR markers. *Crop Sci.* 40: 815-823.

Gupta, R., Sangeetatetwar, and Nair, S.K. 2014. Agro-morphological characterization of rice germplasm of Chhattisgarh. *Int. J. Plant Sci.* 9(1): 257-262.

Guru, T., Padma, V., Reddy, D.V.V., Rao, P.R., and Rao, D.S. 2016. Correlation and path coefficient analysis for grain yield and other component traits in rice genotypes. *Int. J. Agric. Sci. Res.* 6(5): 363-370.

Halder, T., Hoque, M.E., Islam, M.M., Ali, L., and Chowdhury, A.K. 2016. Morpho-molecular characterization of Bangladeshi local Boro rice (*Oryza sativa* L.) genotypes. *Bangladesh J. Plant Breed. Genet.* 29(2): 1-9.

Hanson, W.D., Robinson, H.F., and Comstock, R.E. 1956. Biometrical studies of yield in segregating population of Korean Lespadeza. *Agron. J.* 48: 268-272.

Haque, S., Pradhan, S. K., Anandan, A., and Singh, O. N. 2014. Morphometric diversity studies in rice genotypes for yield and yield attributing characters under drought. *Int. J. Sci. Technol.* 2(8): 139-142.

Hosan, S.M., Sultana, N., Iftekharuddaula, K.M., Ahmed, M.N.U., and Mia, S. 2010. Genetic divergence in landraces of Bangladesh rice (*Oryza sativa* L.). *Agric.* 8(2): 28-34.

Hossain, M.M., Islam, M.M., Hossain, H., Ali, M.S., da Silva, J.A.T., Komamine, A., and Prodhan, S.H. 2012. Genetic diversity analysis of aromatic landraces of rice (*Oryza sativa* L.) by microsatellite markers. *Genes, Genomes and Genomics* 6(1): 42-47.

Hossain, M.Z., Rasul, M.G., Ali, M.S., Iftekharuddaula, K.M., and Mian, M.A.K. 2007. Molecular characterization and genetic diversity in fine grain and aromatic landraces of rice (*Oryza sativa* L.) using microsatellite markers. *Bangladesh J. Genet Plant Breed.* 20(2): 01-10.

IRRI (International Rice Research Institute). 1996. Standard Evaluation System for Rice (3rd Ed.). *International Rice Testing Programme*. Los Banos, Laguna, Philippines, 43p.

Islam, M.A., Raffi, S.A., Hossain, M.A., and Hasan, A.K. 2015.Analysis of genetic variability, heritability and genetic advance for yield and yield associated traits in some promising advanced lines of rice. *Prog. Agric*. 26: 26-31.

Islam, M.M.U., Saha, P.S., Chakrobarty, T., Saha, N.K., Islam, M.S., and Salam, M.A. 2017. Genetic diversity of aromatic rice in Bangladesh. *Res. Agric. Livest. Fish.* 4(1): 1-6.

Jain, S., Jain, R.K., and McCouch, S.R. 2004. Genetic analysis of Indian aromatic and quality rice (*Oryza sativa* L.) germplasm using panels of fluorescently-labeled microsatellite markers. *Theor. Appl. Genet.* 109: 965-977.

Jaccard, P. 1908. *Nourelles recherché sur la distribution florale. Bull. Vaud. Sci. Nat.* 44: 223-270.

Jennings, P.R., Coffman, W.R., and Kauffman, H.E. 1979. *Grain quality, international rice improvement.* International Rice Research Institute, Manila, Philippines, pp. 101-120.

Johnson, H.W., Robinson, H.F., and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J.* 47: 314-318.

Joshi, R.K. and Behera, L. 2006. Identification and differentiation of indigenous non-Basmati aromatic rice genotypes of India using microsatellite markers. *Afr. J. Biotechnol*. 6(4): 348-354.

Kalyan, B., Krishna, K.V.R., and Rao, L.V.S. 2017a. DUS characterization for germplasm of rice. *Int. J. Curr. Microbiol. Appl. Sci.* 6(10): 3480-3487.

Kalyan, B., Krishna, K.V.R., and Rao, L.V.S. 2017b. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.) germplasm. *Int. J. Pure Appl. Biosci.* 5(5): 1619-1624.

Kalyan, B., Krishna, K.V.R., and Rao, L.V.S. 2017c. Path coefficient analysis for yield and yield contributing traits in rice (*Oryza sativa* L.) genotypes. *Int. J. Curr. Microbiol. Appl. Sci.* 6(7): 2680-2687.

Karpagam, V., Jebaraj, S., Rajeswari, S., and Vanniarajan, C. 2014. Role of root and yield characters under drought stress in rice (*Oryza sativa* L.). *Electr. J. Plant Breed.* 5(4): 760-764.

KAU (Kerala Agricultural University). 2011. *Package of Practices Recommendations: Crops* (14th Ed.). Kerala Agricultural University, Thrissur, 360p.

Ketan, R. and Sarkar, G. 2014. Studies on variability, heritability, genetic advance and path analysis in some indigenous Aman rice (*Oryza sativa* L.). *J. Crop Weed.* 10(2): 308-315.

Kioko, W.F., Mawia, M.A., Piero, N.M., Muriira, K.G., Wavinya, N.D., Chemutai, L.R., Felix, M., Makori, A.W., and Mwenda, N.S. 2015. Phenotypic characterization on selected Kenyan and Tanzanian rice (*Oryza sativa* L.) populations based on grain morphological traits. *J. Rice Res.* 3(4): 1-6.

Kole, P.C., Chakraborty, N.R., and Bhat, J.S. 2008. Analysis of variability, correlation and path coefficients in induced mutants of aromatic non-Basmati rice. *Trop. Agril. Res. Ext.* 11: 60-64.

Krupa, K. N., Shashidhar, H.E., Dalawai, N., Reddy, M., and Swamy, H.V. 2017. Molecular marker based genetic diversity analysis in rice genotypes (*Oryza sativa* L.) using SSR markers. *Int. J. Pure Appl. Biosci.* 5(2): 668-674.

Kumar, A., Kumar, S., and Parmhansh, P. 2016. Characterization of rice germplasm of North Bihar for panicle morphology and grain characteristic traits under rainfed lowland and deep water condition. *Ecol. Environ. Conserv.* 22(3): 1233-1236.

Kumar, A. and Senapati, B.K. 2013. Genetic parameters and association studies for important quantitative traits in advanced lines of Sambamahsuri derivatives. *J. Crop Weed* 9(1): 156-163.

Kumar, B., Kour, A., and Laxami, J. 2017. Genetic diversity for agro-morphological traits in rice germplasm. *Electr. J. Plant Breed.* 8(4): 1216-1222.

Kumar, C. and Nilanjaya. 2014. Correlation and path coefficient analysis of yield components in aerobic rice (*Oryza sativa* L.). *Bioscan* 9(2): 907-913.

Kumar, H.R.U., Gangaprasad, S., Raghavendra, P., and Kumar, B.M.D. 2017. Revealing genetic variability and trait association studies in landraces of rice (*Oryza sativa* L.) under controlled and drought conditions. *Int. J. Curr. Microbiol. Appl. Sci. 6*(8): 737-747.

Kumar, R., Babu, G.S., Rai, S.K., and Sandhya. 2015. Genetic variability and divergence studies in elite rice genotypes for biometrical traits. *Ecoscan* 9(1): 209-212.

Kumar, R., Singh, A.K., Kumar, A., and Radha. 2012. Evaluation of genetic diversity in rice using simple sequence repeats (SSR) markers. *Afr. J. Biotechnol.* 11(84): 14956-14995.

Kumar, V., Rastogi, N.K., Sarawgi, A.K., Chandraker, P., Singh, P.K., and Jena, B.K. 2016. Agro-morphological and quality characterization of indigenous and exotic aromatic rice (*Oryza sativa* L.) germplasm. *J. Appl. Nat. Sci.* 8(1): 314-320.

Lakshmi, M.V., Suneetha, Y., Yugandhar, G.Y., and Lakshmi, N.V. 2014. Correlation studies in rice (*Oryza sativa* L.). *Int. J. Genet. Eng. Biotechnol.* 5(2): 121-126.

Latha, M., Nizar, A.M., Abraham, Z., John, J.K., Nair, R.A., Mani, S., and Dutta, M. 2013. Rice landraces of Kerala state of India: a documentation. *Int. J. Biodivers. Conserv.* 5(4): 250-263.

Lenka, D. and Mishra, B. 1973. Path coefficient analysis of yield in rice varieties. *Ind. J. Agric. Sci.* 43: 376-379.

Limbani, P.L., Gangani, M.K., and Pandya, M.M. 2017. Genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.). *Int. J. Pure Appl. Biosci.* 5 (6): 1364-1371.

Madhukar, P., Raju, C.H.S., Senguttuvel, P., and Reddy, S.N. 2017. Association and path analysis of yield and its components in aerobic rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. Appl. Sci.* 6(9): 1335-1340.

Mahalanobis, P.C. 1928. A Statistical Study of Chinese Heads Measurement. *J. Asiatic. Soc. Bengal* 25: 301-317.

Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proceedings of National Institute of Sciences*, India. 12: 49-55.

Mamata, K., Rajanna, M.P., and Savita, S.K. 2018. Assessment of genetic parameters for yield and its related traits in f2 populations involving traditional varieties of rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. Appl. Sci. 7*(1): 2210-2217.

Manjunatha, G.A., Vanaja, T., Vasudevan, N.R., and Rao, G.V.S. 2015a. Organic varietal traits in rice (*Oryza sativa* L.) through farmer participatory evaluation strategy. *Ann. Plant Physiol.* 29(2): 1-5.

Manjunatha, G.A., Vanaja, T., Vasudevan, N.R., and Rao, G.V.S. 2015b. Variability study on physico-chemical and cooking quality of rice (*Oryza sativa* L.) genotypes under organic management. *Ann. Plant. Physiol.* 29(2) 6-10.

Manjunatha, G.A., Vanaja, T., Naik, J., Kumar, A.S.A., and Vasudevan, N.R. 2016. Identification of rice genotypes best suited for the development of organic varieties and identification of current varieties best suited for organic farming. *J. Org.* 3(1): 16-24.

Manjunatha, G.A., Kumar, M.S., and Jayashree, M. 2017. Character association and path analysis in rice (*Oryza sativa* L.) genotypes evaluated under organic management. *J. Pharmacognosy Phytochem.* 6(6): 1053-1058.

Mathure, S., Shaikh, A., Renuka, N., Wakte, K., Jawali, N., Thengane, T., and Nadaf, A. 2011. Characterisation of aromatic rice (*Oryza sativa* L.) germplasm and correlation between their agronomic and quality traits. *Euphytica* 179: 237-246.

McCouch, S.R., Chen, X., Panaud, O., Temnykh, S., Xu, Y., Cho, Y.G., Huang, N., Ishii, T., and Blair, M. 1997. Microsatellite marker development, mapping and applications in rice genetics and breeding. *Plant Mol. Biol.* 35(2): 89-99.

McCouch, S. R., Chen, X., and Cho, Y. G. 2002. Sequence divergence of rice microsatellites in *Oryza* and other plant species. *Mol. Genet. Genomics* 268: 331-343.

Meti, N., Samal, K.C., Bastia, B.N., and Rout, G.R. 2013. Genetic diversity analysis in aromatic rice genotypes using microsatellite based simple sequence repeats (SSR) marker. *Afr. J. Biotechnol.* 12(27): 4238-4250.

Mishra, A., Kumar, P., Sengar, R.S., Kumar, P., Singh, R., Chaudhary, R., Kumar, A., and Fatima, P. 2016. Assessment of diversity by using morphological, biochemical and molecular approaches of selected basmati rice (*Oryza sativa L.*) varieties. *J. Appl. Nat. Sci.* 8(1): 69-76.

Mishra, A.K., Singh, P.K., Kumar, R., Kumar, P., Singh, R., Kumar, P., Kumar, A., and Kumar, A. 2018. Genetic divergence study in advance *indica* rice (*Oryza sativa* L.) lines for yield and quality attributes. *Int. J. Curr. Microbiol. Appl. Sci.* 7: 2924-2933.

Myint, K.M., Courtois, B., Risterucci, A.M., Frouin, J., Soe, K., Thet, K.M., Vanavichit, A., and Glaszmann, J.C. 2012. Specific patterns of genetic diversity among aromatic rice varieties in Myanmar. *Rice* 5(20): 1-13.

Nadia, I., Mohiuddin, A.K.M., Sultana, S., and Ferdous, J. 2014. Diversity analysis of *indica* rice accessions (*Oryza sativa* L.) using morphological and SSR markers. *Ann. Biol. Res.* 5(11): 20-31.

Nagaraju, C., Sekhar, M.R., Reddy, K.H., and Sudhakar, P. 2013. Correlation between traits and path analysis coefficient for grain yield and other components in rice (*Oryza sativa* L.) genotypes. *Int. J. Appl. Biol. Pharma. Technol.* 4(3): 137-142.

Naik, D., Sao, A., Sarawgi, A.K., and Singh, P. 2006. Genetic divergence studies in some indigenous scented rice (*Oryza sativa* L.) accessions of central India. *Asian J. Plant Sci.* 5(2): 197-200.

Nascimento, W.F., Silva, E.F., and Veasey, E.A. 2011. Agro-morphological characterization of upland rice accessions. *Sci. Agric.* 68(6): 652-660.

Naseem, I., Khan, A.S., and Akhter, M. 2014. Correlation and path coefficient studies of some yield related traits in rice (*Oryza sativa* L.). *Int. J. Sci. Res. Pub.* 4(4): 1-5.

Nath, J.K., Sarker, U., Miarr, M.A.K., and Hossain, T. 2008. Genetic divergence in traditional *Aman* rice. *Ann. Bangladesh Agric.* 12(1): 51-60.

Nayak, A.R., Chaudary, D., and Reddy, J.N. 2001. Correlation and path analysis in scented rice (*Oryza sativa* L.). *Indian J. Agric. Res.* 35(3): 186-189.

Olufowote, J.O., Xu, Y., Chen, X., Park, W.O., Beachell, H.M., Dilday, R.H., Goto, M., and McCouch, S.R. 1997. Comparative evaluation of within cultivar variation in rice (*Oryza sativa* L.) using microsatellite and RFLP markers. *Genome* 40: 370-378.

Ovung, C.Y., Lal, G.M., and Rai, P.K. 2012. Studies on genetic diversity in rice (*Oryza sativa* L.). *J. Agril. Technol.* 8(3): 1059-1065.

Pachauri, A.K., Sarawgi, A.K., Bhandarkar, S., and Ojha, G.C. 2017. Agro-morphological characterization and morphological based genetic diversity

analysis of Rice (*Oryza sativa* L.) germplasm. *J. Pharmacognosy Phytochem.* 6(6): 75-80.

Padmaja, D., Radhika, K., Rao, L.V.S., and Padma, V. 2008. Studies on variability, heritability and genetic advance for quantitative characters in rice (*Oryza sativa* L.). *J. Plant Genet. Resour.* 21(3): 196-198.

Pan, R. Z. and Dong, Y. D. 1995. *Plant physiology. Higher Educ. Press*, Beijing, pp. 67-78.

Panigrah, P., Sao, A., and Singh, P. 2016. Genetic divergence study in traditional local landraces of rice (*Oryza sativa* L.) predominant in Bastar Plateau Zone of Chhattisgarh. *Adv. Res. J. Crop Improv.* 7(2): 192-196.

Patel, N.B., Dhirhi, N., Shrivastava, R., and Sahu, M. 2015. Molecular characterization of aromatic rice (*Oryza sativa* L.) using simple sequence repeats (SSR) markers. *Plant Arch.* 15(2): 1151-1156.

Patra, B.C. 2000. Collection and characterization of rice genetic resources from Keonjhar district of Orissa. *Oryza* 34: 324-326.

Patra, N., Agrawal. R.C., and Chawla, H.S. 2010. Assessment of distinctiveness, uniformity and stability of Basmati rice (*Oryza sativa* L.) varieties based on morphological descriptors. *Indian J. Genet.* 70(1): 48-57.

Parikh, M., Motiramani, N.K., Rastogi, N.K., and Sharma, B. 2012. Agro-morphological characterization and assessment of variability in aromatic rice germplasm. *Bangladesh J. Agril. Res.* 37(1): 1-8.

Pervaiz, Z.H., Rabbani, M.A., Pearce, S.R., and Malik, S.A. 2009. Determination of genetic variability of Asian rice (*Oryza sativa* L.) varieties using microsatellite markers. *Afr. J. Biotechnol.* 8(21): 5641-5651.

Powell, W., Machray, G.C., and Provan, J. 1996. Polymorphism revealed by simple sequence repeats. *Trends Plant Sci.* 1: 215-222.

PPV & FRA (Protection of Plant Variety and Farmers Right Act). 2007. Guidelines for the conduct of test for Distinctiveness, Uniformity and Stability on rice (*Oryza sativa* L.). *Plant Variety J. India* 1(1): 25p.

Prabakaran, A., Paramasivam, K., Rajesh, T., and Rajarajan, D. 2010. Molecular characterization of rice landraces using SSR markers. *Electr. J. Plant Breed.* 1(4): 512-516.

Prasad, K.R., Krishna, K.V.R., Bhave, M.H.V., and Rao, L.V.S. 2017. Genetic variability, heritability and genetic advance in *boro* rice (*Oryza sativa* L.) germplasm. *Int. J. Curr. Microbiol. Appl. Sci. 6*(4): 1261-1266.

Priya, A.A. and Joel, A.J. 2009. Grain yield response of rice cultivars under upland condition. *Electr. J. Plant Breed.* 1: 6-11.

Rabara, R.C., Ferrer, M.C., Diaz, C.L., Newingham, M.C.V., and Romero, G.O. 2014. Phenotypic diversity of farmers' traditional rice varieties in the Philippines. *Agron.* 4: 217-241.

Rabbani, M.A., Masood, M.S., Shinwari, Z.K., and Shinozaki, K.Y. 2010. Genetic analysis of Basmati and non-Basmati Pakistani rice (*Oryza sativa* L.) cultivars using microsatellite markers. *Pakist. J. Bot.* 42(4): 2551-2564.

Rahman, M.M., Rasul, M.G., Hossain, M.A., Iftekaruddaula, K.M., and Hasegawa, H. 2012. Molecular characterization and genetic diversity analysis of rice (*Oryza sativa* L.) using SSR markers. *J. Crop Improv.* 26(2): 244-257.

Rai, S.K., Chandra, R., Suresh, B.G., Rai, P.K., Kumar, R., and Sandhya. 2014. Genetic diversity analysis of rice germplasm lines for yield attributing traits. *Int. J. Life Sci. Res.* 2(4): 225-228.

Rajanna, C.M., Narayanaswamy, R.B., Choudhury, M.M., da Silva, J.A.T., and Prasad, R. 2011. Characterization of rice (*Oryza sativa* L.) hybrids and their parental lines based on the seed, seedling, and plant morphological traits. *Seed Sci. Biotechnol.* 5(1): 36-41.

Rajesh, T., Paramasivam, K., and Thirumeni, S. 2010. Genetic divergence in land races of rice. *Electr. J. Plant Breed.* 1(2): 199-204.

Rajkumar, A., Badri, J., Bhadana, V.P., Priyanka, C., Ansari, N.A., Dey, S., and Chary, D.S. 2015. Genetic divergence studies for yield and its components in rice. *J. Rice Res.* 8(1): 33-40.

Ranawake, A.L. and Amarasinghe, U. G. S. 2014. Relationship of yield and yield related traits of some traditional rice cultivars in Sri Lanka as described by correlation analysis. *J. Sci. Res. Rep.* 3(18): 2395-2403.

Rao, C.R. 1952. *Advanced statistical methods in biometrical research*. John Willey and Sons, Inc. New York, 390p.

Rao, L.V.S., Prasad, G.S., Chiranjivi, M., Chaitanya, U., and Surendhar, R. 2013. DUS Characterization for Farmer varieties of rice. *IOSR J. Agric. Veter. Sci.* 4(5): 35-43.

Rashid, M.M., Nuruzzaman, M., Hassan, L., and Begum, S.N. 2017. Genetic variability analysis for various yield attributing traits in rice genotypes. *J. Bangladesh Agril. Univ.* 15(1): 15-19.

Rathod, R., Rao, D.S., Babu, V.R., and Bharathi, M. 2017. Correlation and path coefficient analysis for yield, yield attributing and nutritional traits in rice (*Oryza sativa* L.). *Int. J. Curr. Microbiol. Appl. Sci.* 6(11): 183-188.

Reddy, V. S., Dash, S., and Reddy, A. R., 1995. Anthocyanin pathway in rice (*Oryza sativa* L.): identification of a mutant showing dominant inhibition of anthocyanin leaf and accumulation of pro-anthocaynidins in pericarp. *Theor. Appl. Genet.* 91: 301-312.

Richharia, R. and Govindasamy, S. 1990. *Rices of India. Academy of Development Science*. Karjat, pp. 47-77.

Rohlf, J.F. 2000. NTSYS-pc: *Numerical Taxonomy and Multivariate Analysis System*, Version 2.1e, Exeter Software, New York.

Roy, S.C. and Sharma, B. D. 2014. Assessment of genetic diversity in rice (*Oryza sativa* L.) germplasm based on agro-morphology traits and zinc-iron content for crop improvement. *Physiol. Mol. Biol. Plants*. 20(2): 209-224.

Sabu, K.K., Abdullah, M.Z., Lim, L.S., and Wickneswari, R. 2009. Analysis of heritability and genetic variability of agronomically important traits in *Oryza sativa* x *O. rufipogon* cross. *Agron. Res*. 7(1): 97-102.

Sajib, A.M., Hossain, M.M., Mosnaz, A.T.M.J., Hossain, H., Islam, M.M., Ali, M.S., and Prodhan, S.H. 2012. SSR marker-based molecular characterization and genetic diversity analysis of aromatic landraces of rice (*Oryza sativa* L.). *J. Biosci. Biotech.* 1(2): 107-116.

Salgotra, R.K., Gupta, B.B., Bhat, J.A., and Sharma, S. 2015. Genetic diversity and population structure of Basmati rice (*Oryza sativa* L.) germplasm collected from North Western Himalayas using trait linked SSR markers. *PLoS ONE* 10(7): 1-19.

Samal, K.C., Rout, G.R., and Das, S.R. 2014. Study of genetic divergence of indigenous aromatic rice (*Oryza Sativa* L.): Potentials and consequences of on-farm management in traditional farming. *Int. J. Agril. Sci.* 4(4): 176-189.

Sandhya, G. R., Lavanya, G., Babu, S., Kumar, K., Rai, S. K., and Devi, B. 2014. Study of genetic variability and D^2 analysis in elite rice genotypes. *Int. J. of Agric. Vet. Sci.* 4(2): 12-16.

Sanghera, G.S., Kashyap, S.C., and Parray, G.A. 2013. Genetic variation for grain yield and related traits in temperate red rice (*Oryza sativa* L.) ecotypes. *Not. Sci. Biol.* 5(3): 400-406.

Sanyal, A. and Joshi, M.A. 2016. Establishing distinctiveness among rice (*Oryza sativa* L.) varieties based on DUS descriptors. *Int. J. of Adv. Res. Sci. Eng.* 5(12): 111-121.

Sarawgi, A.K., Parikh, M., Sharma, B., and Sharma, D. 2014. Phenotypic divergence for agro-morphological traits among dwarf and medium duration

rice germplasm and inter-relationship between their quantitative traits. *Bioscan* 9(4): 1677-1681.

Sarawgi, A.K., Rao, L.V.S., Parikh, M., Sharma, B., and Ojha, G.C. 2013. Assessment of variability of rice (*Oryza sativa* L.) germplasm using agro-morphological characterization. *J. Rice Res*. 6(1): 15-28.

Shah, S.M., Naveed, S.A., and Arif, M. 2013. Genetic diversity in Basmati and non-Basmati rice varieties based on microsatellite markers. *Pakist. J. Bot*. 45(1): 423-431.

Sharma, S., Singh, A.K., Kumar, B., and Salgotra, R.K. 2015. Microsatellite marker based genetic diversity analysis in Basmati rice. *Ecoscan* 9(2): 389-392.

Shahidullah, S.M., Hanafi, M. M., Ashrafuzzaman, M., Ismail, M.R., and Khair, A. 2009. Genetic diversity in grain quality and nutrition of aromatic rices. *Afr. J. Biotechnol.* 8(7): 1238-1246.

Shamim, M.Z. and Sharma, V.K. 2014. Assessment of variability and genetic diversity among different rice varieties for qualitative traits. *Indian J. Agric. Res*. 48(3): 237-240.

Siddique, M.A., Islam, M. Z., Khalequzzaman, M., and Ahmed, M. S. 2011. Genetic diversity in rice (*Oryza sativa* L.) landraces of hilly areas in Bangladesh. *Bangladesh J. Plant Breed. Genet.* 24(2): 25-30.

Siddique, M.A., Khalequzzaman, M., Islam, M.Z., Ahamed, M.S., and Rashid, E.S. M.H. 2013. Genetic diversity in local *Boro* rice (*Oryza sativa* L.) genotypes of Bangladesh. *Bangladesh J. Plant Breed. Genet.* 26(1): 19-24.

Siddique, M.A., Khalequzzaman, M., Islam, M.Z., Baktiar, M.H.K., and Ahmed, M.S. 2016. Genetic diversity assessment of quantitative traits in landraces of *Aus* rice. *Bangladesh J. Plant Breed. Genet.* 29(2): 17-24.

Singh, A., Negi, M.S., Rajagopal, J., Bhatia, S., Thomas, U.K., Srivastava, P.S., and Lakshmikumaran, M. 1999. Assessment of genetic diversity in *Azadirachta indica* using AFLP markers. *Theor. Appl. Genet.* 99: 272-279.

Sinha, A.K. and Mishra, P.K. 2013. Agro-morphological characterization of rice landraces variety (*Oryza sativa* L.) of Bankura district of West Bengal. *Res. Plant Biol.* 3(5): 28-36.

Singh, P. and Narayanam, S.S. 2009. *Biometrical techniques in plant breeding. Kalyani Pub.,* New Delhi, 343p.

Singh, S.K., Singh, C.M., and Lal, G.M. 2011. Assessment of genetic variability for yield and its component characters in rice (*Oryza sativa* L.). *Res. Plant Biol.* 1(4): 73-76.

Singh, S.K., Singh, M., Vennela, P.R., Singh, D.K., Kujur, S.N., and Kumar, D. 2018. Studies on genetic variability, heritability and genetic advance for yield and yield components in drought tolerant rice (*Oryza sativa* L.) landraces. *Int. J. Curr. Microbiol. Appl. Sci. 7*(3): 299-305.

Singh, S.P., Singh, R.R., and Singh, R.V. 1980. Combining ability in rice. *Oryza* 17: 104-108.

Siwach, P., Jain, S., Salni, N., Chowdhury, V.K., and Jain, R.K. 2004. Allelic diversity among Basmati and non-Basmati long-grain *indica* rice varieties using microsatellite markers. *J. Plant Biochem. Biotechnol.* 13: 25-32.

Solis, S.H.D, Rivera1, R.M., David, D.L., and Alvarez, R.C. 2015. Morpho-agronomic evaluation of traditional rice cultivars (*Oryza sativa* L.) collected in grower farm from Pinar Del Rio Province. *Cultivos Trop.* 36(2): 131-141.

Song, Z. P., Xu, X., Wang, B., Chen, J. K., and Lu, B. R. 2003 Genetic diversity in the northernmost *Oryza rufipogon* populations estimated by SSR markers. *Theor. Appl. Genet.* 107: 1492-1499.

Soni, S.K., Yadav, V.K., Pratap, N., Bhadana, V.P., and Ram, T. 2013. Selection criteria, yield relationship with component traits and grouping of tropical *japonica, indica* lines and derived hybrids of rice (*Oryza sativa* L.). *SAARC J. Agric.* 11(2): 17-32.

Srinivas, D., Anuradha, C.H., Sujatha, M., and Sivasankar, A. 2018. Assessment of genetic diversity in rice. *Int. J. Trop. Agric.* 33(2): 199-202.

Srujana, G., Suresh, B.G., Lavanya, G.R., Ram, B.J., and Sumanth, V. 2017. Studies on genetic variability, heritability and genetic advance for yield and quality components in rice (*Oryza sativa* L.). *J. Pharmacognosy Phytochem.* 6(4): 564-566.

Subbaiah, P.V., Sekhar, M.R., Reddy, K.H.P., and Reddy, N.P.E. 2011. Variability and genetic parameters for grain yield and its components and kernel quality attributes in cms based rice hybrids (*Oryza sativa* L.). *Int. J. Appl. Biol. Pharma. Technol.* 2(3): 603-609.

Subudhi, H.N., Samantaray, S., Swain, D., and Singh, O.N. 2012. Collection and agro-morphological characterization of aromatic short grain rice in eastern India. *Afr. J. Agric. Res.* 7(36): 5060-5068.

Sumanth, V., Suresh, B.G., Ram, B.J., and Srujana, G. 2017. Estimation of genetic variability, heritability and genetic advance for grain yield components in rice (*Oryza sativa* L.). *J. Pharmacognosy Phytochem.* 6(4): 1437-1439.

Tanksley, S.D., Young, N.D., Paterson, A.H., and Bonierbale, M.W. 1989. RFLP mapping in Plant Breeding- new tools for an old science. *Biotechnol.* 7: 257-264.

Tejaswini, K.L.Y., Srinivas, M., Ravikumar, B.N.V.S.R., Ahamed, M., Raju, S.K., and Rao, P.V.R. 2016. Correlation and path analysis studies of yield and its component traits in F_5 families of rice (*Oryza sativa* L.). *IOSR J. Agric. Veter. Sci.* 9(11): 80-85.

Temnykh, S., Park, W.D., Ayers, N., Cartinhour, S., Hauck, N., Lipovich, L., Cho, Y.G., Ishii, T., and Mccouch, S.R. 2000. Mapping and genome organization of microsatellite sequences in rice (*Oryza sativa* L.) *Theor. Appl. Genet.* 100: 697-712.

Terzi, V., Morcia, C., Gorrini, A., Stanca, M., Shewry, P.R., and Faccioli, P. 2005. DNA based methods for identification and quantification of small grain cereal mixtures and fingerprinting of varieties. *J. Cereal Sci.* 41: 213-220.

Tripathi, N., Verma, O.P., Singh, P.K., and Rajpoot, P. 2018. Studies on genetic variability, heritability and genetic advance in rice (*Oryza sativa* L.) for yield and its components under salt affected soil. *Int. J. Curr. Microbiol. Appl. Sci.* 7: 5316-5324.

Umarani, E., Radhika, K., Padma, V., and Subbarao, L.V. 2017. Agro-morphological characterization of rice (*Oryza sativa* L.) landraces based on DUS descriptors. *Int. J. Pure Appl. Biosci.* 5(4): 466-475.

Vanaja, T. and Babu, L.C. 2006. Variability in grain quality attributes of high yielding rice varieties (*Oryza sativa* L.) of diverse origin. *J. Trop. Agric.* 44(1): 61-63.

Venkanna, V., Lingaiah, N., Raju, C.S., and Rao, V.T. 2014. Genetic studies for quality traits of F_2 population in rice (*Oryza sativa* L.). *Int. J. Appl. Biol. Pharma. Technol.* 5(2): 125-127.

Venkatesan, K. and Bhat, K.V. 2015. Microsatellite marker-based molecular characterization of small and medium-grained aromatic rice germplasm of Odisha, India. *SABRAO J. Breed. Genet.* 47(3): 248-259.

Virk, P.S., Zhu, J., Newbury, H.J., Jackson, M.T., and Ford-Lloyd, B.V. 2000. Effectiveness of different classes of molecular markers for classifying and revealing variation in rice (*Oryza sativa* L.) germplasm. *Euphytica* 112: 275-284.

Vhora, Z., Trivedi, R., Chakraborty, S., Ravikiran, R., and Sasidharan, N. 2013. Molecular studies of aromatic and non-aromatic rice (*Oryza sativa* L.) genotypes for quality traits using microsatellite markers. *Bioscan* 8(2): 359-362.

Wright, S.1923. The theory of path coefficients. *Genet.* 8: 239-355.

Xu, X. H., Wang, G. C., Zheng, X. B., and Wang, H. X. 1974. A report on the vertical distribution of the rice varieties in Simao, Yunnan. *ActaBotanicaSinica* 16: 208-222.

Yadav, S.K., Pandey, P., Kumar, B., and Suresh, B.G. 2011. Genetic architecture, inter relationship and selection criteria for yield improvement in rice. *Pakist. J. Biol. Sci.* 14(9): 540-545.

Yadav, S. and Suresh, B.G. 2018. Path coefficient analysis for yield and yield components in diverse rice genotypes. *Int. J. Curr. Microbiol. Appl. Sci.* 6: 998-1004.

Yang, G.P., Maroof, S.M.A., Xu, C.D., Zhang, Q., and Biyashev, R.M. 1994. Comparative analysis of microsatellite DNA polymorphism in land races and cultivars of rice. *Mol. Gen. Genet.* 245: 187-194.

316

DIVERSITY ANALYSIS IN LANDRACES OF RICE (*Oryza sativa* L.) IN WAYANAD THROUGH MORPHOLOGICAL AND MOLECULAR POLYMORPHISM STUDY

by

MANJUNATHA, G. A.

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ABSTRACT OF THE THESIS

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KERALA, INDIA- 680 656

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ABSTRACT

The present investigation entitled "Diversity analysis in landraces of rice (*Oryza sativa* L.) in Wayanad through morphological and molecular polymorphism study" was conducted at the Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara, Thrissur and Regional Agricultural Research Station, Ambalavayal, Wayanad during the period 2015-2018. The study aimed to collect and characterize the rice landraces of Wayanad at morphological level and also to characterize the popular aromatic genotypes of the area at molecular level.

DUS characterization revealed that, all the landraces under the study exhibited presence of leaf collar, absence of anthocyanin colouration of leaf collar, presence of leaf ligule, split shape of leaf ligule, absence of anthocyanin colouration for plant parts like lemma (keel), area below apex of lemma, stem nodes and presence of secondary branching in panicle. Variability was exhibited for majority of characters namely coleoptile colour, basal leaf sheath colour, intensity of green colour of leaf, anthocyanin colouration of plant parts like leaf, leaf sheath, auricles, ligules, lemma apex, area below apex of lemma, distribution of anthocyanin colouration in leaf, pubescence of leaf blade surface, leaf auricles, culm attitude, density of pubescence of lemma, colour of stigma, attitude of flag leaf blade, curvature of main axis of panicle, lemma and palea colour, presence and colour of awns, distribution of awns in panicle, secondary branching in panicle, attitude of branches in panicle, panicle exsertion, leaf senescence, sterile lemma colour, shape, colour and aroma of decorticated grain, gelatinization temperature and lodging nature. Thavalakannan, Mullan puncha and Sugandhamathi exhibited distinct morphological characters.

Among the 60 landraces, Kanni kayama, Ambalavayal-1, Kothandan, Onamottan, Thondi-2, Chenthadi, Kannali and Thondi-1 exhibited significantly

high grain yield per plant, which was on par with that of Uma and Aathira (high yielding check varieties), indicating the possibility of commercial cultivation of these cultivars.

High PCV value than GCV for all the characters under study, indicated the influences of environmental factors on the characters. High heritability and high genetic gain was exhibited by the characters like length of leaf blade, width of leaf blade, stem thickness, stem length, number of tillers per plant, number of panicles per plant, length of panicle main axis, number of spikelets per panicle, number of grains per panicle, seed setting (per cent), 1000 grain weight, grain length, grain L/B ratio, decorticated grain L/B ratio and grain yield per plant, indicating that these characters could be used in crop improvement programmes.

Character association studies including correlation and path-analysis revealed that, five characters *viz.,* width of leaf blade, stem length, number of panicles per plant, weight of 1000 grains and decorticated grain width showed both positive correlation and positive direct effect on grain yield per plant.

Cluster analysis based on qualitative characters categorized 60 landraces into 11 clusters at 74 percent similarity level. Based on D^2 statistics analysis, the landraces were grouped into seven clusters with variable number of landraces in each cluster, indicating wide genetic diversity in the Wayanad landraces. All the inter-cluster distances were higher than the intra-cluster distance, indicating the wider genetic diversity among landraces of different clusters.

Molecular characterization of aromatic rice genotypes of Wayanad by SSR (RM) profiling revealed high level of genetic polymorphism among the genotypes studied. Out of 86 SSR markers used for molecular characterization, 44 markers were polymorphic and remaining 42 were monomorphic. Maximum number of amplicons was exhibited by RM247 with five amplicons, followed by RM85, RM251, RM248 and RM493 with four amplicons each.

The highest PIC value was exhibited by RM247 (0.90), followed by RM85, RM251 and RM493 with 0.88 PIC value each.

Out of 86 SSR (RM) markers, 21 markers distinguished Basmati from traditional aromatic landraces of Wayanad *viz.*, Gandhakasala and Jeerakasala. Seven SSR markers distinguished Gandhakasala from Jeerakasala, whereas 23 markers distinguished Basmati from Jeerakasala. Twenty-two markers distinguished Basmati from Gandhakasala and 23 markers distinguished aromatic group from non-aromatic group.

Cluster analysis for molecular characterization revealed maximum similarity coefficient (1.00) within all the Jeerakasala morphotypes and all the Gandhakasala morphotypes. Cluster analysis effectively differentiated Basmati, Jeerakasala, Gandhakasala, Uma and Aathira from each other. Among the five clusters formed, cluster III was the largest one comprising all the 12 Gandhakasala morphotypes, followed by cluster IV with all Jeerakasala morphotypes. Cluster I, Cluster II and Cluster V exhibited one genotype each namely Aathira, Uma and Basmati, indicating their genetic distinctness.