GENETIC STUDIES ON ANAEROBIC GERMINATION AND SEEDLING VIGOUR TRAITS IN RICE (*Oryza sativa* L.)

By

P. SRILAKSHMI

B.Sc. (Ag.)

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CHAIRPERSON: Dr. N. CHAMUNDESWARI



DEPARTMENT OF GENETICS AND PLANT BREEDING

AGRICULTURAL COLLEGE, BAPATLA - 522 101

ACHARYA N. G. RANGA AGRICULTURAL UNIVERSITY
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DECLARATION

I, **Ms. P. SRI LAKSHMI,** hereby declare that the thesis entitled **"GENETIC STUDIES ON ANAEROBIC GERMINATION AND SEEDLING VIGOUR TRAITS IN RICE (*Oryza sativa* L.)",** submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that any material in the thesis has not been published earlier.

Place :

Date : **(P. SRI LAKSHMI)**

(ID.No. BAM-15-22)

CERTIFICATE

Ms. P. SRI LAKSHMI has satisfactorily prosecuted the course of research and that the thesis entitled **"GENETIC STUDIES ON ANAEROBIC GERMINATION AND SEEDLING VIGOUR TRAITS IN RICE (*Oryza sativa* L.)"** submitted is the result of original research work and is of sufficiently high standard to warrant it's 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.

Place:
Date:

(**N. CHAMUNDESWARI)**
Chairperson
Scientist (Plant Breeding)
APRRI & RARS
Maruteru - 534 122

CERTIFICATE

This is to certify that thesis entitled **"GENETIC STUDIES ON ANAEROBIC GERMINATION AND SEEDLING VIGOUR TRAITS IN RICE (*Oryza sativa* L.)"** submitted in partial fulfillment of the requirements for the degree of Master of Science in Agriculture in the major field of **Genetics and Plant Breeding** of the Acharya N. G. Ranga Agricultural University, Guntur, is a record of the bonafied research work carried out by **Ms. P. SRI LAKSHMI** 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 by the student for any other degree or diploma. The published part has been fully acknowledged. All assistance and help received during the course of the investigation have been duly acknowledged by the author of the thesis.

Thesis approved by the Student's Advisory Committee

Chairperson : **Dr. N. CHAMUNDESWARI** _____
Scientist (Plant Breeding)
APRRI & RARS
Maruteru - 534 122

Member : **Dr. LAL AHAMED MOHAMMED** _____
Assistant Professor
Department of Plant Molecular Biology and Biotechnology
Advanced Post Graduate Centre
Lam, Guntur - 522 034

Member : **Dr. V. SRINIVASA RAO** _____
Professor and University Head
Department of Statistics and Mathematics
Agricultural College, Bapatla - 522 101

Date of final viva-voce:

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Place: Bapatla ***(P. SRI LAKSHMI)***

Date:

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LIST OF SYMBOLS AND ABBREVATIONS

%	:	Per cent
&	:	And
/	:	Per
$\hat{\sigma}^2$	:	Estimate of Variance
µl	:	Microlitre
viz.,	:	Namely
vs.	:	Against
Σ	:	Standard Deviation
^oC	:	Degree Celsius
AG	:	Anaerobic Germination
AFLP	:	Amplified Fragment Length Polymorphism
APRRI	:	Andhra Pradesh Rice Research Institute
BPT	:	Bapatla
BYD	:	Biological Yield/Plant
C.D	:	Critical Difference
C.V	:	Coefficient Of Variation
Cm	:	Centimeter
Conc.	:	Concentration
Cont.).	:	Continued
Covar.	:	Covariance
CTAB	:	Cetyl Tris Methyl Ammonium Bromide
DDW	:	Double Distiiled Water
d.f	:	Degrees of Freedom
DAS	:	Days After Sowing
DNA	:	Deoxy Ribonucleic Acid
dNTPs	:	Deoxy Nucleotide Triphosphate
DSR	:	Direct seeding of rice
DTF	:	Days to 50% Flowering
DTM	:	Days to Maturity
EDTA	:	Ethylene Diamine Tetra Acetic Acid
et al.,	:	And Coworkers

F_1	:	First Filial Generation
F_2	:	Second Filial Generation
F_3	:	Third filial generation of a cross
FAO,	:	Food and Agriculture Organization
Fig	:	Figure
FS	:	Full Sibs
G	:	Grams
G %	:	Germination Per cent
g stem-1	:	gram per stem
GA	:	Genetic Advance
GAM	:	Genetic Advance As Percent of Mean
GCA	:	General Combining Ability
GCV	:	Genotypic Coefficient of Variation
GY	:	Grain Yield
H%	:	Hulling Per cent
h^2 b	:	Heritability In Broad Sense
HI	:	Harvest Index
HCl	:	Hydrochloric acid
HRR	:	Head Rice Recovery
HS	:	Half Sibs
IRRI	:	International Rice Research Institute
JGL	:	Jagtyal
KLAC	:	Kernal Length After Cooking
L x T	:	Line ×Tester
LAI	:	Leaf Area Index
L/B	:	Length/Breadth ratio
M	:	Molar
M%	:	Milling percent
MABC	:	Marker Assisted Backcrossing
MAS	:	Marker Assisted Selection
Mb	:	Mega Base Pairs
Mg	:	Milligram
Mm	:	Millimeter

MSS	:	Mean Sum of Squares
MTU	:	Maruteru
NA	:	Not Available
No.	:	Number
NACL	:	Sodium Chloride
NS	:	Non-Significant
OD	:	Optical Density
PCR	:	Polymerase Chain Reaction
PCV	:	Phenotypic Coefficient of Variation
Per se	:	As Such With Mean
PHT	:	Plant Height
Ppm	:	Parts per million
PVP	:	Poly Vinyl Pyrrolidone
QTL		Quantitative Trait Loci
RAPD	:	Random Amplified Polymorphic DNA
RARS	:	Regional Agricultural Research Station
RBD	:	Randomized Block Design
RFLP	:	Restriction Fragment Length Polymorphism
Rpm	:	Revolutions Per Minute
SCA	:	Specific Combining Ability
SDW	:	Seedling Dry Weight
SE	:	Standard Error
SEm	:	Standard Error of Mean
SES	:	Standard Evaluation System
SFW	:	Seedling Fresh Weight
SNP	:	Single Nucleotide Polymorphisms
SRL	:	Seedling Root Length
SS	:	Sum of Squares
SSL	:	Seedling Shoot Length
SSR	:	Simple Sequence Repeats
SVI	:	Seedling Vigour Index
TAE	:	Tris acetate EDTA
TE	:	Tris –EDTA

ABSTRACT

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The present investigation, "Genetic studies on anaerobic germination and seedling vigour traits in rice (*Oryza sativa* L.)" was carried out during *kharif* 2016 and *rabi* 2016-17 to obtain information on the nature and extent of variability, heritability, genetic advance as per cent of mean and genetic diversity for yield and its contributing parameters, quality characters, direct seeded traits, seedling vigour and anaerobic germination related traits at Andhra Pradesh Rice Research Institute (APRRI) and Regional Agricultural Research Station (RARS), Maruteru, Andhra Pradesh. Fifty genotypes were collected from Department of Genetics and Plant Breeding, APRRI & RARS, Maruteru. Data was recorded on plant height at maturity (cm), days to 50% flowering, no. of panicles/plant, panicle length (cm), no. of grains/panicle, spikelet fertility (%), grain yield/plant (g), test weight (g), hulling (%), milling (%), HRR (%), kernel length (mm), kernel breadth (mm), kernel L/B Ratio, kernel elongation ratio, volume expansion ratio, culm diameter (mm), bending strength, leaf area index, harvest index, germination % on 10^{th} day, germination % on 14^{th} day (rate of germination), SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SVI -1, SVI -2, AG % after 2 weeks of submergence, plant survival % after 2 weeks, AG % after 3 weeks of submergence and plant survival % after 3 weeks. In *rabi* 2016-17, selection of lines and testers was done based on seedling vigour and anaerobic germination related traits performance among 50 genotypes and crossing was done in Lx T fashion among selected genotypes. Data were recorded on F_1's along with parents for SV and AG traits under lab conditions and combining ability studies were performed. Molecular screening was also done for F_1's along with parents for AG and SV related traits with 24 trait linked SSR markers.

The analysis of variance revealed significant differences among the genotypes for all the characters indicating the presence of sufficient genetic variability in the studied material. High heritability coupled with high genetic advance as per cent of mean was observed for plant height at maturity (cm), days to 50% flowering, no. of panicles/plant, no. of grains/panicle, grain yield/plant, test weight, kernel L/B ratio, culm diameter (mm), bending strength, leaf area index, harvest index, germination % on 10^{th} day, SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SV I -1, SV I -2, AG % after 2 weeks of submergence, plant survival % after 2 weeks, AG % after 3 weeks of submergence, plant survival % after 3 weeks indicating the predominance of additive gene action and their amenability for further improvement through simple selection.

Genetic divergence was high and the 50 genotypes were distributed into eight clusters. Out of eight clusters, maximum number of genotypes (16) included in cluster II. Cluster I is the second largest with 14 genotypes followed by cluster VII and VIII each with 11 and 5 genotypes respectively. The clusters III, IV, V and VI were solitary clusters.

Survival % after 2 weeks, anaerobic germination % after 3 weeks of submergence, anaerobic germination % after 2 weeks of submergence, leaf area index, seedling shoot length on 10^{th} day and seedling shoot length on 14^{th} day together contributed 80% towards total divergence indicating that these characters should be taken into consideration while selecting parents for hybridization.

The analysis of variance for combining ability revealed significant differences among crosses for all the characters studied indicating high degree of variability in the material studied. While, line × tester effects were significant for majority of the characters except for seedling shoot length on 14^{th} day (cm), seedling root length on 14^{th} day (cm), seedling dry weight (mg) and survival % after 2 weeks. The analysis of variance for combining ability also revealed significant differences among the lines for the traits *viz.*, seedling shoot length on 14^{th} day (cm), seedling root length on 10^{th} day (cm), Seedling fresh weight on 14^{th} day (mg), seedling dry weight (mg), seedling vigour Index I**.** While, in testers significant difference was observed only for seedling shoot length on 14^{th} day (cm), seedling fresh weight on 14^{th} day (mg) and survival % after 2 weeks.

Among the eight parents evaluated, based on their gca effects and their per se performance, AC 39416A, N-22 were identified as good general combiners for seedling vigour traits. The genotypes AC 39397, MTU 1140 and AC 39416A were identified as good general combiners for the anaerobic germination.

The ratio of *gca* variance to *sca* variance was high indicating the predominance of additive gene action for seedling shoot length on 10^{th} day (cm), seedling root length on 10^{th} day (cm), seedling root length on 14^{th} day (cm), seedling dry weight (mg) and seedling vigour index I. The traits governed by additive gene action may be improved by hybridization followed by simple selection procedures like pedigree breeding method. For the characters *viz.*, germination % on 10^{th} day, germination % on 14^{th} day, seedling shoot length on 14^{th} day (cm), seedling fresh weight on 14^{th} day (mg), seedling vigour index II, anaerobic germination % after 2 weeks of submergence, plant survival % after 2 weeks, anaerobic germination % after

3 weeks of submergence and plant survival % after 3 weeks, the ratio between *gca* variance and *sca* variance was low and indicated the role of non additive gene action. Non-additive gene action governing characters may be exploited through heterosis breeding.

Based on *sca* effects and *per se* performance, the crosses, Azucena x MTU 1010, AC 39416A x MTU 1010 , N 22 x MTU 1010, AC 39397 x MTU 1121, AC 39416A x MTU 1121, N 22 x MTU 1010 and MTU 1140 x MTU 1010 were identified as promising for seedling vigour and anaerobic germination traits.

Molecular screening was done for F_1's along with parents for anaerobic germination and seedling vigour traits with 24 specific trait linked SSR markers.The markers RM 478, RM 104, RM 341, RM 253 RM 520, RM 105, RM 210, RM 263 and RM 206 were associated with anaerobic germination. The markers RM 231 and RM 7 were associated with rate of germination, where as RM 201 and RM 234 were associated with root length. The markers RM 214, RM 5509, RM 20557, RM 306, RM 152 and RM 208 were associated with culm diameter, RM 17 associated with seedling height, RM 270 associated with seedling vigour. RM 10, RM 172 and RM 346 associated with culm strength. Among these markers 13 markers has shown polymorphism which were used for characterization of F_1 crosses.

Chapter I

INTRODUCTION

Rice, India's most prominent crop is the staple food for the people of the eastern and southern parts of the country. In India, rice is cultivated over an area of 43.95 Mha with a production of 104.80 Mt of milled rice and productivity of 2390 kg ha^{-1} (Indiastat, 2014-15). It is predominant dietary energy source for consumers in 18 Asian countries where 90% of total rice is produced and consumed. Rice provides 18.9% of the global per capita energy per day (Rice Almanac, 2013). Ranking first in area (44mha), India is the second largest producing country in the world after China. Andhra Pradesh is one of the important states contributing to national rice production with productivity of 3126 kg/ha (http://agricop.nic.in/agristatics.html).

In India, the increase in rice production has to come from higher yield per unit area because area under rice is declining. Day by day puddling and transplanting operations require large amount of water and labour, both of which are becoming increasingly scarce and expensive, making rice production less profitable. All these factors demand a major shift from puddled-transplanted rice production to direct seeding of rice (DSR) in irrigated areas.

According to Pandey and Velasco (2005), low wages and adequate availability of water favour transplanting, whereas high wages and low water availability favour direct seeding of rice. Direct seeding in rice can be categorized as (1) Wet-DSR, in which sprouted rice seeds are broadcasted or sown in lines on wet/ puddled soil and (2) Dry-DSR, in which dry rice seeds are drilled or broadcast on unpuddled soil either after dry tillage or zero tillage or on a raised bed.

Direct seeding is a successful method of cultivation in some countries which save labour and is more economical than transplanting and also provides good stand establishment. Direct-seeded rice offers the advantage of faster and easier planting, ensure proper plant population, reduce labour and hence less drudgery, 10-12 days earlier crop maturity, more efficient water use and higher tolerance to water-deficit and often high profit in areas with assured water supply (De Datta, 1986). Gill (2008)

also reported that direct seeding results in early maturity and shorten the crop duration. To date, no specific variety has been developed especially for direct seeding conditions. Hence, there is an urgent need to develop and identify promising rice cultures suitable for direct sowing conditions.

Early vigour is important in DSR systems (Balasubramanian and Hill, 2002 and Cairns *et al.,* 2009). Rapid early growth increases stand establishment and weed competitiveness, both of which are important components for high yields in DSR (Zhao *et al.,* 2006). Rice varieties suitable for direct seeding in irrigated areas must possess early seedling vigour and enhanced foliar growth to combat weeds at the vegetative stage, moderate tillering, less foliar growth and enhanced assimilate export from leaves to stems during the late vegetative and reproductive phases, sustained high foliar N concentration at the reproductive stage, strong stems to withstand lodging and to store assimilates and improved reproductive sink capacity with a prolonged ripening period (Dingkuhn *et al.*, 1991).

Rice crop is frequently prone to flooding in coastal areas due to recent trend of climate change. Three different types of floods *viz.*, submergence during germination (anaerobic germination), flash floods (complete submergence up to 2 weeks) and stagnant flooding (30-50cm water depth) are mostly prevailing types of floods in coastal Andhra Pradesh. Breeding for submergence tolerance during germination (anaerobic germination) is becoming mandatory to get good seedling establishment under direct seeding conditions during monsoon in coastal areas.

In rice besides yield, it is also important to look into the quality aspects for better consumer preference and also to get premium price in the market. The significance of grain quality varies depending upon the requisites established by the international market, ethnic customs, uses *etc.* and is also important for all people involved in supply chain *i.e.*, production, processing and consumption. In rice, the quality parameters play an important role in fetching the foreign currency to the Indian exchequer.

Information on nature and magnitude of variability for these traits present in a population due to genetic and non-genetic causes is an important prerequisite for systematic breeding programs to improve yield potential of the crop. Success of plant breeding depends on understanding the genetic basis of qualitative/quantitative

characters. *i.e.,* due to additive or dominant gene effects since the former is key component for genetic gain by selection and latter determines level of trait heterosis. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme (Vivekanandan and Subramanian, 1993).

Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses for the exploitation of heterosis. The performance of parent may not necessarily reveal it to be a good or poor combiner. Therefore, gathering information on nature of gene effects and their expression in terms of combining ability is necessary for crop improvement. At the same time, it also elucidates the nature of gene action involved in the inheritance of characters. So combining ability studies are also paramount important for selecting best parental lines with good seedling vigour and tolerant to anaerobic germination suitable for wet direct seeded conditions.

Breeding for better germination, greater seedling vigour and higher tolerance to water logging along with good grain quality in rice has been attempted before but with limited success because genotypes with sufficient tolerance are not available. The use of molecular markers **(**DNA markers) provides effective selection technique for crop improvement and has an added advantage to selection based on phenotype and have been extensively used for genetic dissection of agriculturally important traits in rice. Hence, the present study is aimed to identify the suitable genotypes with short stature, non lodging, early vigour and high yield potential along with desirable quality parameters for wet direct sowing method with the following objectives.

1. To assess anaerobic germination (AG) and seedling vigour (SV) traits in rice germplasm.
2. To evaluate rice germplasm for yield, quality and direct seeding traits under wet direct sown conditions.
3. To study gene action and combining ability effects for AG and SV traits.
4. To characterize F_1s and their parents with established molecular markers for AG and SV traits.

Chapter II

REVIEW OF LITERATURE

The present investigation in rice was undertaken to study the extent of variability, heritability, genetic advance and genetic divergence among 50 genotypes for yield and its components, quality traits, direct seeded traits, seedling vigour and anaerobic germination related traits and to know the combining ability affects in 12 crosses generated by mating in L x T design in the experimental material. The literature available on the objectives of the present study has been comprehensively reviewed under the following headings.

2.1 Variability

2.2 Heritability and genetic advance

2.3 Genetic divergence

2.4 Combining ability

2.5 Molecular characterization

2.1 VARIABILITY

Development of high yielding varieties requires the knowledge of existing genetic variability. The large spectrum of genetic variability in segregating population depends on the amount of genetic variability among genotypes and offer better scope for selection. The magnitude of heritable variation in the traits has immense value in understanding the potential of the genotype for further breeding programme. Assessment of variability for yield and its component characters has become absolutely essential before planning for an appropriate breeding strategy of genetic improvement. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm.

Available literature on variability for yield components, quality parameters, direct seeded traits, seedling vigour and anaerobic germination traits in rice is reviewed and presented here under in table 2.1.

2.2 HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

Heritability and genetic advance are important selection parameters. Hanson *et al.* (1956) defined heritability in the broad sense as the ratio of genotypic variance to the total variance in the non- segregating populations. Heritability estimates provide authentic information about the faithfulness with which a particular genetic attribute will be transmitted to the successive generations. The higher heritability makes simpler the selection process and greater the response to selection. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Heritability values are variable depending upon the genetic nature of genotypes for different characters studied.

The available literature pertaining to heritability and genetic advance for yield components, quality parameters, direct seeded traits, seedling vigour and anaerobic germination traits in rice is reviewed and presented here under in Table 2.2.

Table 2.1: Review of literature on variability in rice (*Oryza sativa* L.)

S.No.	Character	Variability	Reference
1.	Days to 50% flowering	High PCV, GCV	Seyoum *et al.* (2012) Shobharani *et al.* (2013)
		Low PCV, GCV	Idris and Mohamed (2013) Gangashetty *et al.* (2013) Sathya and Jebaraj(2013) Dhurai *et al.* (2013) Paikhomba *et al.* (2014) Neha *et al.* (2014) Nikhil *et al.* (2014) Allam *et al.* (2015) Mahendra *et al.* (2015) Harsh *et al.* (2015) Rajkumar and Ibrahim (2015)

Table 2.1 (Cont.).

			Srihima *et al.* (2015) Sameera *et al.* (2015) Islam *et al.* (2015) Shrivastava *et al.* (2015) Karande *et al.* (2015) Islam *et al.* (2016) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016) Tomar *et al.* (2016) Tripathi *et al.* (2017) Onyia *et al.* (2017)
		Moderate PCV, GCV	Kumar and Saravanan (2012) Pratap *et al.* (2012) Dhurai *et al.* (2013) Bekele *et al.* (2013) Vanisree *et al.* (2013) Bhati *et al.* (2015) Kishore *et al.* (2015) Muthuramu and Sakthivel (2016)
		Moderate PCV, Low GCV	Lingaiah (2015)
2.	Plant height at maturity (cm)	High PCV, GCV	Bhadru *et al.* (2012) Seyoum *et al.* (2012) Bhati *et al.* (2015) Neha *et al.* (2014) Bornare *et al.* (2014) Ameenal *et al.* (2016)
		Low PCV, GCV	Sathya and Jebaraj (2013) Paikhomba *et al.* (2014) Nikhil *et al.* (2014) Kishore *et al.* (2015) Mahendra *et al.* (2015) Srihima *et al.* (2015)

Table 2.1 (Cont.).

			Sameera *et al.* (2015) Rajkumar and Ibrahim (2015) Gampala *et al.* (2015) Islam *et al.* (2015) Karande *et al.* (2015) Onyia *et al.* (2017)
		Moderate GCV, PCV	Sravan *et al.* (2012) Pratap *et al.* (2012) Kumar and Saravanan (2012) Ghosh and Sharma (2012) Bekele *et al.* (2013) Dhurai *et al.* (2013) Idris and Mohamed (2013) Allam *et al.* (2015) Harsh *et al.* (2015) Sindhumole *et al.* (2015) Shrivastava *et al.* (2015) Pavan Shankar *et al.* (2016) Tomar *et al.* (2016) Muthuramu and Sakthivel (2016)
		Moderate PCV, Low GCV	Lingaiah (2015) Islam *et al.* (2016)
3.	Number of panicles per plant	High PCV, GCV	Singh *et al.* (2011) Seyoum *et al.* (2012) Tushara *et al.* (2013) Sathya and Jebaraj (2013) Bornare *et al.* (2014) Harsh *et al.* (2015) Sameera *et al.* (2015) Shrivastava *et al.* (2015) Bhati *et al.* (2015) Ameenal *et al.* (2016) Tomar *et al.* (2016)

Table 2.1 (Cont.).

			Onyia *et al.* (2017)
		High PCV, Moderate GCV	Saidaiah *et al.* (2010b) Laxuman *et al.* (2010) Dhurai *et al.* (2013)
		Moderate PCV, Low GCV	Muthuramu and Sakthivel (2016) Tripathi *et al.* (2017)
		Moderate PCV, GCV	Ullah *et al.* (2011) Islam *et al.* (2016) Pavan Shankar *et al.* (2016)
		Low PCV, Moderate GCV	Rukmini Devi *et al.* (2016)
4.	Panicle length (cm)	Low GCV, PCV	Sravan *et al.* (2012) Sathya and Jebaraj (2013) Paikhomba *et al.* (2014) Nikhil *et al.* (2014) Kishore *et al.* (2015) Lingaiah *et al.* (2015) Sameera *et al.* (2015) Sindhumole *et al.* (2015) Karande *et al.* (2015) Islam *et al.* (2016) Pavan Shankar *et al.* (2016) Tomar *et al.* (2016) Tripathi *et al.* (2017)
		High PCV, GCV	Srihima *et al.* (2015)
		Moderate PCV, GCV	Saidaiah *et al.* (2010b) Gangashetty *et al.* (2013) Idris and Mohamed (2013) Dhurai *et al.* (2013) Bhati *et al.* (2015) Harsh *et al.* (2015) Rukmini Devi *et al.* (2016)
		Moderate PCV	Parvathi *et al.* (2011)

Table 2.1 (Cont.).

		low GCV	Ghosh and Sharma (2012) Allam *et al.* (2015) Mahendra *et al.* (2015) Shrivastava *et al.* (2015)
5.	Number of grains per panicle	High PCV, GCV	Dhurai *et al.* (2013) Bhati *et al.* (2015) Islam *et al.* (2015) Karande *et al.* (2015) Sameera *et al.* (2015) Shrivastava *et al.* (2015) Onyia *et al.* (2017)
		Moderate PCV, GCV	Karande *et al.* (2015) Tomar *et al.* (2016)
6.	Spikelet fertility (%)	High PCV,GCV	Bisne *et al.* (2009) Shrivastava *et al.* (2015)
		Low PCV,GCV	Sathya and Jebaraj (2013) Bhati *et al.* (2015) Karande *et al.* (2015)
7.	Test weight (g)	High PCV, GCV	Gangashetty *et al.* (2013) Bhati *et al.* (2015) Nirmaladevi *et al.* (2015) Islam *et al.* (2016)
		Moderate PCV, GCV	Basavaraja *et al* .(2013) Dhurai *et al.* (2013) Bornare *et al.* (2014) Allam *et al.* (2015) Harsh *et al.* (2015) Kishore *et al.* (2015) Lingaiah (2015) Mahendra *et al.* (2015) Srihima *et al.* (2015) Gampala *et al.* (2015) Shrivastava *et al.* (2015)

Table 2.1 (Cont.).

			Nirmaladevi *et al.* (2015) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016) Tomar *et al.* (2016)
		Moderate PCV Low GCV	Karande *et al.* (2015) Onyia *et al.* (2017)
		Low PCV, GCV	Paikhomba *et al.* (2014) Nikhil *et al.* (2014) Islam *et al.* (2015)
		Moderate GCV, High PCV	Sameera *et al.* (2015) Tripathi *et al.* (2017)
8	Grain yield per plant (g)	High PCV, GCV	Bekele *et al.* (2013) Idris and Mohamed (2013) Gangashetty *et al.* (2013) Tushara *et al.* (2013) Dhurai *et al.* (2013) Bhati *et al.* (2015) Allam *et al.* (2015) Harsh *et al.* (2015) Kishore *et al.* (2015) Lingaiah (2015) Shrivastava *et al.* (2015) Sindhumole *et al.* (2015) Tomar *et al.* (2016) Rukmini Devi *et al.* (2016)
		Moderate GCV, PCV	Saidaiah *et al.* (2010b) Paikhomba *et al.* (2014) Sameera *et al.* (2015) Sindhumole *et al.* (2015) Pavan Shankar *et al.* (2016)
		High PCV Moderate GCV	Mahendra *et al.* (2015) Karande *et al.* (2015) Islam *et al.* (2016)

Table 2.1 (Cont.).

		Moderate PCV, GCV	Sameera *et al.* (2015)
		Low PCV, GCV	Sathya and Jebaraj (2013)
9	Hulling (%)	Moderate PCV, GCV	Asish Binodh *et al.* (2007)
		Low PCV, GCV	Mishra and Pravin (2004) Satish Chandra *et al.* (2009) Parvathi *et al.* (2011) Nirmaladevi *et al.* (2015) Sameera *et al.* (2015) Rukmini Devi *et al.* (2016)
		Low GCV, Moderate PCV	Shrivastava *et al.* (2015)
10	Milling (%)	High GCV, PCV	Chaudhary *et al.* (2004)
		Moderate PCV, GCV	Asish Binodh *et al.* (2007)
		Moderate PCV, Low GCV	Mishra and Pravin (2004) Shrivastava *et al.* (2015)
		Low GCV, PCV	Nagajyothi (2001) Krishna Naik (2004) Satish Chandra *et al.* (2009) Parvathi *et al.* (2011) Nirmaladevi *et al.* (2015) Sameera *et al.* (2015) Rukmini Devi *et al.* (2016)
11	Head rice recovery (%)	High GCV, PCV	Chaudhary *et al.* (2004) Mishra and Pravin (2004) Singh and Singh (2005) Asish Binodh *et al.* (2007) Nirmaladevi *et al.* (2015)
		Moderate PCV, GCV	Shrivastava *et al.* (2015) Rukmini Devi *et al.* (2016)

Table 2.1 (Cont.).

		Low GCV, PCV	Patil *et al.* (2003) Satish Chandra *et al.* (2009) Sameera *et al.* (2015)
12	Kernel length (mm)	Moderate PCV, GCV	Asish Binodh *et al.* (2007) Satish Chandra *et al.* (2009) Bhati *et al.* (2015) Nirmaladevi *et al.* (2015)
		Low PCV, GCV	Krishna *et al.* (2008) Pratap *et al.* (2012) Dhurai *et al.* (2013) Sameera *et al.* (2015) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016)
		Low PCV, Moderate GCV	Shrivastava *et al.* (2015)
		High GCV, PCV	Chaudhary *et al.* (2004)
13	Kernel breadth (mm)	Moderate PCV, GCV	Asish Binodh *et al.* (2007) Sameera *et al.* (2015) Nirmaladevi *et al.* (2015)
		Low PCV, GCV	Pratap *et al.* (2012) Dhurai *et al.* (2013) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016)
		Moderate PCV, Low GCV	Bhati *et al.* (2015) Shrivastava *et al.* (2015)
14	Kernel L/B ratio	High PCV, GCV	Chaudhary *et al.* (2004)
		Moderate PCV, GCV	Pratap *et al.* (2012) Dhurai *et al.* (2013) Bhati *et al.* (2015) Shrivastava *et al.* (2015) Nirmaladevi *et al.* (2015) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016)

Table 2.1 (Cont.).

		Low GCV, Moderate PCV	Sameera *et al.* (2015)
		Low PCV, GCV	Krishna Veni *et al.* (2006)
15	Kernel elongation ratio	High GCV, PCV	Chaudhary *et al.* (2004)
		Moderate PCV, GCV	Asish Binodh *et al* .(2007) Satish Chandra *et al.* (2009) Rajeswari *et al.* (2010) Umadevi *et al.* (2010) Dhurai *et al.* (2013) Nirmaladevi *et al.* (2015)
		Low PCV, GCV	Sameera *et al.* (2015) Rukmini Devi *et al.* (2016)
16	Volume expansion ratio	Moderate PCV, low GCV	Rukmini Devi *et al.* (2016)
		Moderate PCV, GCV	Sameera *et al.* (2015)
		Low PCV, Low GCV	Nirmaladevi *et al.* (2015)
17	Leaf area index	High GCV, PCV	Niranjan Murthy *et al.* (1999) Surender Raju (2002)
		Low GCV, PCV	Sathish Chandra *et al.* (2004)
18	Harvest index	Moderate GCV, High PCV	Dhurai *et al.* (2013) Islam *et al.*(2016)
		Hihg GCV, PCV	Bisne *et al.* (2009) Shrivastava *et al.* (2015)
		Moderate GCV, PCV	Sathya and Jebaraj (2013) Sameera *et al.* (2015) Muthuramu and Sakthivel (2016) Tomar *et al.* (2016)

Table 2.2 Review of literature on heritability and genetic advance as per cent of mean in rice (*Oryza sativa* L.)

S. No.	Character	Heritability	Genetic advance as % of mean	Reference
1.	Days to 50% flowering	High	Moderate	Parvathi *et al.* (2011) Gangashetty *et al.* (2013) Dhurai *et al.* (2013) Paikhomba *et al.* (2014) Nikhil *et al.* (2014) Rajkumar and Ibrahim (2015) Srihima *et al.* (2015) Harsh *et al.* (2015) Sindhumole *et al.* (2015) Islam *et al.* (2016) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016) Tripathi *et al.* (2017) Onyia *et al.* (2017)
		High	Low	Mahendra *et al.* (2015) Nikhil *et al.* (2014) Karande *et al.* (2015) Tomar *et al.* (2016)
		High	High	Dhanwani *et al.* (2013) Vanisree *et al.* (2013) Shobharani *et al.* (2013) Neha *et al.* (2014) Bhati *et al.* (2015) Kishore *et al.* (2015) Allam *et al.* (2015) Srihima *et al.* (2015)

Table 2.2 (Cont.).

				Sameera *et al.* (2015) Ameenal *et al.* (2016) Muthuramu and Sakthivel (2016)
		Low	Low	Khare *et al.* (2014)
2.	Plant height (cm)	High	Moderate	Sathya and Jebaraj (2013) Paikhomba *et al.* (2014) Nikhil *et al.* (2014) Rajkumar and Ibrahim (2015) Harsh *et al.* (2015) Kishore *et al.* (2015) Srihima *et al.* (2015) Rajkumar and Ibrahim (2015) Karande *et al.* (2015) Islam *et al.* (2016) Muthuramu and Sakthivel (2016) Tomar *et al.* (2016) Onyia *et al.* (2017)
		High	High	Kumar and Saravanan (2012) Tushara *et al.* (2013) Vanisree *et al.* (2013) Dhurai *et al.* (2013) Bornare *et al.* (2014) Bhati *et al.* (2015) Harsh *et al.* (2015) Lingaiah (2015) Sindhumole *et al.* (2015) Ameenal *et al.* (2016) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016)
		Moderate	Low	Sathya and Jebaraj (2013)

Table 2.2 (Cont.).

		High	Low	Singh *et al.* (2011) Verma *et al.* (2011)
		Low	High	Krishna *et al.* (2008)
		Low	Low	Manna *et al.* (2006)
3.	Number of panicles per plant	High	High	Parvathi *et al.* (2011) Gangashetty *et al.* (2013) Tushara *et al.* (2013) Sathya and Jebaraj (2013) Dhurai *et al.* (2013) Bhati *et al.* (2015) Allam *et al.* (2015) Sameera *et al.* (2015) Ameenal *et al.* (2016) Tomar *et al.* (2016) Rukmini Devi *et al.* (2016) Pavan Shankar *et al.* (2016)
		Moderate	Moderate	Bharadwaj *et al.* (2007) Islam *et al.* (2016)
		High	High to moderate	Kole *et al.* (2008) Bornare *et al.* (2014)
		High	Low	Harsh *et al.* (2015) Onyia *et al.* (2017)
		Low	High	Mishra and Pravin (2004) Krishna *et al.* (2008)
		Moderate	High	Prasad *et al.* (2009) Paikhomba *et al.* (2014)
		Low	Low	Lingaiah (2015) Muthuramu and Sakthivel (2016) Tripathi *et al.* (2017)

Table 2.2 (Cont.).

4.	Panicle length (cm)	High	High	Gangashetty *et al.* (2013) Dhanwani *et al.* (2013) Vanisree *et al.* (2013) Dhurai *et al.* (2014) Allam *et al.* (2015) Sameera *et al.* (2015) Ameenal *et al.* (2016)
		High	Moderate	Saidaiah *et al.* (2010b) Shobharani *et al.* (2013) Nikhil *et al.* (2014) Bhati *et al.* (2015) Lingaiah *et al.* (2015) Rajkumar and Ibrahim (2015) Tomar *et al.* (2016) Rukmini Devi *et al.* (2016) Pavan Shankar *et al.* (2016)
		High	Low	Shobharani *et al.* (2013) Sindhumole *et al.* (2015) Kishore *et al.* (2015) Mahendra *et al.* (2015) Harsh *et al.* (2015) Srihima *et al.* (2015) Islam *et al.* (2016)
		Low	High	Mishra and Pravin (2004)
		Low	Moderate	Manna *et al.* (2006)
		Moderate	Low	Sathya and Jebaraj (2013) Paikhomba *et al.* (2014) Karande *et al.* (2015) Tripathi *et al.* (2017)
		Moderate	High	Patil *et al.* (2003)
		Moderate	Moderate	Parvathi *et al.* (2011)
		Low	Low	Krishna *et al.* (2008) Chandra *et al.* (2009)

Table 2.2 (Cont.).

5.	Number of grains per panicle	High	High	Bhati *et al.* (2015) Allam *et al.* (2015) Sameera *et al.* (2015) Ameenal *et al.* (2016) Tomar *et al.* (2016) Onyia *et al.* (2017)
		Moderate	High	Kishore *et al.* (2015)
		High	High	Dhurai *et al.* (2013) Karande *et al.* (2015)
6.	Spikelet fertility (%)	Moderate	Low	Singh *et al.* (2005) Karande *et al.* (2015)
		High	Low	Singh *et al.* (2011) Verma *et al.* (2011) Bhati *et al.* (2015) Harsh *et al.* (2015) Mahendra *et al.* (2015) Onyia *et al.* (2017)
		High	Moderate	Sathya and Jebaraj (2013) Nikhil *et al.* (2014) Karande *et al.* (2015)
		Low	High	Krishna *et al.* (2008) Paikhomba *et al.* (2014)
		Moderate	Moderate	Kuchanur *et al.* (2009)
7.	Test weight (g)	High	High	Dhurai *et al.* (2013) Tushara *et al.* (2013) Bornare *et al.* (2014) Bhati *et al.* (2015) Kishore *et al.* (2015) Lingaiah (2015) Sameera *et al.* (2015) Allam *et al.* (2015) Srihima *et al.* (2015) Ameenal *et al.* (2016) Islam *et al.* (2016)

Table 2.2 (Cont.).

				Pavan Shankar *et al.* (2016) Tomar *et al.* (2016) Rukmini Devi *et al.* (2016) Tripathi *et al.* (2017)
		High	Low	Singh *et al.* (2011) Verma *et al.* (2011) Harsh *et al.* (2015) Mahendra *et al.* (2015)
		High	Moderate	Nikhil *et al.* (2014)
		Low	High	Paikhomba *et al.* (2014)
		Moderate	Low	Singh *et al.* (2005)
8.	Grain yield per plant (g)	High	High	Dhurai *et al.* (2013) Bhati *et al* .(2015) Karande *et al.* (2015) Sameera *et al.* (2015) Tomar *et al.* (2016) Rukmini Devi *et al.* (2016)
		Low	Moderate	Islam *et al.* (2016)
		High	Moderate	Sathya and Jebaraj (2013) Pavan Shankar *et al.* (2016)
9	Hulling (%)	High	High	Asish Binodh *et al.* (2007)
		High	Low	Nirmaladevi *et al.* (2015) Sameera *et al.* (2015)
		Low	Moderate	Mishra and Pravin (2004)
		Low	Low	Nagajyothi (2001) Rukmini Devi *et al.* (2016)
10	Milling (%)	High	High	Asish Binodh *et al.* (2007) Uma Devi *et al.* (2010) Nirmaladevi *et al.* (2015)
		High	Moderate	Parvathi *et al.* (2011) Rukmini Devi *et al.* (2016)
		High	Low	Krishna Naik (2004)

Table 2.2 (Cont.).

		Low	Moderate	Mishra and Pravin (2004)
		Moderate	Low	Nagajyothi (2001) Sameera *et al.* (2015)
11	Head rice recovery (%)	High	High	Singh and Singh (2005) Asish Binodh *et al.* (2007) Uma Devi *et al.* (2010) Nirmaladevi *et al.* (2015) Rukmini Devi *et al.* (2016)
		Low	Moderate	Patil *et al.* (2003) Mishra and Pravin (2004)
		High	Moderate	Parvathi *et al.* (2011)
		High	Low	Sameera *et al.* (2015)
12	Kernel length (mm)	High	High	Kumar *et al.* (2006) Bhati *et al.* (2015)
		High	Moderate	Dhurai *et al.* (2013) Sameera *et al.* (2015) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016)
		High	Low	Nirmaladevi *et al.* (2015)
		Moderate	Low	Singh *et al.* (2005)
13	Kernel breadth (mm)	High	High	Sameera *et al.* (2015)
		High	Low	Nirmaladevi *et al.* (2015)
		High	High to Moderate	Hossain and Hossain (2001)
		High	Moderate	Dhurai *et al.* (2013) Bhati *et al.* (2015) Pavan Shankar *et al.* (2016) Rukmini Devi *et al.* (2016)
		Moderate	Low	Singh *et al.* (2005)
14	Kernel L/B ratio	High	High	Dhurai *et al.* (2013) Bhati *et al.* (2015) Pavan Shankar *et al.* (2016)

Table 2.2 (Cont.).

				Rukmini Devi *et al.* (2016)
		High	Low	Singh *et al.* (2011) Verma *et al.* (2011) Mohan Lal and Chauan (2011) Nirmaladevi *et al.* (2015)
		Moderate	Moderate	Sameera *et al.* (2015)
15	Kernal elongation ratio	High	Low	Madhavilatha *et al.* (2005)
		High	High	Dhurai *et al.* (2013)
		Moderate	Low	Sameera *et al.* (2015) Rukmini Devi *et al.* (2016)
		High	Moderate	Nirmaladevi *et al.* (2015)
16	Volume expansion ratio	Low	Low	Rukmini Devi *et al.* (2016)
		Moderate	High	Sameera *et al.* (2015)
		High	Low	Nirmaladevi *et al.* (2015)
17	Leaf area index	High	High	Niranjan Murthy *et al.* (1999) Surender Raju (2002)
		High	Moderate	Satya and Jebaraj (2013)
18	Harvest index	Moderate	Moderate	Islam *et al.* (2016) Muthuramu and Sakthivel (2016)
		High	High	Sathya and Jebaraj (2013) Dhurai *et al.* (2013) Sameera *et al.* (2015) Tomar *et al.* (2016)

Akram *et al.* (2001) conducted variability studies on fifty seven diverse genotypes of rice for seed and seedling vigour traits such as germination rate, root length, shoot length and dry weight of seedlings, alpha amylase activity, dehydrogenase activity and 100 seed weight. All the traits were found significant. The genotypes IR50, IR25924-92-1-2, IR31779-19-3-3-2-3, TNAU {AD} 103 and PUSA 510 proved superior in respect of most of the traits studied.

Nirala Ramchiary (2001) assessed genetic divergence among 132 indigenous rice germplasm collection of Western Ghats of Karnataka which revealed high genotypic coefficient of variation, high heritability as well as expected genetic advance for flag leaf, flag leaf length, plant height, number of panicles per plant, grain length, grain breadth, length breadth ratio, 1000-grain weight, root length, dry weight, grain yield per plant and harvest index.

Sunday *et al.* (2007) conducted genetic variability studies for eleven seed vigour traits and seed yield in 24 genotypes of West African rice (*Oryza sativa* L.). Highly significant differences were observed among the genotypes for the seed vigour traits and seed yield per plant in both seasons. GCV, h^2b and GA (as per cent of the mean) as the best estimators of the amount of advance expected from selection. Seedling vigour index (53.02), speed of germination index (0.99) and energy of germination (0.69) gave the highest values in the late season while seedling vigour index (35.75), speed of emergence (0.99) and energy of germination (0.61) gave the highest values in the early season. This shows that a satisfactory selection programme for improvement of these seed quality characters is possible in West African rice at each specific season.

Khriedinuo *et al.* (2011) reported that higher heritability estimates for all the yield and other quality traits except for flag leaf angle. GCV was high for flag leaf area, plant height, number of tillers per plant, number of ear bearing tillers, number of filled grains per panicle, panicle weight, root length, straw weight and grain yield.

Hosseini *et al.* (2012) estimated heritability and genetic advance in 18 diverse rice genotypes under salt stress conditions. Where high heritability estimates associated with high genetic advance were obtained for plant height, root dry weight and shoot length characters and concluded that selection for these characters would be more effective because it has high heritability and genetic advance.

Rajendra Krishna *et al.* (2015) conducted genetic variability studies in F_3 population derived from a cross between BPT5204 / IR88633-1-136-B2 for seedling vigour traits *i.e.* plant height, biomass, vigour index, leaf number and tiller number. Among them plant height, biomass and vigour index shows high heritability and genetic advance at 15 and 30 days stages of crop.

Lakshmi *et al*. (2016) conducted genetic variability studies for 34 genotypes on anaerobic germination and seedling vigour traits such as germination % on 10^{th} day, germination % on 14^{th} day, seedling shoot length on 10^{th} day, seedling shoot length on 14^{th} day, seedling root length on 10^{th} day, seedling root length on 14^{th} day, seedling fresh weight on 14^{th} day seedling dry weight, anaerobic germination and plant survival percent, reported that lower estimates of PCV and GCV were observed for seedling root length on 10^{th} day and 14^{th} day (cm) and seedling dry weight (mg). High heritability coupled with high genetic advance on percent mean was observed for germination % on 10^{th} day, germination % on 14^{th} day, seedling shoot length on 10^{th} day, seedling shoot length on 14^{th} day, seedling fresh weight on 14^{th} day, seedling dry weight, anaerobic germination and plant survival percent.

2.3 GENETIC DIVERGENCE

Knowledge on the nature and magnitude of genetic variability present in the plant material plays an important role in planning a sound breeding programme. It has been well established that genetically diverse parents are likely to yield desirable gene recombinants or to produce high heterotic effect. Information on the nature and degree of genetic divergence would help the plant breeder in choosing the right parents for breeding programme (Vivekanandan and Subramanian 1993). For this, the presence of sufficient amount of genetic variability and diversity in the base population is essential. Mahalanobis's D^2 statistic has proved to be a powerful tool for quantifying genetic divergence in a given population.

Some of the available literature on genetic divergence in rice is reviewed hereunder

Genetic divergence was worked out by Saidaiah *et al.* (2012) in 86 rice germplasm lines. Based on 13 important yield attributes, the genotypes were grouped into ten clusters. Characters such as plant height, 1000 seed weight, days to 50% flowering and number of filled grains per panicle contributed more towards total divergence.

Chanbeni *et al.* (2012) estimated nature and magnitude of genetic divergence among 70 rice genotypes using Mahalanobis D^2 statistic by considering 13 quantitative characters. The results revealed considerable amount of diversity in the material and the genotypes were grouped into nine clusters. Traits like spikelets per panicle, plant height and biological yield were the major contributors to total genetic divergence.

Chakma *et al.* (2012) determined genetic diversity among 39 rice genotypes collected from Bangladesh Rice Research Institute, Lal Teer Seed Ltd. and Chittagong Hill Tracts. The genotypes were grouped into six clusters based on Mahalanobis's D^2 statistic. Number of unfilled grains per panicle, 1000 grain weight and grain yield per plant showed maximum contribution towards total genetic divergence.

Chamundeswari *et al.* (2012) studied genetic diversity among 64 rice germplasm lines using D^2 technique. Based on the genetic distance all the genotypes were grouped into 8 clusters. The trait, days to 50% flowering contributed maximum genetic divergence followed by iron content, grain yield per plant, gel consistency and test weight.

Genetic divergence of 52 traditional lowland rice genotypes from five states of North Eastern Region of India was investigated by Singh *et al.* (2013) using Mahalanobis D^2 statistic. Based on 15 agro-morphological characters, these genotypes were grouped into six clusters. Geographical origin was not found to be a good parameter of genetic divergence. Plant height followed by leaf angle and leaf area, highly contributed (32.43%) to the formation of clusters.

Chakaravorthy and Ghosh (2013) assessed genetic diversity among 51 landraces of rice genotypes using Mahalanobis's D^2 analysis. The 51 rice genotypes were grouped into 11 clusters. Cluster II was found to be the largest comprising 16 genotypes followed by cluster III having 8 genotypes and cluster I included 7 genotypes. The pattern of distribution of genotypes from different ecogeographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters *viz.*, culm diameter, culm length and grain length contributed maximum towards genetic divergence among the genotypes.

Kar *et al.* (2013) studied 65 indigenous aromatic rice genotypes and the genotypes were grouped into thirteen clusters. Based on clustering pattern, the maximum genetic distance among the genotypes existed between the clusters IV, V and XI. The clusters, V and X, were ascertained outstanding on the basis of higher cluster means for most of the component characters.

Girijarani *et al.* (2013) studied 64 rice genotypes under submergence conditions to assess genetic diversity. The genotypes were grouped into eight clusters. Maximum contributions towards total divergence was observed from traits *viz.*, test

weight, relative shoot elongation, grain yield per plant and days to 50% flowering indicating importance of these traits in breeding of rice genotypes for submergence tolerance.

Diversity analysis of 60 rice genotypes was conducted by Patil *et al.* (2013) using D^2 technique. The genotypes were grouped into six clusters based on genetic distance values of yield attributes. Days to 50% flowering had maximum contribution towards total divergence.

Kumar *et al.* (2013) assessed genetic divergence of 62 genotypes and grouped the genotypes into 9 clusters. Maximum contribution towards expression of genetic divergence was exhibited by days to 50 % flowering followed by days to maturity.

Manohara and Singh (2013) studied genetic diversity among the 24 genotypes using D^2 analysis and total 6 clusters were obtained. Days to 50 % flowering followed by 1000 grain weight contributed maximum towards total divergence.

According to Tushara *et al.* (2013), 19 medium duration rice genotypes were grouped into five clusters using D^2 analysis. Protein percentage showed maximum contribution towards total divergence.

Karuppaiyan *et al.* (2013) carried out genetic divergence studies using Mahalanobis D^2 statistics on the basis of 50% flowering, days to maturity, plant height, tiller number, productive tillers, panicle length, number of grains panicle^{-1}, grain length, grain breadth, length / breadth ratio and yield per hectare. The 27 genotypes were grouped into 4 clusters. Yield ha^{-1} (20.80 %) contributed maximum towards divergence followed by plant height (16.81 %), grain breadth (16.52 %) and grain length (15.10%).

Doddabhimappa *et al.* (2014) studied genetic diversity of 208 genotypes and they were grouped into 14 different clusters using Mahalanobis D^2 statistic. The maximum intercluster distance was recorded between clusters X and XI and the maximum intra-cluster distance was found in cluster IX followed by X. The characters like spikelets fertility, number of filled grains per panicle and 100 grain weight contributed maximum towards genetic diversity.

Haque *et al.* (2014) studied Seventy six rice genotypes, landraces and popular varieties consisting of both indigenous and exotic collection for yield and yield related traits. Based on D^2 analysis, the genotypes were grouped into eight clusters.

Maximum numbers of genotypes (35 genotypes) were grouped in cluster I. The maximum inter cluster distance was observed between cluster VI and VII (35.02) followed by clusters III and VII (34.68) and clusters I and VIII possessing wider genetic diversity among the genotypes between these groups. The maximum intra cluster distance was observed in cluster III (6.46) followed by cluster IV (6.32). Among the twelve traits studied, kernel length contributed maximum divergence (34.32%) followed by plot yield (21.02%). Hence, the traits viz., sterility, plot yield, kernel length, kernel breadth, 1000 grain weight contributed 71.52 per cent towards total divergence.

Dash *et al.* (2015) studied genetic diversity in fourty two promising NPT selections along with 6 indica, 4 tropical japonica, 3 temperate japonica and 3 irrigated clusters and grouped them into eight clusters using Mahalanobis D^2 statistic. The clustering pattern indicated that the NPT selections had clustered differently in comparison to the tropical japonicas.

Wijayawardhana *et al.* (2015) evaluated cluster analysis for 16 rice accessions, representing both traditional and improved varieties using 12 vegetative traits. All rice *accessions* were grouped into 3 clusters at 0.5 minimum distances between clusters. Numbers of rice accessions in these 3 clusters were 4, 2 and 10, respectively. Cluster I and II represented the rice accessions of traditional varieties and cluster III represented the rice accessions of new improved variety.

Khokhar and Sarial (2016) studied 25 rice genotypes and grouped them into 6 clusters on the basis of grain yield, days to flowering, days to maturity, plant height, effective tillers/ plant, percent filled spikelets, test weight, biological yield/plant, harvest index, hulling per cent, milling per cent, and head rice recovery using Mahalanobis D^2 statistic.

Bharathi *et al.* (2016) studied genetic divergence among 32 rice (*Oryza sativa* L.) genotypes using D^2 technique for ten characters. The 32 genotypes were grouped into 9 clusters containing 1 to 12 genotypes. Cluster I was the largest with 12 genotypes and cluster III, V, VI, VII and VIII were lowest with one genotype each. In this study filled grains per panicle followed by ear bearing tillers per panicle and days to 50% flowering contributed maximum towards the divergence. The inter-cluster distance was maximum between clusters V and IX and clusters V and VII.

Tripathi *et al.* (2017) studied genetic diversity for 32 genotypes under direct seeded conditions and grouped the genotypes into 7 clusters on the basis of days to 50% flowering, panicle length, tiller no per plant, filled grain per panicle, 1000 grain weight, yield/ ha (kg/ha**)** using Mahalanobis D^2 statistic. Cluster II had maximum number (16) of genotypes. Maximum inter cluster distance was found between clusters IV and VII (984.82). However, intra cluster distance was maximum in cluster III (363.58).

2.4 COMBINING ABILITY FOR ANAEROBIC GERMINATION AND SEEDLING VIGOUR RELATED TRAITS

The ability of a parent to transmit desirable performance to its hybrid progeny is called combining ability. Combining ability helps in the identification of parents with good general and specific combining ability and also to determine the gene action. The concept of combining ability as a measure of gene action was proposed by Sprague and Tatum (1942). They defined general combining ability as an average performance of a strain in a series of hybrid combinations, whereas specific combining ability is the average performance of a specific cross combination expressed as deviation from the population mean. They further reported that general combining ability was primarily due to additive gene effect, while specific combining ability was due to non-additive gene effect.

Seedling vigour is the ability, which enables a seedling upon germination to grow rapidly and well. It is related to all phases of seedling development from seed germination through to plant establishment. Seedling vigour plays a critical role under direct seeded cultivation of rice. It helps in better plant establishment and successful competition with weeds. Seedling vigour is the ability of plant to emerge rapidly from soil or water (Heydecker, 1960). Seed and seedling vigour are genetically controlled and modified by the environment (Perry, 1973) and it is possible to incorporate this trait in high yielding varieties (Seshu and Krishnasamy 1987).

Cultivars having high seedling vigour are desirable for crop establishment in the direct-seeded rice system and in temperate rice-growing areas (Redona and Mackill, 1996b). Under direct seeded rice culture, varieties with high seedling vigour are required for better competitive ability against weeds. Seedling vigour is a trait that expresses itself as an ability of seedlings to rapidly elongate after germination and emerge for escaping and surviving submergence stress (Vu *et al.*, 2010).

Seed vigour is highly complex phenomenon, it is not a single measurable property like germination, but a concept for describing several characteristics associated with various aspects of performance of the seed (Perry, 1981) both in field (Perry, 1978) and storage (Hampton and Coolbear, 1990).

Anaerobic germination

Submergence tolerance is defined as the ability of a rice plant to survive and continue growing after being completely submerged in water for several days. Rice plants are less tolerant to submergence at the early growth stages (Adkin *et al.,* 1990). Submergence tolerance is a rare, genetically determined trait with relatively high heritability that is controlled by one or a few genes with major effects, and minor modifiers (Suprihatno and Coffman, 1981; Mohanty and Khush, 1985 and Haque *et al*., 1989).

Breeding for increased seed and seedling vigour as well as for enhanced tolerance of flooding or anaerobic conditions during germination has been previously attempted by several workers (Yamauchi *et al.,* 1993, Yamauchi and Winn 1996; Redona and Mackill 1996 and Biswas and Yamauchi 1997). However, progress over the years has been slowed by the limited knowledge on the genetics of the trait, the involvement of complex mechanisms, the lack of an effective screening method (Seshu *et al.,* 1988), lack of suitable donors with a high level of tolerance, limited knowledge on the genetics of tolerance, the involvement of several complex mechanisms (Seshu *et al.,* 1988), and complex genetic backgrounds and methods used for measurement (Jiang *et al.,* 2004).

The available literature on the above aspects in rice is reviewed hereunder:

Li and Rutger (1980) reported that under cool temperature (18^oC), shoot length of seedling grown for 14 days was regulated by additive and dominance effects in F_1 and F_2 generations.

Lee *et al.* (1986) reported that dry weight of 12 days old rice-seedling was under the control of additive and dominance effects, with additive effects being higher. High narrow sense heritability value of 65.24% was observed for this trait.

Li *et al.* (1990) observed heterosis for root length in a study involving parents and F_1 hybrids of five crosses of *indica* type. All the F_1 s showed better root length compared to their respective parents.

Jiakui *et al.* (1996) studied heterosis, genetic variance and heritability of root characters and observed significant heterosis for these characters and inferred that they are mainly controlled by non-additive gene effects.

Akram *et al.* (2007) carried out studies on combining ability in 7x7 diallel cross for rate of germination index, seedling root and shoot length and seedling dry weight. The study reported, IR 21820-154-2-2-3 and IR 9764-45-2-2 were best general combiners for seedling root length. However dominant gene effects seem to be more important for seedling root length as supported by low heritability and negative value of dominance to heritability.

Manigbas *et al.* (2008) identified PR33176-1-3 was tolerant to continuous submergence for 14 days in puddled soil and also noticed NSIC Rc146, PR32220-16-1-B-1-2, PR32749-10-1-B-B and PR32750-2-9-2 were intermediate to anaerobic germination, where PR33176-1-3 and PR30536-B-48-1 were having better seedling vigour than the check varieties which are known with good seedling vigour in direct wet seeded rice culture.

Hendawy *et al.* (2011) characterized the response of 56 diverse contrasting rice genotypes to submergence and their recovery following de-submergence. Among these genotypes, nine lines had been developed for anaerobic germination and submergence tolerance (AG + *Sub1*) by IRRI. Further, the study classified tested genotypes into three clusters based on shoot elongation rate of submerged to non-submerged treatments (ratio) during submergence period and chlorophyll contents during recovery period using Ward's method.

Sathya and Jebaraj (2013) reported the traits *viz.*, productive tillers per plant, filled grains per panicle, dry root weight, dry shoot weight, root: shoot ratio and root length, had high heritability accompanied with high genetic advance indicating lesser environmental influence and were under the control of additive gene effect.

Septiningsih *et al.* (2013) conducted QTL study using population derived from a cross between IR 42, a susceptible variety, and Ma-Zhan Red, a tolerant landrace from China. They genotyped 175 F2:3 families with 118 SSR markers and identified

six significant QTLs on chromosomes 2, 5, 6, and 7. The largest QTL on chromosome 7, having a LOD score of 14.5 and an R_2 of 31.7 %, was confirmed using a BC_2F_3 population.

Kretzschmar *et al.* (2015) identified a trehalose-6-phosphate phosphatase gene, OsTPP7, as the genetic determinant in qAG-9-2, a major quantitative trait locus (QTL) for anaerobic germination tolerance.

Toledo *et al.* (2015) improved popular cultivars through introgression of SUB1 an FR13A-derived QTL conferring submergence tolerance at the vegetative stage, using marker-assisted backcrossing (MABC). Ciherang-Sub1, one of these improved near isogenic lines (NILs), showed significantly higher tolerance compared to the original cultivar while retaining its desirable agronomic qualities. They transferred *AG1,* derived from Khao Hlan on to Ciherang-Sub1 via MABC, using IR64-AG1, a closely-related donor.

Vishnuvardhan Reddy *et al.* (2015) screened 48 rice genotypes for anaerobic germination. They identified nine resistant genotypes for 14 days of anaerobic germination (75-95%). Among them, three genotypes Isukaravalu, IR 85956/23-1-2, MTU 1140 co segregated with markers RM 341 to qAG2 on chromosome 2, RM 206 to qAG11 on chromosome 11 indicating presence of genes pertaining to anaerobic germination.

2.5 MOLECULAR CHARACTERIZATION

Molecular markers are being extensively used by plant breeders globally as an effective and appropriate tool for basic and applied studies addressing biological components in agricultural production systems (Jones *et al.*, 1997 and Mohan *et al.*, 1997). Molecular markers allow selection for the traits to be done on the basis of a simple laboratory tests on a small amount of plant tissue, rather than direct measurement of the character itself (Christopher *et al*. 2004).

There are various kinds of molecular markers available including Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLPs), Simple Sequence Repeats (SSRs) and Single Nucleotide Polymorphisms (SNPs). There are merits and

demerits of each type of marker depending on the specific objectives of particular study. Among the marker systems available SSRs have been proved to be more useful in marker assisted selection (Yang *et al*., 1996).

Breeding for better germination, greater seedling vigour and higher tolerance of water logging in rice has been attempted before but with limited success because genotypes with sufficient tolerance were not available. So to identify QTL's further for AG and SV traits, characterization of F_1s and their parents was done with established molecular markers.

The available literature on the above aspects in rice is reviewed hereunder:

Jiang *et al.* (2006) tested USSR5 (*japonica* type) x N22 (*indica* type) for low temperature germinability and anoxia germinability and detected 11 putative QTLs for low temperature germinability. Similarly, Han *et al.* (2006) identified QTLs for low temperature vigour of germination using $F_{2:3}$ population, which included 200 individuals and lines derived from a cross of *indica* and *japonica* Milyang 23/Jileng 1 and detected qLVG2 located in RM29-RM262 on chromosome 2, qLVG7-2 and qCIVG7-2 located in RM336-RM118 on chromosome 7 when the germination periods were 11, 14, and 17 days. qCIVG2 located in RM29-RM262 on chromosome 2 when the germination periods were 11 and 14 days.

Angaji (2008) screened BC_2F_2 population for anaerobic germination and constructed linkage map was constructed with 155 polymorphic SSR markers, resulting in a map of 1483.5 CM with a mean inter-marker distance of 9.6. Four putative QTLs were detected in mapping population, one each on chromosomes 1 (qAG-1), 2 (qAG-2-1), 11 (qAG-11), and 12 (qAG-12). The LOD value of these QTLs was ranged from 3.66 to 5.71 with phenotypic variance in the range of 12 to 29.24%.

Vasanth (2012) conducted an experiment to identity microsatellite markers linked to plant production and root traits under rainfed condition in rice genotypes using association mapping analysis. The study reported that eighty two SSR markers are associated with root traits *viz.*, maximum root length, root thickness, root dry weight and deep root dry weight. Among the markers, RM 316 (ch.9),RM 219 (ch.9),RM 29 (ch.9), RM 574 (ch.5), RM 540 (ch.6), RM 1287(ch.1), RM 318(ch.3), RM 8084(ch.1), RN 3131 (ch. 3), RM 5603 (ch.5), RM 36 (ch.3) and RM 439 (ch.9) showed highly significant association with several root traits under rainfed conditions.

Divya (2013) studied genetic diversity in Karnataka rice land races using SSR markers. A total of 11 microsatellite markers were used to assess the extent of genetic diversity across 26 genotypes and reported markers RM 166, RM 201, RM 234 and RM 302 association with root length.

Baltazar *et al.* (2014) screened $F_{2:3}$ mapping population to identify QTLs associated with tolerance for anaerobic germination. Based on phenotyping, selective genotyping was employed resulting in 234 polymorphic markers in the study. A major QTL for AG, qAG7, was detected on chromosome 7 with an LOD of 13.93 and 22.3 % of the phenotypic variance. A second QTL of smaller effect, qAG11, was also derived.

Girijarani *et al.* (2016) studied genetics of flash flood tolerance and anaerobic germination in MTU 1140, AC 37887, AC 39416 A and flash tolerance in MTU 1064 The study detected presence of sub1 A alleles conferring flash flood tolerance in AC 39416 A and rest of donors might have flash flood tolerance mechanism other than sub1A.Furthur the study also detected donor AC 39416 A co-segregated for alleles of anaerobic germination QTLS linked markers for qAG1-1, qAG3-1, qAG 7-2 and qAG 9-2 and no co-segregation for MTU 1140 indicating another locus might be responsible for anaerobic germination in this donor.

Chapter III

MATERIAL AND METHODS

The present investigation on **"**Genetic studies on anaerobic germination and seedling vigour traits in rice (*Oryza sativa* L.)" was taken up during *kharif* 2016 in field and *rabi* 2016-17 in Quality and Biotechnology Laboratory of Andhra Pradesh Rice Research Institute (APRRI) and Regional Agricultural Research Station (RARS), Maruteru, West Godavari district of Andhra Pradesh. Maruteru is located at 81.440 E longitude, 26.380 N latitude and 5 m above mean sea level. The soils are characterized by black alluvial clay soils, neutral to slightly alkaline in reaction with medium levels of phosphorus and potassium. The annual rainfall of the location is 1100 mm.

3.1 MATERIAL

The experimental material consisted of fifty genotypes obtained from Department of Genetics and Plant Breeding, APRRI & RARS, Maruteru, West Godavari district of Andhra Pradesh. The information on pedigree of the genotypes is given in Table 3.1. Data were recorded on seedling vigour traits, anaerobic germination, yield and its contributing traits, quality characters and direct seeded traits. The experimental material in *rabi* 2016-2017 was 12 crosses ($F_{1's}$) generated by mating 6 lines and 2 testers in Line x Tester (L x T) design and is given in the Table 3.1.1

3.2 METHODS

Experimental Details

The main field was laid out in a randomized block design with two replications in *Kharif* 2016. Each experimental unit consisted of a plot size of 6.4 m^2. All the genotypes were sown separately in each experimental unit having two replications under wet direct sowing conditions in rice through broadcasting method. The same set of genotypes were screened for anaerobic germination and seedling vigour traits. Based on anaerobic germination and seedling vigour data, 6 lines and 2

testers were selected and mated in L x T design. The 12 crosses along with parents were screened for anaerobic germination and seedling vigour traits under lab conditions in completely randomized design during *rabi* 2016-17. Molecular screening was also done for F_1's, along with their parents for anaerobic germination and seedling vigour related traits. The detailed experimental technique for the present investigation is furnished in Table 3.2 and Plate 3.1.Experimental lay out was presented in the Figure 3.1.

Table 3.1: List of rice genotypes included in the study along with their pedigree

S. No.	Designation	Cross combination/ Pedigree
1	Azucena	-
2	N 22	-
3	Mahsuri	Taichung 65 / Mueyana ebos 8012
4	IR-64	IR 5657-33-2-1/IR 2061-465-1-5-5
5	Naveen	Sattari/Jaya
6	Vandhana	C 22/ Kalakeri
7	Luna Suvarna	-
8	Savithri	Pankaj/ Jagannath
9	Varalu	Erramallelu/ CR 544-1-2
10	FL 478	Selection from pokkali
11	Varsha	-
12	MTU 1006	Pure line selection from oodasannalu
13	MTU 1140	MTU 5249 / PLA 85722
14	MTU 2067	Sowbhagya / ARC 5984
15	MTU 1184	PLA 1100 / BM 71
16	MTU 1224	BPT 5204 / NLR 34449 / BPT 5204
17	MTU 1226	MTU3626 / MTU1075
18	MTU 1229	MTU 7029 / NLR 3042
19	MTU 1194	MTU 1081 / MTU 1064
20	MTU 1156	MTU 1010 / MTU 1081
21	MTU 1187	MTU 1075 / IR 64
22	MTU 1112	MTU 1071 / MTU 1003
23	MTU 2716	Vijaya / Mahsuri
24	MTU 1153	MTU1010 / MTU1081

Table. 3.1 (Cont.).

25	MTU 1121	BPT 5204 / MTU IJ 8-24
26	MTU 7029	Vasishta / Mahsuri
27	MTU 1010	Krishnaveni / IR 64
28	MTU 3626	IR 8 / MTU 3
29	MTU 1001	Vajram / MTU 7014
30	MTU 1061	PLA 1100 / MTU 1010
31	MTU 1064	PLA 1100 / MTU 1010
32	MTU1075	MTU 2716 / MTU 1010
33	MTU 2077	Sowbhagya / ARC 5984
34	BPT 5204	GEB 24 / TN (1) / Mahsuri
35	BPT 3291	Sona / Mahsuri
36	Tellahamsa	HR 12 / TN-1
37	BPT 2270	BPT 5204 / CRMR 1523
38	BPT 2231	Surya / IR 64
39	MTU 1078	BPT 5204 / MTU II 104-3
40	MTU 1210	MTU 1001 / KMP 150
41	AC 39416A	Accessions from Cuttack
42	AC 39397	Accessions from Cuttack
43	Pooja	Vijaya / T 141
44	MTU 2344-25-1-3-1	MTU 3626 / MTU 1010
45	MTU 2344-25-2-2-2	BPT 3291 / MTU 1010
46	MTU 2328-37-1-2-1	MTU 3626 / MTU 1075
47	MTU 2344-25-2-2-1	MTU 3626 / MTU 1010
48	MTU 2360-18-2-2	MTU 1081 / IR 72
49	MTU 2360-78-1-1	MTU 1081 / IR 72
50	MTU 2366-97-1-1	MTU 1121 / MTU 1075

Table 3.1.1 Material used in Line × Tester analysis of rice (*Oryza sativa* L.)

Lines	**Testers**	**Crosses**
Azucena BPT 2270 MTU 1140 N 22 AC 39397 AC 39416A	MTU 1121	Azucena x MTU 1121
		BPT 2270 x MTU 1121
		MTU 1140 x MTU 1121
		N 22 x MTU 1121
		AC 39397 x MTU 1121
		AC 39416A x MTU 1121
	MTU 1010	Azucena x MTU 1010
		BPT 2270 x MTU 1010
		MTU 1140 x MTU 1010
		N 22 x MTU 1010
		AC 39397 x MTU 1010
		AC 39416A x MTU 1010

Table 3.2 Experimental details of evaluation of genotypes of rice (*Oryza sativa* L.)

Location	APRRI and RARS, Maruteru, Andhra Pradesh
Season	*Kharif*, 2016
Genotypes	50
Design	Randomized complete block design
Replications	2
Plot size	6.4m^2



Plate 3.1 Experimental field with label indicating all the details of the experimental site

3.2.1 EXPERIMENT I

Screening of lines for early seedling vigour and anaerobic germination

Techniques adopted

This experiment was taken up during *kharif*, August, 2016 at APRRI, RARS, Maruteru, West Godavari with an objective to classify the 50 rice genotypes for anaerobic germination and seedling vigour traits.

3.2.1.1 Seedling Vigour Related Traits

Laboratory assessed parameters of vigour

Seeds of all the genotypes were germinated in 3 replications separately using rolled paper towels at ambient temperature (20^0-30^0 C) in dark condition and kept in glass beakers with little amount of water for regular moisture for germination and growth.

Characters studied and recording of data

Data was recorded on the following characters.

3.2.1.2 Rate on germination (%)

The number of seedlings germinated was recorded on 10^{th} and 14^{th} day after soaking and expressed in per cent.

3.2.1.3 Root length at 10^{th} day (cm)

The root length of five seedlings per replication were measured from collar region down to the tip of longest root and average were expressed in centimeter.

3.2.1.4 Shoot length at 10^{th} day (cm)

Five normal seedlings were randomly selected from each replication of the standard germination test on 10 DAS and length of shoot was measured from collar region to the tip of top most leaf and average was expressed in centimeter.

3.2.1.5 Root length at 14^{th} day (cm)

The root length of five seedlings per replication were measured from collar region down to the tip of the longest root and average was expressed in centimeter.

3.2.1.6 Shoot length at 14^{th} day (cm)

Five normal seedlings were randomly selected from each replication of the standard germination test on 10 DAS and length of shoots average was measured from collar region to the tip of top most leaf and average were expressed in centimeter.

3.2.1.7 Seedling fresh weight at 14th day (mg)

Immediately after taking root length and shoot length of five seedlings per genotype at 14th day fresh weight was measured using weighing balance. The total weight of seedlings divided by number of seedlings taken for observation gave average weight of each seedling and this was expressed in milligrams per seedling.

3.2.1.8 Seedling dry weight (after 14th day) (mg)

Five seedlings per genotype were dried in hot air oven to constant weight and weighed. The total weight of seedlings divided by number of seedlings taken for observation gave average weight of each seedling and this was expressed in milligrams per seedling.

3.2.1.9 Seedling Vigour Index (SVI)

The seedling vigour indices were calculated using the following formula suggested by Kharb *et al*. (1994)

$$\text{Seedling vigour index-I:} \quad \frac{\text{Seedling germination per cent x seedling length (cm)}}{100}$$

$$\text{Seedling vigour Index-II:} \quad \frac{\text{Seedling germination per cent x seedling dry weight (mg)}}{100}$$

ANAEROBIC GERMINATION TEST

3.2.1.10 Phenotypic screening

Fifty rice genotypes were screened for anaerobic germination in wet season of 2016 at Andhra Pradesh Rice Research Institute and RARS, Maruteru to identify genotypes tolerant to anaerobic germination by sub surface seeding of pre germinated seeds (3 days after sowing) in puddled soil using pot trays of size 35 X 10 cm as per Manigbas *et al*., (2008). Pot trays were submerged up to 10 cm depth in concrete tank for 14 days, 21 days and plants survived 7 days after desubmergence was counted.

EXPERIMENT II: Evaluation of rice germplasm for yield, quality and direct seeding traits under wet direct sown conditions.

OBSERVATIONS RECORDED

Observations were recorded on five randomly selected plants for fifty genotypes per methodology given in SES, 2014 without border effect of each genotype in each replication and the average values were subjected for statistical analysis. Details of the different characters studied were as follows.

3.2.1.11 Plant height (cm) at maturity

The plant height was measured in centimeters from ground level to the tip of the panicle of the mother tiller excluding awns at the time of harvest.

3.2.1.12 Days to 50% flowering

The number of days taken from the day of sowing to opening of panicles in 50 per cent of the plants in a plot was taken as days to 50 per cent flowering.

3.2.1.13 Number of panicles per plant

Total number of panicles per plant were counted and recorded.

3.2.1.14 Panicle length (cm)

Length from the base of panicle (neck node) to the tip of last spikelet was taken as panicle length and is measured in centimeters.

3.2.1.15 Number of grains per panicle

Total number of filled grains and unfilled grains per each panicle was counted for five randomly selected panicles from each sample and the average was calculated.

3.2.1.16 Spikelet Fertility (%)

Spikelet fertility per cent was calculated as the ratio of fertile grains per panicle to the total number of grains in a panicle and was expressed as percentage.

3.2.1.17 Grain yield per plant (g)

Panicles from a square metre area was harvested at maturity, threshed, cleaned and dried to 12-14 percent moisture content and weight was recorded in grams. Then weight was divided by number of plants per square metre and weight was taken as grain yield per plant.

3.2.1.18 Test weight (g)

Thousand well filled grains were counted at random and weight was recorded in grams.

QUALITY CHARACTERS

3.2.1.19 Hulling (%)

Weigh desired amount of paddy minimum hundred grams and subject to dehusking in a standard dehusker .After cleaning, the dehusked kernels (brown rice) is weighed and percentage is determined by using the following formulae:

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

3.2.1.20 Milling (%)

The dehusked kernels were transferred to standard polisher.Time of the polisher is adjusted in such a way that percent polishing is 5% (approx) and then milling was carried out. The milled rice obtained was weighed in grams and the milling per cent was calculated by using the formulae:

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

3.2.1.21 Head rice recovery (%)

The polished kernels were separated into whole grains and broken grains in order to quantify the head rice recovery. Full grains and ¾ size grains were considered as whole grains and the percentage of the head rice recovery was calculated as per the following formula.

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

3.2.1.22 Kernel length (mm)

Ten grains of milled rice were selected by hand randomly and the length in millimetre was recorded using INDOSCAN software of Rice Analyzer version 4.0.

3.2.1.23 Kernel breadth (mm)

Ten grains of milled rice were selected by hand randomly and the breadth in millimetre was recorded using INDOSCAN software of Rice Analyzer version 4.0.

3.2.1.24 L/B ratio

The L/B ratio was recorded in millimetre using INDOSCAN software of Rice Analyzer version 4.0.

Based on the L/B ratio, the following categories were made for grain shape.

Grain type	**L/B Ratio**
Long slender (LS)	Length 6 mm and above, L/B ratio 3 and above.
Short slender (SS)	Length less than 6 mm, L/B ratio 3 and above.
Medium slender (MS)	Length less than 6 mm, L/B ratio 2.5 to 3.0.
Long bold (LB)	Length 6 mm and above, L/B ratio less than 3.0.
Short bold (SB)	Length less than 6 mm, L/B ratio less than 2.5.

3.2.1.25 Kernel Elongation Ratio and Volume Expansion Ratio

Take 5 gm of rice sample in a 50 ml graduated centrifuge tubes and add 15 ml water. After soaking 10 minutes take the volume of water raised as (Y-15). Cook for 20 minutes on a water bath. Put the cooked rice on a bloating paper. Select ten cooked grains and measure the length of the kernel using the millimeter scale for computing the kernel length after cooking (KLAC). After that for measuring volume expansion ratio take 50 ml water in 100ml measuring cylinder (X). Dip the cooked rice in measuring cylinder and note the raise in volume of water as (X-50). The following formulas are used to calculate the kernel elongation ratio and volume expansion ratio, expressed in percentage.

Initial	Y	Y-15	X	X-50
Water taken	Increase in vol. After adding 5gm rice	Increase in volume before cooking	Increase in volume of cooked rice in 50 ml water	Increase in volume after cooking

$$\text{Volume Expansion Ratio} = \frac{\text{Increase in volume after cooking (X-50)}}{\text{Increase in volume before cooking (Y-15)}} \times 100$$

$$\text{Kernel Elongation Ratio} = \frac{\text{Kernel length after cooking (mm)}}{\text{Kernel length before cooking (mm)}}$$

Direct Seeded Traits:

3.2.1.26 Leaf Area Index (LAI)

Leaf area index is the total leaf area present for unit land area .it is dimension less figure. It is calculated by using the formula

$$\text{LAI} = \frac{\text{Total leaf area}}{\text{Land area}}$$

3.2.1.27 Harvest Index (HI)

It was computed by dividing the grain yield with biological yield per plant.

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

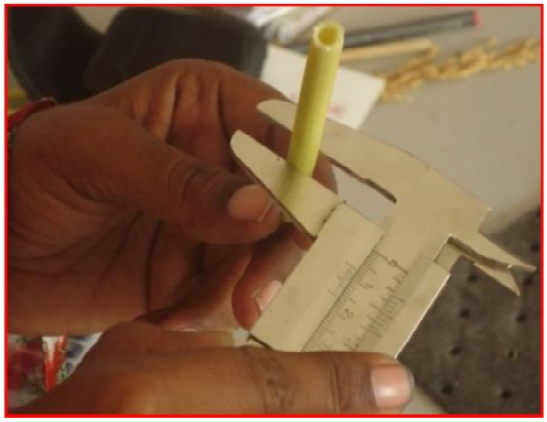
3.2.1.28 Culm Diameter (mm)

Stem lodging occurs due to breakage at lower internodes. Culm diameter was measured at 4^{th} inter node from the top at 20 days after heading using Vernier calipers and expressed in millimeters (mm).(Plate 2a).

3.2.1.29 Bending Strength (g stem^{-1})

It was measured by pushing hill at 20 cm above the ground at 45^0 angle using Prostrate tester (DIK 7401, Daiki Rika Kogyo Co. Lt d., Tokyo, Japan) and it was expressed in g/stem using the following formula as per Bhagat *et al*. (2011).(Plate 2b)

Bending strength = [(Test reading / 40) x (1000 / Number of tillers)]



a) Measurement of culm diameter at 4th internode using vernier calipers



b) Measurement of bending strength using diaki prostrate tester

Plate 3.2 Evaluation of elite rice lines for direct seeding traits during *kharif* 2016

3.3 DNA Extraction and Quantification

DNA was extracted from leaf tissue from all the genotypes using the modified Cetyl Tris Methyl Ammonium Bromide (CTAB) method of Dellaporta *et al.* (1983) as described under.

Reagents

CTAB Extraction Buffer, composition and concentration of CTAB extraction buffer is given in Table 3.3.

Table 3.3 Composition and concentrations of CTAB extraction buffer

S. No.	Components	Stock concentration	Working concentration	Volume for 500 ml
1	Tris HCL	1 M	200 mM	100 ml
2	EDTA	0.5 M	20 mM	20 ml
3	NACL	5 M	1.4 mM	140 ml
4	CTAB	2%	2 g	10 g
5	PVP	2%	2 g	10 g

- RNase-10 mg/ml
- Absolute ethanol
- Agarose gel (3%)
- 1X TAE Buffer which contains

  Tris acetate (pH 8.0)-40 mM

  Acetic acid-20 mM

  EDTA-1mM
- Ethidium bromide-10 mg/ml
- 10X DNA Tracking dye which contains

  Glycerol-5 ml

  10X TAE Buffer-1 ml

  Bromophenol blue-1 ml

  DDW-3 ml

Methodology

- Healthy leaf samples were collected in a sterile plastic bag or cover and were labeled with plant number. It was then sealed and placed on ice or freezer.
- The leaf tissue was cut into 0.5 cm long pieces.
- 400 µl DNA Extraction buffer was added using micropipette and the tissue was grinded until the buffer turns dark green.
- The dark green colour solution obtained was transferred into a micro centrifuge tube labelled with the plant number or variety name.
- To this tube 200 µl of Tris saturated phenol and 200 µl of chloroform: isoamyl alcohol mixture (24:1) was added and centrifuged at 10,000 rpm for about 10 min in a cooling centrifuge.

- The supernatant thus obtained was transferred into another labelled tube using a micropipette.
- To the aqueous supernatant, 10 µl of RNase was added and incubated at 37 ^{0}C for about 30-45 min.
- After incubation, 400 µl of chloroform: isoamyl alcohol mixture (24:1) was added and mixed gently and centrifuged at 10,000 rpm for 10 min.
- The top aqueous phase *i.e.,* supernatant was transferred to another labelled tube.
- To this solution, equal volume of chilled isopropanol was added, mixed well and centrifuged at 10,000 rpm.
- After centrifugation the supernatant was discarded and the DNA pellet settled at the bottom of the tube. 200 µl of 70% ethanol was added and centrifuged at 10,000 rpm for 10 min.
- The supernatant was discarded and the tubes containing DNA pellet were air dried at room temperature for about 1-2 hr till the smell of ethanol completely goes off.
- After the pellet was completely dried with no smell of alcohol the DNA pellet was suspended in 100-200 µl of $T_{10}E_1$ Buffer and stored at -20 ^{0}C.
- The DNA thus obtained was subjected to quantification.

3.3.1 Estimation of Quality and Quantity of DNA

The isolated genomic DNA was quantified by Nano Drop 8000 Spectrophotometer. This instrument provides the amount of concentration present in the genomic DNA as ng /µl. The instrument was initialized with 2.0 µl of Milli Q® water. Then, 2.0 µl of low salt Tris-EDTA buffer was used as blank. The unknown concentration DNA (2.0 µl) was added to the instrument and the quantity of DNA was measured. To ensure accuracy, the quantification of each unknown concentration sample was repeated twice. After quantification, the final concentration of DNA was adjusted to 30 ng /µl.

The ratio of OD 260 to OD 280 provided information on the purity of the DNA

1) If the ratio is 1.8 to 2.0 the sample of DNA is relatively pure

2) If the ratio is < 1.8 the sample of the DNA is either contaminated with phenol or protein

3.3.2 Polymerase Chain Reaction

The *in vitro* amplification of DNA by repeated cycles of strand separation and polymerization, by DNA polymerase activity is called polymerase chain reaction (PCR). This technique was developed by Kary.B.Mullis at Cites Corporation, California in 1985 and he was awarded with the noble prize in chemistry in 1993. PCR is now considered as a basic tool for molecular biology. The polymerase chain reaction technique is used for generating large quantities of a specified DNA segment of interest. The Reagents for PCR for 10 µL reaction are presented in table 3.3.

Table 3.4 Reagents for PCR for 10 µL reaction

DNA	3 µL
10X Buffer	1µL
Taq polymerase	0.2 µL
dNTP Mix	0.5µL
Forward primer	1µL
Reverse primer	1µL
Water	3.3µL

3.3.3 PCR with Microsatellite Markers

SSR markers are very powerful tools in Marker Assisted Selection (MAS) due to their hyper polymorphism, abundance in the genome, co-dominant inheritance; simplicity of assay, most important being already mapped both physically and genetically in the rice genome. Amplification of single SSR involves two different primers- F (Forward) and R (Reverse) primers. SSR primers are usually in the size range of 18 to 25 bases. *Taq* DNA polymerase is the most vital ingredient of a PCR reaction. *Taq* DNA polymerase is a special category of DNA polymerase, which is obtained from a thermophilic bacterium, *Thermus aquaticus* and is highly thermo stable. The steps involved in PCR were given below

- Master Mix consisting of PCR buffer, dNTPs, Forward primer, Reverse primer, Milli Q water, *Taq* DNA polymerase was prepared.
- Inorder to avoid minor pippeting errors, a little extra quantity of master mix was prepared to ensure that adequate quantity was available for the samples. Empirically, for every 10 reactions, one extra reaction was taken.
- The tube containing master mix was spun for about 10 to 15 seconds and kept in ice until added to PCR tubes.
- Master Mix was added equally to all the wells in the PCR plate, given a spin and kept inside the thermocycler (Applied Biosystem's Veriti PCR machine).

The actual technique of PCR involves repeated cycles for amplification of target DNA.

Each cycle has 3 stages.

1. Denaturation
2. Annealing
3. Extension

On raising the temperature to 94 ^{0}C for about 5.0 minutes, the DNA gets denatured and the two strands were separated. When the temperature of mixture was slowly cooled to about 58^{0}C for 0.5 minutes the primers base pair with the complementary regions flanking the target DNA segments. The initiation of DNA synthesis occurs at 3-hydroxyl end of each primer by the enzyme *Taq* DNA polymerase. The primers were extended by joining the bases complementary to DNA strands. However, the temperature has to be kept optimal as required by the enzyme *Taq* DNA polymerase, the optimum temperature was around 72 ^{0}C for 1 minute. It was estimated that the end of 35 cycles of PCR, about a million fold target DNA was synthesized. The thermo profile for PCR is given in Table 3.5.

Table 3.5. The thermo profile for Polymerase Chain Reaction

Activity	Temperature (^{0}C)	Duration (minutes)	Number of cycles
Initial Denaturation	94	5.0	1
Denaturation	94	0.5	35
Annealing	58	0.5	35
Extension	72	1.0	35
Final Extension	72	7.0	1

After completion of 35 cycles, PCR plate was taken out and stored at 4 ^{0}C.

3.3.4 Agarose Gel Electrophoresis

The migration of charged particles under the influence of direct electric field is known as electrophoresis. Many important biological molecules such as amino acids, peptides, proteins, nucleic acids and nucleotides possess ionizable groups. When they are subjected to electric field the charged molecules migrate towards either cathode or anode under the influence of electric field. Agarose gel electrophoresis is useful in identification and separation of DNA molecules.

3.3. 5 Gel Preparation

- Prepared 1X TAE buffer by diluting 50X TAE buffer.
- Agarose gel was prepared by adding 15 g agarose to 500 ml of 1X TAE buffer (3%) and boiled till agarose dissolves completely and a clear solution is formed.
- The electrophoresis apparatus and the combs were washed with distilled water and the combs were placed approximately 2 cm away from the cathode.
- When the temperature of molten Agarose was around 50 ^{0}C, ethidium bromide was added at a concentration of 15 µl/500 ml mixed and poured into the central part of the tank without any air bubbles.
- The gel casting set was kept undisturbed till the Agarose solidified.
- Upon solidification, 1X TAE buffer was poured into the gel tank till the level reached 0.6-0.8 cms above the gel surface.
- The combs were lifted gently ensuring that the wells remained intact

3.3.6 Loading DNA

PCR plate was taken out from the refrigerator and tracking dye, bromophenol blue (0.25% bromophenol blue and 40% sucrose mixed in water) was added and given one spin for uniform mixing of bromophenol blue. The samples were then loaded carefully into the wells.

3.3.7 Electrophoresis

- After loading all DNA samples into the wells electrophoresis unit was made air tight with the lid and power supply was switched on.

- DNA molecules with in an Agarose gel matrix were subjected to steady electric field; it will migrate through the gel towards the positive electrode, anode since DNA has a strong negative charge at neutral p_H. The pores in the gel separate the linear fragments of DNA according to their size.
- The gel was run at 80 to120 V till the dye front reached 3/4th of the gel.

3.3.8 Gel Documentation and scoring the gels

The resolved PCR bands were documented using Syngene Gel Documentation system and finally scoring of the population was done.

3.3.9 Screening with Microsatellites

The 12 F_1's generated by mating 6 lines with 2 testers in L x T design were screened using SSR markers. The list of the SSR primers used is given in Table 3.3.9.1.

Table 3.3.9.1 Primers used in screening in rice (*Oryza sativa* L.)

S. No.	SSR marker	Forward primer	Reverse primer	Trait associated
1	RM206	CCCATGCGTTTAACTATTCT	CGTTCCATCGATCCGTATGG	Anaerobic germination
2	RM263	CCCAGGCTAGCTCATGAACC	GCTACGTTTGAGCTACCACG	Anaerobic germination
3	RM231	CCAGATTATTTCCTGAGGTC	CACTTGCATAGTTCTGCATTG	Rate of germination
4	RM201	CTCGTTTATTACCTACAGTACC	CTACCTCCTTTCTAGACCGATA	Root length
5	RM210	TCACATTCGGTGGCATTG	CGAGGATGGTTGTTCACTTG	Anaerobic germination
6	RM214	CTGATGATAGAAACCTCTTCTC	AAGAACAGCTGACTTCACAA	Culm diameter
7	RM105	GTCGTCGACCCATCGGAGCCAC	TGGTCGAGGTGGGGATCGGGTC	Anaerobic germination
8	RM520	AGGAGCAGAAAAGTTCCCC	GCCAATGTGTGACGCAATAG	Anaerobic germination
9	RM7	TTCGCCATGAAGTCTCTCG	CCTCCCATCATTTCGTTGTT	Rate of germination

10	RM234	ACAGTATCCAAGGCCCTGG	CACGTGAGACAAAGACGGAG	Root length
11	RM346	CGAGAGAGCCCATAACTACG	ACAAGACGACGACGAGGAGGGAC	Culm strength
12	RM17	TGCCCTGTTATTTTCTTCTCTC	GGTGATCCTTTCCCATTTCA	Seedling height
13	RM172	TGCAGCTGCGGCACAACCATAG	CAACCACGACACCGCCGTGTTG	Culm strength
14	RM270	GGCCGTTGGTTCTAAAATC	TGCGCAGTATCATCGGCGAG	Seedling vigour
15	RM253	TCCTTCAAGAGTGCAAAACC	GCATTGTCATGTCGAAGCC	Anaerobic germination
16	RM5509	GATGATCCATGCTTTGGCC	TTCCAGCAGAAAGAAGACAC	Culm diameter
17	RM20557	TCATGAGGGTTATGGGAGTCAAGG	AGTGGTCGTTGAAATCCTTGTGC	Culm diameter
18	RM341	CAAGAAACCTCAATCCGAGC	CTCCTCCCGATCCCAATC	Anaerobic germination
19	RM306	CAAGGTCAAGAATGCAATGG	GCCACTTTAATCATTGCATC	Culm diameter
20	RM104	GGAAGAGGAGAGAAAGATGTGTGTCG	TCAACAGACACACCGCCACCGC	Anaerobic germination
21	RM152	GAAACCACCACACCTCACCA	CCGTAGACCTTCTTGAAGTAG	Culm diameter
22	RM10	TTGTCAAGAGGAGGCATCG	CAGAATGGGAAATGGGTCC	Culm strength
23	RM478	CAGCTGGGGAAGAGAGAGAG	TCAGAAACTAAACGCACCCC	Anaerobic germination
24	RM208	TCTGCAAGCCTTGTCTGATG	TAAGTCGATCATTGTGTGGACC	Culm diameter

3.4 STATISTICAL ANALYSIS

3.4.1 Analysis of Variance

The analysis of variance for each character was done as per the standard statistical procedure given by Cochran and Cox (1950) for Randomized Block Design.

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

Where,

Y_{ij} = Performance of the j^{th} genotype in the i^{th} block

μ = General mean

b_i = Effect of i^{th} block

t_j = Effect of j^{th} genotype

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

The analysis of variance of randomized block design for each character was carried out as indicated below

Source of variation	**d.f**	**SS**	**MSS**	**F.ratio**
Replications	r-1	RSS	RSS/r-1 [Mr = $\sigma^2_e + \sigma^2_r$]	Mr / Me
Treatments	g-1	TrSS	TrSS/g-1 [Mt = $\sigma^2_e + \sigma^2_g$]	Mg / Me
Error	(r-1)(g-1)	ESS	ESS/(g-1)(r-1) [Me = σ^2_e]	
Total	(rg-1)	TSS		

Where,

r = Number of replications

g = Number of genotypes

d.f = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

TSS = Total sum of squares

ESS = Error sum of squares

σ^2_e = Error variance

σ^2_g = Variance due to genotypes

σ^2_r = Variance due to replications

Mr = Mean sum of squares due to replications

Mt = Mean squares due to treatments

Me = Mean squares due to error

Genotypic variance (σ^2_g) = TrMSS – EMSS/r

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

The genotypes mean sum of squares were tested against error mean sum of square to find out the significance. The significance test was carried out by referring to 'F' table values (Fisher and Yates, 1963).

3.4.2 Estimation of Genetic Parameters

The mean sums of squares obtained from analysis of variance were utilized for estimating genetic parameters.

3.4.2.1 Coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed using the formulae adopted by Burton and Devane (1953).

Phenotypic standard deviation (σ_p) = $\sqrt{\sigma^2 p} = \sqrt{\sigma^2 g + \sigma^2 e}$

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

Genotypic standard deviation (σ_g)

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation } (\sigma g)}{\text{General mean } (\overline{X})} \times 100$$

Categorization of the range of variation as suggested by Subramanian and Menon (1973).

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

3.4.2.2 Heritability in broad sense [h^2 (b)]

Heritability in broad sense was estimated according to the formula given by Allard (1960).

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma^2_g)}{\text{Phenotypic variance } (\sigma^2_p)} \times 100$$

The range of heritability in broad sense [h^2 (b)] estimates were classified as suggested by Johnson *et al.* (1955).

Low	=	0 - 30%
Moderate	=	31 - 60%
High	=	61% and above

3.4.2.3 Genetic advance (GA)

Genetic advance was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

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

Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value of 2.06

σ^2_p = Phenotypic standard deviation

h^2 (b) = Heritability in broad sense

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\text{Grand mean } (\overline{X})} \times 100$$

Where,

GA = Genetic Advance

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%

3.4.3 Estimation of genetic divergence using Mahalanobis's generalized distance (D^2)

A measure for group distance based on multiple characters was given by Mahalanobis (1928) using D^2 statistic. With the help of this, genetic divergence between genotypes was estimated.

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

$$D^2_{ij} = \sum_{t=1}^{p} (\bar{Y}_i^t - \bar{Y}_j^t)\, 2$$

Where,

Y_i^t = Uncorrelated mean values of i_{th} genotype for't' character

Y_j^t = Uncorrelated mean values of j_{th} genotype for't' character

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

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

3.4.3.1 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., $\sum d_i^2$. Therefore, transformation of correlated variables into uncorrelated one was done before working out the D^2 values. Transformation was done by using pivotal consideration method.

3.4.3.2 Computation of D^2 values

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

Where,

$$D^2_{ij} = \sum_{t=1}^{P} (\bar{Y}_i^t - \bar{Y}_j^t)^2$$

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

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

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

3.4.3.3 Testing of significance of D^2 values

The D^2 values obtained for a pair of populations is taken as the calculated value of $\chi 2$ and is tested against the tabulated value of χ^2 for P degrees of freedom, where P is the number of characters considered.

3.4.3.4 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their combination towards divergence between two entries ($di=Yi^t-Yj^t$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where P is the total number of characters. 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 contribution where the character was ranked first

M = All possible combinations of number of genotypes considered

3.4.3.5 Grouping of genotypes into various clusters

Grouping of populations 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 varieties belonging to the same cluster should at least on an average

show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of magnitude in a tabular form as described by Singh and Chaudhary (1979). To start with two populations having the smallest distance from each other were considered to which a third population having the smallest D^2 value from the first two populations was added. Similarly, next nearest fourth population was considered and this procedure was continued. At certain stage where it was felt that after adding a particular population 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 the genotypes were included into one or other cluster.

3.4.3.6 Average intra cluster distance

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

Where,

$\sum D^2 i$ = Sum of distances between all possible combinations (n) of the populations included in a cluster

n = Number of clusters

3.4.3.7 Average inter-cluster distance

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

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

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

n_1 and n_2 are the number of genotypes of two clusters

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

3.4.4 Combining ability analysis

The variation among the hybrids was further partitioned into genetic components attributable to general combining ability (*gca*) and specific combining ability (*sca*) as per the method suggested by Kempthorne (1957).

Mathematical model for combining ability analysis is

$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$

Where, Y_{ijk} = Any measurable character of the cross i ×j in the k^{th} replication

μ = Population mean effect

g_i = General combining ability effect of the female parent

g_j = General combining ability effect of the male parent

s_{ij} = Specific combining ability effect of $(i \times j)^{th}$ cross

r_k = Effect due to K^{th} replication

e_{ijk} = Environmental effect on $(ijk)^{th}$ individual

Table 3.5. ANOVA of Line × Tester mating design for combining ability in rice (*Oryza sativa* L.)

Source of variation	Degrees of freedom	MSS Expected	MSS
Replications	(r-1)	M_r	
Entries (genotypes)	(e-1)	M_g	
Parents	(p-1)	M_p	
Crosses	(c-1)	M_c	
Parents vs Crosses	1	M_{pc}	
Lines	(l-1)	M_l	$\sigma^2 + r\sigma^2 s + rt\sigma^2_r$
Testers	(t-1)	M_t	$\sigma^2 + r\sigma^2_s + rl\sigma^2_m$
Line × tester	(l-1)(t-1)	M_{lt}	$\sigma^2 + r\sigma^2_s$
Error	(e-1)(r-1)	M_e	σ^2

Where,

r = Number of replications

e = Number of entries

p = Number of parents

l = Number of lines or female parents

t = Number of testers or male parents

c = Number of crosses

σ^2 = Random error

σ^2_s = Variance of interaction between lines and testers

σ^2_f = Variance due to lines

σ^2_m = Variance due to testers

3.4.4.1Estimation of combining ability effects

(i) *gca* effect of line and tester

$$\text{Line } g_i = \frac{x_{i..}}{tr} - \frac{x_{...}}{ltr}$$

$$\text{Tester } g_j = \frac{x_{.j.}}{lr} - \frac{x_{...}}{ltr}$$

(ii) *sca* effect of cross

$$s_{ij} = \frac{x_{ij.}}{r} - \frac{x_{i..}}{tr} - \frac{x_{.j.}}{lr} + \frac{x_{...}}{ltr}$$

Where,

x_i = Total of i^{th} line over all testers and replications

x_j = Total of j^{th} tester over all lines and replications

x_{ij} = X_{ij} th combination total over all replications

x…. = Total of all hybrid combinations over all replications

l = Number of lines

t = Number of testers

r = Number of replications

Standard Errors for combining ability effects

Standard errors pertaining to *gca* and *sca* effects of different combinations were calculated as follows:

$$SE_{gi}\ (\text{Lines}) = \sqrt{\frac{Me}{tr}}$$

$$SE_{gj}\ (\text{Testers}) = \sqrt{\frac{Me}{lr}}$$

$$SE_{gi-gj}\ (\text{Lines}) = \sqrt{2Me/tr}$$

$$SE_{gi-gj}\ (\text{Testers}) = \sqrt{2Me/lr}$$

$$SE_{gij}\ (\text{line x tester combination}) = \sqrt{\frac{Me}{r}}$$

$$S_{ij} - S_{kl} = \sqrt{\frac{2Me}{r}}$$

The *gca* and *sca* effects were tested against zero for significance by calculating‘t’ value by using the following formulae.

$$t\ \text{cal (lines)} = \frac{|gi-0|}{SE(gi)}$$

$$t\ \text{cal (testers)} = \frac{|gj-0|}{SE(gj)}$$

$$t\ \text{cal (crosses)} = \frac{|sij-0|}{SE(sij)}$$

‘t’ calculated value is compared with ‘t’ table value at error degrees of freedom.

3.4.4.2 Estimation of genetic components of variation

Estimation of Covariances

Covariance of full-sibs and half-sibs were estimated using the formula as given below:

Cov HS (Line) = $\frac{Ml-Mlt}{rt}$

Cov HS (Tester) = $\frac{Mt-Mlt}{rl}$

Cov HS (pooled) = $\frac{1}{r(2lt-l-t)}\left[\frac{(l-1)(Ml)+(t-1)Mt)}{(l+t-2)}-Mlt\right]$

Cov FS = $\frac{(Ml-Me)+(Mt-Me)+(Mlt-Me)}{3r}+\frac{6rCovHS-r(l+t)CovHS}{3r}$

According to King *et al.* (1961) average Cov HS over testers and lines were calculated.

Cov HS (average) = $\frac{\mathrm{M}l+\mathrm{M}t-2\,\mathrm{M}lt}{\mathrm{r}\,(l+t)}$

Estimation of combining ability variances

$\sigma^2 gca$ = Cov HS average = $\left[\frac{1+\mathrm{F}}{4}\right]\sigma^2\mathrm{A}$

$\sigma^2 sca$ = $\frac{Mlt-Me}{r}$ = $\left[\frac{1+F}{4}\right]^2\sigma^2\mathrm{D}$

Ratio of combining ability variances

$\sigma^2 gca$ to $\sigma^2 sca$ ratio was calculated to know the type of gene action involved *i.e.,* additive or non-additive (Singh and Chaudhary, 1977)

3.4.4.3 Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines} = \frac{\text{SS } (l) \times 100}{\text{SS (crosses)}}$$

$$\text{Contribution of testers} = \frac{\text{SS } (t) \times 100}{\text{SS (crosses)}}$$

$$\text{Contribution of } l \times t = \frac{\text{SS } (l \text{ x } t) \times 100}{\text{SS (crosses)}}$$

(Where, SS is sum of squares).

Chapter IV

RESULTS AND DISCUSSION

The data collected on 50 rice genotypes for characters pertaining to yield and its components, quality traits, direct seeded traits, seedling vigour and anaerobic germination related traits was statistically analyzed and calculated mean, variability, heritability, GA as % mean and genetic diversity. Combining ability analysis was done for AG and SV traits collected from 12 crosses generated in L x T design along with parents. These lines, testers and crosses were characterized using microsatellite (SSR) markers for AG and SV traits. The results obtained are presented and discussed under the following heads.

4.1 Mean, variability, heritability and genetic advance as per cent of mean

4.2. Genetic divergence

4.3 Combining ability

4.4 Molecular characterization

ANALYSIS OF VARIANCE

The analysis of variance revealed significant differences among the genotypes for all the 34 characters studied, indicating the sufficient variability in the material (Table 4.1)

4.1 MEAN, VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PERCENT OF MEAN

The mean performance of genotypes is presented in Table 4.2. The estimates of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2 broad sense) and genetic advance as per cent of mean (GAM) are presented in Table 4.3 and described character wise here under.

Table 4.1: Analysis of variance for yield and yield components, quality traits, direct seeded traits, seedling vigour traits and anaerobic germination among 50 genotypes of rice (*Oryza sativa* L.)

Source	Degrees of freedom	Plant height at maturity(cm)	Days to 50% flowering	Number of panicles/ plant	Panicle length (cm)	Number of Grains/ panicle	Spikelet fertility (%)	Grain yield/ plant(g)	Test weight (g)
		Mean sum of squares							
Replication	1	40.44	2.89	1.00	0.28	169.00	2.28	0.93	0.26
Treatment	49	415.03 **	181.24 **	7.82 **	6.94 **	1165.00 **	27.45 **	15.99 **	24.73 **
Error	49	18.01	2.80	1.18	0.28	76.38	4.90	0.68	0.24

Source	Degrees of freedom	Hulling (%)	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio	Kernel elongation ratio	Volume expansion ratio
		Mean sum of squares							
Replication	1	2.25	5.29	9.00	0.01	0.01	0.01	0.01	0.02
Treatment	49	3.43 **	6.76**	26.42**	0.48**	0.11**	0.23**	0.02**	0.03**
Error	49	1.47	1.88	2.46	0.02	0.01	0.01	0.01	0.01

**** Significant at 1 % level**

Table. 4.1 (Cont.).

Source	Degrees of freedom	Culm diameter (mm)	Bending strength (g/stem)	Leaf area index	Harvest index	G % on 10th day	G % on 14th day	SSL on 10th day (cm)	SSL on 14th day (cm)	SRL on 10th day (cm)	SRL on 14th day (cm)
		Mean sum of squares									
Replication	1	0.01	83.33	0.01	0.01	0.36	0.20	0.01	0.15	0.15	0.07
Treatment	49	1.30**	422.99**	0.99**	0.02**	194.65**	96.17**	11.85**	13.9**	11.21**	9.62**
Error	49	0.21	82.93	0.01	0.01	4.95	2.18	0.37	0.92	0.89	0.82

Source	Degrees of freedom	SFW on 14th day (mg)	SDW (mg)	SVI -1	SVI -2	AG % after 2 weeks of submergence	Plant survival % after 2 weeks	AG % after 3 weeks of submergence	Plant survival % after 3 weeks
		Mean sum of squares							
Replication	1	66.25	2.59	1.94	0.10	2.01	1.81	1.53	7.81
Treatment	49	127.90**	10.60**	10.31**	10.83**	344.68**	248.87**	220.65**	132.50**
Error	49	32.06	2.42	2.11	0.80	10.06	5.94	3.75	4.06

**** Significant at 1 % level**

G% -germination per cent, SSL –seedling shoot length, SSR- seedling root length, SFW – seedling fresh weight, SDW- seedling dry weight, SVI- 1 seedling vigour index-1, SVI –II seedling vigour index –II, AG % - anaerobic germination per cent.

Table 4.2: **Mean performance of 50 genotypes of rice for yield and yield components, quality traits, direct seeded traits, seedling vigour traits and anaerobic germination**

S. No	Character	Plant height at maturity (cm)	Days to 50% flowering	Number of panicles/ plant	Panicle length (cm)	Number of grains/ panicle	Spikelet fertility (%)	Grain yield/ plant (g)	Test weight (g)	Hulling (%)	Milling (%)	HRR (%)	Kernel length (mm)
		1	2	3	4	5	6	7	8	9	10	11	12
1	Azucena	158.40	82.50	9.00	28.90	233.50	85.40	11.10	22.40	74.00	67.00	54.00	5.70
2	N22	140.70	91.50	5.50	31.10	207.00	82.05	12.00	21.15	77.00	67.00	60.00	5.11
3	Mahsuri	124.00	98.00	8.50	23.25	171.00	84.75	12.00	17.65	77.00	70.00	69.00	5.40
4	IR-64	114.80	78.50	7.50	23.95	175.50	83.50	15.50	24.80	78.00	67.00	60.00	6.57
5	Naveen	113.60	75.50	7.00	25.75	165.00	84.25	11.00	18.40	76.00	70.00	63.00	5.09
6	Vandhana	115.00	77.00	7.50	25.45	175.50	83.85	12.00	25.45	77.00	70.00	63.00	5.81
7	Luna Suvarna	143.90	88.50	9.50	25.40	190.50	84.15	11.00	24.50	78.00	69.00	65.00	5.67
8	Savithri	110.30	98.50	13.00	23.35	222.00	85.15	13.75	22.20	80.00	75.00	72.00	4.78
9	Varalu	111.10	85.00	6.50	21.65	201.00	83.05	10.00	19.80	78.00	68.00	60.00	5.46
10	FL478	89.90	89.00	7.50	24.50	172.50	81.25	10.15	18.95	79.00	69.00	65.00	6.27
11	Varsha	134.20	88.50	8.00	21.15	162.50	77.65	11.00	16.90	77.00	68.00	63.50	4.94
12	MTU1006	117.50	67.00	10.00	24.70	147.00	83.25	12.50	15.10	79.00	69.00	63.50	6.00
13	MTU1140	121.50	98.00	10.00	26.70	247.00	88.25	15.10	25.20	78.00	68.00	65.00	5.10
14	MTU2067	102.40	109.00	7.50	25.25	197.50	85.65	14.15	20.00	77.00	67.00	64.00	5.30
15	MTU1184	129.50	97.50	9.50	24.75	201.00	83.05	15.50	18.10	78.50	70.50	68.50	5.11
16	MTU1224	95.20	95.00	6.00	24.75	223.50	93.00	18.80	15.00	78.00	69.00	68.00	5.06
17	MTU1226	110.00	105.50	8.00	25.90	245.00	90.00	21.20	25.80	78.00	70.00	65.00	5.89
18	MTU1229	107.00	109.50	10.50	24.65	250.00	96.00	19.75	15.50	77.50	71.00	66.00	5.18
19	MTU1194	115.30	94.50	9.50	23.80	204.00	83.75	14.00	16.50	78.50	70.00	66.00	5.18
20	MTU1156	113.50	81.00	8.50	27.90	221.00	91.00	18.00	23.70	81.00	71.00	66.00	5.97
21	MTU1187	118.90	90.50	8.00	25.10	225.00	92.00	17.00	21.15	77.00	70.00	67.00	5.97
22	MTU1112	101.90	108.00	13.00	24.00	215.00	85.65	15.00	16.00	77.00	72.00	71.00	4.84
23	MTU2716	105.10	100.00	11.50	23.70	206.50	83.80	15.00	20.70	78.00	69.00	63.00	4.53
24	MTU1153	114.50	83.00	9.50	27.25	215.00	93.00	19.45	22.80	79.00	68.00	67.00	6.16
25	MTU1121	110.40	91.50	8.50	27.75	225.00	95.00	19.00	19.10	78.00	70.00	68.00	5.61
26	MTU7029	107.00	99.50	9.00	23.35	217.00	90.00	17.00	19.30	78.00	71.00	66.00	5.35

Table. 4.2 (Cont.).

		1	2	3	4	5	6	7	8	9	10	11	12
27	MTU1010	106.30	79.00	8.50	23.90	183.50	86.40	14.00	23.95	78.50	66.50	59.00	6.10
28	MTU3626	91.60	91.00	7.50	24.15	160.00	83.80	14.25	25.00	77.00	69.00	56.00	5.82
29	MTU1001	107.75	91.50	6.50	23.55	187.50	86.55	14.10	24.80	77.00	64.00	55.00	5.90
30	MTU1061	111.00	107.00	12.00	25.45	219.50	89.55	16.00	19.30	78.00	71.00	69.00	5.27
31	MTU1064	110.25	105.50	11.00	24.75	206.00	87.40	16.45	18.75	79.00	70.00	67.00	5.27
32	MTU1075	113.40	92.00	9.00	25.45	222.50	92.00	18.10	22.00	79.00	70.00	65.00	5.80
33	MTU2077	95.10	106.50	6.00	25.75	222.50	88.10	16.45	21.00	78.00	67.00	66.00	4.99
34	BPT5204	106.05	103.00	6.50	22.75	230.50	85.85	16.10	13.10	78.00	70.00	64.00	4.99
35	BPT 3291	98.00	98.00	5.50	20.95	187.00	87.70	15.20	18.35	78.00	69.00	65.00	5.39
36	Tellahamsa	94.80	92.50	6.50	22.00	184.50	85.35	14.00	19.80	78.00	71.00	65.00	6.13
37	BPT2270	113.90	108.00	6.50	24.55	250.00	83.90	17.00	14.50	81.50	73.00	68.00	5.05
38	BPT2231	106.00	108.50	11.00	25.70	210.00	83.05	16.10	17.25	76.00	70.00	65.00	5.21
39	MTU1078	102.50	99.50	10.00	24.25	210.00	87.60	18.19	17.75	77.00	70.00	65.00	4.83
40	MTU1210	111.60	93.50	8.50	26.50	250.00	92.10	20.80	17.10	78.00	72.00	69.00	5.10
41	AC39416A	132.20	91.00	13.00	26.40	210.00	85.75	14.00	28.60	79.00	68.50	65.50	5.38
42	AC39397	155.95	89.50	10.00	23.00	210.00	82.60	13.20	25.60	77.00	67.00	62.00	6.70
43	Pooja	108.00	95.50	7.50	24.50	210.00	85.80	13.80	20.40	77.00	68.00	64.00	5.20
44	MTU 2344-25-1-3-1	108.30	96.50	7.50	22.70	215.00	88.15	17.30	18.70	77.00	69.00	62.00	5.45
45	MTU 2344-25-2-2-2	113.80	95.00	7.00	24.85	202.00	86.00	18.25	19.10	77.00	70.00	65.00	4.85
46	MTU 2328-37-1-2-1	118.10	98.00	7.50	25.00	203.00	88.50	16.00	17.25	81.00	71.00	67.00	4.84
47	MTU 2344-25-2-2-1	111.40	93.00	6.50	24.25	202.00	87.45	16.75	19.10	77.00	69.00	63.00	5.15
48	MTU 2360-18-2-2	104.10	93.00	6.50	24.20	201.00	89.75	17.45	16.25	76.00	70.00	67.00	5.44
49	MTU 2360-78-1-1	102.70	91.50	6.50	23.25	209.00	87.30	19.00	17.90	77.00	68.00	66.00	5.95
50	MTU 2366-97-1-1	106.00	93.00	6.50	25.25	204.00	87.60	17.80	17.05	78.00	69.00	64.00	5.14
	Mean	113.09	93.87	8.44	24.74	206.10	86.73	15.42	19.97	77.85	69.35	64.64	5.44
	C.V.	3.75	1.79	12.89	2.14	4.24	2.55	5.36	2.46	1.56	1.98	2.43	2.65
	S.E.	3.00	1.18	0.77	0.37	6.18	1.57	0.58	0.35	0.86	0.97	1.11	0.10
	C.D. 5%	8.53	3.37	2.19	1.06	17.56	4.45	1.66	0.99	2.44	2.76	3.16	0.29

C.V % = Coefficient of Variation per cent C.D. = Critical Difference

Table. 4.2 (Cont.).

S.No	Character	Kernel breadth (mm)	Kernel L/B Ratio	Kernel elongation ratio	Volume expansion ratio	Culm diameter (mm)	Bending strength (g/stem)	Leaf area index	HI	G % on 10th day	G % on 14th day	SSL on 10th day (cm)	SSL on 14th day (cm)
		13	14	15	16	17	18	19	20	21	22	23	24
1	Azucena	2.11	2.71	1.53	3.83	5.70	53.33	3.00	0.31	72.00	80.00	16.63	18.25
2	N22	2.18	2.35	1.54	3.69	5.50	93.60	2.25	0.35	72.00	82.00	15.25	16.41
3	Mahsuri	2.39	2.28	1.66	3.72	5.72	60.02	2.70	0.38	92.50	93.00	10.87	12.70
4	IR-64	2.09	3.15	1.63	3.77	5.92	77.39	2.25	0.51	89.50	91.00	14.15	15.50
5	Naveen	1.96	2.59	1.68	3.56	5.85	79.82	2.35	0.40	74.50	85.00	12.60	15.50
6	Vandhana	2.49	2.34	1.61	3.66	6.67	66.57	1.70	0.34	88.50	89.00	13.70	15.20
7	Luna Suvarna	2.24	2.54	1.66	3.59	6.21	64.65	2.85	0.36	72.00	73.50	15.00	16.00
8	Savithri	2.61	1.83	1.60	3.66	6.21	52.60	2.85	0.40	89.00	90.50	13.75	15.72
9	Varalu	2.19	2.51	1.51	3.49	6.15	79.42	2.20	0.32	92.00	92.50	8.94	9.31
10	FL478	2.22	2.82	1.68	3.64	5.92	63.64	2.00	0.39	84.50	85.00	7.60	10.50
11	Varsha	2.01	2.46	1.64	3.41	5.95	70.30	2.90	0.38	84.00	84.50	7.60	10.92
12	MTU1006	1.61	3.74	1.60	3.44	5.26	54.96	1.60	0.47	70.00	71.00	13.40	14.50
13	MTU1140	2.42	2.11	1.79	3.43	8.22	58.03	2.20	0.38	91.00	92.00	9.65	10.50
14	MTU2067	2.17	2.44	1.44	3.56	6.33	61.72	2.50	0.47	82.00	85.00	8.07	10.10
15	MTU1184	1.87	2.74	1.60	3.64	7.51	61.80	2.85	0.45	92.50	93.00	9.80	10.98
16	MTU1224	1.83	2.76	1.70	3.68	6.65	82.08	3.55	0.61	86.50	92.00	9.55	10.60
17	MTU1226	2.67	2.20	1.64	3.97	7.78	67.28	3.30	0.64	74.00	89.00	12.19	14.50
18	MTU1229	2.21	2.35	1.46	3.80	7.50	44.10	2.80	0.54	78.50	80.50	9.35	14.10
19	MTU1194	2.01	2.59	1.75	3.64	7.26	50.70	2.70	0.44	97.00	97.50	9.05	12.25
20	MTU1156	2.16	2.76	1.55	3.55	7.10	66.35	3.00	0.60	93.50	94.00	12.50	17.25
21	MTU1187	2.20	2.70	1.58	3.71	7.93	68.99	2.45	0.48	71.00	91.25	8.80	13.25
22	MTU1112	1.97	2.47	1.79	3.63	6.32	48.08	2.75	0.52	80.00	86.50	6.15	9.95
23	MTU2716	1.93	2.34	1.81	3.45	5.85	49.46	2.85	0.52	82.50	86.00	8.22	10.40
24	MTU1153	1.98	3.11	1.50	3.34	5.78	59.45	3.50	0.66	97.00	97.50	11.39	14.75
25	MTU1121	2.15	2.61	1.65	3.72	7.60	73.60	3.30	0.59	87.00	95.00	9.50	14.06

Table. 4.2 (Cont.).

		13	14	15	16	17	18	19	20	21	22	23	24
26	MTU7029	2.34	2.28	1.62	3.56	4.90	63.80	3.30	0.60	72.00	93.00	9.30	12.15
27	MTU1010	1.88	3.24	1.70	3.64	5.46	66.95	3.05	0.45	95.00	95.50	9.30	15.95
28	MTU3626	2.47	2.38	1.65	3.70	5.60	66.36	2.30	0.45	92.50	93.00	12.50	15.00
29	MTU1001	2.38	2.48	1.74	3.94	6.15	104.17	4.40	0.44	93.50	94.00	8.70	9.65
30	MTU1061	2.13	2.48	1.57	3.52	6.00	43.15	3.70	0.50	94.50	95.50	7.75	9.57
31	MTU1064	2.13	2.48	1.71	3.81	5.68	40.45	3.70	0.53	93.50	94.50	8.80	10.77
32	MTU1075	1.95	2.97	1.56	3.63	6.00	60.65	2.50	0.62	80.00	85.00	8.75	11.05
33	MTU2077	2.26	2.22	1.50	3.59	5.60	76.67	2.35	0.55	65.00	86.00	8.98	11.25
34	BPT5204	1.74	2.88	1.57	3.72	5.40	75.32	2.80	0.53	95.50	96.50	7.49	10.45
35	BPT 3291	2.17	2.48	1.52	3.43	5.57	95.42	4.05	0.63	76.50	78.50	6.85	9.05
36	Tellahamsa	2.24	2.74	1.54	3.56	5.83	71.74	4.50	0.53	89.00	90.50	10.10	11.90
37	BPT2270	1.80	2.80	1.55	3.72	7.12	71.54	3.80	0.59	68.00	91.00	7.65	9.50
38	BPT2231	1.99	2.63	1.68	3.69	6.60	43.08	4.50	0.54	97.00	97.50	8.25	9.80
39	MTU1078	1.99	2.43	1.68	3.85	6.96	50.72	2.70	0.59	89.00	90.50	8.18	10.58
40	MTU1210	2.05	2.49	1.60	3.88	8.10	57.20	1.90	0.62	68.00	70.50	10.15	11.64
41	AC39416A	2.88	1.87	1.67	3.59	7.39	36.22	1.65	0.39	72.50	91.50	10.45	11.30
42	AC39397	2.13	3.16	1.62	3.78	5.98	48.75	1.85	0.38	87.50	93.00	9.90	10.85
43	Pooja	2.14	2.43	1.58	3.81	6.16	75.69	3.55	0.47	92.00	93.00	12.95	17.60
44	MTU 2344-25-1-3-1	2.20	2.49	1.62	3.70	5.02	70.40	3.20	0.61	98.00	100.00	8.86	10.10
45	MTU 2344-25-2-2-2	2.05	2.36	1.71	3.70	6.27	81.79	3.00	0.63	97.00	98.00	8.89	10.03
46	MTU 2328-37-1-2-1	2.13	2.27	1.72	3.73	6.48	61.92	2.45	0.52	96.00	96.00	9.14	9.90
47	MTU 2344-25-2-2-1	2.02	2.55	1.62	3.66	6.00	82.32	2.45	0.51	95.00	96.50	8.28	9.20
48	MTU 2360-18-2-2	1.83	2.98	1.37	3.88	6.52	77.92	3.20	0.60	90.00	91.00	9.10	12.15
49	MTU 2360-78-1-1	2.22	2.68	1.41	3.64	6.85	78.95	2.55	0.63	96.00	98.00	11.86	13.71
50	MTU 2366-97-1-1	2.05	2.51	1.31	3.66	6.45	71.88	3.30	0.61	96.00	97.00	6.29	7.65
	Mean	2.14	2.58	1.61	3.66	6.34	65.62	2.86	0.50	85.64	90.04	10.04	12.28
	C.V.	5.43	4.19	2.93	3.33	7.28	13.88	3.54	7.62	2.60	1.64	6.07	7.82
	S.E.	0.08	0.08	0.03	0.09	0.33	6.44	0.07	0.03	1.57	1.04	0.43	0.68
	C.D. 5%	0.23	0.22	0.09	0.25	0.93	18.30	0.20	0.08	4.47	2.97	1.23	1.93

C.V % = Coefficient of Variation per cent C.D. = Critical Difference

Table. 4.2 (Cont.).

S.No	Character	SRL on 10th day (cm)	SRL on 14th day (cm)	SFW on 14th day (mg)	SDW (mg)	SVI -1	SVI -2	AG % after 2 weeks of submergence	Plant survival % after 2 weeks	AG % after 3 weeks of submergence	Plant survival % after 3 weeks
		25	26	27	28	29	30	31	32	33	34
1	Azucena	8.75	11.60	30.00	14.56	11.65	14.60	46.99	34.43	27.95	14.47
2	N22	9.05	14.00	33.00	15.70	12.63	13.45	50.46	32.88	27.44	24.33
3	Mahsuri	5.27	9.50	30.00	8.38	7.80	11.82	30.94	24.33	26.59	10.51
4	IR-64	5.25	9.80	54.00	13.58	12.35	14.10	37.15	39.22	26.17	18.43
5	Naveen	6.85	7.65	29.00	10.86	9.23	13.18	48.72	31.92	29.88	26.55
6	Vandhana	5.66	10.30	45.00	11.57	10.30	13.53	75.47	30.94	35.35	24.72
7	Luna Suvarna	6.65	9.70	38.00	12.42	9.13	11.76	66.94	37.75	35.34	18.43
8	Savithri	6.90	11.45	41.00	15.78	14.30	14.23	58.99	33.19	35.35	31.29
9	Varalu	8.13	8.85	44.00	10.53	9.74	8.61	63.77	30.94	48.72	24.34
10	FL478	8.05	9.32	56.00	16.60	14.10	8.94	58.67	48.43	46.42	22.78
11	Varsha	5.35	7.75	28.50	8.44	7.14	9.24	48.72	22.87	15.11	10.51
12	MTU1006	4.26	5.30	44.50	8.62	6.11	10.30	21.54	16.94	14.95	10.51
13	MTU1140	11.80	13.00	44.00	14.25	13.18	9.66	65.71	55.83	46.71	32.89
14	MTU2067	7.65	9.55	40.00	11.70	9.95	8.58	29.32	25.08	21.38	15.34
15	MTU1184	7.95	8.68	25.00	9.39	8.73	10.21	50.46	37.44	43.14	21.54
16	MTU1224	7.90	8.20	30.00	8.03	7.39	9.75	48.81	16.40	23.94	10.51
17	MTU1226	8.25	10.75	42.00	11.58	10.29	12.91	49.01	37.15	29.98	15.34
18	MTU1229	6.99	8.50	26.00	10.40	8.35	11.35	48.81	17.45	12.73	12.73
19	MTU1194	8.45	9.70	38.00	10.33	10.07	11.94	50.46	37.44	32.89	21.13
20	MTU1156	7.31	8.60	36.00	13.05	12.26	16.22	49.01	42.40	23.95	14.76
21	MTU1187	7.07	8.55	36.00	10.64	9.71	12.09	52.51	24.31	41.15	18.90
22	MTU1112	6.42	7.70	38.50	8.75	7.52	8.56	50.46	37.44	37.15	20.69
23	MTU2716	12.65	13.45	37.00	9.86	8.49	8.95	29.32	25.08	10.51	12.73
24	MTU1153	5.15	7.30	43.00	12.84	12.49	14.39	56.77	35.05	26.55	18.90
25	MTU1121	8.99	10.85	43.00	12.88	12.25	13.38	63.41	32.89	35.25	18.43
26	MTU7029	5.90	10.85	41.00	10.75	9.99	11.30	52.81	39.22	33.20	26.90
27	MTU1010	8.60	9.34	47.00	12.10	11.56	15.23	63.41	28.64	30.31	18.71
28	MTU3626	7.50	9.80	49.00	12.63	11.74	13.95	59.65	42.68	38.93	21.11

Table. 4.2 (Cont.).

		25	26	27	28	29	30	31	32	33	34
29	MTU1001	5.00	9.10	48.00	11.53	10.84	9.07	61.09	51.92	28.99	18.41
30	MTU1061	6.17	7.50	36.00	10.34	9.91	9.15	39.80	24.31	23.95	14.76
31	MTU1064	7.14	8.55	36.00	11.07	10.47	10.17	57.40	48.14	41.15	15.30
32	MTU1075	5.84	8.30	34.00	11.68	9.93	9.40	48.43	24.02	46.71	20.24
33	MTU2077	6.90	7.70	37.00	10.88	9.35	9.67	48.81	39.21	37.15	21.11
34	BPT5204	7.63	8.75	26.00	8.08	7.80	10.09	44.69	39.21	30.97	26.90
35	BPT 3291	6.50	7.95	39.00	11.73	9.21	7.11	65.25	26.90	14.95	10.51
36	Tellahamsa	6.53	8.05	37.00	11.71	10.60	10.78	43.07	33.20	14.95	12.73
37	BPT2270	10.64	12.20	29.00	7.29	6.64	8.65	67.60	53.71	38.33	28.97
38	BPT2231	8.20	10.50	34.00	10.22	9.96	9.55	71.54	39.21	35.25	20.24
39	MTU1078	6.61	7.91	32.00	8.15	7.38	9.57	33.20	30.31	28.75	10.51
40	MTU1210	8.65	10.25	28.20	8.48	5.97	8.20	65.30	26.55	40.38	21.54
41	AC39416A	13.65	14.80	43.00	15.34	14.05	10.34	72.54	60.99	53.32	46.33
42	AC39397	12.38	13.95	36.00	15.00	13.96	10.09	76.42	61.67	48.82	43.46
43	Pooja	7.35	8.90	30.00	12.50	11.64	16.38	63.41	39.21	41.25	20.24
44	MTU 2344-25-1-3-1	14.13	15.04	45.50	12.72	12.72	10.10	64.86	44.98	38.40	13.56
45	MTU 2344-25-2-2-2	9.58	11.65	48.50	12.55	12.30	9.83	69.21	52.74	31.60	16.48
46	MTU 2328-37-1-2-1	11.47	12.20	29.50	12.31	11.82	9.51	52.73	39.16	20.69	5.26
47	MTU 2344-25-2-2-1	11.78	12.77	40.00	10.92	10.54	8.88	82.48	49.59	38.10	20.92
48	MTU 2360-18-2-2	11.15	13.10	35.50	13.00	11.85	11.06	59.07	35.25	38.40	20.69
49	MTU 2360-78-1-1	8.80	11.51	60.00	16.15	15.83	13.43	63.41	48.82	28.59	10.51
50	MTU 2366-97-1-1	11.35	12.00	30.00	10.36	10.05	7.41	63.41	52.89	12.34	5.26
	Mean	8.12	10.05	38.05	11.56	10.42	11.01	54.84	36.81	31.80	19.23
	C.V.	11.62	9.04	14.88	13.45	13.95	8.14	5.78	6.62	6.10	10.49
	S.E.	0.67	0.64	4.00	1.10	1.03	0.63	2.24	1.72	1.37	1.43
	C.D. 5%	1.90	1.83	11.38	3.13	2.92	1.80	6.38	4.90	3.90	4.05

C.V % = Coefficient of Variation per cent C.D. = Critical Difference

Table. 4.2 (Cont.).

Table 4.3: **Estimates of mean, variability, heritability and genetic advance as % of mean for yield components, quality traits, direct seeded traits, seedling vigour traits and anaerobic germination among 50 genotypes of rice (*Oryza sativa* L.)**

S.No.	Character	Mean	Range		Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5% level)
			Minimum	Maximum	GCV	PCV		
1	Plant height at maturity (cm)	113.09	89.90	158.40	12.46	13.01	91.70	24.57
2	Days to 50% flowering	93.87	67.00	109.50	10.06	10.22	96.90	20.41
3	Number of panicles/plant	8.44	5.50	13.00	21.60	25.15	73.70	38.20
4	Panicle length (cm)	24.74	21.00	31.10	7.38	7.68	92.20	14.59
5	Number of grains/panicle	206.10	147.00	250.00	11.32	12.09	87.70	21.84
6	Spikelet fertility (%)	86.73	77.70	96.00	3.87	4.64	69.70	6.66
7	Grain yield/ plant (g)	15.42	10.00	21.20	17.94	18.72	91.80	35.40
8	Test weight (g)	19.97	13.10	28.60	17.52	17.69	98.10	35.74
9	Hulling (%)	77.85	74.00	81.50	1.27	2.01	39.90	1.65
10	Milling (%)	69.35	64.00	75.00	2.25	3.00	56.40	3.49
11	HRR (%)	64.64	54.00	72.00	5.35	5.88	82.90	10.04
12	Kernel length (mm)	5.44	4.50	6.70	8.85	9.24	91.80	17.47
13	Kernel breadth (mm)	2.14	1.60	2.90	10.47	11.79	78.80	19.14
14	Kernel L/B Ratio	2.58	1.80	3.70	12.94	13.60	90.50	25.35
15	Kernel elongation ratio	1.61	1.30	1.80	6.13	6.80	81.40	11.39
16	Volume expansion ratio	3.66	3.30	4.00	2.94	4.44	43.7	4.00
17	Culm diameter (mm)	6.34	4.90	8.20	11.68	13.76	72.10	20.43
18	Bending strength (g/stem)	65.62	36.20	10.42	19.87	24.24	67.20	33.56
19	Leaf area index	2.86	1.60	4.50	24.52	24.78	98.00	50.00
20	Harvest index	0.50	0.30	0.70	19.06	20.53	86.20	36.45

Table. 4.3 (Cont.).

S.No	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean (5% level)
			Minimum	Maximum	GCV	PCV		
21	Germination % on 10^{th} day	85.64	65.00	98.00	11.37	11.67	95.00	22.84
22	Germination % on 14^{th} day	90.04	70.50	100.00	7.61	7.79	95.60	15.33
23	SSL on 10^{th} day (cm)	10.04	6.20	16.60	23.86	24.62	93.90	47.63
24	SSL on 14^{th} day (cm)	12.28	7.70	18.30	20.79	22.21	87.60	40.08
25	SRL on 10^{th} day (cm)	8.12	4.30	14.10	27.97	30.28	85.30	53.20
26	SRL on 14^{th} day (cm)	10.05	5.30	15.00	20.86	22.73	84.20	39.43
27	SFW on 14^{th} day (mg)	38.05	25.00	60.00	18.19	23.50	59.90	29.00
28	Seedling dry weight (mg)	11.56	7.30	16.60	17.55	22.12	63.00	28.70
29	SVI -1	10.42	6.00	15.80	19.43	23.92	66.00	32.50
30	SVI -2	11.01	7.10	16.40	20.33	21.90	86.20	38.89
31	AG% after 2 weeks of submergence	54.84	21.50	82.50	23.59	24.29	94.30	47.19
32	Plant survival % after 2 weeks	36.81	16.40	61.70	29.94	30.67	95.30	60.23
33	AG% after 3 weeks of submergence	31.80	10.50	53.30	32.75	33.31	96.60	66.32
34	Plant survival % after 3 weeks	19.23	5.30	46.30	41.68	42.98	94.00	83.26

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

4.1.1 Yield and yield component traits

4.1.1.1 Plant height at maturity (cm)

A wide range of variation from 89.9 cm (FL 478) to 158.4 cm (Azucena) with a mean value of 113.09 cm was observed for this trait. Under wet direct sowing conditions in irrigated areas, genotypes with short stature and non lodging trait are suitable. Moderate genotypic (12.46) and phenotypic (13.01) coefficients of variation coupled with high heritability (91.7) and high genetic advance as per cent of mean (24.57) was observed for this trait. The estimates of both GCV and PCV were moderate indicating that variation among the genotypes is medium. These results are in agreement with the findings of Pavan Shankar *et al.* (2016) and Tomar *et al.* (2016). Mean performance for plant height (cm) is graphically represented in fig. 4.2.1.

High heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the operation of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Pavan Shankar *et al.* (2016).

4.1.1.2 Days to 50% Flowering

Among the fifty genotypes studied, days to 50% flowering varied from 67.00 days (MTU 1006) to 110.00 days (MTU 1229) with a mean value of 94.00 days. Moderate genotypic (10.06) and phenotypic (10.22) coefficients of variation were observed for this trait. These findings are in agreement with the results reported by Pratap *et al.* (2012) and Muthuramu and Sakthivel (2016).

High heritability (96.9) coupled with high genetic advance as per cent of mean (20.41) was observed for this trait revealing the operation of additive gene action in the inheritance of this trait and simple selection may be effective. These findings are in agreement with the results reported by Sameera *et al.* (2015), Ameenal *et al.* (2016) and Muthuramu and Sakthivel (2016).

4.1.1.3 Number of panicles/plant

The trait, number of panicles/plant showed variation from 5.50 (N-22, MTU 3291) to 13.00 (MTU1112) with a mean value of 8.44. High genotypic (21.6) and phenotypic (25.15) coefficients of variation along with high heritability (73.7) and high

genetic advance as per cent of mean (38.2) were noticed indicating that variation among the genotypes is high and the predominance of additive gene action in the inheritance of this trait. Hence, simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Tomar *et al.* (2016), Rukmini Devi *et al.* (2016) and Pavan Shankar *et al.* (2016).

4.1.1.4 Panicle length (cm)

Panicle length among all the genotypes varied from 21.00 cm (BPT 3291) to 31.10 cm (N 22) with a mean value of 24.74 cm. Low genotypic (7.38) and phenotypic (7.68) coefficients of variation with high heritability (92.2) and moderate genetic advance as per cent of mean (14.59) were observed for this trait. Pavan Shankar *et al.* (2016), Tomar *et al.* (2016) and Tripathi *et al.* (2017) also reported low estimates for both GCV and PCV.

In this trait, high heritability and moderate genetic advance as per cent of mean was observed indicating the operation of both additive and non additive gene actions in the inheritance of this trait which are in agreement with the results reported by Tomar *et al.* (2016), Rukmini Devi *et al.* (2016) and Pavan Shankar *et al.* (2016).

4.1.1.5 Number of grains/panicle

For number of grains per panicle a wide range of variation was observed among the genotypes studied. The minimum value observed was MTU 1006 (147) while the entries MTU 1229 and MTU1210 recorded maximum value (250) with a mean value of 206.1. Moderate genotypic (11.32) and phenotypic (12.09) coefficients of variation were observed for this trait. Narrow differences between phenotypic and genotypic coefficients of variation (PCV and GCV) for most of the characters revealed less environmental influence on the expression of these traits and the chance of high selection gain. These findings are in agreement with the results reported by Karande *et al.* (2015) and Tomar *et al.* (2016).

High heritability (87.7) coupled with high genetic advance as per cent of mean (21.84) was observed for this trait indicating the operation of additive gene action. Hence simple section would be effective for improving this character. These findings are in agreement with the results reported by Tomar *et al.* (2016) and Onyia *et al.* (2017).

4.1.1.6 Spikelet fertility (%)

Spikelet fertility among all the genotypes varied from 77.70 (Varsha) to 96.00 (MTU 1229) with a mean value of 86.73. Among the genotypes, low estimates of genotypic (3.87) and phenotypic (4.64) coefficients of variation, high heritability (69.7) and low genetic advance as per cent of mean (6.66) were recorded for this trait. The estimates of both GCV and PCV were low for this trait indicating that the variation among the genotypes is low. Similar results were reported by Bhati *et al.* (2015) and Karande *et al.* (2015).

High heritability coupled with low genetic advance as per cent of mean indicated the involvement of both additive and non additive gene actions for this trait and selection for such traits may not be rewarding. This trait can be improved by intermating superior genotypes of segregating population developed from combination breeding. Similar results were reported by Mahendra *et al.* (2015) and Onyia *et al.* (2017).

4.1.1.7 Grain yield/plant (g)

Grain yield/plant exhibited variation from 10g (Varalu) to 21.2g (MTU 1226) with a mean value of 15.42g. Moderate genotypic (17.94) and phenotypic (18.72) coefficients of variation were observed for this trait. The difference between PCV and GCV was low indicating the less influence of environment on the expression of the trait. Similar results are recorded by Sameera *et al.* (2015), Sindhumole *et al.* (2015) and Pavan Shankar *et al.* (2016).

High heritability (91.8) and high genetic advance as per cent of mean (35.4) were observed for this trait, which indicated the role of additive gene action in the inheritance of this trait and directional selection could be profitably applied for improvement of this trait. These results are in accordance with the results ofTomar *et al.* (2016) and Rukmini Devi *et al.* (2016). Mean performance for grain yield/plant (g) is graphically represented in fig. 4.2.2.

4.1.1.8 Test weight (g)

Test weight exhibited wide variation from 13.1g (BPT 5204) to 28.6g (AC 39416A) with a mean value of 19.97g. Moderate genotypic (17.52) and moderate phenotypic (17.69) coefficients of variation were recorded for this trait. Similar results are also recorded by Pavan Shankar *et al.* (2016) and Rukmini Devi *et al.* (2016).). Mean performance for test weight (g) is graphically represented in fig. 4.2.3.

Estimates of heritability (98.1) and genetic advance as per cent of mean (35.74) were high suggesting the role of additive gene effects in controlling this trait. Similar findings were earlier reported by Pavan Shankar *et al.* (2016) and Tomar *et al.* (2016).

4.1.2 Quality Parameters

4.1.2.1 Hulling (%)

Hulling percentage values varied from 74.0 % (Azucena) to 81.5% (BPT 2270) with a mean value of 77.85%. Low genotypic (1.27) and phenotypic (2.01) coefficients of variation were observed for this trait. These results suggested less variation for hulling percentage among the genotypes studied. These results are in agreement with Nirmaladevi *et al.* (2015), Sameera *et al.* (2015) and Rukmini Devi *et al.* (2016).

Moderate heritability (39.9) coupled with low genetic advance as per cent of mean (1.65) was recorded for this trait indicating the presence of both additive and non additive gene action.

4.1.2.2 Milling (%)

Among 50 genotypes studied the values of milling % ranged from 64% (MTU 1001) to 75% (Savithri) with a mean value of 69.35%. Low genotypic (2.25) and phenotypic (3.00) coefficients of variation were recorded for this trait. Low GCV and PCV indicated less variation among the genotypes studied. These results are in accordance with the results given by Sameera *et al.* (2015) and Rukmini Devi *et al.* (2016).

Moderate heritability (56.4) and low genetic advance as per cent of mean (3.49) were recorded for this trait indicating the operation of non-additive gene action. The moderate heritability is being exhibited due to favorable influence of environment rather than genotype indicating the possibility of improvement of these traits through heterosis breeding rather than simple selection. Similar results were also reported by Nagajyothi (2001) and Sameera *et al.* (2015).

4.1.2.3 Head rice recovery (%)

Head rice recovery percentage varied from 54 % (Azucena) to 72% (Savithri) with a mean value of 64.64%. Low genotypic (5.35) and phenotypic (5.88) coefficients of variation with high heritability (82.9) and moderate genetic advance as per cent of mean (10.04) were observed for this trait. Satish Chandra *et al.* (2009) and Sameera *et al.* (2015) also reported low estimates for both GCV and PCV.

High heritability coupled with moderate genetic advance as per cent of mean was observed for this trait indicating the operation of both additive and non additive gene action in the inheritance of this trait which is in agreement with the results reported by Parvathi *et al.* (2011).

4.1.2.4 Kernel length (mm)

Variation for kernel length ranged from 4.5 mm to 6.7 mm with a mean value of 5.44 mm. Among the genotypes studied minimum kernel length was observed in MTU 2716 while maximum value was exhibited by AC 39397. Low estimates were manifested by this trait for both GCV (8.85) and PCV (9.24) indicating that the variation among the genotypes are low. These results are in conformity with Pratap *et al.* (2012), Sameera *et al.* (2015), Pavan Shankar *et al.* (2016) and Rukmini Devi *et al.* (2016). High heritability (91.8) coupled with moderate genetic advance as per cent of mean (17.47) was recorded for this trait indicating the operation of both additive and non additive gene action.

4.1.2.5 Kernel breadth (mm)

Kernel breadth among all the genotypes varied from 1.6 mm (MTU 1006) to 2.9 mm (AC 39416A) with a mean value of 2.14 mm. For kernel breadth, the estimates of GCV (10.47) and PCV (11.79) were moderate. These results are in conformity with Sameera *et al.* (2015) and Nirmaladevi *et al.* (2015). The estimates of heritability were high (78.8) for this trait whereas moderate values were recorded for genetic advance as per cent of mean (19.14). Similar results were previously reported by Pavan Shankar *et al.* (2016) and Rukmini Devi *et al.* (2016).

4.1.2.6 Kernel L/B ratio

Kernel L/B ratio in the genotypes studied ranged from 1.8 (Savithri) to 3.7 (MTU 1006) with a mean value of 2.58. Moderate genotypic (12.94) and phenotypic (13.6) coefficients of variation were recorded for this trait and the less difference between them indicated less influence by the environment. These results are in accordance with Pavan Shankar *et al.* (2016) and Rukmini Devi *et al.* (2016).

High heritability (90.5) and high genetic advance as per cent of mean (25.35) were observed for this trait indicating the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. These results are in accordance with Pavan Shankar *et al.* (2016) and Rukmini Devi *et al.* (2016).

4.1.2.7 Kernel elongation ratio

This trait exhibited the range from 1.3 (MTU 2366-97-1-1) to 1.8 (MTU 1112, MTU 1140, MTU 2716) with a mean value of 1.61. Low genotypic (6.13) and phenotypic (6.8) coefficients of variation were recorded for this trait. Similar results are also recorded by Sameera *et al.* (2015) and Rukmini Devi *et al.* (2016).

High heritability (81.4) coupled with moderate genetic advance as per cent of mean (11.39) was observed for this trait indicating the operation of both additive and non-additive gene actions and desired results may not be possible by simple selection methods. Nirmaladevi *et al.* (2015) also recorded high heritability for this character in their studies.

4.1.2.8 Volume expansion ratio

Volume expansion ratio in the genotypes studied ranged from 3.3 (MTU 1153) to 4.0 (MTU 1226) with a mean value of 3.66. Low estimates for genotypic (2.94) and phenotypic (4.44) coefficients of variation were recorded for this trait. The heritability estimates were moderate (43.7) while genetic advance as per cent of mean (4.0) was low for this trait.

The estimated values of GCV and PCV were low for this character indicating that variations among the genotypes are low. These results are in agreement with Nirmaladevi *et al.* (2015). Moderate heritability coupled with low genetic advance as per cent of mean was recorded for this trait indicating the presence of both additive and non additive gene action.

4.1.3 Direct Seeded Traits

4.1.3.1 Culm diameter (mm)

This trait exhibited the range from 4.9 mm (MTU 7029) to 8.2 mm (MTU 1140) with the mean value of 6.34 mm. Moderate estimates for genotypic (11.68) and phenotypic (13.76) coefficients of variation were recorded for this trait. These results are in agreement with the findings of Islam *et al.* (2016).

High heritability (72.1) coupled with high genetic advance as per cent of mean (20.43) were observed for this trait which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Mean performance for culm diameter (mm) is graphically represented in fig. 4.2.7.

4.1.3.2 Bending strength (g/stem)

A wide range of variation from 36.2 (AC 39416A) to 104.2 (MTU 1001) with a mean value of 65.62 was observed for this trait. Moderate GCV (19.87) and high PCV (24.24) were recorded for this trait. This suggests that environmental effects constitute a major portion of the total phenotypic variation of this trait. High heritability (67.2) coupled with high genetic advance (33.56) as per cent of mean was recorded for this trait indicating the presence of additive gene action in the inheritance of this trait.

4.1.3.3 Leaf area index

This trait exhibited the range from 1.6 (MTU 1006) to 4.5 (Tellahamsa, BPT 2231) with a mean value of 2.86. High GCV (24.52) and high PCV (24.78) were recorded for this trait.

High heritability (98) and high genetic advance as per cent of mean (50.0) were observed for this trait which indicated the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

4.1.3.4 Harvest index

The genotypes Azucena, Vandhana, Varalu had lowest harvest index of 0.3 while MTU 1153 had highest value of 0.7 with a mean value of 0.5. This trait manifested moderate genotypic (19.06) and high phenotypic (20.53) coefficients of variation. These findings are in accordance with the results of Dhurai *et al.* (2013) and Islam *et al* (2016).

The estimates of heritability are high (86.2) which amounted to high genetic advance as percent of mean (36.45). High heritability coupled with high genetic advance as per cent of mean was recorded for this trait indicating the presence of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Sathya and Jebaraj (2013), Sameera *et al.* (2015) and Tomar *et al* (2016).

4.1.4 Seedling Vigour Traits

4.1.4.1 Germination % on 10th day

Minimum value of 65% for germination on 10th day was recorded by MTU 2077 while MTU 2344-25-1-3-1 manifested maximum germination on 10th day (98%) and the overall mean were 85.64%. This trait manifested moderate genotypic (11.37) and phenotypic (11.67) coefficients of variation. The estimate of heritability was high (95) which accounted to high genetic advance as per cent of mean (22.84).

High heritability coupled with high genetic advance as per cent of mean was recorded for this trait indicating the presence of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Lakshmi *et al. (*2016).

4.1.4.2 Germination % on 14th day

Germination % on 14th day varied from 70.5 (MTU 1210) to 100 (MTU 2344-25-1-3-1) with a mean value of 90.04 under lab conditions. This trait showed low variability which is evident from the estimates of genotypic (7.61) and phenotypic (7.79) coefficients of variation. This trait exhibited low variability with low GCV and PCV indicating the presence of low variability in the material and less scope for improvement of this character through selection.

High heritability (95.6) coupled with moderate genetic advance as per cent of mean (15.33) recorded for this trait indicates the involvement of both additive and non additive gene actions in the expression of this trait.

4.1.4.3 SSL on 10th day (cm)

Variability for this character ranged from 6.2 cm (MTU 1112) to 16.6 cm (Azucena) with a mean value of 10.04 cm. All the genetic parameters manifested high values *viz.*, GCV (23.86), PCV (24.62), heritability (93.9) and genetic advance as per cent of mean (47.63) suggesting the role of additive gene effects in controlling this trait. Similar results were earlier reported by Lakshmi *et al. (*2016).

4.1.4.4 SSL on 14th day (cm)

Under laboratory conditions, the trait, shoot length at 14 DAS, showed variation which ranged from 7.7 cm (MTU 2366-97-1-1) to 18.3 cm (Azucena) with a mean value of 12.28 cm. High genotypic (20.79) and high phenotypic (22.21) coefficients of variation were recorded indicating the presence of high variation among the genotypes studied.

High heritability (87.6) coupled with high genetic advance as per cent of mean (40.08) was recorded for this trait indicating heritability is due to additive effects and selection may be effective for these characters, based on phenotypic values in order to obtain maximum genetic gain for yield improvement in rice by simple selection process. These findings are in agreement with the results reported by Lakshmi *et al. (*2016).

4.1.4.5 SRL on 10th day (cm)

Variability for this character ranged from 4.3 cm (MTU 1006) to 14.1 cm (MTU 2344-25-1-3-1) with a mean value of 8.12 cm. All the genetic parameters manifested high values *viz.*, GCV (27.97), PCV (30.28), heritability (85.3) and genetic advance as per cent of mean (53.2) suggesting the role of additive gene effects in controlling this trait. Similar results were earlier reported by Sathya and Jebaraj (2013).

4.1.4.6 SRL on 14th day (cm)

The range of variation for this trait was high which varied from 5.3 cm (MTU 1006) to 15 cm (MTU 2344-25-1-3-1) with a mean value of 10.05 cm. This trait manifested high genotypic (20.8) and phenotypic (22.73) coefficients of variation coupled with high heritability (84.2) and high genetic advance as per cent of mean (39.43).

High heritability (84.2) coupled with high genetic advance as per cent of mean (39.43) was observed for this trait indicating the operation of additive gene action. Hence, simple section would be effective for improving this character. These findings are in agreement with the results reported by Sathya and Jebaraj (2013).

4.1.4.7 SFW on 14th day (mg)

The variation for this trait ranged from 25 mg (MTU 1184) to 60 mg (MTU 2360-78-1-1) with a mean value of 38.05 mg. This trait manifested moderate genotypic (18.19) to high phenotypic (23.50) coefficients of variation. Moderate heritability (59.9) coupled with high genetic advance (29) was observed for this trait. Mean performance for seedling fresh weight on 14th day (mg) is graphically represented in fig. 4.2.4.

4.1.4.8 Seedling dry weight (mg)

Genotypes showed values for this trait from 7.3 mg (BPT 2270) to 16.6 mg (FL 478) with a mean value of 11.56 mg under lab conditions. This trait manifested moderate genotypic (17.55) to high phenotypic (22.12) coefficients of variation.

High heritability (63) coupled with high genetic advance (28.7) as per cent of mean was recorded for this trait suggesting the role of additive gene action in the inheritance of this trait. These findings are in accordance with the results reported by Lakshmi *et al.* (2016) and Subbarao *et al.* (1996).

4.1.4.9 Seedling vigour index -1

The range of variation for this trait is high which varied from 6 (MTU 1210) to 15.8 (MTU 2360-78-1-1) with a mean value of 10.42. This trait manifested moderate genotypic (19.43) and high phenotypic (23.92) coefficients of variation coupled with

high heritability (66) and high genetic advance as per cent of mean (32.5). These findings are in accordance with the results reported by Rajendra Krishna *et al.* (2015).Mean performance for seedling vigour index -1 is graphically represented in fig. 4.2.5.

High heritability coupled with high genetic advance as per cent of mean was recorded for this trait suggesting the role of additive gene action in the inheritance of this trait. These findings are in accordance with the results reported by Ramadevi (1998).

4.1.4.10 Seedling vigour index -2

Vigour index recorded a mean value of 11.01 with a range of 7.1 (BPT 3291) to 16.4 (Pooja). All the genetic parameters studied manifested high value for this trait. High genotypic (20.33) and phenotypic (21.90) coefficients of variation along with high heritability (86.2) and high genetic advance as per cent of mean (38.89) indicated that variation among the genotypes is high and the predominance of additive gene action in the inheritance of this trait. Hence, simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Ramadevi (1998).

4.1.4.11 AG% after 2 weeks of submergence

Variability for this character ranged from 21.5 (MTU 1006) to 82.5 (MTU 2344-25-2-2-1) with a mean value of 54.84. Both genotypic (23.59) and phenotypic (24.29) coefficients of variation manifested high estimates for AG% after 2 weeks of submergence. Similar results were also reported previously by Lakshmi *et al.* (2016). Estimates of heritability (94.3) and genetic advance as per cent of mean (47.19) were high suggesting the role of additive gene effects in controlling this trait. Similar findings were earlier reported by Lakshmi *et al.* (2016). Mean performance for AG% after 2 weeks of submergence is graphically represented in fig. 4.2.6.

4.1.4.12 Plant survival% after 2 weeks

Genotypes for this trait showed variation from 16.4 (MTU 1224) to 61.7 (AC 39397) with a mean value of 36.81. All the genetic parameters manifested high values *viz.*, GCV (29.94), PCV (30.67), heritability (95.3) and genetic advance as per cent of mean (60.23) suggesting the role of additive gene effects in controlling this trait. Similar results were earlier reported by Lakshmi *et al.* (2016).

4.1.4.13 AG % after 3 weeks of submergence

Wide range of variation was observed for this trait. Among the genotypes studied MTU 2716 (10.5) manifested low value for this trait while AC 39416A (53.3) exhibited the maximum value with a mean value of 31.8. This trait observed high estimates for both GCV (32.75) and PCV (33.31) indicating that variation among the genotypes is high.

High heritability (96.6) coupled with high genetic advance as per cent of mean (66.32) was observed for this trait indicating the operation of additive gene action. Hence, simple section would be effective for improving this character.

4.1.4.14 Plant survival % after 3 weeks

Plant survival % after 3 weeks recorded a mean value of 19.23 with a range of 5.3 (MTU 2328-37-1-2-1) to 46.3 (AC 39416A). High genotypic (41.6) and phenotypic (42.98) coefficients of variation, high heritability (94.0) and high genetic advance as per cent of mean (83.26) were recorded for this trait.

The estimates of both GCV and PCV were high indicating that the variations among the genotypes are high. High heritability coupled with high genetic advance as per cent of mean was recorded for this trait indicating that most likely heritability is due to additive gene effects and selection may be effective.

In the present investigation, a total of 34 characters in rice related to yield, quality, seedling vigour, anaerobic germination were studied. High heritability coupled with high genetic advance as per cent of mean was observed for plant height at maturity (cm), Days to 50% flowering, number of panicles/Plant, number of grains/panicle, grain yield/plant (g), test weight (g), kernel L/B ratio, culm diameter (mm), bending strength (g/stem), leaf area index, harvest index, germination % on 10^{th} day, SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SV I -1, SV I -2, AG % after 2 weeks of submergence, plant survival % after 2 weeks, AG % after 3 weeks of submergence, plant survival % after 3 weeks indicating the predominance of additive gene action and their amenability for further improvement through simple selection.

4.2 GENETIC DIVERGENCE

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence would more likely to yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. However, this is an inferential criterion and may not be useful for discrimination among the population occupying ecologically marginal habitats.

The multivariate analysis using Mahalanobis' D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. Further selection of diverse parents for hybridization programme can be effective by the identification of characters responsible for the genetic diversity among the populations (Singh and Chaudhary, 1977).

The multivariate analyses like Mahalanobis' D^2 statistic and principal component analysis provide useful statistical tool for measuring the genetic diversity in a given population with respect of the characters that were considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discriminations between the populations.

The quantitative and quality assessment of genetic divergence was made by adopting Mahalanobis' D^2 statistic for yield and its contributing characters, quality parameters, direct seeded traits, seedling vigour traits and anaerobic germination. Genetic divergence was estimated for 34 characters in 50 rice genotypes and the results obtained from the study are discussed below.

4.4.1 Mahalanobis'D^2 analysis

Test with Wilk's criterion

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by per cent (%) at 1666 degrees of freedom. The 'V' statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of 50 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

Mahalanobis' D^2 values

In order to assess the genetic diversity among 50 genotypes, D^2 statistic was used following the procedure given by Rao (1952). Since the entire 34 yield component characters, quality parameters, direct seeded traits, seedling vigour and anaerobic germination traits were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. The statistical distance (D^2) between the pairs of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated values of any two genotypes considered at one time.

4.4.1.1 Relative contribution of individual characters towards divergence

The per cent contribution towards genetic divergence by all the 34 characters is presented in Table 4.4. The trait plant survival % after 2 Weeks (30.12) showed maximum contribution towards genetic divergence followed by anaerobic germination % after 3 weeks of submergence (25.71), anaerobic germination % after 2 weeks of submergence (10.12), leaf area index (6.86), seedling shoot length on 10^{th} day (5.55), seedling shoot length on 14^{th} day (5.31), survival% after 3 weeks (3.76) , seedling dry weight (mg) (3.10), germination % on 10^{th} day (2.45), seedling vigour index I (1.88), test weight (g) (1.55), seedling fresh weight on 14^{th} day (1.06), kernel elongation ratio (0.49), bending strength (0.41), seedling root length on 10^{th} day (0.41), seedling vigour index II (0.41), harvest index (0.24), germination % on 14^{th} day (0.24) , Days to 50%

flowering (0.16) , kernel L/B ratio (0.08), seedling root length on 14th day (0.08), Plant height at maturity (cm) (0.01), number of panicles/plant (0.01), Panicle Length (cm) (0.01) , number of grains/panicle (0.01), spikelet fertility(%) (0.01), grain yield/plant (g) (0.01), hulling (%) (0.01), milling (%) (0.01), head rice recovery (%) (0.01), kernel length (mm) (0.01), kernel breadth (mm) (0.01), volume expansion ratio (0.01) and culm diameter (0.01).

4.4.1.2 Grouping of genotypes into various clusters

The 50 genotypes were grouped into 8 clusters using the Tocher's method with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values. The distribution of 50 genotypes into 8 clusters is presented in Table 4.5.

The distribution of 50 genotypes into eight clusters was at random with maximum number of 16 genotypes in cluster II. Cluster I was the second largest with 14 genotypes followed by cluster VII and VIII each with 11 and 5 genotypes respectively. The clusters III, IV, V and VI were with 1 genotype each and are solitary clusters. As could be seen in the results, cluster III, IV, V, VI were solitary clusters. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity. These results were in accordance with Adebisi *et al*. (2013), Karuppaiyan *et al.* (2013) and Beevi and Venkatesan (2015).

4.4.1.3 Average intra and inter cluster D^2 values

The average intra and inter cluster D^2 values estimated as per the procedure given by Singh and Chaudhary (1977) and were presented in Table 4.6. Intra- and inter cluster distance of 50 rice genotypes showed in Fig. 4.3. Dendrogram represented relationship among 50 rice genotypes in eight clusters based on Mahalanobis's D^2 values are presented in Fig. 4.4.

The maximum intra cluster D^2 value was 1750.148 for cluster VIII followed by 1334.415 for cluster VII, 1012.594 for cluster II, 570.977 for cluster I, while it was zero for cluster III, IV, V and VI. The high intra cluster distance in cluster VIII indicated the presence of wide genetic diversity among the genotypes *viz.*, BPT 3291, Tellahamsa, MTU 1001, IR- 64, MTU 1006. Cluster mean values showed wide range among the

clusters studied, which indicates the presence of variation among the clusters present in the genotypes.

Cluster I comprised of 14 genotypes and was the closest to cluster VI (799.468) followed by cluster III (868.2) and it was the farthest from cluster VIII (2229.460) followed by cluster VII (1636.768).

Cluster II comprised of 16 genotypes and it was the closest to cluster I (1029.814) followed by cluster VI (1406.091) and it was the farthest from cluster VIII (2334.931) followed by cluster VII (2019.687).

Cluster III comprised of 1 genotype and it was the closest to cluster IV (480.875) followed by cluster VI (629.507) and it was the farthest from cluster VIII (2211.285) followed by clusterV (2024.702).

Cluster IV comprised of 1 genotype and was the closest to cluster III (480.875) followed by cluster VI (1099.085) and it was the farthest from cluster VII (2506.154) followed by cluster V (2034.941).

Cluster V comprised of 1 genotype and was the closest to cluster I (1031.071) followed by cluster II (1910.592) and it was the farthest from cluster VIII (2886.549) followed by cluster VII (2678.859).

Cluster VI comprised of 1 genotype and was the closest to cluster III (629.507) followed by cluster I (799.468) and it was the farthest from cluster VIII (2719.182) followed by cluster V (1992.858).

Cluster VII comprised of 11 genotypes and was the closest to cluster VI (1377.298) followed by cluster I (1636.768) and it was the farthest from cluster VIII (3749.427) followed by cluster V (2678.859).

Cluster VIII comprised of 5 genotypes and it was the closest to cluster IV (1882.096) followed by cluster III (2211.285) and it was the farthest from cluster VII (3749.427) followed by cluster V (2886.549).

The intra and inter cluster D^2 values revealed that inter cluster D^2 values were greater than intra cluster D^2 values. The maximum inter cluster D^2 values was observed between clusters V and VIII (2886.549) followed by cluster VI and VIII (2719.182).

Based on these studies crosses may be made between genotypes of clusters V (BPT 2231) and cluster VIII (BPT 3291, Tellahamsa, MTU 1001, IR- 64, MTU 1006.) followed by genotypes of clusters VI (MTU 2328-37-1-2-1) and VIII (BPT 3291, Tellahamsa, MTU 1001, IR- 64, MTU 1006) to obtain new desirable recombinants in rice.

Table 4.4 Contribution of different characters towards genetic divergence among 50 genotypes of rice (*Oryza sativa* L.)

S.No.	Characters	Contribution %
1	Plant survival % after 2 weeks	30.12
2	Anaerobic germination % after 3 weeks of submergence	25.71
3	Anaerobic germination % after 2 weeks of submergence	10.12
4	Leaf area index	6.86
5	Seedling shoot length on 10^{th} day	5.55
6	Seedling shoot length on 14^{th} day	5.31
7	Survival% after 3 weeks	3.76
8	Seedling dry weight (mg)	3.10
9	Germination % on 10^{th} day	2.45
10	Seedling vigour index I	1.88
11	Test weight (g)	1.55
12	Seedling fresh weight on 14^{th} day	1.06
13	Kernel elongation ratio	0.49
14	Bending strength (g / stem)	0.41
15	Seedling root length on 10^{th} day	0.41
16	Seedling vigour index II	0.41
17	Harvest index	0.24
18	Germination % on 14^{th} day	0.24
19	Days to 50% flowering	0.16
20	Kernel L/B ratio	0.08
21	Seedling root length on 14^{th} day	0.08
22	Plant height at maturity (cm)	0.01
23	Number of panicles/plant	0.01
24	Panicle length (cm)	0.01
25	Number of grains/panicle	0.01
26	Spikelet fertility (%)	0.01
27	Grain yield/ plant(g)	0.01
28	Hulling (%)	0.01
29	Milling (%)	0.01
30	HRR (%)	0.01
31	Kernel length (mm)	0.01
32	Kernel breadth (mm)	0.01
33	Volume expansion ratio	0.01
34	Culm diameter (mm)	0.01

Table 4.6 Average Inter and intra cluster D^2 values of eight clusters in 50 rice (*Oryza sativa* L.) genotypes during *kharif* 2015-16

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**570.977**	1029.814	868.200	1104.650	1031.071	799.468	1636.768	2229.460
Cluster II		**1012.594**	1406.496	1547.017	1910.592	1406.091	2019.687	2334.931
Cluster III			**0.000**	480.875	2024.702	629.507	1828.113	2211.285
Cluster IV				**0.000**	2034.941	1099.085	2506.154	1882.096
Cluster V					**0.000**	1992.858	2678.859	2886.549
Cluster VI						**0.000**	1377.298	2719.182
Cluster VII							**1334.415**	3749.427
Cluster VIII								**1750.148**

Diagonal bold values indicate intra cluster distances

Table 4.5 Distribution of 50 rice genotypes into different clusters based on Mahalonobis D^2 (Tocher's method) analysis during *kharif* 2015-16

Cluster no.	No. of genotypes	Genotypes included in the cluster
1	14	MTU 2344-25-2-2-2, MTU 2344-25-2-2-1, MTU 2344-25-1-3-1, MTU 1064, MTU 7029, MTU 2360-78-1-1, MTU 1184, MTU 1194, BPT 5204, MTU 2360-18-2-2, MTU 1061, MTU 1078, Pooja, MTU 1121
2	16	MTU 1187, MTU 1075, MTU 1153, MTU 1156, MTU 1010, Varalu, MTU 1224, FL 478 Vandhana, MTU 3626, MTU 1226, Mahsuri, Naveen, Luna Suvarna, MTU 2077, MTU 1112
3	1	MTU 2067
4	1	Varsha
5	1	BPT 2231
6	1	MTU 2328-37-1-2-1
7	11	MTU 1140, AC 39416A, AC 39397, Azucena, N 22, Savithri, MTU 1210, MTU 1229, MTU 2716, BPT 2270, MTU 2366-97-1-1
8	5	BPT 3291, Tellahamsa, MTU 1001, IR- 64, MTU 1006.

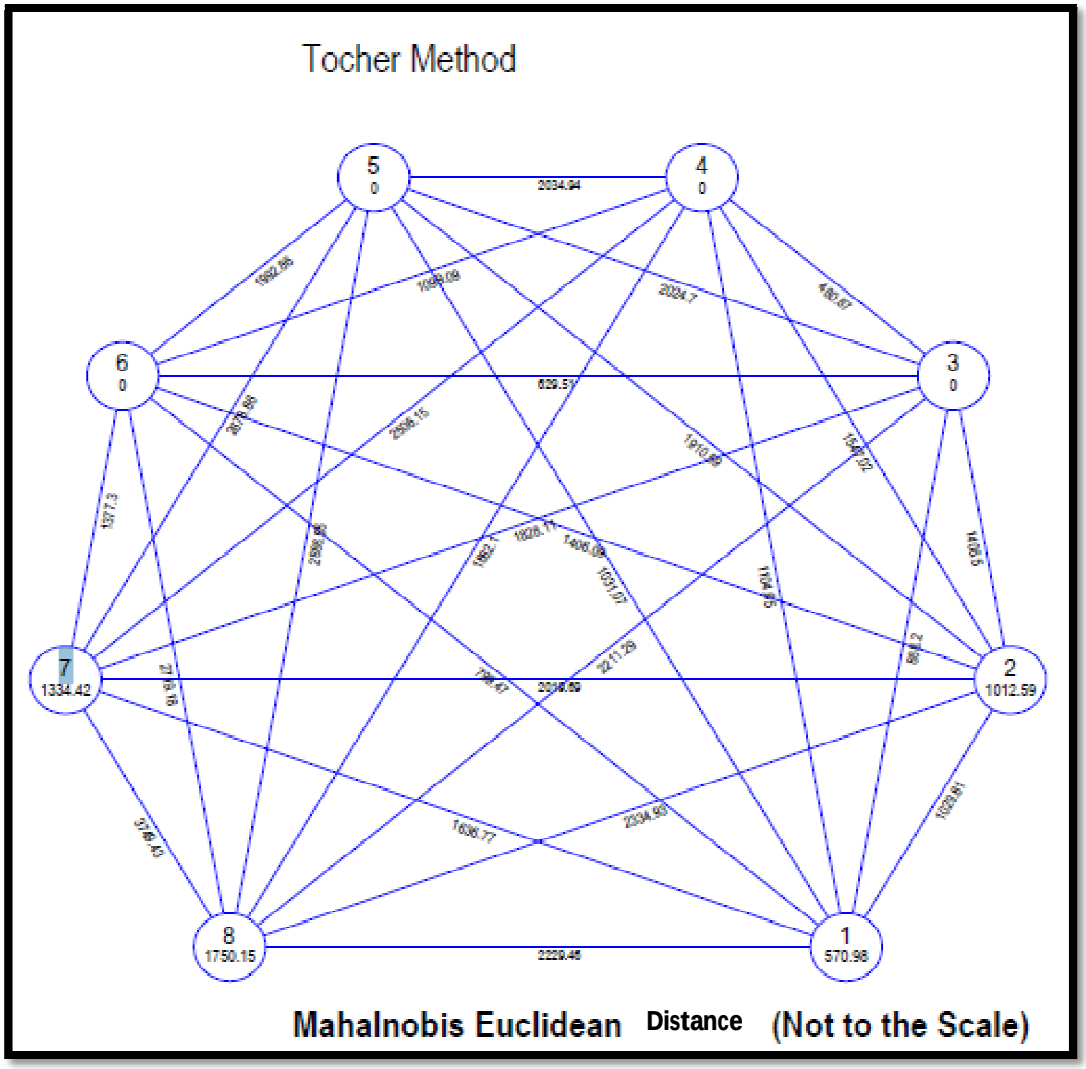


Fig. 4.3 Intra-and Inter-cluster distances of 50 rice (*Oryza sativa* L.) genotypes in eight clusters based on Euclidean^2 distances

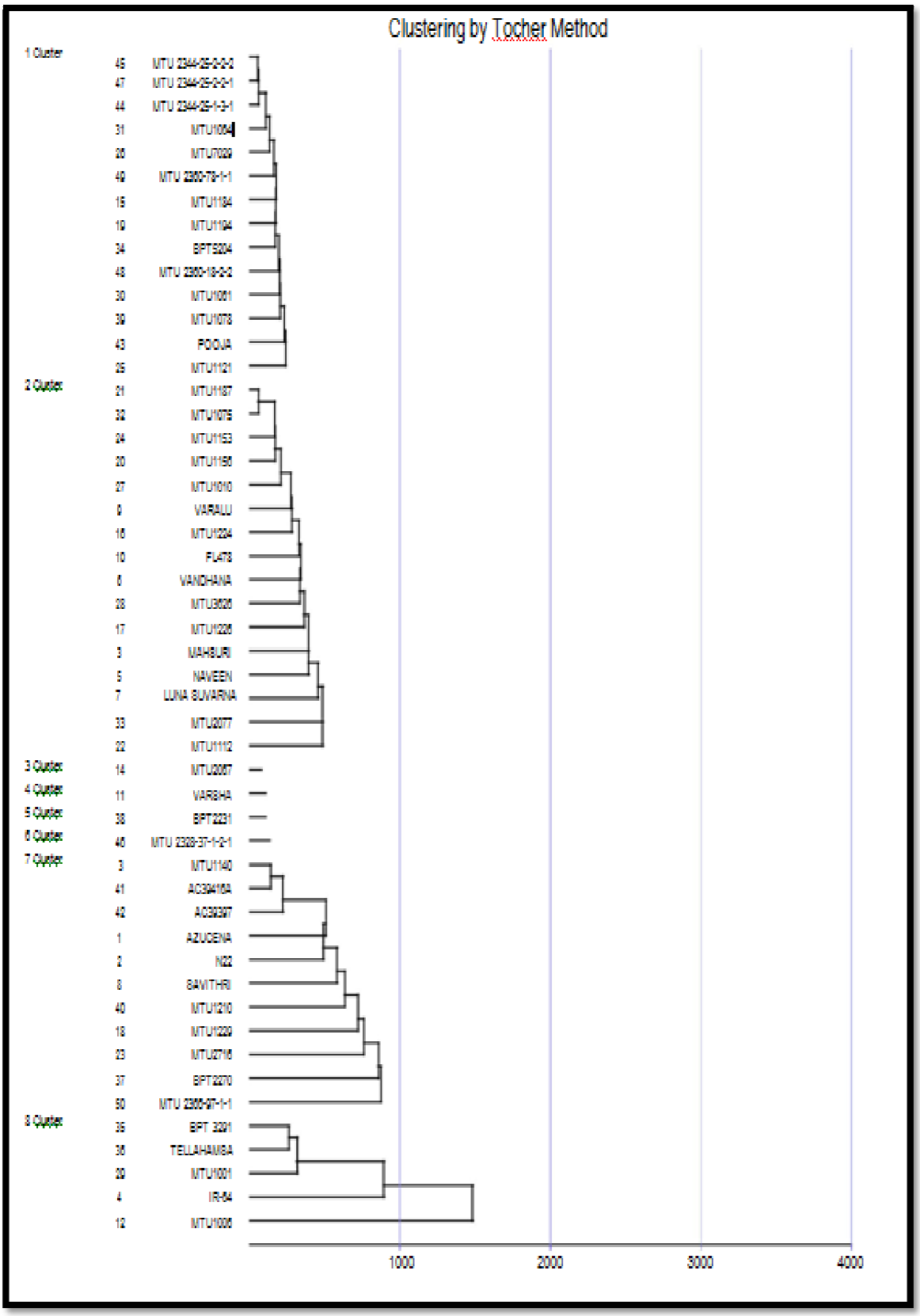


Fig. 4.4 Dendrogram showing relationship among 50 rice (*Oryza sativa* L.) genotypes in eight clusters based on Mahalanobis's D^2 values

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Table 4.7 Mean values of 8 clusters by Tocher's method for 50 genotypes of rice (Oryza sativa L.)

Character /Cluster number	Plant height at maturity(cm)	Days to 50% flowering	Number of panicles/ plant	Panicle length (cm)	Number of grains/ panicle	Spikelet fertility (%)	Grain yield/ plant(g)	Test weight (g)	Hulling (%)
1 Cluster	110.021	97.321	8.393	24.329	210.857	87.618	**16.770**	18.096	77.571
2 Cluster	109.869	90.281	8.156	25.009	200.531	87.266	14.900	**21.322**	77.969
3 Cluster	**102.400**	**109.000**	7.500	25.250	197.500	85.650	14.150	20.000	77.000
4 Cluster	**134.200**	88.500	8.000	**21.150**	**162.500**	**77.650**	**11.000**	**16.900**	77.000
5 Cluster	106.000	108.500	**11.000**	25.700	210.000	83.050	16.100	17.250	**76.000**
6 Cluster	118.100	98.000	7.500	25.000	203.000	**88.500**	16.000	17.250	**81.000**
7 Cluster	123.877	95.909	9.455	**25.827**	**226.364**	86.600	15.409	20.909	78.000
8 Cluster	106.570	**85.500**	**7.200**	23.030	176.300	85.270	14.260	20.570	78.000

Character /Cluster number	Milling (%)	Head rice recovery (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio	Kernel elongation ratio	Volume expansion ratio	Culm diameter(mm)	Bending strength	Leaf area index	Harvest index
1 Cluster	69.750	65.750	5.262	2.058	2.570	1.603	3.704	6.295	66.186	3.071	**0.549**
2 Cluster	69.281	64.688	5.644	2.179	2.619	1.623	3.631	6.296	67.310	2.659	0.486
3 Cluster	**67.000**	64.000	5.295	2.170	2.440	**1.440**	3.560	6.330	61.720	2.500	0.465
4 Cluster	68.000	63.500	4.940	2.010	2.460	1.645	**3.410**	5.950	70.300	2.900	**0.385**
5 Cluster	70.000	65.000	5.210	**1.990**	2.635	1.685	3.690	6.600	**43.080**	**4.500**	0.540
6 Cluster	**71.000**	**67.000**	**4.840**	2.130	**2.270**	**1.720**	**3.730**	6.480	61.915	**2.450**	0.525
7 Cluster	69.682	64.409	5.251	**2.215**	2.410	1.589	3.681	**6.729**	57.883	2.586	0.463
8 Cluster	68.000	**61.700**	**5.998**	2.095	**2.918**	1.605	3.629	**5.746**	**80.733**	3.360	0.517

Table. 4.7 (Cont.).

Character /Cluster number	Germination % on 10th day	Germination % on 14th day	Seedling shoot length on 10th day (cm)	Seedling shoot length on 14th day (cm)	Seedling root length on 10th day (cm)	Seedling root length on 14th day (cm)	Seedling fresh weight on 14th day (mg)	Seedling dry weight (mg)	Seedling vigour index I	Seedling vigour index II
1 Cluster	92.071	95.143	9.272	11.686	8.688	10.411	38.321	11.345	10.820	11.106
2 Cluster	83.656	89.234	10.551	**13.297**	6.972	8.848	39.656	11.408	10.158	**11.875**
3 Cluster	82.000	85.000	8.075	10.100	7.650	9.550	40.000	11.700	9.955	**8.580**
4 Cluster	84.000	**84.500**	**7.600**	10.920	**5.350**	**7.750**	**28.500**	**8.440**	**7.140**	9.240
5 Cluster	**97.000**	**97.500**	8.250	**9.800**	8.200	10.500	34.000	10.220	9.960	9.550
6 Cluster	96.000	96.000	9.140	9.900	**11.470**	12.200	29.500	12.310	**11.820**	9.505
7 Cluster	**79.727**	86.727	**10.661**	12.393	10.255	**12.291**	34.291	**12.457**	10.841	10.631
8 Cluster	83.700	85.000	10.640	12.120	5.508	8.040	**44.500**	11.434	9.822	10.271

Character /Cluster number	Anaerobic germination % after 2 weeks of submergence	Plant survival % after 2 weeks	Anaerobic germination % after 3 weeks of submergence	Plant survival% after 3 weeks
1 Cluster	56.761	39.967	34.689	18.419
2 Cluster	54.461	33.226	34.882	19.224
3 Cluster	**29.320**	25.085	21.380	15.340
4 Cluster	48.715	**22.870**	**15.110**	10.510
5 Cluster	**71.540**	39.210	**35.250**	20.245
6 Cluster	52.730	39.160	20.695	**5.255**
7 Cluster	58.685	**41.334**	32.170	**24.908**
8 Cluster	45.621	33.636	20.002	14.117

Bold figures are indicated maximum and minimum mean values for each character.

4.4.1.4 Cluster mean values of the characters studied

The cluster mean values for 34 characters are presented in Table 4.9. The data indicated a wide range of mean values between the characters. Plant height at maturity (cm) had a range of 134.20 cm for cluster IV to 102.40 cm for cluster III; Days to 50% flowering had a range of 109.00 for cluster III to 85.50 for cluster VIII; No. of panicles/plant had a range of 11.00 for cluster V to 7.20 for cluster VIII; Panicle length (cm) had a range of 25.82 cm for cluster VII to 21.15 cm for cluster IV; No. of grains/panicle had a range of 226.36 for cluster VII to 162.50 for cluster IV; spikelet fertility (%) varied from 88.50 % for cluster VI to 77.65 % for cluster IV; grain yield/plant(g) had a range of 16.77 g for cluster I to 11.00 g for cluster IV; test weight (g) had a range of 21.32 g for cluster II to 16.90 g for cluster IV; hulling (%) varied from 81.00 for cluster VI to 76.00 for cluster V; milling (%) had a range of 71.00 for cluster VI to 67.00 for cluster III; head rice recovery (%) had a range of 67.00 for cluster VI to 61.70 for cluster VIII; kernel length (mm) had a range of 5.99 mm for cluster VIII to 4.84 mm for cluster VI; kernel breadth (mm) had a range of 2.21 mm for cluster VII to 1.99 mm for cluster V ; kernel L/B ratio had a range of 2.91 for cluster VIII to 2.27 for cluster VI ; kernel elongation ratio had a range of 1.72 for cluster VI to 1.44 for cluster III; volume expansion ratio had a range of 3.73 for cluster VI to 3.410 for cluster IV; culm diameter (mm) varied from 6.72 mm for cluster VII to 5.74 mm for cluster VIII; bending strength had a range of 80.73 for cluster VIII to 43.08 for cluster V; leaf area index had a range of 4.50 for cluster V to 2.45 for cluster VI ; Harvest index had a range of 0.54 for cluster I to 0.38 for cluster IV; germination % on 10^{th} day had a range of 97.00 for cluster V to 79.72 for cluster VII; germination % on 14^{th} day had a range of 97.50 for cluster V to 84.50 for cluster IV; seedling shoot length on 10^{th} day (cm) had a range of 10.66 for cluster VII to 7.60 for cluster IV; seedling shoot length on 14^{th} day (cm) had a range of 13.29 for cluster II to 9.80 for cluster V ; seedling root length on 10^{th} day (cm) had a range of 11.47 for cluster VI to 5.35 for cluster IV; seedling root length on 14^{th} day (cm) had a range of 12.29 for cluster VII to 7.75 for cluster IV; seedling fresh weight on 14^{th} day (mg) had a range of 44.50 for cluster VIII to 28.50 for cluster IV; seedling dry weight (mg) had a range of 12.45 mg for cluster VII to 8.44 mg for cluster IV; seedling vigour index I varied from 11.82 for cluster VI to 7.14 for cluster IV; seedling vigour index II had a range of 11.87 for cluster II to8.58 for cluster III; anaerobic germination %

after 2 weeks of submergence had a range of 71.54 for cluster V to 29.32 for cluster III; plant survival % after 2 weeks had a range of 41.33 for cluster VII to 22.87 for cluster IV; anaerobic germination % after 3 weeks of submergence varied from 35.25 for cluster V to 15.11 for cluster IV; Plant survival % after 3 weeks had a range of 24.90 for cluster VII to 5.25 for cluster VI. Cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes present in different clusters.

4.3 COMBINING ABILITY STUDIES

The analysis of variance for combining ability revealed significant differences for all the characters studied indicating high degree of variability in the material studied (Table 4.8). The mean performance of parents and crosses for different characters are presented in Table 4.9. Line × tester effects were significant for majority of the characters except for seedling shoot length on 14th day (cm), seedling root length on 14th day (cm), seedling dry weight (mg) and plant survival % after 2 weeks (Table 4.9). The analysis of variance for combining ability also revealed significant differences among the lines for the traits *viz*., seedling shoot length on 14th day (cm), seedling root length on 10th day (cm), Seedling fresh weight on 14th day (mg), seedling dry weight (mg) and seedling vigour Index I **.** While, in testers significant difference was observed only for seedling shoot length on 14th day (cm), seedling fresh weight on 14th day (mg), Plant survival % after 2 weeks.

The estimates of genetic components of variance and proportional contribution of lines, testers and line × tester interaction to total variance are presented in Table 4.10.The character wise estimates of *gca* effects of parents and *sca* effects of crosses are presented in Table 4.11 and Table 4.12 respectively. Summary of top ranking general combiners was depicted in the Table 4.13. Top ranking hybrids with high *sca* effects coupled with per se performance was depicted in the Table 4.14. Individual character wise results are discussed here under.

4.3.1 Germination % on 10th day

The estimates of *gca* effects were positive and significant for AC 39397 (3.13) and AC 39416A (10.63) suggesting that these lines were good general combiners with

favourable genes for germination per cent. These parents may be used in future breeding programmes for desirable germination percentage. Among testers, none were found to be superior.

The proportional contribution by line × tester (63.6112 %) towards total genetic variance was high as compared to lines (35.7033%) and testers (0.6855%) components which indicated lower estimates of variances due to general combining ability. The estimated component of variance due to *sca* (137.9550) was greater than variance due to *gca* (10.3283). The ratio of general combining ability component of variance to specific combining ability component of variance was low 0.074867 which indicated the preponderance of non-additive gene action. Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait.

Among the crosses, AC 39397 x MTU 1121 (9.04), AC 39416A x MTU 1121 (4.54), Azucena x MTU 1010 (12.21), BPT 2270 x MTU 1121 (5.79) and N-22 x MTU 1010 (7.96) showed significant positive *sca* effects which are desirable for this trait. Based on the *per se* performance and *sca* effects the crosses Azucena x MTU 1010 (high x low), AC39397 x MTU 1121 (high x low) and AC 39416A x MTU 1121 (high x low) were identified as superior cross combinations. The crosses involving high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action as it is likely to produce desirable transgressive segregants.

4.3.2 Germination % on 14th day

The estimates of *gca* effects were positive and significant for AC 39416A (9.75) among lines and MTU 1010 (1.42) in testers. The proportional contribution to total genetic variance due to line x tester (59.3715) was high followed by lines (37.6507) and testers (2.9778) which indicates this trait is influenced by non additive gene action. The estimated component of variance due to *sca* (93.8156) greater than variance due to *gca* (10.0685). The ratio of general combining ability component of variance to specific combining ability component of variance was low 0.107322 which indicated the preponderance of non-additive gene action. Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait.

Among the crosses, AC 39397 x MTU 1121 (7.92), Azucena x MTU 1010 (10.33), N-22 x MTU 1010 (6.58) and BPT 2270 x MTU 1121 (3.42), showed significant positive *sca* effects which are desirable for this trait. Based on the *per se* performance and *sca* effects the crosses *viz.*, Azucena x MTU 1010 (low x high), AC 39397 x MTU 1121 (high x low) and N 22 x MTU 1010 (low x high) were identified as superior cross combinations. The crosses between high × low or low × high combiners resulted in superior cross combinations due to complementary gene action which has arisen out of both additive and non-additive gene actions. These crosses may likely throw superior transgressive segregants. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system.

4.3.3 Seedling shoot length on 10th day (cm)

The estimates of *gca* effects revealed that AC 39416A (1.20), Azucena (1.15), N-22 (1.25) among lines, MTU 1010 (0.60) among testers were found to be good general combiners. These parents may be utilized in future hybridization programmes for improving shoot length. Maximum proportional contribution towards total genetic variance was shared by lines (72.1718 %) followed by line × tester (14.7610 %) and testers (13.0672 %). Female parents play an important role which indicates predominant maternal influence towards this trait. The variance due to *gca* (1.1234) was greater than the *sca* variance (0.9237) for this trait. The ratio of *gca* variance to *sca* variance was greater than unity (1.21626) which indicated the presence of additive gene action. Hybridization followed by simple selection through pedigree breeding method may help to improve this character. Similar results were also reported by Li and Rutger (1980).

Among the crosses MTU 1140 x MTU 1121 (0.55), N-22 x MTU 1010 (1.35) showed significant positive *sca* effects which are desirable for this trait. Based on the *per se* performance and *sca* effects the crosses *viz.*, N 22 x MTU 1010 (high x high), AC 39416A x MTU 1010 (high x high) were identified as superior cross combinations. Involvement of additive variance was predominant in the cross combination of high x high general combiners.

4.3.4 Seedling shoot length on 14th day (cm)

AC 39416A (1.63), Azucena (1.50), N-22 (1.75) among lines, MTU 1010 (0.43) in testers, exhibited significant positive *gca* effects and these were identified as good general combiners for improving this trait. The proportional contribution by lines (95.5128 %) towards total genetic variance was high as compared to testers (3.2748 %) and line × tester (1.2123 %) components which indicated higher estimates of variances due to general combining ability. The estimated component of variance due to *gca* (1.8728) was significant and greater than variance due to *sca* (-0.0405). The ratio of general combining ability component of variance to specific combining ability component of variance was low (-46.27). This indicated the predominance of non additive gene action involved in the inheritance of this character which may be exploited through heterosis breeding. These results were in accordance with the results of Li and Rutger (1980).

Among the crosses studied none of them shown significant results for *sca* effects. But based on the *per se* performance and *sca* effects the crosses N 22 x MTU 1010 (high x low) and AC 39416A X MTU 1010 (high x low) were found to be superior. The high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.5 Seedling root length on 10th day (cm)

The estimates of *gca* effects revealed that AC 39416A (1.87) among lines exhibited significant positive *gca* effects and this was identified as good general combiner for improving this trait. Among testers, none were found to be superior. The proportional contribution by lines (82.9507 %) towards total genetic variance was high as compared to line × tester (14.0206 %) and testers (3.0287 %) components. The estimated component of variance due to *gca* (0.2361) was significant and greater than variance due to *sca* (0.2117). The ratio of general combining ability component of variance to specific combining ability component of variance was high (1.115631). This indicated the predominance of additive gene action involved in the inheritance of this character which may be exploited through pedigree breeding. These results were in accordance with the results of Jiakui *et al*. (1996).

Among the crosses studied none of them shown significant results for *sca* effects. But based on the *per se* performance and *sca* effects the crosses *viz.*, AC 39416A x MTU 1010 (high x low) and MTU 1140 x MTU 1121 (low x high), showed superior performance for this trait. The high × low *gca* effects or low x high *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.6 Seedling root length on 14th day (cm)

Among lines AC 39416A (1.74), exhibited significant positive *gca* effect and this was identified as good general combiner for improving this trait. Among testers, none were found to be superior. The proportional contribution by lines (79.5265 %) towards total genetic variance was high as compared to line × tester (17.6055 %) and testers (2.8680 %) components. The component of variance due to *gca* variance (0.1945) was greater than the *sca* (0.1627). The ratio of general combining ability component of variance to specific combining ability component of variance was high (1.19521) which indicated the preponderance of additive gene action. This trait may be improved by hybridization followed by simple selection procedures like pedigree breeding method. These results were in accordance with the results of Jiakui *et al*. (1996) and Akram *et al.* (1993).

Among 12 crosses studied none of them found significant for *sca* effects. Based on their *sca* effects and *per se* performance the crosses, AC 39416A x MTU 1010 (high x low) and AC 39416A x MTU 1121(high x low) were found to be good for seedling root length. The high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.7 Seedling fresh weight on 14th day (mg)

Higher positive significant *gca* effect was recorded from the line AC 39416A (13.92) and significant in negative direction was observed in Azucena (10.58) and BPT 2270 (11.83). Mean performance of AC 39416A and MTU 1140 coupled with *gca* effect for high seedling fresh weight indicated these lines can contribute high seedling fresh weight in hybrids with their higher general combining ability.

The proportional contribution to total genetic variance due to lines was high (72.2805 %) followed by testers (20.1613 %) and line × tester (7.5582 %). Female parents play an important role which indicated predominant maternal influence towards this trait. The component of variance due to general combining ability (49.6769) was greater than variance due to specific combining ability (-13.4342). The ratio of *gca* variance to *sca* variance was low (-3.6978) which indicated the predominance of non additive gene action which may be exploited through heterosis breeding.

The estimates of *sca* effects pertaining to seedling fresh weight on 14th day ranged from -5 to 4.75. None of the crosses exhibited positive significant *sca* effects Based on per se performance and positive significant *sca* effects the crosses, MTU 1140 x MTU 1010 (high x low) and AC 39416A x MTU 1010 (high x low) were identified as superior cross combinations for earliness. The crosses between high x low general combiners resulted in superior cross combinations due to additive and non additive gene actions.

4.3.8 Seedling dry weight (mg)

The mean values of seedling dry weight ranged from 8.6 mg to 16.25 mg with general mean of 15.15mg. Highest seedling dry weight was observed in the line MTU 1140 (16.25 mg), and lowest in the line BPT 2270 (8.6 mg) with parental mean of 14.55 mg. In case of hybrids, N-22 x MTU 1121 recorded highest Seedling dry weight of 17.9 mg and lowest value of 9.55 mg in BPT 2270 x MTU 1121 with cross mean of 13.65 mg. Positively significant *gca* effects were observed for AC 39397 (1.83), AC 39416A (1.02), MTU 1140 (1.27) and N 22 (2.00) among the lines.

The proportional contribution by lines (96.4060) towards total genetic variance was high as compared to line × tester (3.0524) and tester (0.5417) components. The estimated component of variance due to *gca* (11.9447) was greater than variance due to *sca* (0.2094). The ratio of general combining ability component of variance to specific combining ability component of variance was high (9.2871). This indicated the predominance of additive gene action involved in the inheritance of this character. This trait may be improved by hybridization followed by simple selection procedures like pedigree breeding method.

None of the crosses recorded significant positive *sca* effects, but based on their *sca* effects and *per se* performance the cross, N 22 x MTU 1121 (high x low), was found to be good for seedling dry weight. The high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.9 Seedling Vigour Index I

AC 39397 (1.58), AC 39416A (2.33), N-22 (0.92) in lines recorded significant positive *gca* effects and these were identified as good general combiners for improving this trait. None of the testers showed significant *gca* effects.

The proportional contribution to total genetic variance due to lines was high (86.0772) followed by testers (11.4955) and line × tester (2.4273). The component of variance due to *gca* (1.6897) was higher than the *sca* variance (1.3886). The ratio of general combining ability component of variance to specific combining ability component of variance was high (1.2168) revealing the role of additive gene action. Hybridization followed by simple selection through pedigree breeding method may help to improve this character.

The crosses *viz.*, AC 39397 x MTU 1121 (1.27) and Azucena x MTU 1010 (1.45) recorded significant positive *sca* effects. Based on the *sca* effects and *per se* performance, the crosses, AC 39416A x MTU 1010 (high x low), AC 39397 x MTU 1121 (high x low) and Azucena X MTU 1010 (low x high) were found to be good. High × low or low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene actions.

4.3.10 Seedling Vigour Index II

The estimates of *gca* effects revealed that AC 39416A (2.7), Azucena (1.36), N 22 (0.87) among lines and MTU 1010 (0.60) in testers were found to be good general combiners. Maximum proportional contribution towards total genetic variance was shared by lines (76.769) followed by line × tester (17.7322) and testers (5.4985). Female parents play an important role which indicates predominant maternal influence towards this trait. The variance due to *sca* (2.5165) was greater than the *gca* variance (1.9711) for this trait. The ratio of *gca* variance to *sca* variance was low 0.783253 which indicated the presence of non additive gene action and could be better exploited through biparental mating or diallel selective mating or heterosis breeding.

Three out of twelve crosses *viz.*, AC 39397 x MTU 1121 (1.37), Azucena x MTU 1010 (1.52), N-22 x MTU 1010 (1.39), recorded significant positive *sca* effects. Out of the above three crosses, Azucena x MTU 1010 (high × low), N 22 x MTU 1010 (high × low), were found to be promising based on positive significant *sca* effects and *per se* performance. Low × high or high × low *gca* effects resulted in superior cross combinations which might be due to complementary gene action.

4.3.11 Anaerobic Germination % after 2 weeks of submergence

Out of six lines and two testers, none have showed positive significant *gca* effects. The proportional contribution to total genetic variance due to line × tester was high (79.1233) followed by lines (11.2087) and testers (9.6680) which indicated lower estimates of variances due to general combining ability.The component of variance due to *sca* (29.0115) was higher than the *gca* variance (1.4134). The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.048719) revealing the role of non additive gene action and could be better exploited through biparental mating or diallel selective mating or heterosis breeding.

The cross *viz.*, Azucena x MTU 1121 (6.60) recorded significant positive *sca* effects. Based on the *sca* effects and *per se* performance, the crosses, N 22 x MTU 1010 (high x low), Azucena x MTU 1121(low x low), were found to be good for this trait. The high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action. The low x low general combiners in the cross showed the non additive gene action and can be exploited through hybridization. Superiority of low × low *gca* combination was due to high nicking ability/genetic diversity of parents.

4.3.12 Plant survival % after 2 weeks

The estimates of *gca* effects were positive and significant for MTU 1140 (3.59) among lines. The proportional contribution to total genetic variance due to lines was high (62.4280%) followed by testers (24.0188 %) and line × tester (13.5532 %).

The component of variance due to general combining ability (1.9631) was significant and greater than variance due to specific combining ability (-2.6258). The ratio of *gca* variance to *sca* variance was low (-0.74761) which indicated the predominance of non additive gene action and suggested good prospects of the exploitation of the variation for this trait through hybrid breeding.

`None of the crosses recorded significant positive *sca* effects. Based on their *sca* effects and *per se* performance the cross, MTU 1140 x MTU 1010 (high x low), was found to be good for this trait. The high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action.

4.3.13 Anaerobic Germination % after 3 weeks of submergence

Azucena (4.63), N-22 (2.20) among lines and MTU 1010 (2.09) in testers recorded significant positive *gca* effects and these were identified as good general combiners for improving this trait.

The proportional contribution to total genetic variance due to line x tester was high (62.3668) followed by lines (25.6572) and testers (11.9760). The component of variance due to *gca* (9.1280) was lower than the *sca* variance (53.7224). The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.169) revealing the role of non additive gene action.

The crosses *viz.*, AC 39397 x MTU 1121 (3.83), Azucena x MTU1010 (3.71), BPT 2270 x MTU 1121 (3.30), MTU 1140 x MTU1121 (3.49) and N-22 x MTU 1010 (9) recorded significant positive *sca* effects. Based on their *sca* effects and *per se* performance the crosses, N22 XMTU 1010 (low x high), Azucena x MTU 1010 (high x high) and AC 39397 x MTU 1121(low x high) were found to be good for this trait. High × low or low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene action.

4.3.14 Plant survival % after 3 weeks

Among six lines, AC 39397 (3.96), AC 39416A (1.93) and MTU 1140 (4.18), showed significant positive *gca* effects suggesting that these lines were good general combiners with favourable genes for this trait. Among testers, none were found to be superior.

The proportional contribution by lines (79.5752 %) towards total genetic variance was high as compared to line × tester (17.6632 %) and testers (2.7616 %) components. The estimated component of variance due to *gca* (4.4828) was lower than variance due to *sca* (6.3800). The ratio of general combining ability component of variance to specific combining ability component of variance was low (0.702631). This indicated the predominance of non additive gene action in the inheritance of this character which may be exploited through heterosis breeding.

Among the crosses, AC 39397 x MTU 1121 (2.68), Azucena x MTU 1010 (2.87), showed significant positive *sca* effects which are desirable for this trait. Based on the *per se* performance and *sca* effects the crosses *viz.*, MTU 1140 x MTU 1010 (high x low), AC 39397 x MTU 1121 (high x low) and Azucena x MTU 1010 (low x high) were identified as superior cross combinations. High × low or low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene actions.

The results revealed that the proportional contribution of lines towards total genetic variance was more for the characters *viz.*, SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SVI -1, SVI -2, plant survival % after 2 weeks and plant survival % after 3 weeks. The contribution of line × tester component was more for germination % on 10^{th} day, germination % on 14^{th} day (Rate of germination), AG % after 2 weeks of submergence and AG % after 3 weeks of submergence.

The ratio of *gca* variance to *sca* variance was high indicating the predominance of additive gene action for seedling shoot length on 10^{th} day (cm), seedling root length on 10^{th} day (cm), seedling root length on 14^{th} day (cm), seedling dry weight (mg), seedling vigour index I. The traits governed by additive gene action may be improved by hybridization followed by simple selection procedures like pedigree breeding method. For the characters germination % on 10th day, germination % on 14^{th} day, seedling shoot length on 14^{th} day (cm), seedling fresh weight on 14^{th} day (mg), seedling vigour index II, anaerobic germination % after 2 weeks of submergence, plant survival % after 2 weeks, anaerobic germination % after 3 weeks of submergence, survival% after 3 weeks, the ratio between *gca* variance and *sca* variance was low and indicated the role of non additive gene action. Non-additive gene action governing characters may be exploited through heterosis breeding.

Table 4.11 Estimates of general combining ability effects of lines and tester for seedling vigour and anaerobic germination related traits during *rabi* 2016-17

Parents	Germination % on 10th day	Germination % on 14th day	Seedling shoot length on 10th day (cm)	Seedling shoot length on 14th Day (cm)	Seedling root length on 10th day (cm)	Seedling root length on 14th day (cm)	Seedling fresh weight on 14th day (mg)
AC39397	3.13**	1.25	0.15	0.33	-0.60 *	-0.71*	3.92
AC39416A	10.63**	9.75**	1.20**	1.63**	1.87**	1.74**	13.92**
Azucena	0.88	1.50	1.15**	1.50**	-0.50*	-0.71*	-10.58 *
BPT2270	-4.13**	-4.75**	-2.40**	-4.97**	-0.23	0.07	-11.83 *
MTU 1140	-5.63**	-4.50**	-1.35**	-0.22	-0.15	-0.36	4.92
N-22	-4.88**	-3.25*	1.25**	1.75**	-0.38	-0.03	-0.33
CD 95% GCA(Line)	1.98	2.32	0.36	0.71	0.44	0.71	9.04
MTU1010	0.79	1.42*	0.60**	0.43*	-0.16	-0.16	4.75
MTU1121	-0.79	-1.42*	-0.60**	-0.43*	0.16	0.16	-4.75
CD 95% GCA(Tester)	1.14	1.34	0.21	0.41	0.26	0.41	5.22

Table. 4.11 (Cont.).

Parents	Seedling dry weight (mg)	Seedling vigour index I	Seedling vigour index II	Anaerobic germination % after 2 weeks of submergence	Plant survival % after 2 weeks	Anaerobic germination % after 3 weeks of submergence	Plant survival% after 3 weeks
AC39397	1.83**	1.58**	0.34	-2.53	0.61	0.57	3.96 **
AC39416A	1.02*	2.33**	2.70**	-0.38	-1.37	-3.20**	1.93**
Azucena	-0.78	-0.39	1.36**	-0.75	0.50	4.63**	-1.00
BPT2270	-5.35**	-4.66**	-4.38**	1.24	-1.86	-4.41 **	-4.54**
MTU 1140	1.27**	0.22	-0.88*	0.32	3.59 *	0.22	4.18**
N-22	2.00**	0.92*	0.87*	2.12	-1.48	2.20*	-4.54**
CD 95% GCA(Line)	0.83	0.78	0.78	4.52	3.28	1.59	1.25
MTU1010	0.19	0.38	0.60*	1.38	1.16	2.09 **	0.68
MTU1121	-0.19	-0.38	-0.60 *	-1.38	-1.16	-2.09**	-0.68
CD 95% GCA(Tester)	0.48	0.45	0.45	2.61	1.90	0.92	0.72

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

Table 4.13 Top ranking desirable parents for general combining ability with their *per se* performance

S. No.	Characters	Parents	GCA	*Per se* Performance
1	**Germination % on 10th day**	AC 39416A	10.63	95
		AC 39397	3.13	81
		MTU 1010	0.79	97
2	**Germination % on 14th day**	AC 39416A	9.75	95.5
		MTU 1010	1.42	97
		MTU 1121	1.42	96
3	**Seedling shoot length on 10th day (cm)**	N-22	1.25	16
		Azucena	1.15	15.8
4	**Seedling shoot length on 14th day (cm)**	N-22	1.75	17.1
		Azucena	1.5	16.8
		AC 39416A	1.63	12.8
5	**Seedling root length on 10th day (cm)**	AC 39397	0.60	13.4
		AC 39416A	1.87	12.45
6	**Seedling root length on 14th day (cm)**	AC 39416A	1.74	14.7
		N-22	0.0.3	15.4
7	**Seedling fresh weight on 14th day (mg)**	AC 39416A	13.92	132
		MTU 1140	3.92	81

Table. 4.13 (Cont.).

8	**Seedling dry weight (mg)**	MTU 1140 N-22 AC 39397	1.27 2 1.83	16.25 15.75 16.1
9	**Seedling vigour index I**	MTU 1140 N-22 AC 39416A	0.22 0.92 2.33	14.92 13.6 14.8
10	**Seedling vigour index II**	N-22 AC 39416A Azucena	0.87 2.7 1.36	14.79 12.22 13.5
11	**Anaerobic germination % after 2 weeks of submergence**	AC 39416A AC 39397	0.38 2.53	74.29 73.57
12	**Plant survival % after 2 weeks**	AC 39397 MTU 1140	0.61 3.59	63.97 54.32
13	**Anaerobic germination % after 3 weeks of submergence**	AC 39397 MTU 1010 Azucena	0.57 2.09 4.63	54.32 45.55 33.5
14	**Plant survival% after 3 weeks**	AC 39397 AC 39416A MTU 1140	3.96 1.93 4.18	35.2 43.8 31.92

Table 4.12 Estimates of specific combining ability effects of hybrids for seedling vigour and anaerobic germination related traits during *rabi* 2016-17

Hybrids	Germination % on 10th day	Germination % on 14th day	Seedling shoot length on 10th day (cm)	Seedling shoot length on 14th Day (cm)	Seedling root length on 10th day (cm)	Seedling root length on 14th day (cm)	Seedling fresh weight on 14th day (mg)
AC39397*MTU1010	-9.04**	-7.92**	0.10	-0.23	0.34	0.61	0.25
AC39397*MTU1121	9.04 **	7.92**	-0.10	0.23	-0.34	-0.61	-0.25
AC39416A*MTU1010	-4.54**	-2.92	-0.15	0.07	0.26	0.21	4.75
AC39416A*MTU1121	4.54**	2.92	0.15	-0.07	-0.26	-0.21	-4.75
Azucena*MTU1010	12.21**	10.33**	-0.35	-0.06	-0.36	-0.34	-1.25
Azucena*MTU1121	-12.21**	-10.33**	0.35	0.06	0.36	0.34	1.25
BPT2270*MTU1010	-5.79**	-3.42 *	-0.40	-0.23	0.41	-0.27	0.00
BPT2270*MTU1121	5.79**	3.42*	0.40	0.23	-0.41	0.27	0.00
MTU 1140*MTU1010	-0.79	-2.67	-0.55*	-0.08	-0.46	-0.49	1.25
MTU 1140*MTU1121	0.79	2.67	0.55*	0.08	0.46	0.49	-1.25
N-22*MTU1010	7.96**	6.58**	1.35**	0.54	-0.19	0.28	-5.00
N-22*MTU1121	-7.96**	-6.58**	-1.35**	-0.54	0.19	-0.28	5.00
CD 95% SCA	2.80	3.28	0.50	1.00	0.63	1.00	12.78

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

Table. 4.12 (Cont.).

Hybrids	Seedling dry weight (mg)	Seedling vigour index I	Seedling vigour index II	Anaerobic germination % after 2 weeks of submergence	Plant survival % after 2 weeks	Anaerobic germination % after 3 weeks of submergence	Plant survival% after 3 weeks
AC39397*MTU1010	0.08	-1.27*	-1.37*	3.14	0.95	-3.83**	-2.68**
AC39397*MTU1121	-0.08	1.27 *	1.37 *	-3.14	-0.95	3.83 **	2.68**
AC39416A*MTU1010	0.48	-0.03	-0.39	3.47	-1.03	-2.09	0.06
AC39416A*MTU1121	-0.48	0.03	0.39	-3.47	1.03	2.09	-0.06
Azucena*MTU1010	-0.02	1.45*	1.52 *	-6.60*	-1.16	3.71**	2.87**
Azucena*MTU1121	0.02	-1.45 *	-1.52 *	6.60*	1.16	-3.71**	-2.87 **
BPT2270*MTU1010	0.06	-0.39	-0.63	-3.61	0.71	-3.30 **	-0.68
BPT2270*MTU1121	-0.06	0.39	0.63	3.61	-0.71	3.30**	0.68
MTU 1140*MTU1010	0.33	-0.20	-0.52	-0.29	-0.29	-3.49**	1.11
MTU 1140*MTU1121	-0.33	0.20	0.52	0.29	0.29	3.49**	-1.11
N-22*MTU1010	-0.94	0.44	1.39 *	3.88	0.82	9.00***	-0.68
N-22*MTU1121	0.94	-0.44	-1.39*	-3.88	-0.82	-9.00***	0.68
CD 95% SCA	1.18	1.11	1.10	6.39	4.64	2.25	1.77

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

Table 4.14 Top ranking desirable crosses for specific combining ability with their *per se* performance

S. No.	Character	Predominant gene action, GCA/SCA variance	Crosses	GCA of Parents	Value of SCA effect
1	**Germination % on 10th day**	0.07 Non additive	Azucena x MTU 1010 AC 39397 x MTU 1121 AC 39416A x MTU 1121	high x low high x low high x low	12.21 9.04 4.54
2	**Germination % on 14th day**	0.11 Non additive	Azucena x MTU 1010 AC 39397 x MTU 1121 N 22 x MTU 1010	low x high high x low low x high	10.33 7.92 6.58
3	**Seedling shoot length on 10th day (cm)**	1.22 Additive	N 22 x MTU 1010 AC 39416A x MTU 1010	high x high high x high	1.35 0.15
4	**Seedling shoot length on 14th day (cm)**	-46.27 Non additive	N 22 x MTU 1010 AC 39416A x MTU 1010	high x low high x low	0.54 0.07
5	**Seedling root length on 10th day (cm)**	1.12 Additive	AC 39416A x MTU 1010 MTU 1140 x MTU 1121	high x low low x high	0.26 0.46
6	**Seedling root length on 14th day (cm)**	1.19 Additive	AC 39416A x MTU 1010 AC 39416A x MTU 1121	high x low high x low	0.34 0.34
7	**Seedling fresh weight on 14th day (mg)**	-3.69 Non additive	MTU 11140 x MTU 1010 AC 39416A x MTU 1010	high x low high x low	1.25 4.75

Table. 4.14 (Cont.).

8	**Seedling dry weight (mg)**	9.28 Additive	N22 x MTU 1121	high x low	0.94
9	**Seedling vigour index I**	1.2 Additive	AC 39416A x MTU 1010 AC 39397 x MTU 1121 Azucena x MTU 1010	high x low high x low low x high	0.03 1.27 1.45
10	**Seedling vigour index II**	0.78 Non additive	Azucena x MTU 1010 N 22 x MTU 1010	high x low high x low	1.52 1.39
11	**Anaerobic germination % after 2 weeks of submergence**	0.04 Non additive	N 22 x MTU 1010 Azucena x MTU 1121	high x low low x low	3.88 6.60
12	**Plant survival % after 2 weeks**	-0.74 Non additive	MTU 1140 x MTU 1010	high x low	0.29
13	**Anaerobic germination % after 3 weeks of submergence**	0.16 Non additive	N 22 x MTU 1010 Azucena x MTU 1010 AC 39397 x MTU 1121	low x high high x high low x high	9.00 3.71 3.83
14	**Plant survival% after 3 weeks**	0.70 Non additive	MTU 1140 x MTU 1010 AC 39397 x MTU 1121 Azucena x MTU 1010	high x low high x low low x high	1.11 2.68 2.87

Table 4.10 The estimates of genetic components of variance and proportional contribution of lines, testers and line × tester interaction to total variance during *rabi* 2016-17

Source	Germination % on 10th day	Germination % on 14th day	Seedling shoot length on 10th day (cm)	Seedling shoot length on 14th Day (cm)	Seedling root length on 10th day (cm)	Seedling root length on 14th day (cm)	Seedling fresh weight on 14th day (mg)
Due to lines	35.70	37.65	72.17	95.51	82.95	79.52	72.28
Due to testers	0.68	2.97	13.06	3.27	3.02	2.86	20.16
Line x Tester	63.61	59.37	14.76	1.21	14.02	17.60	7.55
σ^2 GCA	10.32	10.06	1.12	1.87	0.23	0.19	49.67
σ^2 SCA	137.95	93.81	0.92	-0.04	0.21	0.16	-13.43
σ^2 GCA/ σ^2 SCA	0.07	0.10	1.21	-46.27	1.11	1.19	-3.69

Source	Seedling dry weight (mg)	Seedling vigour index I	Seedling vigour index II	Anaerobic germination % after 2 weeks of submergence	Plant survival % after 2 weeks	Anaerobic germination % after 3 weeks of submergence	Plant survival% after 3 weeks
Due to lines	96.40	86.07	76.76	11.20	62.42	25.65	79.57
Due to testers	0.54	2.42	5.49	9.66	24.01	11.97	2.76
Line x Tester	3.05	11.49	17.73	79.12	13.55	62.36	17.66
σ^2 GCA	11.94	1.68	1.97	1.41	1.96	9.12	4.48
σ^2 SCA	0.20	1.38	2.51	29.01	-2.62	53.72	6.38
σ^2 GCA/ σ^2 SCA	9.28	1.21	0.78	0.04	-0.74	0.16	0.70

Table 4.9 Mean performance of parents and crosses for different characters in rice (*Oryza sativa* L.)

L × T	Germination % on 10th day	Germination % on 14th day	Seedling shoot length on 10th day (cm)	Seedling shoot length on 14th Day (cm)	Seedling root length on 10th day (cm)	Seedling root length on 14th day (cm)	Seedling fresh weight on 14th day (mg)
AC 39397	81.00	82.00	11.00	14.85	13.40	14.60	88.00
AC 39416A	95.00	95.50	10.75	12.80	12.45	14.70	132.00
Azucena	79.00	80.50	15.80	16.80	8.65	13.65	65.50
BPT 2270	87.50	88.00	6.05	8.17	10.55	12.15	65.50
MTU 1140	91.00	92.00	9.80	13.65	12.00	13.30	81.00
N-22	85.00	86.50	16.00	17.10	9.70	15.40	70.50
Lines mean	86.42	87.41	11.56	13.89	11.12	13.96	83.75
MTU 1010	97.00	97.00	7.20	9.05	8.95	10.25	68.50
MTU 1121	95.00	96.00	6.85	9.85	9.10	10.55	65.00
Tester mean	96.00	96.50	7.02	9.45	9.02	10.40	66.75
AC 39397*MTU1010	69.00	72.50	10.25	14.50	10.70	11.60	72.50
AC 39397*MTU1121	85.50	85.50	8.85	14.10	10.35	10.70	62.50
AC 39416A*MTU 1010	81.00	86.00	11.05	16.10	13.10	13.65	87.00
AC 39416A*MTU 1121	88.50	89.00	10.15	15.10	12.90	13.55	68.00
Azucena*MTU 1010	88.00	91.00	10.80	15.85	10.10	10.65	56.50

Table. 4.9 (Cont.).

Azucena*MTU 1121	62.00	67.50	10.30	15.10	11.15	11.65	49.50
BPT 2270*MTU 1010	65.00	71.00	7.20	9.20	11.15	11.50	56.50
BPT 2270*MTU 1121	75.00	75.00	6.80	8.80	10.65	12.35	47.00
MTU 1140*MTU 1010	68.50	72.00	8.10	14.10	10.35	10.85	74.50
MTU 1140*MTU 1121	68.50	74.50	8.00	13.40	11.60	12.15	62.50
N-22*MTU 1010	78.00	82.50	12.60	16.70	10.40	11.95	63.00
N-22*MTU 1121	60.50	66.50	8.70	14.75	11.10	11.70	63.50
Parental mean	88.81	89.68	10.43	12.78	10.60	13.07	79.50
General mean	80	82.52	9.81	13.49	10.91	12.34	69.95
Cross mean	74.12	77.75	9.40	13.97	11.12	11.85	63.58
CD at 5%	3.70	4.40	0.60	1.30	0.85	1.350	17.30
CV %	2.20	2.50	3.20	4.77	3.70	5.20	11.70

Table. 4.9 (Cont.).

L × T	Seedling dry weight (mg)	Seedling vigour index I	Seedling vigour index II	Anaerobic germination % after 2 weeks of submergence	Plant survival % after 2 weeks	Anaerobic germination % after 3 weeks of submergence	Plant survival% after 3 weeks
AC39397	16.10	13.20	12.18	73.57	63.97	54.32	35.24
AC39416A	15.49	14.80	12.20	74.29	55.48	52.81	43.83
Azucena	13.38	10.76	13.52	54.92	35.03	33.51	17.94
BPT2270	8.60	7.57	7.19	68.85	53.42	36.83	28.27
MTU 1140	16.25	14.92	12.55	68.01	54.32	45.55	31.92
N-22	15.75	13.62	14.79	57.64	32.94	27.18	23.95
Lines mean	14.26	12.47	12.07	66.21	49.19	41.70	30.19
MTU 1010	11.10	10.76	8.78	61.36	28.62	45.55	12.73
MTU 1121	12.60	12.10	9.45	44.98	32.86	35.05	18.43
Testers mean	11.85	11.43	9.12	53.17	30.74	40.30	15.58
AC39397*MTU1010	17.25	12.51	10.52	33.77	16.69	14.95	6.50
AC39397*MTU1121	16.70	14.28	12.05	24.74	12.46	18.43	10.51
AC39416A*MTU1010	16.85	14.49	13.85	36.26	12.73	12.92	7.20
AC39416A*MTU1121	15.50	13.80	13.44	26.55	12.46	12.92	5.74
Azucena*MTU1010	14.55	13.24	14.43	25.82	14.47	26.55	7.09
Azucena*MTU1121	14.20	9.58	10.19	36.26	14.47	14.95	0.00
BPT2270*MTU1010	10.05	7.13	6.53	30.80	13.98	10.51	0.00
BPT2270*MTU1121	9.55	7.16	6.60	35.25	10.24	12.92	0.00
MTU 1140*MTU1010	16.95	12.20	10.15	33.20	18.43	14.95	10.51

Table. 4.9 (Cont.).

MTU 1140*MTU1121	15.90	11.85	9.99	31.01	16.69	17.74	6.93
N-22*MTU1010	16.40	13.55	13.80	39.17	14.47	29.42	0.00
N-22*MTU1121	17.90	11.90	9.83	28.65	10.51	7.23	0.00
Parental mean	14.55	11.97	11.10	44.25	26.21	26.21	13.34
General mean	15.15	11.80	10.94	31.78	13.96	16.12	4.54
Cross mean	13.65	12.21	11.33	62.95	44.58	41.35	26.54
CD at 5%	1.59	1.50	1.49	8.66	6.29	3.00	2.40
CV %	5.20	5.90	6.37	9.28	11.38	5.51	8.53

Table 4.8 Analysis of variance for combining ability for 14 different characters during *rabi* 2016-2017

	Df	Germination % on 10th day	Germination % on 14th day	Seedling shoot length on 10th day (cm)	Seedling shoot length on 14th Day (cm)	Seedling root length on 10th day (cm)	Seedling root length on 14th day (cm)	Seedling fresh weight on 14th day (mg)
Replicates	1.00	1.60	4.22	0.01	0.09	0.00	0.53	0.10
Treatments	19.00	258.37**	187.55 **	14.87**	16.76 **	3.64**	4.59 **	651.99**
Parents	7.00	91.99**	82.56**	29.46**	23.89**	6.52**	7.42**	1038.57**
Parents (Line)	5.00	72.88**	65.88**	28.85**	21.46**	6.47**	2.74**	1278.15**
Parents (Testers)	1.00	4.00	1.00	0.12	0.64	0.02	0.09	12.25
Parents (L vs T)	1.00	275.52**	247.52**	61.88**	59.27**	13.23**	38.16**	867.00**
Parents vs Crosses	1.00	2070.94**	1368.04 **	10.21**	13.62 **	2.69**	14.21**	2432.07**
Crosses	11.00	199.47**	147.05**	6.01**	12.51**	1.90**	1.91**	244.17**
Line Effect	5.00	156.68	121.80	9.54	26.29**	3.47*	3.34	388.27*
Tester Effect	1.00	15.04	48.17	8.64	4.51 *	0.63	0.60	541.50*
Line * Tester Eff.	5.00	279.14**	192.07**	1.95**	0.33	0.59*	0.74	40.60
Error	19.00	3.23	4.44	0.10	0.41	0.16	0.41	67.47
Total	39.00	127.49	93.64	7.30	8.37	1.85	2.45	350.51

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

Table. 4.8 (Cont.).

	Df	Seedling dry weight (mg)	Seedling vigour index I	Seedling vigour index II	Anaerobic germination % after 2 weeks of submergence	Plant survival % after 2 weeks	Anaerobic germination % after 3 weeks of submergence	Plant survival% after 3 weeks
Replicates	1.00	0.16	0.32	0.42	17.17	36.84	8.96	1.82
Treatments	19.00	15.35**	12.10**	13.23**	591.46**	616.06 **	436.96**	343.77**
Parents	7.00	15.35**	12.22**	13.41**	205.73**	367.48**	187.76**	212.54**
Parents (Line)	5.00	17.56**	16.09**	13.44**	132.27**	306.65**	239.61**	162.92**
Parents (Testers)	1.00	2.25	1.78	0.45	268.47**	17.98	110.36 **	32.49**
Parents (L vs T)	1.00	17.45**	3.29*	26.21**	510.32**	1021.12**	5.87	640.65**
Parents vs Crosses	1.00	21.35**	1.61	1.45	9324.19**	8997.99**	6109.80**	4646.05**
Crosses	11.00	14.80**	12.98**	14.19**	43.03*	12.26	79.83**	36.17**
Line Effect	5.00	31.38**	24.58*	23.96	10.61	16.84	45.06	63.33
Tester Effect	1.00	0.88	3.47	8.58	45.76	32.39*	105.17	10.99
Line * Tester Eff.	5.00	0.99	3.28**	5.53**	74.90**	3.66	109.54**	14.06**
Error	19.00	0.57	0.51	0.50	16.88	8.91	2.09	1.30
Total	39.00	7.76	6.15	6.70	296.81	305.42	214.13	168.16

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

4. Molecular Characterization

The Morphological marker characters may be qualitative or quantitative in nature. They may be governed by one or more genes. The quantitative characters are influenced by environment, which indicates that such characters are not stable hence cannot be used as marker trait whereas qualitative traits may be used as morphological markers with low reliability in characterization of germplasm because they are less influenced by environment. The molecular markers are DNA based markers and represent the genetic constitution of any individual. DNA of any individual does not get influenced by environment; hence the DNA based markers are supposed to be stable marker to diagnose any trait. Molecular markers are powerful tools in the assessment of genetic variation, elucidation of genetic relationships within and among species and to aid in the management of plant genetic resources. In the present study, 8 parents (6 lines, 2 testers) and 12 F_1's generated by mating in Line x Tester (L x T) design are used for molecular characterization.

The F_1's along with parents were screened with 24 linked SSR markers for specific traits *viz.*, RM 478, RM 104, RM 341, RM 253 RM 520, RM 105, RM 210, RM 263 and RM 206 associated with anaerobic germination, RM 231 and RM 7 associated with rate of germination, RM 201 and RM 234 associated with root length, RM 214, RM 5509, RM 20557, RM 306, RM 152 and RM 208 associated with culm diameter, RM 17 associated with seedling height, RM 270 associated with seedling vigour. RM 10, RM 172 and RM 346 associated with culm strength. Among 24 SSR markers used, 13 were found polymorphic for specific parental combinations *viz.*, RM 231, RM 206, RM 520, RM 346, RM 17, RM 263, RM 172, RM 253, RM 5509, RM 341, RM 208, RM 152 and RM 478 for those specific traits.

Table 4.13 List of markers that have shown polymorphism between parents

S. No.	F_1's	Markers
1	AC 39416 A x MTU 1010	RM 231, RM 520, RM 341, RM 208, RM 478, RM 152
2	AC 39397 x MTU 1010	RM 253
3	MTU 1140 x MTU 1010	RM 206, RM 172, RM 208, RM 152, RM 478
4	Azucena x MTU 1010	RM 231, RM 520, RM 346
5	BPT 2270 x MTU 1010	RM 206, RM 172, RM 253
6	N 22 x MTU 1010	RM 231, RM 206, RM 346, RM 17, RM 253, RM 341, RM 208
7	AC 39416 A x MTU 1121	RM 478, RM 152, RM 208, RM 253, RM 5509, RM 341, RM 231, RM 206, RM 520, RM 346, RM 17
8	AC 39397 x MTU 1121	RM 206, RM 346, RM 17, RM 263, RM 5509
9	MTU 1140 x MTU 1121	RM 346, RM 17, RM 172, RM 253, RM 208, RM 478, RM 152
10	Azucena x MTU 1121	RM 231, RM 206, RM 520, RM 17, RM 253
11	BPT 2270 x MTU 1121	RM 172
12	N 22 x MTU 1121	RM 231, RM 17, RM 5509, RM 341, RM 208

RM 231

The marker, RM 231, was associated with rate of germination and is located on the chromosome number 3. It showed parental polymorphism between these lines and testers *viz.*, Azucena x MTU 1010, AC 39416 A x MTU 1010, N 22 X MTU 1010, Azucena x MTU 1121, AC 39416A x MTU 1121 and N 22 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing.

RM 206

The marker, RM 206 associated with anaerobic germination, is located on the chromosome number 11, showed parental polymorphism between these lines and testers *viz.*, MTU 1140 x MTU 1010, N 22 x MTU 1010, BPT 2270 x MTU 1010,

Azucena x MTU 1121, AC 39416A x MTU 1121 and AC 39397 x MTU 1121. So this marker was used for screening F_1's of respective crosses to identify heterozygous plants shown in (plate 4.1B).

RM 520

The marker, RM 520 associated with anaerobic germination, is located on the chromosome number 3, showed parental polymorphism between these lines and testers *viz*., Azucena x MTU 1010, AC 39416 A x MTU 1010, AC 39416A x MTU 1121 and Azucena x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants.

RM 346

The marker, RM 346, was associated with culm strength and is located on the chromosome number 7. It showed parental polymorphism between these lines and testers *viz*., Azucena x MTU 1010, N 22 x MTU 1010,MTU 1140 x MTU 1121, AC 39416A x MTU 1121and AC 39397 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing shown in (plate 4.1 A).

RM 17

The marker, RM 17 associated with rate of germination showed parental polymorphism between these lines and testers *viz*., N 22 x MTU 1010, N 22 x MTU 1121, AC 39397 x MTU 1121, MTU 1140 x MTU 1121, Azucena x MTU 1121and AC 39416A x MTU 1121. So this marker was used for screening F_1's of respective crosses to identify heterozygous plants.

RM 263

The marker, RM 263 associated with anaerobic germination, is located on the chromosome number 2, showed parental polymorphism between this line and tester *viz*., AC 39397 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing.

RM 172

The marker, RM 172 associated with culm strength and is located on the chromosome number 7 showed parental polymorphism between these lines and testers *viz.*, MTU 1140 x MTU 1121, MTU 1140 x MTU 1010, BPT 2270 x MTU 1010 and BPT 2270 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants.

RM 253

The marker, RM 253 associated with anaerobic germination and is located on the chromosome number 6, showed parental polymorphism between these lines and testers *viz.*, MTU 1140 x MTU 1121, Azucena x MTU 1121, AC 39416A x MTU 1121, AC 39397 x MTU 1010, N 22 X MTU 1010 and BPT 2270 x MTU 1010. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing.

RM 5509

The marker, RM 5509 associated with culm diameter, is located on the chromosome number 6, showed parental polymorphism between these lines and testers *viz.*, AC 39416A x MTU 1121, AC 39397 x MTU 1121 and N 22 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing.

RM 341

The marker, RM 341 associated with anaerobic germination, is located on the chromosome number 2, showed parental polymorphism in (plate 4.1 C) between these lines and testers *viz.*, AC 39416 A x MTU 1010, AC 39416A x MTU 1121, N 22 X MTU 1010 and N 22 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing.

RM 208

The marker, RM 208 associated with culm diameter, is located on the chromosome number 2, showed parental polymorphism between these lines and testers *viz.*, MTU 1140 x MTU 1121, MTU 1140 x MTU 1010, AC 39416 A x MTU

1010, AC 39416A x MTU 1121, N 22 X MTU 1010 and N 22 x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants.

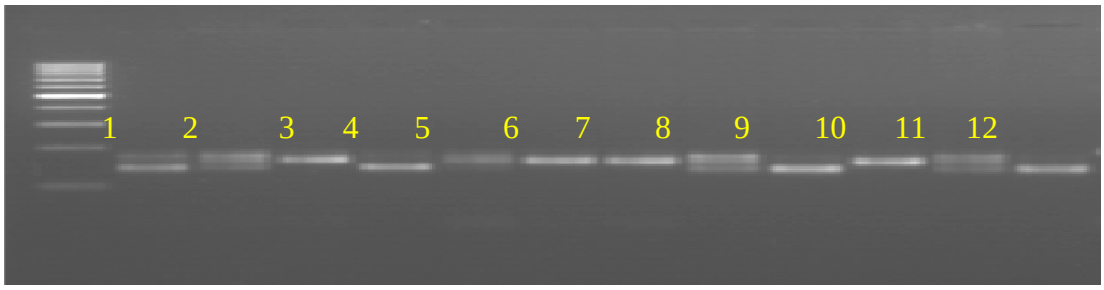
RM 152

The marker, RM 152, was associated with culm diameter and is located on the chromosome number 8. It showed parental polymorphism between these lines and testers *viz*., MTU 1140 x MTU 1121, MTU 1140 x MTU 1010, AC 39416A x MTU 1010 and AC 39416A x MTU 1121. So this marker was used for screening F_1's of respective crosses to identify heterozygous plants.

RM 478

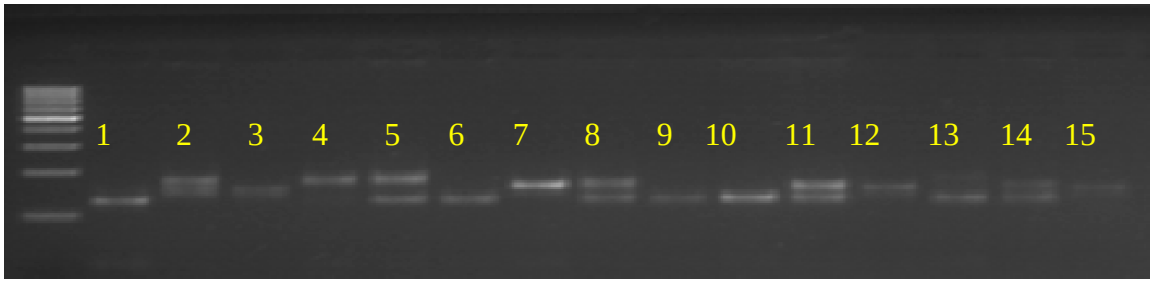
The marker, RM 478, was associated with anaerobic germination and is located on the chromosome number 7. It showed parental polymorphism between these lines and testers *viz*., MTU 1140 x MTU 1121, MTU 1140 x MTU 1010, AC 39416 A x MTU 1010 and AC 39416A x MTU 1121. So this marker was used for screening F_1's of respective crosses, identified heterozygous plants and tagged for selfing.

A) Confirmation of F_1's with RM 346



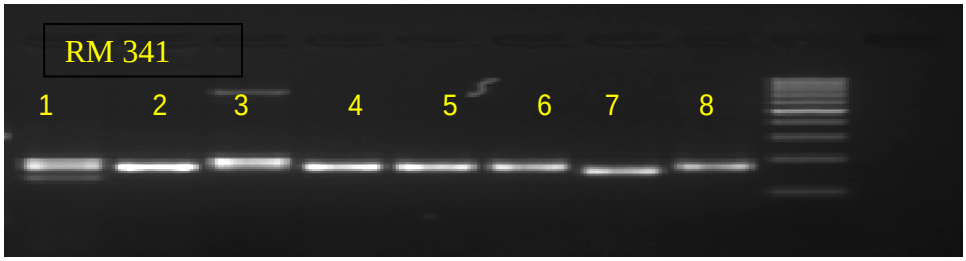
1. Azucena, **2.** Azucena x MTU 1010, **3.** MTU 1010, **4.** N22, **5.** N 22 x MTU 1010, **6.** MTU 1010, **7.** AC 39416A, **8.** AC 39416 A x MTU 1121, **9.** MTU 1121, **10.** MTU 1140, **11.** MTU 1140 x MTU 1121, **12.** MTU 1121.

B) Confirmation of F_1's with RM 206



1. BPT 2270, 2. BPT 2270 x MTU 1010, 3. MTU 1010, 4.Azucena, 5.Azucena x MTU 1121, 6. MTU 1121, 7. AC 39416A, 8.AC 39416A x MTU 1121, 9. MTU 1121, 10.N 22, 11. N 22 x MTU 1010, 11. MTU 1010, 12.MTU 1140, 13.MTU 1140, 14.MTU 1140 x MTU 1010, 15. MTU 1010.

C) Plate showing polymorphism among Lines and Testers



1. BPT 2270 (L), 2. MTU 1140 (L), 3. Azucena (L), 4. AC 39416 A (L), 5. MTU 1010 (T), 6. MTU 1121(T), 7. AC 39397 (L), 8.N 22 (L), 9. BPT 2270 (L).

Plate 4.1 Molecular Characterization of F_1's with established SSR markers

Chapter V

SUMMARY AND CONCLUSIONS

Rice (*Oryza sativa* L.) is an important food crop for over half of the world's population. Transplantation of rice seedlings is the most common practice in intensive rice cultivation. Alternatively, various pattern of direct seeding method are also used depending on the agro ecological conditions. Transplanting rice has some drawbacks, including increased labour requirement and exposure of 'transplant shock' that delays rice harvesting for 7-15 days. The adoption of the direct-seeding method would significantly reduce the cost of rice production in the lowland cultivation system in South East Asia and some other parts of the world including India. Faster and easier planting reduced requirements for water and labour makes the direct seeding method economically more profitable. In addition, the significance of grain quality varies depending upon the requisites established by the international market, ethnic customs, uses *etc* and is also important for all people involved in supply chain *i.e.,* production, processing and consumption. In rice, the quality parameters play an important role in fetching the foreign currency to the Indian exchequer.

However, direct seeded rice practice has been hindered by poorly levelled fields, heavy rainfall and poor drainage which cause accumulation of water in the fields shortly after sowing leading to poor crop establishment. There is also high weed infestation and potential damage possible by rodents and birds which reduce the plant stand. So there is a need for varieties that can germinate in flooded soils with high seedling vigour, as it is beneficial for direct seeded systems not only in low land areas but also for intensive irrigated systems where early flooding can suppress weeds.

Information on nature and magnitude of variability for these traits present in a population due to genetic and non-genetic causes is an important prerequisite for systematic breeding programs to improve yield potential of the crop. To date no specific variety was released for direct sowing conditions.Hence this study was undertaken to study variability parameters, diversity for yield and yield components in field, early vigour traits and anaerobic germination in lab for fifty genotypes. The present investigation "Genetic studies on anaerobic germination and seedling vigour

traits in rice (*Oryza sativa* L.)" was carried out during *kharif* 2016 at APRRI& RARS, Maruteru, Andhra Pradesh. Fifty genotypes were collected from Department of Genetics and Plant Breeding, APRRI& RARS, Maruteru and evaluated during *kharif* 2016. In *rabi* 2016-17 to study combining ability and gene action for seedling vigour and anaerobic germination traits, crossing was done in L x T fashion by taking 6 lines and 2 testers (12 F_1's) among 50 diverse genotypes based on seedling vigour and anaerobic germination performance in earlier season. Molecular screening was also done for F_1's along with parents for AG and SV related traits with 24 trait linked SSR markers.

Data was recorded on plant height at maturity (cm), days to 50% flowering, number of panicles/plant, panicle length (cm), number of grains/panicle, spikelet fertility (%), grain yield/Plant (g), test weight (g), hulling (%), milling (%), head rice recovery (%), kernel length (mm), kernel breadth (mm), kernel L/B Ratio, kernel elongation ratio, volume expansion ratio, culm diameter (mm), bending strength, leaf area index, harvest index, germination % on 10^{th} day, germination % on 14^{th} day (Rate of germination), SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SVI -1, SVI -2, AG % after 2 weeks of submergence, survival % after 2 weeks, AG % after 3 weeks of submergence, Survival % after 3 weeks. In *rabi* 2016-17 data was collected on germination % on 10^{th} day, germination % on 14^{th} day (Rate of germination), SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SVI -1, SVI -2, AG % after 2 weeks of submergence, survival % after 2 weeks, AG % after 3 weeks of submergence and survival % after 3 weeks for F_1 ' s along with parents.

The analysis of variance indicated significant differences among fifty treatments for all the 34 characters studied. The genetic variability studies indicated that the material used in the present investigation possessed considerable variability which provides sufficient basis for selection by the breeder. The results of genetic parameters revealed that moderate to high GCV, PCV coupled with high heritability and high genetic advance as percent of mean were observed for plant height at maturity (cm), days to 50% flowering, number of panicles/plant, number of grains/panicle, grain yield/plant (g), test weight, kernel L/B ratio, culm diameter,

bending strength, leaf area index, Harvest index, germination % on 10^{th} day, SSL on 10^{th} day (cm), SSL on 14^{th} day (cm), SRL on 10^{th} day (cm), SRL on 14^{th} day (cm), SFW on 14^{th} day (mg), SDW (mg), SV I -1, SV I -2, AG % after 2 weeks of submergence, plant survival % after 2 weeks, AG % after 3 weeks of submergence, plant survival % after 3 weeks suggesting the predominance of additive type of gene action in controlling these traits. Thus apparently important contribution of additive genetic variance is involved in the expression of these traits. Hence, good response to selection can be attained in early generations in improving these traits.

The remaining characters under study showed low to moderate estimates for genotypic and phenotypic coefficient of variation, moderate to high heritability estimates and low to high genetic advance as percent of mean indicating the role of both additive and non-additive gene effects in the expression of these traits. Hence, instead of simple selection, other methods like heterosis breeding or recurrent selection could be better.Based on high mean performance 6 lines were selected for crossing programme among 50 genotypes to test the combining ability. Genotypes exhibited significant mean performance for anaerobic germination (AC 39397, AC 39416A, MTU 1140) for shoot length (N 22, Azucena), for root length (AC 39397, AC 39416A), for dry weight (MTU 1140, AC 39416A, AC 39397), for seedling vigour index (AC 39416A, Azucena).

The distribution of 50 genotypes into eight clusters was at random with maximum number of 16 genotypes in cluster II. Cluster I was the second largest with 14 genotypes followed by cluster VII and VIII each with 11 and 5 genotypes respectively. The clusters III, IV, V and VI were with 1 genotype each and are solitary clusters. As could be seen in the results, cluster III, IV, V, VI were solitary clusters. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity.

As Survival % after 2 Weeks, Anaerobic germination % after 3 weeks of submergence, Anaerobic germination % after 2 weeks of submergence, Leaf area index, Seedling shoot length on 10^{th} day, Seedling shoot length on 14^{th} day together contributed 80% towards total divergence suggested that these characters should be taken into consideration while selecting parents for hybridization.

The maximum intra cluster D^2 value was 1750.148 for cluster VIII followed by 1334.415 for cluster VII, 1012.594 for cluster II, 570.977 for cluster I, while it was zero for cluster III, IV, V and VI. The high intra cluster distance in cluster VIII indicated the presence of wide genetic diversity among the genotypes *viz.*, BPT 3291, Tellahamsa, MTU 1001, IR- 64, MTU 1006. Cluster mean values showed wide range among the clusters studied, which indicates the presence of variation among the clusters present in the genotypes.

The analysis of variance for combining ability revealed significant differences among crosses for all the characters studied indicating high degree of variability in the material studied. While, line × tester effects were significant for majority of the characters except for seedling shoot length on 14th day (cm), seedling root length on 14th day (cm), seedling dry weight (mg), Survival % after 2 weeks. The analysis of variance for combining ability also revealed significant differences among the lines for the traits, seedling shoot length on 14th day (cm), seedling root length on 10th day (cm), Seedling fresh weight on 14th day (mg), seedling dry weight (mg), seedling vigour Index I **.** While, in testers significant difference was observed only for seedling shoot length on 14th day (cm), seedling fresh weight on 14th day (mg), survival % after 2 weeks.

Among the eight parents evaluated, based on their gca effects and their per se performance AC 39416A, AC 39397, MTU 1010, MTU 1121 were identified as good general combiners for rate of germination (%). While N-22, Azucena, AC 39416A were identified as good general combiners for shoot length (cm), AC 39397, AC 39416A, N 22 were identified as good general combiners for root length (cm). The parents AC 39416A, MTU 1140 were identified as good general combiners for seedling fresh weight (mg), while MTU 1140, N-22, AC 39397 were identified as good general combiners for seedling dry weight (mg). MTU 1140, N-22, AC 39416A were identified as good general combiners for seedling vigour index- I, N-22, AC 39416A, Azucena were identified as good general combiners for seedling vigour index –II, AC 39416A, AC 39397 were identified as good general combiners for anaerobic germination % after 2 weeks of submergence. The parents AC 39397, MTU 1140 were identified as good general combiners for plant survival % after 2 weeks while AC 39397, MTU 1010, Azucena were identified as good general combiners for anaerobic germination % after 3 weeks of submergence. For survival % after 3 weeks AC 39397, AC 39416A and MTU 1140 were identified as good general combiners.

The ratio of *gca* variance to *sca* variance was high indicating the predominance of additive gene action for Seedling shoot length on 10^{th} day (cm), Seedling root length on 10^{th} day (cm), Seedling root length on 14^{th} day (cm), Seedling dry weight (mg), Seedling vigour index I. These traits governed by additive gene action and may be improved by hybridization followed by simple selection procedures like pedigree breeding method. For the characters, germination % on 10^{th} day, germination % on 14^{th} day, seedling shoot length on 14^{th} day (cm), seedling fresh weight on 14^{th} day (mg), seedling vigour index II, anaerobic germination % after 2 weeks of submergence, plant survival % after 2 weeks, anaerobic germination % after 3 weeks of submergence, plant survival% after 3 weeks the ratio between *gca* variance and *sca* variance was low and indicated the role of non additive gene action. Non-additive gene action governing characters may be exploited through heterosis breeding.

Based on *sca* effects and *per se* performance, the crosses, Azucena x MTU 1010, AC 39397X MTU 1121, AC 39416A x MTU 1121, N 22 x MTU 1010 were found to be superior for rate of germination. While, N 22 x MTU 1010, AC 39416A x MTU 1010 were detected as good specific crosses for seedling shoot length (cm), AC 39416A x MTU 1010, MTU 1140 x MTU 1121, AC 39416A x MTU 1121 were found to be superior for seedling root length (cm), MTU 11140 x MTU 1010, AC 39416A x MTU 1010 were found to be superior for seedling fresh weight (mg). For seedling dry weight (mg), N 22 x MTU 1121, cross was found superior. The crosses, AC 39416A x MTU 1010, AC 39397 x MTU 1121, Azucena x MTU 1010 were detected as good specific crosses for seedling vigour index –I. While, Azucena x MTU 1010, N22 x MTU 1010 were found to be superior crosses for seedling vigour index –II, N22 x MTU 1010, Azucena x MTU 1121 were detected as good specific crosses for anaerobic germination % after 2 weeks of submergence, MTU 1140 x MTU 1010 was found to be superior cross for plant survival % for 2 weeks. The crosses N 22 X MTU 1010, Azucena X MTU 1010 and AC 39397 X MTU 1121 were detected as good specific crosses for anaerobic germination % after 3 weeks of submergence. For plant survival % for 3 weeks MTU 1140 x MTU 1010, AC 39397 x MTU 1121 and Azucena x MTU 1010 crosses were found superior.

Among the eight parents evaluated, based on their gca effects and their per se performance, AC 39416A, N-22 were identified as good general combiners for seedling vigour traits. The genotypes AC 39397, MTU 1140 and AC 39416A were identified as good general combiners for the anaerobic germination. These parents though they belong to same cluster based on Mahalanobis D^2 analysis their intra cluster distance is sufficient enough to use them in the breeding programme.

Molecular screening was done for F_1's along with parents for anaerobic germination and seedling vigour traits with 24 specific trait linked SSR markers *viz*., RM 478, RM 104, RM 341, RM 253 RM 520, RM 105, RM 210, RM 263 and RM 206 associated with Anaerobic germination , RM 231 and RM 7 associated with rate of germination, RM 201 and RM 234 associated with root length, RM 214, RM 5509, RM 20557, RM 306, RM 152 and RM 208 associated with culm diameter, RM 17 associated with seedling height, RM 270 associated with seedling vigour. RM 10, RM 172 and RM 346 associated with culm strength. Further, the markers which have shown parental polymorphism were used for screening to identify heterozygous plants in F_1 crosses.

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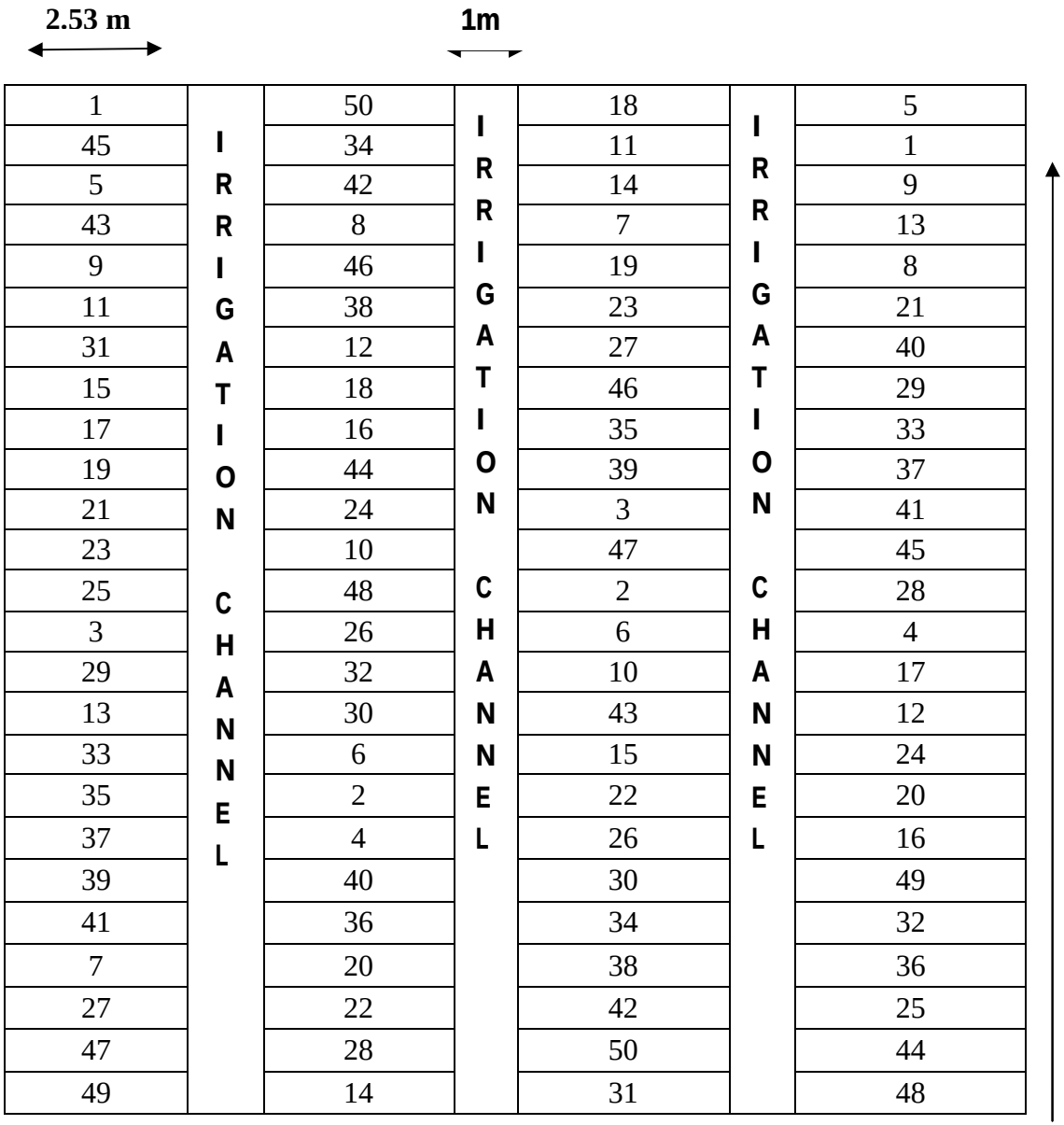
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Note: The literature is cited as per the "Thesis Guidelines" prescribed by Acharya N. G. Ranga Agricultural University, Guntur.



1	IRRIGATION CHANNEL	50	IRRIGATION CHANNEL	18	IRRIGATION CHANNEL	5
45		34		11		1
5		42		14		9
43		8		7		13
9		46		19		8
11		38		23		21
31		12		27		40
15		18		46		29
17		16		35		33
19		44		39		37
21		24		3		41
23		10		47		45
25		48		2		28
3		26		6		4
29		32		10		17
13		30		43		12
33		6		15		24
35		2		22		20
37		4		26		16
39		40		30		49
41		36		34		32
7		20		38		36
27		22		42		25
47		28		50		44
49		14		31		48

N

E

Design : Randomized Block Design (folded)

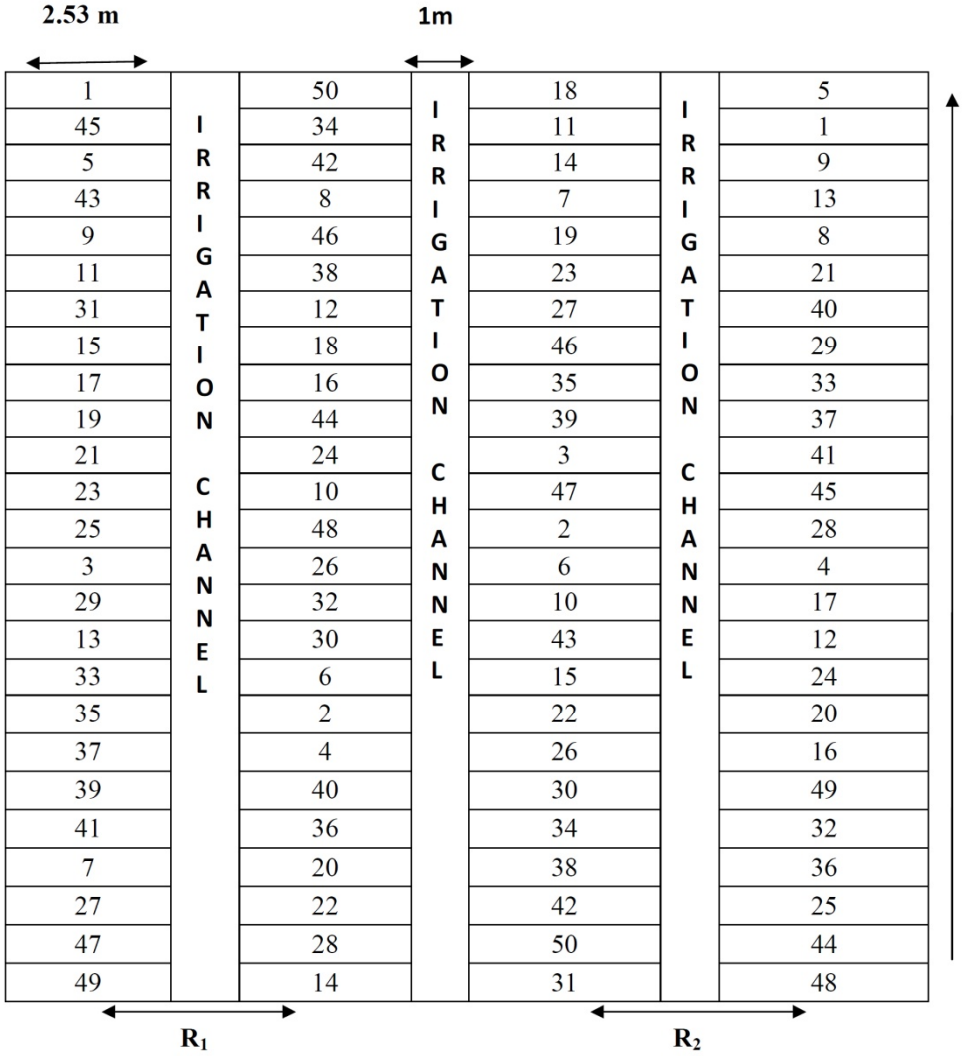
Replications : 2

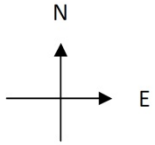
Genotypes : 50

Season : *Kharif*, 2016

Plot size : 6.4 m^2

Fig. 3.1 Experimental lay out





Design : Randomized Block Design (folded)

Replications : 2

Genotypes : 50

Season : *Kharif*, 2016

Plot size : 6.4 m^2

Fig. 3.1 Experimental lay out

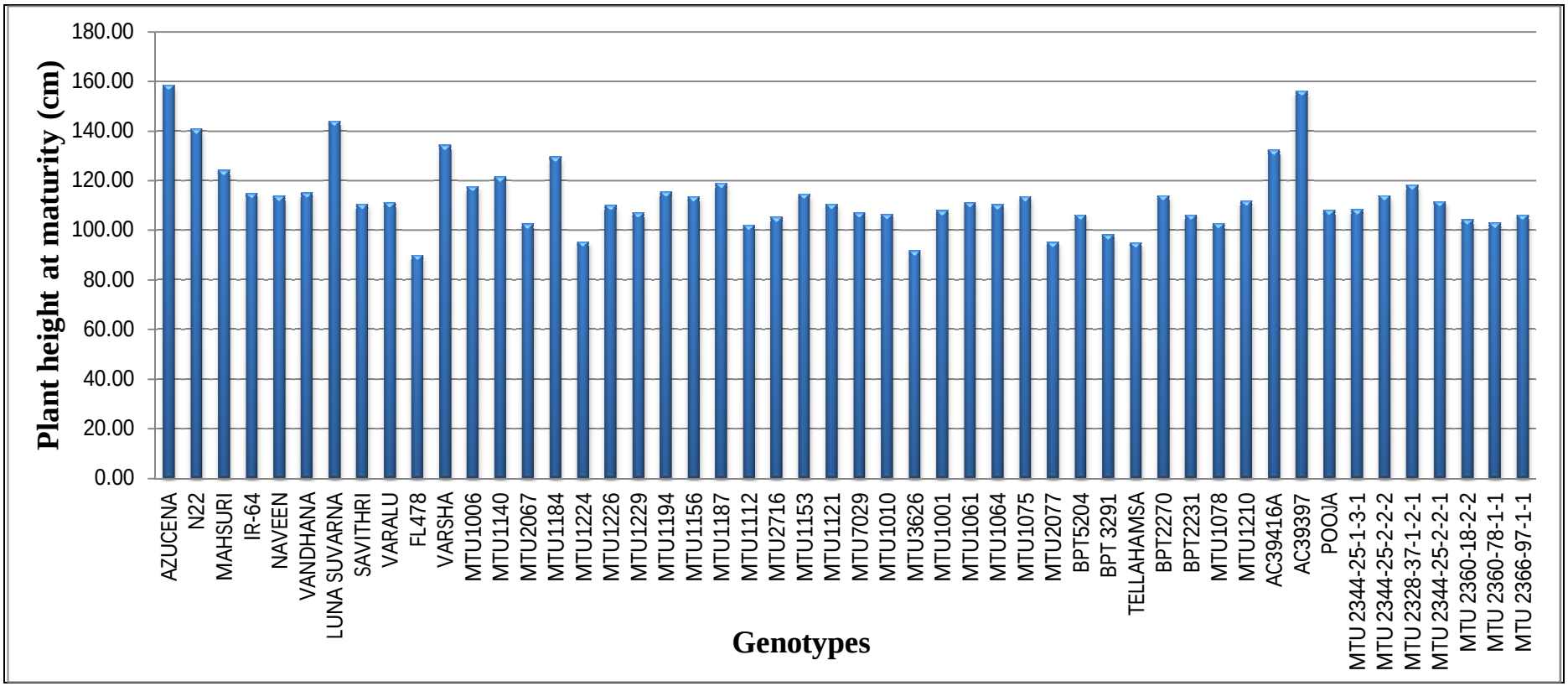


Fig. 4.2.1: Mean performance of 50 genotypes for plant height (cm)

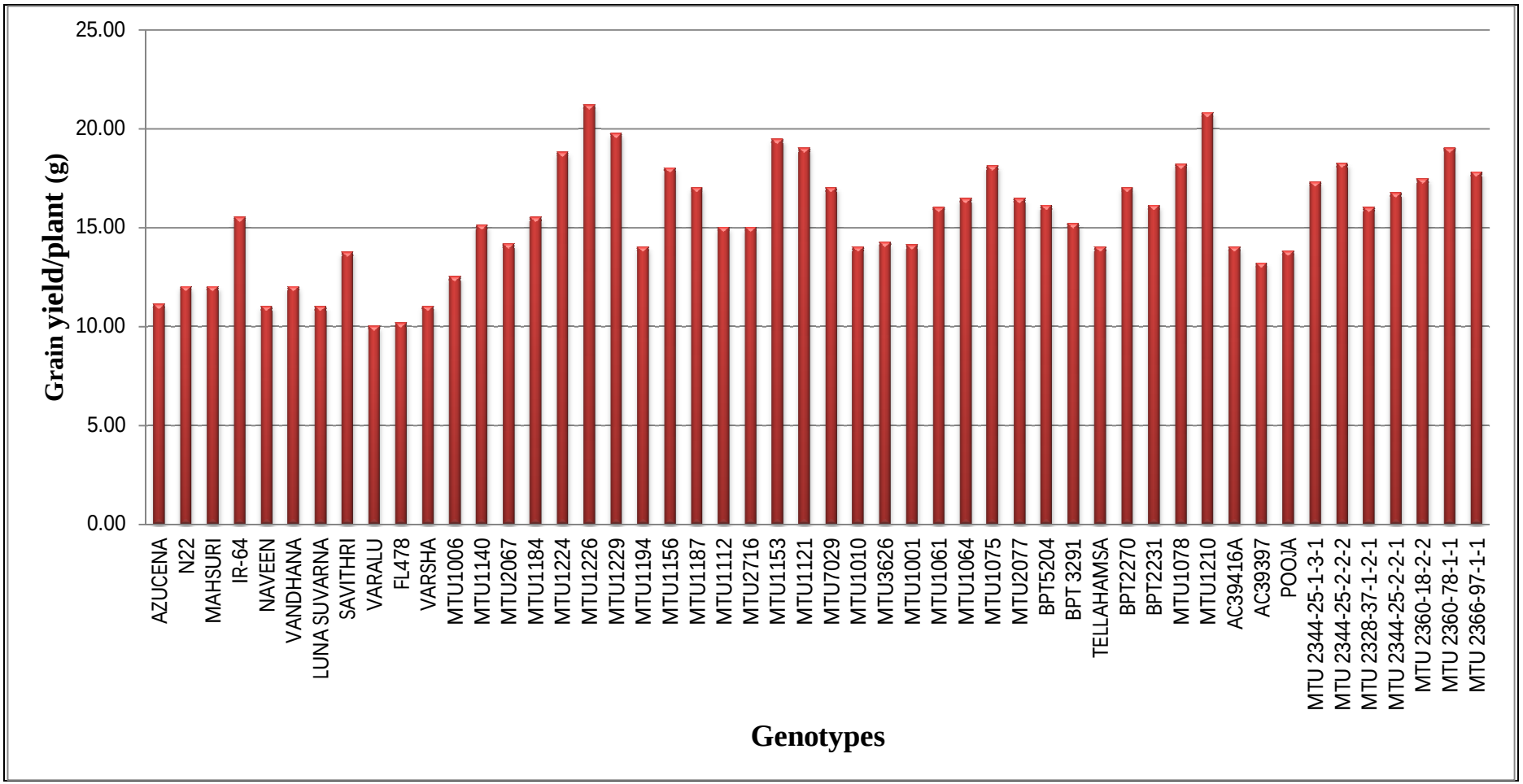


Fig. 4.2.2: Mean performance of 50 genotypes for Grain yield (g)

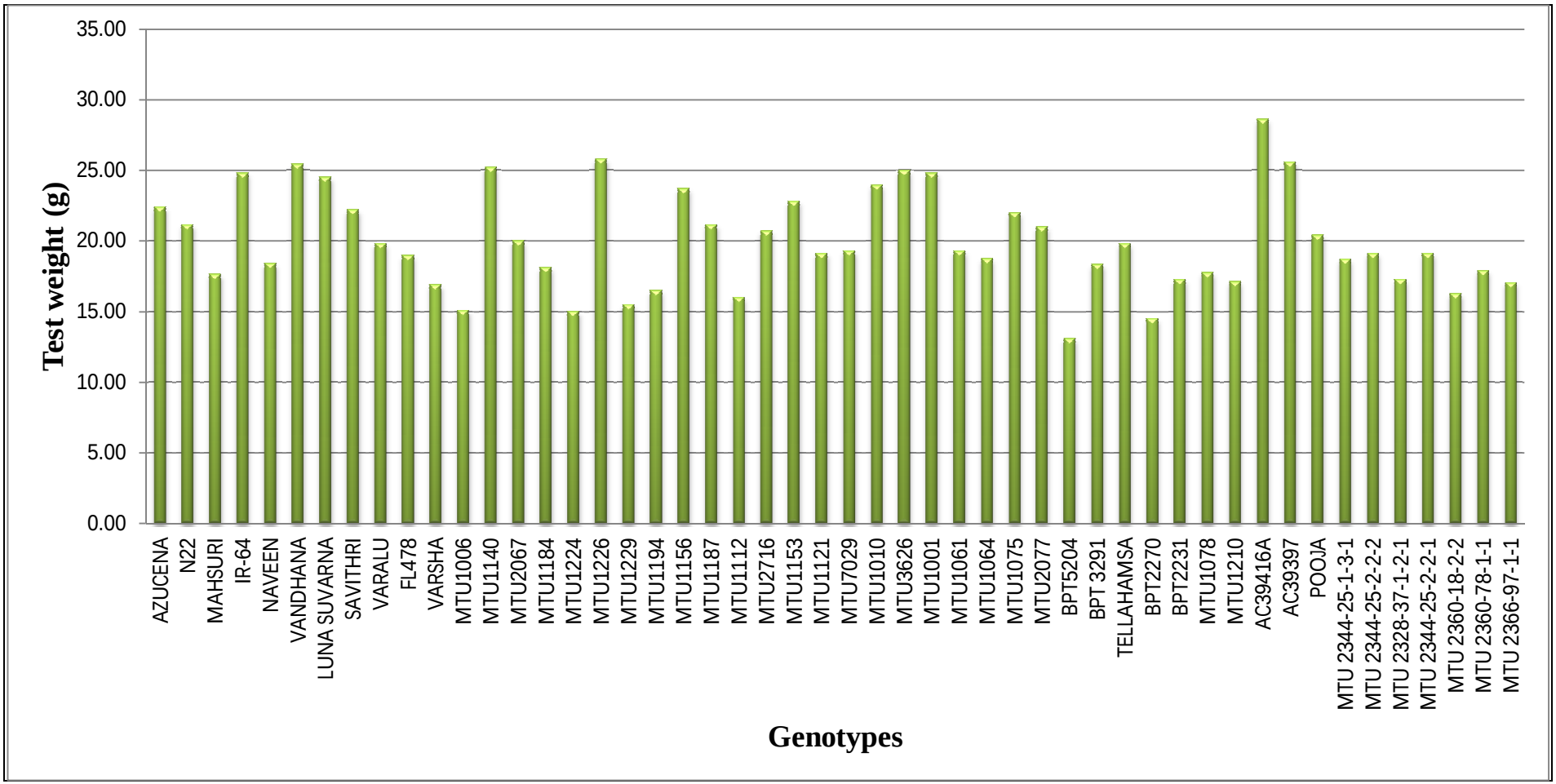


Fig. 4.2.3: Mean performance of 50 genotypes for Test weight (g)

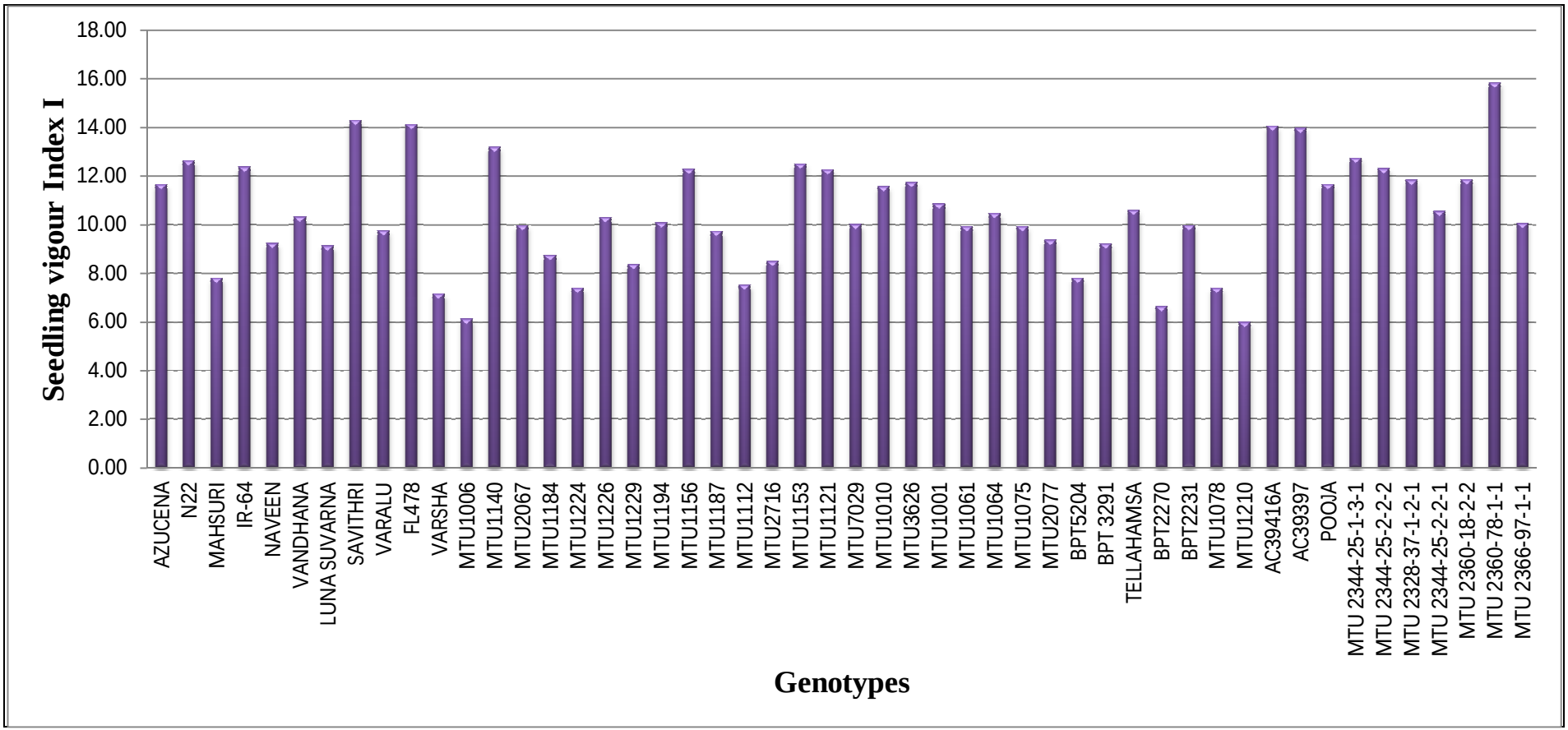


Fig. 4.2.4: Mean performance of 50 genotypes for seedling vigour index I

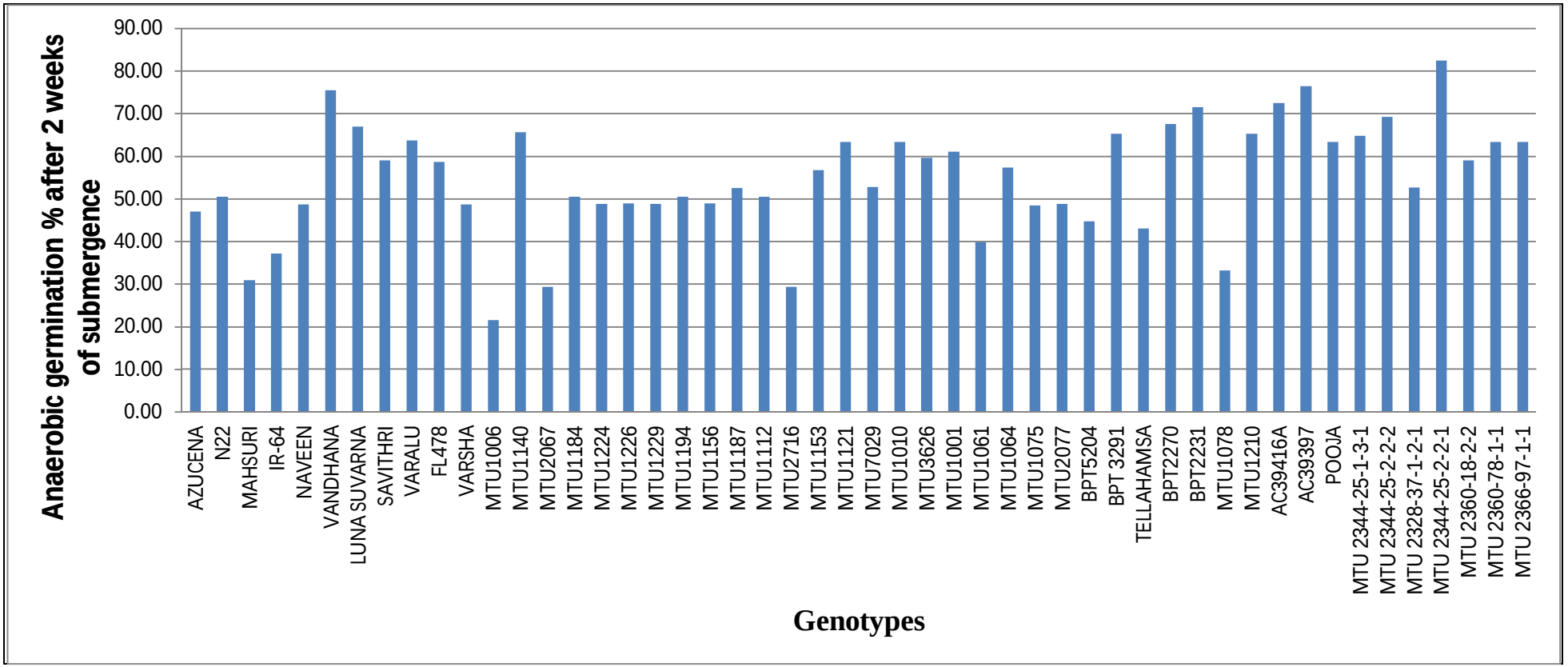


Fig. 4.2.6: Mean performance of 50 genotypes for Anaerobic germination % after 2 weeks of submergence

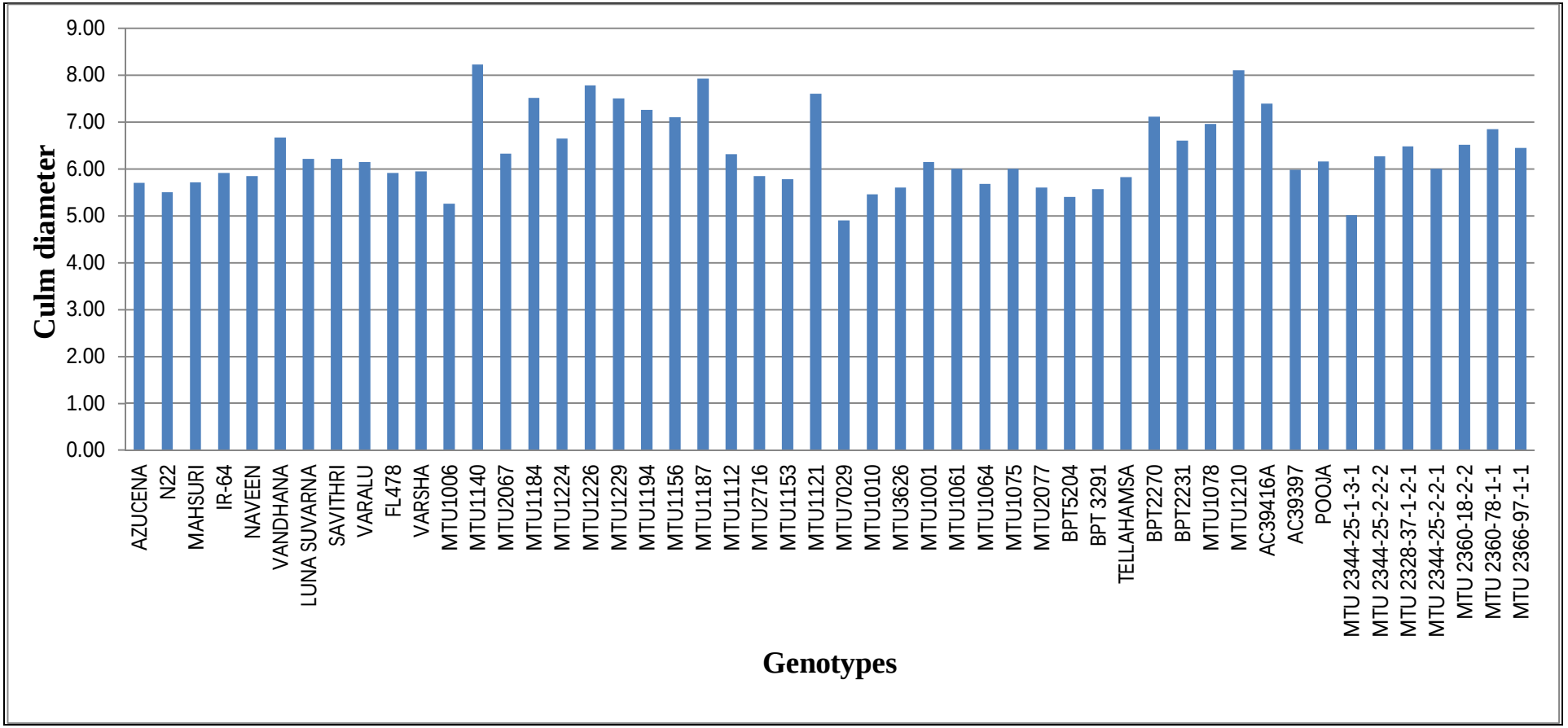


Fig. 4.2.6: Mean performance of 50 genotypes for culm diameter (mm)