STUDIES ON GENETIC DIVERSITY IN RICE GERMPLASM (*Oryza sativa* L.)

By
D.PADMAJA
B.Sc. (Ag.)

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ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY
RAJENDRANAGAR, HYDERABAD-500 030,
ANDHRA PRADESH

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CERTIFICATE

Ms. D. PADMAJA has satisfactorily prosecuted the course of research and that the thesis entitled **“STUDIES ON GENETIC DIVERSITY IN RICE GERMPLASM (*Oryza sativa* L.)”** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by her for a degree of any University.

Date: **(K. RADHIKA)**
Place: Hyderabad Chairman of the Advisory Committe

CERTIFICATE

This is to certify that the thesis entitled **"STUDIES ON GENETIC DIVERSITY IN RICE GERMPLASM (*Oryza sativa* L.)"** submitted in partial fulfillment of the requirements for the degree of **'MASTER OF SCIENCE IN AGRICULTURE'** of **Acharya N. G. Ranga Agricultural University,** Hyderabad, is a record of the bonafide research work carried out by **Ms. D. PADMAJA** under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

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

(Dr. K. RADHIKA)
Chairman of the Advisory Committee

Thesis approved by the Student's Advisory Committee.

Chairman : **Dr. K. RADHIKA**
Assistant Professor --------------------------------------
Dept. of Genetics & Plant Breeding
College of Agriculture
Rajendranagar, Hyderabad-30.

Member : **Dr. L. V. SUBBA RAO**
Senior Scientist **--------------------------------------**
Dept. of Plant Breeding & Genetics
Directorate of Rice Research
Rajendranagar, Hyderabad-30.

Member : **Dr. V. PADMA**
Associate Professor --------------------------------------
Dept. of Plant Physiology
College of Agriculture
Rajendranagar, Hyderabad-30.

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LIST OF ABBREVIATIONS

%	:	Percentage
°C	:	Degree Celsius
µg	:	micro gram
µl	:	microlitre
AFLP	:	Amplified fragment length polymorphism
ANOVA	:	Analysis of variance
bp	:	Base pairs
CD	:	Critical Difference
CE	:	Coefficiet of variationss
cm	:	centi meter
cM	:	Centi Morgan
CTAB	:	Cetyl Trimethyl Ammonium Bromide
D^2	:	Genetic distance
dNTP	:	deoxy Nucleotide Tri-Phosphate
DRR	:	Directorate of Rice Research
DUS	:	Distinctness, Uniformity and Stability
EDTA	:	Ethylene Diamine Tetra Acetic Acid
EST'S	:	Expressed sequence tagged sites
et al.	:	and others
F_1	:	First Filial generation
F2	:	Second Filial generation

Fig.	:	Figure
g	:	gram
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
h^2(bs)	:	Heritability in broad sense
ha	:	hectare
IRRI	:	International Rice Research Institute
ISSR	:	Inter Simple Sequence Repeats
M	:	Molar
m.ha	:	million hectare
m.t	:	million tonnes
mg	:	milli gram
ml	:	milliliter
mM	:	Micro molar
mm	:	millimeter
ng	:	nano gram
No.	:	Number
PCR	:	Polymerase Chain Reaction
PCV	:	Phenotypic coefficient of variation
PIC	:	Polymorphic Information Content
PPV &FR,Act	:	Protection of Plant Variety and Farmers Rights, Act
RAPD	:	Random Amplified Polymorphic DNA
RFLP	:	Restriction Fragment Length Polymorphism
RM	:	Rice microsatellite

rpm	:	revolutions per minute
SEM	:	Standard Error between Means
SNP	:	Single nucleotide polymorphism
SSLP	:	Simple sequence length polymorphism
SSR	:	Simple Sequence Repeats
TAE	:	Tris Cl, acetic acid, EDTA
TE	:	Tris.Cl, EDTA
TRIPS	:	Trade Related Intellectual Property Rights
Tris.Cl	:	Tris (hydroxy methyl) aminomethane hydro chloride
U	:	Units
UPGMA	:	Unweighted Pair Group Method with Arithmetic Averages
σ^2g	:	Genotypic variance
σ^2p	:	Phenotypic variance

DECLARATION

I, **Ms. D. PADMAJA** hereby declare that the thesis entitled **"STUDIES ON GENETIC DIVERSITY IN RICE GERMPLASM (*Oryza sativa* L.)"** submitted to Acharya N.G. Ranga Agricultural University for the degree of **'MASTER OF SCIENCE IN AGRICULTURE'** is the result of original research work done by me. It is further declared that the thesis or any part thereof has not been published earlier in any manner.

Date: **(D.PADMAJA)**
Place: Hyderabad.

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(D.Padmaja)

Author : **D. PADMAJA**

Title of the thesis : **“STUDIES ON GENETIC DIVERSITY IN RICE GERMPLASM (*Oryza satva* L) “**

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Major advisor : **Dr. K. RADHIKA**

University : **A. N. G. R. AGRICULTURAL UNIVERSITY**

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ABSTRACT

The present investigation consisting of one hundred and fifty diverse genotypes of rice (*Oryza sativa* L.) was undertaken to evaluate the morphological characters, variability, heritability, genetic advance as percent of mean, character association and genetic divergence of eleven qualitative characters and eleven quantitative characters. The experiment was laid out at DRR Farm, ICRISAT Campus, Patancheru, Hyderabad in a randomized block design with three replications during R*abi*, 2007. Visual observations were recorded on single plant basis as per standard descriptors on eleven qualitative characters *viz*., early plant vigour, basal leaf sheath colour, leaf colour, leaf pubescence, ligule shape, ligule colour, panicle exsertion, panicle type, stigma colour, awning and threshability. All these traits were found to exhibit a wide range of variability among the genotypes under study. The data were recorded on days to 50% flowering, plant height, leaf length, leaf width, total number of tillers per plant, productive tillers per plant, panicle length, number of grains per panicle, spikelet fertility, 100-grain weight and single plant yield.

Analysis of variance indicated the existence of significant differences among genotypes for all the characters studied except leaf width and 100 grain weight. Detection of minor difference between GCV and PCV for all the characters indicated less influence of environment on these characters. The characters *viz*., plant height, leaf length, leaf width, total number of tillers per plant, Productive tillers per plant, number of grains per panicle and single plant yield exhibited high heritability estimates coupled with high genetic advance as per cent of mean indicating that simple selection could be effective for improving these characters.

The results of D^2 statistic revealed that the material used in the present investigation possessed high genetic diversity and all the one hundred and fifty genotypes were grouped into sixteen clusters using Tocher’s method. Cluster analysis grouped the genotypes into thirteen clusters. The characters *viz.*, grains per panicle, spikelet fertility, plant height, days to 50% flowering, single plant yield and

100-seed weight contributed 99.01% of the total divergence and these traits were found to be potential factors for genetic differentiation in genotypes.

Based on the divergence estimates and the clustering pattern in the present genetic material, it was found that the genotypes of clusters I and IX possesed high genetic diversity for the characters *viz.*, leaf length, total tillers per plant, panicle length and grains per panicle. Hence these could be used in hybridization programme for the development of superior recombinants.

Character association studies revealed significant and positive association of single plant yield with total tillers per plant, productive tillers per plant, panicle length, grains per panicle, spikelet fertility and 100-seed weight, while significant negative association of single plant yield with leaf length was noticed at genotypic level. Therefore, these characters could be used as criteria for selection of genotypes with high seed yield. Productive tillers per plant exhibited strong positive direct effect on seed yield at genotypic level and 100-seed weight exhibited high positive direct effect on seed yield at phenotypic level.

Genotyping of seventy-two germplasm lines of rice was done using 23 SSR markers. Seven markers exhibited polymorphism by generating 20 alleles. JGT 12 amplified a maximum number of four alleles. The number of alleles ranged from 2 - 4 with a mean of 2.85, while the polymorphic information content (PIC) for these seven markers ranged from 1.021 (JGT 06) to 1.839 (RM 151). Based on the information generated through SSR markers, the genotypes were grouped according to their genetic relatedness.

CHAPTER - I

INTRODUCTION

Rice (*Oryza sativa* L.) is the most important staple food crop for more than 60% of the global population and forms the cheapest source of food energy and protein. In India rice cultivation is very closely inter woven with livelyhood and culture of millions of people and is not only the major staple food but gained the status of major export commodity for the last ten years.

Rice is grown in an area of 44.3 m ha with the production and productivity levels of 91.8 m tonnes and 2074 kg/ha, respectively in India. In AndhraPradesh rice is grown in an area of 39.82 lakh ha with the production and productivity levels of 11.70 lakh tonnes and 2939 kg/ha (CMIE 2006), respectively.

To meet the food demands of the growing population and to achieve food security in the country, the present production levels need to be increased by 2 m.tonnes every year. It is estimated that 120 m. tonnes of rice is required to feed the increasing population by 2020.

The development and cultivation of semi- dwarf, photo-insensitive, fertilizer responsive varieties like IR 8 and Jaya in large scale in mid sixties had resulted in green revolution by increasing the productivity levels by 2.0-2.5 times, which was a great land mark in the history of development of rice varieties. But, since then, there is no substantial increase in the yield. Therefore, the other crop improvement methods like heterosis breeding, identification and introduction of QTL's for yield improvement are being employed. To increase the present levels of heterosis for yield, there is a need to identify and utilize genetically divergent parents for inter and intra sub-specific crosses in rice. A systematic evaluation and characterization of germplasm lines helps in identification of superior and genetically divergent germplasm lines. Characterization of germplasm provides the information on morphological and agronomic aspects of the material that is essential for gene bank management.

Yield is a complex character which is genetically influenced by a large number of quantitative characters (Nickell and Grafius, 1969), which are especially important in plant breeding, because majority of the economic traits are of this nature. Application of biometrical techniques in plant breeding has led to the greater understanding of genetics of quantitative characters and proved to be extremely useful to the plant breeder for systematic genetic analysis.

A thorough knowledge of nature and magnitude of genetic variability and association of characters in a crop species is a pre-requisite for a successful breeding programme. Information on direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection process.

In addition to the above information, quantification of degree of divergence in a given experimental material is of immense value in identification of divergent genotypes for further use in hybridization to create new variability. Mahalanobis's D^2 statistic has proved to be a powerful tool for quantifying genetic divergence in a given population. Divergent genotypes could be obtained by collection from different eco-geographical regions or it could be induced by combination breeding.

The advent of molecular markers in detecting variation at DNA level has opened up new horizons in clustering the germplasm and widening the scope for crop improvement. RAPD, SSR and ISSR markers are useful in studies on genetic diversity, gene tagging and genome mapping. Hence, detecting genetic diversity among germplasm lines using the polymorphism developed by these markers and correlating with agro- morphological characters will be a potential tool in identifying elite parental lines for future crossing programmes.

Keeping in view the importance of the aforesaid aspects, an attempt has been made in the present investigation to characterize and identify the promising rice germplasm lines collected from Directorate of Rice Research, Hyderabad with the following objectives.

1. To study the general pattern of variation for agro-morphological characters.
2. To assess the extent of genetic diversity among different accessions of rice germplasm using molecular markers.
3. To group these accessions into suitable clusters and study the inter and intra cluster variations.
4. To study the character association among yield attributes.

CHAPTER II

REVIEW OF LITERATURE

2.1 DIVERSITY STUDIES ON GERMPLASM ACCESSIONS OF RICE THROUGH FIELD EVALUATION

The exploitation of genetic diversity for crop improvement should be the ultimate objective of exploration and conservation of genetic resources. While it is important to ensure that plant genetic resources are adequately safeguarded for future generations, they simply can not be placed in a gene bank and forgotten about. A systematic evaluation of the genetic resources and the utilization of the promising germplasm lines possessing valuable traits such as resistance to biotic and abiotic stresses into crop improvement programmes is of paramount importance. The immediate value of genetic resources depends to a considerable extent upon the ease with which a breeder can utilize them.

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

The available literature on morphological characterization, genetic variability, heritability and genetic advance, character association, path coefficient analysis and genetic divergence in rice are summarized below under the following categories:

1. Morphological characterization
2. Genetic variability
3. Heritability and genetic advance
4. Genetic divergence
5. Character association

2.1.1. Morphological characterization

Bhag Singh and Kochhar (1994) suggested the following criteria for selecting germplasm lines for characterization.

i) New collections through explorations.

ii) New exotic introductions.

iii) New accessions generated from parasexual methods/ vegetative propagules/ tissue culture raised propagules etc.

iv) Samples redrawn from gene bank after long intervals to monitor the changes in expression of stable (characterization) traits may also be included, and

v) Samples procured from other gene bank as duplicate sets to monitor the changes due to the location effect in character expression.

Ramaiah (1953) classified rice varieties on the basis of pigment distribution in different plant parts.

Ramaiah (1953) and Hadgal (1980) reported that both linkage and pleiotrophy are responsible for simultaneous occurrence of anthocyanin in different plant parts.

Richharia and Seetharaman (1962) observed the inheritance of colouration in the apiculus in the intervarietal rice crosses involving three *glaberrima* varieties. The expression of colour in the apiculus was found to be governed by two pairs of dominant genes.

Seetharaman *et al.* (1974) classified rice varieties using relatively fewer characters.

Das *et al.* (1981) while classifying *ahu* rice germplasm in Assam explained the relevance of broad categorization of characters and choice of a few rather than several characters in varietal characterization.

Klakhaeng *et al.* (1991) studied 36 agronomic characters in 198 local genotypes from the National Rice Seed Storage Laboratory for Genetic Resources. The apiculus was white in most rices but red at the apex in Sao Nueng and Niaw Nak.

Ahmed and Das (1994) made an attempt for characterization and grouping of 85 indigenous glutinous rice varieties on the basis of pigment distribution in 11 plant parts. Except two, all the varieties were pigmented in one or more plant parts and anthocyanin pigmentation was a dominant trait. On the basis of pigment distribution the entire rice germplasm was grouped into 47 groups.

Cunha and Nascimento (1995) studied the inheritance of anthocyanin colouration from the crosses between IR 8 x Sagrimao and reported the ratio of 39 colourless; 25 coloured suggesting that presence of pigment in the leaf sheath was controlled by two duplicate genes with additive effects (R_1 and R_2), interacting with one non dominant inhibitor gene.

Dharmendra Kumar *et al.* (1997) studied variability for different characters in 112 samples of wide rice. Grouping was done according to their habit. Four were placed in erect, 26 in semi erect, 49 in semi spreading 34 were kept in spreading type. Pigmentation range was observed for 1 to 12 different plant parts.

Diaz *et al.* (2000) studied 19 rice germplasm entries using the system of Standard Evaluation for Rice and Varietal Description form and there were varietal differences for most of the characters evaluated.

Subba Rao *et al.* (2001) studied 123 native cultivars and land races which were characterized using morpho-agronomic descriptors (IRRI, 1996) to estimate variability. Based on the frequency distribution for 11 morphological characters, a majority of cultivars were found to posses green basal leaf sheath (65%), light green collar (60%),white stigma (57%).

Subbarao *et al.* (2006) Studied one thousand and fifty six accessions were characterized using morpho-agronomic descriptors (IRRI, 1996) to estimate variability for 21 agro-morphological characters the results revealed that 54 percent of them showed very good early plant vigour, 41 per cent exhibited intermediate vigour while 4.5 per cent accessions were found to exhibit poor plant vigour. The study revealed that 57 percent accessions exhibited green basal leaf sheath colour, 18 per cent possessed purple colour and 12 per cent showed light purple colour while another 12 per cent accessions exhibited purple lines.

2.1.2 Genetic variability

The information on the extent of variability available in crops could be of immense value to the breeder to efficiently design the breeding programme. Superior genotypes can be isolated by selection if considerable genetic variation exists within the population. It is essential to partition the overall variability into heritable and non-heritable components with the help of genetic parameters like genotypic and phenotypic coefficients of variation.

The available literature on variability shows the existence of either low, moderate or high estimate of coefficients of variation exists as per the reports by different scientists with different material and at various locations. So, to avoid the redundancy in presentation, the literature is furnished below in a tabular form to make it convenient to the reader.

Character	**Coefficient of variation**		**References**
	GCV	**PCV**	
Days to 50% flowering	High	High	Chookar *et al.* (1994) Surendrasingh and choudary (1996) Kaw *et al.*(1999) Awasti and Pandey (2000)
	Moderate	--	Manonmani *et al.* (1996) Vange and Ojo (1997) Chikkalingaiah *et al.* (1999)
	Low	Low	Nayak *et al.*(2002) Patil *et al.*(2003) Suman *et al.*(2003) Sinha *et al.*(2004)
	Low	--	Balan *et al.*(1999)
Plant height (cm)	High	High	Nath and Talukdar (1997) Debchoudhary and Das (1998) Tripathi *et al.*(1999) Awasthi and Pandey (2000) Sinha *et al.*(2004)
	--	High	Remabai *et al.* (1992) Chookar *et al.* (1994)
		Moderate	Ganesan and Subramanian (1990) Manonmani *et al.* (1996) Surendra singh and Choudhary (1996) Vange and Ojo (1997) Nagajyothi (2001) Tarasatyavathi (2001) Nayak *et al.* (2002) Patil *et al.* (2003)
	Low	--	Chikkalingaiah *et al.* (1999) Patil *et al.* (2003)
Leaf length	High	High	Souroush *et al.* (2004)
Leaf width	High	High	Souroush *et al.* (2004)
Total number of tillers per plant	High	High	Sinha *et al.* (2004)
	High	--	Amirthdevarathinam (1990)
	--	High	Rahangdale and Khorgade (1988)
	High	Low	Shanta kumar *et al.* (1998)
Number of productive tillers per plant	High	High	Sardana *et al.* (1989) Chookar *et al.* (1994) Manonmani *et al.* (1996) Surendra singh and Choudhary (1996) Saravanan and Senthil (1997) Chikkalingaiah (1999) Sinha *et al.* (2004)

Contd….

Character	Coefficient of variation		References
	GCV	**PCV**	
	--	High	Chudhary and Motiramani (2003)
	Moderate	Moderate	Vange and Ojo (1997) Nagajyothi (2001)
	Low	Low	Niranjana Murthy *et al.* (1999) Tarasatyavathi *et al.* (2001) Surender Raju (2002)
Panicle length	High	High	Tripati *et al.* (1999)
	--	High	Rahangdale and Khorgade (1998)
	High	--	Chaubey and Richaria (1993) Chaubey and Singh (1994) Sawanth and Patil (1995) Mani *et al.* (1997) Deb Choudhary and Das(1998) Yadav (2000) Bharadwaj *et al.* (2001)
	Moderate	--	Nayak *et al.* (2002)
	Low	Low	Manonmani *et al.* (1996) Vange and Ojo (1997) Chikkalingaiah *et al.* (1999) Nagajyothi (2001) Tarasatyavathi *et al.* (2001) Patil *et al.* (2003)
Total number of grains per panicle	High	High	Rao and Shrivastav (1994) Reddy and De (1996) Borbora and Hazarika(1998) Debchoudhary and Das (1998) Nagajyothi (2001) Nayak *et al.* (2002) Madhavilatha (2002)
	High	--	Suman (2003)
	Moderate	Moderate	Sarma and Roy (1993) Tarasatyavathi *et al.* (2001)
	Low	Low	Nath and Talukdar (1997)

Contd….

Character	Coefficient of variation		References
	GCV	PCV	
Spikelet fertility	High	High	Saravanan and Senthil (1997) Kumar *et al.* (1998)
100-grain weight (g)	High	High	Chaubey and Singh (1994) Mani *et al.* (1997) Bharadwaj *et al.* (2001)
	Low	Low	Ganeshan and Subramanian (1990) Rama Rao (1990)
Grain yield per plant	High	High	Chookar *et al.* (1994) Rao and Shrivastav (1994) Balan *et al.* (1999) Satyapriya Lalitha and Sreedhar (1999) Nayak *et al.* (2002) Patil *et al.* (2003) Suman (2003)
	High	--	Sinha *et al.* (2004) Hasib *et al.* (2005) Madhavilatha *et al.* (2005)
	--	High	Chaudhary and Motiramani (2003)
	Moderate	High	Borkakati *et al.* (2005)
	Moderate	Moderate	Nagajyothi (2001) Tarasatyavathi *et al.* (2001)
	Low	--	Supriyo and Chakraborthy and Hazarika (1994)

GCV = Genotypic coefficient of variation, **PCV** = Phenotypic coefficient of variation

2.1.3 Heritability and genetic advance

Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance.

Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population.

High heritability coupled with high genetic advance suggests that character improvement could be made by selection based on phenotypic performance. This estimation of broad sense heritability and genetic advance for different characters by different workers are reviewed below.

2.1.3.1 Days to 50 per cent flowering

Marimuthu *et al.* (1990) and Rao and Shrivastav (1994) studied high heritability coupled with moderate genetic advance for days to 50 per cent flowering.

Chikkalingaiah *et al*. (1999) and Patil *et al.* (2004) reported high heritability estimates for days to 50 per cent flowering.

Madhavilatha (2002) Nayak *et al.* (2002) and Paramesha *et al*. (2005) observed high heritability coupled with high genetic advance to 50 per cent flowering in rice.

Balan *et al.* (1999), Niranjana Murthy *et al*. (1999), Suman (2003), Patil *et al.* (2003) and Sinha *et al.* (2004) and obtained high heritability coupled with low genetic advance.

2.1.3.2 Plant height (cm)

Mokate *et al.* (1998), Chikkalingaiah (1999) Kaw *et al* (1999) and Souroush *et al.* (2004) reported high heritability estimates for plant height, while high heritability coupled with high genetic advance for plant height in rice was recorded by Mahto *et al.* (2003) Mall *et al.* (2005) Paramesha *et al*. (2005) and Singh *et al.* (2005). Nagajyothi (2001), Venkata Suresh (2001), Nayak *et al.* (2003), Patil *et al.* (2003), Suman (2003) and Sinha *et al*. (2004) observed high heritability along with moderate or low genetic advance.

Sahdev Singh *et al.* (1996) reported low to high heritability and low genetic advance in F_3 populations of the cross Jhona-349 x IR-8.

2.1.3.3 Total number of tillers per plant

Amrithadevarathinam (1983) observed high heritability and high expected genetic advance for total number of tillers/m^2 in upland rice.

Srikrishnadevarayalu (1993) reported high heritability coupled with low genetic advance for this trait in rice. Similar reports were further confirmed by Mehetre *et al.* (1996) in eight upland rice varieties.

Shantha Kumar *et al.* (1998), Suman (2003) and Mall *et al*. (2005) observed high heritability coupled with high genetic advance for total tiller number of tillers per hill.

Swathi *et al.* (2004) obtained moderate heritability for total number of tillers/hill.

2.1.3.4 Number of productive tillers per plant

Borbora and Hazarika (1998), Chikkalingaiah *et al.* (1999), Nagajyothi (2001), Nayak *et al.* (2002), Suman (2003), Patil *et al.* (2003), Patil and Sarawgi (2005) and Mall *et al*. (2005) recorded high heritability coupled with high genetic advance as per cent of mean for number of productive tillers per plant in rice.

Satya Priya Lalitha and Sreedhar (1996) and Venkata Suresh (2001) noticed moderate heritability coupled with moderate genetic advance.

Medium to high heritability and low genetic advance for number of productive tillers per plant in rice were reported by Sahdev Singh *et al.* (1996).

Ramesh Kumar (1989) and Niranjana Murthy *et al.* (1999) recorded low heritability with very low genetic advance.

2.1.3.5 Panicle length (cm)

Paramasivam *et al*. (1995), Chikkalingaiah *et al*. (1999) and Nayak *et al*. (2002) reported high heritability coupled with high genetic advance for panicle length.

Borbora and Hazarika (1998), Nagajyothi (2001) and Suman (2003) noticed high heritability and low genetic advance for panicle length in rice.

Satya Priya Lalitha and Sreedhar (1996) and Venkata Suresh (2001) observed moderate heritability and moderate genetic advance for panicle length in rice.

2.1.3.6 Number of grains per panicle

Satyapriyalalitha and Sreedhar (1996) studied moderate heritability and moderate genetic advance for number of grains per panicle in rice.

Borbora and Hazarika (1998), Venkata Suresh (2001), Nayak *et al*. (2002) Patil *et al*. (2003), Madhavilatha *et al*. (2005) and Monalisa *et al*. (2006), reported high heritability coupled with high genetic advance for this trait in rice.

2.1.3.7 Spikelet fertility (%)

Kumar *et al*. (1998) reported high heritability coupled with high genetic advance for this trait in rice.

Madhavilatha *et al.* (2005) reported high heritability and low genetic advance for **s**pikelet fertility in rice.

Saravanan and Senthil (1997) reported high heritability and moderate genetic advance for spikelet fertility in rice.

2.1.3.8 100-grain weight (g)

Awasthi and Borhtakur (1986) observed high heritability (92.13%) and low expected genetic advance (5.37) for 100-grain weight in 12 upland rice varieties. High heritability with moderate to low genetic advance was reported to 100-grian weight in F_2 population of six inter varietal crosses was noticed by (Marimuthu *et al.,* 1990).

Lok Prakash *et al.* (1992) and Suman (2003) reported high heritability coupled with moderate to high genetic advance.

Vanniarajan *et al.* (1996) reported comparatively high heritability coupled with high genetic advance for 100-grain weight in a cross MS 37A x IR 50 out of three crosses.

2.1.3.9 Single plant yield (g)

Balan *et al.* (1999), Niranjana Murthy *et al.* (1999), Yadav (2000), Nagajyothi (2001), Nayak *et al.* (2002), Patil *et al.* (2003), Sinha *et al.* (2004), Madhavilatha (2005), Paramesha *et al.* (2005) and Patil and Sarawgi (2005) obtained high heritability estimates coupled with high genetic advance as percentage of mean.

Studies of Satya Priya Lalitha and Sreedhar (1999) revealed moderate heritability and moderate genetic advance, while Ramesh Kumar (1989), Suman (2003) and Singh *et al.* (2005) recorded high heritability with very low expected genetic advance.

Sinha *et al.* (2004) revealed high heritability with moderate genetic advance for this trait.

2.1.4 Genetic divergence

Genetic improvement in any crop mainly depends upon the amount of genetic variability present in the population. The importance of genetic diversity in crop plants was first realized by Darwin (1859) and the term “morphism” employing genetic morphs was given by Huxley (1955), which means the existence of distinct genetic forms in balance in a population.

2.1.4.1 Mahalanobis’s D^2 analysis

Mahalanobis’s D^2 analysis is a powerful tool in quantifying the degree of divergence between biological populations at genetic level and provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

Estimation of degree of divergence between populations and contribution of different characters to total divergence was done by Mahalanobis’s D^2 statistic (Maurya and Singh, 1977) which is a more reliable method in selection of parents for hybridization programme.

Murthy and Arunachalam (1966) emphasized the importance of genetic diversity in selection of parents for hybridization in different crops and concluded that the greatest contributing characters to genetic diversity in grain crops were flowering time, plant height and number of tillers per plant.

Kotaiah *et al.* (1987) grouped thirty six long duration genotypes into 10 clusters by D^2 analysis. Days to 50% flowering and 1000-grain weight were found to be the main contributors to total divergence.

Studies of Gomathinayagam *et al*. (1990) grouped 40 rice entries into four different clusters and revealed that there was a lack of parallelism between geographic distribution and genetic divergence. Similarly, Pradhan and Roy (1990) conducted D^2 analysis in 25 rice cultures and grouped them into 6 clusters. Test weight contributed maximum to genetic divergence.

Vivekanandan and Sukanya Subramanian (1993) carried out genetic divergence studies using D^2 analysis in 28 genotypes of rainfed rice and grouped them into five clusters. Plant height and grain yield contributed considerably (85 %) to the total divergence. The geographical diversity was found to be not related to genetic diversity.

Barauah *et al.* (1994) grouped 144 rice varieties into 55 clusters and noticed that there was a lack of correspondence between ecological situation and genetic divergence. They further emphasized that days to 50% flowering, plant height, ear bearing tillers per hill, test weight and grain yield contributed maximum towards divergence.

Kaw (1995) from his investigation on genetic divergence in 94 cold tolerant rice varieties grouped the genotypes into 18 clusters using D^2 statistic and canonical analysis. The maximum contribution of plant height, days to 50 per cent flowering and fertility percentage towards genetic divergence was observed.

Genetic divergence was assessed by using 40 rice genotypes at two different locations by Rao and Gomatinayagam (1997). Genetic divergence was found to be not related to geographic diversity. They also noted the differential response of genotypes to different environment which had altered the clustering pattern too. It was also observed that stable genotypes having less interaction with environment were tend to group into one cluster and such genotypes were found to be best breeding material for heterosis.

Sardana *et al*. (1997) conducted D^2 analysis in 82 local rice varieties and categorized them into 18 clusters based on 15 agro-morphological characters. Cluster I with 15 genotypes was the largest one. They observed that number of grains per panicle, number of effective tillers per plant and single plant yield were major characters contributing to the genetic diversity.

Ushakumari and Rangaswamy (1997) carried out genetic divergence among 74 rice genotypes and classified them into six clusters by multivariate analysis using D^2 statistic. The characters single plant yield and plant height contributed maximum towards divergence. There was no relation between geographic distribution and genetic diversity.

Hanamaratti *et al.* (1998) evaluated fifty rice genotypes for 10 yield components in low and upland environments by D^2 statistic and grouped them into 18 and 17 clusters, respectively.

Genetic divergence among 85 indigenous glutinous rice varieties of Assam was worked out by Ahmed and Borah (1999) using Mahalanobis's D^2 analysis. The genotypes were grouped into 12 clusters based on the 13 agronomic characters. Cluster X and XII were the largest, while cluster I was the smallest. Tiller number, number of effective tillers per plant, grains per panicle, spikelet fertility and grain yield accounted for major portion of divergence.

Studies on fifty rice genotypes by Pandey *et al.* (1999) using Mahalanobis's D^2 statistic assigned the genotypes into six clusters and revealed no correlation between genetic diversity and geographical diversity. The characters, days to 50 per cent flowering, Plant height and 1000-seed weight contributed maximum to the genetic diversity.

Kandhola and Panwar (1999) grouped 52 indigenous and exotic genotypes of rice using D^2 statistic into 11 clusters based on 16 agro-morphological and quality characters. Cluster I with 26 genotypes was the largest, while clusters VII, VIII, IX and XI were monogenotypic and revealed no association between genetic and geographic diversity. The inter-cluster distance was maximum between genotypes of clusters V and XI. Hybridization among the genotypes drawn from widely divergent clusters with high yield potential is likely to produce more heterotic effect.

Hegde and Patil (2000) assessed the genetic divergence in 40 genotypes of rainfed rice and grouped into seven clusters. The average inter cluster D value was highest (51.88) between the clusters V and VII indicating high genetic divergence between cultivars of these two clusters. Total spikelets per panicle, photosynthetic rate and 1000-grain weight contributed maximum to total genetic divergence.

D^2 analysis of divergence grouped the 56 diverse rice cultivars into eight clusters. Geographical origin was found to be a good parameter of genetic divergence. The 100 grain weight was important component of divergence. Based on mean performance for plant height, grain yield and inter-cluster distance, the genotypes from clusters II and IV may be used for initiating the hybridization programme (Rather *et al.*, 2001).

Surender Raju (2002) assessed the genetic divergence among 42 genotypes by Mahalanobis's D^2 statistic and grouped them into 12 clusters. The characters 100-grain weight and days to 50% flowering had contributed maximum to the genetic divergence.

Manonmani *et al*. (2003) studied nature and magnitude of genetic divergence among fourteen *indica* rice genotypes and grouped them into five clusters. The cluster I consisted of ten genotypes and the clusters II, III, IV and V had one genotype each. Days to 50 per cent flowering and plant height showed maximum contribution to the genetic divergence.

Vanaja *et al.* (2003) carried out genetic divergence among 56 high yielding rice genotypes representing different eco-geographical regions and grouped them into nine clusters. It was concluded that there was no association between geographical distribution and genetic diversity. At the same time the relationship between genetic divergence and geographical origin also exists to some extent.

Nayak *et al.* (2004) assessed nature and magnitude of genetic divergence among 200 rice genotypes of scented rice for the quantitative traits and grouped the genotypes into 10 clusters. No relationship was found between clustering pattern and geographic distribution. Days to 50 per cent flowering played an important role in the formation of clusters.

Swati *et al.* (2004) evaluated fifty-nine rice genotypes based on 18 agronomic characters and grouped them into 10 clusters based on Euclidean cluster analysis. The genotypes Bengawan, Red-awned mutant, Surya, IR-65598-112, Palghat-1 and Pant Dhan-12 recorded high values for one or more yield components and hence can be used in multiple crossing programmes to recover transgressive segregants.

Bose and Pradhan (2005) studied the nature and the magnitude of genetic divergence in 35 deep water rice genotypes using Mahalonobis's D2 statistics. The genotypes were grouped into 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Cluster IV showed the maximum intracluster divergence, while intercluster divergence was maximum between clusters IX and X. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Traits such as plant yield, days to 50% flowering and plant height were the major contributors to genetic divergence

Chand *et al.* (2005) studied the genetic divergence among 19 genotypes of Aman rice using Mahalanobis's D2 statistic for 12 characters. Based on D^2 values, the genotypes were grouped into six clusters. Cluster I was the largest with eight genotypes followed by cluster II with four genotypes. Intra-cluster distance was highest in cluster VI and lowest in cluster IV. The maximum inter-cluster distance was found between clusters IV and VI suggesting wide diversity between these groups. The major part of total divergence was imparted by single trait i.e. 1000-grain weight. Panicle length and plant height were also very important in this regard.

Chaturvedi and Maurya (2005) studied the genetic divergence analysis in 26 genotypes of rice belonging to 7 ecotypic situations for 20 characters .The genotypes were grouped in 8 clusters. Comparison of cluster means revealed that cluster VIII gave exceptionally high values for 7 characters followed by cluster VII. The maximum inter-cluster D^2 value was obtained between cluster III and VI and III and VIII. It is suggested that for developing better cultivar, the genotypes of cluster III could be utilized in hybridization programme with the genotypes of cluster VI and VIII.

Genetic divergence studies carried out with 54 rice genotypes which were grouped them into nine clusters. The mode of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters, plant height and days to 50 per cent flowering contributed maximum towards genetic divergence (Madhavi Latha *et al.* 2005).

Mundhe *et al.* (2006) studied the genetic diversity for 39 mid late rice genotypes. These genotypes were grouped into seven clusters. Intra-cluster distance was maximum in cluster III. Inter cluster distance maximum between cluster V and VII. Number of tillers per plant, days to 50% flowering, 1000-grain weight and yield per plant were major contributing characters towards the genetic divergence.

2.1.5 Character association

Study of character associations helps the breeder in fixing criteria for selection of elite parental lines having maximum grain yield coupled with desired combination of characters. Phenotypic correlation is the correlation of phenotypic values and is subjected to changes in the environment. It measures the environment deviation together with non-additive gene action. Genotypic correlation is the correlation of breeding value (Additive + Additive x Additive + Epistatic) gene action. Hence, knowledge of association between different characters is highly essential for planning a sound breeding programme.

2.1.5.1 Correlation coefficients

Several workers have studied the correlation coefficients in rice and contradictory association have been reported for almost all the character pairs which may be due to the different experimental material handled by them.

A brief review of studies on the association of characters in rice is presented hereunder:

2.1.5.1.1 Association of yield component characters with single plant yield in rice

Character	Nature of association	Reference
Days to 50% flowering	Positive significant	Selvarani and Rangaswamy (1998) Balan *et al.* (1999) Sakthivel (2001) Madhavilatha (2002) Mahto *et al.* (2003) Kuldeep *et al.* (2004) Patil and Sarawgi (2005) Suman *et al.*(2006) Tayeng and Singh (2006)
	Positive non-significant	Kumar *et al.* (1998) Rao and Shrivastav (1999) Vange *et al.* (1999)
	Negative non-significant	Sarma and Roy (1993) Yolanda and Vijendra Das (1995) Meenakshi *et al.* (1999)
Plant height	Positive significant	DebChaudhury and Das (1998) Bala (2001) Janardhanam *et al.*(2001) Nayak *et al.* (2001) Sakthivel (2001) Madhavilatha (2002) Oad *et al.*(2002) Patil and Sarawgi (2005) Sandya kishore (2005)
	Positive non-significant	Suman (2003)
	Negative significant	Yolanda and Vijendra Das (1995) Reddy *et al.* (1997) Rao and Shrivastav (1999) Tarasatyavathi *et al.* (2001) Mahto *et al.* (2003) Borbora *et al.* (2005) Paramesha *et al.* (2005)

(Contd…. 2.1.5.1.1)

Character	Nature of association	Reference
	Negative non-significant	Chauhan *et al.* (1993) Gupta *et al.* (1998) Meenakshi *et al.* (1999)
Total number of tillers per plant	Positive significant	Allahgholipour *et al.* (2003)
No. of productive tillers per plant	Positive significant	Janardhanam *et al.* (2001) Nayak *et al.* (2001) Sakthivel (2001) Tarasatyavathi *et al.* (2001) Madhavilatha (2002) Chaudhary and Motiramani (2003) Suman (2003) Kuldeep *et al.* (2004) Patil and Sarawgi (2005) Sandya kishore (2005)
	Positive and non-significant	Chaubey and Singh (1994) Yolanda and Vijendra Das (1995) Reddy *et al.* (1997) Selvarani and Rangaswamy (1998) Deb choudhary and Das (1998) Khedikar *et al.* (2004) Suman *et al.* (2006)
	Negative Non-significant	Awasthi and Borthakur (1986) Haque *et al.* (1991)
Panicle length	Positive significant	Chandra and Das (2000) Bala (2001) Nayak *et al.* (2001) Sakthivel (2001) Madhavilatha (2002) Somnath Bhattacharya and Ghosh (2004)
		Kuldeep *et al.* (2004) Suman *et al.* (2006) Tayengh and Singh (2006)
	Positive Non-significant	Rao and Shrivastav (1999) Tarasatyavathi *et al.* (2001) Suman *et al.* (2006)

(Contd…. 2.1.5.1.1)

Character	Nature of association	Reference
	Negative significant	Sukanya Subramaniyan and Rathinam (1984)
	Negative Non-significant	Chauhan *et al.* (1993) Ramesh Babu (1999) Sandya kishore (2005)
Number of grains per panicle	Positive significant	Reddy *et al.* (1997) Deb chaudhary and Das (1998) Tarasatyavathi *et al.* (2001) Madhavilatha (2002) Allahgholipour *et al.* (2003) Monalisa *et al.* (2006)
	Positive Non-significant	Sarma and Roy (1993) Chaubey and Singh (1994) Paul and Sarmah (1997)
Spikelet fertility	Positive significant	Chauhan *et al.*(1993) Kumar *et al.*(1998) Rao and Shrivastav (1999) Borkakati *et al.* (2005)
	Positive non-significant	Yolanda and Vijendra Das (1995) Madhavilatha (2002)
	Negative Non-significant	Supriyo chakravarthy and Hazarika (1994)
100-grain weight	Positive Non-significant	Suman *et al.* (2006)
	Positive significant	Prasad *et al.*(1988) Babu and Soundarapandian (1990)
1000-grain weight	Positive significant	Sakthivel (2001) Madhavilatha (2002) Tarasatyavathi *et al.* (2002) Sinha *et al.* (2004) Kuldeep *et al.* (2004)
	Positive Non-significant	Supriyo Chakraborty and Hazarika (1994) Gupta *et al.* (1998) Vange *et al.* (1999)
	Negative Non-significant	Geeta *et al.* (1994)

2.1.5.1.2 Association of yield component traits with days to 50 per cent flowering in rice

Character	Nature of association	Reference
Plant height	Positive significant	Meenakshi *et al*. (1999) Kavitha and Sree Rama Reddi (2001) Sakthivel (2001) Madhavilatha (2002)
	Positive Non-significant	Chauhan *et al*. (1993) Ramesh Babu (1999)
	Negative Non-significant	Debchoudhary and Das (1998) Rao and Shrivastav (1999)
Number of productive tillers per plant	Positive significant	Sawant *et al*. (1995) Sakthivel (2001)
	Positive Non-significant	Kavitha and Sree Rama Reddi (2001) Reddy (2001) Surendar Raju (2002)
	Negative Non-significant	Yolanda and Vijendra Das (1995) Meenakshi *et al*. (1999) Madhavilatha (2002)
Panicle length	Positive significant	Vange *et al*. (1999) Nayak *et al*. (2001) Sakthivel (2001) Madhavilatha (2002) Paramesha *et al*. (2005) Suman *et al*. (2006)
	Positive Non-significant	Sarma and Roy (1993) Sawant *et al*. (1995) Kavitha and Sri Rama Reddi (2001)
	Negative Non-significant	Chauhan *et al*. (1993) Ramesh Babu (1999)
Number of grains per panicle	Positive significant	Debchoudhury and Das (1998) Kavitha and Sree Rama Reddi (2001) Nayak *et al*. (2001) Madhavilatha (2002)

(Contd…. 2.1.5.1.2)

Character	**Nature of association**	**Reference**
	Positive Non-significant	Chauhan *et al.* (1993) Yolanda and Vijendra Das (1995) Vange *et al.* (1999)
	Negative Non-significant	Sawant *et al.* (1995) Meenakshi *et al.* (1999)
Spikelet fertility	Positive Non-significant	Rao and Shrivastav (1999)
	Negative significant	Yolanda and Vijendra Das (1995)
	Negative non – significant	Madhavilatha (2002)
1000-grain weight	Positive significant	Ravindranath *et al.* (1982)
	Positive and non-significant	Roy *et al.* (1995)
	Negative significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddi (2001) Nayak *et al.* (2001) Sakthivel (2001)
	Negative non-significant	Sawant *et al.* (1995) Vange *et al.* (1999)

2.1.5.1.3 Association of yield component characters with plant height in rice

Character	Nature of association	Reference
Number of productive tillers per plant	Positive significant	Janardhanam *et al*. (2001) Kavitha and Sree Rama Reddi (2001) Sakthivel (2001) Surender Raju (2002)
	Positive Non-significant	Roy *et al*. (1995) Yolanda and Vijendra Das (1995)
	Negative significant	Satya Priaya Lalitha and Sreedhar (1996) Meenakshi *et al*. (1999) Nayak *et al*. (2001) Paramesha *et al*. (2005)
	Negative non-significant	Sandyakishore (2005)
Panicle length	Positive significant	Janardhanam *et al*. (2001) Sakthivel (2001) Tarasatyavathi *et al*. (2001) Madhavilatha (2002) Sinha *et al*. (2004) Suman *et al*. (2006)
	Positive non-significant	Reddy *et al*. (1997) Debchaudhury and Das (1998) Rao and Shrivastav (1999)
	Negative significant	Ananda Kumar (1992)
Number of grains per panicle	Positive significant	Yolanda and Vijendra Das (1995) Satya Priya Lalitha and Sreedhar (1996) Nayak *et al*. (2001) Madhavilatha (2002)
	Positive non-significant	Geeta *et al*. (1994) Meenakshi *et al*. (1999) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Debchoudhury and Das (1998) Surender Raju (2002)
	Negative non-significant	Chauhan *et al*. (1993) Sawant *et al*. (1995) Reddy *et al*. (1997)

(Contd…. 2.1.5.1.3)

Character	Nature of association	Reference
Spikelet fertility	Positive significant	Yolanda and Vijendra Das (1995)
	Positive non-significant	Satpaty and Nanda (1978) Rao and Shrivastav (1999) Madhavilatha (2002)
100-grain weight	Positive and significant	Suman *et al.* (2006)
1000-grain weight	Positive and significant	Reddy *et al.* (1997) Suman (2003) Yogameenakshi *et al.* (2004)
	Positive and non-significant	Awasthi and Borthakur (1986) Ramesh Babu (1999)
	Negative significant	Sukanya Subramanian and Rathinam (1984)
	Negative non-significant	Roy *et al.* (1995) Meenakshi *et al.* (1999) Nayak *et al.* (2001)

2.1.5.1.4 Association of yield component traits with number of total tillers per plant in rice

Character	Nature of association	Reference
Number of productive tillers per plant	Positive significant	Shanta kumar *et al.*(1998) Babu and Soundarapandian (1990) Suman (2003)
Panicle length	Negative significant	Suman (2003)
Single plant yield	Positive significant	Suman (2003)

2.1.5.1.5 Association of yield component traits with number of productive tillers per plant in rice

Character	Nature of association	Reference
Plant height	Positive significant	Sakthivel (2001)
	Negative significant	Suman *et al.* (2006)
Panicle length	Positive significant	Roy *et al.* (1995) Janardhanam *et al.* (2001) Sakthivel (2001)
	Positive non-significant	Yolanda and Vijendra Das (1995) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Chaubey and Richharia (1993) Tarasatyavathi *et al*. (2001) Paramesha *et al.* (2005) Suman *et al.* (2006)
	Negative non-significant	Satya Priya Lalitha and Sreedhar (1996) Reddy *et al.* (1997) Sandyakishore (2005)
Number of grains per panicle	Positive significant	Sundaram *et al.* (1990) Meenakshi *et al.* (1999) Janardhanam *et al.* (2001)
	Positive non-significant	Geetha *et al.* (1994) Yolande and Vijendra Das (1995) Satya Priya Lalitha and Sreedhar (1996) Sandyakishore (2005)
	Negative significant	Chaubey and Richharia (1993) Tarasatyavathi *et al*. (2001)
	Negative non-significant	Roy *et al.* (1995) Reddy *et al.* (1997) Kavitha and Sree Rama Reddy (2001) Nayak *et al.* (2001)
Spikelet fertility (%)	Positive significant	Suryanarayana (2000)

(Contd…. 2.1.5.1.5)

Character	Nature of association	Reference
	Positive non-significant	Satpaty and Nanda (1978) Madhavilatha (2002)
	Negative non-significant	Verma *et al.*(1997)
100-grain weight	Negative significant	Mahto *et al*. (2003)
1000-grain weight	Positive and significant	Suryanarayana (2000) Sakthivel (2001)
	Positive and non-significant	Yolanda and Vijendra Das (1995) Meenakshi *et al*. (1999) Kavitha and Sree Rama Reddy (2001) Tarasatyavathi *et al*. (2001)
	Negative significant	Gopinath *et al*. (1984) Nayak *et al*. (2001)
	Negative non-significant	Nanja Reddy *et al*. (1995) Roy *et al*. (1995) Reddy *et al*. (1997) Sandyakishore (2005)

2.1.5.1.6 Association of yield component traits with panicle length in rice

Character	Nature of association	Reference
Days to 50 per cent flowering	Positive significant	Bala (2001) Sakthivel (2001)
Plant height	Positive significant	Bala (2001) Sakthivel (2001) Suman *et al.* (2006)
Total number of tillers per plant	Negative significant	Suman *et al.* (2006)
Number of productive tillers per plant	Positive significant	Bala (2001)
	Negative significant	Suman *et al.* (2006)
Number of grains per panicle	Positive significant	Satya Priya Lalitha and Sreedhar (1996) Ganesan *et al.* (1997) Janardhanam *et al.* (2001) Kavitha and Sree Rama Reddy (2001) Yogameenakshi *et al.* (2004)
	Positive non-significant	Reddy *et al.* (1997) Deb Choudhury and Das (1998) Tarasatyavathi *et al.* (2001)
	Negative significant	Gopinath *et al.* (1984) Paramesha *et al.* (2005)
	Negative non-significant	Sawant *et al.* (1995)
Spikelet fertility (%)	Positive significant	Yolanda and Vijendra Das (1995)
	Positive non-significant	Rao and Shrivastav (1999) Suryanarayana(2000) Madhavilatha (2002) Sandyakishore (2005)
1000-grain weight	Positive significant	Gopinath *et al.* (1984) Yogameenakshi *et al.* (2004)
	Positive and non-significant	Reddy *et al.* (1997) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Sukanya Subramanian and Rathinam (1984) Sandyakishore (2005)
	Negative and non-significant	Roy *et al.* (1995) Vange *et al.* (1999) Nayak *et al.* (2001)

2.1.5.1.7 Association of the yield component traits with number of grains per panicle in rice

Character	Nature of association	Reference
Spikelet fertility (%)	Positive significant	Yolanda Vijendra Das (1995)
	Positive non-significant	Verma *et al.*(1997) Suryanarayana (2000) Madhavilatha (2002)
100-seed weight	Positive significant	Meenakshi *et al.*(1999)
1000-grain weight	Positive significant	Ravindranath *et al.* (1982)
	Positive non-significant	Nanja Reddy *et al.* (1995) Meenakshi *et al.* (1999)
	Negative significant	Geetha *et al.* (1994) Nayak *et al.* (2001)
	Negative non-significant	Reddy *et al.* (1997) Vange *et al.* (1999) Kavitha and Sree Rama Reddi (2001)

2.1.5.1.8 Association of yield component traits with spikelet fertility in rice

Character	Nature of association	Reference
1000-grain weight	Positive significant	Ravindranath *et al.* (1982)
	Positive non-signifiant	Nanja Reddy *et al.* (1995) Meenakshi *et al.* (1999)
	Negative significant	Geetha *et al.* (1994) Nayak *et al.* (2001)
	Negative non-significant	Reddy *et al.* (1997) Vange *et al.* (1999) Kavitha and Sree Rama Reddi (2001)

2.1.5.2 Path coefficient analysis

Path coefficient analysis, a statistical device developed by Wright (1921) helps in partitioning the correlation coefficients into direct and indirect effects of independent variable on dependent variable. As grain yield is a complex character influenced by several factors, selection based on simple correlation without taking into consideration between the component characters is not effective. Hence, path analysis is of much importance in any plant breeding programme. Correlation in combination with path analysis would give a better insight into cause and effect relationship between different pairs of characters. Dewey and Lu (1959) and Frakes (1961) demonstrated the utility of path coefficient analysis in plant selection and since then its application has been extended to almost every crop.

The findings of earlier workers on the relative contribution of different characters to grain yield in rice are furnished hereunder in a tabular form:

2.1.5.2.1 Direct effects of yield contributing characters on grain yield in rice

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Days to 50 per cent flowering	Saravanan *et al*., (1996) Rather *et al*., (1997) Selvarani and Rangaswamy (1998) Balan *et al.* (1999) Bala (2001) Mahto *et al.* (2003) Khedikar *et al.* (2004) Sandya kishore (2005) Patil and Sarawgi (2005) Manonmani and Ranganathan (2006)	Debchoudhury and Das (1998) Gupta *et al.* (1998) Kavitha and Sree Rama Reddi (2001) Nayak *et al.* (2001) Borbora *et al.* (2005) Samonte *et al.* (2006)
Plant height	Meenakshi *et al.* (1999) Bala (2001) Janardhanam *et al.* (2001) Kavitha and Sree Rama Reddi (2001) Nagajyothi (2001) Nayak *et al.* (2001) Babu *et al*. (2002) Madhavilatha (2002) Mishra and Verma (2002) Borbora *et al.* (2005) Sandya kishore (2005) Samonte *et al.* (2006)	Genctan *et al.*(1994) Gupta *et al.* (1998) Tarasatyavathi *et al*. (2001) Paramesha *et al.* (2005) Suman *et al.* (2006)
Total number of tillers per plant	Singh *et al.* (2002) Srikrishnadevarayalu (1993) Samonte *et al.* (2006)	
Number of productive tillers per plant	Meenakshi *et al.* (1999) Nayak *et al.* (2001) Satish *et al*. (2003) Khedikar *et al.* (2004) Yogameenakshi *et al.* (2004) Madhavilatha *et al.* (2005) Patil and Sarawgi (2005) Sandya kishore (2005) Monalisa *et al.* (2006)	Valarmathi and Leenakumary (1998) Kavitha and Sree Rama Reddi (2001) Somnath Bhattacharya and Ghosh (2004) Tayeng and Singh (2006)
Panicle length	Kavitha and Sree Rama Reddi (2001) Nagajyothi (2001) Mishra and Verma (2002) Suman (2003) Khedikar *et al.*(2004) Suman *et al.*(2006) Tayeng and Singh (2006)	Ganesan *et al.* (1997) Nayak *et al.* (2001) Madhavilatha (2002) Sandya kishore (2005)

(Contd…. 2.1.5.2.1)

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Number of grains per panicle	Janardhanam *et al.* (2001) Nayak *et al.* (2001) Madhavilatha (2002) Satish *et al.* (2003) Yogameenakshi *et al.* (2004) Paramesha *et al.* (2005) Sandya kishore (2005) Manonmani and Ranganathan (2006) Monalisa *et al.* (2006) Tayeng and Singh (2006)	Amirthadevarathinam (1990) Gupta *et al.* (1998)
Spikelet fertility (%)	Kumar *et al.*(1998) Madhavilatha (2002) Paramesha *et al.* (2005)	Yolanda and Vijendra Das (1995) Saravanan *et al.*(1996)
100- grain weight	Manonmani and Ranganathan (2006)	---
1000-grain weight	Nayak *et al.* (2001) Tarasatyavathi *et al.* (2001) Madhavilatha (2002) Suman (2003) Khedikar *et al.* (2004) Yogameenakshi *et al.* (2004)	Reddy *et al.* (1997) Gupta *et al.* (1998) Selvarani and Rangaswamy (1998) Kavitha and Sree Rama Reddi (2001) Borbora *et al.* (2005)

2.1.5.2.2 Indirect effects of yield contributing characters on grain yield in rice

2.1.5.2.2.1 Indirect effects of days to 50 per cent flowering on grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Plant height	Meenakshi *et al.* (1999) Nayak *et al*. (2001) Madhavilatha (2002) Manonmani and Ranganathan (2006)	Saravanan *et al*. (1996) Debchoudhury and Das (1998)
Number of productive tillers per plant	Gupta *et al*. (1998) Madhavilatha (2002)	Meenakshi *et al*.(1999) Kavitha and Sree Rama Reddi (2001)
Panicle length	Gupta *et al*. (1998) Kavitha and Sree Rama Reddi (2001)	Nayak *et al*. (2001) Madhavilatha (2002)
Number of grains per panicle	Debchoudhury and Das (1998) Nayak *et al*. (2001) Madhavilatha (2002) Sandya kishore (2005)	Gupta *et al*. (1998) Meenakshi *et al*. (1999)
Spikelet fertility (%)	Suryanarayana (2000)	Saravanan *et al*.(1996) Madhavilatha (2002)
1000-grain weight	Kavitha and Sree Rama Reddi (2001) Madhavilatha (2002)	Meenakshi *et al*. (1999) Nayak *et al*.(2001)

2.1.5.2.2.2 Indirect effects of plant height on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Gupta *et al.* (1998) Madhavilatha (2002) Sandya kishore (2005)	Sinha *et al.* (1999) Kavitha and Sree Rama Reddi (2001)
Number of productive tillers per plant	Valarmathi and Leenakumary (1998) Janardhanam *et al.* (2001) Nagajyothi (2001) Madhavilatha (2002) Suman *et al.* (2006)	Ganesan *et al.* (1997) Nayak *et al.* (2001) Tarasatyavathi *et al.* (2001)
Panicle length	Genctan *et al.* (1994) Nagajyothi (2001) Tarasatyavathi *et al.* (2001) Babu *et al.* (2002) Suman *et al.* (2006)	Nayak *et al.* (2001) Madhavilatha (2002)
Number of grains per panicle	Genctan *et al.* (1994) Debchoudhury and Das (1998) Babu *et al.* (2002) Madhavilatha (2002) Sandya kishore (2005)	Valarmathi and Leenakumary (1998) Suryanarayana (2000)
Spikelet fertility (%)	Babu *et al.* (2002) Madhavilatha (2002)	Saravanan *et al.*(1996) Suryanarayana (2000)
100 - grain weight		Suman *et al.* (2006)
1000-grain weight	Sarvanan *et al.* (1996) Nagajyothi (2001) Madhavilatha (2002)	Reddy *et al.* (1997) Nayak *et al.* (2001)

2.1.5.2.2.3 Indirect effects of total number of tillers per plant on grain yield through

Character	Positive indirect effect	Negative indirect effect
Panicle length	Singh *et al.* (2002)	---
Number of grains per panicle	Singh *et al.* (2002)	---

2.1.5.2.2.4 Indirect effects of number of productive tillers per plant on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Nayak *et al*. (2001) Madhavilatha (2002) Sandya kishore (2005)	Amirthadevarathinam (1990) Kavitha and Sree Rama Reddi (2001)
Plant height	Janardhanam *et al*. (2001) Nagajyothi (2001) Madhavilatha (2002)	Ravindra Babu (1996) Reddy *et al*. (1997)
Panicle length	Gupta *et al*. (1998) Nagajyothi (2001) Madhavilatha (2002)	Kavitha and Sree Rama Reddi (2001) Nayak *et al*. (2001) Manonmani and Ranganathan (2006)
Number of grains per panicle	Gupta *et al*.(1998) Janardhanam *et al*. (2001) Tarasatyavathi *et al*. (2001) Sandya kishore (2005)	Valarmathi and Leenakumary (1998) Nayak *et al*. (2001) Madhavilatha (2002)
Spikelet fertility (%)	Saravanan *et al*.(1996) Suryanarayana (2000) Madhavilatha (2002)	---
1000-grain weight	Reddy *et al*. (1997) Nagajyothi (2001) Tarasatyavathi *et al*. (2001)	Ganesan *et*. *al*. (1997) Nayak *et al*. (2001) Madhavilatha (2002)

2.1.5.2.2.5 Indirect effects of panicle length on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per-cent flowering	Bala (2001) Kavitha and Sree Rama Reddi (2001) Madhavilatha (2002) Sandya kishore (2005)	Debchoudhury and Das (1998)
Plant height	Valarmathi and Leenakumary (1998) Bala (2001) Nayak *et al.* (2001) Madhavilatha (2002) Sandya kishore (2005)	Tarasatyavathi *et al.* (2001) Janardhanam *et al.* (2001)
Number of productive tillers per plant	Valarmathi and Leenakumary (1998) Bala (2001) Nayak *et al.* (2001)	Tarasatyavathi *et al.* (2001) Madhavilatha (2002)
Number of grains per panicle	DebChoudhury and Das (1998) Nayak *et al.* (2001)	Amirthadevarathinam (1990)
Spikelet fertility (%)	Saravanan *et al.*(1996) Madhavilatha (2002)	Suryanarayana (2000)
1000-grain weight	Ganesan *et al.* (1997) Nagajyothi (2001) Madhavilatha (2002)	Nayak *et al.* (2001)

2.1.5.2.2.6 Indirect effects of number of grains per panicle on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Gupta *et al.* (1998) Madhavilatha (2002) Sandya kishore (2005)	Kavitha and Sree Rama Reddi (2001) Nayak *et al.* (2001) Manonmani and Ranganathan (2006)
Plant height	Valarmathi and Leenakumari (1998) Nayak *et al.* (2001) Madhavilatha (2002) Sandya kishore (2005)	Reddy *et al.* (1997) Debchoudhury and Das (1998) Manonmani and Ranganathan (2006)
Number of productive tillers per plant	Amrithadevarathinam (1990) Valarmathi and Leenakumary (1998) Sandya kishore (2005)	Satya Priya Lalitha and Sreedhar (1996) Ganesan *et al.* (1997) Nayak *et al.* (2001) Madhavilatha (2002) Manonmani and Ranganathan (2006)

(Contd…. 2.1.5.2.2.6**)**

Panicle length	Amirthadevarathinam (1990) Satya Priya Lalitha and Sreedhar (1996) Reddy *et al.* (1997)	Nayak *et al.* (2001) Madhavilatha (2002) Manonmani and Ranganathan (2006)
Spikelet fertility (%)	Suryanarayana (2000) Madhavilatha (2002)	Saravanan *et al.*(1996)
1000-grain weight	Ganesan *et al.* (1997) Reddy *et al.* (1997) Madhavilatha (2002)	Tarasatyavathi *et al.* (2001)

2.1.5.2.2.7 Indirect effects of spikelet fertility on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Saravanan *et al.*(1996) Suryanarayana (2000)	
Plant height	Suryanarayana (2000) Madhavilatha (2002)	Saravanan *et al.*(1996)
Number of productive tillers per plant	Madhavilatha (2002)	Saravanan *et al.*(1996) Suryanarayana (2000)
Panicle length		Saravanan *et al(*1996) Suryanarayana (2000) Madhavilatha (2002)
Number of grains per panicle	Saravanan *et al.*(1996) Madhavilatha (2002)	Suryanarayana (2000)
1000-seed weight	Saravanan *et al.*(1996) Suryanarayana (2000)	Madhavilatha (2002)

2.1.5.2.2.8 Indirect effects of 100-grain weight on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering		Manonmani and Ranganathan (2006)
Plant height	Manonmani and Ranganathan (2006)	---
Number of productive tillers per plant	Manonmani and Ranganathan (2006)	---

(Contd…. 2.1.5.2.2.8)

Panicle length	Manonmani and Ranganathan (2006)	
Number of grains per panicle		Manonmani and Ranganathan (2006)

2.1.5.2.2.9 Indirect effects of 1000-grain weight on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Nayak *et al.* (2001) Madhavilatha (2002)	Sinha *et al.* (1999)
Plant height	Reddy *et al.* (1997) Nagajyothi (2001) Madhavilatha (2002)	Ganesan *et al.* (1997)
Number of productive tillers per plant	Tarasatyavathi *et al.* (2001) Nagajyothi (2001)	Kavitha and Sree Rama Reddi (2001) Madhavilatha (2002)
Panicle length	Nagajyothi (2001) Nayak *et al.* (2001)	Gupta *et al.* (1998) Madhavilatha (2002)
Number of grains per panicle	Tarasatyavathi *et al.* (2001) Madhavilatha (2002)	Reddy *et al.* (1997) Nayak *et al.* (2001)

2.2 GENOTYPING OF SELECTED GERMPLASM LINES OF RICE USING SSR MARKERS

Initially, morphological markers were used for the identification of genetic diversity. Later, the biochemical markers like proteins and isozymes were used for the purpose since they provided for rapid analysis which can be done during early stages of crop growth. However, their reliability is questionable due to environmental influences. Recently, the molecular markers have gained prominence as they are heritable, discriminate between the individuals examined, easy to measure and evaluate, provide comparable results, and known to be either neutral or unlinked.

Wide arrays of molecular techniques that can be used to detect polymorphism at the DNA level have been described in the recent times. Most molecular markers fall into one of three basic categories that use either hybridization based (non-PCR) techniques, arbitrarily primed PCR or other PCR based multilocus profiling techniques and sequence targeted and single locus PCR. Some techniques are also derivatives or combinations of other techniques.

Rice, a member of the gramineae family, has a genome size of 0.45 x 10^{-9} bp (Arumungathan and Earle, 1991), which is one tenth the size of the human genome and is a model system for cereal genome analysis. A wide variety of DNA markers have been extensively used in rice for genetic diversity analysis, cultivar identification, phylogenetic and evolutionary studies and tagging genes and quantitative traits of agronomic importance and marker assisted selection.

One of the DNA markers, simple sequence repeats which hold greater promise in varietal identification, genetic purity assessment and diversity studies in near future are discussed.

Simple sequence repeats (SSRs), commonly referred to as microsatellites are DNA sequences that are randomly repeated mono to hexa nucleotide units such as (AT), (CTT) and (AT & T).These small repetitive DNA sequences are ubiquiotous in eukaryotic genomes and exhibit highly variable numbers of repeats at a locus and referred as simple sequence length polymorphism (SSLP). Their abundance and hypervariability make them valuable as genetic markers (Weber and May, 1989). They provide the basis of polymerase chain reaction (PCR) based multi-allelic and co dominant marker system. PCR primers complementary to the flanking region are used to amplify SSR containing DNA fragment. Length polymorphism is created when PCR product from different individuals vary in length as a result of variation in the number of repeat units in the SSR (Cregan, 1992). Of the several DNA markers available, microsatellites or SSRs are considered to be the ideal genetic markers. The first published study on microsatellites in plants was made by Candit and Hubbell (1991) who reported abundant occurrence of microsatellites in plants. There after, SSR markers have been developed for several plant species including rice (Zhao and Kochert, 1992; Wu and Tanksley, 1993), soybean (Akkaya *et al*., 1992), barley (Saghai-Maroof *et al*., 1994), etc. The first application of microsatellite in plants has been in cultivar identification and purity assessments and they are markers of choice in genotyping cultivars and for germplasm characterization (Weising *et al*., 1991; Beyermann *et al*., 1992). The structure and length of simple sequence repeats are considered to be the major factors affecting microsatellite variability (Mc Murry 1995). In general, SSLP loci with more repeats tend to be more polymorphic and have larger amplitude of variation (Weber 1990; Goldstein and Clark 1995; Innan *et al*., 1997; Schug *et al*., 1998)

In rice, more than 2740 microsatellite markers have been developed and used to construct genetic maps (Wu and Tanksley, 1993; Akagi *et al*., 1996; Panaud *et al*., 1996; Chen *et al*., 1997; Temnykh *et al*., 2000; 2001). These markers provide important landmarks that are well distributed throughout the rice genome. SSRs have been widely used in rice genetics to fingerprint accessions, analyse diversity, identify introgressions in interspecific crosses, trace pedigrees, genetic purity assessments, etc. They are valuable as genetic markers because they are codominant, detect high level of allelic diversity, and are assayed efficiently by the polymerase chain reaction (Mc Couch *et al*., 1997).

Zhou and Gustafson (1995) were able to identify and fingerprint 57 rice cultivars released in USA using microsatellites. They demonstrated the discriminating power of the microsatellites by distinguishing 40 colours related one out of the total 57 varieties. Akagi *et al*., (1997), based on microsatellite analysis of closely related *japonica* varieties, recommended an identification system based on three highly polymorphic microsatellite markers to maintain genetic purity of rice seeds by eliminating contamination. Garland *et al*., (1999) was able to uniquely identify 43 rice cultivars using 10 microsatellite markers and they have also shown that most cultivars were uniquely identified by atleast one microsatellite marker. Bligh *et al.* (1999) recommended SSLP as the method of choice using 29 SSLP sets to identify premium quality rices through DNA isolated from milled and brown rice.

Many studies have reported significantly greater allelic diversity of microsatellites over RFLPs (Mc Couch *et al*., 1997) and high numbers of alleles for rice microsatellite markers. It has been found that genetically mapped microsatellite markers cover the whole rice genome with atleast one microsatellite for every 157 kb (<1 cM) (Chen *et al*., 1997; Mc Couch *et al*., 2002). Rice microsatellites have been demonstrated to be polymorphic between (Yang *et al*., 1994; Akagi *et al*., 1997; Olufowote *et al*., 1997) and within rice varieties (Olufowote *et al*., 1997). Akagi *et al*. (1997) found 5 to 10 alleles among 59 closely related *Japonica* cultivars. Panaud *et al*. (1996) found 2 to 9 alleles for microsatellite markers in 22 *Japonica* and *Indica* cultivars and Yang *et al*. (1994) found 3 to 25 alleles for 10 microsatellite markers among 238 accessions of *Indica* and *Japonica* cultivars and landraces.

Mackill *et al.* (1996) found that microsatellites have average polymorphisms atleast 1.5 times higher than AFLP and RAPD markers in a comparison of 12 *Japonica* cultivars. Provan *et al.* (1997) using SSR detected intra and inter cultivar polymorphism between the cultivated and wild rice and the extent of chloroplast genomic differentiation was quantified. Olufowote *et al.* (1997) found microsatellite to be more powerful for the assessment of within cultivar variation. Sebastian *et al*. (1998) studied the molecular diversity of Philippine landraces and cultivars and found that diversity is more in land races compared to modern cultivars. Subudhi *et al*. (1998) classified 71 cytoplasmic genetic male sterile lines of rice into different groups. Use of microsatellite polymorphisms for the identification of Australian breeding lines of rice was investigated by Garland *et al*. (1999) and most of the cultivars could be uniquely identified by atleast one microsatellite marker. These markers are useful for assessment of hybrid seed purity and for genotype identification (Temnykh *et al*., 2000). Application of SSR markers in estimation of diversity among cultivars, inbreds and parental lines have been reported in rice (Enoki *et al*., 2002; Naveenkumar, 2003).

CHAPTER III

MATERIAL AND METHODS

The present study work was conducted during *Rabi*, 2007 at Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad, A.P., India, situated at 17.53°N latitude, 78.27°E longitude and altitude of 545m above mean sea level. The meteorological data pertaining to weekly rainfall, minimum and maximum temperature, relative humidity, wind velocity, evaporation and bright sunshine hours of the entire crop growing period have been presented in Table 3.1 and Fig. 3.1.

The experimental materials used and methods adopted in the present study are outlined below:

3.1 MATERIAL

The materials comprised of one hundred and fifty rice germplasm accessions including five improved varieties viz., Jaya, Mandya vijaya, Prasanna, Rasi and Vasumathi as standard checks, collected from Directorate of Rice Research, Rajendranagar, Hyderabad. The details of genotypes are furnished in Table 3.2.

3.2 METHODS

The entire investigation was carried out by conducting two experiments.

Experiment 1: Diversity studies on germplasm accessions of rice through field evaluation.

Experiment 2: Diversity studies of selected germplasm lines of rice using SSR Markers.

3.2.1 Diversity studies on germplasm accessions of rice through field evaluation

The experiment was laid out in a Randomized Block Design (RBD) with three replications. The material consisted of one hundred and fifty rice germplasm lines including five check varieties. Thirty days old seedlings were transplanted 20 cm apart between rows and 15 cm within the row. Each accession was grown in three rows and in each row 25 hills were maintained. All necessary precautions were taken to maintain uniform plant population in each treatment per replication (plate 3.1). All the recommended package of practices were adopted besides providing necessary prophylactic plant protection measures to raise a good crop.

3.2.1.1 Collection of data

Single plant observations were recorded on five plants selected at random in each genotype from the middle row in each replication. The mean of five plants for all the characters except days to 50% flowering were utilized for statistical analysis. Days to 50% flowering was recorded replication wise on plot basis. Following observations were recorded at appropriate growth stages.

3.2.1.1.1 Qualitative characters

Visual observations were recorded on single plant basis on ten randomly selected plants in each genotype as per standard descriptors of IRRI (Table 3.3) on eleven qualitative characters *viz*., early plant vigour, basal leaf sheath colour, leaf colour, leaf pubescence, ligule shape, ligule colour, panicle exsertion, panicle type, stigma colour, awning and threshability at appropriate growth stage.

3.2.1.1.2 Quantitative characters

Data on eleven yield and its attributing characters were recorded on five randomly selected plants in each plot. These characters were measured as per the standard techniques and the mean of five plants for all the characters except days to 50% flowering was utilized for carrying out statistical analysis. For days to 50% flowering the data was recorded on plot basis.

3.2.1.1.2.1 Days to 50% flowering

The number of days taken from sowing to the days when primary panicles in 50 per cent plants in each plot and in each replication were in heading was recorded.

3.2.1.1.2.2 Plant height (cm)

Plant height was measured in centimeters from ground level to the tip of the tallest panicle in each hill at the time of harvest.

3.2.1.1.2.3 Leaf length (cm)

Leaf length (cm) was measured on the penultimate leaf with small scale in centimeters from base of leaf to the tip of the leaf in each plant at the time of harvest.

3.2.1.1.2.4 Leaf width (cm)

Leaf width (cm) was measured on the penultimate leaf with small scale in centimeters each plant at the time of harvest.

3.2.1.1.2.5 Number of tillers per plant

Number of tillers in each hill at maturity was recorded.

3.2.1.1.2.6 Number of productive tillers per plant

Number of ear bearing tillers in each hill at maturity was counted.

3.2.1.1.2.7 Panicle length (cm)

It was measured in centimeters with a scale from the panicle base node to the tip of last spikelet prior to harvesting.

3.2.1.1.2.8 Number of grains per panicle

Numbers of grains were counted from five panicles of each selected plant and this average was recorded.

3.2.1.1.2.9 Spikelet fertility (%)

Number of filled grains and chaffy grains in each panicle were counted and fertility percentage was calculated by dividing the filled grains with total number of grains per panicle and expressed in percentage.

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled grains per panicle}}{\text{Total Number of grains per panicle}} \times 100$$

3.2.1.1.2.10 100-grain weight (g)

One hundred well filled grains were counted at random from each genotype per replication and weighed after thorough drying at 13 per cent moisture content and recorded in grams, with the help of electronic top pan balance (Precision of 0.001 g).

3.2.1.1.2.11 Single plant yield (g)

The weight of filled grains harvested from each plant was recorded in grams after drying the grains to the required moisture content (13%).

3.2.1.2 Statistical analysis

The data with respect to the above characters were subjected to the following analysis with the help of standard statistical procedures:

1. Analysis of variance
2. Genotypic and phenotypic coefficients of variation
3. Heritability and genetic advance
4. Estimation of genetic divergence using Mahalanobis's generalized distances (D^2)
5. Estimation of correlation coefficients
6. Direct and indirect effects of characters using path coefficient analysis

3.2.1.2.1 Analysis of variance

Analysis of variance was computed based on randomized block design for each of the character separately as per standard statistical procedure (Panse and Sukhatme, 1978). The significance was tested by referring to the values of 'F' table (Fisher and Yates, 1967).

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

Where,

y_{ij} = Phenotypic observation of i^{th} genotype and j^{th} replication

μ = General mean

g_i = Effect of i^{th} genotype

r_j = Effect of j^{th} replication

e_{ij} =Rrandom error associated with i^{th} genotype and j^{th} replication

The analysis of variance for each character was carried out as indicated below:

Source	**Degrees of freedom**	**Mean sum of squares**	**F-ratio**
Replications	(r-1)	M's	M's/M'e
Treatments	(t-1)	M't	M't/M'e
Error (e)	(r-1) (t-1)	M'e	
Total	(tr-1)	TMSS	

Where,

r and t = Number of replications and treatments, respectively

M's, M't and M'e = Mean sum of squares due to replications, treatments and error respectively

Variance

The genotypic and phenotypic variances were calculated as per the following formulae given by Burton and Devane, 1953.

$$\text{Genotypic variance } (\sigma^2 g) = \frac{(\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error})}{\text{Number of replications}}$$

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

Where $(\sigma^2 e)$ = Error variance

3.2.1.2.2 Genotypic and phenotypic coefficients of variation

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

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

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

Categorization of the range of variation was effected as proposed by Sivasubramanian and Madhavamenon (1973).

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

3.2.1.2.3 Heritability and genetic advance

i) Heritability (Broad sense)

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

h^2 = Heritability in broad sense

$\sigma^2 g$ = Genotypic variance

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

$\sigma^2 e$ = Environmental variance

As suggested by Johnson *et al*. (1955) the estimates of heritability in broad sence were categorized as:

Low	:	0-30%
Medium	:	30-60%
High	:	above 61%

ii) Genetic advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

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

Where,
GA = Expected genetic advance
K = Selection differential, the value of which is 2.06 at 5 per cent selection intensity
σp = Phenotypic standard deviation
$h^2\ (b)$ = Heritability in broad sense

In order to visualize the relative unity of genetic advance among the characters, genetic advance as per cent for mean was computed.

$$\text{Genetic advance as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

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

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

3.2.1.2.4 Genetic diversity

The genetic divergence between one hundred and fifty genotypes was estimated using Mahalanobis (1936) using D^2 statistic technique.

D^2 value between i^th^ and j^th^ genotypes for 'P' characters was calculated as:

$$D^2_{ij} = \sum_{t=1}^{P} (\overline{Y}_{it} - \overline{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of ith genotype for 't' character

Y_{jt} = Uncorrelated mean values of jth genotype for 't' characters

and D^2_{ij} = D^2 between ith and jth genotype

The various steps involved in estimation of D^2 values are given below:

3.2.1.2.4 .1 Test of significance:

Variances were calculated for all eleven characters investigated and Test of significance was carried. Analysis of covariance (ANCOVA) for the character pairs was estimated on the basis of mean values. From these estimates, a dispersion table was prepared. After testing the differences between the genotypes for each of the characters, a simultaneous test of significance of differences between the mean values of a number of correlated variables was done by using V statistic which in turn utilizes Wilk' s criterion (Rao, 1952)

Wilk's criterion '^' $|E| / |E+V|$

$|E|$ = Determinant of error matrix

$|E+V|$ = Determinant of (genotypes + error) sum of squares and sum of product

Matrix.

Then the value of 'V' statistic was worked out using Wilk' s lambda criterion

'V' $_{(stat)}$ = -m log $_e$'^'

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

p = number of characters

q = number of genotypes

n = degrees of freedom (for error +genotypes)

e = 2.7183

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

3.2.1.2.4.2 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation values of the differences in mean values of various characters of the two genotypes i.e., di^2. Therefore, transformation of correlated variables to uncorrelated one was done before working out the D^2 values. Transformation was done by using pivotal consideration method.

3.2.1.2.4.3 Computation of D^2 values

For a given combination of 'i' and 'j' genotype, the mean deviation *i.e.,* $\overline{Y_{it}} - \overline{Y_{jt}}$ for t = 1, 2 …….. P variables were computed and D^2 values were calculated as sum of squares deviations:

$$D^2_{ij} = \sum_{t=1}^{P} (\overline{Y}_{it} - \overline{Y}_{\underline{jt}})^2$$

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for‘t’ character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for‘t’ character

D^2_{ij} = D^2 between i^{th} and j^{th} genotype

3.2.1.2.4.4 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of X^2 and was tested against the tabulated value of X^2 for P degrees of freedom, where P was the number of characters considered.

3.2.1.2.4.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries (di = yit-yjt). Rank 1 was given to the highest mean difference and rank P to the lowest difference, where P is the total number of characters considerd. Percentage contribution of each character towards genetic divergence was calculated using the formula:

$$\text{Percentage contribution of character X} = \frac{N \times 100}{M}$$

Where,

N = Number of genotype contributions where the character was ranked first

M = All possible combinations of genotypes considered

3.2.1.2.4.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should at least on an average show an average of smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other.For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of their magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with the two genotypes having the smallest distance from each other were considered first to which a third population having the smallest average D^2 value from the first two genotypes was added. Similarly, next nearest fourth genotype was considered and this procedure was continued. At certain stage where it was felt that after adding a particular genotype, there was abrupt increase in the average D^2 value, that population was not considered for including in that cluster. The group of the first cluster was then omitted and the rest was treated in a similar way. This process was continued till all the genotypes were included into one or other clusters.

3.2.1.2.4.7 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D^2_i/n$

Where,

ΣD^2_i = Sum of distances between all possible combinations (n) of the Populations included in a cluster

n = Number of clusters

3.2.1.2.4.8 Average inter-cluster distance

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

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

$$\text{Average inter cluster distance} = \frac{D^2}{n_1 \text{ x } n_2}$$

When n_1 and n_2 are the number of genotypes in cluster 1 and cluster 2, respectively. Based on the ‘D’ values, the genotypes were categorised as indicated below

3.2.1.2.4.9 Canonical analysis

Canonical analysis was used to compare the clustering pattern obtained by Mahalanobis’s D^2 statistic. The canonical roots vectors were calculated to present the genotypes in the graphical form (Rao, 1952).

3.2.1.2.4.10 Calculation of sum of squares and sum of products

The correlated means were transformed into uncorrelated variables. From the transformed variables, sum of squares and sum of product for each character and character combinations were computed to obtain the matrix of variances and co-variance (matrix-A). Matrix $(A)^p$ was then divided from matrix A where P is the number of characters.

3.2.1.2.4.11 Calculation of first vector

Taking the sum column totals of matrix $(A)^p$, dividing by the highest quantity among them, the first approximate trial vector was estimated. The first approximate trial vector can be checked by interaction, multiply each column of matrix $(A)^p$ with the first trial vector to get another column vector. Dividing each value of the second column vector by the highest value among then, the second approximation vector was obtained. This new vector was taken them as a trial vector and the procedure was repeated till the elements of the second approximation vectors were the same. Then the vectors were standardized by dividing them by correlated sum of squares of these vectors. The first root ‘n’ was calculated p^{th} root of the highest column total of the last approximation.

3.2.1.2.4.12 Calculation of second vector

For getting the second vector ϖ^2, the original $(A)^p$ matrix was transformed and represented $(B)^p$. In $(B)^p$, each $(i, j)^{th}$ element was calculated as follows:

$(I,j)^{th}$ element = $(A)^p - \lambda_1 X_1^{th}$ element X_j^{th} element of the first vector

The procedure followed in case of matrix A was repeated to obtain the second canonical root.

3.2.1.2.4.13 Estimation of Z values

From the values of Y_1, Y_2 . . . . Y_{ij} the mean values of characters considered Z_1, Z_2, Z_3 were calculated as:

$$Z_1 = (Y)(V_1); \qquad Z_2 = (Y)(V_2)$$

Where,

(Y) = mean transformed value

V_1, V_2 = the first and second vectors, respectively

The mean values Z_1, and Z_2 for each genotype were represented in a 2-dimensional diagram.

3.2.1.2.4.14 Contribution of Vectors towards divergence

Total contribution of all the vectors was given by the sum of diagonal elements in matrix A.

$$\text{Per cent contribution of vector '1' } (X_1) = \frac{\lambda_1 \times 100}{\text{Total contribution of all vectors}}$$

$$\text{Per cent contribution of vector '2' } (X_2) = \frac{\lambda_2 \times 100}{\text{Total contribution of all vectors}}$$

$$\text{Per cent contribution of vector '3' } (X_3) = \frac{\lambda_3 \times 100}{\text{Total contribution of all vectors}}$$

Where, ‘λ’ are canonical roots.

3.2.1.2.5 Character Association

Correlation coefficients were calculated to determine the degree of association of yield components with seed yield and also with seed yield and also among themselves.

Correlation coefficients were calculated at genotypic and phenotypic level using the formulae suggested by Falconer (1964).

$$\text{Genotypic coefficient of correlation } (r_g) = r(x_i . x_j)g = \frac{\text{Cov.}(x_i . x_j)g}{\sqrt{v(x_i)g . v(x_j)g}}$$

Where,

$r(x_i.x_j)g$ = Genotypic correlation between ith and jth characters

$\text{Cov.}(x_i . x_j)g$ = Genotypic covariance between ith and jth characters

$v(x_i)g$ = Genotypic variance of ith character

$v(x_j)g$ = Genotypic variance of jth character

$$\text{Phenotypic coefficient of correlation } (r_p) = r(x_i . x_j)p = \frac{\text{Cov.}(x_i . x_j)p}{\sqrt{v(x_i)p . v(x_j)p}}$$

Where,

$r(x_i.x_j)p$ = Phenotypic correlation between ith and jth characters

$\text{Cov.}(x_i . x_j)p$ = Phenotypic covariance between ith and jth characters

$v(x_i)p$ = Phenotypic variance of i^{th} character

$v(x_j)p$ = Phenotypic variance of j^{th} character

The phenotypic and genotypic correlation coefficients were compared against 'r' values given in Fisher and Yates (1967) tables for n-2 degrees of freedom at 0.05 and 0.01 level of probability to test their significance.

3.2.1.2.5.1 Path coefficient analysis

The direct and indirect effects of yield components on yield both at genotypic and phenotypic level were estimated by taking seed yield as dependent variable, using path coefficient analysis suggested by Wright (1921) and is illusrated by Dewey and Lu (1959). The path coefficients were obtained by solving the 'P' normal equations following the matrix method given by Singh and Choudhary (1977). Correlations among all the variables were utilized to set up the simultaneous equations.

$$r_{1y} = P_{1y} r_{11} + P_{2y} r_{12} + P_{3y} r_{13} \dots\dots\dots\dots + P_{ny} r_{1n}$$

$$r_{2y} = P_{1y} r_{21} + P_{2y} r_{22} + P_{3y} r_{23} \dots\dots\dots\dots + P_{ny} r_{2n}$$

$$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \dots\dots\dots\dots + P_{ny} r_{nn}$$

Where,

1, 2 .... n = Independent variable

y = Dependent variable (yield per plant)

$r_{1y}\ r_{2y} \dots\dots\dots\ r_{ny}$ = Coefficient of correlation between causal factors '1' to 'n' on dependent character 1

$p_{1y}\ P_{2y} \ldots\ldots\ P_{ny}$ = Direct effect of characters 1 to n on character

The above equations can be written in matrix form as:

$$\overset{A}{\begin{pmatrix} r_{1y} \\ r_{2y} \\ : \\ : \\ r_{ny} \end{pmatrix}} = \overset{C}{\begin{pmatrix} 1 & r_{12} & r_{13} & \ldots\ldots\ r_{1n} \\ r_{21} & 1 & r_{23} & \ldots\ldots\ r_{2n} \\ : & : & : & \\ : & : & : & \\ r_{n1} & r_{n2} & r_{n3} & \ldots\ldots\ 1 \end{pmatrix}} = \overset{B}{\begin{pmatrix} p_{1y} \\ p_{24} \\ : \\ : \\ p_{ny} \end{pmatrix}}$$

Then

$$B=[C]^{-1}A \text{ where } C^{-1} = \begin{pmatrix} c_{11} & c_{12} & c_{13}\ldots\ldots & c_{1n} \\ c_{21} & c_{22} & c_{23}\ldots\ldots & c_{2n} \\ : & : & : & \\ : & : & : & \\ c_{n1} & c_{n2} & c_{n3}\ldots\ldots & c_{nn} \end{pmatrix}$$

Direct effects were as follows:

$$p_{1y} = \sum_{i=1}^{k} c_{1i}\ r_{iy}$$

$$p_{2y} = \sum_{i=1}^{k} c_{2i}\ r_{iy}$$

$$p_{ny} = \sum_{i=1}^{k} c_{nj}\ r_{iy}$$

Residual effect, which measures the contribution of characters not considered, was obtained as:

$$p_{ry} = \sqrt{1-(p_{1y}\,r_{iy} + p_{2y}\,r_{iy} + \ldots\ldots + p_{ny}\,r_{ny}}$$

Where, p_{ny} = Direct effect of x_n on Y

r_{iy} = Correlation coefficient of x_n on y.

3.2.2 Genotyping of selected germplasm lines of rice using SSR markers

Based on diversity studies on germplasm accessions of rice through field evaluation, seventy one genotypes including five indica check varieties *viz.*, Jaya, Mandya vijaya, Prasanna, Rasi and Vasumathi with diversified morphological characters were selected and utilized for genotyping using SSR markers. One Japonica variety Nipponebare in which the complete genome sequence has been identified, was also included for genetic diversity analysis using rice microsatellite markers. The details of the genotypes selected are presented in the Table 3.4. The seeds of all the seventy two genotypes were obtained from the Directorate of Rice Research (DRR), Hyderabad

3.2.2.1 DNA isolation

Genomic DNA was extracted from all the seventy two genotypes by following the procedure given by Zheng *et al.* (1995) with few modifications as described below:

Leaves were collected from 15-30 days old rice seedling for DNA extraction. Leaves were cut into small pieces and taken in the well of a spot test plate (Thomas Scientific, USA). 400 µl of extraction buffer (50 mM Tris HCl, pH 8.0, 25 mM EDTA, 300 mM NaCl and 10% SLS) was added and the leaf bits were ground thoroughly using an alcohol sterilized blunt ended glass rod. Then 400 µl more of extraction buffer added. Entire content from the well of spot test plate was transferred into a sterile 1.5 ml micro centrifuge tube using a micropipette tip of 1 ml capacity (cut at the bottom using a sterile scissors).

To the micro-centrifuge tube 300-400 µl of Phenol: Chloroform: Isoamyl alcohol (25:24:1) was added and the contents were mixed well by inversion for about 10 minutes and centrifuged at 13,000 rpm for about 10 minutes at room temperature. The supernatant was transferred to fresh 1.5 ml centrifuge tube with out disturbing the intermediate layer. The purification step was repeated until the supernatant was clear. To the supernatant, ~10µl of RNase (10 mg/ml) was added and incubated at room temperature (37^{o}C) for 30-45 minutes. After incubation 400 µl of chloroform was added to the micro-centrifuge tube and mixed well by invertion for 5 minutes. The contents were centrifuged at 13000 rpm for 10 minutes and the supernatant layer was collected into a fresh 1.5 ml micro-centrifuge tube with out disturbing the chloroform layer. Then 500-600 µl of chilled Isopropyl alcohol was added to the supernatant and mixed gently and centrifuge at 13000 rpm for 10 minutes at room temperature. The supernatant was drained gently and add about 150-200 µl of 70% ethanol was added to the pellet collected at the bottom of the micro centrifuge tube. It was ensured that the pellet was drained out and washed with 70% alcohol by gently tapping the tube. Then the contents were micro-centrifuged for 10 minutes at 13000 rpm. The supernatant was drained out and washed with 70% ethanol once again. Finally, after centrifugation and draining out the supernatant the pellet was left for air drying at room temperature for 6-8 hours.. After complete drying of the pellet 100-200 μl of sterile T.E. buffer (10 mM Tris-HCl, pH 8.0 and 1 mM EDTA) was added to the tube for dissolving the pellet.

Approximately 5 μl of dissolved DNA was loaded in a 0.8 % ethidium bromide stained Agarose-TBE (0.5 X TBE) gel and subjected to electrophoresis to check the quality and quantity of DNA.

3.2.2.2 Electrophoresis of genomic DNA

The isolated genomic DNA was verified for size, intactness, homogeneity and purity through ethidium bromide stained agarose gel electrophoresis.

Tris-Borate buffer (TBE) – 0.5X was prepared by mixing 0.9 M Tris-HCl, 0.025M EDTA Na^{2+}, 0.9M boric acid. Agarose 1 per cent W/V (Biogene, USA) was melted in 0.5X TBE buffer and 5μl of ethidium bromide (1 mg/ml) was added when hot.The gel was cooled under running tap water and casted in sealed plates with the combs fitted. Genomic DNA samples of seventy two rice genotypes were loaded in each well along with 2 μl of tracking dye (40 per cent W/V sucrose: 0.25 per cent W/V bromophenol blue; 0.25 per cent W/V xylene cyanol FF in sterile distilled water) and run at a constant voltage of 100 volts. The gel was placed over an UV trans-illuminator and viewed at 300 nm. The bands appeared as orange-coloured intact bands owing to the florescence of ethidium bromide and the gel was photographed using ALPHA IMAGER Gel documentation System (Alpha innotech, USA).

3.2.2.3 Selection of simple sequence repeat (SSR) markers

A total of twenty three rice microsatellite markers (which are also called SSR markers) listed in Table 3.5 were used in the present study. The forward and reverse primer sequences are also provided in Table 3.5. These markers were selected based on their high polymorphic information content value as inferred from rice SSR data base (http://www.gramene.org).

3.2.2.4 Polymerase Chain Reaction (PCR) amplification

The genomic DNA of the seventy two rice samples isolated as described earlier were subjected to PCR amplification as per the procedure described by Panaud *et al.*, (1996). Briefly, 10 µl reaction mixture contained 0.2 µM of each primer (both forward and reverse primers), 200 µM of deoxyribonucleotides, 50 mM KCl, 10 mM Tris HCl (pH 8.3), 1.5 mM $MgCl_2$, 0.1 per cent gelatin, 40-50 ng of DNA and 0.5 unit of *Taq* DNA polymerase (Bangalore Genei Pvt. Ltd., Bangalore). The following thermal profile was followed for SSR markers:

Initial denaturation	94^{o}C for 5 minutes	
Denaturation	94^{o}C for 30 seconds	35 cycles
Annealing	55^{o}C for 30 seconds	
Elongation	72^{o}C for 1 minute	
Final elongation	72^{o}C for 7 minutes.	

3.2.2.5 Agarose Gel Electrophoresis of PCR products

PCR amplified products were resolved in 3 % Seakem LE agarose gels in 0.5X TBE buffer at 100-150V for 3.5 hrs using Submarine Horizontal

Electrophoresis Unit (CBS Scientific, USA). Before loading, the PCR amplified products were mixed with 1/6th volume of gel loading dye (40% sucrose; 0.25% bromophenol blue). The gel documentation was done using ALPHA IMAGER gel documentation system. The sizes of amplified fragments were determined by comparing with 100 bp ladder (MBI Fermentas, Lithuania).

3.2.2.6 Data Analysis

Scoring:

Qualitative multistate traits that depict an array of characters were converted into binary characters (Sneath and Sokal, 1973) based on the variations present. Only the clear and unambiguous bands of SSR markers were scored. Markers were scored for the presence and absence of the corresponding band among the genotypes, in binary digits of 1 and 0, respectively. A data matrix comprising of '1' and '0' were formed depending upon the marker allele and this data matrix was subjected to further analysis.

Marker polymorphism analysis

To measure the informativeness of the markers, the polymorphism information content (PIC) for each SSR marker was calculated according to the formula:

$$PIC=1-\Sigma Pi^2 - \Sigma\Sigma Pi^2\ Pj^2$$

where 'i' is the total number of alleles detected for SSR marker and 'Pi' is the frequency of the i^{th} allele in the set of 72 genotypes investigated and j = i+1. This formula gives us an indicator of how many alleles a certain marker has, and how much these alleles divide evenly. The PIC value was calculated using the online software- 'Polymorphism Information Content Calculator' available at www.agri.huji.ac. The heterozygosity of each marker was calculated by using the formula:

$$H = 1 - \sum (fi)^2$$

Where ‘fi’ is the frequency of the i^{th} allele.

Cluster analysis

Presence of bands was scored as ‘1‘ and absence of bands as‘0‘ to construct a binary data matrix .The binary data matrix was analysed using TREECONW software (Peer and Wachter, 1994) to cluster the genotypes based on the dissimilarity co-efficients utilizing the the Unweighted Pair Group Method with Arithmetic Averages (UPGMA) method.

Table 3.1: Weekly mean meteorological data at ICRISAT Campus during *Rabi* 2007

Std. week	Date	Temperature ^{0}C		Relative humidity (%)		Weekly Rain fall (mm)	Sunshine hours per day	Wind velocity (km per hr)	Evaporation (mm day^{-1})
		Maximum temperature	Minimum temperature	Maximum	Minimum				
1	Jan. 01-07	28.1	11.1	95.9	42.7	9.0	0.0	1.4	3.5
2	Jan. 08-14	27.6	11.9	97.6	42.7	8.7	0.0	3.1	4.0
3	Jan. 15-21	30.3	13.0	94.6	39.1	9.5	0.0	2.2	4.3
4	Jan. 22-28	30.8	14.7	96.6	49.7	9.2	0.0	2.8	4.7
5	Jan.29-Feb.4	31.1	14.9	89.7	43.3	9.0	0.0	4.7	6.4
6	Feb. 5-11	31.6	15.8	91.1	35.3	9.3	0.0	4.8	6.0
7	Feb. 12-18	30.2	14.7	83.4	35.7	8.6	0.0	4.0	5.6
8	Feb. 19-25	30.6	14.0	82.4	34.6	10.0	0.0	4.3	6.9
9	Feb. 26-Mar. 4	33.5	15.7	74.3	38.6	10.6	0.0	3.3	8.1
10	Mar. 5-11	34.5	19.8	86.4	35.6	8.8	0.0	3.9	7.6
11	Mar. 12-18	34.4	18.6	76.3	31.9	9.6	0.0	7.7	9.1
12	Mar. 19-25	37.1	21.4	71.3	28.3	7.5	0.0	6.2	8.5
13	Mar. 26-Apr. 1	37.5	19.4	76.0	27.4	10.1	0.0	5.7	9.3
14	Apr.2-Apr.8	38.7	21.1	80.6	25.6	10.1	0.0	6.5	9.4
15	Apr. 9-Apr.15	37.3	21.5	87.0	40.9	8.5	1.3	9.4	8.7
16	Apr.16-Apr.22	34.9	21.6	82.1	38.0	8.7	4.9	7.1	8.0
17	Apr.23-Apr.29	39.0	22.4	69.3	24.1	10.6	0.0	6.5	10.6
18	Apr.30-May 6	39.4	25.4	74.9	29.3	9.3	0.3	8.9	10.3
19	May 7-May 13	40.2	26.4	68.6	30.6	9.5	0.1	9.5	12.0
20	May14-May20	40.2	25.1	58.6	31.6	11.2	0.0	10.3	14.2
21	May21-May27	38.9	25.7	69.9	39.1	10.1	1.7	9.7	11.4
22	May28-June 3	37.3	24.4	76.9	38.3	6.7	1.3	8.0	8.3

Std. week	**Date**	**Temperature (^{o}C)**		**Relative humidity (%)**		**Weekly rain fall (mm)**	**Sun shine hours per day**	**Wind velocity (km per hr)**	**Evaporation (mm day^{-1})**
		Maximum	**Minimum**	**RH I**	**RH II**				
44	Oct. 29-Nov. 4	29.4	17.9	89	49	0.0	5.7	3.4	3.2
45	Nov. 5-11	29.1	18.1	87	47	0.6	6.1	2.9	3.2
46	Nov.12-18	31.1	17.0	90	41	0.0	7.8	2.7	3.5
47	Nov.19-25	30.0	11.4	82	29	0.0	9.6	2.5	3.4
48	Nov.26-Dec.2	29.0	10.7	84	29	0.0	9.6	2.8	3.5
49	Dec. 3-9	28.7	9.2	86	31	0.0	9.6	2.2	3.5
50	Dec. 10-16	28.8	10.7	85	33	0.0	9.3	1.9	2.8
51	Dec. 17-23	30.2	11.0	87	30	0.0	9.4	1.6	3.2
52	Dec. 24-31	29.0	12.4	84	37	0.0	8.8	2.5	3.9
1	Jan. 01-07	29.6	15.9	85	36	0.0	8.0	3.2	3.6
2	Jan. 08-14	30.2	12.5	80	27	0.0	9.3	1.6	3.1
3	Jan. 15-21	29.4	14.8	72	33	0.0	9.3	3.0	2.9
4	Jan. 22-28	30.7	19.6	91	43	4.2	6.9	4.2	3.2
5	Jan.29-Feb.4	27.9	17.4	88	47	19.6	6.5	4.3	3.0
6	Feb. 5-11	31.3	15.4	88	25	0.0	9.1	3.4	4.1
7	Feb. 12-18	35.1	14.9	70	17	0.0	10.0	4.3	4.6
8	Feb. 19-25	34.3	18.8	80	26	0.0	9.3	3.3	5.3
9	Feb. 26-Mar. 4	35.0	17.3	75	17	0.0	9.6	3.4	6.0

Table 3.2: Details of 150 genotypes of rice used in the present investigation (All these genotypes were collected from Chattisgarh except check varieties)

SNo	Genotype	Duration (days)
1	IC-114007	115
2	IC-114009	120
3	IC-114012	114
4	IC-114016	104
5	IC-114017	109
6	IC-114018	114
7	IC-114019	111
8	IC-114027	109
9	IC-114035	104
10	IC-114039	120
11	IC-114040	117
12	IC-114058	119
13	IC-114061	105
14	IC-114063	111
15	IC-114064	105
16	IC-114085	120
17	IC-114114	119
18	IC-114117	116
19	IC-114126	119
20	IC-114149	118
21	IC-114150	109
22	IC-114156	121
23	IC-114157	116
24	IC-114160	133
25	IC-114162	135
26	IC-114164	133
27	IC-114177	128
28	IC-114196	124
29	IC-114237	140
30	IC-114250	126
31	IC-114251	124
32	IC-114253	127
33	IC-114256	122
33	IC-114256	122
34	IC-114261-1	135
35	IC-114278	119
36	IC-114285	128
37	IC-114286	127
38	IC-114309	136
39	IC-114313	125
40	IC-114316	114
41	IC-114321	126
42	IC-114325	111
43	IC-114338	121
44	IC-114339	116
45	IC-114341	119
46	IC-114344	115
47	IC-114346	119
48	IC-114349	120
49	IC-114350	121
50	IC-114351	115
51	IC-114354	118
52	IC-114362	110
53	IC-114369	114
54	IC-114384	112
55	IC-114386	116
56	IC-114389	121
57	IC-114400	118
58	IC-114407	111
59	IC-114410	119
60	IC-114411	120
61	IC-114419	117
62	IC-114421	117
63	IC-114425	136
64	IC-114430	129
65	IC-114441	119
66	IC-114458	120
67	IC-114485	115
68	IC-114511	115
69	IC-114513	114
70	IC-114514	112
71	IC-114515	109
72	IC-114526	118
73	IC-114527	127
74	IC-114530	123
75	IC-114538	112
76	IC-114543	111
77	IC-114558	117
78	IC-114562	115
79	IC-114571	108
80	IC-114583	136
81	IC-114587	115
82	IC-114588	118
83	IC-114589	116
84	IC-114612	135
85	IC-114655	124
86	IC-114680	121
87	IC-114712	118
88	IC-114723	117
89	IC-114725	111

SNo	Genotype	Duration (days)
90	IC-114730	119
91	IC-114732	139
92	IC-114736	119
93	IC-114740	140
94	IC-114752	125
95	IC-114766	112
96	IC-114784	127
97	IC-114785	126
98	IC-114797	117
99	IC-114831	121
100	IC-114840	118
101	IC-114847	116
102	IC-114851	112
103	IC-114852	112
104	IC-114864	119
73	IC-114527	127
74	IC-114530	123
75	IC-114538	112
76	IC-114543	111
77	IC-114558	117
78	IC-114562	115
79	IC-114571	108
80	IC-114583	136
81	IC-114587	115
82	IC-114588	118
83	IC-114589	116
84	IC-114612	135
85	IC-114655	124
86	IC-114680	121
87	IC-114712	118
88	IC-114723	117
89	IC-114725	111
90	IC-114730	119
91	IC-114732	139
92	IC-114736	119
93	IC-114740	140
94	IC-114752	125
95	IC-114766	112
96	IC-114784	127
97	IC-114785	126
98	IC-114797	117
99	IC-114831	121
100	IC-114840	118
101	IC-114847	116
102	IC-114851	112
103	IC-114852	112
104	IC-114864	119

SNo	Genotype	Duration (days)
105	IC-114882	134
106	IC-114889	139
107	IC-114921	114
108	IC-114984	125
109	IC-114992	126
110	IC-114999	123
111	IC-115000	113
112	IC-115001	114
113	IC-115004	127
114	IC-115006	111
115	IC-115050	112
116	IC-115063	136
117	IC-115074	129
118	IC-115078	125
119	IC-115090	119
120	IC-115108	112
121	IC-115114	121
122	IC-115116	112
123	IC-115118	121
124	IC-115131	114
125	IC-115170	125
126	IC-115208	110
127	IC-115623	121
128	IC-115625	122
129	IC-115628	122
130	IC-115630	116
131	IC-115733	123
132	IC-115734	115
133	IC-115738	120
134	IC-115743	115
135	IC-115744	116
136	IC-115757	127
137	IC-115760	128
138	IC-115868	121
139	IC-115888	124
140	IC-115897	116
141	IC-115905	122
142	IC-115907	132
143	IC-115909	121
144	IC-115914	111
145	IC-115921	109
146	Jaya	132
147	M.V.	143
148	Prasanna	99
149	Rasi	122
150	Vasumathi	136

Table 3.3: Description of qualitative characters (IRRI, 1996)

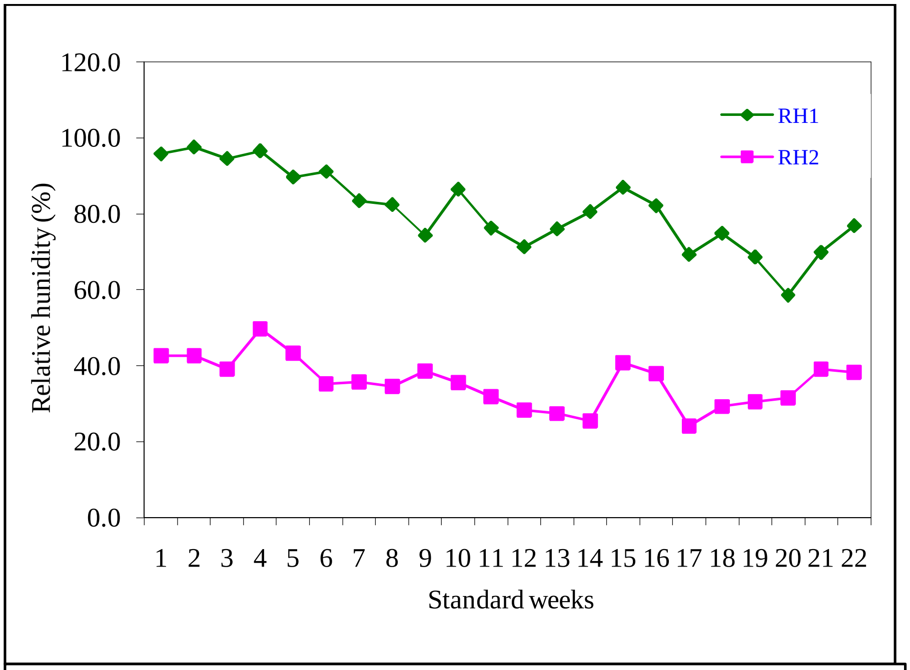
S.NO.	Character		Categories
1	Early plant vigour	1 2 3	Poor Good Very Good
2	Basal leaf sheath colour	1 2 3 4 5	Green Purple lines Light purple Purple Others
3	Leaf colour	1 2 3 4 5 6 7 8	Light green Green Dark green Purple tips Purple margin Purple blotch Purple Others
4	Leaf pubescence	1 2 3	Glabrous Intermediate Pubescent
5	Ligule shape	1 2 3	Acute Cleft Truncate
6	Ligule colour	1 2 3 4	White Purple lines Purple Others
7	Panicle exsertion	1 2 3 4 5	Well exs Moderate exs Just eks Partly exs Enclosed
8	Panicle type	1 5 9	Compact Intermediate Open
9	Stigma colour	1 2 3 4 5 7	White Light green Yellow Light purple Purple Purple apex
10	Awning	0 1 3 5 7 9	Absent Short & partly awned Short & fully awned Long & partly awned Long & fully awned Awned
11	Threshability	1 2 3	Easy Intermediate Difficult

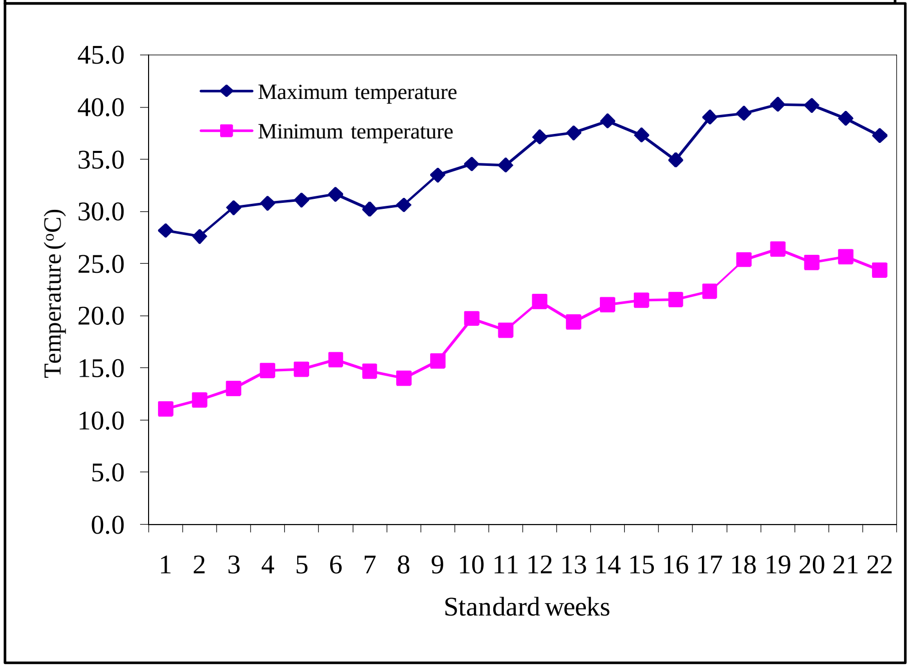
Table 3.4 : List of the selected genotypes utilized for genotyping through SSR markers

S.No.	Genotype	S.No.	Genotype
1	IC-114009	37	IC-114543
2	IC-114256	38	IC-114430
3	IC-115131	39	IC-115170
4	IC-114017	40	IC-114587
5	IC-114362	41	IC-114882
6	IC- 114261-1	42	IC-115628
7	IC-115625	43	IC-115623
8	IC-114740	44	IC-115063
9	IC-114027	45	IC-115108
10	IC-114349	46	IC-114407
11	IC-114278	47	IC-114162
12	IC-114571	48	IC-114612
13	IC-115001	49	IC-114732
14	IC-114752	50	IC-115000
15	IC-114680	51	IC-115909
16	IC-114441	52	IC-114019
17	IC-115905	53	IC-114723
18	IC-114852	54	IC-115738
19	IC-114325	55	IC-115897
20	IC-114237	56	IC-115744
21	IC-114196	57	IC-114589
22	IC-115888	58	IC-114149
23	IC-114253	59	IC-115743
24	IC-115004	60	IC-115114
25	IC-115090	61	IC-114766
26	IC-115116	62	IC-114341
27	IC-114386	63	IC-114354
28	IC-114035	64	IC-115208
29	IC-114513	65	IC-114064
30	IC-115733	66	IC-114058
31	IC-114921	67	Prasanna
32	IC-114313	68	Vasumathi
33	IC-114583	69	Rasi
34	IC-114889	70	Jaya
35	IC-115006	71	M.Vijaya
36	IC-114992	72	Nipponebare

Table 3.5: List of SSR primers along with their forward and reverse primers selected for genetic diversity analysis in rice

S.No.	Primer Name	Forward Primer	Reverse Primer
1	RM1384	TGGTACGGGAGAACTGGTACGC	AATCGAGCCAGCCTAGCAAGC
2	RM3019	AAAGGTGTTGTAGGAGTCGAGGTTGG	ACGCATTCGCCTTTGACATGC
3	RM5923	ATTCGGTCGATCGAGATAGTTGG	TGTCCGGTTTGCACAGTTGG
4	RM6690	AGGGAGTACCTTGTAACGAATTGC	GCATCAATTACACCAGTGAGTAGC
5	RM7163	NA	NA
6	RM7446	CGTTGAGCCAAGAAGAAGAAAGG	TTTGAAGGCAGTTTCACTGACG
7	RM1384	TGGTACGGGAGAACTGGTACGC	AATCGAGCCAGCCTAGCAAGC
8	RMES 3-1	GCAAGGAAGAAACCAGCGTA	TTGTGGGCAAAAACAAATGA
9	RMES 3-2	ACGGATTCACTGGGTTCTGT	CACCAGAAAGCATCACCTCA
10	RM 151	GGCTGCTCATCAGCTGCATGCG	TGCGCAGTGGTAGAGTTTGATCTGC
11	RM 5862	CCTCCTGAAGGGTAAAGGATTGG	TCCACACATGATCGCTACTCG
12	JGT 01-15.9	GGGTGCCACTTGACGGTTTG	GGCGCTCCAACAAATGCTG
13	JGT 02-9.1	CCATGTGGCGGTCTAGGAGTATTTGT	TGCCCTTGCTAAATAAATGCTACCC
14	JGT 03-0.01	CCGATGCACCAACACCCTCAC	GACGCATGGTGAGTTTGGAGTGAT
15	JGT 04-11.5	AGGGCTCGTAGAAAGTGTCCAATTAG	CCGCTGGGTATTGCCTAACTG
16	JGT 05-7.8	ACGGTGAGATTAGGTATTGCCA	AGTTCGGACAAGGGGGAGTACT
17	JGT 06-18.1	GAAGAACGTGGTTTGCATCGT	TGTACCGTCGGCGAAGAACGCACC
18	JGT 07-22.8	TGGCGATCTAGGAGCGTCTGT	TGTAAACATTTCAAAAGGGCACTAA
19	JGT 08-10.2	GTACTAAACAGATGGAGCAGTACG	GTGGTACTGCTAATTAGGGGGTA
20	JGT 09-4.8	CGGGATACTAACAGCAAGCAAAT	TCTCGCACCACTAACAGGGAACA
21	JGT 10-4.3	TGGCGACTTAGGAGCGTTTGTAG	GCGGCACTTCCCCAAACAA
22	JGT 11-15.3	GATCGCCCGTTAGCCTTTTCGA	GAACAGTTTTGCTGGCAACAA
23	JGT 12-18.6	ATGGCAGCGTAGGAGCGTTTGTAG	AACGTACCTAGGCAGCAAAATTCT


RH1
RH2
Relative hunidity (%)
120.0
100.0
80.0
60.0
40.0
20.0
0.0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
Standard weeks


Maximum temperature
Minimum temperature
Temperature (°C)
45.0
40.0
35.0
30.0
25.0
20.0
15.0
10.0
5.0
0.0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22
Standard weeks

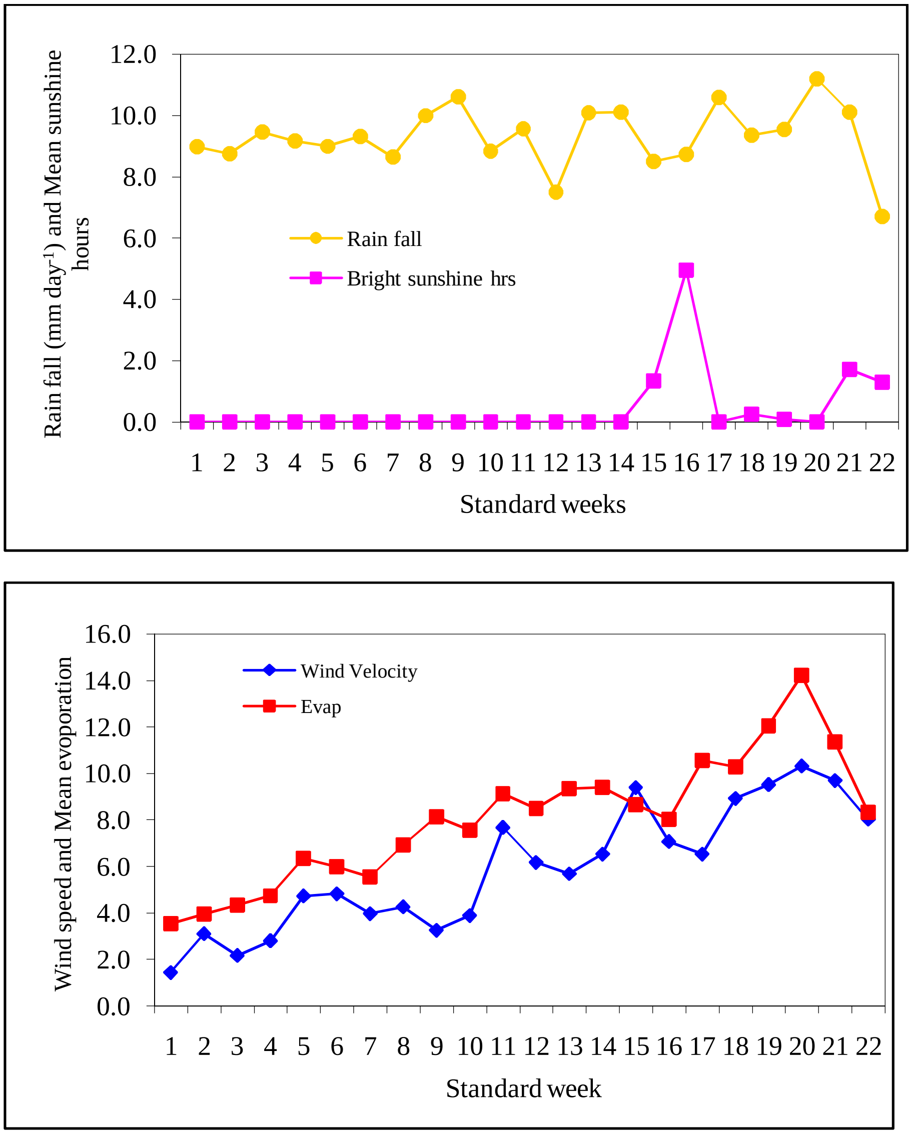


Fig. 3.1 : Weekly meteorological data at ICRISAT campus during Rabi 2007

Plate 3.1: An overview of experimental plot

CHAPTER IV

RESULTS

The present investigation was carried out by conducting two experiments, one through field evaluation and other through SSR markers. Hence, the results obtained are presented experiment wise separately here under:

4.1 DIVERSITY STUDIES ON GERMPLASM ACCESSIONS OF RICE THROUGH FIELD EVALUATION

The experimental findings obtained from the present study on evaluation of one hundred and fifty rice germplasm lines along with the five standard checks for twelve qualitative characters and eleven quantitative characters are presented under the following heads in this chapter.

1. Morphological characterization
2. Analysis of variance
3. Mean, Genetic variability, Heritability and Genetic advance
4. Genetic divergence
5. Character association
6. Path coefficient analysis

4.1.1 Morphological characterization

One hundred fifty genotypes were characterized using eleven morphological characters as per standard evaluation system (IRRI, 1996) (Table 4.1). These descriptors are highly heritable, unambiguous and easily identifiable. The study of morphological traits was carried to describe each genotype and establish their diagnostic characteristics. The experimental material showed great variability for the eleven morphological traits (Fig.4.1). All the traits *viz*. early plant vigour, basal leaf sheath colour, leaf blade colour, leaf pubescence, ligule shape, ligule colour, panicle exsertion, panicle type, stigma colour, awning and threshability exhibited wide variation among the genotypes under study.

4.1.1.1 Early plant vigour:

Agro-morphological characterization of 150 genotypes revealed that 81 genotypes showed very good plant vigour, 60 genotypes exhibited good plant vigour, while the remaining 9 genotypes were found to exhibit poor plant vigour.

4.1.1.2 Basal leaf sheath colour:

The study revealed that 75 genotypes exhibited green basal leaf sheath colour, 33 genotypes showed purple colour, 24 genotypes exhibited purple lines and 18 genotypes showed light purple.

4.1.1.3 Leaf blade colour:

Leaf blade colour of 120 genotypes was found to be green in colour, while 12 genotypes showed purple margins, 11 genotypes exhibited dark green colour, 5 genotypes had light green colour and the remaining 2 exhibited purple tips.

4.1.1.4 Leaf pubescence:

The study revealed that 117 genotypes exhibited leaf pubescence, 27 intermediate and 6 glabrous leaf.

4.1.1.5 Ligule shape:

145 genotypes showed cleft ligule, 3 genotypes exhibited acute ligule and 2 genotypes had truncate ligule.

4.1.1.6 Ligule colour:

89 genotypes showed white ligule colour, 35 exhibited purple lines, 20 showed purple and 6 genotypes others.

4.1.1.7 Panicle exertion:

138 genotypes showed well panicle exertion, 12 genotypes exhibited moderate panicle exertion.

4.1.1.8 Panicle type:

64 genotypes exhibited compact type of panicle, 67 genotypes showed intermediate type of panicle and 19 genotypes showed open type of panicle.

4.1.1.9 Stigma colour:

76 genotypes exhibited white stigma, 55 genotypes showed purple colour, 18 had light purple colour and one exhibited yellow stigma colour.

4.1.1.10 Awning:

The 150 rice genotypes were divided into three groups on the basis of awning character. Maximum number of genotypes (143) were found to be awnless, 6 genotypes were having short and partly awned, while a single genotype was with full of long awns.

4.1.1.11 Threshability:

Majority (71) genotypes exhibited intermediate threshability sixty seven genotypes were found to have easy threshability while twelve genotypes exhibited difficult threshability.

4.1.2 Analysis of variance

Analysis of variance showed highly significant differences among the genotypes for most of the traits *viz.*, days to 50% flowering, plant height, leaf length, total number of tillers per plant, productive tillers per plant, panicle length, total number of grains per panicle, Spikelet fertility and single plant yield except leaf width and 100-grain weight. The results of analysis of variance are presented in Table 4.2

4.1.3 MEAN, GENETIC VARIABILITY, HERITABILITY, GENETIC ADVANCE AND GENETIC ADVANCE AS PERCENT OF MEAN:

The genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV), heritability, genetic advance and genetic advance as per cent of mean were estimated for one hundred and fifty genotypes including five standard checks. The results obtained for various morphological traits are furnished in Table 4.3.

The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among the metric characters, productive tillers per plant recorded highest PCV (31.31) followed by single plant yield (24.15) and the lowest PCV (9.27) was recorded for days to 50% flowering. Highest GCV values were recorded for the productive tillers per plant (27.44) followed by single plant yield (23.44) whereas lowest GCV value (9.20) was recorded for days to 50% flowering.

Heritability is classified as low (below 30%), medium (30-60%) and high (above 61%). The characters studied in the present investigation expressed high heritability estimates ranging from 62% to 99%. Among the metric characters, highest heritability was obtained for spikelet fertility (99.46%), followed by total grains per panicle (99.38%) and plant height (99.05%).

4.1.3.1 Mean

The mean performance of 11 characters is presented in Table 4.4.

4.1.3.2 Metric characters

4.1.3.2.1 Days to 50% flowering

Days to 50% flowering ranged from 69.0 (Prasanna) to 113.0 (Mandya vijaya) with mean of 89.83. The genotypic and phenotypic coefficients of variability were low i.e. 9.20 and 9.27 respectively. The heritability estimate for this trait was high (98.52 %) while low genetic advance (6.91) and genetic advance as per cent of mean (18.82) were moderate.

4.1.3.2.2 Plant height (cm)

Plant height showed high genetic variability varying from 78.33 cm (Rasi) to 155.43 cm (IC- 114344) with a mean of 115.70 cm. The estimates of genotypic and phenotypic coefficients of variation estimates recorded for this trait were moderate i.e. 11.88 and 11.93 respectively. The observed heritability for this character was high (99.05) with high genetic advance (28.18) and genetic advance as per cent of mean (24.35).

4.1.3.2.3 Leaf length (cm)

The range of variation observed for this character was 26.02 cm (IC-115114) to 50.35 (IC-114766) with a mean value of 38.86 cm. The observed genotypic and phenotypic coefficients of variability for this trait were moderate i.e. 13.72 and 14.33 respectively. This character recorded a high heritability of 91.66 and moderate genetic advance of 10.51. However, genetic advance as per cent of mean was high (27.05)

4.1.3.2.4 Leaf width (cm)

The range of variation observed for this character was 0.68 cm (IC-114058) to 1.45 cm (IC-114156) with a mean value of 1.15. The observed genotypic and phenotypic coefficients of variability for this trait were moderate i.e. 12.52 and 15.83 respectively. This character recorded a high heritability of 62.56 and very low genetic advance of 0.23 and genetic advance as per cent of mean was moderate (20.40).

4.1.3.2.5 Total number of tillers per plant

The range of variation obtained for this character was 7.30 to 20.21 (IC-114831, IC-115868) with a mean value of 13.14. The observed genotypic and phenotypic coefficients of variability for this trait were high i.e. 20.17 and 22.73, respectively. This character recorded a high heritability of 78.72 and low genetic advance of 4.84 coupled with high genetic advance as per cent of mean (36.85).

4.1.3.2.6 Productive tillers per plant

Productive tillers per plant was found to vary from 3.23 (IC-114831) to 13.36 (IC-115208) with a mean value of 6.86. The genotypic and phenotypic coefficients of variability for this trait were high i.e. 27.44 and 31.31, respectively. The observed heritability estimate was high (76.82) with a very low genetic advance (3.40) and high genetic advance as per cent of mean (49.54).

4.1.3.2.7 Panicle length (cm)

The mean panicle length was 23.17 cm with a minimum of 17.13 cm (IC-114040) and maximum of 28.87 cm (IC-115630). The GCV (9.32) and PCV (10.33) were found to be low. The heritability noticed for this trait was high (81.54). This character recorded low genetic advance (4.02) and the moderate expected genetic advance as per cent of mean (17.34).

4.1.3.2.8 Total number of grains per panicle

The wide range of variability was obtained for total grains per panicle ranging from 73.81 (IC-114400) to 297.23 (IC-114344) with a mean value of 151.88. High genotypic and phenotypic coefficients of variability values of i.e. 22.27 and 22.34, respectively were recorded for this trait with very high heritability (99.38), with high genetic advance (69.47) and high genetic advance as per cent of mean (45.74).

4.1.3.2.9 Spikelet fertility (%)

Spikelet fertility ranged from 52.39 (IC-114587) to 97.35 (IC-115108) with a mean value of 86.18. The estimates of genotypic (12.16) and phenotypic (12.19) coefficients of variability were found to be moderate. The heritability estimate was very high (99.46) with high genetic advance (21.52) and high genetic advance as per cent of mean (24.97).

4.1.3.2.10 100-Grain weight (g)

100-Grain weight ranged from 1.42 g (IC-114538) to 3.60 g (IC-114039) with a mean value of 2.46 g. Moderate genotypic (14.66) and phenotypic (15.70) coefficients of variations were recorded with high heritability estimate of 87.21. The genetic advance was very low (0.69) while genetic advance as per cent of mean was high (28.20).

4.1.3.2.11 Single plant yield (g)

The yield per plant,which ranged from 6.19 g (IC-114012) to 26.17 g (IC-114085) exhibited with a mean value of 17.37 g, high heritability (94.21). A high genotypic coefficient of variation (23.44) coupled with high phenotypic coefficient of variation (24.15) were observed for this trait. The genetic advance was low (8.14) while genetic advance as per cent of mean was high (46.87).

4.1.4 Genetic divergence

The quantitative assessment of genetic divergence was taken up by adopting Mahalonibis's D^2 statistic using all the yield contributing characters including yield. Genetic divergence was estimated for one hundred and fifty rice genotypes and the results obtained from the study are presented below.

4.1.4.1 Wilk's '^' criterion test

Wilk's '^' criterion test was done to determine whether significant differences existed among the genotypes for individual characters and later the significant differences between genotypes based on the pooled effects of all the characters were determined.

4.1.4.2 Mahalanobis's generalized distance D^2

In order to assess the genetic diversity among one hundred and fifty genotypes, D^2 statistic was used following the procedure given by Rao (1952). Since the eleven yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. The statistical distance (Mahalanobis's D^2) between a pair of genotypes was obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated values of any two genotypes considered at a time.

4.1.4.3 Grouping of genotypes into various clusters

a. Tocher's method

Cluster composition

Tocher's method distributed one hundred and fifty genotypes into sixteen clusters (Table 4.5 and Fig.4.2). Among the different clusters, cluster I had maximum (73) genotypes followed by cluster III (29), cluster IV (16), cluster VIII (15), cluster IX (4) and cluster XVI (3). Clusters II, V, VI, VII, X, XI, XII, XIII, XIV and cluster XV contained single genotype each. Each of the five check varieties utilized in the present investigation had found place in five different clusters, i.e., Vasumathi in cluster XI, Rasi in cluster XII, Prasanna in cluster XIV, Mandya vijaya in cluster III and Jaya in cluster IV.

Intra and Inter-cluster distances

The cluster IX had a large distance (69.19) from cluster XVI. The cluster VI had a lowest distance (9.82) from cluster VII.The clusters II, V,VI, VII, X, XI, XII, XIII, XIV, XV had no intra-cluster distance. While the cluster XVI had highest (21.60) intra cluster distance followed by cluster VIII (20.18). (Table 4.6).

Cluster means for various characters

A wide range of variation was observed in cluster means for all the characters studied Table 4.7. Cluster II was characterized by the highest (96.34) and lowest (30.23) mean values for spikelet fertility and leaf length respectively. The cluster VI had the highest value (1.33) for leaf width. Lowest and highest values (8.23) and (13.13) for total tillers and productive tillers were recorded in cluster VII and cluster XI respectively. While the least values for number of grains per panicle (93.97) and spikelet fertility (49.16) were noticed in cluster IX. The lowest (78.33) and highest (146.87) values of plant height were observed in cluster XII and cluster XIII, respectively. ClusterXIII was further characterized by the highest value of days to 50% flowering (109.00) and lowest and values of panicle length (17.92) and 100-seed weight (1.55). Cluster XIV had lowest values of leaf width (0.76) and days to 50% flowering (69.00). While cluster XV exhibited highest values of 100-seed weight (2.93) and single plant yield (22.22). Cluster X had lowest single plant yield (9.41g). The cluster XVI is having highest mean values and a maximum of three characters leaf length (46.04), panicle length (24.38) and grains per panicle (286.21) among all the other clusters.

b. Canonical analysis

Canonical analysis was carried out in one hundred and fifty genotypes the values of four canonical roots and percentage of variation by them are presented in Table 4.8.

Table 4.8: Canonical root values, per cent variation observed and cumulative total variation for one hundred and fifty genotypes of rice

Canonical root	Value of canonical root	Percentage of variation observed	Cumulative total per cent variation
1	16119.75	42.83	42.83
2	10235.69	27.19	70.03
3	5244.062	13.93	83.96
4	3004.189	7.98	91.94

The first canonical root accounted for 42.83 % of total variability, second for 27.19%, third for 13.93% and fourth for 7.98%. The four canonical roots were responsible for 91.94% of total variability hence, the canonical means were obtained in three dimensions. The first three vectors contributed 83.96% of the total variability only.

The coefficients attached to different characters in four canonical roots are presented in Table 4.9 and mean values of canonical variates for one hundred and fifty genotypes in three roots Z_1, Z_2, and Z_3 were furnished in Table 4.10. The mean values of the canonical variates Z_1 on x-axis, Z_2 on y-axis were plotted in a 2-D graph (Fig.4.3). The figure clearly depicted the sixteen distinct clusters.

The characters *viz.*, grains per panicle (0.24584) and spikelet fertility (0.81172) contributed highest towards divergence in vector Z_1, 100-seed weight (0.21542) and grains per panicle (0.92813) in vector Z_2, productive tillers per plant (0.08101) and plant height (0.94066) in $Z_{3,}$ plant height (0.15980) and days to 50 %flowering (0.95727) in Z_4 contributed more towards genetic divergence. This was in conformity with the relative contribution of characters through D^2 statistic.

c. Cluster analysis

The quantum of genetic divergence was also assessed by cluster analysis using Mahalanobis's euclidean squared distances which grouped the entire material into more précised clusters and estimates the average distance between them. The euclidean squared distance grouped the material into 13 clusters. The cluster composition is given in Table 4.11. The clustering pattern was depicted by Ward's minimum variance dendrogram (Fig.4.4). Among the clusters, cluster XI was the largest comprising of 28 genotypes followed by cluster IV (18), cluster VIII (17), cluster XII (16) and XIII with 15, cluster V (14), cluster III (10), cluster VI and cluster VII (8) cluster II and cluster X (6), Cluster IX (3), and cluster I (2) genotypes. The standard checks Jaya, Vasumathi and Rasi were grouped in cluster XIII while Mandya vijaya and Prasanna had fallen in cluster VIII and X, respectively.

4.1.4.4 Intra and inter euclidean cluster average distances

The average intra and inter cluster D^2 values are presented in Table 4.12 and Fig.4.5. Most of the intra clusters were closely related and cluster D^2 values ranged from 203.902 (cluster I) to 1400.294 (cluster (IX).

From the inter cluster D^2 values of the thirteen clusters, it can be observed that the highest divergence was between cluster I and IX (16373.400) while, lowest divergence was noticed between cluster IV and V (459.951). The clusters III and XI, II and X and V and III were moderately divergent, while rest of the clusters were closely related.

Mean values of clusters for yield contributing characters are presented in Table 4.13. From the data it can be concluded that considerable differences existed for all the characters studied. The cluster I was characterized by the lowest cluster mean values for five characters leaf width (1.040 cm), productive tillers (5.028), grains per panicle (96.758), spikelet fertility (41.057) and yield per plant (9.858). Highest cluster mean values for productive tillers per plant (8.218), single plant yield (21.446) and spikelet fertility (94.301) were noticed in cluster XIII, III and V respectively. The highest plant height (129.879) and lowest total tillers per plant (11.234) were recorded in cluster VI. The lowest leaf length (36.731 cm) and panicle length

(21.948 cm) were obtained in cluster VII. Cluster VIII had highest leaf width (1.222) and days to 50% flowering (102.922) and lowest seed weight (2.2481). The cluster IX was found to be the superior among all the clusters by recording highest cluster means for leaf length (46.036 cm), total tillers per plant (15.242), panicle length (24.377 cm) and grains per panicle (286.212). Highest 100-seed weight (2.640 g) and lowest days to 50% flowering (79.833) were recorded in cluster X, while the least plant height (89.742 cm) was obtained in cluster XIII

4.1.5 Relative contribution of characters towards genetic divergence

The number of times that each of yield component appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.14. The results showed that the contribution of grains per panicle towards genetic divergence was highest (28.70%) by taking 3207 times ranking first, followed by fertility (24.84%) by 2776 times, plant height (22.06%) by 2525 times, days to 50% flowering (14.33%) by 1601 times, single plant yield (5.35%) by 598 times, 100-grain weight (3.19%) by 356 times, leaf length (0.66%) by 74 times, panicle length (0.30 %) by 33 times, total tillers per plant (0.04 %) by five times. Leaf width and productive tillers per plant did not contribute towards genetic divergence among the genotypes under investigation.

4.1.5 Character association

Phenotypic and genotypic correlations between yield and yield components *viz.*, days to 50% flowering, plant height, leaf length, leaf width, total number of tillers per plant, productive tillers per plant, panicle length , number of grains per panicle, spikelet fertility, 100-grain weight and single plant yield of rice genotypes were estimated and presented in Table 4.15.

The results revealed that the estimates of genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the characters under study. The results obtained from the phenotypic and genotypic correlation coefficients are presented character wise here under.

4.1.5.1 Metric characters

4.1.5.1.1 Days to 50% flowering

Days to 50 per cent flowering registered positive and significant correlations with total number of grains per panicle (0.1840**/0.1866**) and spikelet fertility (0.1237**/0.1243**). Single plant yield had positive association with this character (0.0372/0.0374).

4.1.5.1.2 Plant height (cm)

This trait exhibited a positive and significant association with leaf width (0.1802**/0.2258**) and leaf length (0.0926*/ 0.0980*) while a negative and significant association with total number of tillers per plant (-0.2272**/-0.1608**), productive tillers per plant (-0.1438**/-0.2602**), days to 50% flowering (-0.1074*/-0.1081*) and spikelet fertility (-0.0967*/-0.0969*). Plant height had positive and non-significant association with number of grains per panicle (0.0661/0.0678).

4.1.5.1.3 Leaf length:

This trait showed a positive and significant association with days to 50% flowering (0.1305**/0.1342**), while a negative and significant association with panicle length (-0.1556**/-0.1885**), leaf width

(-0.1355**/-0.1599**), single plant yield (-0.1227**/-0.1313**) and total tillers per plant (-0.0995*/-0.1186*).

4.1.5.1.4 Leaf width

This trait showed a positive and significant association with panicle length (0.1491**/0.2103**), days to 50% flowering (0.0958*/0.1222**) and spikelet fertility (0.0951*/0.1187*). Single plant yield was positively correlated with leaf width (0.0005/0.0077)

4.1.5.1.5 Total number of tillers per plant

This trait had a positive and significant correlation with productive tillers per plant (0.7184**/0.8241**), single plant yield (0.1267**/0.1732**), panicle length (0.0939*/0.0457) while 100-seed weight (-0.1970**/-0.2073**) recorded negative and significant association with this trait.

4.1.5.1.6 Productive tillers per plant

This trait exhibited positive and significant association with Single plant yield (0.2063**/0.2780**), panicle length (0.1283**/0.0504), days to 50% flowering (0.1015*/0.1141*) and a negative and significant association with 100-seed weight (-0.1890/-0.1859).

4.1.5.1.7 Panicle length (cm)

Panicle length recorded a positive and significant association with 100-seed weight (0.2411**/0.3330**) number of grains per panicle (0.1181*/0.1181*), single plant yield (0.1178*/0.1729**). Spikelet fertility was positively correlated with this trait (0.0610/0.0780).

4.1.5.1.8 Total number of grains per panicle

This trait had a positive and significant correlation with single plant yield (0.1229**/0.1305**) and positive association with 100-Grain weight (0.0014/0.0074). Spikelet fertility showed negative correlation with this trait (-0.0417/-0.0403).

4.1.5.1.9 Spikelet fertility (%)

This trait had a positive and significant correlation with single plant yield (0.1414**/0.1365**).100-seed weight showed positive association with this character (0.0194/0.0052)

4.1.5.1.10 100-Grain weight (g)

100-Grain weight recorded positive and significant correlation with single plant yield (0.2549**/0.2243**).

4.1.5.1.11 Single plant yield (g)

This trait registered positive and significant correlation with 100-grain weight (0.2549**/0.2243) productive tillers per plant (0.2063**/0.2780**), spikelet fertility (0.1414**\0.1365**), total tillers per plant (0.1267**/0.1732**), total number of grains per panicle (0.1229**/0.1305**) and panicle length (0.1178*/0.1729**). It exhibited negative and significant correlation with leaf length (-0.1227**/-0.1313**) positive and non- significant association with days to 50% flowering (0.0372/0.0374) and leaf width (0.0005/0.0077)

4.1.5.2 Path coefficient analysis

Path coefficient analysis was done for single plant yield and its component characters in rice genotypes for partitioning the correlation coefficients into the corresponding direct and indirect effects and are furnished Table 4.16.

4.1.5.2.1 Metric characters

4.1.5.2.1.1 Days to 50% flowering

Days to 50% flowering expressed a positive direct effect of 0.0052 on single plant yield. It had shown positive indirect effects on single plant yield via leaf length (0.0007) and spikelet fertility (0.0006).

4.1.5.2.1.2 Plant height (cm)

Plant height exhibited a positive direct effect of 0.0488 on single plant yield. It recorded positive indirect effects on yield per plant via leaf width (0.0088), leaf length (0.0045) and number of grains per panicle (0.0032), while rest of the characters showed negative indirect effects.

4.1.5.2.1.3 Leaf length

Leaf length showed negative direct effects of -0.1217 on single plant yield. It had shown negative indirect effects on single plant yield via days to 50% flowering (-0.0159) and plant height (-0.0113).

4.1.5.2.1.4 Leaf width

Leaf width expressed a negative direct effect of -0.0177 on single plant yield. It had shown positive indirect effects on single plant yield via leaf length (0.0024) total tillers per plant (0.0015) and productive tillers per plant (0.0015).While rest of the characters showed negative indirect effects.

4.1.5.2.1.5 Total number of tillers per plant

Total number of tillers per plant expressed a negative direct effect of -0.0167 on single plant yield. It showed a positive indirect effect on single plant yield via plant height (0.0038) and 100-grain weight (0.0033). While rest of the characters expressed negative indirect effects.

4.1.5.2.1.6 Productive tillers per plant

Productive tillers per plant expressed a positive direct effect of 0.2796 on single plant yield. It had a positive indirect effect via total tillers per plant (0.2009) and panicle length (0.0359) on single plant yield.

4.1.5.2.1.7 Panicle length (cm)

Panicle length expressed a negative direct effect of -0.0305 on single plant yield. It had shown positive indirect effects on single plant yield via leaf length (0.0048) and productive tillers per plant (0.0039). Negative indirect effects on single plant yield was noticed via spikelet fertility (-0.0019) at phenotypic level and positive indirect effect (0.0012) at genotypic level.

4.1.5.2.1.8 Number of grains per panicle

Number of grains per panicle exhibited a positive direct effect (0.1370) on single plant yield and positive indirect effects were manifested through days to 50% flowering (0.0252) and panicle length (0.0162).

4.1.5.2.1.9 Spikelet fertility (%)

Spikelet fertility expressed positive direct effect (0.1470) on single plant yield and positive indirect effects were manifested through days to 50% flowering (0.0182), panicle length (0.0090) and 100 grain weight (0.0029).

4.1.5.2.1.10 100-grain weight (g)

100-grain weight expressed positive direct effect (0.3097) on single plant yield. It had shown positive indirect effects via panicle length (0.0747), spikelet fertility (0.0063) and number of grains per panicle (0.0004) on single plant yield.

4.2 DIVERSITY STUDIES OF SELECTED GERMPLASM LINES OF RICE USING SSR MARKERS

In the present investigation, genetic diversity among seventy two rice genotypes was assessed using 23 SSR markers. Intact, high molecular weight DNA was isolated from all the genotypes and used for amplification with 23 SSR markers, which were selected based on their polymorphic information content (PIC) value from rice SSR data base (http:/www.gramene.org)

4.2.1 Analysis using SSR markers

Out of the 23 SSR markers used in the present study, 7 were found to be polymorphic and generated a total of 20 alleles in the seventy two genotypes studied. The number of alleles per SSR marker ranged from 2-4 with an average value of 2.85. The polymorphic information content (PIC) for these seven SSR markers ranged from 1.021 (JGT 06) to 1.839 (RM 151) with an average of 1.487. Information regarding the polymorphism status of the SSR markers is given in Table 4.17 along with their PIC values. Gel images of the SSR markers are given in Plate no.4.1. Each amplicon (band) was considered as an allele in SSR analysis. A maximum number of 4 alleles were amplified by JGT 12. The primers JGT 01, JGT 04, JGT 06 and JGT 07 amplified three alleles while JGT 05 and RM 151 amplified two alleles each. The markers JGT 08, JGT 02, JGT 11 and RM 5862 were monomorphic among the genotypes under investigation. The allelic distribution of the 23 SSR markers among the seventy two genotypes is given in Table 4.18.

4.2.2 Genetic relationship among the Rice genotypes Cluster analysis

Cluster analysis was performed using similarity coefficient matrices, calculated from SSR markers. A dendrogram of genotypes was generated with UPGMA algorithm (Fig. 4.6). The similarity coefficient values ranged from 0.1 to 0.9. The dendrogram showed the grouping pattern of rice genotypes analyzed. All the seventy two genotypes were grouped into two clusters (with 68% similarity among them). Nipponebare, a Japonica genotype was found in separate cluster, while all the other indicas were grouped into one major cluster. This major cluster had two sub-clusters; the first sub-cluster consisted of thirty nine genotypes including four checks Vasumathi, Rasi, Jaya and Mandya vijaya and the second sub-cluster comprised of thirty two genotypes including one check i.e. Prasanna. The first sub cluster had two sub sub clusters, the first sub sub cluster with thirty six genotypes including two standard check varieties and the second sub sub cluster with three genotypes. The second sub cluster has two sub sub clusters. The first sub sub cluster had eleven genotypes including one check Prasanna. Second sub sub cluster had twenty one genotypes.

Table 4.1 : Morphological characterization of rice genotypes

	EarlyPlant vigour	**Basal leaf sheath colour**	**Leaf colour**	**Leaf pubescence**	**Ligule shape**	**Ligule colour**	**Panicle exsertion**	**Panicle type**	**Stigma colour**	**Awning**	**Threashability**
IC-114007	Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Short and partly awned	Intermediate
IC-114009	Good	Green	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Intermediate
IC-114012	Good	Purple lines	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	Light purple	Absent	Intermediate
IC-114016	V.Good	Purple lines	Green	Intermediate	Cleft	Purple lines	Well exs	Compact	Light purple	Absent	Intermediate
IC-114017	Poor	Purple	Purple lines	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-114018	Poor	purple	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Easy
IC-114019	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Light purple	Absent	Intermediate
IC-114027	V.Good	Light purple	Green	Pubescent	Cleft	Others	Well exs	Intermediate	Purple	Absent	Easy
IC-114035	Good	purple	Green	Intermediate	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114039	Good	Green	Green	Pubescent	Cleft	Purple lines	Just exs	Open	White	Short and partly awned	Easy
IC-114040	Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-114058	V.Good	Purple lines	Green	Intermediate	Acute	Purple lines	Well exs	Open	Light purple	Absent	Intermediate
IC-114061	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Light purple	Short and partly awned	Easy
IC-114063	V.Good	Light purple	Green	Pubescent	Cleft	White	Well exs	Open	Purple	Absent	Easy
IC-114064	Poor	purple	Green	Pubescent	Cleft	Purple	Well exs	Open	Purple	Absent	Difficult
IC-114085	Good	purple	Dark green	Intermediate	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114114	Poor	Green	Dark green	Glabrous	Cleft	White	Well exs	Open	White	Absent	Easy
IC-114117	Good	Green	Green	Glabrous	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-114126	Good	Green	Light green	Pubescent	Cleft	White	Well exs	Intermediate	Yellow	Absent	Intermediate
IC-114149	V.Good	Green	Green	Intermediate	Cleft	White	Just exs	Intermediate	White	Absent	Easy
IC-114150	Good	Purple lines	Green	Intermediate	Cleft	White	Well exs	Intermediate	White	Absent	Difficult
IC-114156	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114157	Good	Green	Light green	Pubescent	Cleft	Purple	Just exs	Compact	Purple	Absent	Easy

	EarlyPlant vigour	Basal leaf sheath colour	Leaf colour	Leaf pubescence	Ligule shape	Ligule colour	Panicle exsertion	Panicle type	Stigma colour	Awning	Threashability
IC-114160	Good	purple	Dark green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Easy
IC-114162	Good	purple	Dark green	Pubescent	Cleft	White	Well exs	Compact	Purple	Absent	Easy
IC-114164	V.Good	purple	Dark green	Pubescent	Cleft	Purple	Just exs	Intermediate	Purple	Absent	Easy
IC-114177	Good	purple	Green	Pubescent	Cleft	White	Well exs	Open	Purple	Absent	Difficult
IC-114196	Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Open	Light purple	Absent	Intermediate
IC-114237	V.Good	Green	Green	Pubescent	Cleft	Others	Well exs	Intermediate	White	Absent	Intermediate
IC-114250	V.Good	purple	Green	Pubescent	Cleft	Others	Well exs	Intermediate	Purple	Short and partly awned	Easy
IC-114251	Good	Purple lines	Green	Pubescent	Cleft	Others	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114253	V.Good	Purple lines	Purple margin	Pubescent	Cleft	Purple	Just exs	Open	White	Absent	Easy
IC-114256	Good	Purple lines	Purple margin	Intermediate	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Difficult
IC-114261-1	Poor	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-114278	Good	Purple lines	Green	Intermediate	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-114285	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-114286	V.Good	Green	Green	Glabrous	Cleft	White	Just exs	Intermediate	White	Absent	Difficult
IC-114309	V.Good	purple	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Light purple	Absent	Intermediate
IC-114313	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114316	Poor	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114321	Good	purple	Green	Intermediate	Cleft	Purple	Well exs	Intermediate	Light purple	Absent	Easy
IC-114325	Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	Purple	Absent	Easy
IC-114328	V.Good	Green	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114332	V.Good	Light purple	Green	Pubescent	Cleft	Others	Well exs	Compact	Purple	Absent	Easy
IC-114334	V.Good	Green	Green	Pubescent	Acute	White	Well exs	Intermediate	White	Absent	Easy
IC-114335	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114338	V.Good	Purple lines	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114339	V.Good	Purple lines	Green	Intermediate	Cleft	Purple lines	Well exs	Intermediate	White	Absent	Easy
IC-114341	V.Good	Green	Light green	Pubescent	Cleft	Others	Well exs	Open	White	Absent	Intermediate
IC-114344	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Difficult

	EarlyPlant vigour	**Basal leaf sheath colour**	**Leaf colour**	**Leaf pubescence**	**Ligule shape**	**Ligule colour**	**Panicle exsertion**	**Panicle type**	**Stigma colour**	**Awning**	**Threashability**
IC-114346	V.Good	Green	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	White	Absent	Intermediate
IC-114349	Good	purple	Green	Pubescent	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Easy
IC-114350	V.Good	purple	Purple margin	Intermediate	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114351	V.Good	Light purple	Purple margin	Pubescent	Truncate	Purple	Well exs	Compact	Purple	Absent	Intermediate
IC-114354	Good	purple	Dark green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114362	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Easy
IC-114369	V.Good	Green	Green	Intermediate	Cleft	Purple lines	Well exs	Intermediate	White	Absent	Easy
IC-114384	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Light purple	Absent	Easy
IC-114386	V.Good	purple	Purple margin	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114389	V.Good	Light purple	Dark green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114400	V.Good	purple	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114407	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-114410	Good	purple	Green	Intermediate	Cleft	Purple	Just exs	Compact	Purple	Absent	Intermediate
IC-114411	V.Good	purple	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114419	Poor	Light purple	Dark green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114421	V.Good	Purple lines	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	White	Absent	Intermediate
IC-114425	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114430	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Difficult
IC-114441	V.Good	purple	Purple margin	Pubescent	Cleft	Purple lines	Just exs	Compact	Purple	Absent	Easy
IC-114458	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114485	V.Good	Purple lines	Green	Glabrous	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114511	Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114513	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114514	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Purple	Absent	Easy
IC-114515	Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114526	Good	purple	Purple margin	Pubescent	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Difficult
IC-114527	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate

	EarlyPlant vigour	Basal leaf sheath colour	Leaf colour	Leaf pubescence	Ligule shape	Ligule colour	Panicle exsertion	Panicle type	Stigma colour	Awning	Threashability
IC-114530	V.Good	Light purple	Green	Pubescent	Cleft	White	Just exs	Intermediate	Purple	Absent	Easy
IC-114538	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114543	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114550	V.Good	Green	Green	Pubescent	Truncate	White	Well exs	Intermediate	Purple	Absent	Easy
IC-114558	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114562	V.Good	purple	Dark green	Glabrous	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Easy
IC-114571	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114583	V.Good	Light purple	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114587	Good	Light purple	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114588	V.Good	Light purple	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114589	V.Good	purple	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Light purple	Absent	Intermediate
IC-114612	Good	purple	Green	Pubescent	Cleft	Purple	Well exs	Intermediate	Light purple	Absent	Easy
IC-114655	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114680	Good	purple	Purple margin	Pubescent	Cleft	Purple	Well exs	Intermediate	Light purple	Absent	Intermediate
IC-114712	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114723	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114725	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Light purple	Absent	Easy
IC-114730	V.Good	Purple lines	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Easy
IC-114732	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114736	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114740	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114752	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114766	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114784	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Intermediate	Purple	Absent	Easy
IC-114785	Poor	Green	Green	Pubescent	Acute	White	Well exs	Compact	White	Absent	Easy
IC-114797	V.Good	purple	Green	Pubescent	Cleft	White	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114831	Poor	Green	Green	Pubescent	Cleft	White	Just exs	Compact	White	Absent	Easy

	EarlyPlant vigour	**Basal leaf sheath colour**	**Leaf colour**	**Leaf pubescence**	**Ligule shape**	**Ligule colour**	**Panicle exsertion**	**Panicle type**	**Stigma colour**	**Awning**	**Threashability**
IC-114840	Good	Light purple	Purple margin	Intermediate	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Intermediate
IC-114847	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-114851	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-114852	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114864	Good	Green	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-114882	Good	purple	Purple margin	Pubescent	Cleft	Purple	Well exs	Compact	Purple	Absent	Intermediate
IC-114889	V.Good	purple	Purple margin	Pubescent	Cleft	Purple lines	Well exs	Compact	Light purple	Absent	Intermediate
IC-114921	Good	purple	Purple tips	Pubescent	Cleft	Purple	Just exs	Compact	Light purple	Absent	Easy
IC-114984	Good	purple	Purple margin	Pubescent	Cleft	Purple	Well exs	Intermediate	Purple	Absent	Easy
IC-114986	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-114999	Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Intermediate	Purple	Absent	Easy
IC-115000	Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-115001	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-115004	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Difficult
IC-115006	V.Good	Purple lines	Purple blotch	Intermediate	Cleft	White	Well exs	Intermediate	White	Long and fully awned	Easy
IC-115050	Good	Green	Light green	Pubescent	Cleft	White	Well exs	Compact	White	Short and partly awned	Easy
IC-115063	V.Good	Purple lines	Green	Pubescent	Cleft	Purple	Well exs	Compact	Light purple	Absent	Easy
IC-115074	V.Good	Light purple	Dark green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Intermediate
IC-115078	V.Good	Purple lines	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Easy
IC-115090	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-115108	V.Good	purple	Dark green	Pubescent	Cleft	Purple	Well exs	Compact	Purple	Short and partly awned	Intermediate
IC-115114	V.Good	Light purple	Light green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Difficult
IC-115116	V.Good	purple	Green	Pubescent	Cleft	White	Well exs	Compact	Purple	Absent	Easy

	EarlyPlant vigour	Basal leaf sheath colour	Leaf colour	Leaf pubescence	Ligule shape	Ligule colour	Panicle exsertion	Panicle type	Stigma colour	Awning	Threashability
IC-115118	V.Good	purple	Green	Intermediate	Cleft	White	Well exs	Intermediate	Purple	Absent	Easy
IC-115131	V.Good	Light purple	Green	Intermediate	Cleft	White	Well exs	Intermediate	Purple	Absent	Easy
IC-115170	V.Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-114208	Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Easy
IC-115623	Good	Green	Green	Intermediate	Cleft	White	Well exs	Open	White	Absent	Easy
IC-115625	Good	Green	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Intermediate
IC-115628	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-115630	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Easy
IC-115733	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Purple	Absent	Intermediate
IC-115734	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Compact	White	Absent	Intermediate
IC-115738	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	Light purple	Absent	Easy
IC-115743	V.Good	Green	Green	Glabrous	Cleft	White	Well exs	Intermediate	Purple	Absent	Intermediate
IC-115744	V.Good	Light purple	Green	Pubescent	Cleft	Purple lines	Well exs	Open	Purple	Absent	Difficult
IC-115757	Good	Light purple	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Easy
IC-115760	V.Good	Purple lines	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Easy
IC-115868	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-115888	V.Good	Purple	Green	Pubescent	Cleft	Purple lines	Moderately	Compact	White	Absent	Intermediate
IC-115897	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
IC-115905	Good	Light purple	Green	Pubescent	Cleft	Purple lines	Well exs	Intermediate	Purple	Absent	Intermediate
IC-115907	Good	Light purple	Green	Pubescent	Cleft	Purple lines	Well exs	Compact	Purple	Absent	Difficult
IC-115909	Good	Green	Green	Pubescent	Cleft	White	Well exs	Intermediate	White	Absent	Easy
IC-115914	Good	Green	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Easy
IC-115921	V.Good	Green	Green	Pubescent	Cleft	White	Well exs	Open	White	Absent	Easy
Jaya	Good	Green	Green	Intermediate	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate
M. Vijaya	Good	Green	Green	Intermediate	Cleft	White	Well exs	Compact	White	Absent	Intermediate
Prasanna	V. Good	Green	Light green	Intermediate	Cleft	White	Well exs	Open	White	Absent	Intermediate
Rasi	Good	Green	Green	Intermediate	Cleft	Others	Well exs	Intermediate	Purple	Absent	Intermediate
Vasumati	Good	Green	Dark grren	Intermediate	Cleft	White	Well exs	Intermediate	White	Absent	Intermediate

Table 4.2: ANOVA for important morphological characters and yield in different rice genotypes

S.No.	Character	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=149)	Error (d.f.=258)
1.	Days to 50% flowering	1.78	206.12**	1.02
2.	Plant height (cm)	6.98	568.60**	1.81
3.	Leaf length (cm)	7.16	87.86**	2.58
4.	Leaf width (cm)	0.014	0.07	0.01
5.	Number of tillers/plant	5.17	22.95**	1.89
6.	Number of productive tillers/plant	3.19	11.69**	1.07
7.	Panicle length (cm)	8.43	15.05**	1.05
8.	Number of grains/panicle	8.86	3440.24**	7.14
9.	Spikelet fertility (%)	5.62	329.87**	0.59
10.	100-grain weight (g)	0.29	0.40	0.02
11.	Single plant yield (g)	4.61	50.76**	1.01

** Significant at 1 per cent level

*Significant at 5 per cent level

Table 4.3: Estimates of variability, heritability (broad sense), genetic advance and genetic advance as per cent mean for various characters in rice genotypes

S.No.	Character	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (h^2) (%)	GA (5%)	GA as per cent mean
1.	Days to 50% flowering	69.39	68.37	9.27	9.20	98.52	16.91	18.82
2.	Plant height (cm)	190.74	188.93	11.94	11.88	99.05	28.18	24.35
3.	Leaf length (cm)	31.01	28.43	14.33	13.72	91.66	10.52	27.05
4.	Leaf width (cm)	0.03	0.02	15.83	12.52	62.56	0.23	20.40
5.	Total tillers per plant	8.92	7.02	22.73	20.17	78.72	4.84	36.85
6.	Productive tillers per plant	4.61	3.54	31.31	27.44	76.82	3.40	49.54
7.	Panicle length (cm)	5.72	4.67	10.33	9.32	81.54	4.02	17.34
8.	Grains per panicle	1151.51	1144.37	22.34	22.27	99.38	69.47	45.74
9.	Spikelet fertility (%)	110.35	109.76	12.19	12.16	99.46	21.52	24.97
10.	100-seed weight (g)	0.15	0.13	15.70	14.66	87.21	0.69	28.20
11.	Single plant yield (g)	17.60	16.58	24.15	23.44	94.21	8.14	46.87

Table 4.4: Mean performance of rice genotypes for various quantitative characters

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility (%)	100-seed weight (g)	Single plant yield (g)
1	IC-114007	85.33	124.63	36.93	1.25	9.32	3.68	22.23	129.50	62.30	2.49	9.04
2	IC-114009	89.67	124.30	36.83	0.94	13.46	6.59	23.24	96.89	41.33	2.24	6.52
3	IC-114012	84.00	118.40	39.33	1.21	15.42	7.31	21.31	90.60	57.23	2.53	6.19
4	IC-114016	74.33	118.54	38.10	1.16	15.43	10.23	23.84	113.95	61.37	2.32	10.80
5	IC-114017	79.33	127.59	46.72	1.15	10.29	4.99	23.63	144.37	87.22	2.85	11.38
6	IC-114018	83.67	120.03	38.93	0.77	14.57	9.45	26.74	148.14	96.38	3.02	23.62
7	IC-114019	81.00	115.28	38.32	0.81	18.22	12.58	24.08	127.89	63.21	2.47	21.39
8	IC-114027	79.33	121.76	39.06	1.14	9.54	3.47	22.57	96.63	40.79	2.67	13.20
9	IC-114035	74.00	134.77	48.93	1.28	11.55	5.30	20.65	91.75	57.29	2.42	16.24
10	IC-114039	90.00	115.40	45.95	0.72	14.35	4.36	20.95	114.37	62.43	3.60	20.83
11	IC-114040	87.33	123.87	49.37	1.03	7.42	5.79	17.13	146.73	96.31	2.25	23.27
12	IC-114058	88.67	119.00	40.71	0.68	13.34	6.23	20.62	115.58	85.39	2.55	24.94
13	IC-114061	75.00	115.05	38.96	1.42	8.62	5.28	22.52	122.84	84.14	3.00	25.44
14	IC-114063	80.67	120.94	36.66	1.17	10.49	5.28	21.55	129.97	90.43	2.89	22.62
15	IC-114064	75.00	122.25	40.36	1.41	11.19	7.23	23.22	119.66	88.26	2.43	24.47
16	IC-114085	90.33	110.31	36.62	1.11	17.39	9.49	26.66	235.10	68.16	2.51	26.17
17	IC-114114	89.33	120.01	30.66	1.23	12.46	7.23	25.71	125.82	96.45	2.46	24.37
18	IC-114117	86.33	116.40	32.66	1.32	11.28	5.19	24.75	122.97	94.50	2.34	24.13
19	IC-114126	88.67	128.26	35.02	1.22	16.39	12.38	24.42	166.44	85.17	2.40	22.57
20	IC-114149	87.67	127.56	33.15	1.22	9.58	7.37	24.35	150.54	95.54	2.25	22.30
21	IC-114150	78.67	127.75	35.89	0.81	13.31	7.47	23.63	141.64	69.48	2.21	20.24
22	IC-114156	91.33	129.04	37.98	1.45	7.83	4.18	22.81	177.66	73.50	2.72	22.53

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility (%)	100-seed weight (g)	Single plant yield (g)
23	IC-114157	86.00	117.39	40.62	1.24	11.36	6.99	23.07	164.45	92.44	2.55	18.99
24	IC-114160	103.00	121.60	37.68	1.17	14.37	7.47	21.48	180.94	94.82	2.64	20.32
25	IC-114162	105.00	103.17	40.51	1.05	10.48	6.27	21.10	168.15	93.03	2.52	20.07
26	IC-114164	103.00	117.44	39.57	1.32	15.24	7.34	21.56	183.55	85.74	2.85	16.64
27	IC-114177	98.00	104.45	46.09	0.98	8.58	3.25	22.45	133.65	91.36	2.28	10.34
28	IC-114196	94.00	87.93	45.19	0.88	13.44	7.35	21.65	155.77	93.43	2.75	15.00
29	IC-114237	109.67	124.41	49.83	1.30	8.34	6.33	23.09	134.45	91.15	2.51	14.98
30	IC-114250	96.00	116.24	41.30	1.01	12.61	7.25	24.51	159.77	96.71	2.45	17.95
31	IC-114251	94.00	120.03	35.67	1.34	10.31	5.25	22.31	119.94	96.46	2.51	16.72
32	IC-114253	97.00	114.63	34.93	1.23	12.03	7.24	22.35	128.40	82.88	2.60	15.33
33	IC-114256	92.00	113.40	49.80	0.96	10.01	5.48	19.36	143.69	88.40	2.31	10.72
34	IC-114261-1	105.00	111.10	42.26	1.22	13.29	7.38	24.10	165.93	79.54	2.65	12.40
35	IC-114278	88.67	122.43	43.42	0.99	12.04	6.19	21.03	124.73	88.67	2.82	13.34
36	IC-114285	98.00	119.43	35.42	1.39	14.26	7.26	22.55	141.59	79.40	2.34	15.35
37	IC-114286	96.67	136.13	41.34	1.36	8.47	4.34	21.75	125.75	88.48	1.94	15.34
38	IC-114309	105.67	122.33	43.71	1.13	13.34	7.45	22.42	146.05	80.75	2.33	18.18
39	IC-114313	94.67	115.23	40.53	1.39	10.37	6.36	21.89	143.04	78.23	2.12	16.34
40	IC-114316	84.33	120.30	45.65	1.21	14.41	8.40	20.53	133.03	90.32	1.66	14.01
41	IC-114321	96.33	126.43	49.18	1.33	12.23	7.33	23.73	123.34	95.30	2.95	18.98
42	IC-114325	81.00	129.28	45.85	1.03	8.23	3.55	21.42	176.43	78.38	2.46	14.92
43	IC-114338	90.67	82.50	44.60	0.95	12.39	6.29	18.48	221.69	84.13	2.93	22.22
44	IC-114339	85.67	133.37	38.93	1.37	13.35	7.42	25.30	155.46	87.72	2.96	22.37
45	IC-114341	89.33	126.57	42.26	1.30	15.30	8.23	27.10	147.82	92.14	3.13	23.28
46	IC-114344	85.00	155.43	47.86	1.20	10.26	5.42	27.03	297.23	89.25	2.95	17.18
47	IC-114346	89.33	130.61	38.72	1.20	10.47	5.27	21.59	147.59	89.54	2.89	20.33
48	IC-114349	89.67	138.27	47.63	1.08	13.58	7.44	21.76	143.87	95.63	2.51	13.25

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility (%)	100-seed weight (g)	Single plant yield (g)
49	IC-114350	91.00	116.50	43.40	1.10	13.14	7.40	23.40	138.95	96.49	2.18	17.40
50	IC-114351	85.33	114.50	36.08	1.25	13.44	8.18	23.62	148.89	89.39	2.50	14.48
51	IC-114354	87.67	118.37	39.10	1.09	13.27	6.33	21.03	142.85	88.32	1.93	23.80
52	IC-114362	79.67	122.20	39.73	1.04	11.20	6.26	23.01	164.65	87.08	1.78	11.85
53	IC-114369	83.67	143.23	32.64	1.20	8.46	5.32	22.05	150.74	92.34	2.34	9.64
54	IC-114384	81.67	122.58	39.53	1.10	13.22	7.20	22.89	154.93	84.56	2.67	11.46
55	IC-114386	86.33	136.33	31.48	1.40	8.24	4.29	24.26	158.97	75.81	2.52	15.66
56	IC-114389	91.00	107.88	31.39	1.20	12.34	6.32	20.76	139.02	87.28	2.24	16.19
57	IC-114400	88.33	118.83	38.80	0.85	10.59	5.27	22.62	73.81	94.44	2.50	16.32
58	IC-114407	80.67	120.20	32.23	1.25	12.85	6.29	22.37	104.31	96.22	3.02	19.64
59	IC-114410	88.67	124.50	38.36	1.19	12.33	6.39	24.45	147.07	91.30	2.82	14.14
60	IC-114411	90.33	126.67	32.77	1.33	11.44	6.29	22.83	198.01	76.42	2.24	15.31
61	IC-114419	87.00	122.30	41.63	1.18	12.47	6.21	25.00	171.71	84.12	2.50	14.01
62	IC-114421	86.67	95.47	35.36	1.01	11.23	5.38	24.80	216.62	68.28	2.46	18.66
63	IC-114425	105.67	119.60	40.95	1.26	10.60	5.43	23.01	156.11	86.20	2.45	16.61
64	IC-114430	99.33	117.40	35.27	1.06	13.53	7.29	21.89	167.86	84.37	2.64	17.59
65	IC-114441	89.33	98.40	36.49	0.95	12.00	6.85	24.07	168.48	88.58	2.84	14.21
66	IC-114458	89.67	95.93	42.00	1.24	13.54	7.27	24.76	158.41	88.25	2.37	15.90
67	IC-114485	85.33	108.80	30.82	1.01	15.49	7.23	19.93	165.03	89.09	2.68	18.27
68	IC-114511	84.67	110.67	37.20	1.23	15.08	5.40	18.81	163.26	96.32	2.17	17.22
69	IC-114513	84.00	111.87	48.77	1.11	11.06	5.46	18.37	103.93	95.47	2.04	16.27
70	IC-114514	82.00	101.06	33.30	1.13	18.28	9.30	19.36	150.14	82.33	2.23	16.63
71	IC-114515	78.67	108.50	33.56	1.02	13.74	7.30	23.68	123.07	95.69	2.36	17.50
72	IC-114526	87.67	115.37	32.39	0.96	12.29	7.20	22.61	175.52	84.89	2.75	18.73
73	IC-114527	96.67	95.60	44.41	1.16	13.62	5.58	22.89	167.71	88.38	2.59	18.31
74	IC-114530	92.67	106.63	36.23	1.29	12.43	7.38	22.79	185.13	87.55	2.55	17.52
75	IC-114538	82.33	111.33	46.27	1.23	13.07	5.50	20.75	120.71	92.45	1.42	11.42

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility (%)	100-seed weight (g)	Single plant yield (g)
76	IC-114543	80.67	99.47	38.70	0.99	12.79	4.33	25.97	137.15	88.03	2.40	17.45
77	IC-114558	87.33	132.07	36.37	1.23	14.27	5.34	20.90	153.39	93.31	2.33	8.93
78	IC-114562	84.67	110.23	41.47	1.35	13.20	7.49	25.18	144.53	88.38	2.51	17.28
79	IC-114571	78.33	113.40	45.46	0.96	12.28	6.35	21.93	180.14	95.44	2.86	13.39
80	IC-114583	105.67	103.73	37.96	1.29	14.62	8.31	22.68	130.31	90.36	2.44	16.47
81	IC-114587	84.67	115.67	36.46	1.23	11.98	4.32	23.11	234.18	52.39	2.66	17.75
82	IC-114588	88.33	110.57	45.73	1.01	14.27	7.17	25.38	103.68	89.17	3.00	19.18
83	IC-114589	86.33	111.52	33.03	1.26	13.07	4.41	24.04	204.00	74.44	2.68	21.84
84	IC-114612	105.33	123.33	40.43	1.21	16.05	9.21	26.42	158.76	84.35	2.46	20.38
85	IC-114655	94.00	114.60	41.23	0.74	15.19	7.38	24.66	179.93	74.92	2.64	23.51
86	IC-114680	91.33	116.43	31.91	1.33	16.53	8.35	22.32	157.00	91.64	1.91	14.18
87	IC-114712	88.33	127.97	36.27	1.20	15.02	7.34	20.41	162.39	90.38	2.28	21.22
88	IC-114723	87.00	133.17	30.23	0.96	11.77	6.00	22.67	149.98	96.34	2.42	21.59
89	IC-114725	80.67	127.80	37.15	0.85	13.81	7.28	18.63	149.19	86.30	2.03	14.19
90	IC-114730	89.33	114.53	42.11	0.96	12.37	5.89	25.06	126.18	91.29	2.51	20.00
91	IC-114732	109.00	146.87	32.25	1.25	12.75	7.23	17.92	148.88	81.49	1.55	20.39
92	IC-114736	88.67	139.11	41.73	0.99	13.09	6.30	20.34	173.40	79.36	1.94	14.70
93	IC-114740	109.67	121.70	42.82	0.98	11.77	5.36	22.63	184.03	79.30	1.78	12.77
94	IC-114752	94.67	115.83	44.92	1.10	18.02	9.13	23.46	117.74	91.33	1.67	13.85
95	IC-114766	82.33	133.37	50.35	1.21	15.83	8.30	19.12	184.22	68.25	2.11	22.84
96	IC-114784	97.00	128.53	46.31	1.19	19.45	9.14	20.85	257.04	88.52	1.93	23.31
97	IC-114785	96.00	124.33	40.50	1.14	13.46	7.27	21.50	217.86	65.86	2.11	20.77
98	IC-114797	87.00	129.69	33.33	1.25	16.92	9.39	24.36	194.06	83.30	2.62	18.37
99	IC-114831	91.00	126.61	31.47	1.12	7.30	3.23	22.00	194.52	87.49	2.30	15.43
100	IC-114840	88.33	129.04	39.82	1.20	12.17	6.38	24.46	178.44	86.47	2.68	14.12
101	IC-114847	86.33	96.82	35.33	0.94	17.97	11.20	24.10	157.49	85.46	3.15	22.22
102	IC-114851	82.00	125.04	42.11	1.10	10.31	5.11	24.97	155.01	88.79	2.03	12.56

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility (%)	100-seed weight (g)	Single plant yield (g)
103	IC-114852	82.33	130.97	39.71	1.24	12.90	5.50	22.40	123.30	96.81	1.95	14.21
104	IC-114864	89.33	105.13	30.10	1.32	9.32	4.38	25.30	120.27	94.35	3.21	17.21
105	IC-114882	104.00	111.29	39.97	1.03	10.08	5.32	22.70	119.50	88.62	3.20	18.16
106	IC-114889	109.33	108.58	39.88	1.23	10.82	4.75	24.32	158.10	95.95	2.55	16.52
107	IC-114921	83.67	89.32	26.96	1.13	12.93	7.20	25.70	149.73	90.56	2.63	16.29
108	IC-114984	95.33	80.33	37.15	1.22	10.41	4.33	27.97	155.14	86.18	2.56	16.75
109	IC-114992	96.00	85.08	41.03	1.21	10.51	5.22	28.44	154.60	87.22	2.60	17.20
110	IC-114999	93.33	126.27	39.04	1.18	12.07	6.23	24.00	153.73	92.74	2.82	10.69
111	IC-115000	83.00	113.80	38.83	1.07	12.35	5.23	24.53	130.56	85.05	2.83	21.16
112	IC-115001	84.33	118.23	30.89	1.08	14.32	7.40	22.04	156.34	84.29	1.55	13.53
113	IC-115004	97.00	107.77	42.13	1.10	18.65	9.25	23.16	158.27	77.18	1.52	15.40
114	IC-115006	81.00	124.03	40.24	1.20	10.51	4.95	28.43	154.07	88.29	2.74	16.96
115	IC-115050	82.33	124.23	32.80	1.40	13.65	7.42	25.19	129.66	91.95	2.69	19.81
116	IC-115063	106.33	131.70	46.18	1.20	13.42	7.26	21.59	144.69	94.32	2.59	19.34
117	IC-115074	99.33	101.81	43.94	0.99	16.02	6.88	25.24	296.86	92.87	2.29	13.48
118	IC-115078	94.67	124.46	47.00	1.05	9.46	7.20	24.10	183.90	91.62	2.56	18.31
119	IC-115090	88.67	113.58	43.37	1.20	10.11	4.66	21.35	140.17	94.57	2.40	15.44
120	IC-115108	81.67	109.21	42.93	1.13	12.21	5.21	24.38	138.25	97.35	2.82	19.53
121	IC-115114	91.00	118.31	26.02	1.30	10.08	6.28	25.78	129.79	88.97	2.73	22.71
122	IC-115116	82.00	116.72	40.23	1.32	12.36	5.53	27.27	143.63	94.96	2.60	15.53
123	IC-115118	90.67	121.98	28.22	1.12	11.25	6.31	24.36	141.04	86.58	2.93	15.48
124	IC-115131	84.00	116.98	32.18	1.25	12.83	4.43	23.67	173.98	91.66	2.45	11.35
125	IC-115170	94.67	110.98	41.43	1.24	13.31	6.25	25.67	177.08	81.63	2.35	17.63
126	IC-115208	80.00	123.53	41.97	1.13	19.50	13.36	24.77	123.53	94.81	2.34	24.28
127	IC-115623	91.33	121.87	37.87	1.26	12.59	7.41	26.47	160.97	92.38	2.19	19.11
128	IC-115625	92.33	110.83	35.96	1.44	17.93	6.54	23.62	130.46	94.41	2.58	12.64
129	IC-115628	91.67	135.09	33.43	1.34	17.15	9.13	26.41	163.85	95.54	2.22	18.93

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility (%)	100-seed weight (g)	Single plant yield (g)
130	IC-115630	86.00	125.99	36.66	1.20	14.50	9.39	28.87	134.96	90.14	2.54	20.61
131	IC-115733	93.00	107.97	38.39	1.12	12.47	4.68	21.91	141.70	93.41	2.41	16.28
132	IC-115734	85.00	103.97	32.10	1.24	16.41	7.43	22.34	129.62	87.49	1.97	18.54
133	IC-115738	90.00	96.07	42.70	1.30	15.04	5.76	23.57	115.01	96.91	2.62	21.64
134	IC-115743	85.33	112.17	33.40	0.97	14.17	8.47	25.57	152.42	91.13	2.52	22.50
135	IC-115744	86.33	103.10	26.98	1.32	17.28	6.86	24.67	175.19	86.50	2.32	21.83
136	IC-115757	97.33	111.98	28.37	1.20	14.39	6.35	24.33	161.12	95.58	2.57	22.14
137	IC-115760	98.33	104.83	33.23	1.24	16.88	9.27	26.26	190.33	70.39	2.62	20.14
138	IC-115868	91.33	96.01	28.11	0.97	20.21	9.97	22.23	136.01	96.81	1.96	19.45
139	IC-115888	94.00	126.60	44.47	1.30	17.78	8.43	25.57	152.77	86.27	2.93	15.27
140	IC-115897	85.67	84.87	39.06	1.00	13.08	7.82	24.71	149.79	83.85	2.82	21.71
141	IC-115905	91.67	106.77	35.99	1.42	14.33	4.30	24.60	151.00	97.10	2.71	14.21
142	IC-115907	101.67	89.50	42.58	1.05	12.39	6.34	21.31	140.63	94.63	2.48	15.91
143	IC-115909	91.33	87.27	36.93	1.21	13.91	7.25	22.87	163.29	94.01	2.44	21.17
144	IC-115914	80.67	95.97	45.20	1.13	12.76	6.32	21.50	191.48	91.96	2.21	9.41
145	IC-115921	78.67	105.80	40.46	1.12	18.79	9.92	28.19	127.69	89.39	1.92	16.44
146	Jaya	102.00	89.49	43.48	1.17	18.36	11.94	21.40	150.84	85.93	2.45	21.07
147	Mandya Vijaya	113.00	112.54	46.54	1.13	16.03	11.12	23.27	150.00	86.09	1.55	17.60
148	Prasanna	69.00	93.45	34.03	0.76	12.67	6.85	21.68	98.82	82.39	2.03	10.29
149	Rasi	91.67	78.33	34.53	1.00	17.72	12.48	18.13	109.35	86.12	2.16	15.73
150	Vasumathi	106.33	86.20	35.70	1.15	19.16	13.13	22.35	115.85	84.66	2.32	15.52
	Mean	89.83	115.7	38.86	1.15	13.14	6.86	23.17	151.88	86.18	2.46	17.37
	C.V.	1.13	1.16	4.14	9.69	10.48	15.08	4.44	1.76	0.89	5.61	5.81
	S.E.	0.58	0.78	0.93	0.06	0.8	0.6	0.59	1.54	0.44	0.08	0.58
	C.D. 5(%)	1.63	2.16	2.58	0.18	2.21	1.66	1.65	4.29	1.24	0.22	1.62

Table 4.5: Clustering pattern among 150 rice genotypes under study (Tocher's method)

Cluster No.	No. of genotypes	Name of the genotype
I	73	IC- 114984, IC- 114992, IC- 115897, IC- 114458, IC- 114527, IC-114921, IC- 115909, IC- 114237, IC- 114441, IC- 114847, IC-114543, IC- 114389, IC- 114562, IC- 114514, IC- 115733, IC-114485, IC- 115743, IC- 114351, IC- 114530, IC- 115170, IC-114526, IC- 115001, IC- 115000, IC- 114730, IC- 114157, IC-114354, IC- 115114, IC- 114680, IC- 115090, IC- 114864, IC-114063, IC- 115118, IC- 115625, IC- 114256, IC- 115905, IC-115108, IC-115006, IC-115116, IC-114410, IC-115623, IC-115050, IC-114419, IC-114341, IC-115630, IC- 114384, IC- 114018, IC-114117, IC- 114851, IC- 114350, IC- 114278, IC- 114346, IC-114362, IC- 114316, IC- 115888, IC- 115757, IC- 114712, IC-114114, IC- 114250, IC-114511, IC- 114251, IC- 114725, IC-115757, IC- 114425, IC-115131, IC-114177, IC-114339, IC- 114149, IC-114752 , IC-115921, IC- 114126, IC-114430, IC- 114253
II	1	IC- 114723
III	29	IC-114285, IC-114313, IC-114309, IC-115004, IC- 114261-1, IC-114612, IC-114425, IC-114882, Mandya vijaya, IC- 114583, IC-114164, IC-114740, IC-114162, IC-114237, IC- 114889, IC-115063, IC- 114286, IC-114321, IC-114999, IC- 115078, IC-114160, IC- 114840, IC- 114736, IC-114831, IC- 114797, IC-115628, IC- 114558, IC- 114040, IC-114017.
IV	16	IC- 114513, IC- 114538, IC- 114407, IC- 114852, IC- 115208, IC-114064, IC- 114400, IC- 114588, IC- 115738, IC- 114058, IC-114061, IC- 115868, IC- 115907, IC- 114349, IC- 114571, Jaya.
V	1	IC- 114369
VI	1	IC- 114411
VII	1	IC-.114325
VIII	15	IC- -114156, IC-- 114655, IC-- 114589, IC-- 115760, IC- -114785 , IC--114085, IC--114421, IC--114766, IC--114386, IC-- 114150, IC-- 114007, IC-- 114019, IC-- 114587, IC--114039, 114016.
IX	4	IC- 114009, IC- 114027, IC- 114012, IC- 114035.
X	1	IC- 115914
XI	1	Vasumathi
XII	1	Rasi
XIII	1	IC- 114732
XIV	1	Prasanna
XV	1	IC- 114338
XVI	3	IC- 114784, IC- 115074, IC- 114344

Table 4.6: Intra (diagonal) and inter –cluster average of D values of 150 genotypes of rice (in Tocher's method)

Cluster	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**	**XIII**	**XIV**	**XV**	**XVI**
I	**12.98**	15.21	16.22	16.25	19.19	19.78	17.24	27.71	45.00	17.32	21.80	22.49	23.50	23.56	24.39	38.78
II		**0.00**	16.52	18.34	10.40	20.53	18.34	32.48	51.57	20.25	30.04	31.16	19.66	30.72	30.10	34.58
III			**15.25**	20.35	19.09	17.81	17.44	27.69	45.74	21.16	24.01	27.44	18.59	30.18	25.90	36.20
IV				**17.01**	22.18	26.20	22.18	31.66	45.63	21.78	22.71	22.11	27.07	22.10	29.94	44.54
V					**0.00**	21.27	17.80	34.03	51.08	22.22	34.32	35.48	21.61	32.63	34.24	35.32
VI						**0.00**	9.82	20.03	42.01	21.84	29.59	32.32	18.47	33.15	20.84	30.08
VII							**0.00**	20.61	39.38	19.87	29.33	30.21	20.83	27.62	23.61	34.17
VIII								**20.18**	32.97	32.19	30.07	31.84	28.47	31.99	27.47	44.22
IX									**16.18**	52.59	40.28	40.89	45.08	37.11	49.95	69.19
X										**0.00**	27.89	26.33	31.94	27.29	17.92	32.75
XI											**0.00**	10.14	30.25	22.61	27.76	51.25
XII												**0.00**	35.44	15.55	28.03	53.61
XIII													**0.00**	38.36	33.87	37.82
XIV														**0.00**	33.62	55.90
XV															**0.00**	32.90
XVI																**21.60**

Table 4.7 : Cluster means for various characters (in Tocher's Method)

Characters	Days to 50% Flowering	Plant Height (cm)	Leaf Length (cm)	Leaf Width (cm)	Total Tillers/Plant	Productive tillers/Plant	Panicle Length (cm)	Total number of Grains /Panicle	Spiklet Fretility (%)	100 - Seed weight (g)	Single plant yield (g)
Cluster I	88.11	112.86	37.39	1.16	13.20	6.80	23.80	148.26	89.99	2.49	17.61
Cluster II	87.00	133.17	30.23	0.96	11.77	6.00	22.67	149.98	96.34	2.42	21.59
Cluster III	98.68	121.77	41.21	1.19	12.50	6.81	22.78	157.21	87.66	2.41	16.41
Cluster IV	86.10	112.90	41.47	1.12	13.70	7.19	22.20	123.62	92.66	2.45	18.80
Cluster V	83.67	143.23	32.64	1.20	8.46	5.32	22.05	150.74	92.34	2.34	9.64
Cluster VI	90.33	126.67	32.77	1.33	11.44	6.29	22.83	198.01	76.42	2.24	15.31
Cluster VII	81.00	129.28	45.85	1.03	8.23	3.55	21.42	176.43	78.38	2.46	14.92
Cluster VIII	87.04	118.47	38.10	1.10	13.45	6.84	23.46	175.08	67.39	2.54	19.48
Cluster IX	81.75	124.81	41.04	1.14	12.49	5.67	21.95	93.97	49.16	2.47	10.54
Cluster X	80.67	95.97	45.20	1.13	12.76	6.32	21.50	191.48	91.96	2.21	9.41
Cluster XI	106.33	86.20	35.70	1.15	19.16	13.13	22.35	115.85	84.66	2.32	15.52
Cluster XII	91.67	78.33	34.53	1.00	17.72	12.48	18.13	109.35	86.12	2.16	15.73
Cluster XIII	109.00	146.87	32.25	1.25	12.75	7.23	17.92	148.88	81.49	1.55	20.39
Cluster XIV	69.00	93.45	34.03	0.76	12.67	6.85	21.68	98.82	82.39	2.03	10.29
Cluster XV	90.67	82.50	44.60	0.95	12.39	6.29	18.48	221.69	84.13	2.93	22.22
Cluster XVI	93.78	128.59	46.04	1.12	15.24	7.15	24.38	286.21	90.21	2.39	17.99

Table 4.9: Canonical root vectors for different characters contributing to genetic diversity (D^2) in rice

Character	Vector 1	Vector 2	vector 3	vector 4
Plant height (cm)	0.04395	0.20350	0.94066	0.15980
Leaf length (cm)	0.00951	0.0143	0.05938	0.07055
Leaf width (cm)	0.01018	-0.00240	-0.01110	0.02648
Total tillers per plant	- 0.00596	-0.01205	-0.11041	-0.01709
Number of productive tillers/plant	0.00272	0.01283	0.08101	0.02757
Days to 50% flowering	0.08985	0.13447	-0.20849	0.95727
Panicle length (cm)	0.01901	0.01996	-0.03788	0.06149
Number of grains/panicle	0.24584	0.92813	-0.16228	-0.18530
Spikelet fertility per cent	0.81172	-0.16498	-0.05621	-0.08554
100-seed weight (g)	-0.46627	0.21542	-0.07969	-0.00435
Single plant yield (g)	-0.22949	0.06728	-0.10958	0.07690

Table 4.10: Mean values of Canonical variates in 150 genotypes of rice

S.No.	Genotype	Z_1 Vector	Z_2 Vector	Z_3 Vector
1	IC-114007	82.42	35.03	34.88
2	IC-114009	60.26	33.35	35.24
3	IC-114012	73.33	26.74	34.17
4	IC-114016	79.03	28.94	34.37
5	IC-114017	106.73	30.94	36.91
6	IC-114018	112.82	29.54	32.01
7	IC-114019	80.09	32.39	30.79
8	IC-114027	57.02	32.69	35.03
9	IC-114035	73.38	27.82	41.66
10	IC-114039	76.16	32.52	30.16
11	IC-114040	114.61	30.45	34.04
12	IC-114058	99.69	26.65	32.03
13	IC-114061	97.22	26.46	31.81
14	IC-114063	105.53	27.94	33.40
15	IC-114064	102.84	24.74	35.10
16	IC-114085	94.62	54.58	22.72
17	IC-114114	111.47	25.79	31.83
18	IC-114117	109.03	24.86	30.89
19	IC-114126	106.39	37.67	33.80
20	IC-114149	114.73	31.75	34.59
21	IC-114150	89.37	35.28	35.74
22	IC-114156	95.88	44.39	33.17
23	IC-114157	112.09	33.82	30.49
24	IC-114160	116.71	39.99	29.03
25	IC-114162	112.03	35.47	22.17
26	IC-114164	108.11	42.20	27.32
27	IC-114177	108.89	26.80	25.91
28	IC-114196	109.63	28.90	18.40
29	IC-114237	110.07	30.92	32.31
30	IC-114250	116.30	32.48	29.10
31	IC-114251	112.23	25.10	32.35
32	IC-114253	99.86	30.01	29.27
33	IC-114256	107.86	30.18	30.03
34	IC-114261-1	100.92	38.54	25.68
35	IC-114278	105.59	27.55	34.19
36	IC-114285	98.93	34.11	30.37
37	IC-114286	108.41	29.96	38.59
38	IC-114309	100.87	35.71	30.60
39	IC-114313	97.65	33.42	29.37

S.No.	Genotype	Z_1 Vector	Z_2 Vector	Z_3 Vector
40	IC-114316	109.66	26.73	33.77
41	IC-114321	111.09	26.55	34.72
42	IC-114325	102.06	40.76	35.74
43	IC-114338	105.33	45.27	13.19
44	IC-114339	107.00	35.42	36.66
45	IC-114341	109.31	31.95	33.78
46	IC-114344	127.39	68.48	40.56
47	IC-114346	108.26	33.98	35.73
48	IC-114349	116.55	31.20	40.01
49	IC-114350	114.36	27.24	30.82
50	IC-114351	108.12	30.70	30.11
51	IC-114354	106.44	30.78	30.96
52	IC-114362	110.09	34.10	33.79
53	IC-114369	115.36	34.07	42.36
54	IC-114384	105.21	33.77	33.83
55	IC-114386	98.36	39.78	37.87
56	IC-114389	104.72	29.73	26.78
57	IC-114400	105.45	14.76	34.59
58	IC-114407	108.52	20.96	34.20
59	IC-114410	110.41	31.68	33.84
60	IC-114411	102.70	46.89	31.99
61	IC-114419	106.50	37.66	32.19
62	IC-114421	92.46	48.49	18.72
63	IC-114425	106.76	36.34	29.24
64	IC-114430	105.37	38.87	28.30
65	IC-114441	107.26	33.86	22.34
66	IC-114458	106.12	30.65	21.72
67	IC-114485	107.96	34.83	26.50
68	IC-114511	115.86	32.07	27.88
69	IC-114513	109.49	18.94	31.63
70	IC-114514	100.16	31.24	24.51
71	IC-114515	110.33	22.25	29.33
72	IC-114526	105.66	38.87	28.53
73	IC-114527	106.58	34.03	20.10
74	IC-114530	108.88	39.15	24.28
75	IC-114538	110.19	21.94	31.12
76	IC-114543	103.47	25.89	24.75
77	IC-114558	115.56	33.31	37.15
78	IC-114562	105.66	29.01	28.53
79	IC-114571	116.40	34.84	29.86
80	IC-114583	106.34	27.78	23.79

S.No.	Genotype	Z_1 Vector	Z_2 Vector	Z_3 Vector
81	IC-114587	81.06	59.00	26.04
82	IC-114588	101.18	21.00	29.73
83	IC-114589	97.66	46.92	25.27
84	IC-114612	105.05	37.28	30.15
85	IC-114655	96.22	42.37	26.80
86	IC-114680	112.62	32.72	29.62
87	IC-114712	111.28	36.10	34.01
88	IC-114723	115.89	32.76	36.73
89	IC-114725	107.59	33.02	36.17
90	IC-114730	106.77	25.81	30.26
91	IC-114732	105.68	40.49	39.53
92	IC-114736	105.05	41.84	38.68
93	IC-114740	105.49	43.96	28.77
94	IC-114752	108.89	23.56	31.04
95	IC-114766	93.03	45.48	36.07
96	IC-114784	120.04	56.76	29.40
97	IC-114785	94.07	54.06	29.14
98	IC-114797	107.87	44.30	33.47
99	IC-114831	112.76	43.91	32.30
100	IC-114840	109.86	39.88	34.45
101	IC-114847	100.96	32.22	21.59
102	IC-114851	110.45	32.19	35.00
103	IC-114852	115.25	24.70	38.43
104	IC-114864	107.05	23.87	26.49
105	IC-114882	102.67	27.63	27.40
106	IC-114889	114.95	33.32	24.34
107	IC-114921	105.93	27.71	19.60
108	IC-114984	101.72	29.47	14.47
109	IC-114992	103.07	29.46	16.50
110	IC-114999	113.44	33.40	34.06
111	IC-115000	100.16	28.12	30.15
112	IC-115001	106.40	33.65	31.30
113	IC-115004	98.88	35.20	25.33
114	IC-115006	107.59	32.35	34.11
115	IC-115050	108.16	27.29	34.53
116	IC-115063	113.96	33.50	34.57
117	IC-115074	126.53	60.47	17.55
118	IC-115078	114.59	39.59	31.89
119	IC-115090	112.16	27.91	30.02
120	IC-115108	112.38	25.49	28.72
121	IC-115114	104.38	29.06	30.61

S.No.	**Genotype**	**Z_1 Vector**	**Z_2 Vector**	**Z_3 Vector**
122	IC-115116	112.55	27.52	31.65
123	IC-115118	104.64	32.41	32.27
124	IC-115131	113.68	35.89	30.24
125	IC-115170	103.31	38.91	26.02
126	IC-115208	110.13	23.86	34.92
127	IC-115623	112.95	33.66	31.58
128	IC-115625	110.85	26.01	28.29
129	IC-115628	117.68	35.38	36.46
130	IC-115630	107.52	28.56	34.66
131	IC-115733	110.57	28.67	26.70
132	IC-115734	103.39	25.92	26.00
133	IC-115738	108.32	20.05	22.96
134	IC-115743	108.52	31.03	28.26
135	IC-115744	105.84	36.41	22.97
136	IC-115757	113.86	33.91	26.06
137	IC-115760	92.54	44.90	21.70
138	IC-115868	112.21	24.84	21.65
139	IC-115888	106.21	34.58	33.54
140	IC-115897	97.94	28.93	17.45
141	IC-115905	114.53	29.28	25.90
142	IC-115907	109.87	26.63	18.53
143	IC-115909	110.15	30.26	17.30
144	IC-115914	114.28	35.44	22.39
145	IC-115921	105.52	22.72	28.11
146	Jaya	101.89	30.82	17.45
147	M.V.	107.13	33.52	26.00
148	Prasanna	95.19	17.02	25.97
149	Rasi	97.74	19.72	16.24
150	Vasumathi	98.04	23.72	17.15

Table 4.11: Clustering pattern among different rice genotypes under study (cluster-analysis)

Cluster No.	No. of genotypes	Name of the genotype
I	2	IC-114009, IC-114027
II	6	IC-114012, IC- 114039, IC- 114016, IC-114019, IC-114007, IC-114035
III	10	IC-114085, IC-114785, IC-114421, IC-114589, IC-115760, IC-114587, IC-114150, IC- 114766, IC-114156, IC- 114655
IV	18	IC-114017, IC- 114384, IC- 114362, IC- 114851, IC- 115006, IC-114725, IC-115001, IC- 114256, IC- 114278, IC-114410, IC-114999, IC-115118, IC- 115888, IC-114126, IC- 1144712, IC-114339, IC- 114346, IC- 114341
V	14	IC-114149, IC- 114723, IC-115628, IC-114157, IC-115623, IC-114680, IC- 114511, IC-114250, IC-115757, IC-114160, IC-115078, IC- 114369, IC- 114558, IC- 114349.
VI	8	IC-114325, IC- 114736, IC- 114386, IC-114411, IC- 114797, IC-114419, IC- 114840, IC- 114831.
VII	8	IC-114485, IC-114526, IC- 114530, IC- 115744, IC-114338, IC-114571, IC- 115131, IC- 115914
VIII	17	IC-114164, IC- 114430, IC- 114261-1, IC-114740, IC-114425, IC-114612, IC- 114309, Mandya Vijaya, IC-114285, IC-114313, IC- 114253, IC-115004, IC-115170, IC-114237, IC-115063, IC-114286, IC- 114732
IX	3	IC-114784, IC- 115074, IC- 114344
X	6	IC-114058, IC- 114588, IC- 114061, IC-115000, IC-114064, Prasanna.
XI	28	IC-IC-114114, IC- 114117, IC-115208, IC- 115050, IC-115630, IC-114063, IC-115114, IC-114351, IC-114562, IC-114389, IC-114354, IC- 115743, IC-114543, IC- 115734, IC-114350, IC-115090, IC-114316, IC- 114040, IC-114852, IC-115108, IC-115116, IC-114018, IC- 114513 IC-, 114538, IC-114515, IC- 115921, IC-114407, IC-114400
XII	16	IC-114162, IC-114889, IC- 114583, IC-114882, IC-114251, IC-114321, IC- 114730, IC-114752, IC-115625, IC-115733, IC-115905, IC-114177, IC-114864, IC- 115738, IC-115868
XIII	15	IC-114196, IC- 115907, IC- 114458, IC- 114527, IC-1144 41, IC-114921, IC- 115909, IC-114984, IC- 114992, IC-114514, IC-114847, IC-115897, Jaya, Vasumathi, Rasi.

Table 4.12: Intra (diagonal) and Inter cluster average of D values of 150 genotypes of rice (in cluster analysis)

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**	**Cluster XII**	**Cluster XIII**
Cluster I	**203.902**	1405.426	4885.366	7565.931	9843.099	7112.541	8713.493	6812.305	16373.400	5794.006	8163.571	8448.660	7286.883
Cluster II		**490.703**	2329.518	3166.917	4688.272	3129.628	4063.998	3013.679	10422.710	2104.044	3493.381	3827.519	3232.485
Cluster III			**774.777**	1996.989	2692.803	1291.812	1880.312	1708.580	4574.577	2393.084	2736.764	2825.431	2205.273
Cluster IV				**266.364**	459.951	515.666	746.734	702.223	4027.763	900.749	505.556	660.129	1126.132
Cluster V					**348.463**	769.152	830.926	921.190	3360.060	1505.494	680.004	738.022	1430.862
Cluster VI						**302.936**	815.801	773.717	3026.544	1531.354	1153.641	1295.294	1583.957
Cluster VII							**556.561**	1123.110	3246.139	1491.412	1001.941	1008.052	936.747
Cluster VIII								**481.699**	4302.633	1375.533	1057.662	840.234	1152.491
Cluster IX									**1400.294**	6949.024	5279.971	5163.124	5552.739
Cluster X										**470.923**	677.654	1000.462	1037.284
Cluster XI											**364.111**	549.151	970.559
Cluster XII												**415.128**	771.396
Cluster XIII													**443.032**

Table 4.13: Cluster means for different characters (in cluster analysis)

Cluster	Days to 50% Flowering	Plant Height (cm)	Leaf Length (cm)	Leaf Width (cm)	Total Tillers/Plant	Productive tillers/Plant	Panicle Length (cm)	Grains/ Panicle	Spiklet fertility (%)	100 Seed weight (g)	Single plant yield (g)
Cluster I	123.032	37.943	1.040	11.502	5.028	84.500	22.908	96.758	41.057	2.457	9.858
Cluster II	121.170	41.262	1.072	14.047	7.244	81.444	22.178	111.342	60.638	2.636	14.081
Cluster III	116.688	38.065	1.119	13.618	6.746	88.867	23.659	198.154	68.568	2.472	21.446
Cluster IV	124.968	39.492	1.142	12.760	6.826	86.519	23.400	151.184	88.079	2.553	15.630
Cluster V	125.001	36.814	1.180	12.944	6.930	90.810	23.087	160.270	94.301	2.365	17.347
Cluster VI	129.879	37.260	1.186	11.234	5.705	87.458	23.085	180.693	81.420	2.407	15.315
Cluster VII	105.343	36.731	1.108	13.468	6.508	85.708	21.948	183.521	88.903	2.595	16.590
Cluster VIII	120.741	40.918	1.222	13.028	7.181	102.922	22.662	153.790	83.595	2.248	16.605
Cluster IX	128.591	46.036	1.124	15.242	7.147	93.778	24.377	286.212	90.213	2.388	17.990
Cluster X	112.354	39.769	1.057	12.073	6.332	79.833	22.992	115.188	85.733	2.640	20.912
Cluster XI	115.847	38.334	1.158	13.029	6.942	84.607	23.582	130.603	92.648	2.364	18.906
Cluster XII	108.722	39.169	1.193	13.121	6.074	96.267	23.270	132.759	93.780	2.543	16.836
Cluster XIII	89.742	38.277	1.097	14.489	8.218	92.778	23.313	149.814	87.973	2.558	17.574

Table 4.14: Relative contribution of different traits to genetic diversity in rice

S.No.	Character	Times ranked first	Contribution (%)
6	Days to 50% flowering	1601	14.33
1	Plant height (cm)	2525	22.60
2.	Leaf length (cm)	74	0.66
3	Leaf width (cm)	0	0.00
4	Total tillers per plant	5	0.04
5	productive tillers per plant	0	0.00
7	panicle length (cm)	33	0.30
8	Grains per panicle	3207	28.70
9	Spikelet fertility (%)	2776	24.84
10	100-seed weight (g)	356	3.19
11	Single plant yield (g)	598	5.35

Table 4.15: Estimates of phenotypic and genotypic correlation coefficients

	Days to 50% flowering	**Plant height (cm)**	**Leaf length (cm)**	**Leaf width (cm)**	**Total tillers per plant**	**Productive tillers / plant**	**Panicle length (cm)**	**Grains per panicle**	**Spikelet fertility %**	**100-seed weight (g)**	**Single plant yield (g)**
Days to 50% flowering	1.0000	-0.1074 * (-0.1081)	0.1305 ** (0.1342)	0.0958 (0.1222	0.0623 (0.0707)	0.1015 * (0.1141)	-0.0482 (-0.0494)	0.1840 ** (0.1866)	0.1237 ** (0.1243)	-0.0563 (-0.0608)	0.0372 (0.0374)
Plant height (cm)		1.0000	0.0926 (0.0980)	0.1802 ** (0.2258)	-0.2272 ** (-0.2602)	-0.1438 ** (-0.1608)	-0.0413 (-0.0459)	0.0661 (0.0678)	-0.0967 * (-0.0969)	-0.0591 (-0.0654)	-0.0248 (-0.0654)
Leaf length (cm)			1.0000	-0.1355 ** (-0.1599)	-0.0995 * (-0.1186)	-0.0545 (-0.0712)	-0.1566 ** (-0.1885)	0.0447 (0.0428)	-0.001 (0.0002)	-0.0186 (-0.0257)	-0.1227** (-0.1313)
Leaf width (cm)				1.0000	-0.0878 (-0.1011)	-0.0784 (-0.1432)	0.1491 ** (0.2103)	0.0277 (0.0333)	0.0951 * (0.1187)	-0.0014 (-0.0066)	0.0005 (0.0077)
Total tillers per plant					1.0000	0.7184 ** (0.8241)	0.0939 * (0.0457)	0.0557 (0.0587)	-0.0280 (-0.0257)	-0.1970 ** (-0.2073)	0.1267** (0.1732)
Productive tillers / plant						1.0000	0.1283 ** (0.0504)	-0.0075 (-0.0195)	0.0040 (0.0143)	-0.1890 ** (-0.1859)	0.2063** (0.2780)
Panicle length (cm)							1.0000	0.1181 * (0.1181)	0.0610 (0.0780)	0.2411 ** (0.3330)	0.1178* (0.1729)
Grains per panicle								1.0000	-0.0417 (-0.0403)	0.0014 (0.0074)	0.1229** (0.1305)
Spikelet fertility %									1.0000	0.0194 (0.0052)	0.1414** (0.1365)
100-seed weight (g)										1.0000	0.2549** (0.2243)

Figures in parenthesis are genotypic correlation coefficients
* Significant at 5% level
** Significant at 1% level

Table 4.16: Direct and indirect effects between yield and its component traits in rice

	Days to 50% flowering	Plant height (cm)	Leaf length (cm)	Leaf width (cm)	Total tillers per plant	Productive tillers / plant	Panicle length (cm)	Grains per panicle	Spikelet fertility %	100-seed weight (g)	Single plant yield (g)
Days to 50% flowering	**0.0052 (-0.0149)**	-0.0006 (0.0016)	0.0007 (-0.0020)	0.0005 (-0.0018)	0.0003 (-0.0011)	0.0005 (-0.0017)	-0.0003 (0.0007)	0.0010 (-0.0028)	0.0006 (-0.0019)	-0.0003 (0.0009)	0.0372 (0.0374)
Plant height (cm)	-0.0052 (-0.0035)	**0.0488 (0.0325)**	0.0045 (0.0032)	0.0088 (0.0073)	-0.0111 (-0.0085)	-0.007 (-0.0052)	-0.0020 (-0.0015)	0.0032 (0.0022)	-0.0047 (-0.0032)	-0.0029 (-0.0021)	-0.0248 (-0.0275)
Leaf length (cm)	-0.0159 (-0.0153)	-0.0113 (-0.0111)	**-0.1217 (0.1137**)	0.0165 (0.0182)	0.0121 (0.0135)	0.0066 (0.0081)	0.0191 (0.0214)	-0.0054 (-0.0049)	0.0001 (0.0000)	0.0023 (0.0029)	-0.1227 (-0.1313)
Leaf width (cm)	-0.0017 (0.0014)	-0.0032 (0.0025)	0.0024 (-0.0018)	**-0.0177 (0.0111)**	0.0015 (-0.0011)	0.0014 (-0.0016)	-0.0026 (0.0023)	-0.0005 (0.0004)	-0.0017 (0.0013)	0 (-0.0001)	0.0005 (0.0077)
Total tillers per plant	-0.0010 (-0.0113)	0.0038 (0.0416)	0.0017 (0.0190)	0.0015 (0.0162)	**-0.0167 (0.1598)**	-0.012 (-0.1317)	-0.0016 (-0.0073)	-0.0009 (-0.0094)	0.0005 (0.0041)	0.0033 (0.0331)	0.1267 (0.1732)
Productive tillers / plant	0.0284 (0.0525)	-0.0402 (-0.0740)	-0.0153 (-0.0328)	-0.0219 (-0.0659)	0.2009 (0.3793)	**0.2796 (0.4602)**	0.0359 (0.0232)	-0.0021 (-0.0090)	0.0011 (0.0066)	-0.0528 (-0.0856)	0.2063 (0.2780)
Panicle length (cm)	0.0015 (-0.0008)	0.0013 (0.0016)	0.0048 (-0.0030)	-0.0045 (0.0034)	-0.0029 (0.0007)	-0.0039 (0.0008)	**-0.0305 (0.0160)**	-0.0036 (0.0019)	-0.0019 (0.0012)	-0.0073 (0.0053)	0.1178 (0.1729)
Grains per panicle	0.0252 (0.0290)	0.0091 (0.0105)	0.0061 (0.0067)	0.0038 (0.0052)	0.0076 (0.0091)	-0.001 (-0.0030)	0.0162 (0.0184)	**0.1370 (0.1555)**	-0.0057 (-0.0063)	0.0002 (0.0011)	0.1229 (0.1305)
Spikelet fertility %	0.0182 (0.0166)	-0.0142 (-0.0129)	-0.0001 (0.0000)	0.014 (0.0158)	-0.0041 (-0.0034)	0.0006 (0.0019)	0.0090 (0.0104)	-0.0061 (-0.0054)	**0.1470 (0.1332**)	0.0029 (0.0007)	0.1414 (0.1365)
100-seed weight (g)	-0.0174 (-0.0163)	-0.0183 (-0.0175)	-0.0058 (-0.0069)	-0.0004 (-0.0018)	-0.061 (-0.0556)	-0.0585 (-0.0498)	0.0747 (0.0892)	0.0004 (0.0020)	0.0060 (0.0014)	**0.3097 (0.2679)**	0.2549 (0.2243)

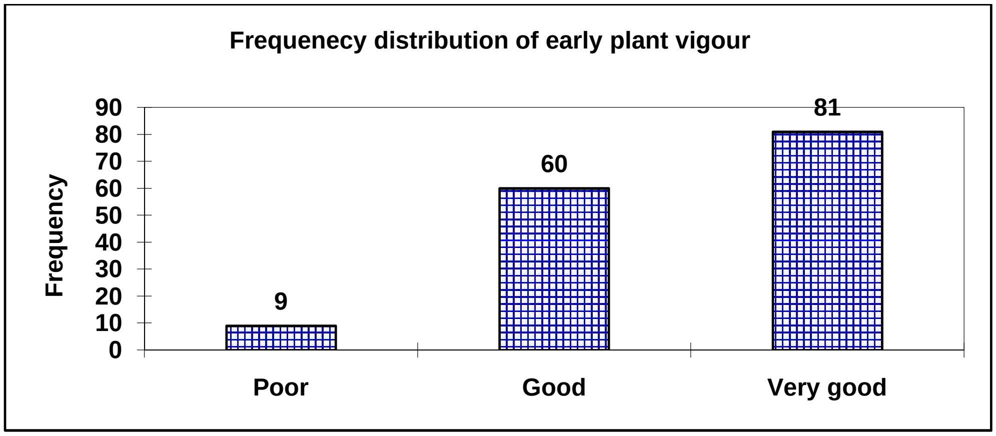
Bold values are direct effects and all other values are indirect effects. Figures in parenthesis indicate genotypic estimates.

Table 4.17: Polymorphic information Content of SSR markers

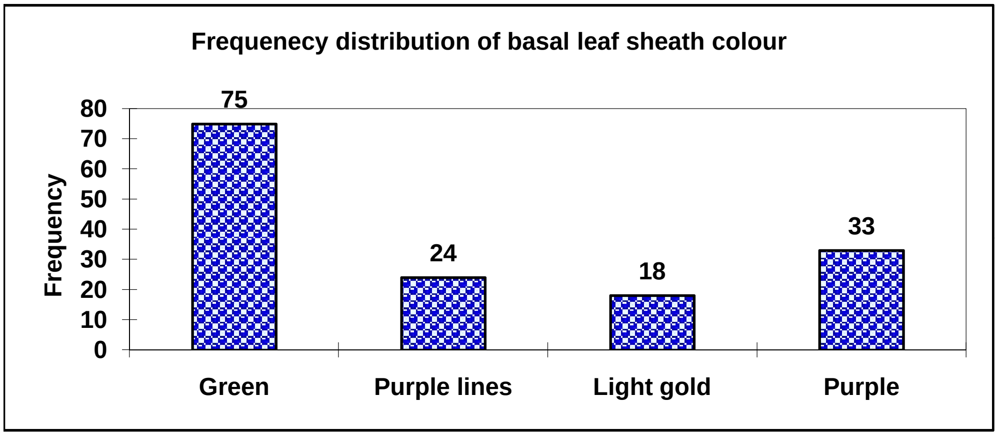
SSR marker	Total alleles	No. of genotypes with polymorphism	Polymorphic Information Content
JGT 01	3	58	1.136
JGT 04	3	62	1.283
JGT 05	2	43	1.316
JGT 06	3	71	1.021
JGT-07	3	66	1.230
RM-151	2	71	1.839
JGT-12	4	67	1.289

Table 4.18: Allelic distribution of SSR markers among 72 rice genotypes

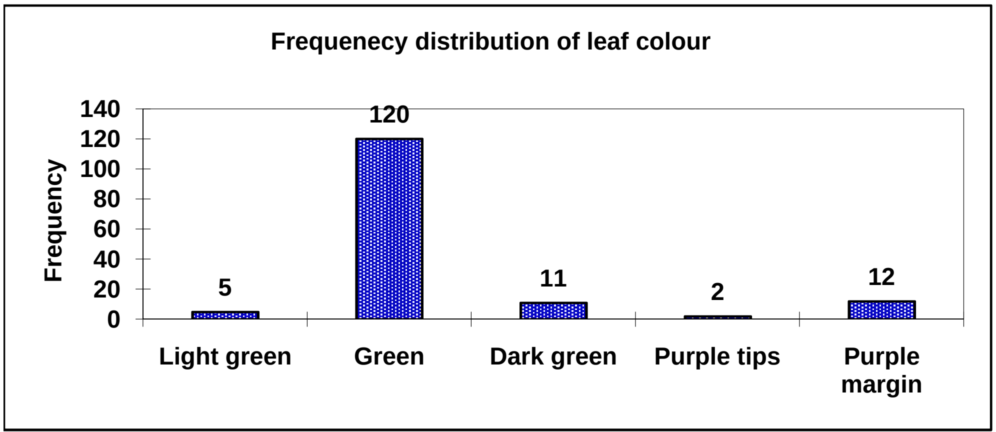
SSR marker	No. of alleles	No. of genotypes with polymorphism for each allele			
		Allele 1	**Allele 2**	**Allele 3**	**Allele 4**
JGT 01	3	3	54	6	-
JGT 04	3	10	32	22	-
JGT 05	2	38	9	-	-
JGT 06	3	60	14	2	-
JGT-07	3	11	41	18	-
RM-151	2	45	31	-	-
JGT-12	4	21	40	6	4



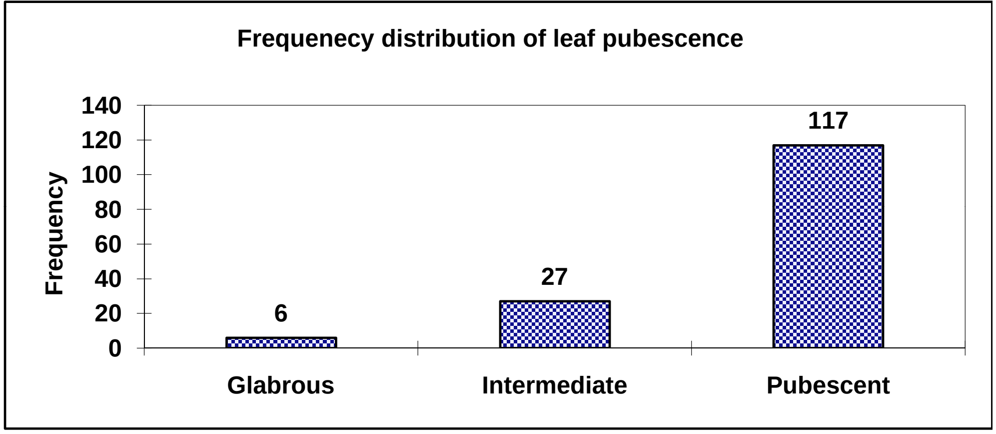
Frequenecy distribution of early plant vigour



Frequenecy distribution of basal leaf sheath colour



Frequenecy distribution of leaf colour



Frequenecy distribution of leaf pubescence

Fig. 4.1 : Frequenecy distribution of various morphological attributes of 150 genotypes of rice

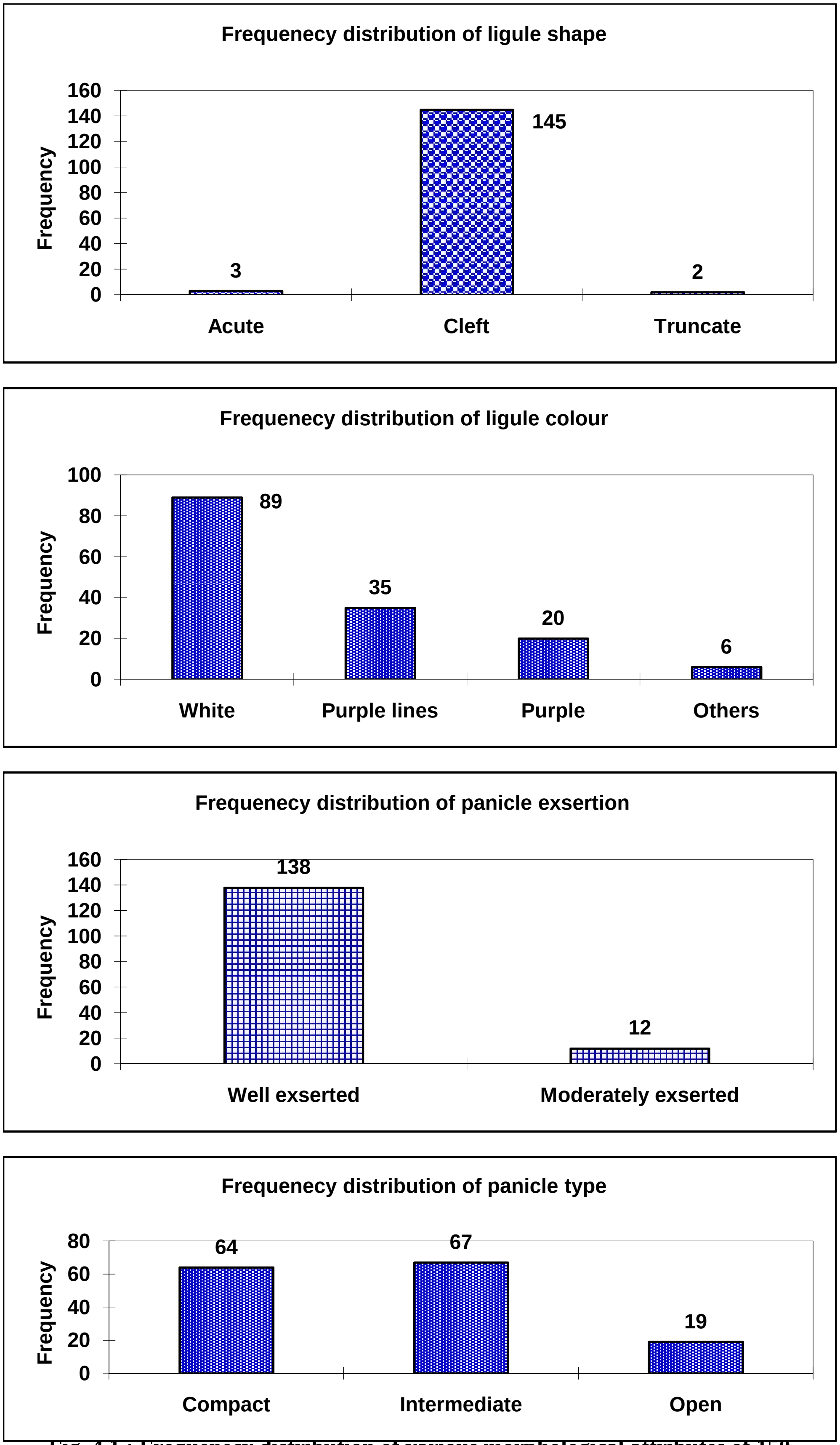
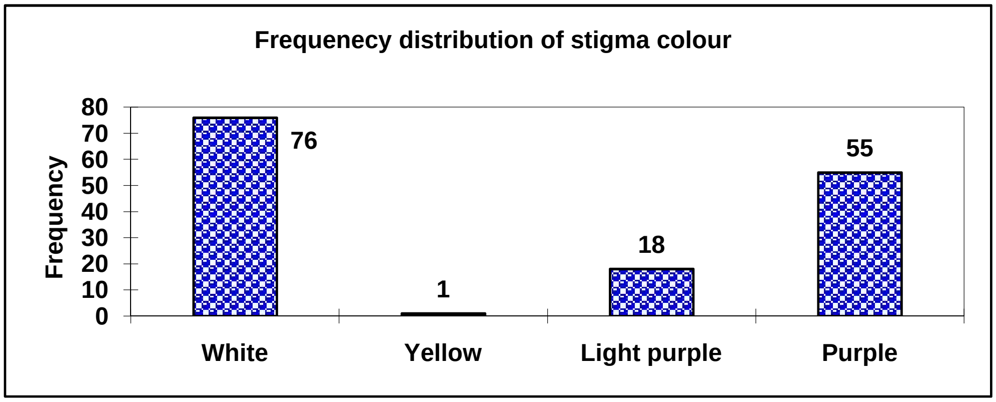
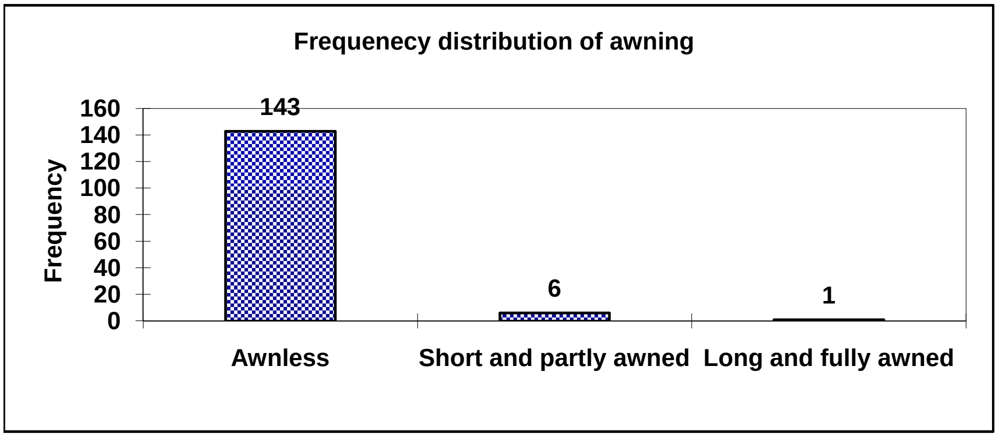


Fig. 4.1 : Frequenecy distribution of various morphological attributes of 150 genotypes of rice





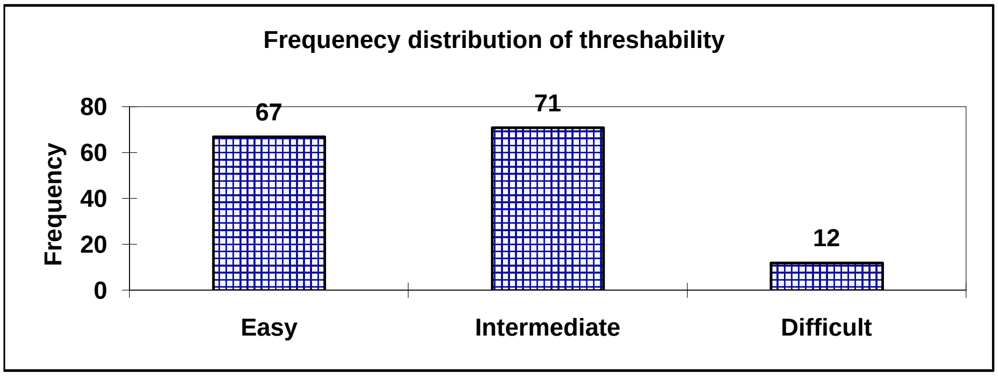


Fig. 4.1 : Frequenecy distribution of various morphological attributes of 150 genotypes of rice

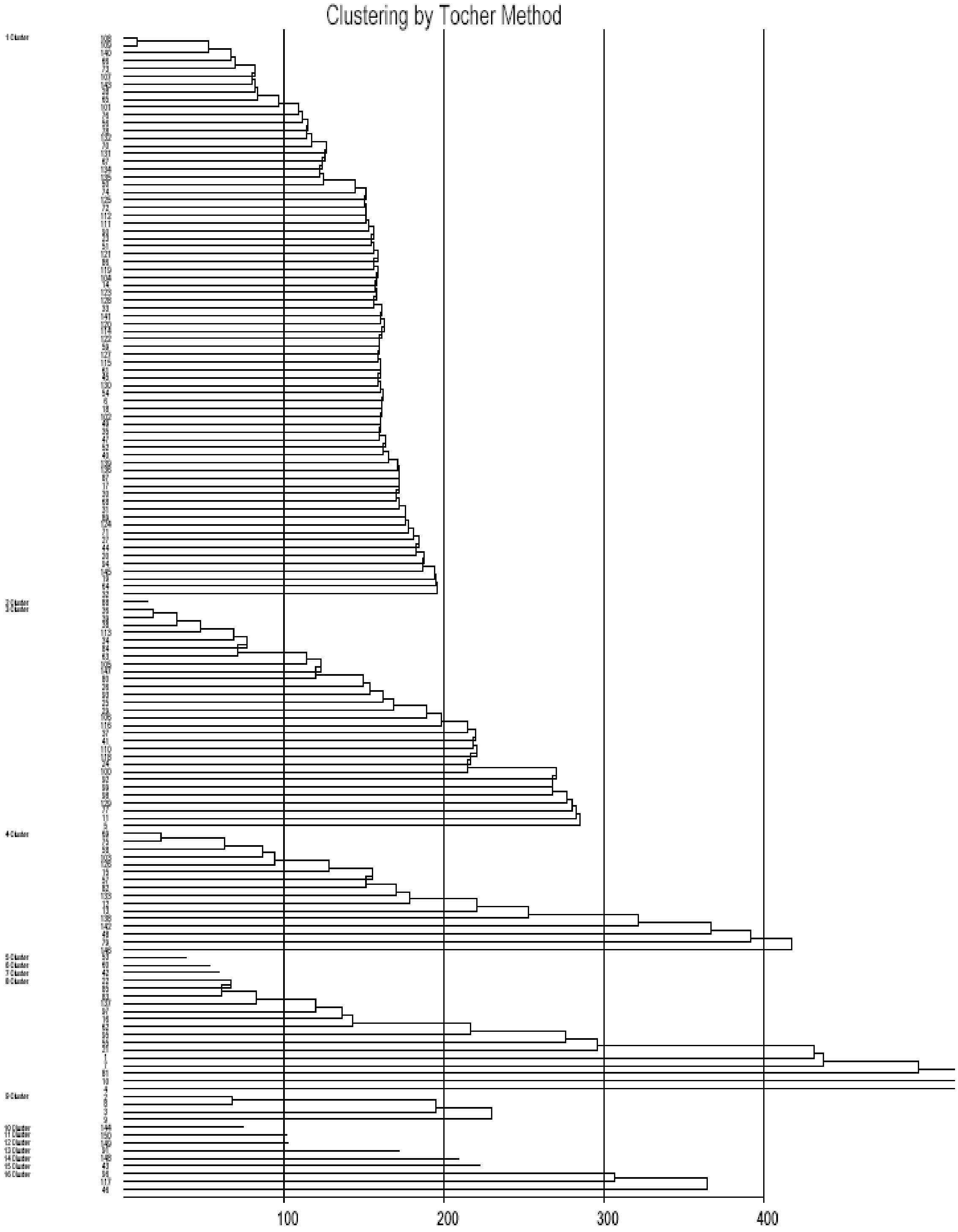


Fig 4.2: Clustering pattern by Tocher's method

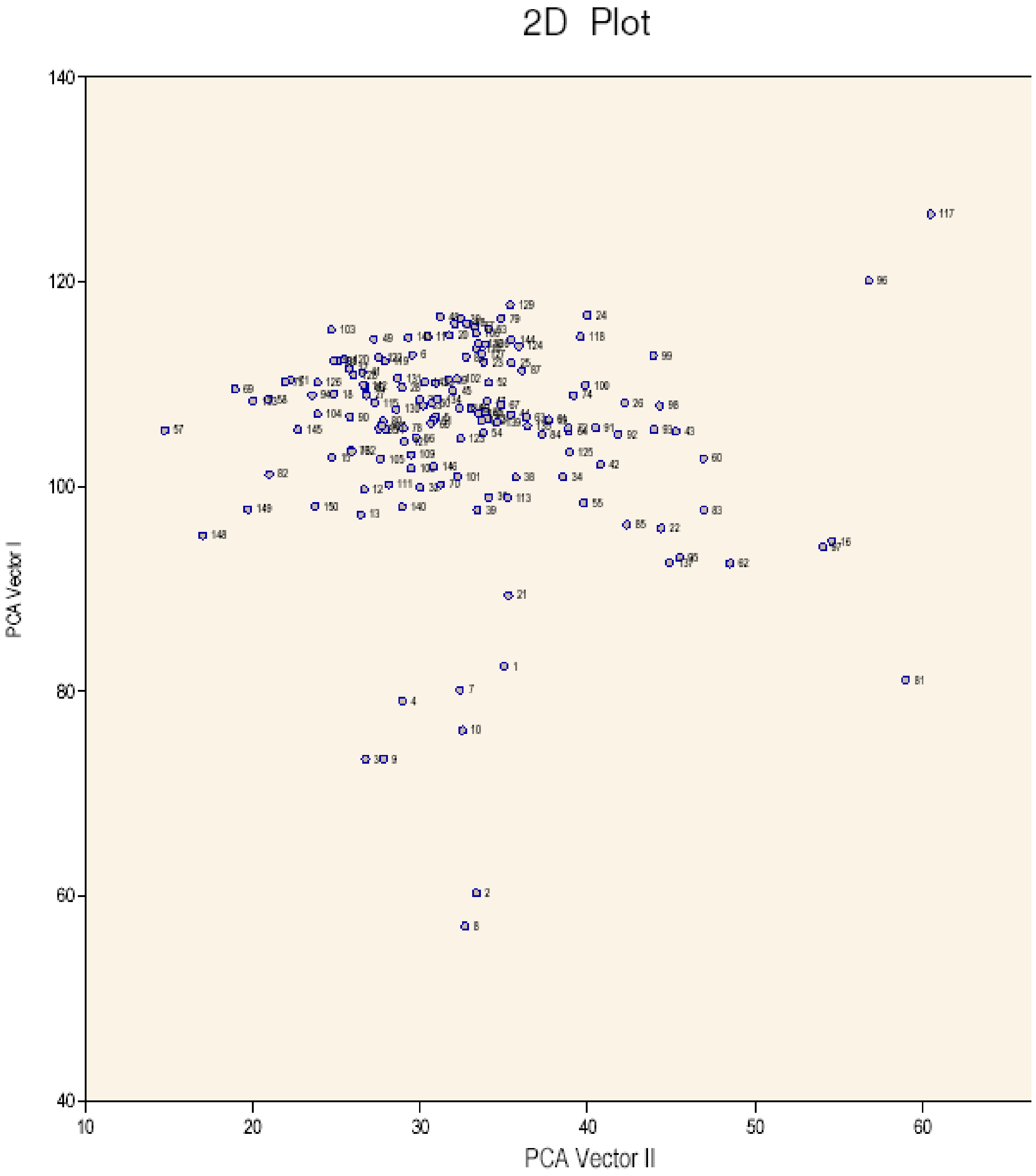
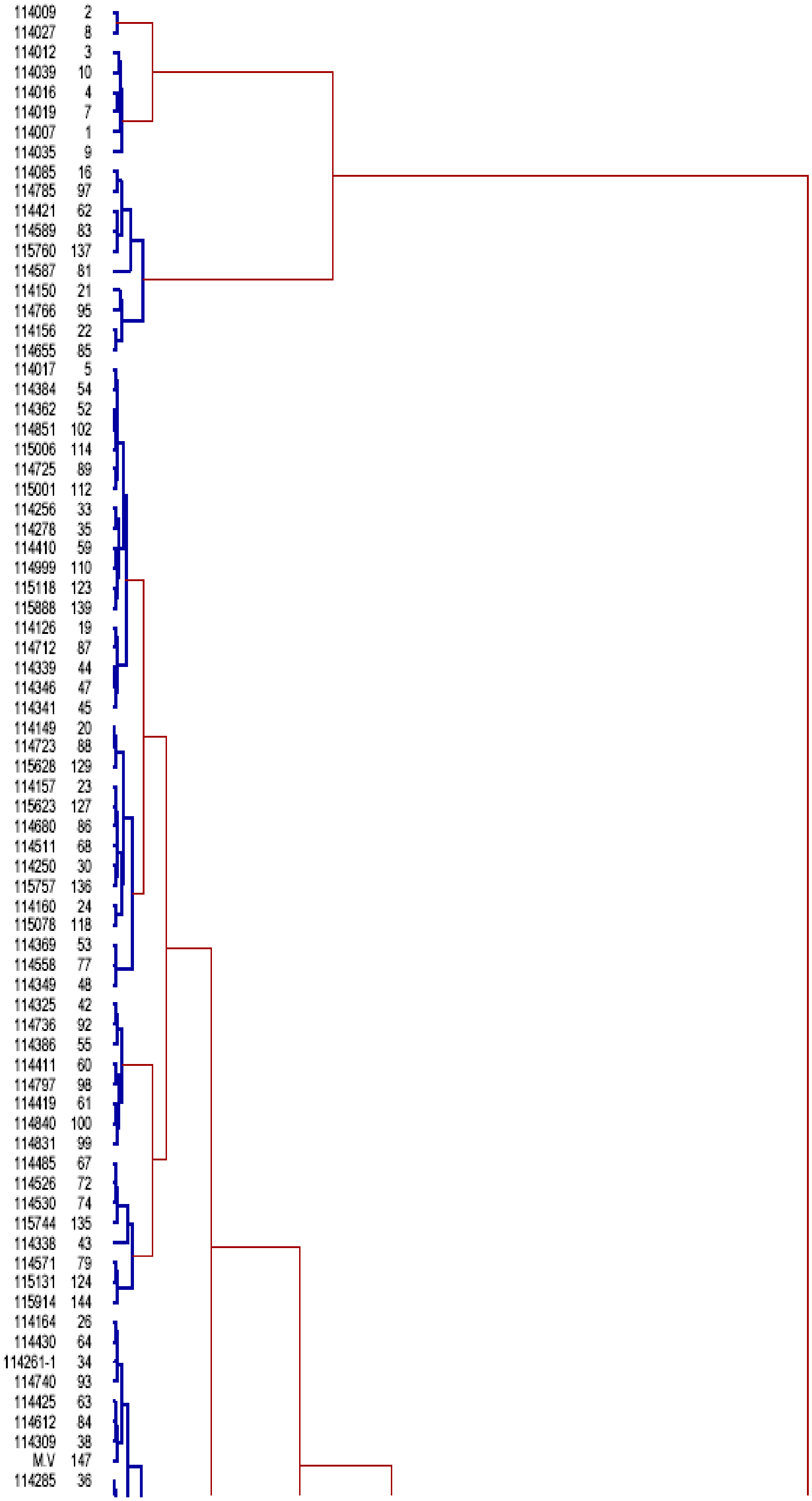


Fig 4.3: Graphical representation of divergence of 150 genotypes using Canonical vectors (Z_1, Z_2) after superimposing grouping obtained by Tocher’s method

Ward's Minimum Variance Dendrogram



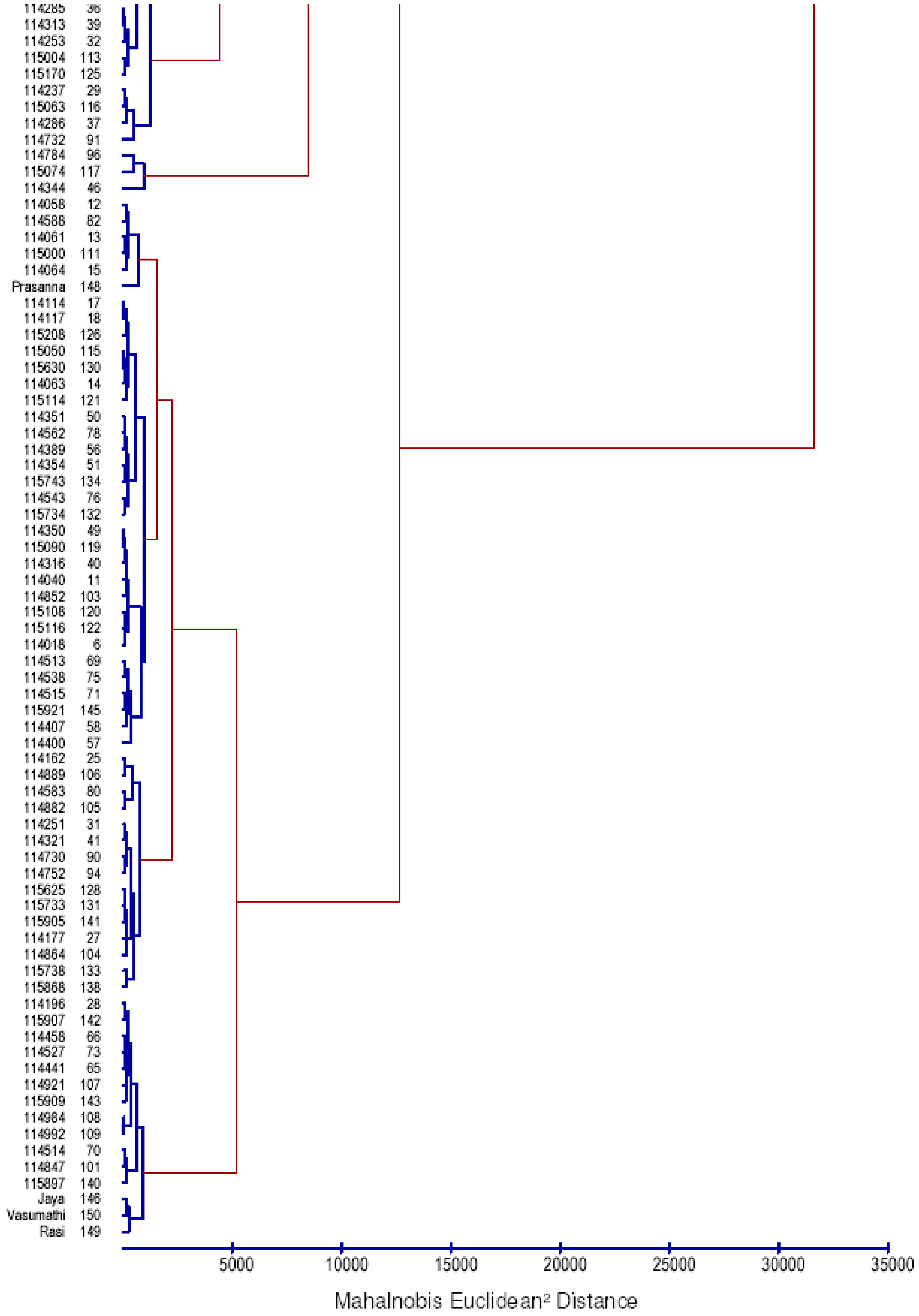


Fig 4.4: Clustering pattern by cluster analysis (Ward's minimum variance dendrogram

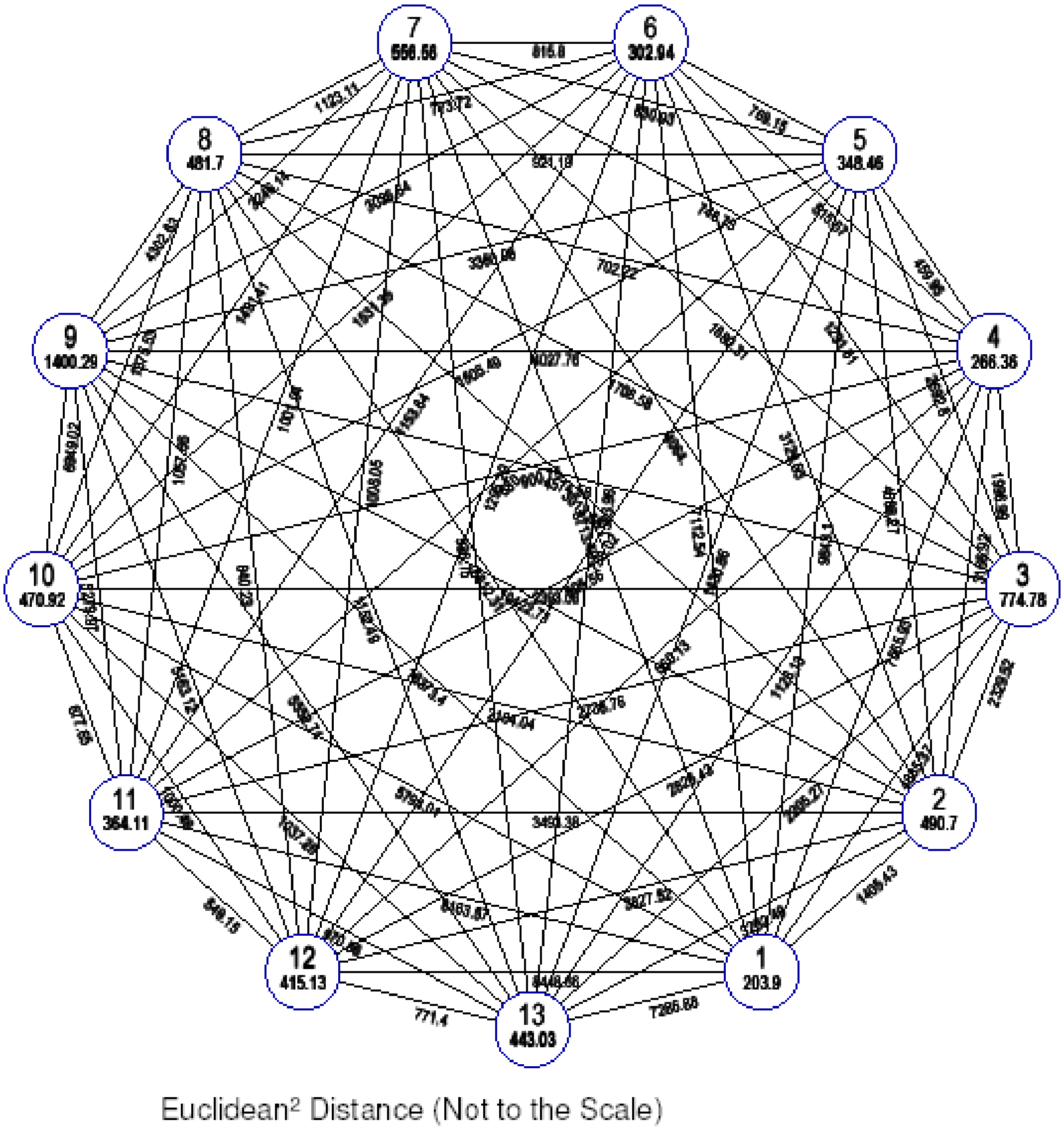


Fig 4.5: Statistical distance among 150 genotypes of rice

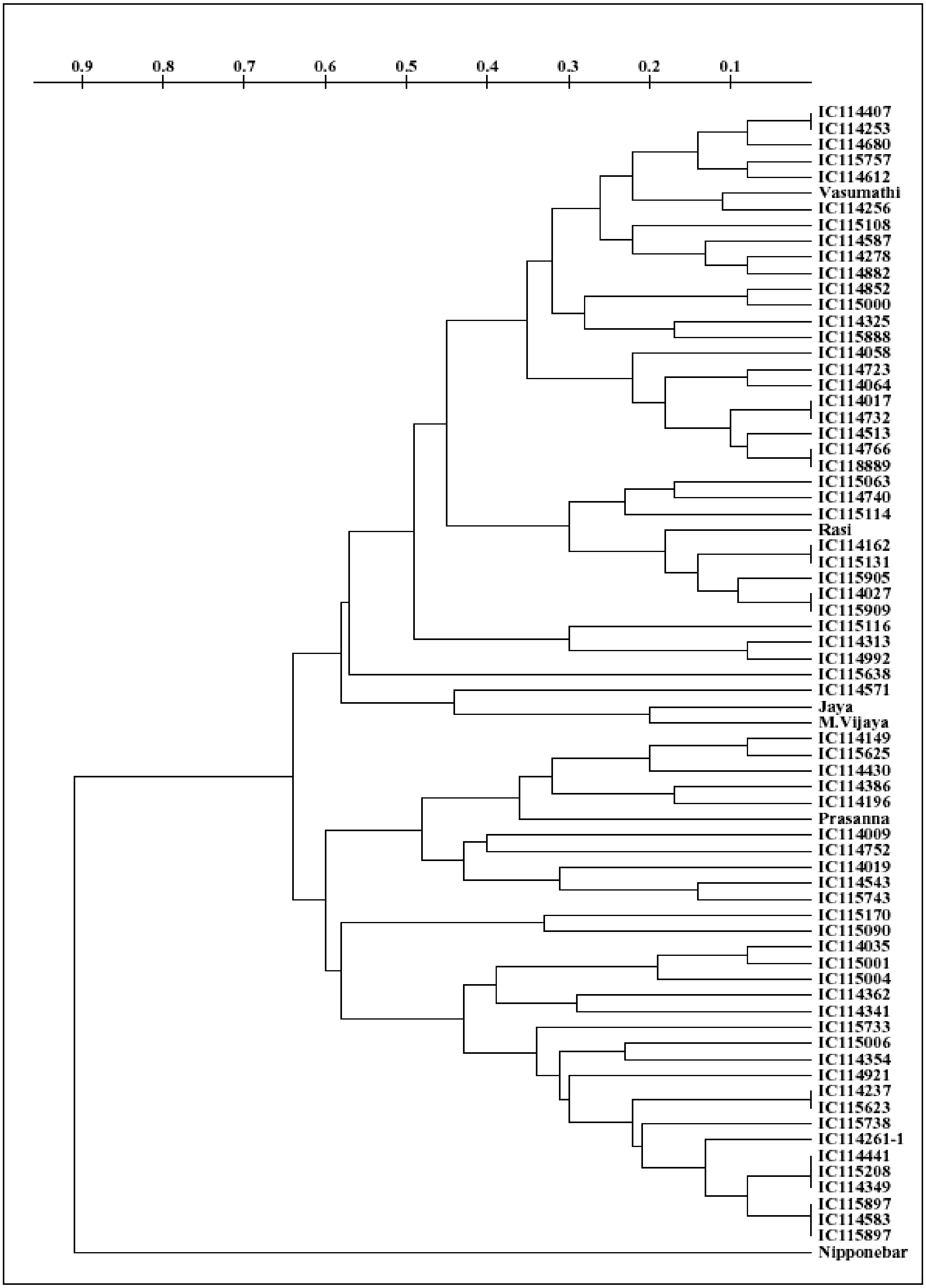


Fig 4.6: Dendrogram showing grouping pattern of 72 genotypes using UPGMA method

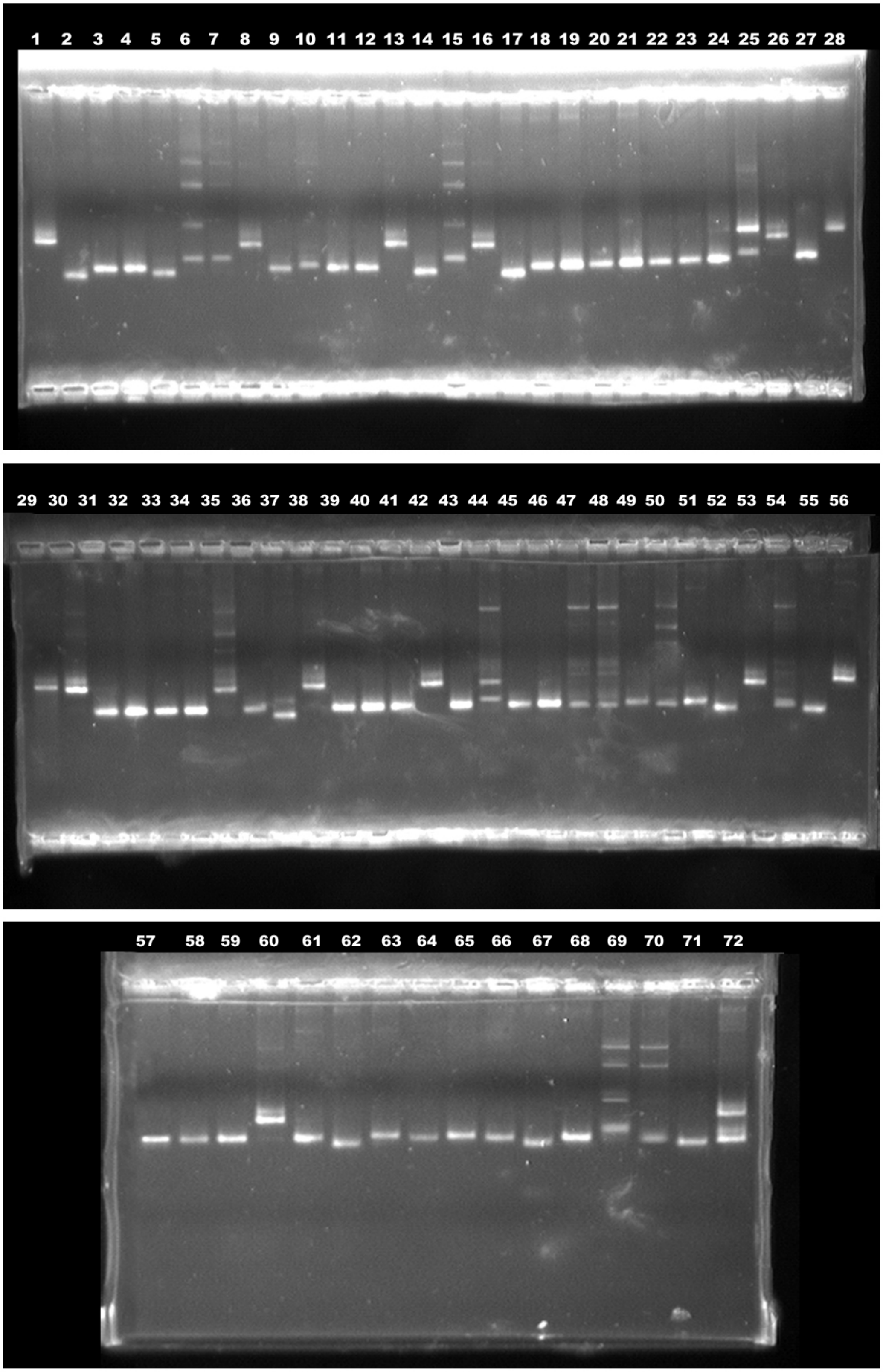


Plate 4.1: Gel photograph showing banding pattern with primer JGT 12

CHAPTER V

DISCUSSION

Rice is a highly polymorphic crop species with wide geographic dispersal and ecogenetic differentiation. The large germplasm of rice includes many land races and related wild species. The success of any breeding programme depends upon the selection of the parents for hybridization. Genetic divergence among the genotypes plays an important role in selection of the parents having wider variability for different characters. The broad spectrum of genetic diversity among the rice genotypes offer better scope for crop improvement through appropriate selection techniques. Hence in the present study one hundred and fifty rice genotypes including five checks were evaluated to assess the extent of genetic divergence using field evaluation through agro- morphological characterization and also molecular markers. The results obtained in the present study have been discussed here under experiment wise:

5.1 DIVERSITY STUDIES ON GERMPLASM ACCESSIONS OF RICE THROUGH FIELD EVALUATION

The results of this experiment were discussed here under the following heads:

1. Morphological characterization
2. Variability, heritability and genetic advance
3. Genetic divergence
4. Character association

5.1.1 Morphological characterization

Utilization of any genetic resource for crop improvement depends upon its desirable traits. Nature of traits is known only when the genetic resources are characterized. Therefore agro-morphological characterization was done as per SES, IRRI (1996), which revealed that a wide range variability existed for all the morphological characters studied. In view of the Protection of Plant Varieties and Farmers Rights Act (2001), DUS testing assumed greater importance. The objective of doing DUS testing is to establish the distinctness of a particular genotype from others in the same species, specifically based on essential or astonished characters, which are highly heritable having least environmental influence. Therefore, the identification of a particular genotype based on its morphological characters is need of the hour. Similar study was conducted by Suman (2003) and Subbarao *et al.*(2006).

5.1.2 Variability, heritability and genetic advance

The efficiency of selection in plant breeding programmes largely depends on the extent of genetic variability present in a given crop species for the character under consideration. The genotypic coefficient of variation measures the range of inherent variability available in the crop and also enables a breeder to exploit this variability either through selection or hybridization. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study.

Heritability is a good index of the transmission of characters from parents to their offspring. The heritability estimates will help the plant breeder in the selection of elite genotypes from diverse genetic populations. High heritability values indicate that the characters under study are less influenced by environment, and such traits could be improved by adopting simple selection techniques. Further, the information on genetic variability, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. Further the heritability estimates coupled with genetic advance will specify the mode of gene action in the expression of a trait, which helps in choosing an appropriate breeding methodology for crop improvement.

5.1.2.1 Metric characters

Analysis of variance Table 4.2 revealed highly significant differences among the genotypes for all the characters studied except leaf width and 100 grain weight indicating the presence of high variability among genotypes utilized in present investigation.

5.1.2.1.1 Days to 50% flowering:

Significant genetic variability for days to 50% flowering was noticed among the genotypes under investigation. The low genotypic and phenotypic coefficients of variation with minute numerical differences between them showed less influence of environment on this character. High heritability with moderate genetic advance revealed that the expression of this trait was mostly influenced by additive type of gene action. Thus selection for this trait is likely to accumulate more additive genes leading to further improvement. These results are in conformity with the findings of Rao and Shrivastav (1994), Nayak *et al*. (2004) and Sinha et *al*. (2004).

5.1.2.1.2 Plant height (cm)

Plant height showed significantly high genetic variability, while the estimates of genotypic and phenotypic coefficients of variation were moderate. But the differences between the estimates of PCV and GCV were low, indicating the stability of this trait over environments. The heritability estimate was high coupled with high genetic advance, which indicated the preponderance of additive gene action in controlling this trait. Hence, the direct selection of this character would be effective in improving seed yield. Similar results were also reported by Venkata suresh (2001), Nayak *et al.* (2003), Patil *et al.*(2003), Suman (2003), Sinha *et al.*(2004) and Sandya kishore (2005).

5.1.2.1.3 Leaf length (cm)

Leaf length showed significantly high genetic variability, while the estimates of genotypic and phenotypic coefficients of variation were moderate with a minor difference in their numerical values indicating the less environmental influence on the expression of this trait. High heritability along with high genetic advance estimates for this trait showed that the expression of this trait was mostly influenced by additive type of gene action.

5.1.2.1.4 Leaf width (cm);

Leaf width exhibited significant genetic variability with moderate genotypic and phenotypic coefficients of variation. The difference between the genotypic and phenotypic coefficients of variation was moderate indicating less influence of environment on this character. High heritability with moderate genetic advance estimates suggested that the expression of this trait was mostly influenced by additive type of gene action.

5.1.2.1.5 Total number of tillers per plant

Total number of tillers per plant showed significant differences among the genotypes. The genotypic and phenotypic coefficients of variation were high. The small difference between these two estimates might be due to less environmental influence on this character. It had high heritability coupled with high genetic advance indicating that expression of this trait was mostly influenced by additive type of gene action. Hence its response to selection would be effective in improving the seed yield. The present findings are in conformity with the results of Amrithadevarathinam (1983), Shanta kumar *et al.* (1998) and Sinha *et al.*(2004).

5.1.2.1.6 Productive tillers per plant

The genetic variability for this trait was found to be significant among the genotypes under study. The genotypic and phenotypic coefficients of variation were high with high heritability and genetic advance, which revealed that the expression of this trait was mostly influenced by additive type of gene action. Hence selection for this character would be effective in improving seed yield. Similar results were obtained by Amrithadevarthinam (1983), Rama Rao (1990) and Suman (2003).

5.1.2.1.7 Panicle length (cm)

The estimates of genotypic and phenotypic coefficients of variation were low with small difference between these two estimates indicating less influence of environment on this character. High heritability coupled with moderate genetic advance as per cent of mean were obtained for this character which indicated that the expression of this trait was influenced by additive type of gene action. Hence, the selection for panicle length would be effective in improving seed yield. Marimuthu *et al.* (1990) and Mehetre *et al.* (1996) also earlier reported similar findings.

5.1.2.1.8 Number of grains per panicle

The wide range of variability was observed for this character. This character showed high genotypic and phenotypic coefficients of variation coupled with a very high heritability and high genetic advance as per cent of mean, which revealed preponderance of additive type of gene action in expression of this trait. Therefore, the selection of this trait would be very effective in improving seed yield. These results are in agreement with the findings of Patil *et al.* (2003), Sandya kishore (2005), and Monalisa *et al.* (2006).

5.1.2.1.9 Spikelet fertility (%)

Significant variation in spikelet fertility was observed among the genotypes**.** The genotypic and phenotypic coefficients of variation observed were moderate and the minor difference between these two estimates indicates the less influence of environment on this character. It had high heritability with high genetic advance as per cent of mean which indicated that the expression of this trait was due to the presence of additive type of gene action. Hence its response to selection would be effective in improving yield. Similar results were reported earlier by Saravanan and Senthil (1997), Kumar et *al*. (1998) and Madhavilatha *et al*. (2005).

5.1.2.1.10 100-Grain weight (g)

A wide range of variability was observed for this character. The genotypic and phenotypic coefficients of variation observed were moderate, with a minute difference between these two estimates suggesting the less influence of environment on this character. The high heritability coupled with high genetic advance as per cent of mean indicated that the expression of this trait was due to the involvement of additive gene action in controlling this trait Vanniarajan *et al*. (1996), Mani *et al*.(1997) and Bharadwaj *et al*.(2001) also obtained similar results.

5.1.2.1.11 Single plant yield (g)

This trait exhibited a high genetic variability along with high genotypic and phenotypic coefficients of variation. The heritability estimate observed was high coupled with high genetic advance as per cent of mean which indicated the involvement of additive type of gene action in controlling of this trait. Further, yield is a complex character and is highly influenced by environment (PCV > GCV). Selection for this trait is likely to accumulate more additive genes leading to further improvement. Results are in unison with findings of Amrithadevarthinam (1983), Nayak *et al.*(2002), Patil *et al.*(2003), Madhavilatha *et al.*(2005) and Paramesha *et al.*(2005).

5.1.3 Genetic divergence

Crop improvement mainly depends upon the amount of genetic variability present among the different genotypes of a species . The success of any hybridization programme mainly depends on the selection of suitable parents which is a difficult task for plant breeders unless the information on the genetic divergence in the available germplasm of a given crop species is available. The crosses between the divergent parents generally display a greater heterosis than those between closely related strains.

Earlier, when no specific tools were available for the measurement of diversity, geographical diversity was considered as a measure of genetic diversity. However, this is an inferential criterion and may not be used for discriminating the populations, which occupy the ecologically marginal habitats.

Currently, the multivariate D^2 analysis using Mahalanobis's D^2 statistic is a potential technique for assessing the genetic diversity in a given population. D^2 statistic also helps in measuring the degree of diversification and in determining the relative proportion of each component character to the total divergence. This technique measures the forces of differentiation at two levels namely, intracluster and inter cluster levels and thus helps in the selection of genetically divergent parents for exploitation in hybridization programmes.

Mahalanobis's D^2 analysis has been successfully used in studies on genetic divergence by Singh *et al.* (1977), Ushakumari and Rangaswamy (1997), Ahmed and Borah *et al.* (1999), Hegde and Patil (2000), Rather *et al.* (2001), Surender Raiu (2002), Madhavilatha *et al.* (2005), Sandyakishore (2005), Suman *et al.* (2005) and Mundhe *et al.* (2006) in rice genotypes.

The data were collected on eleven quantitative characters along with yield from one hundred and fifty genotypes including five standard checks. Three techniques *viz.*, Tocher's method, Canonical analysis and Cluster analysis were used to measure genetic divergence quantitatively.

Clustering of entries was done based on D^2 values as it represents the index of genetic diversity among genotypes and clusters. Further the magnitude of D^2 values suggests that there was considerable diversity in the material used in the present investigation.

In the first technique, Tocher's method, among the different clusters, cluster I comprised of maximum number of genotypes fallowed by cluster III, cluster IV, cluster VIII, cluster IX, and cluster XVI (Table 4.5). Clusters II, V, VI, VII, X, XI, XII, XIII, XIV and cluster XV contained single genotype each. Each of the five check varies utilized in the present investigation had found place in different clusters, Vasumathi in cluster XI, Rasi in cluster XII, Prasanna in cluster XIV, Mandya Vijaya in cluster III and Jaya in cluster IV.

The intra cluster distance ranged from 0 to 21.60 Table 4.6. The existence of a single genotype in each of clusters II, V, VI, VII, X, XI, XII, XIII, XIV and XV might be the reason for the zero intra cluster distance in these clusters. The maximum intra -cluster distances observed in cluster XVI (21.60) and cluster VIII (20.18) revealed the existence of some genetic divergence among cluster constituents. It was reported that genotypes with in a cluster with high degree of divergence would produce more desirable breeding material for acheiving with maximum genetic advance with regard to yield per se, provided that there is an adequate complementation. (Mundhe *et al.*,2006). Therefore due emphasis would be given on the constituents of cluster XVI and cluster VIII for selection of parents for hybridization programme. These findings were in agreement with the earlier reports of Kandhola and Panwar (1999). Maximum inter cluster distance (69.19) was noticed between clusters IX and XVI followed by that between clusters XIV and XVI (55.90) (Table 4.6). The greater the distance between the two clusters, the wider the genetic diversity among the genotypes of those clusters. The crosses involving genotypes from these clusters would give wider and desirable recombinants. Chand *et al.*, (2005) and Chaturvedi and Maurya (2005) also recommended that the parents should be selected from two clusters having wider inter cluster distance to realize much variability and high heterotic effect.

A wide range of variation was observed in cluster means Table 4.7 for all the characters studied. Cluster II was characterized by the highest and lowest mean values for spikelet fertility and leaf length, respectively. The cluster VI had the highest value for leaf width. Lowest and highest values for total tillers and productive tillers were recorded in cluster VII and cluster XI, respectively. While the least number of grains per panicle and spikelet fertility were noticed in cluster IX. The lowest and highest values of plant height were observed in cluster XII and cluster XIII respectively. Cluster XIII was further characterized by the highest value of days to 50% flowering , lowest values of panicle length and 100-seed weight and single plant yield . The cluster XVI is having highest mean values for a maximum of three characters (leaf length, panicle length, and grains per panicle) among all other clusters.

The canonical root analysis in the present study accounted for the total variance of 91.94% (Table 4.8). For getting clear association of two dimensional representation of variation, the first three Canonical roots should be more than 95 per cent (Patel *et al*., 1989). On the contrary the first three canonical vectors as a whole contributed only 83.96% towards genetic diversity because of which discernible overlapping was observed in group constellations of canonical vectors (Fig.4.3).

The third method, Cluster analysis grouped the 150 genotypes very precisely into thirteen clusters (Table 4.11 and Fig 4.4). The distinct genotypes (IC-114009, IC-114027) were grouped in cluster I and IC-114784, IC- 115074 and IC-114344 were included in cluster X, while the check varieties Mandya Vijaya and Prasanna were found in cluster X and Jaya, Vasumathi and Rasi were placed in cluster XIII.

Statistical distances represent the index of genetic diversity among clusters. The maximum genetic divergence was observed between clusters I and IX indicating wider genetic diversity between genotypes in these groups (Table 4.12). Clusters showing maximum inter-cluster distances were also considerably diverse for the various characters studied. Selection of parents from such clusters for hybridization programme would help in achieving novel recombinants.

Among eleven characters including yield considered for the estimation of genetic divergence, six characters were considered to be potential contributors for genetic divergence. The maximum genetic divergence was contributed by number of grains per panicle (28.70%), followed by spikelet fertility (24.84%), plant height (22.60%), days to 50% flowering (14.33%), single plant yield (5.35%) and 100-seed weight (3.19%). Leaf width and number of productive tillers per plant did not contributed to the genetic divergence (Table 4.14). The results are in conformity with those of Madhavilatha *et al*. (2005) and Mundhe *et al*. (2006)

5.1.4 Character association

Character association studies are of primary importance to know the suitability of various characters for selection, because selection of a particular trait may induce desirable or undesirable changes in the associated characters. Generally, direct selection for yield was not aimed at, as it is a complex quantitative character which is highly influenced by environment. As a consequence, high genotypic and environmental interactions are likely to restrict the improvement. Some of the yield components are less influenced by environment and also simple in inheritance.

If the relationship of characters is due to manifold effect of gene or genes, it is difficult to separate these characters by selecting a particular character so related. If the correlation is due to linkage it is possible to reverse the correlation, provided the linkage is not very close. It is therefore important to establish the genetic basis of correlations before launching any breeding programme. Further, the component characters of yield show different associations among themselves and also with yield. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, knowledge on the magnitude of association between the yield and yield components and also among the yield components themselves is essential for planning a sound breeding programme.

In the present investigation a number of yield components were investigated and their relationships with yield as well as among themselves were examined using correlation analysis (Table 4.15). High genotypic correlations were obtained in general when compared to their phenotypic counterparts which indicated a strong inherent association between the characters.

5.1.4.1 Metric characters

5.1.4.1.1 Days to 50% flowering

This trait recorded a positive and significant correlation with total number of grains per panicle and spikelet fertility. Kavitha and Sree Ramareddi (2001), Nayak *et al.* (2001) and Madhavilatha (2002) also earlier made similar reports.

5.1.4.1.2 Plant height (cm)

A positive and significant association of plant height with leaf width and leaf length was observed, which is in agreement with the findings of Chauhan *et al.* (1993), Gupta *et al.* (1998) and Meenakshi *et al.* (1999). Negative and significant association with total number of tillers per plant, productive tillers per plant, days to 50% flowering and spikelet fertility was observed, which confirms the findings of Nayak *et al.* (2001) and Paramesha *et al.* (2005).

Plant height had positive and non-significant association with number grain grains per panicle, which was in agreement with the earlier works of Yolanda and Vijendra das (1995) and Madhavilatha (2002)

5.1.4.1.3 Leaf length (cm)

This trait had a positive and significant correlation with days to 50% flowering. Total tillers per plant, leaf width and panicle length showed negative and significant association with yield.

5.1.4.1.4 Leaf width (cm)

This trait had a positive and significant correlation with days to 50% flowering, panicle length and spikelet fertility. Single plant yield had positive and non significant association with leaf width.

5.1.4.1.5 Total number of tillers per plant

This trait had a positive and significant correlation with productive tiller per plant, panicle length and single plant yield. From the results it was evident that an increase in number of tillers per plant would further help in increasing the grain yield due to production of more panicles and grains. The results are in accordance with the findings of Amrithadevarathinam (1983), Babu and Soundarapandian (1990) and Shantha Kumar *et al*. (1998), Allahgholipur *et al*. (2003) and Suman (2003).

5.1.4.1.6 Productive tillers per plant

Productive tillers per plant registered positive and significant association with days to 50% flowering, panicle length, single plant yield. which confirms the findings of Bala (2001), Janardhanam *et al*.(2001), Sakthivel (2001) and Kuldeep *et al*. (2004).

Productive tillers per plant exhibited negative and significant association with 100-seed weight, the results are in conformity with the findings of Mahto *et al*. (2003).

5.1.4.1.7 Panicle length (cm)

Panicle length had a positive and significant association with number of grains per panicle, single plant yield and 100-grain weight. These results are in unison with the findings of Kuldeep *et al.* (2004). From the results it was evident that increase in panicle length would always contribute to more number of grains per panicle and there by increase in grain yield.

Panicle length had a positive and non-significant association with spikelet fertility which is in agreement with the findings of Madhavilatha (2002) and Sandya kishore (2005)

5.1.4.1.8 Number of grains per panicle

Number of grains per panicle registered positive and significant association with single plant yield and it had a negative correlation with spikelet fertility which confirms the findings of of Allahgholipour *et al.* (2003) and Monalisa *et al* .(2006)

This trait had shown positive and non-significant association with 100-grain weight which is in agreement with the findings of Meenakshi *et al.* (1999).

5.4.1.9 Spikelet fertility (%)

Spikelet fertility had positive and significant association with single plant yield and positive association with 100-grain weight. Chauhan *et al.* (1993), Meenakshi *et al.* (1999) and Borkakati *et al.* (2005) also obtained similar results.

5.1.4.1.10 100-grain weight (g)

100-grain weight exhibited positive and significant association with single plant yield, which confirms the findings of Prasad *et al.* (1988) and Babu and Soundarapandian (1990)

5.1.4.1.11 Single plant yield (g)

Single plant yield exhibited positive and significant correlation with total tillers per plant, productive tillers per plant, panicle length, number of grains per panicle, spikelet fertility and 100-seed weight. These results are in agreement with the findings of Allahgholipour *et al.* (2003) Khedikar *et al.*

(2004), Borkakati *et al.* (2005), Monalisa *et al.*(2006) and Tayeng and Singh (2006).

Single plant yield exhibited positive and non - significant correlation with leaf width and days to 50% flowering. These results are in agreement with the findings of Kumar *et al.* (1998) and Vange *et al.*(1999).

5.1.4.2 Path coefficient analysis

The observed correlation between yield and a particular yield component is the net result of direct effect of that component and indirect effects through various other yield attributes. The direct effect may be different from the observed correlations. The total correlation between grain yield and component characters may sometimes be misleading since it may be an over estimate or under estimate because of its indirect association with other characters. Hence, direct selection by considering correlated response may not be fruitful. Further, if many characters are affecting a given trait, it is necessary to separate the total correlation estimate into direct and indirect effects of cause as devised by Wright (1921) and utilized by Dewey and Lu (1959) in selection programmes.

If the correlation coefficient between caused factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and direct selection of this trait will be effective. The correlation coefficient is positive, and the direct effects are negative or negligible, the indirect effects seem to be the cause of correlation. In such situations the other factors influencing the trait have to be considered simultaneously. Correlation coefficient may be negative but the direct effect may be positive and high. Under these conditions a restricted simultaneous selection model is to be followed i.e., restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

Based on the above considerations, the results obtained from the above investigation from the 145 rice germplasm lines along with five check varieties on eleven metric characters with yield were subjected to path coefficient analysis and the estimates of direct and indirect contribution with yield are discussed hereunder for formulating sound selection programmes along with character associations (Table 4.16).

5.1.4.2.1 Metric characters

5.1.4.2.1.1 Days to 50% flowering

Days to 50 per cent flowering exhibited negligible positive direct effect on single plant yield. It had shown positive indirect effects on single plant yield via spikelet fertility and leaf length. Both direct effects and correlation coefficients are positive. Hence direct selection of this character would be effective in improving single plant yield because it nullifies the negative indirect effects. These results are in accordance with the findings of Babu *et al.* (2002), Patil and Sarawgi (2005) and Sandyakishore (2005).

5.1.4.2.1.2 Plant height (cm)

Plant height showed a negligible, positive direct effect on single plant yield and correlation coefficient was positive. It had shown negligible positive indirect effects on single plant yield via leaf length, leaf width and number of grains per panicle, while rest of the characters showed negligible negative indirect effects. These results are in agreement with the findings of Deb-choudhary and Das *et al.* (1998), Bala (2001), Janardhanam *et al.* (2001), Madhavilatha (2002), Sandyakishore (2005) and Samonte *et al.* (2006) but in contrary with the findings of Suryanarayana (2000), Tarasatyavathi *et al.* (2001), Babu *et al*. (2002), Paramesha *et al*. (2005) and Suman *et al.* (2006)

5.1.4.2.1.3 Leaf length (cm)

Leaf length exhibited low negative direct effect on single plant yield correlation coefficient was also negative and significant. It had shown negligible negative indirect effects on single plant yield via days to 50% flowering and plant height.

5.1.4.2.1.4 Leaf width

Leaf width exhibited negligible negative direct effect on single plant yield but correlation coefficient was positive. It had shown negligible positive indirect effects on single plant yield via leaf length, total number of tillers per plant and productive tillers per plant. While rest of the characters showed negligible negative indirect effects.

5.1.4.2.1.5 Total number of tillers per plant

The direct contribution of this trait on single plant yield was negligible and negative. Its indirect effects were positive and manifested through plant height and 100-seed weight. While rest of the characters expressed negligible indirect effects. The correlation coefficient estimate was also positive and significant. This indicated that negative direct effects manifested through various other traits were nullified by the positive indirect effects. These results are in agreement with the findings of Srikrishnadevarayalu (1993), Allahgholipour *et al.* (2003) and Suman (2003).

5.1.4.2.1.6 Productive tillers per plant

This trait had moderate positive direct effect on single plant yield and and positive indirect effects via total tillers per plant and panicle length. The correlation coefficient estimate was positive and significant. These results are in accordance with the findings of Madhavilatha (2005), Sandyakishore (2005) and Monalisa *et al.*(2006).

5.1.4.2.1.7 Panicle length (cm)

This character exhibited a negligible, negative direct effect on single plant yield, while correlation coefficient for this trait was positive and significant. It had a positive indirect effect via leaf length and productive tillers per plant on single plant yield. while rest of the characters exhibited negative indirect effects. Similar results were also reported by Nayak *et al.* (2001), Madhavilatha (2002), Sandyakishore (2005).

5.1.4.2.1.8 Number of grains per panicle

Number of grains per panicle showed low positive direct effect and its indirect positive effects were manifested through days to 50% flowering and panicle length. This trait had significant positive correlation with single plant yield. Hence, simple selection would be effective for improving single plant yield if it is based on this trait. The results obtained are in agreement with the findings of Madhavilatha (2002) Sandyakishore (2005) and Monalisa *et al.*(2006).

5.1.4.2.1.9 Spikelet fertility (%)

Spikelet fertility had a low positive direct effect and its indirect positive effects were manifested through days to 50% flowering, panicle length and 100-grain weight.This trait had significant positive correlation with single plant yield. The results obtained are in agreement with the findings of Kumar *et al.* (1998) Borkakati *et al.*(2005) and Paramesha *et al.*(2005).

5.1.4.2.1.10 100-Grain weight (g)

This trait showed high positive direct effect on single plant yield. It has positive indirect effects were manifested through spikelet fertility, panicle length and grains per panicle. Rest of the characters exhibited negative indirect effect on yield. It had positive and significant correlation with single plant yield. Hence, selection based on this character for the improvement of single plant yield was effective. These results are in accordance with the findings of Sawant *et al.* (1995), Tarasatyavathi *et al.* (2001) and Khedikar *et al.* (2004).

5.2 GENOTYPING OF SELECTED GERMPLASM LINES OF RICE USING SSR MARKERS

The extent of genetic diversity in the germplasm can be estimated by adopting various methods like morphological, biochemical and/or molecular analyses. Since morphological evaluation is influenced by environment and time consuming, isozymes, which are basically biochemical markers are being used widely for characterization of cultivated varieties and their wild relatives in rice (Endo and Morishima, 1983, Glaszmann, 1987 and De Kochko, 1987a, b).

Though morphological and isozyme markers have been employed in assessing the genetic diversity of a species, the accuracy of the assessment is questionable. The availability of low number of morphological and biochemical markers, their poor or unknown genetic control, environmental influence on the phenotypic expression, stage specific expression and procedural difficulties are known impediments in using these as potential markers in genetic diversity analysis (Ainsworth and Sharp, 1989 and Aldrich, 1992).

The above-mentioned problems associated with morphological and isozyme markers have necessitated the development of alternative tools. The recent developments in molecular biology has resulted in development of simple, easily assayable PCR based DNA markers. Multi-locus markers like RAPD, ISSR, AFLP etc., are the most popularly used markers for genetic diversity analysis (Phillips and Vasil, 2001). Among the different markers, SSR markers are useful for a variety of applications in plant genetics and breeding because of their reproducibility, multiallelic nature, co-dominant inheritance, relative abundance and good genome coverage (Powell et al., 1996). Microsatellites or Simple sequence repeats (SSRs) are single locus markers that are mapped to chromosomes unlike the ISSRs, which are unmapped multi-locus markers. While ISSRs are amplified using anchored SSR sequences as primers, SSRs are amplified using specific conserved sequences flanking the repeat elements as primers . SSR primers have been used for assessing the genetic diversity (Wang and Tanksley, 1989; Fukuoka *et asl*., 1992; Yu and Nguyen, 1994; Virk *et al*., 1994; Subudhi *et al*., 1998; Agarwal *et al*., 1999)

In the present investigation, genetic diversity among the seventy two rice genotypes was assessed using 23 SSR markers. Seven SSR markers have generated 20 alleles. A maximum number of 4 alleles were amplified by JGT 12 (Table 4.17). The primer JGT 01, JGT 04, JGT 06 and JGT 07 amplified three alleles while JGT 05 and RM 151 amplified two alleles each. The polymorphic information content (PIC) for these seven SSR markers ranged from 1.021 (JGT 06) to 1.839 (RM 151). The PIC values are dependent on the genetic diversity of the accessions chosen and the present investigation had a high proportion of closely related cultivars that might be the reason for a lower PIC when compared to earlier published reports. Evaluation of germplasm with SSRs derived from genes or ESTs might enhance the role of genetic markers by assaying the variation in transcribed and known-function genes, although there is a higher probability of bias owing to selection.

The use of SSR markers in genetic diversity studies helped in grouping the genotypes according to their genetic relatedness. When more clusters are obtained with fewer genotypes in each cluster, the significance in clustering is higher because of the presence of smaller genetic differences between the genotypes in a cluster. The multi-allelic nature of SSR markers has the advantage of discriminating the individual genotype more precisely. For example, the SSR loci JGT 12 exhibited 4 alleles across the 72 genotypes studied grouping them into 4 allelic groups.

CHAPTER VI

SUMMARY

The present investigation entitled "Studies on genetic diversity in rice germplasm (*Oryza sativa* L.)" was carried out with one hundred and forty five diverse germplasm lines and five checks, namely Jaya, Mandya vijaya, Prasanna, Rasi and Vasumathi obtained from DRR, Hyderabad with a view to study the agro-morphological characterization, nature and magnitude of variability, degree of association between yield and its components and direct and indirect effects of the different quantitative characters on seed yield and categorization of the genotypes into different clusters to identify the promising genotypes possessing desirable traits besides their yielding ability.

The experimental material was sown in a randomized block design with three replications during *Rabi*, 2007 at DRR farm, ICRISAT Campus, Patancheru, Hyderabad. Visual observations were made on single plant basis as per standard evaluation system on eleven qualitative characters *viz.*, early plant vigour, basal leaf sheath colour, leaf colour, leaf pubescence, ligule shape, ligule colour, panicle exsertion, panicle type, stigma colour, awning and threshability. A wide range of variability existed among the genotypes under investigation for all the above-mentioned characters among the genotypes studied.

Data were recorded on five randomly selected plants for eleven metric characters *viz.*, days to 50% flowering, plant height, leaf length, leaf width, total number of tillers per plant, productive tillers per plant, panicle length, number of grains per panicle, Spikelet fertility, 100-grain weight and single plant yield.

Analysis of variance indicated highly significant differences among genotypes for all the traits under the study except leaf width and 100 grain weight, suggesting the presence of considerable amount of variability among the genotypes studied. A perusal of genetic parameters *viz.*, PCV and GCV for all the characters studied indicated less influence of the environment on the characters. The PCV and GCV values were highest for productive tillers per plant and lowest for days to 50% flowering. The characters *viz.*, plant height, leaf length, total number of tillers per plant, productive tillers per plant, number of grains per panicle, spikelet fertility, 100-grain weight and single plant yield exhibited high heritability estimates coupled with high genetic advance as per cent of mean which suggested that these characters were amenable for further improvement by following simple selection methods.

Genetic diversity studies using D^2 statistic revealed the presence of considerable diversity among the genotypes through the formation of large number of clusters with wide range of inter-cluster distances. Three techniques *i.e.*Tocher's method, canonical analysis and cluster analysis were used to measure genetic divergence quantitatively. A wide range of variation was observed in cluster means for all the traits under study. Cluster analysis through Euclidean D^2 distances revealed that the one hundred and fifty genotypes were categorized into thirteen clusters.

The mode of distribution of genotypes into various clusters was at random indicating that geographical distribution and genetic diversity were not related to each other. The characters *viz.,* grains per panicle, spikelet fertility, plant height, days to 50% flowering, single plant yield, and 100-grain weight contributed 99.01%

of the total divergence and these traits were found to be important factors for genetic differentiation in genotypes.

Based on the divergence estimates and clustering pattern in the present genetic material, it was observed that the genotypes included in cluster I and IX exhibited maximum genetic divergence. Therefore the genotypes from these clusters can be used as parents in hybridization programme for yielding good recombinants for the characters *viz*., number of grains per panicle, spikelet fertility, plant height, single plant yield and 100-grain weight. Presence of high amount of genetic diversity in a population is essential to take up hybridization programme for isolating good recombinants. In addition to the above information, it is also essential to have the knowledge on the general combining ability of the selected parents for obtaining success in hybridization programmes.

Character association studies revealed that the genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients indicating that strong inherent associations were some what masked at the phenotypic level due to environmental effect. Single plant yield exhibited significant positive association with total tillers per plant, productive tillers per plant, panicle length, number of grains per panicle, spikelet fertility and 100-grain weight. Hence, selection for improvement of these traits would simultaneously improve the yield.

Critical analysis of results obtained from character association and path analysis revealed that days to 50% flowering, plant height, productive tillers per plant, number of grains per panicle, spikelet fertility and 100-grain weight exhibited positive direct effect on grain yield. Among these characters, grains per panicle, productive tillers per plant, spikelet fertility and 100-grain weight possessed both positive associations and positive direct effects. Hence preference should be given to these traits to isolate superior lines with genetic potentiality for high yield.

A preliminary effort towards application of SSR markers to characterize germplasm and to group them according to their genetic relationship was made in the present investigation. A small set of 23 SSR markers was used in the present study, of which seven exhibited polymorphism by generating 20 alleles among the seventy two rice lines studied. The number of alleles ranged from 2 - 4 with a mean of 2.85, while the PIC for these seven SSR markers ranged from 1.021 to1.839 with an average of 1.487. The PIC values are dependent on the genetic diversity of the accessions chosen, which could be due to two reasons: (i) the lines considered may be genetically very closely related to each other or (ii) the SSR markers selected may not be highly polymorphic. In the present study, all the SSR markers selected were observed to have high polymorphic information content when checked in the Gramene SSR database (http://www.gramene.org). Thus in all probability, the low polymorphism observed in the present study could be because the accessions selected were close to each other genetically.

LITERATURE CITED

Agarwal, R.K., D.S. Brar, S. Nandi, N. Huang and G.S. Khush. 1999. Phylogenetic relationship among *Oryza* species revealed by AFLP markers. Theor. Appl. Genet., 98 : 1320-1328.

Ahmed T and Borah P 1999 Genetic diversity in glutinous rice germplasm of Assam. Oryza 36(1) : 74-75.

Ahmed T and Das G R 1994 Evaluation of characterization of glutinous rice germplasm of Assam. Oryza 31 : 77-83.

Ainsworth C C and Sharp P J 1989 The potential role of DNA probes in plant variety identification. Plant Var. Seeds, 2 : 27-34.

Akagi A Y Yokozeki A Imagaki A Nakamura and Fujimura J 1996 A codominant DNA marker closely linked to the rice nuclear restorer gene Rf-1, identified with inter-SSR fingerprinting. Genome, 39(6) : 1205-1209.

Akagi H Y Yokozeki A Inagaki and T Fujimura 1997 Highly polymorphic microsatellites of rice consist of AT repeats and a classification of closely related cultivars with these microsatellite lici. Theor. Appl. Genet., 94 : 61-67.

Akkaya M S Bhagwat A A and Cregan P B 1992 Length polymorphisms of simple sequence repeat DNA in soybean. Genetics, 132 : 1131-1139.

Aldrich P R J Doebley K F Schertz and A Stec 1992 Patterns of allozyme variation in cultivated and wild *Sorghum bicolour*. Theor. App. Genet., 85 : 451-460.

Allahgholipour M and Salehi M S M 2003 Factor and path analysis in different rice genotypes. Seed and plant 19(1) : 76-86.

Allard R W 1960 Principles of Plant Breeding. John Wiley and Sons Inc., New York, USA pp. 485.

Amirthadevarathinam A 1983 Genetic variability, correlation and path analysis of yield components in upland rice. Madras Agricultural Journal 70 : 781-785.

Amirthadevarathinam A 1990 Genetic variability interrelationship and path analysis of yield characters in early maturing *indica* and *japonica* rice genotypes. Madras Agricultural Journal 77(9-12) : 363-368.

Ananda Kumar C R 1992 Variability and character association studies in upland rice. Oryza 29: 11-13.

Arumungathan, K and Earle E D 1991 Nuclear DNA content of some important plant species. Plant Mol. Biol. Rep. 9:208-218.

Awasthi L P and Pandey V K 2000 Genetic variation in morphological traits of aromatic rice. Crop Research, Hisar 19(2) : 361-363.

Awasthi R P and Borhthakur D N 1986 Agronomic evaluation of rice varieties in upland terraces of Meghalaya. Indian Journal of Agricultural Sciences 56(10): 700-703.

Babu J R K and Soundarapandian G 1990 Correlation and path analysis in F_3 generation of rice crosses. Madras Agricultural Journal 77 : 542-544.

Babu S, Netaji S V S R K, Phillip B and Rangaswamy 2002 Intercorrelation and path coefficient analysis in rice. Research On Crops. 3(1) : 67-71.

Bala A 2001 Genetic variability, association of characters and path coefficient analysis of saline and alkaline rice genotypes under rainfed condition. Madras Agricultural Journal 88(4-6) : 356-357.

Balan A, Muthaiah and Ramachandra Boopathi S N M 1999 Genetic variability, correlation and path coefficient analysis in upland early rice genotypes. Madras Agricultural Journal 86(1-3) : 7-9.

Barauah R K S M, Das G R and Hazarika M H 1994 Diversity of ahu rice of Assam and its characterization. Oryza 31: 163-168.

Beyermann B P, Nurenberg A, Wiehe M, Meixner J T, Epplen and Borner T 1992 Fingerprinting plant genome with oligonucleotide probes specific for repetitive DNA sequences. Theor. Appl. Genet., 83 : 691-694.

Bhag Singh and Kochhar S 1994 Guide lines for characterization and evaluation of plant genetic resources In : R S Rana *et al* (ed) pp.51-59. Plant Genetic Resources : Exploration, Evaluation and Maintenance. NBPGR, New Delhi.

Bharadwaj C, Satyavathi C T and Subramanyam D 2001 Evaluation of different classificatory analysis methods in some rice (*Oryza sativa* L.) collections. Indian Journal of Agricultural Sciences 71(2) : 123-125.

Bligh, H F J, Blackhall N A., Edwards K J and Mc Clung A M 1999 Using amplified fragment length polymorphism to identify cultivar of brown and white milled rice. Crop Sci., 39 : 1715-1721.

Borbora T K and Hazarika G N 1998 Study of genetic variability, heritability and genetic advance for panicle characters in rice. Oryza 35(1): 19-21.

Borbora T K, Hazarika G N and Medhi 2005.Correlation and Path analysis for plant and panicle charactes in rice.Crop –Research Hisar 30(2):215-220

Borkakati R P, Chowdhury R K, Kurmi K 2005 Studues on genetic variability and correlation in some rice hybrids. National Journal of plant improvement. 7(2):119-121

Bose L K and Pradhan S K (2005) Genetic divergence in deepwater rice genotypes. Journal-of-Central-European-Agriculture. 2005; 6(4): 635-640

*Burton G W 1952 Quantitative inheritance in grasses. Proceedings on 6th International Grassland Congress Journal 1: 277-283.

*Burton G W and Devane E H 1953 Estimating heritability in tall fescue (*Festuca arundinaceae)* from replicated clonal material. Agronomy Journal 45: 478-481.

Candit, R. and S.P. Hubbel. 1991. Abundance and DNA sequence of two base repeat regions in tropical genomes. Genome, 34 : 66-71.

Chand S P, Roy S K and Senapati B K (2005) Genetic divergence in Aman rice under semi-deep rainfed condition. Crop-Research-Hisar. 2005; 30(1): 46-49

Chandra K and Das A K 2000. Correlation and inter correlation of physiological parameters in rice (*Oryza sativa*) under rainfed trans planted condition. Crop Research Hisar 19(2) : 251-254

Chaturvedi,H P and Maurya D M (2005) Genetic divergence analysis in rice (Oryza sativa L). Advances-in-Plant-Sciences. 2005; 18(1): 349-353

Chaubey P K and Richharia A K 1993 Genetic variability, correlations and path coefficients. Indian Journal of Genetics 53(4): 356-360.

Chaubey P K and Singh R P 1994 Genetic variability, correlation and path analysis of yield components in rice. Madras Agricultural Journal 81(9): 468-470.

Chaudhary M and Motiramani N K 2003 Variability and association among yield attributes and grain quality in traditional aromatic rice accessions. Crop Improvement 30(1) : 84-90.

Chauhan J S Chauhan V S and Variar M 1993 Genetic variation and character association in upland rice. Oryza 30: 116-119.

Chen X S Temnykh Y Xu YG Cho and S R Mc Couch 1997 Development of a microsatellite frame work map providing genome wide coverage in rice (*Oryza sativa* L.). Theor. Appl. Genet., 95 : 553-567.

Chikkalingaiah Shridhara S, Lingaraju S and Radhakrishna R M 1999 Genetic variability of plant and quality traits in promising genotypes of scented rice (*Oryza sativa* L.). Mysore Journal of Agricultural Sciences 33 (4) : 338-431.

Chookar S K, Marekar R V and Siddiqui M A 1994 Genetic variability for grain yield and yield contributing characters in rice. Journal of Maharashtra Agricultural Universities 19(2) : 236-238.

CMIE 2006 Centre for Monitoring Indian Economy Pvt. Ltd. Apple Heritage, Mumbai Ltd.

Cregan P B 1992 Simple sequence repeat DNA length polymorphisms. Probe 2 : 18-22.

Cunha Filho L A Da and Nascimento L S Do 1995 Inheritance of anthocyanin colouration of the leaf sheath in rice (*Oryza sativa* L.). Revista Universidade Rural Serie Ciencias da Vida 17(1) : 25-30

*Darwin C 1859 The origin of species. Wolfe and Company, London

Das G R, Ahmed T, Bhattacharya H C and Borthakur B C 1981 Evaluation of rice germplasm : 1. Characterization and evaluation of *ahu* rice for important quantitative characters in relation to yield. Journal of Research Assam Agricultural University 2 : 156-164.

De Kochko, A. 1987a. Isozymic variability of traditional rice (*Oryza sativa* L.) in Africa. Theor. Appl. Genet., 73 : 675-682.

De Kochko, A. 1987b. A classification of traditional rice varieties (*Oryza sativa* L.) from Africa using isozymic variability. Trends Plant., 1 : 105-110.

Debchoudhury P K and Das P K 1998 Genetic variability, correlation and path coefficient analysis in deep water rice. Annals of Agricultural Research 19(2): 120-124.

*Dewey J R and Lu K H 1959 Correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal 51: 515-518.

Dharmendra Kumar, Shrivstava M N Sahu R K and Shau V N 1997 Morphological variability in wild rices of Raipur. Oryza 34(4) : 288-291.

Diaz S H, Castro R and Morejon R 2000 Morpho-agronomic characterization of varieties of rice (*Oryza sativa* L.). Cultivars Tropicales 21(3) : 81-86.

Endo T and Morishima H 1983 Rice In: S.D. Tanksley and T.J. Ortan (eds) isozymes in plant genetics and breeding. Vol. B. Elsiever, Amsterdam, pp.129-146.

Enoki, H., H. Sato and K. Kolhuma. 2002. SSR analysis of genetic diversity among maize inbred lines adapted for cold regions of Japan. Theo. Appli. Genet., 104 : 1270-1277.

*Falconer D S 1964 Introduction to quantitative genetics. Longmann, London and New York pp.294-300.

*Falconer D S 1981 Introduction to quantitative genetics. Oliver and Boyd, London, pp.340.

*Fisher R A and Yates F 1967 Statistical tables for biological, agricultural and medical research. Olive Boyd, Edinburgh.

*Frakes R V, Davis R L and Patterson F L 1961 The breeding behaviour of yield and related variables in Alfalfa 11 association between characters. Crop Science 1: 207-209.

Fukuoka, S., K. Hosaka and O. Kamijima. 1992. Use of random amplified polymorphic DNAs (RAPDs) for identification of rice accessions. Jpn. J. Genet., 67 : 243-252.

Ganesan K and Subramanian 1990 Genetic studies of the F_2 and F_3 of tall semi-dwarf rice varieties. International Rice Research Newsletter 15 : 4-7.

Ganesan K, Wilfred Manuel W, Vivekanandan P and Arumugam Pillai 1997 Character association and path analysis in rice. Madras Agricultural Journal 84(10): 614-615.

Garland S H L, Lewin M, Abedinia R, Henry and. Blakeney A 1999 The use of microsatellite polymorphisms for the identification of Australian breeding lines of rice (*Oryza sativa* L.). Euphytica, 108(1): 53-63.

Geetha S, Kirubakaran Soundaraj A P M, Giridharan S and Selvi B 1994 Association of yield component characters of medium duration rice genotypes. Annals of Agricultural Research 15(4): 410-412.

Genctan T, Aygun I O and Base I 1994 Determination of relations of same characters of rice with grain yield by means of path analysis . Journal of Tekridag Agricultural faculty 3 (1/2):158-165.

Glaszmann J C 1985 A varietal classification of Asian cultivated rice (*Oryza sativa* L.) based on isozyme polymorphism. In: Rice Genetics, International Rice Research Institute, Manila, Philippines, pp.83-90.

Glaszmann, J C 1987. Isozymes and classification of Asian rice varieties. Theor. Appl. Genet., 74 : 21-30.

Goldstein D B and Clark A G 1995 Microsatellite variation in North American populations of *Drosophila melanogaster*. Nucleic Acide Res., 23 : 3882-3886.

Gomathinayagam P, Nagarajan M and Guruswamy Raja V D 1990 D^2 statistic on upland rice varieties. Madras Agricultural Journal 77 (9-12): 547-548.

Gopinath M, Sree Rama Reddi N and Subramanyam P 1984 Studies on character association in rice (*Oryza sativa* L.). The Andhra Agricultural Journal 31(2): 102-105.

Gupta J C, Kotoch P C, Kaushik R P and Sharma S L 1998 Cause and effect relationship of yield and its components under cold stress condition in rice (*Oryza sativa* L.). Indian Journal of Agricultural Sciences 68(1): 13-15.

Hadgal B N, Manjunath A and Goud J V 1980 Linkage of genes for anthocyanin pigmentation in rice. Euphytica 30 : 747-754.

Hanamaratti N G, Patil S J, Nadaf S K, Naresh Dronavalli and Dronavalli N 1998 Genetic divergence in upland rice (*Oryza sativa* L.) genotypes under lowland and upland conditions. Karnataka Journal of Agricultural Sciences 11(1) : 220-222.

*Haque M E, Baset A, Zeenat Z and Miah N M 1991 Path coefficient analysis of seven characters in cold tolerant rice (*Oryza sativa* L.). Bangladesh Rice Journal 2: 1-7.

Hasib K M 2005 Genetic variability, interrelations and path analysis for panicle characters in scented rice. Crop Research Hissar. 30 (1): 37-39

Hegde S G and Patil C S 2000 Genetic divergence in rainfed rice. Karnataka Journal of Agricultural Sciences 13(3) : 549-553.

*Huxley J 1955 Morphism and evolution. Heredity 9: 1-62.

Innan, H., R. Terauchi and T. Miyashita. 1997. Microsatellite polymorphism in natural populations of the wild plant *Arabidopsis thaliana*. Genetics, 146 : 1441-1452.

IRRI 1996 Standard Evaluation System for Rice. International Rice Research Institute, Manila, Philippines.

Janardhanam V, Nadarajan N and Jebaraj S 2001 Correlation and path analysis in rice (*Oryza sativa* L.). Madras Agricultural Journal 88 : 719-720.

Johnson H W, Robinson H F and Comstock R E 1955 Estimates of genetic and environmental variability in soybean. Agronomy Journal 47(7) : 314-318.

*Kandhola S S and Panwar D V S 1999 Genetic divergence in rice. Annals of Biology Ludhiana 15(1): 35-39.

Kavitha S and Sree Rama Reddi N 2001 Correlation and path analysis of yield components in Rice. The Andhra Agricultural Journal 48(3-4): 311-314.

Kaw R N 1995 Analysis of divergence in some cold tolerant rices. Indian Journal of Genetics and Plant Breeding 55(1): 84-89.

Kaw R N, Aquino R C, Moon H P, Yae J D and Haq N 1999 Variability and interrelations in rice under cold stress environments. Oryza 36(1) : 1-4.

Khedikar V P, Bharose A A, Sharma D, Khedikar Y P and Killare A S 2004 Path coefficient analysis of yield components of scented rice. Journal of Soils and Crops 14(1): 198-201.

Klakhaeng K, Chitrakon S and Luangsodsai H 1991 Evaluation of rice germplasm in Bangkhen. International Rice Research Newslettr 16 : 3-55.

Kotaiah K C, Panduranga Rao C, Ramachandra Reddy J and Reddy M V 1987 Comparison of Mahalanobis's D^2 and Metroglyph analysis in long duration genotypes of rice (*Oryza sativa* L.). Indian Journal of Genetics 47(1): 55-60.

Kuldeep T, Bathshwar Kumar, Ramesh B and Ajay J 2004 Genetic variability and correlations for some seedling and nature plant traits in 70 genotypes of rice. Research on Crops 5(1) : 60-65.

Kumar G S, Mahadevappa M and Rudraradhya M 1998 Studies on genetic variability, correlation and path analysis in rice during winter across the locations. Karnataka Journal of Agricultural Sciences 11(1): 73-77

Lok Prakash R, Shivasankar G, Mahadevappa M, Gowda B T S and Kulkarni R S 1992 Study on genetic variability, heritability and genetic advance in rice. The Indian Journal of Genetics and Plant Breeding 52 : 416-721.

Mackill D J, Zhang Z, Redona E D and. Colowit P M 1996 Level of polymorphism and genetic mapping of AFLP markers in rice. Genome, 39 : 969-977.

Madhavilatha L 2002 Studies on genetic divergence and isozyme analysis in rice (*Oryza sativa* L.). M.Sc. (Ag.) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Madhavilatha L, Sekhar M R, Suneetha Y and Srinivas T 2005 Genetic variability, correlation and path analysis for yield and quality traits in rice. Research on crops. 6(3) : 527-534.

Madhavilatha L, Sekhar M R,Suneetha Y and Srinivas T 2005 Studies on genetic divergence and isozyme variability in Rice (*Oryza sativa* L.). Research on Crops 6(3): 520-526.

*Mahalanobis P C 1936 On the generalized distance in statistics. Proceedings of National Institute of Sciences, India 12: 49-55.

Mahto R N, Yadava M S and Mohan K S 2003 Genetic variation, character association and path analysis in rainfed upland rice. Indian Journal of Dryland Agricultural Research and Development 18(2) : 196-198.

Mall A K , Babu J D P and Babu G S 2005 Estimation of genetic variability in rice. Journal of Maharastra Agricultural universities 30(2) : 166-168.

Mani S C, Verma S K and Sharma R K 1997 Genetic variability and character association for panicle traits in Basmati rice. Agricultural Science Digest 17(3) : 155-157.

Manonmai S and Fazlullah Khan A K 2003 Analysis of genetic diversity for selection of parents in rice. Oryza 40(3&4) : 54-56.

Manonmani S and T B Ranganathan 2006 Path analysis in early x very early crosses of rice.Oryza : 43(1), 62-63

Manonmani S, Sree Rangasamy S R and Ranganathan B 1996 Variability and heritability in early lines of Indian rice. Madras Agricultural Journal 83(1): 75-76.

Marimuthu R, Rajesekharan S and Soundarapandian G 1990 Variability, heritability and genetic advance in rice. Madras Agricultural Journal 77 : 443-446.

Maurya D M and Singh D P 1977 Combining in rice for yield and fitness. Indian Journal of Agricultural Sciences 47(2): 65-70

Mc Couch S R L, Teytelman Y, Xu K B, Lobos K, Clare M, Walton B, Fu R, Maghirang Z, Li Y, Xing Q, Zhang I, Kano M, Yano R, Fjellstrom G De Clerk, Schneider D, Cartinhour, Ware D and Stein L 2002 Development and mapping of 2240 new SSR markers for rice (*Oryza sativa* L.). DNA Res., 9 : 199-207.

Mc Couch S R, Chen X, Panaud U, 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 : 89-99.

Mc Murry C T 1995 Mechanisms of DNA expansion, chromosome, 104 : 2-13.

Meenakshi T, Amirthadevarathinam A and Backiyarani S 1999 Correlation and path analysis of yield and some physiological characters in rainfed rice. Oryza 36(2): 154-156.

Mehetre S S, Patil P A, Mahajan C R and Shinde R B 1996 Variability, heritability, character association and genetic divergence studies in M_2 generation of gamma irradiated upland paddy. Crop Research 12 (2) : 155-161.

Mishra L K and Verma R K 2002.Correlation and path coefficient analysis for morphological and quality traits in rice (*Oryza sativa* L.) Plant Archives 2 (2) : 275-284.

Mokate A S, Bendale V W and Birari S P 1998 Variability, heritability, correlation and path analysis studies in rice (*Oryza sativa* L.). Crop Research 15 : 243.

Monalisa Manna, Ali M N and Sasmal B G 2006 Variability, correlation and path analysis in some important traits of low land rice. Crop Reseach Hisar 3(1) : 153-156.

Mundhe B S Jundhale N D and Bendale V W 2006 Genetic divergence in midlate genotypes of rice. Journal of Maharastra Agricultural Universities (2006) 31(1):21-23

Murthy B R and Arunachalam V 1966 The nature of genetic divergence in relation to breeding system in crop plants. Indian Journal of Genetics 26A: 188-198.

Nagajyothi B 2001 Studies on performance and heterosis of rice hybrids for yield. yield components and certain grain quality characters. M.Sc. (Ag.) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Nanja Reddy Y A, Prasad T G and Udaya Kumar M 1995 Genetic variation in yield attributes and yield of rice. Madras Agricultural Journal 82(4): 310-313.

Nath N and Talukdar P 1997 Genetic variability and correlation studies in segregating populations of indigenous Scented x High yielding non-scented crosses of rice. Oryza 34(2): 91-93.

Naveenkumar, B. 2003. Molecular characterization of parental lines of rice hybrids using PCR based DNA markers. M.Sc. (Ag.) Thesis submitted to ANGRAU, Hyderabad.

Nayak A R, Chaudhary D and Reddy J N 2001 Correlation and path analysis in scented rice (*Oryza sativa* L.). Indian Journal of Agricultural Research 35(3): 186-189.

Nayak A R, Chaudhary D and Reddy J N 2002 Genetic variability, heritability and genetic advance in scented rice. Indian Agriculturist 46(1&2) : 45-47.

Nayak A R, Chaudhary D and Reddy J N 2003 Genetic variability and correlation study among quality characters in scented rice. Agricultural Science Digest 23(3) : 175-178.

Nayak A R, Chaudhary D and Reddy J N 2004 Genetic divergence in scented rice. Oryza 41(3&4) : 79-82.

Nickell C D and Grafius 1969 Analysis of negative response to selection for high yield in winter barley. Crop Science 9 : 447-451.

Niranjana Murthy, Kulkarni R S and Uday Kumar M 1999 Genetic variability, heritability and genetic advance for morpho-physiological traits in rice. Oryza 36(2): 159-160.

Oad F C, Sano M A, Zia U I Hassan, Sta Cruz P and Oad N L 2002 Correlation and path analysis of quantitative characters of rice ratoon cultivars and advance lines. International Journal of Agriculture and Biology 4(2) : 204-207

Olufowote O, Yuhbixu, Xiuli Chen, William D, Park M, Henry R H, Beachell H, Dilday, Mazk Goto and Mc Couch R M 1997 Comparative evaluation of within-cultivar variation of rice (*Oryza sativa* L.) using microsatellite and RFLP markers. Genome., 40 : 370-378.

Panaud O, Chen X and Mc Couch S R 1996 Development of microsatellite markers and characterization of simple sequence length polymorphism (SSLP) in rice (*Oryza sativa* L.). Mol. Gen. Genet., 252 : 597-607.

Pandey D K, Gupta H S and Pandey P S 1999 Assessment of divergence in rice grown in iron toxic soil of Meghalaya. Indian Journal of Agricultural Sciences 69(1): 69-70.

*Panse V G and Sukhatme P V 1978 Statistical methods for Agricultural Workers. ICAR, New Delhi pp.235-246.

Paramasivam K, Giridharan S and Kirubakaran Soundararaj 1995 Genetic variability and character association of derived panicle characteristics of rice genotypes. Crop Research 10(3) : 285-290

Paramesha K, Rao M R G and Rajanna M P 2005 Evaluation of stabilized selections of different crossesof rice for yield and yield related components.Mysore Journal of Agricultural Sciences 39(1):31-36.

Patel M Z, Redd M V, Rana B S and Reddy B J 1989 Genetic variability and character association studies in semi-dry rice. Madras Agricultural Journal 83 (3): 185-188.

Patil P V, Sarawgi A K and Shrivastava M N 2003 Genetic analysis of yield and quality traits in traditional aromatic accessions of rice. Journal of Maharashtra Agricultural Universities 28(3) : 255-258.

Patil P V, Sarawgi A K, Nichal S S and Shrivastava M N 2004 Genetic divergence in aromatic traditional rice accessions from Chattisgarh and Madhya Pradesh (*Oryza sativa* L.). P K V Research Journal 28(1) : 67-72.

Patil PV and Sarawgi A K 2005 Studies on genetic variability, correlation and path analysis in traditional aromatic rice accessions. Annals of Plant Physiology 19 91):92-95.

Patil S G, Marin N R, Sahu V N 2005 Genetic divergence of traditional rice germplasm accessions. Journal of soils and crops 15 (2) : 308-314

Paul S K and Sarmah A K 1997 Interrelationship of yield and yield contributing characters in upland ahu rice. Journal of the Agricultural Science Society of North East India 10(2): 164-167.

Peer and Wachter, 1994. TREECON for Windows: a software package for the construction and drawing of evolutionary trees for the Microsoft Windows environment. Bioinformatics. Vol 10, Pp. 569-570

Philips, R L and Vasil I K eds (2001) DNA-Based Markers in Plants, Kluwer Academic Publishers.

Powell W, Michele Morgante, Chaz Andre, Michael Hanafey, Julie Vogal, Tingey and Antani Rafalski. 1996. The comparison of RFLP, RAPD, AFLP and SSR (microsatellite) markers for germplasm analysis. Mol. Breed., 2 : 225-238.

Pradhan K and Roy A 1990 Genetic divergence in rice. Oryza 27(4) : 415-418.

Prasad G S V, Prasad A S R, Sastry M V S and Srinivasan T E 1988 Genetic relationship among yield components in rice (*Oryza sativa* L.). The Indian Journal of Agricultural Sciences 58 : 470-472.

Provan, J G, Corbott J W, Mc Niol and Powell W 1997 Chloroplast DNA variability in wild and cultivated rice (*Oryza sativa*) revealed by polymorphic chloroplast simple sequence repeats. Genome, 40 : 104-110.

Rahangdale S L and Khorgade P W 1988 Studies on genetic variability, correlation and path analysis in upland rice. PKV Research Journal 12(2) : 98-101.

Rama Rao M V 1990 Genetic analysis of yield and its components in rice crosses (*Oryza sativa* L.). M.Sc. (Ag.) Thesis, Andhra Pradesh Agricultural University, Hyderabad (unpublished).

Ramaiah K 1953 Rice Breeding and Genetics. Science Monograph No.19 ICAR, New Delhi.

Ramesh Babu P 1999 Genetic analysis of yield and grain quality attributes in Rice (*Oryza sativa* L.). Ph.D. Thesis Acharya N.G. Ranga Agricultural University Hyderabad.

Ramesh Kumar V V 1989 Genetic analysis of yield and its components in four rice crosses. Journal of Research APAU 17(1) : 11.

*Rao C R 1952 Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York pp.236-272.

Rao S S and Shrivastav M N 1994 Genetic variation and correlation studies in rainfed upland rice. Oryza 31: 288-291.

Rao S S and Shrivastav M N 1999 Association among yield attributes in upland rice. Oryza 36(1): 13-15.

Rao T P and Gomathinayagam P 1997 Genetic divergence in semi-dry rice under different environments. Madras Agricultural Journal 84(6): 314-317.

Rather A G, Mir G N and Raina R L 1997.Cause and effect relation ship of yield and other characters in rice. Madras Agricultural Journal 84 :311-313

Rather A G, Zarger M A and Sheikh F A 2001 Genetic divergence in rice under temperate conditions. Indian Journal of Agricultural Sciences 71(5) : 344-345.

Ravindra Babu V 1996 Study of genetic parameters, correlations and path coefficient analysis of rice (*Oryza sativa* L.) under saline conditions. Annals of Agricultural Research 17(4): 370-374.

Ravindranadh B, Peraiah A, Sreerama Reddy N, Subramanyam D, Ramayya B and Murthy K R K 1982 Interrelationships between yield and yield components in rice. The Andhra Agricultural Journal 29(4) : 287-290.

Reddy J N and De R N 1996 Genetic variability in low land rice. Madras Agricultural Journal 83(4): 269-270.

Reddy J N, De R N and Suriya Rao A V 1997 Correlation and path analysis in low land rice under intermediate (0-50 cm) water depth. Oryza 34(3): 187-190.

Reddy S R 2001 Principles of Agronomy. Kalyani Publishers, Ludhiana, pp.65-72.

Remabai N, Ahmed Regina Devika R and Joseph C A 1992 Genetic variability and association of characters in medium duration rice genotypes. Oryza 29 : 19-22.

Richharia R H and Seetharaman R 1962 Studies in (*Oryza glaberrima steud* L.). Inheritance of colour in apiculus and stigma, interrelationship of genes and their significance. The Nucleus, Calcutta 5 : 87-94.

Roy A, Panwar D V S and Sarma R N 1995 Genetic variability and causal relationships in rice. Madras Agricultural Journal 82(4): 251-255.

Saghai Maroof, M.A., R.M. Biyashav, G.P. Yang, Q. Zhang, R.W. Allard. 1994. Extraordinary polymorphic microsatellite DNA in barley : species diversity, chromosomal locations and population dynamics. Proc. Natl. Acad. Sci., USA, 91 : 5466-5470.

Sahdev Singh, Dhaka R P S and Malik S S 1996 Heritability and genetic advance in irradiated population of rice. Crop Research 11(2) : 184-188.

Sakthivel P 2001 Genetic divergence and genetic analysis of yield attributes and certain quality traits in rice (*Oryza sativa* L.). M.Sc. (Ag) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Samonte S O P B, Wilson L T and Tabien R E 2006 Maximum node production rate and main culm node number contributions to yield and yield related traitsin rice. Field Crops Research 96 (2/3): 313-319.

Sandyakishore N 2005 Studies on genetic diversity of quality parameters in rice (Oryza sativa L.).Msc.(Ag.) Thesis, Acharya N.G. Ranga Agricultural university, Hyderabad.

Saravanan R and Senthil N 1997 Genotypic and phenotypic variability heritability and genetic advance in some important traits in Rice. Madras Agricultural Journal.84(5) : 276-277.

Saravanan R, Palanisamy S and Senthil N 1996 Path analysis in Rice. Madras Agricultural Journal 83(8): 528-529.

Sardana S, Borthakur D N and Lakhanpal T N 1997 Genetic divergence in rice germplasm of Tripura. Oryza 34(3): 201-208.

Sardana S, Sasi Kumar and Modak D 1989 Variability and path analysis in Fixed cultures of rice. Oryza 26 : 250-251

Sarma R N and Roy A 1993 Studies on variability and inter-relationship of yield attributes in jhum rice. Annals of Agricultural Research 14(3): 311-316.

Satish Y, Seetha Ramaiah K V, Srinivasulu R and Sree Rami Reddi N 2003 Correlation and path analysis of certain quantitative and physiological characters in rice (*Oryza sativa* L.). The Andhra Agricultural Journal 50(3&4) : 231-234.

Satpaty D and Nanda A K (1978) Inter relationship between yield and some associated characters in upland rice grown under rainfed conditions.Oryza 15 (1): 12-19.

Satya Priya Lalitha V and Sreedhar N 1996 Heritability and correlation studies in rice. The Andhra Agricultural Journal 43(2-4): 158-161.

Satya Priya Lalitha V and Sreedhar N 1999 Estimates of genetic parameters for quality traits in rice. Annals of Agricultural Research 20(1): 18-22.

Sawant D S, Patil S L, Jadhav B B and Bhave S G 1995 Genetic divergence, character association and path analysis in Rice. Journal of Maharashtra Agricultural Universities 20(3): 412-414.

Schug M D, Hutler C M, Wetter-Strand K A, Gaudette M S, Mackay Ts F C and Aquadro C F 1998 The mutation rates of di-, tri-and tetranucleotide repeats in *Drosophila melanogaster*. Nat. Genet., 15 : 99-102.

Sebastian L S, Hipolito L R and Gracia J S 1998 Molecular markers analysis of the contribution made by landraces to modern Philippine rice cultivars. J. of Breed. Genet., 30 : 73-81.

Seetharaman R, Shrivastava D P and Ghori D P 1974 Preliminary studies in rice cultivars from N E. Indian Journal of Genetics 34 : 143-149.

Selvarani M and Rangasamy P 1998 Correlation and Path analysis in Rice. Madras Agricultural Journal 85(1): 57-58.

Shantha Kumar G, Mahadevappa M and Rudraradhya M 1998 Studies on genetic variability, correlation and path analysis in rice during winter across the locations. Karnataka Journal of Agricultural Sciences 11(1) : 73-77.

Singh S P, Singhara G S, Parray G A and Bhat G N 2005 Genetic variability and heritability in rice. Environment and Ecology 23s (549-551).

Singh L, Singh J D, Sachan N S 2002 Intercharacter association and path analysis in paddy. Annals of Biology 18(2) : 125-128.

Singh R K and Chaudhary B D 1977 Biometrical methods in quantitative genetic analysis Kalyani Publishers New Delhi pp. 215-218.

Sinha S K , Tripathi A K and Bisen U K 2004 Study of genetic variability and correlation co efficient analysis sin midland landraces of rice. Annals of Agricultural Research 25 (1) : 1-3

Sivasubramanian S and Madhavamenon P 1973 Combining ability in rice. Madras Agricultural Journal 60 : 419-421.

Sneath P H A and Sokal R R 1973 Numerical taxonomy. W.H. Freeman Ed. San Fransisco.

Somnath Bhattascharya and Ghosh S K 2004 Association among yield related traits of twenty four diverse land races of rice.Crop Research Hisar 27(1) : 90-93

Souroush H R, Mesbah M, Hossainzadeh A and Bozorgipour R 2004 Genetic and Phenotypic variability and cluster analysis for quantitative and qualitative traits of rice.

Srikrishnadevarayalu B 1993 Genetic variability and character association of some physiological and quantitative traits in rice (*Oryza sativa* L.). M.Sc. (Ag.) Thesis Andhra Pradesh Agricultural University, Hyderabad (unpublished).

Subba Rao L V, Prasad G S V, Rama Prasad A, Acharyulu T L and Rama Krishna S 2001. Collection, characterization and evaluation of rice germplasm from Bastar Region. Indian Journal of Plant Genetic Resources 14(2) : 222-224.

Subbarao L V, Ram T, Shobharani N, Ravindra Babu V, Pasalu I C, Reddy C S, Ramaprasad A S, Viraktmath and Subbaiah S V 2006. Agro-morphological characterization and evaluation of rice germplasm for major biotic stress tolerance.In Proceedings of National Plant Breeding Congress on Plant Breeding in post genomics Era :Organized by Indian Society of Plant Breeders & TNAU. March, 1-3 pp:83

Subudhi P K, Nandhi S, Casal C, Virmani S S and Huang N 1998 Classification of germplasm. II. High resolution fingerprinting of cytoplasmic genetic male sterile (CGMS) lines with AFLP. Theor. Appl. Genet., 96 : 941-949.

Sukanya Subramanian and Rathinam M 1984 Genetic components of variation in rice. Madras Agricultural Journal 71: 561-565.

Suman A , Shankar V G and Rao L V S 2005 Analysis of genetic divergesnce in rice germplasm. Research on crops 6 (3) 487-491

Suman A 2003 Studies on genetic diversity and agro-morphological characterization of rice (*Oryza sativa* L.) germplasm. M.Sc. (Ag.) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Suman A, Sreedhar N and Subbarao L V 2006 Correlation and Path analysis of yield and its components in Rice. International Journal of Tropical Agriculture.24(1-2)

Sundaram T, Ganesan K and Wilfred Manuel W 1990 Correlation studies in rice varieties and cultures. Madras Agricultural Journal 77(9-12): 546-547.

Supriyo Chakraborty and Hazarika M K (1994) Estimation of various genetic parameters for yield and yield components in rice. Oryza 31: 226-227.

Surender Raju C H 2002 Study of genetic divergence, variability, stability, gene action and character association for certain physiological quality and yield components in Rice (*Oryza sativa* L.) Ph.D. Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Surendra Singh and Chaudhary B S 1996 Variability, heritability and genetic advance in cultivars of rice (*Oryza sativa* L.). Crop Research (12(2) : 165-167.

Suryanarayana Y 2000 Genetic studies on drought tolerance in Rice (*Oryza sativa* L.) Ph.D. Thesis, Acharya N. G. Ranga Agricultural University Hyderabad.

Swathi Prashanth Goel, Ramesh BR 2004 The nature and divergence in relation to yield traits in rice germplasm. Annals of Agricultural Research 25 (4) : 598-602.

Tarasatyavathi C, Bharadwaj C H and Subramanyam D 2001 Variability, correlation and path analysis in rice varieties under different spacings. Indian Journal of Agricultural Research 35(2): 79-84.

Tayeng T and Singh M R K 2006 Correlation and path analysis in some early rice genotypes under pre kharif conditions of Manipur valley. Environment and Ecology. 24(2) 265-267.

Temnykh S G, Declerck A, Lukashova L, Lipovich L, Cartinhour S, and. Mc Couch. 2001. Computational and experimental analysis of microsatellites in rice (*Oryza sativa* L.) : frequency, length variation, transposan associations and genetic marker botanical. Genome Res., 11 : 1441-1452.

Temnykh S, Cartinhour S, Park W, Ayres N, Hauck N, Lipovich L,. Cho Y G and Mc Couch 2000 Mapping and genome organization of microsatellite sequence in rice (*Oryza sativa* L.). Theor. Appl. Genet., 100 : 697-712.

Tripathi A K, Sinha S K and Bhandarkar S 1999 Studies on variability, heritability and genetic advance of semideep water rice. Advance in Plant Sciences 12(1): 235.

Ushakumari R and Rangaswamy P 1997 Studies on genetic diversity in international early rice genotypes. Annals of Agricultural Research 18(1): 29-33.

Valarmathi G and Leenakumari S 1998 Character association analysis in rice varieties under upland conditions. Madras Agricultural Journal 85(10-12): 679-680.

Vanaja T, Babu L C, Radhakrishnan V V and Unnithan V K G 2003 Genetic divergence in high yielding rice genotypes. Oryza 40(1&2) : 40-42.

Vange T and Ojo A A 1997 Variability and heritability estimates of yield and yield components in some Nigerian low land rice genotypes. International Rice Research Newsletter : 6.

Vange T, Ojo A A and Bellow L L 1999 Genetic variability, stability and correlation studies in lowland rice (*Oryza sativa* L.) genotypes. Indian Journal of Agricultural Sciences 69(1): 30-3.

Vanniarajan C, Rangasamy P, Ramalingam J, Nandarajan N and Arumugampillai M 1996 Studies on genetic variability in hybrid rice derivatives. Crop Research 12 (1) : 24-27.

Venkata Suresh A 2001 Genetic analysis for certain quantitative and qualitative traits in F_2 populations of rice (*Oryza sativa* L.). M.Sc. (Ag) Thesis, Acharya N.G. Ranga Agricultural University, Hyderabad.

Verma D K Thakur R and Mishra S B 1997 Correlation and path analysis of yield and yield component s in deep water rice. Indian Journal of Genetics and Plant breeding .57 : 19-24

Virk P S, Ford-Llyod B V, Jackson M T and. Newburry H J 1994 Use of RAPD for the study of diversity within the plant germplasm collections. Heredity, 74 : 170-179.

Vivekanandan P and Sukanya Subramanian 1993 Genetic divergence in rainfed rice. Oryza 30: 6-62.

Wang Z Y and. Tanksley S D 1989 Restriction fragment length polymorphism in *Oryza sativa* L. Genome., 32 : 1113-1118.

Weber J L 1990 Informativeness of human (dC-dA)n (dG-dT)n polymorphisms. Genomics, 7 : 524-530.

Weber J L, and May P E 1989 Abundant class of human DNA polymorphisms, which can be typed using the polymerase chain reaction. Am. J. Hum. Genet., 44:388-396.

Weising J, Beyermann B, Ramsat J and Kahl G 1991 Plant DNA fingerprinting with radioactive and digoxygenated oligonucleotide probes complementary to simple repetive DNA sequences. Electrophoresis, 12 : 159-169.

*Wright S 1921 Correlation and causation. Journal of Agricultural Research 20 : 557-585.

Wu K S and Tanksley S D 1993 Abundance, polymorphism and genetic mapping of microsatellites in rice. Mol. Gen. Genet., 241 : 225-235.

Yadav R K 2000 Studies on genetic variability for some quantitative characters in rice (*Oryza sativa* L.). Advances in Agricultural Research in India 13 : 205-207.

Yang G P, Saghai Maroof M A, Xu C G, Zhang Q and Biyashav R M 1994 Comparative analysis of microsatellite DNA polymorphosim in land races and cultivar rice.Mol.Genetics 245: 187-194.

Yogameenakshi P, Nadarajan N and Anbumalarmathi J 2004 Correlation and path analysis on yield and drought tolerant attributes in rice (*Oryza sativa* L.) under drought stress. Oryza 41(3&4) : 68-70.

Yolanda J L Vijendra Das L D 1995 Correlation and path analysis in rice (Oryza sativa) Madras Agricultural Journal 82(11) : 576-578.

Yu LX, and Nguyen H T 1994 Genetic variation detected with RAPD markers among upland and low land rice cultivars (*O. sativa* L.). Theor. Appl. Genet., 87 : 668-672.

Zhao X and Kochert G 1992 Phylogenic distribution and genetic mapping of a (GCG)n microsatellite from rice (*Oryza sativa* L.). Plant Mol. Biol., 21 : 607-614.

Zheng K L, Shen and. Quian H R, 1995 DNA polymorphisms generated by arbitrary primed PCR in rice. Rice Genet. Newslet., 8: 134-136.

Zhou Z and Gustafson J P 1995. Characterization of minisatellite sequences in rice and application for DNA fingerprinting induced mutations and molecular technique for crop imrpvoement proceedings, Vienna, Austria, pp.205-214

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