BIOMETRICAL STUDIES
IN
LOWLAND RICE (*Oryza sativa* L.)

BY

HANUMAN PRASAD CHATURVEDI

DEPARTMENT OF GENETICS & PLANT BREEDING

SUBMITTED

IN FULFILMENT OF THE REQUIREMENT OF THE DEGREE OF

DOCTOR OF PHILOSOPHY
IN
GENETICS & PLANT BREEDING

NAGALAND UNIVERSITY

2008

DEDICATED TO

MY

LOVING MOTHER

NAGALAND UNIVERSITY
SCHOOL OF AGRICULTURAL SCIENCES
AND RURAL DEVELOPMENT
MEDZIPHEMA CAMPUS

DECLARATION

I, Hanuman Prasad Chaturvedi hereby declare that the subject matter of thesis is the record of research work done by me, that the contents of this thesis did not form basis for the award of any previous degree to me or to the best of my knowledge to anybody else and that the thesis has not been submitted by me for any degree in any other University/ Institute.

This is being submitted to the Nagaland University for the degree of Doctor of Philosophy in Genetics and Plant Breeding.

Chaturvedi

DATE :30TH. OCTOBER 2008 ***(HANUMAN PRASAD CHATURVEDI)***

Countersigned:

(P.TALUKDAR)
Joint Supervisor
Professor
Deptt. of Plant Breeding & Genetics
Assam Agricultural University

(SAPU CHANGKIJA)
Supervisor
Reader & Head
Deptt. of Genetics & Plant Breeding
Nagaland University

CERTIFICATE

*This is to certify that the thesis entitled "**Biometrical Studies in Lowland Rice (Oryza sativa. L)**" submitted to the School of Agricultural Sciences and Rural Development, Nagaland University, in partial fulfillment of the requirement for the degree of Doctor of Philosophy in Genetics and Plant Breeding is a record of bonafide research carried out by Mr. Hanuman Prasad Chaturvedi, under our personal guidance and supervision. The findings of the investigation have not been submitted for award of any degree in this or any other university or institute of learning.*

The assistance of all kind received by him has been duly acknowledged

(P.TALUKDAR)
Joint Supervisor
Professor
Deptt. of Plant Breeding & Genetics
Assam Agricultural University

Date : 30th. Oct. 2008
Place : Medziphema.

(SAPU CHANGKIJA)
Supervisor
Reader & Head
Deptt. of Genetics & Plant Breeding
Nagaland University

Date : 30th. Oct. 2008
Place: Medziphema.

ACKNOWLEDGEMENT

I take this opportunity to express my heartfelt gratitude to Dr. Sapu Changkija, Reader & Head of the Department of Genetics and Plant Breeding, School of Agricultural Sciences & Rural Development, Nagaland University, Medziphema for his enlightened guidance and constant encouragement which helped successful pursuance of this endeavour.

I would like to extend special thanks to Prof. P. Talukdar, Department of Plant Breeding & Genetics, Assam Agricultural University for his valuable suggestions, useful comments and critically reviewing the manuscript.

The author is highly indebted to Prof. K.K. Singh, (Retired) who, in fact, had initiated this research study and guided me in carrying out the present work.

My sincere thanks are also due to Dr C. Rajkhowa, the then Joint Director, ICAR, Research Complex, Jharanapani, Nagaland for allowing me to carry out field works in the research farm. Credit also goes to Mr T. Gohain, Farm Manager of ICAR for his help rendered during experimentation.

I extend my cordial thanks to Prof. R. C. Nayak for going through the manuscript thoroughly in short time.

I also would like to express my thanks and gratitude to Prof Imnayongdang, Dean, SASRD for providing necessary facilities for conducting the experiment.

My sincere thanks are due to Prof. V. B. Singh, Prof. V. B. Sharma, Prof. R. C. Gupta, Prof. S. K. Sharma, Dr Kigwe Seyei, Dr. P.L.Singh, Dr. A. K. Makar, Dr. V. K. Vidyarthi, Dr. Amod Sharma, Dr.(Mrs) Malini Sharma for the encouragement and moral support during the course of investigation.

My sincere thanks are due to Mr. Mbonbemo Ngullie, Assistant Librarian and other staff members for enabling me to utilize the library facility.

I am equally indebted to Dr. V. H. Gupta, Scientist, Indian Agricultural Statistical Research Institute, New Delhi for analyzing the data during the course of investigation.

I also extend my sincere thanks to all my colleagues and other staff members for their helps during the course of investigation of the work.

The author wishes to express his deep sense of gratitude to his wife, Mrs. Mamta Chaturvedi for her support and other family members for being the source of constant encouragement.

Dated: 30th, Oct. 2008
Place: Medziphema

(HANUMAN PRASAD CHATURVEDI)

CONTENTS

3.4.2 Combining ability and genetic analysis

4. Experimental findings

4.1 Genetic variability and genetic divergence

4.1.3 Mean performance for grain yield and other related parameters

4.1.4 Association among characters

4.1.5 Path coefficient analysis

4.2 Combining ability and genetic analysis

5. Discussion

5.1 Genetic variability, correlation and path coefficient

5.3 Combining ability and genetic analysis

5.3.3 Combining ability analysis

5.3.4 Genetic analysis

6. Summary and conclusion

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

&	and
@	at the rate of
cm	centimeter
cv	coefficient of variation
ECV	environmental coefficient of variation
Et al.	Et allia (and others/ co- workers)
Fig.	Figure
gca	general combining ability
GCV	genotypic coefficient of variation
G x E	Genotype x Environment
gms	grams
ha	hectare
h^2_{bs}	heritability (in broad sense)
h^2_{ns}	heritability (in narrow sense)
mm	millimeter
M.T.	meteric ton
N.S.	non significant
PCV	phenotypic coefficient of variation
/	per
%	percent
SE	standard error
TRC/WRC	terrace rice culture/ wet rice culture
Vr	variances of arrays
Wr	co variances between parents and their offspring

LIST OF PLATES

INTRODUCTION

1. INTRODUCTION

For more than half of humanity, rice is life. It is the grain that has shaped the cultures, diets, and economies of billions of people. For them, life without rice is simply unthinkable. Rice provides more calories per hectare than any other cereal crop grown in the world. It meets as much as 40% of the requirement of the calories of the global population. In India, rice is taken along with pulses in various preparations where complementation of protein and carbohydrates as well as essential amino acids is made.

Rice is the most important food crop of India. Of the total area under rice, around 35% is under rainfed lowland. In North Eastern Region of India, rice is the major crop occupying 3.5 million hectares, accounting for 10.48% of the total rice area and 6.46% of the total rice production in the country (Bujarbaruah *et al.,* 2006). In Nagaland rice is grown in an area of 151 thousand hectares, out of which 65.7 thousand hectares is under TRC/WRC paddy with a production of 1.22 M.T. (Statistical Hand Book of Nagaland, 2006).

By 2020, 1.2 billion new rice consumers will be added to the population of this continent. Rice production must be increased by one third from current 320 million tons to 420 million tons. Farmers will have to grow an extra 3.7 million tons every year even though rice land is decreasing and the remaining fields seem to be wearing out (Asia Rice Foundation). This has necessitated a major thrust to generate improved rice varieties for vast rainfed lowlands to ensure sustainable higher rice production.

The plant breeder's success in devising suitable effective breeding program for incorporating useful gene(s) in a single genotype depends to a large extent on nature and magnitude of genetic variability existing in a given species. Greater the variability in the initial material better would be chances of evolving desirable types (Vavilov, 1951). Therefore, knowledge of nature and extent of genetic variation, inter- relationship of characters and causal relationship could provide necessary guidelines for plant breeders in developing useful and improved varieties.

Correlation measures the mutual relationship among various plant characters and helps in determining the yield components on which indirect selection can be based for improvement in yield. Path analysis splits the correlation coefficients into the measures of direct and indirect effects and determines the direct and indirect contribution of various characters towards yield.

The presence of potential genetic variability in early and advanced generations is an important pre- requisite for the success of selection procedures in attaining objectives of breeding programs. The varieties which come from widely separated localities are usually presumed to be diverse and are utilized in hybridization program. However, several workers have emphasized that there is no parallelism in geographical distribution and genetic diversity (Murthy and Anand 1966, in linseed; Maurya and Singh 1977 and De *et al.* 1992 in rice), advocating that varieties with the same geographical origin could have under- gone changes under selection pressure. Thus the extent of genetic diversity between populations can be judged by following methods to study genetic diversity like D^2 analysis. In this method the genotypes could be classified into different clusters each accommodating similar genotypes within and dissimilar genotypes in different clusters.

Hybridization is the most potent technique for breaking yield barriers and evolving varieties having built- in high yield potential. The selection of suitable parents for hybridization is one of the most important steps in a breeding program. Selection of parents on the basis of phenotypic performance alone is not a sound procedure since phenotypically superior lines may yield poor recombinants in the segregating generation. It is therefore, essential that parents should be chosen on the basis of their genetic value. The parents are chosen on the basis of their combining ability and the breeding procedure is decided on the basis of gene action involved in the expression of various quantitative characters.

Combining ability refers to the ability of a genotype to transmit superior performance to its crosses. It is of two types, viz., general combining ability (gca) and specific combining ability (sea). The gca refers to the average performance of a genotype in a series of hybrid combinations and the sea refers to the performance of a parent in a specific cross, i.e. deviation of a particular cross from the average performance in a series of crosses. The gca is due to additive genetic variance and additive x additive interactions and sea is due to dominance variance and all three types of non- allelic interactions. The estimates of combining ability provide information about the components of genetic variance involved in the expression of various polygenic characters and thus help in the selection of desirable parents for hybridization and also in deciding the breeding procedure for genetic improvement of such characters.

In the pursuit of rendering a permanent genetic improvement in crop plants, an adequate knowledge of gene action, especially components of genetic variance (i.e. additive, dominance and epistatic) and allied parameters (such as heritability, degree of dominance & genetic correlations between relatives, etc.) are necessary. Fortunately, the demands of plant breeding with respect to the genetic composition of the breeding material are fully matched by the biometrical approach.

Varietal adaptability to environmental fluctuations is important for the stabilization of crop production both over regions and years. Estimation of phenotypic stability, which involves regression analysis, has proved to be a valuable technique in the assessment of varietal adaptability. Stability analysis is useful in the identification of adaptable genotypes and in predicting the response of various genotypes over changing environments. It is generally agreed that the more stable genotypes can some how adjust their phenotypic responses to provide some measure of uniformity in spite of environmental fluctuations.

In Nagaland an array of local genotypes are in cultivation since long. Though many of them are low yielding but they are valuable with reference to many rare physiological and quantitative traits. Systematic attempts are rare in proper evaluation and characterization of these landraces. Keeping these views in mind the present investigation "Biometrical Studies in Lowland Rice (*Oryza sativa* L.)" has been taken up with the following broad objectives:

1. To study the nature and extent of genetic variability in the lowland rice landraces.
2. To estimate genetic diversity present within the population on the basis of morphological and agronomical characteristics.
3. To study the combining ability effects and variances of a 6 x 6 diallel cross for different quantitative characters.
4. To study the genetic architecture of different quantitative characters through genetic analysis of diallel.
5. To study the phenotypic stability of the landraces in order to identify high yielding phenotypically stable genotypes over variable environments.

REVIEW OF LITERATURE

2. REVIEW OF LITERATURE

2.1 Genetic variability, correlation & path coefficient

The development of an effective plant breeding program depends upon the presence of genetic variability. Thus the success of genetic improvement for any character depends on the nature of variability present in the gene pool for that character. Hence an insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding program. Further, the efficiency of selection in improving a plant character depends largely on the extent of transmissibility of the character in question. The presence of high magnitude of variability in the germplasm or breeding materials only indicates the greater possibility of improvement through selection but the existence of high transmissibility is an important pre- requisite for realization of such possibility. The direct selection parameters like heritability in broad sense, genetic advance as percent of mean are helpful in assessment of transmissibility of characters.

Gomathinayagam *et al.* (1990) studied genetic variability in 40 upland rice genotypes. The coefficient of variation was high for number of effective tillers per plant & grain yield per plant. High heritability estimate and genetic advance was observed for the characters and may be considered reliable for selection under rainfed condition.

Ibrahim *et al.* (1990) reported that the number of productive tillers had high direct effect on grain yield while panicle length and flowering duration had moderate direct effects. The effect of plant height was slightly negative.

Bai *et al.* (1992) found that the grain yield per plant was positively correlated with number of productive tillers, plant height, panicle length and number of grains per panicle at genotypic and phenotypic levels. The genotypic correlations were greater than the phenotypic ones.

Ganesan *et al.* (1995) evaluated twenty-eight rice hybrids and their 11 parents for genetic variability, heritability and genetic advance as percentage of mean. The characters grains per panicle and grain yield per plant had high genotypic coefficients of variation, heritability and genetic advance as percentage of mean indicating the predominance of additive gene effects. Days to panicle emergence showed moderate genetic variability along with high heritability and genetic advance indicating the existence of scope for further improvement through phenotypic selection.

Chauhan (1996) studied genetic variability, phenotypic, genotypic and environmental correlations for 11 morpho-agronomic characters. Grain yield, straw yield & biological yield per plant and spikelets per panicle showed substantial genetic variability. Grain yield, panicle weight, spikelets per panicle, grain weight, biological yield and harvest index had high expected genetic advance associated with high heritability values suggesting the preponderance of additive gene effects in their expression & thus offer scope for selection.

Reddy *et al.* (1997) studied genetic and phenotypic correlations and path-coefficient analysis among 12 quantitative traits in 36 genotypes of rainfed lowland rice. The grain yield per hill showed significant positive correlation with panicle weight and number of grains per panicle at both genetic and phenotypic levels and with 1000 grain weight, panicle length and length of flag leaf at genetic level. Path coefficient analysis revealed that panicle weight was the most important character for increasing the grain yield.

Ali *et al.* (2000) studied genetic variability and the estimates of broad sense heritability observed in F_2 population of *Oryza sativa* L. were significant for all the traits evaluated except for number of tillers per plant and panicle length. Heritability estimates were high for plant height, 100 seed weight, number of tillers per plant and panicle length but maximum genetic gain relative to the mean was expected for number of tillers per plant and plant height.

Goswami *et al.* (2000) in a study of 9 lowland rice varieties reported significant positive correlation of grain yield with panicle number per unit area, grain number per panicle and filled grain percent.

Yadav (2000) studied genetic variability for yield and its components for days to 50% flowering, days to maturity, plant height, tillers per plant, panicle length, spikelets per panicle, total grains per panicle and per plant, 1000 grain weight and grain yield per plant. Appreciable amount of genotypic coefficient of variation, heritability and genetic advance were observed for total grains per panicle, total grains per plant and grain yield per plant.

Chakraborty *et al.* (2001) studied twenty-nine *boro* rice genotypes for estimating genotypic and phenotypic correlation coefficients and path effects of plant height, panicles per plant, panicle length, fertile grains per panicle, 100 grain weight and harvest index on grain yield per plant. All the characters except 100 grain weight showed significant positive genotypic correlation, phenotypic correlation or both with the grain yield per plant. Path analysis revealed high positive direct effects of harvest index, panicle length and 100 grain weight on the grain yield per plant.

Ganesan (2001) studied direct and indirect effects of yield component characters of 48 rice hybrids. Filled grains per panicle (0.895) had the highest significant positive direct effect on yield per plant followed by numbers of tillers per plant (0.688), panicle exertion (0.172), panicle length (0.167) and plant height (0.149). Plant height, days to flowering, number of tillers per plant and productive tillers per plant had both positive and negative indirect effects on yield.

Nayak *et al.* (2001) studied genotypic and phenotypic correlation and path analysis in 10 quantitative traits of 200 scented rice genotypes including 1 scented rice control, Ratna. Grain yield per plant showed positive correlation with plant height, panicle number per plant, panicle length, total number of spikelets per panicle and total number of grains per panicle at both genotypic and phenotypic levels. Path coefficient analysis revealed that panicle number per plant, total number of grains per panicle and 1000 grain weight contributed to the grain yield of the plant.

Patra *et al.* (2001) in a study of root and shoot characteristics in rice cultivar reported higher PCV than GCV for all the characters. Moderate to high heritability coupled with high genetic advance for number of tillers per plant reported.

Bhandarkar *et al.* (2002) evaluated genetic parameters of variability for yield and its components in 52 early duration genotypes of rice. Heritability estimates were high for days to 50% flowering, maturity and panicle length, high heritability coupled with high genetic advance as percent of mean were observed for plant height. Correlation analysis revealed that yield per plant had positive significant association with days to 50% flowering, maturity, plant height, number of total grains per panicle and number of filled grains per panicle.

Khedikar *et al.* (2003) assessed genetic variability for 9 characters viz., days to 50% flowering, plant height, effective tillers per plant, panicle length, test weight, sterile percentage, spikelet density, head rice recovery and grain yield per plant in 20 scented rice genotypes. The PCV was higher than GCV for all the characters. Days to 50% flowering followed by plant height recorded low GCV and PCV values.

Sarma and Bhuyan (2004) studied genetic variability in a set of 58 *Ahu* rice genotypes. Highest genotypic as well as phenotypic coefficient of variation was exhibited by number of grains per panicle followed by grain yield per plant and number of effective panicles per plant. Heritability (broad sense) was highest for plant height followed by days to flowering and number of effective panicles per plant. Highest genetic advance was observed for number of grains per panicle followed by grain yield per plant and number of effective panicles per plant. Grains per panicle and number of effective panicle per plant showed both high heritability and high genetic advance and, therefore, selection would be effective for these two traits.

Chitra *et al.* (2005) in correlation and path coefficient analysis studies conducted with sixteen parents and their sixty four hybrids revealed that number of tillers per plant, number of productive tillers per plant and harvest index had strong positive association with yield. Besides, their inter-correlations were positive and significant, indicating the possibility of improving these characters simultaneously. The path analysis indicated that the contribution of harvest index was much through direct effects and their indirect effects by way of other traits were also much pronouncing.

Das et al (2005) assessed 22 semi deep- water rice genotypes including advanced generation breeding lines and locally recommended high yielding varieties for genetic variability, heritability and genetic advance for grain yield and flood tolerance. Amongst the traits under study, highest GCV was recorded for effective ear bearing tillers followed by grain yield and plant height. Heritability in broad sense was observed to be high for days to maturity, plant height, effective ear bearing tillers, panicle length, grain yield and flood tolerance. The traits effective ear bearing tillers, grain yield and plant height exhibited both high heritability and high genetic advance.

Hasib (2005) evaluated 12 F_1 hybrids of scented rice and their seven parents involving induced mutants and basmati varieties for eight important panicle characters. The values of phenotypic and genotypic coefficients of variation, heritability and genetic advance were high for panicle weight, secondary branches per panicle, spikelet number per panicle, test weight and grain yield per panicle indicating important role of additive gene action for the expression of these traits. Character association analysis revealed significant positive association of all the panicle traits, except test weight, with grain yield per panicle. Path coefficient analysis revealed that panicle weight had highest positive direct effect followed by panicle length and secondary branches per panicle.

Hence, selection on higher panicle weight and higher number of secondary branches per panicle could be effective for yield improvement in scented rice.

Mankesh *et al.* (2005) in a study on correlation and path coefficient in rice under rainfed lowland condition reported that phenotypic coefficient of variation were higher than those of genotypic coefficient of variation for all the traits viz., days to 50% flowering, plant height panicle length, number of tillers per hill, fertile spikelets per panicle, 1000 grain weight and grain yield per plant. Grain yield was positively and significantly correlated with fertile spikelets per panicle & 1000 grain weight for direct sowing condition and number of tillers per hill & fertile spikelets per panicle for normal transplanting condition. The path analysis indicated a greater contribution of number of tillers per hill & fertile spikelets per panicle in normal transplanting condition.

Suman *et al.* (2005) studied genetic variability and heritability of different characters using 114 genotypes and three checks. Reported high coefficients of variation for seedling dry weight followed by number of spikelets per panicle, number of filled grains per panicle and biological yield. High values of heritability coupled with high genetic advance as percent of mean were observed for the characters total number of tillers per plant, productive tillers per plant, number of spikelets per panicle, number of filled grains per panicle, plant yield, biological yield, harvest index and seedling vigour index.

Ramakrishnan *et al.* (2006) in correlation studies indicated that for improvement in rice grain yield, the intensive selection on the positive side should be made for grains per panicle and spikelet fertility since these traits showed significantly positive correlation with seed yield and also among themselves. Panicles per plant, panicle length and grain weight though had positively non-significant correlation with grain yield also be utilized for improvement of yield. Partitioning through path coefficient analysis revealed that grains per panicle played an important role in the improvement of grain yield in rice.

Kishore *et al.* (2007) studied path- coefficient analysis among plant height, days to 50% flowering, productive tillers per plant, panicle length, number of filled grains per panicle, 1000 grain weight and grain yield per plant in 70 rice genotypes. Correlation studies revealed that genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the characters. Significantly positive association of grain yield per plant with number of grains per panicle and 1000 grain weight was reported. Path coefficient analysis revealed that 1000 grain weight, number of grains per panicle, productive tillers per plant, days to 50% flowering and plant height showed positive direct effects on grain yield.

Panwar and Ali (2007) investigated association among yield components, their direct and indirect influence on grain yield in 47 genotypes of rice under two sowing dates. Grain yield per plant had significant positive association with grain yield per panicle, harvest index, filled grains per panicle, biological yield per plant, primary branch number per panicle, productive tillers per plant and secondary branch number per panicle in both the environments. Path coefficient analysis revealed that grain yield per panicle had the highest direct effect on grain yield per plant in both the environments followed by harvest index, biological yield per plant and productive tillers per plant suggesting that the improvement in grain yield could be efficient if the selection is based on these component characters.

Singh *et al.*, (2007) studied thirty-four genotypes for their genotypic, phenotypic and environmental coefficient of variation. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) for all the traits. PCV was highest for grain yield (33.15%) followed by biological yield (26.67%) and effective tillers per plant (25.87%). GCV was highest for grain yield / plant (26.19%) followed by effective tillers per plant (21.46%). High heritability coupled with high genetic advance was recorded for spikelets per panicle. Genetic advance as percent of mean ranged from 8.39- 40.19.

Das and Borah (2008) initiated the experiment to assess the genotypic variability for yield attributing characters as well as certain quality characters in 28 traditional rice varieties of *Nalbari* district of Assam. Among these varieties, PCV was found to be higher than GCV for all the six characters studied. Number of fertile grains per panicle had maximum GCV followed by grain weight per plant. A moderate to high heritability estimates associated with moderate to high genetic advance was observed for grain weight per plant followed by plant height. Highest L/B ratio of grains was observed in the varieties *Kharika Jaha* (4.13) and *Rupsundari* (4.12) and lowest L/B ratio was observed in *Koni Dhan* (1.30).

2.2 **Genetic divergence**

Charles Darwin (1959) used the expression divergence in characters to record variation in genera, species and varieties. Huxley (1955) used other term genetic polymorphism which means co- existence of different genetic forms in a population.

A number of scientists (Griffing and Lindstrom 1954; Moll *et al.* 1962; Arunachalam 1981 and Hawkes 1981) have emphasized the importance of genetic diversity in plant breeding for obtaining broad spectrum of desirable variability in segregating generations. The presence of potential genetic variability in early and advanced generation is an important pre- requisite for the success of selection procedures in attaining objectives of breeding programs.

The varieties which come from widely separated localities are usually presumed to be diverse and are utilized in hybridization program. Earlier workers regarded this geographical isolation as a reasonable index of genetic diversity (Joshi and Dhawan

1966). However, several workers have emphasized that there is no parallelism in geographical distribution and genetic diversity (Murthy and Anand 1966, in linseed; Maurya and Singh 1977 and De *et al.* 1992 in rice), advocating that varieties with the same geographical origin could have under- gone changes under selection pressure. Thus for estimation of variation within the germplasm in divergence study in the form of classification into different homogeneous groups is an important practice.

De *et al.* (1992) observed no correlation between geographical distribution and genetic divergence.

Mishra *et al.* (1994) reported that number of fertile grains per panicle, number of sterile grains per panicle and plant height were the highest contributors of Mahalanobis D^2 values.

Rahaman *et al.* (1997) estimated nature and magnitude of genetic divergence in 52 lowland rice collections under 40-50 cm water depth situation. The cultivars were grouped into eight clusters showing no relationship between geographic distribution and genetic divergence.

Roy and Das (2000) assessed nature and magnitude of genetic divergence in 28 hill rice genotypes of Karbi Anglong district of Assam using Mahalanobis's D^2 statistic. The population was grouped into six clusters. Grains per panicle, effective panicles per plant and grain yield per plant were the major contributing traits for divergence.

Shiv Datt and Mani (2003) studied degree and nature of genetic divergence among a set of 61 elite basmati rice genotypes. All the genotypes were grouped into 4 clusters and clustering pattern indicated that there was no association between eco-geographical distribution of genotypes and genetic divergence as genotypes selected under diverse locations clustered together. Plant height contributed maximum towards genetic divergence followed by days to 50% flowering and grain yield per plant.

Manonmani (2004) studied fourteen indica rice genotypes for the genetic diversity and grouped into five clusters using Mahalanobis D^2 analysis. Cluster I consisted of ten genotypes, cluster II, III, IV and V consisted of single genotype each viz. ADT 40, CR 1009, HA 891037 and Improved White Ponni respectively. Filled grains number per panicle followed by days to 50 per cent flowering contributed the maximum to the genetic divergence. Cluster III exhibited relatively high mean value for days to 50 per cent flowering and grain yield. The highest contribution to the maximum divergence was made by filled grains number per panicle followed by days to 50 per cent flowering and plant height. Hybrids between parents from inter clusters produced higher heterosis than the parents from intra cluster.

Sarma and Bhuyan (2004) studied genetic divergence in a set of 58 *Ahu* rice genotypes. D^2 analysis indicated presence of good amount of genetic diversity amongst the genotypes. The entries were grouped into six clusters, the largest one containing 28 genotypes and the smallest one having only two. Hybridization between genotypes belonging to diverse groups may be undertaken to obtain desirable segregants.

Awasthi *et al.* (2005) studied twenty- one genotypes for their genetic divergence and grouped them into six clusters for different characters. The genotypes of one cluster indicates overall genetic similarity among them. Number of grains per panicle, grain yield per plant, days to 50% flowering, leaf length and leaf width showed high percent contribution towards total divergence.

Bose and Pradhan (2005) studied nature and the magnitude of genetic divergence in 35 deepwater rice genotypes using Mahalonobis's D^2 – statistics. The genotypes were grouped onto 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Cluster IV showed maximum intra cluster divergence while inter cluster divergence was maximum between clusters IX and X. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. Traits like plant yield, days to 50% flowering, EBT/m2 and plant height were the major contributors to genetic divergence.

Chand et al (2005) grouped nineteen genotypes into six clusters based on D^2 values. 1000 grain weight contributed maximum towards genetic divergence followed by panicle length, grain length and plant height.

Chaturvedi and Maurya (2005) evaluated twenty- six genotypes of rice belonging to seven ecotypic situations for genetic divergence. The genotypes were grouped in eight clusters. Comparison of cluster mean revealed that cluster eight gave exceptionally high values for seven characters followed by cluster VII. The maximum inter- cluster D^2 value was obtained between cluster III & VI and III & VIII.

Madhavilatha and Suneetha (2005) evaluated fifty four elite rice germplasm lines being maintained at Agricultural Research Station, Nellore for their genetic diversity with regard to yield, yield components and quality trails. The genotypes were grouped into nine clusters, based on Mahalanobis D2 statistics. Geographical and genetic diversity were observed to be unrelated, as genotypes from diverse geographical regions were placed in the same cluster, while genotypes from the same centre were grouped into different clusters. Results on inter-cluster distances revealed maximum diversity between genotypes of clusters IV and VIII. Intra-cluster distance was maximum for Cluster V, indicating the existence of variability with in the cluster. A perusal of the results on cluster means revealed high yield, number of grains per panicle, panicle length, plant height and days to 50 per cent (lowering for Cluster IV, indicating the desirability of genotypes from the cluster for improvement of grain yield and the above yield components. Further, plant height and days to 50 per cent flowering, together accounted for 82.04 per cent of the total genetic divergence, indicating their importance in the choice of parents for hybridization programs.

Babu *et al*., (2005) studied genetic divergence for yield and quality traits in 19 aromatic rice genotypes. Based on the genetic distance, 19 genotypes were grouped into 5 clusters. The distribution of genotypes into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like water uptake, days to 50% flowering contributed maximum towards genetic divergence.

Sobita Devi *et al*., (2006) in their studies on genetic divergence, fifty-four standard varieties of rice grouped into nine clusters on the basis of D^2 analysis. Plant height (40.60%) followed by flag leaf width (20.12%), yield per plant (15.79%) and maturity duration (15.58%) contributed maximum towards the genetic divergence.

Chandra et al (2007) assessed Fifty-seven upland rice genotypes including 32 local rice germplasm for the nature and magnitude of genetic divergence among them based on 14 agro- morphological traits following Mahalanobis' D^{2-} statistic and Anderson's canonical analysis. On the basis of D^2 values, the 57 genotypes were grouped into five clusters flowing Tocher's method. The clustering patterns of the genotypes were quite at random indicating that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were grain L/B ratio, 1000- grain weight, grain length, grain yield and biological yield.

2.3 Combining ability and genetic analysis

Sprague and Tatum (1942) defined general combining ability (gca) as the average performance of a line involved in hybrid combination and specific combing ability (sea) designates those cases in which certain combinations do relatively better or worse than would be expected on the basis of the gca of their parents. Good general combining parents result in higher frequency of heterotic hybrids than poor combining parents. From the genetic points of view, general combining ability measures additive gene effects and specific combing ability measures non additive gene effects, depending on genes with dominance(intra-allelic interactions) and epistasis (inter-allelic interactions). In a hybrid breeding program, plant breeders generally identify parental lines with good general combining ability, and crosses with high specific combining ability.

Griffing (1956, a) gave the generalized concept and methodologies for combining ability analysis. He pointed out that gca involved both additive effects and additive X additive interaction effects. Griffing (1956, b) outlined the procedure for determining the gca and sea effects and variances from diallel sets of varied composition.

Singh and Nanda (1976) studied a set of diallel cross of six rice varieties and their F_1 progenies (excluding reciprocals) and reported the significance of both general combining ability (gca) and specific combining ability (sea) variances for most of the characters studied viz., grain yield per plant, grains per panicle, panicle length and panicle number. They further reported that the crosses with high sea generally involved high x low combinations.

Maurya and Singh (1977) in study of diallel cross of seven rice varieties (excluding reciprocals) reported significance of both gca and sea variances for all the thirteen characters such as days to heading, plant height, ear bearing tillers, panicle length, number of grains per panicle, test weight, grain yield etc. Further, they reported that the best parent was also the best general combiner for a particular trait but none of the parents or specific cross combinations was good combiner for all the characters.

Rahman *et al.* (1981) studied nature of gene effects in a 5 x 5 diallel cross of rice for heading time, plant height, panicle number, panicle length, grains per panicle and yield per plant. They detected additive and non- additive gene effects with predominance of additive genes.

Singh and Shrivastava (1982) in a diallel cross involving five varieties of rice observed additive gene action for tillers per plant, panicle length, number of primary branches and length & breadth of grains and non- additive gene action for grain yield per plant, number of grains per panicle, effective tillers per plant, panicle density and sterility.

Shrivastava and Seshu (1983) from the study of 15 x 15 diallel cross (excluding reciprocals) of rice for sixteen traits found the variance of gca to be significant for all the traits

Dhaliwal and Sharma (1990) studied the gca and sea for grain length, grain thickness, L/B ratio, grain density, 100 grain weight, days to 50% flowering, number of panicles per plant, panicle length, grains per panicle and grain yield in 7x7 diallel mating system. Mean squares due to gca and sea were significant for all the characters except sea for grain density. The genotype IR 8 and China 27 were judged as good general combiners for grain yield and a number of component characters. Non- additive genetic variances were predominant for all the traits except grain density where additive gene effects were more important. The predominance of non- additive genetic variances for agronomic characters suggested the improvement of these traits through hybridization.

Mohanty et el. (1995) evaluated a set of diallel crosses involving seven rice varieties of different duration groups for six yield attributing characters. The additive nature of gene action was predominant for all the characters. The high heritability in narrow sense was also established for all the characters.

Sharma *et al.* (1995) studied combining ability with 5 lines and 3 testers on eight quantitative traits. Preponderance of additive gene action for days to 50% flowering, plant height, number of grains and grain weight per panicle and non- additive gene action for number of productive tillers per plant, 1000 grain weight and yield per plant were reported.

Sharma *et al.* (1995) studied eighteen hybrids generated from crossing six lines with three testers along with the parents for combining ability. Preponderance of non-additive gene action for plant height, grain weight per panicle and grain yield per plant was observed. Additive gene action was found important for panicle bearing tillers per plant, panicle length and fertile spikelets per panicle.

Verma *et al.* (1995) in the study of 9 x 9 diallel analysis in F_2 generation (excluding reciprocals) in rice for various yield components revealed significant differences for general and specific combining abilities for all the characters. The magnitude of gca variance was relatively higher than sea variance and thus predominance of additive gene action was observed for all the characters except for biological yield per plant and number of effective tillers per plant.

Katre, N.B. and Jambhale, N.D. (1996) studied combining ability in 9 x 9 diallel set in rice for grain yield and related characters. The magnitude of variance due to gca was lower than that due to sea for all the characters i.e. plant height, days to maturity, tillers per plant, grain yield per plant, grains per panicle, 1000 grain weight, grain length and grain breadth indicating predominance of non- additive gene action.

Lavanya (2000) reported majority of the superior combiners for grain yields (72%) involved at least one good combiner and the other either good or low combining parent indicating additive x additive and additive x dominance type of gene interaction.

Mehla *et al.* (2000) in a study with five lines, six testers and their thirty hybrids reported high values of sca revealing the predominance of non- additive gene action for all the characters.

Reddy (2002) studied combining ability in a set of diallel crosses (excluding reciprocals) with eight lowland rice genotypes for grain yield per plant and its components i.e. 1000 grain weight, panicle weight, number of filled grains per panicle, panicle length, number of effective panicles per plant and plant height. Analysis of variance for combining ability revealed that both gca and sea variances were significant for both the F_1 & F_2 generations for grain yield and its components, indicating the importance of additive and non- additive genetic variance in the inheritance of these characters.

Verma (2003) carried out genetic components and combining ability analyses of various physiological traits by using seven parents diallel mating design excluding reciprocals. Results revealed that both additive and non-additive gene effects were important for the inheritance of characters studied with preponderance of latter for all traits, except plant height and harvest index in both F1 and F2 generations. The significance of gene distribution indicated the presence of gene asymmetry. At least one major group of genes controlled the inheritance of each trait. High narrow-sense heritability further supported the importance of additive gene effects for harvest index and plant height. NDR 359, Sarjoo 52, Mahsuri, T 21 and Jal Lahari were good general combiners. The promising cross combinations were NDR 359/Jal Lahari, NDR 359/T 21, Mahsuri/ T 21, Sarjoo 52/NDR 359 and Sarjoo 52/T 21. Since non-additive/dominance components were higher than the additive for all the characters in both Fl and F2 generations, therefore, biparental mating and/or reciprocal recurrent selection could be used for genetic improvement of these characters.

Kumar *et al.* (2004) evaluated twenty seven crosses represented by a 3 lines x 9 testers design along with parents for grain yield and related characters. Analysis of variance indicated significant variations among the crosses and parents for all the traits. Combining ability analysis showed both additive and non-additive gene action, but the latter was predominantly operative for most of the traits studied. Among the three Cytoplasmic male sterile (CMS) lines, IR 58025A and among the nine testers, PSRM-1-16-48-1, Pusa 1040 and RAU 1411-4 were found to be good general combiners for yield and other yield attributes. The hybrids IR 68886A x Pusa 1040, IR 58025A x Gautam, IR 68886A x PSRM-1-16-48-1 were identified as good specific combinations for grain yield plant-1 and related characters.

Singh et al (2005) from the study of line x tester analysis involving 4 well adopted CMS lines and 18 testers of different eco-geographic origin in rice revealed significant role of non-additive gene action for seedling height, leaves per seedlings, days to 50% flowering (earliness), Plant height (dwarfness), ear bearing tillers per plant, biological yield per plant, harvest index and grain yield per plant. NDR358 & Pankaj were found to be good general combiners. Three heterotic hybrids viz., PMS1A/NDR3026, PMS2A/Pankaj and PMS2A/NDR1014 were identified as potential hybrids based on high SCA effects for few desired traits.

Murugan and Ganesan (2006) from study involving 3 lines and 6 testers observed preponderance of additive gene action for grain yield per plant. The resultant 18 hybrids were studied in line x tester design for gca of parents and sea of crosses for seven economic traits, viz., days to flower, plant height, productive tillers per plant, panicle length, filled grains per panicle, 100 grain weight and grain yield per plant. The estimates of gca effects of parents revealed that L_3 among the lines and T_1, T_2, & T_3 among the testers were found to be superior for most of the traits including grain yield per plant. Among hybrids L_2 x L_3 had significant sea effect for six traits including grain yield per plant. The combining ability variance indicated the preponderance of additive gene action for grain yield per plant.

Pradhan *et al.* (2006) studied combining ability and gene action by crossing 3 lines with 12 testers along with parents. The gca and sea were significant for all the characters indicating the importance of both additive and non- additive genetic components. But it was found that there was a predominance of the non additive genetic components for expression of different traits.

Raju et al (2006) from the study of 7x7 diallel (without reciprocal) of rice found that the inheritance of days to 50% flowering, productive tillers per plant, filled grains per panicle and grain yield per plant were pre- dominantly under the control of non-additive gene action. Whereas 100 grain weight was largely governed by additive gene action. The parents RDR 763 for productive tillers per plant, and Lunisree for 100 grain weight were identified as good general combiner. The per se performance of the parents was found to be good indicator of their general combining ability. The best specific crosses with high SCA effects mostly involved parents with high x low or low x low GCA effects.

Sadhukhan and Chattopadhyay (2006) in a 5x5 parent's diallel cross involving local aromatic rice cultivars studied nature of gene action and combining ability effects on yield and some related metric characters in two environments. Both additive and non-additive gene action were found significant for all the characters. However, additive gene action was predominant in expression of most of the characters. For yield per plant, harvest index, panicles per plant and unproductive tiller percent non additive genetic variance action was higher in magnitude with low heritability in narrow sense and predictability ratio. Randhunipagal was good general combiner for short grain character. Among the cross combinations none was found good for all the characters. IET4786 x Basmati 370, Basmati 370 x Kataribhog and Kataribhog x Randhunipagal had significant and positive sca effects for yield per plant and harvest index and showed high x low, low x high and low x low combinations for gca effects respectively.

Saravanan et al (2006) from study involving 7 lines and 4 testers observed that non- additive gene action was important in controlling grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, kernel L/B ratio and grain yield per plant in rice.

Sharma et al (2006) in F_1 & F_2 diallel of seven varieties resistant to bacterial blight of rice for yield and other agronomic traits found highly significant combining ability variances for plant height, panicle number per plant, panicle length, spikelet number per panicle, grain number per panicle, total dry matter, harvest index and grain yield per plant indicating importance of non- additive gene action in their expression. The parent BJ1 was the best combiner for most of the characters including yield.

Senguttuvel and Bapu (2007) from study involving 4 lines and 10 testers observed that additive gene action was important in controlling days to flowering, plant height, number of productive tillers, panicle length, number of grains per panicle, 100 grain weight and single plant yield. The crosses with significant sca were due to the combinations of the parents, both of which were good or poor general combiners or any one of them was a good general combiner.

Singh *et al*., (2007) carried out combining ability analysis for grain yield and its components in 7 parental diallel crosses of rice excluding reciprocal. The GCA and SCA were significant for all the seven characters indicating the importance of additive and non-additive genetic components for these traits. The per se performance was observed to be a good indication of GCA effects of the parents and SCA effects of the crosses. Among parents studied, Vaidehi and Rajshree were observed to be good general combiners for grain yield. The superior specific cross combinations Saket 4 x Vaidehi, Rajshree x Kamini, Prabhat x Rajshree and Sita x Vaidehi appeared promising for further exploitation in rice breeding program.

Torres and Geraldi (2007) in rice (*Oryza sativa* L.) breeding program seeking to combine high productivity and cold tolerance for the temperate Latin America region, estimated some useful parameters which can be used to investigate the genetic control of agronomic characters in crosses combining cold tolerance and productivity. A partial diallel design was used in crosses between six tropical indica rice cold susceptible genotypes (group 1) and seven japonica or indica/japonica cold tolerant rice genotypes (group 2). Parents and crosses were evaluated for agronomic characters under field conditions in two different experiments in 2005. The results showed significant mid-parent heterosis for all characters (plant height, tiller number, days to 50% flowering, panicle length, grains per panicle, sterility, and one-hundred grain weight). The predominant direction of dominance effects was negative for days to 50% flowering, and positive for all the other characters. General combining ability (GCA) and specific combining ability (SCA) were significant for all characters, although the GCA effects of the two groups were more important .than the SCA effects.

Shukla and Pandey (2008) analyzed combining ability and heterosis over optimum (120N : $60P_2O_5$: $40K_2O$ kg/ha) and high (200N : $90P_2O_5$: $60K_2O$ kg/ha) fertility environments for six traits made in 2 years (2001 and 2002) using 120 hybrids of inter- and intra-subspecific nature derived from hybridization of 30 elite indica TGMS lines and four cultivars, viz., 'Pant Dhan 4' and 'Ajaya' (I = indica), 'Taichung 65' (J = japonica) and 'IR 65598-112-2' (TJ = tropical japonica) in line × tester mating design. Predominance of non-additive genetic variance suggested good prospects of hybrid breeding. Pooled analysis revealed highly significant variances for lines, general combining ability (GCA), specific combining ability (SCA) and line x tester. TGMS line 365-8S was the best general combiner for all the six traits including grain yield.

2.4 Phenotypic stability

Information about phenotypic stability is useful for the selection of crop varieties as well as for breeding programs. The phenotypic performance of a genotype is not necessarily the same under diverse agro-ecological conditions (Ali *et al*., 2003). Some genotypes may perform well in certain environments, but, fail in several others. Genotype-environment (GE) interactions are extremely important in the development and evaluation of plant varieties because they reduce the genotypic- stability values under diverse environments.

De et al (1990) evaluated 28 rice genotypes of early maturity (110 days) for three yield components over 4 environments in Orissa. Significant G x E interaction was observed. Genotypes TNAU81804, RP1714-111-732 and NDR312-1 were stable and produced the highest grain yields (means/ hill of 14.1, 12.2 and 11.8 g respectively).

Ramlingam *et al.* (1990) evaluated twelve short duration rice genotypes for stability parameters with respect to four quantitative traits recorded for three years. The pooled analysis of variance showed that the genotype- environment interactions were significant for all the four traits indicating differential behaviour of some genotypes. The genotype ACM 24 was a stable variety for grain yield and can be utilized for developing high yielding stable rice lines.

Jamadagni & Birari (1990) grew 18 genotypes at 7 sites in Maharashtra state. The genotypes RTN 144-1-2 and TR-17 were best adapted to the test sites in the state.

Reddy (1991) estimated stability parameters of 25 genotypes in 6 different environments according to the method of Eberhart & Russell. Genotypes CR628-2, Akashi, Keshari and Cavery were the most stable to changes in environmental conditions with good yield (3.58- 3.8 t/ ha).

De at al (1992) provided information on stability of rice yield under different lowland situations. Out of 47 lowland genotypes only 3 were most stable giving overall mean grain yield of 432.2, 404.8 & 380.8 g/mt^2 respectively.

Das et al (1995) evaluated 10 promising breeding lines & 5 cultivars for yield, plant height, days to maturity & number of productive tillers in 4 significantly different environments. There was significant G x E interaction for the 4 traits. ACK-85 was recommended for favorable environments in view of its above average stability for plant height, productive tillers & grain yield.

Singh et al (1995) provided information on G x E interaction derived from the data on 6 yield components in 15 genotypes grown in 6 environments. Only three genotypes showed stable performance and were recommended for cultivation in Sikkim.

Singh et al (1995) found significant differences due to genotypes, environments and G x E interaction for days to 50% flowering, plant height, grain weight and grain yield in 20 tall indica rice genotypes under three showing dates.

Kumar *et al.* (2005) evaluated twenty rainfed low land rice genotypes for their stability to grain yield and its component traits under three predictable environments created by changing the method of sowing and date of transplanting viz. direct sowing, normal transplanting and delayed transplanting. The pooled analysis of variance indicated that the mean differences due to genotypes and genotype x environment interaction were significant indicating that the genotypes differ in their adaptability and stability. The pooled deviations were also significant for all the characters studied, suggested that these genotypes differed in their deviation from linearity. Most of the characters were influenced by non-linear components of G x E interaction, but magnitude of linear components was greater than non-linear types. On the basis of linear components characters, the genotypes RAU 1401-12-2, Satyam, Kishori expressed average response and relative stability under different environment for yield and yield components. Stability for grain yield and its components were also exhibited by the genotypes TTB 517-16-SBIR 70149- 33 and Satyam under favourable environment whereas, genotypes RAU 1305-6-3-2-3 had higher stability under poor environmental condition. The genotypes RAU 1401-12-2 and RAU 1314-3-3-3 were found to be stable under average environment for grain yield per plant. These genotypes are suitable for the rainfed low land condition which will also serve as good parents for the development of high yielding stable lines.

Shanmuganathan and Ibrahim (2005) evaluated 11 rice hybrids in six different environments for their stability. The data were analyzed using Eberhart and Russell (1996) approach for yield and its contributing characters. Significant mean sum of square due to genotypes, environments and G x E interaction was observed. Linear and non- linear components of G x E interaction were important for the expression of most of the traits; however, linear component was larger in magnitude than the non- linear component. The hybrid CORH 2 was found to be stable for maximum of five characters. Among the six environments, Madurai (*kharif* 2000) was the most suitable environment for the expression of most of the characters.

Deshpande and Dalvi (2006) evaluated 12 rice hybrids in respect of grain yield and other characters under five environments. Variation due to genotypes (G), environments (E) and G x E interaction was highly significant in all the traits. Stability parameters $\overline{X}$, b_i and S^2_d were estimated for yield and other characters. By regression model it was revealed that stability in yield of the hybrid appeared to differ in respect of level of stability in the component traits. It was found that stability in grain yield was due to stability in yield components only and plasticity in others.

Arumugam *et al*., (2007) evaluated twelve rice genotypes for stability of grain yield and its components in six environments of sowing dates. Genotype-environment (GE) interaction was significant for grain yield and its components. Genotypes IET8116, KMP101, IR30864, CTH1, CTH3 and IR64 were stable for grain yield.

Dushyantha Kumar and Shadakshari (2007) evaluated thirty-six red rice genotypes for stability of yield and yield components under three environments. The significant G x E interaction for most of the traits suggested that the major portion of interaction was linear in nature and prediction over the environment was possible. The considerable genotypic difference was observed for the yield and its components when tested against the pooled error. The linear and nonlinear components were significant by apportioning of the G x E interaction indicating their importance in the expression of the trait grain yield in red rice.

Acuña *et al*., (2008) Genotype by environment (G × E) interactions were investigated in Vandana and a subset of 13 BC2 and BC3 lines of an improved *indica* upland rice cultivar, Vandana, backcrossed with a drought-tolerant traditional *japonica* cultivar, Moroberekan, which has a thick and extensive root system, in response to eight hydrological field environments conducted at Los Baños, in the Philippines, between 2001 and 2003. The G × E interaction accounted for 13% of the total sum of squares with environment and genotype responsible for 84 and 3%, respectively. Cluster analysis identified four environment and six genotype groups, which accounted for 70% of the G × E sums of squares. Of this, AX1, AX2 and AX3 accounted for 27, 22 and 21% of the G × E-SS, respectively. AX1 represented yield potential; AX2 was related to soil conditions, aerobic status and possibly VPD; and AX3 to change in phenology (days to flowering) with stress. The four environment groups were considered as broadly representative of contrasting rice production environments, including lowland-type, upland-wet season and upland-aerobic environments that experienced vegetative- or anthesis-stage drought stress. Genotype groups differed in adaptation to these diverse environments. For genotype groups G1–G6, G3 (VM150) had stable yields across environments; G1 (VM134) had the greatest grain yield in lowland-type environments (E2); G5 (VM135) in wet season environments (E3); G6 (VM168) in anthesis-stage drought (E4); G2 (Vandana and VM26) in vegetative- and anthesis-stage drought (E1 and E4); G4 had average yields across environments. Implications for breeding of rice adapted to contrasting hydrological environments are discussed, with the caution that adaptation to more than one environment type is desirable, because, as is demonstrated in this paper, an untimely climatic event can transform one environment type into another. Our results suggest that selection in one environment type may not give benefit in other environment types, so testing in more than one environment type is essential.

Parray *et al.*, (2008) estimated stability performance for ten rice cultivars across five random environments in the valley. Analysis of variance revealed presence of significant genetic variability for all traits studied. G × E interaction was significant for head rice recovery. Mean squares due to environment plus cultivars × environments was significant for plant height, productive tillers m^{-2}, grains $panicle^{-1}$ and grain yield $plot^{-1}$ Stability analysis for grain yield $plot^{-1}$ revealed that the mean square deviation from regression was significant and the prediction of stability of grain yield across environments would be precise and reliable.

MATERIALS & METHODS

3. MATERIALS AND METHODS

3.1. Location of the trial

The present investigation on "Biometrical Studies in Lowland Rice (*Oryza sativa* L)" was carried out in the experimental farm of ICAR research Complex, Jharnapani during the period 2003 to 2005. The details of the material used and methods employed in the present investigation are as follows:

3.2. Metrological observation during the investigation

The relevant metrological observations during the period of investigation are presented in the Appendix - A. The metrological data were obtained from ICAR research Complex, Jharnapani.

3.3. Experimental material

The experimental material in the present study comprised of thirty-two local genotypes of rice namely Mekrilha, Ngoba, Mekninya Khol, Thevuru(Kelo-u), Kuki Chaushi, Wonder rice, Krumiavinya, Tevuru(white), Keituo-ulha, Nyapie, N.S.Keniese-u, Kewhi Vuru, Rulonya, Rhineinya, Khezharhi, Ngobanya, Mekrilha(Kepei-u), Thevuru(Kezha-u), Chamben(N.S.Kumelo-u), Kencnya Kumui(Red), Tsorenya, Rosholha, Khenou, Nyuceimo, Kemony Kehnau(white), Kekhnie-LHE-Kenelo-u, Thevurie Tieca, Petkoti, Malong, Teke, Aboru, Mehuru, collected from different parts of Nagaland along with three improved genotypes Ranjit, Bahadur and Piolee from Assam.

3.4. Layout of experiment

The experiments were laid out for studying different aspects as indicated below:

3.4.1. Genetic variability & genetic divergence

3.4.1.1. Field experimentation

The present investigation was conducted on the experimental farm of ICAR Research Complex NEH Region (Jharnapani) during the period 2003-2004. Thirty-two local genotypes of rice of Nagaland namely Mekrilha, Ngoba, Mekninya Khol, Thevuru(Kelo-u), Kuki Chaushi, Wonder rice, Krumiavinya, Tevuru(white), Keituo-ulha, Nyapie, N.S.Keniese-u, Kewhi Vuru, Rulonya, Rhineinya, Khezharhi, Ngobanya, Mekrilha(Kepei-u), Thevuru(Kezha-u), Chamben(N.S.Kumelo-u), Kencnya Kumui(Red), Tsorenya, Rosholha, Khenou, Nyuceimo, Kemony Kehnau(white), Kekhnie-LHE-Kenelo-u, Thevurie Tieca, Petkoti, Malong, Teke, Aboru, Mehuru, along with three improved genotypes Ranjit, Bahadur and Piolee from Assam were grown in Randomized Complete Block Design with three replications in plots of 2m x Im size at a spacing of 20cm between rows and 15cm between plants in a row. All the recommended agronomic practices were followed for raising a good crop. Observations were recorded on 5 plants sampled randomly in each replication for different quantitative characters.

3.4.1.2. Observations recorded

The observations were recorded for the following characters:

3.4.1.2.1. Days to 50% flowering

Number of days was counted from the date of nursery sowing to the date of 50% panicle emergence on plot basis in each replication.

3.4.1.2.2. 50% flowering to maturity

The number of days from 50% flowering to date of ripening was recorded on plot basis in each replication.

3.4.1.2.3. Effective tillers per plant

The total number of ear bearing panicles per plant was recorded at maturity on sampled plants within a plot and average was worked out.

3.4.1.2.4. Plant height (cm)

From the sampled plants of each plot, plant height was recorded in cm from the ground level to the top of the tallest tiller and average was worked out.

3.4.1.2.5. Panicle weight (gm)

From the sampled plants of each plot panicle weight was recorded in gms using an electronic balance and average was worked out.

3.4.1.2.6. Panicle length (cm)

From the sampled plants of each plot panicle length was recorded in cm from the base of panicle to the top of the panicle and average was worked out.

3.4.1.2.7. Grains per panicle

The number of grains per panicle was counted at maturity in each of the sampled plant and average was worked out.

3.4.1.2. 8. Grain filling percent

The number of filled grains per plant was counted at maturity by removing chaffy grains in each of the sampled plants and average was worked out and expressed in percentage.

3.4.1.2.9. Length- breadth ratio

Length and breadth was measured in millimeters with the help of dial thickness gauge on 5 seeds in each replication.

3.4.1.2.10. 1000 grain weight

Three random samples of 1000 well filled grains each from the bulk produce of each replication were counted and weighed in grams.

3.4.1.2.11. Yield per plant

Panicles harvested from each hill were hand threshed, grains cleaned and dried, and weighed in grams.

3.4.1.3. Statistical analysis of data

The mean data over the sampled plants of each plot for different characters were subjected to various statistical and biometrical analyses like analysis of variance and covariance; estimation of genotypic, phenotypic and environmental variances and coefficients of variation; heritability and genetic advance; genotypic and phenotypic correlation coefficients; path coefficient analysis and genetic divergence.

3.4.1.3.1. Analysis of variance

In order to find out the significance of differences between the genotypes for each trait, the data were subjected to analysis of variance in the following manner.

Analysis of Variance Table

Source of variation	Degree of freedom	MSS	Expected MSS	F values
Replication	(r-1)	Mr	$\sigma^2e + v\,\sigma^2r$	
Genotype	(v-1)	Mv	$\sigma^2e + r\,\sigma^2g$	Mv/Me
Error	(r-1)(v-1)	Me	σ^2e	

Where,

r = Number of replications, v = Number of genotypes

σ2e = Error mean squares, σ2g = Genotypic variance

The calculated F values were tested at 5% and 1% level of significance.

3.4.1.3.2. Estimation of mean and standard error

Mean values of each characters was worked out by dividing the totals by corresponding number of observations (x = xi/n). Standard error of differences of two means was calculated as follows:

$$SE = \pm\sqrt{\frac{2Mse}{r}}$$

Where, r = Number of replications

Mse= Error mean squares

3.4.1.3.3. Coefficient of variation

The phenotypic, genotypic and environmental coefficients of variation were calculated according to Burton, (1952).

(a) Phenotypic coefficient of variation, $PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}}$

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

(b) Genotypic coefficient of variation, $GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}}$

Genotypic variance ($\sigma^2 g$) $= Mv - Me/r$

(c) Environmental coefficient of variation, $ECV = \frac{\sqrt{\sigma^2 e}}{\bar{x}}$

$\bar{x}$ = grand mean of the character

3.4.1.3.4. Heritability

Heritability in broad sense (h^2_{bs}) was computed as the ratio of genotypic variance ($\sigma^2 g$) to the phenotypic variance ($\sigma^2 p$) and expressed in percentage (Allard, 1960).

$h^2_{bs} = \sigma^2 G / \sigma^2 G + \sigma^2 E$

Where,

$\sigma^2 G$ = genotypic variance (Mv- Me)/r
$\sigma^2 E$ = environmental variance (Me)
$\sigma^2 G + \sigma^2 E = \sigma^2 P$ = phenotypic variance

3.4.1.3.5. Genetic advance (GA)

Genetic advance possible through selection was computed following Johnson et al; (1955).

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

Where,

K = selection differential at 5% selection intensity, the value of which is 2.06.

σ_p = phenotypic standard deviation

h^2_{bs} = heritability in broad sense

The genetic advance was expressed as percent of the mean to facilitate the comparison between different characters.

3.4.1.3.6. Correlation

Phenotypic and genotypic correlation coefficients were worked out to study the inter-relationship between various pairs of characters as suggested by Al-Jibouri *et al* (1958).

(a) Phenotypic correlation coefficients (rp)

$$rp = \frac{\text{Phenotypic Cov. of } x, y}{\sqrt{\text{Phenotypic } \sigma^2 x.\ \text{Phenotypic } \sigma^2 y}}$$

(b) Genotypic correlation coefficients (rg)

$$rg = \frac{\text{Genotypic Cov. of } x, y}{\sqrt{\text{Genotypic} \sigma^2 x.\ \text{Genotypic } \sigma^2 y}}$$

The significance of r values were tested at 5% and 1% from r table using (v – 2) degrees of freedom. Here, v is the number of genotypes on which the observations were recorded.

3.4.1.3.7. Path coefficient analysis

The path coefficient analysis was worked out by the formula applied by Dewey and Lu (1959). In general form, path coefficient is determined from the equation.

$$\sum_{j=1}^{n-1} r_{ij}\, p_{jN} = r_{iN} \quad \dots (1)$$

Where,

N is the character taken as the effect and all the character as possible cause, r and p are the correlations and the path coefficients respectively, i and j are column and rows indices respectively and N is the total number of characters considered for analysis.

The path coefficients were obtained by solving a set of simultaneous equations of the formula:

$$r_{ny} = P_{ny} + r_{n1}P_{1y} + r_{n3}\, P_{2y} + \text{-----------} + r_{n\,(n-1)}P_{\,(n-1)\,y}$$

Where,

r_{ny} = correlation between one component character and grain yield.

P_{ny} = path coefficient between the character and grain yield.

r_{n1}, r_{n2} --$r_{n(n-1)}$ = correlation between character and each of the other yield components in turn.

In matrix notation, equation (1) can be written as:

$$\begin{vmatrix} r_{11N} \\ r_{21N} \\ \\ r_{(n-1)N} \end{vmatrix} = \begin{vmatrix} r_{11} & r_{12} & r_{13} & ---- & r_{1(n-1)} \\ r_{21} & r_{22} & r_{23} & ---- & r_{2\,(n-1)} \\ & & & & \\ r_{(n-1)1} & r_{(n-1)2} & r_{(n-1)3} & ---- & r_{(n-1)\,(n-1)} \end{vmatrix} \begin{vmatrix} P_{11N} \\ P_{21N} \\ \\ P_{(n-1)N} \end{vmatrix}$$

Or,

$r_{iN} = (r_{ij})\ (P_{jN})$

$P_{jN} = (r_{ij})^{-1}\ (r_{iN})$

To determine the values of inverse matrix $(r_{ij})^{-1}$, original square matrix was transformed in rows and columns. The factors of the elements were then determined and divided by the determinant of the entire original matrix with the value of the matrix, P_{JN} was calculated.

Indirect effects for a particular character through other character were obtained by multiplication of direct path and particular correlation coefficients between those characters respectively.

Indirect effects= $r_{ij} \times P_{iy}$

Where,

r_{iy} = correlation between the i^{th} and j^{th} characters
P_{ij} = correlation between the i^{th} and j^{th} characters
P_{iy} = direct path of i^{th} character on dependent character.

Residual effect (x) is given by

$$P_x^{\,2} = 1 - \sum_{i=1}^{P} r_{iy}.P_{iy}$$

Where,

P = number of characters
riy = correlations between the ith character and yield (dependent character)
Piy = direct effect of the ith character on yield.

3.4.1.3.8. Genetic divergence

Genetic divergence among 35 genotypes of experiment was analyzed by using Mahalanobis D^2 statistics (Rao, 1952). D^{2-} statistics is a measure of genetic distances among groups or varieties based on multiple characters. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related parents. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability. The purpose of D^2- statistics is to identify genotypes which can be grouped together as one genetic group. If there are 'p' characters measured on each individual, and 'ds' are the difference between means of two groups, then D_2- statistics (Mahalanobis, 1928)is defined as:

$$pD^2 = b_1d_1 + b_2d_2 + \text{---------} + b_pd_p \qquad \text{... (1)}$$

Where,

The bi values are to be estimated such that the F ratio of variance 'between groups' and 'within groups' is maximized. In terms of variances and covariances of the i^{th} and j^{th} traits of two groups, 1and 3, the D^2 value is obtained as follows:

$$pD^2 = W^{ij}\,(x^1i - x^2i)\,(x^1j - x^2j)$$

Where,

W^{ij} is the inverse of estimated variance- covariance matrix.

For each pair of mean deviation i.e. Yi^{1-} $Yi1$ with i =1,2,----P. is computed and the D_2 is calculated as the sum of these deviation i.e.

$$D^2 = \sum (Yi^1 - Yi^2)^2$$

Traits					
Group	1	2	3		P
1	Y_{11}	Y_{21}	Y_{31}	----------	Y_{p1}

2	Y_{12}	Y_{22}	Y_{32}	---------	Y_{p2}
-----	-----	-----	-----	---------	-----
Difference	$Y_{11}-Y_{12}$	$Y_{21}-Y_{22}$	$Y_{31}-Y_{32}$	---------	$Y_{p1}-Y_{p2}$

$$D^2 = (Y_{11}-Y_{12})^2 + (Y_{21}-Y_{22})^2 + \text{--------} (Y_{p1}-Y_{p2})^2$$

$$= \sum (Yi^{1}-Yi^{2})^{2}$$

Similarly, the D^2 values for all the other combination of group pairs\, 1 and 3, land 4, 2and 3, etc. are calculated. The D^2 values obtained for a pair of group is taken as the calculated value of x^2 for p degrees of freedom, where p is the number of character considered.

Each character is ranked on the basis of di $=Y_{ij} - Y_{ik}$ values. Rank one is given to the highest mean difference, where p is the number of characters. These ranks are given in the parenthesis in the calculation of D^2 values for all the contribution of pairs.

Percent contribution is calculated taking pq = 100.

Tocher's method of cluster grouping.

A table is made with each group heading a column and changing their group in the same column in order of their distances. First column is headed by group or variety 1. in this column, the group or variety nearest to the group or variety 1 is placed next row below and so on for the 3rd, 4th, ---- pth rows of the same column. Second column is headed by group 2 and the group nearest to the group 2 is placed in the 2nd row and so on. In this ways all the columns and rows are flied by groups' with D^2 statistics values in parenthesis. The groups belonging to the same are now grouped into different clusters according to D^2 values.

The average D^2 value in the first row is arbitrarily taken as the maximum permissible value for being placed in the same cluster. The first two are automatically of the same cluster. When the third is added, the average D^2 value due to addition of the third and fourth group from the previous average should not exceed the permissible limit set above. If the increase in the average D^2 value over the previous combination is less than the permissible value, it is excluded in the cluster, otherwise stays out. The rest of the group is then considered for making a second cluster. Any pair which shows least distances between them is taken and the same procedure is followed for the inclusion of other group.

Forces of differentiation at genotypic and inter cluster levels are demonstrated by CV values.

3.4.2. Combining ability and genetic analysis

3.4.2.1. Field experimentation

The hybridization work was carried out in wet season 2003. In 2004 wet season, six parents (Malong, Mehuru, Teke, Piolee, Ranjit and Bahadur) along with 15 F_1 hybrids (Malong x Mehuru, Malong x Teke, Malong x Piolee, Malong x Ranjit, Malong x Bahadur, Mehuru x Teke, Mehuru x Piolee, Mehuru x Ranjit, Mehuru x Bahadur, Teke x Piolee, Teke x Ranjit, Teke x Bahadur, Piolee x Ranjit, Piolee x Bahadur and Ranjit x Bahadur) of a 6 x6 diallel cross (excluding reciprocals) were grown in Randomized Complete Block Design with three replications. Thirty days old single seedling per hill was planted at a spacing of 20 X 15 cm with three-meter length row having three rows in each entry. The experiment was conducted with normal package of practices and need based plant protection measures. Observations were recorded on ten sampled plants of the middle row of each plot avoiding the border rows and border plants for different quantitative characters.

COMBINING ABILITY & GENETIC ANALYSIS

P-1

GENETIC VARIABILITY & GENETIC DIVERGENCE

Data pertaining to the parents and F_1's of 6 x 6 diallel cross (excluding reciprocals) were analyzed according to Griffing (1956) Model I, Method II and Hayman- Jinks method (Jinks & Hayman, 1953; Hayman, 1954 and Jinks, 1954).

3.4.2.2. Observations recorded

The observations were recorded for days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, plant weight, panicle length, grains per panicle, grain filling percent, length- breadth ratio, 1000 grains weight and yield per plant as per the procedures indicated in 3.4.1.2.

3.4.2.3. Analysis of variance

The mean data for each character was subjected to analysis of variance. The partitioning of variance into different components was done in accordance with the following model:

$$Pijk = \mu + Gij + b_k + e_{ijk}$$

Where,

Pijk is the phenotype of the ijth genotype grown in the kth block.

μ is the general mean, Gij is the effect of the ijth genotype

b_k is the effect of kth block, e_{ijk} is the random error associated with the ijkth observation

The variance of the genotypes was further partitioned into different components as indicated below:

Sources of Variation	Degrees of Freedom	Mean sum of squares
Replication	(r-1)	M r
Genotype	(g-1)	M g
Parent	(p-1)	M p
Cross	(c-1)	M c
Parent Vs Cross	(p-1) (c-1)	M p x g
Error	(r-1) (g-1)	M e
Total	rg-1	

Where,

r is the number of replications, g is the number of genotypes,

p is the number of parents, c is the number of crosses,

M r is the replication mean sum of squares; M g is the genotype mean sum of squares,

M p is the parent mean sum of squares, M c is the cross mean sum of squares,

Me is the error mean sum of squares

The different variances were tested against error mean squares by F- test for appropriate degrees of freedom.

3.4.2.4. Griffing's method for combining ability analysis

The general combining ability and specific combining ability analyses were carried out according to the procedure outlined by Griffing (1956) using Model I, Method II where variety and block effects are assumed fixed and only one set of crosses with the parents is used. The analysis of variance for combining ability (Method II, Model I) developed by Griffing (1956b) was based on the following mathematical model:

$\text{Pijk} = m + g_i + g_j + S_{ij} + e_{ijk} / r$

Where,

P_{ijk} = phenotype of the cross of ith and jth parents in the kth block.
m = population mean
g_i = general combining ability (gca) effect of the i^{th} parent
g_j = general combining ability (gca) effect of the j^{th} parent
S_{ij} = specific combining ability (sea) effect of the ij^{th} combinations such that Sij = Sji
r = number of replications, e_{ijk} = random error for the ijk^{th} observations

3.4.2.4.1. Analysis of variance

The analysis of variance for combining ability showing the expectations of mean sum of squares is as follows:

Sources of Variation	Degree of freedom	Sum of Squares	Mean Sum of Squares	Expected Mean Sum of Squares
gca	p-1	Sg	Mg	$\sigma^2_e + \frac{P+2}{P-2}\sum g_i^2$
sea	$\frac{P(P-1)}{2}$	Ss	Ms	$\sigma^2_e + \frac{2}{P(p-1)}\sum_i \sum_j S_{ij}^2$
Error	m	Se	M'e	σ^2_e

Where, p = number of parents

Sg = Sum of squares due to gca

$$= \frac{1}{P+2}\left[\sum_i (X_i + X_{ii})^2 - \frac{4}{P} X_{..}\right]$$

Ss = Sum of squares due to sca

$$= \sum_i \sum_j X_{ij}^2 - \frac{1}{(P+2)}(X_i + X_{ii})^2 + \frac{2}{(P+1)(P+2)} X^2..$$

Mg, Ms= Mean sum of squares (variance) due to GCA and SCA

M'e = Mean sum of squares due to error

$$= \frac{Mse}{r} = \sigma^2_e$$

m = d.f. for error

Model I:

Component due to gca variance; σ^2 gca

$$= \frac{1}{(p-1)} \sum_i g_i^2 = (Mg - M'e)/(p+2)$$

Component due to sca variance, σ^2 sca

$$= \frac{2}{p(p-1)} \sum\sum_{i<j} S_{ij}^2 = Ms - M'e$$

The ratio of gca variance to sca variance

$$= \frac{(Mg - M'e)/(p+2)}{(Ms - M'e)}$$

3.4.2.4.2. Combining ability effects

The general combining ability (GCA) effect of the i^th^ parent was calculated as

$$G_i = \frac{1}{P+2}\left[\sum (X_{i.} + X_{ii})^2 - \frac{2}{P} X..\right]$$

The specific combining ability (SCA) effect of the ij^th^ cross was calculated as

$$S_{ij} = X_{ij} - \frac{1}{p+2}(X_{i.} + X_{ii} + X_j + Y_{jj}) + \frac{2}{(p+1)(p+2)} X..$$

Where,

$X_{i.}$ = total of array involving ith parent, $X_{.j}$ = total array involving jth parent

X_{ii} = mean value of ith parent, X_{jj} = mean value of jth parent, $X_{..}$ = grand total

3.4.2.4.3. Standard errors

To test significance of gca and sea effects, S.E. was calculated as follows:

$$\text{S.E.}(g_i) = \left(\frac{p-1}{p(p+2)}6^2\right)^{\frac{1}{2}}$$

$$\text{S.E.}(g_i\text{-}g_j) = \left(\frac{2}{p+2}6^2\right)^{\frac{1}{2}}$$

$$\text{S.E.}(Sij) = \left(\frac{p^2+p+2}{(p+1)(p+2)}6^2\right)^{\frac{1}{2}} \text{ and}$$

$$\text{S.E.}(S_{ij}\text{- } S_{kl}) = \left(\frac{2p}{p+2}6^2\right)^{\frac{1}{2}}$$

Where,

g_i = general combining ability for the ith parent

S_{ij} = specific combining ability for the ijth cross

g_i-g_j = comparison of any two gca estimates

S_{ij}- S_{kl} = comparision of any two sea estimates

3.4.2.5. Hayman's method of genetic analysis of diallel

The genetic analysis of diallel was carried out following Hayman- Jinks method (Jinks & Hayman, 1953; Hayman, 1954 and Jinks, 1954). A 6 x 6 diallel table was prepared from the means of the parents and their F_1's over all the replications to calculate the following second- degree statistics:

V_oL_o= Variance of the parents

W_oL_o= Covariance between the parents and their offspring in a given array

V_2= Mean variance of a given array

V_oL_2= Variance of the mean of the arrays, and

M_{L2} - M_{Lo}= Difference of the parental and progeny means.

The validity of assumptions underlying the diallel hypothesis postulated by Jinks and Hayman (1953) and Hayman (1954) was tested by the V_r, W_r (Variance, Covariance) homogeneity and also by the F- Test with (n-2) degrees of freedom. The testing was done by using the following formula.

$$t^2 = \frac{(n-2)}{4} \text{ X } \frac{(\text{VarVr} - \text{VarWr})^2}{(\text{VarVrxVrWr}) - \text{cov}^2(\text{VrWr})}$$

Further, joint regression test was also conducted before constructing a Vr, Wr graph.

3.4.2.5.1. Genetic parameters

With the assumptions validated, estimates of genetic parameters according to Hayman (1954) were obtained as given below.

E=environmental variance

$D = VoLo - E$

$F = 2\ VoLo - 4\ WoLo_1 - 2(n-2)\ E/n$

$H_1 = VoLo - 4\ WoLo_1 + 4\ V_1L_1 - (3n-2)\ E/n$

$H_2 = 4\ V_1L_1 - 4\ VoL_1 - 2E$

$h_2 = 4\ (M_{L1} - M_{Lo})^2 - 4\ (n-1)\ E/n_2$

The expressions were defined by Jinks (1954) as given below:

$VoLo = D + E$

$WoLo_1 = D/2 - F/8 + E/n$

$V_1L_1=D/4-F/8 + H_1/ 16 + E$

$VoL_1=D/4-F/8 - H_1/ 16-H_2 / 16 + (n\text{-}1) E/n^2$

$(M_{L1} - M_{Lo})^2=h^2 / 4 - (n\text{-}1) E /n^2$

Where,

E = Environmental variance from ANOVA

D = Estimate of additive and additive x additive genetic variance

H_1 & H_2 = Estimates of dominance and dominance x dominance interactions, respectively.

h2=Overall dominance effect

F=Estimate of relative frequencies of dominant and recessive alleles in the parents

3.4.2.5.2. Standard errors

Standard errors of above estimates were calculated using the common multipliers from Hayman (1954) as follows:

$$S.E._{E} = \left[\frac{N^{4}}{N^{5}} S^{2}\right]^{½}$$

$$S.E._{D} = \left(\frac{n^{5}+n^{4}}{n^{5}} S^{2}\right)^{\frac{1}{2}}$$

$$S.E._{H_1} = \left(\frac{n^{5}+41n^{4}-12n^{3}+4n^{2}}{n^{5}} S^{2}\right)^{\frac{1}{2}}$$

$$S.E._{H_2} = \left(\frac{36n^{4}}{n^{5}} S^{2}\right)^{\frac{1}{2}}$$

$$S.E._{h^2} = \left(\frac{16n^{4}+16n^{2}-32n+16}{n^{5}} S^{2}\right)^{\frac{1}{2}}$$

$$S.E._{\cdot F} = \left(\frac{4n^5 + 20n^4 - 16n^3 + 16n^2}{n^5} S^2 \right)^{\frac{1}{2}}$$

Where,

N = Number of parents

S_2 = Sample variance

Significance of each statistics was tested by t- test at n-2 df as t =parameter/SE of the parameter.

The proportion of genes with positive and negative effects in the parents is expressed as the ratio, $H_2/4H_1$ and mean degree of dominance as the ratio $(H_1/D)_{1/2}$. The proportion of dominant and recessive genes in the parents was obtained by the ratio (KD/KR) = $[(4DH_1)^{1/}{}_2 + F]/\ [(4DH_1)_{1/2} - F]$. The number of group of genes which control the character and exhibit dominance was computed as h^2/H_2.

Heritability (h$^{2)}$ estimates in narrow sense were computed following the formula of Mather and Jinks (1982).

$$h^2_{(ns)} = \frac{(1/2)D+(1/2)H_1 -(1/2)H_2 -(1/2)F}{(1/2)D+(1/2)H_1 -(1/4)H_2 -(1/2)F+E}$$

3.4.2.5.3. Graphical analysis

The relationship of Wr (covariance) with Vr (variance) provides information regarding (i) degree of dominance and (ii) distribution of dominance and recessive genes among the parents. Therefore, the Wr values were plotted against the corresponding Vr values to obtain such information. For drawing limiting parabola, corresponding Wri values were calculated against each Vri.

Wri = (Vri x VoLo)$^{1/}{}_2$

For drawing regression line, the expected Wrei values were calculated as follows:

$Wrei = Wr - b\,Vr + b\,Vri$

The calculated values of Wrei were plotted against Vr to draw the regression line. The point of interception of the regression line with Wr ordinate i.e., 'a' was obtained as follows:

$a = Wr - bVr$

3.4.3 Phenotypic stability

3.4.3.1 Field experimentation

In the present investigation 32 local along with three improved genotypes of rice were grown in six environments. The details of six environments are as under

SN	Environment	Date of sowing	Year
1	E_1	1st June	2003
2	E_2	25th June	2003
3	E_3	1st June	2004
4	E_4	25th June	2004
5	E_5	1st June	2005
6	E_6	25th June	2005

In each environment, these genotypes were planted in a Randomized Complete Block Design with three replications.

3.4.3.2 Observation recorded

Data were recorded on grain yield per plot in gms for each genotype replication wise in each environment.

3.4.3.3 Analysis of variance

The data were subjected to analysis of variance at individual environments and also pooled analysis of variance.

3.4.3.4 Stability analysis

Genotype- environment (G x E) interaction and phenotypic stability were studied following the model of Eberhart and Russell (1966).The model developed by Eberhart and Russell is expressed as :

$Y_{ij} = m + b_i I_j + \delta_{ij}$ ($i = 1, 2, 3, \ldots t$ and $j = 1, 2, 3, \ldots s$)

Where,

Y_{ij}= the mean of the i^{th} genotype at the j^{th} environment,

m=the mean of all the genotypes over all the environments,

b_i=The regression coefficient of the i^{th} genotype on the environmental index which measures the response of this genotype to varying environments.

I_j=the environmental index which is defined as the deviation of the mean of all the genotypes at a given environment from the overall mean and is calculated as:

=, with $\sum_{j} I_j = 0$,=

δ_{ij} = The deviation from regression of the i^{th} genotype at the j^{th} environment.

PLATE-3


STABILITY EXPERIMENT


STABILITY EXPERIMENT

3.4.3.4.1 Analysis of variance

The format for analysis of variance according to Eberhart and Russell (1966) model is as given below:

Source	Degrees of freedom	Sum of squares
Total	$(st-1)$	$\sum_i \sum_j Y_{ij}^2$ CF
Genotypes (G)	$(t-1)$	$\frac{1}{s}\sum_i Y_i^2$ CF
Environment (E) + G × E	$(s-1)+(t-1)(s-1)$	$t(s-1) \sum_i \sum_j Y_{ij}^2 \frac{1}{s}\sum_i Y_i^2$
Environment (linear)	1	$1/t \left(\sum_i Y_j I_j\right)^2 / \sum_j I_j^2$
G × E (Linear)	$(t-1)$	$\sum_i \left(\sum_j Y_{ij} I_j\right)^2 / \sum_j I_j^2$ -Envt. (lin.) SS
Pooled deviation	$t(s-2)$	$\sum_i \sum_j \delta_{ij}^2$
Genotype 1	$(s-2)$	$\left[\sum_j Y_{ij}^2-(Y_i)^2/s\right]-\left(\sum_j Y_{ij} I_j\right)^2/\sum_j I_j^2$ $=\sum_j \delta_{1j}^2$
Genotypes	$(s-2)$	$\left[\sum_j Y_{tj}^2-(Y_1)^2/s\right]-\left(\sum_j Y_{1j} I_j\right)^2/\sum_j I_j^2$ $=\sum_j \delta_{tj}^2$
Pooled error	$St(r-1)$	

3.4.3.4.2 Calculation of pooled error

Pooled error was calculated as

$$\text{Pooled error} = \frac{(n_1 - 1)(MSeE_1) + \ldots + \ldots + (ns - 1)(MSeE_1)}{(n_1 - 1) + (n_2 - 1) + \ldots + \ldots + (n_s - 1)}$$

Where,

$(n_1 - 1)$ = The d.f. for error in environment, 1

$(n_s - 1)$ = The d.f. for error in environment, s

M.S. error E_1 = the mean sum of squares due to error in environment, 1

and M.S. error E_s = the mean sum of squares due to error in environment, s

Pooled error M.S. was calculated as

$$\text{Pooled error M.S} = \frac{\text{Pooled error}}{r}$$

Where, r = number of replications

3.4.3.4.3 Testing of variances

S.E. and C.D. for comparing varietal means in the individual environments were calculated as

$$\text{S.E. of means} = \sqrt{\frac{2\,MSe}{r}}$$

Where, r = number of replications

C.D. was calculated as: $SE_{(means)} \times t_{5\%}$ at error d.f.

3.4.3.4.4 Stability parameters

The three stability parameters were calculated as follows:

(1) Mean (m) = the mean of the i^{th} genotype over all the environments

(2) Regression coefficient (b_i) = $\dfrac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$

Where,

$\sum_j Y_{ij} I_j$ is the sum of products of value of i^{th} genotype at j^{th} environment and environmental index

$\sum_j I_j^2$ is the sum of the squares of environmental indices

(3) Deviation mean square (s_2d_i) = $\dfrac{\sum_j \delta^2_{ij}}{S-2} - \dfrac{S^2_e}{r}$

Where,

$\sum_j \delta^2_{ij}$ = the estimate of pooled error, and

$$Ij = \left(\sum_j Yij/t\right)\left(\sum_i \sum_j Yij/ts\right)$$

To test the significance of b_i values from unity, 't' test is followed.

$t = \dfrac{b-1}{s_b}$, Where,

b = regression coefficient of ith genotype

s_b = The standard error of 'b' and is calculated as

$$\sqrt{\frac{\text{MS due to pooled deviations}}{\sum_j I_j^2}}$$

To test the significance of deviation mean square (s^2d_i) of each genotype from its regression, the appropriate F test is

$$F = \frac{s^2 d_i}{\text{Mean square for pooled error}}$$

3.4.3.4.5 Phenotypic index (Pi)

Phenotypic index (Pi) was estimated (Ram *et al.* 1970) for each genotype in order to determine the genotypes with high mean as reflected by positive indices.

$Pi = X_{i.} - X_{..}$

Where, $X_{i.}$ is the mean of ith genotype over environments

and $X_{..}$ is the grand mean

EXPERIMENTAL FINDINGS

4. EXPERIMENTAL FINDINGS

The results obtained in the present investigation are presented below:

4.1 Genetic variability and genetic divergence

4.1.1 Analysis of variance

The analysis of variance for the 11 characters under study is presented in Table 1. The mean sums of squares for genotypes (treatments) were found highly significant for all the characters.

4.1.2 The extent of genetic variation

Owing to the presence of sufficient variation among the genotypes different variance components and related genetic parameters were estimated and presented in Table 2.

4.1.2.1. Days to 50% flowering

The estimates of genotypic variance (127.62) and the phenotypic variance (138.85) were higher than environmental variance (11.23). The phenotypic coefficient of variation (11.21) was higher than genotypic coefficient of variation (10.74). The estimates of heritability in broad sense was found to be high (91.90) with high genetic advance (21.22).

4.1.2.2. 50% flowering to maturity

The estimate of genotypic variance (22.89) was lower than phenotypic variance (26.74) and higher than environmental variance (3.85). The phenotypic coefficient of variation (17.76) was higher than genotypic coefficient of variation (16.43).The estimates of heritability in broad sense was found to be high (85.60) with high genetic advance (31.31).

Table: 1 Analysis of Variance for 11 characters of Rice (*Oryza sativa* L)

Sources of Variation	Degree Of Freedom	MEAN SQUARES										
		Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Replication	2	53.625	15.238	0.319	65.375	0.227	11.464	97.062	40.125	0.036	27.093	0.340
Genotype	34	394.09**	72.55**	10.44**	1833.30**	11.936**	12.378**	1348.506**	212.112**	0.344**	36.132**	37.301**
Error	68	11.236	3.855	0.271	198.851	0.195	4.329	169.272	49.761	0.025	3.741	1.997

** Significant at 1% level

Table: 2. Mean, Range, Variance, Coefficient of Variation, Heritability, Genetic Advance and GA as percent of Mean

Characters	Mean ±SE	Range	Variance			Coefficient of Variation		Heritability (Broad sense) (%)	Genetic Advance	GA as % of Mean
			6^2_g	6^2_e	6^2_p	(GCV)	(PCV)			
Days to 50% Flowering	105.11± 2.73	82.00-124.00	127.62	11.23	138.85	10.74	11.21	91.90	22.31	21.22
50% Flowering To Maturity	29.12± 1.60	20.33-38.67	22.89	3.85	26.74	16.43	17.76	85.6	9.12	31.31
Effective Tillers / Plant	5.76± 0.42	3.13-10.40	3.39	0.27	3.66	31.97	33.23	92.6	3.65	63.37
Plant Height	136.99± 11.51	76.33-187.33	544.90	198.85	743.75	17.04	19.91	73.3	41.16	30.04
Panicle Weight	4.83± 0.36	1.88-9.53	3.91	0.20	4.11	40.93	41.96	95.13	3.96	81.98
Panicle Length	27.19± 1.69	24.33-32.33	2.68	4.33	7.01	6.02	9.73	38.23	2.08	7.64
Grains Per Panicle	115.43± 10.62	79.33-169.67	393.07	169.27	562.34	17.17	20.54	69.89	34.13	29.56
Grain Filling Percent	74.88± 5.75	58.47-87.41	54.11	49.76	103.87	9.81	13.61	52.09	10.93	14.59
Length-Breadth Ratio	2.70± 0.12	1.90-3.16	0.11	0.03	0.14	12.28	13.85	78.57	0.60	22.22
1000 Grains Weight	27.18± 1.57	22.48-33.80	10.79	3.74	14.53	12.06	14.01	74.26	5.82	19.42
Yield Per Plant	12.75± 1.15	9.17-23.55	11.76	1.99	13.75	26.82	29.01	85.55	6.52	51.13

4.1.2.3. Effective tillers per plant

The estimates of genotypic variance (3.39) and the phenotypic variance (3.66) were higher than environmental variance (0.27). The phenotypic coefficient of variation (33.23) was higher than genotypic coefficient of variation (31.97). The estimates of heritability in broad sense was found to be high (92.60) with high genetic advance (63.37).

4.1.2.4. Plant height

The estimate of genotypic variance (544.90) was lower than phenotypic variance (743.75) and higher than environmental variance (198.85). The phenotypic coefficient of variation (19.91) was higher than genotypic coefficient of variation (17.04).The estimates of heritability in broad sense was found to be high (73.30) with high genetic advance (30.04).

4.1.2.5. Panicle weight

The estimates of genotypic variance (3.91) and the phenotypic variance (4.11) were higher than environmental variance (0.20). The phenotypic coefficient of variation (41.96) was higher than genotypic coefficient of variation (40.93). The estimates of heritability in broad sense was found to be high (95.13) with high genetic advance (81.98).

4.1.2.6. Panicle length

The estimate of genotypic variance (2.68) was lower than both phenotypic variance (7.01) and environmental variance (4.33). The phenotypic coefficient of variation (9.73) was higher than genotypic coefficient of variation (6.02).The estimates of heritability in broad sense was found to be moderate (38.23) with low genetic advance (7.64).

4.1.2.7. Grains per panicle

The estimates of genotypic variance (393.07) and the phenotypic variance (562.34) were higher than environmental variance (169.27). The phenotypic coefficient of variation (20.54) was higher than genotypic coefficient of variation (17.17). The estimates of heritability in broad sense was found to be high (69.89) with high genetic advance (29.56).

4.1.2.8. Grain filling percent

The estimate of genotypic variance (54.11) was lower than phenotypic variance (103.87) and higher than environmental variance (49.76). The phenotypic coefficient of variation (13.61) was higher than genotypic coefficient of variation (9.81).The estimates of heritability in broad sense was found to be moderate (52.09) with moderate genetic advance (14.59).

4.1.2.9. Length- breadth ratio

The estimates of genotypic variance (0.11) and the phenotypic variance (0.14) were higher than environmental variance (0.03). The phenotypic coefficient of variation (13.85) was higher than genotypic coefficient of variation (12.28). The estimates of heritability in broad sense was found to be high (78.57) with high genetic advance (22.22).

4.1.2.10. 1000 grain weight

The estimate of genotypic variance (10.79) was lower than phenotypic variance (14.53) and higher than environmental variance (3.74). The phenotypic coefficient of variation (14.01) was higher than genotypic coefficient of variation (12.06).The estimates of heritability in broad sense was found to be high (74.26) with moderate genetic advance (19.42).

4.1.2.11. Yield per plant

The estimates of genotypic variance (11.76) and the phenotypic variance (13.75) were higher than environmental variance (1.99). The phenotypic coefficient of variation (29.01) was higher than genotypic coefficient of variation (26.82). The estimates of heritability in broad sense was found to be high (85.55) with high genetic advance (51.13).

4.1.3 Mean performance for grain yield per plant and other related parameters

The present investigation was also aimed to assess the mean performance of the genotypes for grain yield per plant and other related traits. The mean performance for grain yield and yield attributing characters are presented in Table 3

4.1.3.1. Days to 50% flowering

The mean value for days to 50% flowering ranged from 82 (Piolee) to 124 (Chamben- N.S.Kumelo-u). The general mean was 105.11 ± 2.73.

4.1.3.2. 50% flowering to maturity

The mean value for 50% flowering to maturity ranged from 20.33 (Mekninya Khol) to 38.67 (Nyceimo). The general mean was 29.12 ± 1.60.

4.1.3.3. Effective tillers per plant

The mean value for effective tillers per plant ranged from 3.13 (Khenon) to 10.40(Ngoba). The general mean was 5.76 ± 0.42.

4.1.3.4. Plant height

The mean value for plant height ranged from 76.33 (Kekhnie-LHE-Kenelo-u) to 187.33 (Mekrilha). The general mean was 136.99 ± 11.51.

TABLE: 3. Mean performance of 35 genotypes of rice for 11 characters

Genotypes	Days to 50% flowering	50% flowering to maturity	Effective tillers per plant	Plant height	Panicle weight	Panicle length	Grains per panicle	Grain filling percent	Length-Breadth ratio	1000 Grain weight	Yield per plant
Mekrilha	117.33	35.67	9.07	187.33	5.47	29.00	154.00	61.87	3.09	33.51	10.50
Ngoba	114.00	25.33	10.40	145.67	3.60	24.67	79.33	75.06	2.85	27.31	12.85
Mekninya Khol	86.00	20.33	4.07	149.00	8.30	29.67	159.33	79.35	2.27	32.59	17.53
Thevuru(Kelo-u)	93.00	35.67	4.40	139.00	9.53	28.00	113.00	83.60	3.14	31.41	17.07
Kuki Chaushi	94.67	21.33	3.37	102.33	2.18	25.00	99.00	66.99	2.61	23.00	9.17
Wonder rice	112.33	35.00	4.87	150.00	6.90	25.33	151.67	85.12	2.81	28.33	14.46
Krumiavinya	116.67	33.00	4.67	133.00	2.47	25.00	110.00	66.44	2.12	22.60	16.86
Tevuru(white)	105.67	30.00	5.47	156.67	2.04	27.33	99.33	73.44	2.45	27.60	10.20
Keituo-ulha	105.00	33.00	6.27	150.67	3.40	32.33	89.00	71.40	3.06	23.38	10.76
Nyapie	112.00	36.00	6.27	103.00	2.82	27.67	111.67	65.70	2.74	30.63	11.63
N.S.Keniese-u	98.67	32.33	5.53	140.00	1.88	25.67	169.67	87.41	3.10	22.93	12.01
Kewhi Vuru	109.33	25.00	5.17	152.00	8.37	27.00	97.33	84.88	1.90	30.35	13.14
Rulonya	110.00	33.67	4.67	141.00	7.37	27.00	110.00	61.77	2.24	30.35	11.06
Rhineinya	118.00	27.00	4.27	152.00	5.27	26.67	99.33	59.13	2.92	30.00	11.89
Khezharhi	106.33	24.33	5.87	141.33	3.23	24.67	112.33	66.10	2.98	23.36	11.55
Ngobanya	118.67	29.00	5.87	143.33	2.82	25.67	120.33	58.47	2.73	26.79	11.40
Mekrilha(Kepei-u)	107.33	33.00	8.20	163.67	5.33	28.00	117.33	74.16	2.83	24.86	11.68
Thevuru(Kezha-u)	116.67	23.33	6.20	143.33	5.13	28.00	119.00	76.54	2.82	25.69	11.63
Chamben(N.S.Kumelo-u)	124.00	30.00	5.20	105.00	4.87	27.00	97.67	83.33	2.92	29.37	10.22

Contd.

Genotypes	Days to 50% flowering	50% flowering to maturity	Effective tillers per plant	Plant height	Panicle weight	Panicle length	Grains per panicle	Grain filling percent	Length-Breadth ratio	1000 Grain weight	Yield per plant
Kencnya Kumui(Red)	97.33	35.33	4.53	154.33	5.30	27.33	111.00	85.37	3.05	25.47	10.65
Tsorenya	114.00	24.33	7.43	152.00	5.03	30.00	120.00	71.72	2.92	26.26	10.55
Rosholha	113.33	26.33	8.00	156.00	5.66	28.00	127.33	68.22	2.84	28.34	10.63
Khenou	112.00	25.67	3.13	155.00	6.17	29.00	134.67	77.23	2.53	30.88	10.85
Nyuceimo	110.00	38.67	4.60	154.33	5.90	29.33	124.67	64.53	2.96	29.41	11.28
Kemony Kehnau(white)	103.33	23.00	4.50	162.00	3.47	30.00	104.33	76.55	2.61	26.40	11.59
Kekhnie-LHE-Kenelo-u	86.67	33.67	3.70	76.33	4.00	29.00	100.67	75.29	2.54	22.48	10.19
Thevurie Tieca	110.33	26.00	6.40	159.67	2.65	31.33	91.33	78.70	3.14	30.81	10.81
Petkoti	112.67	28.00	4.00	105.00	3.87	26.00	106.67	76.66	2.76	22.68	10.18
Malong	97.67	34.00	4.00	101.00	7.80	25.00	108.00	82.14	2.32	28.25	11.05
Teke	88.00	30.33	4.20	138.67	7.45	25.33	141.33	85.85	3.02	33.80	13.42
Aboru	112.33	25.67	4.07	151.33	4.80	26.67	134.00	74.74	2.25	27.48	10.43
Mehuru	103.67	28.67	7.63	122.00	3.97	26.00	132.33	85.61	3.16	26.78	12.69
Ranjit	86.00	29.67	9.17	101.00	3.10	24.33	89.67	73.15	2.31	22.73	21.31
Bahadur	84.00	25.00	8.40	106.67	5.60	25.00	108.00	80.09	2.48	22.87	23.55
Poilee	82.00	22.00	8.03	101.00	3.56	25.67	97.00	84.27	2.25	22.80	21.63
Grand Mean	105.11	29.12	5.76	136.99	4.83	27.19	115.43	74.88	2.70	27.18	12.75
CV	3.18	6.74	9.04	10.29	9.14	7.65	11.27	9.42	5.84	7.11	11.08

4.1.3.5. Panicle weight

The mean value for panicle weight ranged from 1.88g (N.S.Keniese-u) to 9.53g (Thevuru- Kelo-u). The general mean was 4.83 ± 0.36.

4.1.3.6. Panicle length

The mean value for panicle length ranged from 24.33cm (Ranjit) to 32.33cm (Keituo-ulha). The general mean was 27.19 ± 1.69.

4.1.3.7. Grains per panicle

The mean value for grains per panicle ranged from 79.33(Ngoba) to 169.67(N.S.Keniese-u). The general mean was 115.43 ± 10.62.

4.1.3.8. Grain filling percent

The mean value for grain filling percent ranged from 58.47% (Ngobanya) to 87.41% (N.S.Keniese-u).The general mean was 74.88 ± 5.75.

4.1.3.9. Length- breadth ratio

The mean value for length- breadth ratio ranged from 1.90mm (Kewhi Vuru) to 3.16mm (Mehuru).The general mean was 2.70 ± 0.12.

4.1.3.10. 1000 grain weight

The mean value for 1000 grain weight ranged from 22.48g (Kekhnie-LHE-Kenelo-u) to 33.80g (Teke).The general mean was 27.18 ± 1.57.

4.1.3.11. Yield per plant

The mean value for yield per plant ranged from 9.17g (Kuki Chaushi) to 23.55g (Bahadur).The general mean was 12.75 ± 1.15.

4.1.4 Association among characters

The association of grain yield per plant with yield attributes as well as among the attributes was studied by estimating the correlation co-efficient at genotypic and phenotypic levels. These are presented in Table 4.

4.1.4.1 Genotypic correlation

At genotypic level, days to 50% flowering showed positive and significant correlation with plant height (0.455**), however, grain filling percent (-0.524**) and yield per plant (-0.626**) showed negative and significant correlation.

Effective tillers per plant exhibited positive and significant correlation with yield per plant (0.356*). Plant height exhibited positive and significant correlation with panicle length (0.609**), grains per panicle (0.392*) and 1000 grains weight (0.519**). However, yield per plant (0.325*) showed negative and significant correlation.

Panicle weight exhibited positive and significant correlation with 1000 grains weight (0.633**).

Panicle length showed positive and significant correlation with length- breadth ratio (0.339*) and 1000 grain weight (0.368*) whereas it had negative and significant correlation with yield per plant (-0.437**).

Grains per panicle exhibited positive and significant correlation with 1000 grain weight (0.378*).

Length- breadth ratio showed negative and significant correlation with yield per plant (-0.360*).

Table: 4. Estimates of Genotypic and Phenotypic Correlation Coefficients between different characters of Rice

Characters	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers / Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Days to 50% Flowering	**G** **P**	0.154 0.059	0.021 0.025	0.475** 0.411*	-0.136 -0.113	0.227 0.082	0.021 -0.022	-0.524** -0.335*	0.225 0.186	0.250 0.239	-0.626** -0.527**
50% Flowering To Maturity		**G** **P**	-0.083 -0.085	0.036 -0.001	0.149 0.121	0.075 0.038	0.151 0.129	-0.066 -0.113	0.299 0.250	0.178 0.113	-0.160 -0.179
Effective Tillers / Plant			**G** **P**	0.111 0.089	-0.248 -0.231	-0.107 -0.090	-0.173 -0.145	-0.092 -0.050	0.193 0.158	-0.166 -0.142	0.356* 0.316
Plant Height				**G** **P**	0.196 0.170	0.609** 0.268	0.392* 0.280	-0.245 -0.125	0.298 0.232	0.519** 0.378*	-0.325 -0.245
Panicle Weight					**G** **P**	0.113 0.088	0.310 0.244	0.313 0.233	-0.123 -0.131	0.633** 0.566**	0.152 0.142
Panicle Length						**G** **P**	-0.047 0.093	-0.192 -0.014	0.339* 0.180	0.368* 0.233	-0.437* -0.258
Grains Per Panicle							**G** **P**	0.185 0.107	0.198 0.181	0.378* 0.258	-0.048 -0.044
Grain Filling Percent								**G** **P**	0.033* 0.017	-0.016 -0.028	0.298 0.245
Length-Breadth Ratio									**G** **P**	0.150 0.093	-0.360* -0.334*
1000 Grains Weight										**G** **P**	-0.231 -0.133

*, ** significant at 5 and 1% levels.

4.1.4.2 Phenotypic correlation

At phenotypic level, days to 50% flowering showed positive and significant correlation with plant height (0.411**), however, grain filling percent (-0.335*) and yield per plant (-0.527**) showed negative and significant correlation.

Plant height exhibited positive and significant correlation with 1000 grains weight (0.378*).

Panicle weight exhibited positive and significant correlation with 1000 grains weight (0.566**).

Length- breadth ratio showed negative and significant correlation with yield per plant (-0.334*).

4.1.5 Path coefficient analysis

Path coefficient analysis was employed to work out the direct and indirect effects of different yield contributing characters on yield at genotypic level (Table 5). The results of various causes influencing seed yield per plant are described below:

4.1.5.1 Direct effect

Effective tillers per plant (0.4040) contributed maximum direct effect on yield per plant followed by panicle weight (0.244), plant height (0.123) and 50% flowering to maturity (0.021). However, days to 50% flowering (-0.546), panicle length (-0.266), length- breadth ratio (-0.217), 1000 grain weight (-0.115), grain filling percent (-0.040) and grains per panicle (-0.012) contributed negative direct effect on yield per plant.

4.1.5.2 Indirect effect

Positive indirect effect of days to 50% flowering on yield per plant was observed via plant height (0.058), grain filling percent (0.021), effective tillers per plant (0.008) and 50% flowering to maturity (0.003). Negative indirect effect was shown by panicle

Table: 5. Direct and indirect effect of different characters at genotypic level in rice

Characters	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers / Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Genotypic Correlation for Yield/ Plant
Days to 50% Flowering	**-0.546**	0.003	0.008	0.058	-0.033	-0.060	0.000	0.021	-0.049	-0.029	-0.626
50% Flowering To Maturity	-0.084	**0.021**	-0.033	0.004	0.036	-0.020	-0.002	0.003	-0.065	-0.021	-0.160
Effective Tillers / Plant	-0.011	-0.002	**0.404**	0.014	-0.061	0.028	0.002	0.004	-0.042	0.019	0.356
Plant Height	-0.259	0.001	0.045	**0.123**	0.048	-0.162	-0.005	0.010	-0.065	-0.060	-0.325
Panicle Weight	0.074	0.003	-0.100	0.024	**0.244**	-0.030	-0.004	-0.012	0.027	-0.073	0.152
Panicle Length	-0.124	0.002	-0.043	0.075	0.028	**-0.266**	0.001	0.008	-0.074	-0.042	-0.437
Grains Per Panicle	-0.012	0.003	-0.070	0.048	0.076	0.012	**-0.012**	-0.007	-0.043	-0.044	-0.048
Grain Filling Percent	0.286	-0.001	-0.037	-0.030	0.076	0.051	-0.002	**-0.040**	-0.007	0.002	0.298
Length-Breadth Ratio	-0.123	0.006	0.078	0.037	-0.030	-0.090	-0.002	-0.001	**-0.217**	-0.017	-0.360
1000 Grains Weight	-0.136	0.004	-0.067	0.064	0.155	-0.098	-0.005	0.001	-0.033	**-0.115**	-0.231

Residual = 0.3108

length (-0.060), length- breadth ratio (-0.049), panicle weight (-0.033) and 1000 grain weight (-0.029).

Positive indirect effect of 50% flowering to maturity on yield per plant was observed via panicle weight (0.036), plant height (0.004) and grain filling percent (0.003); whereas negative indirect effect was shown by days to 50% flowering (-0.084), length- breadth ratio (-0.065), effective tillers per plant (-0.033), 1000 grain weight (-0.021), panicle length (-0.020) and grains per panicle (-0.002).

For effective tillers per plant positive indirect effect on yield per plant was observed via panicle length (0.028), 1000 grain weight (0.019), plant height (0.014), grain filling percent (0.004) and grains per panicle (0.002). Negative indirect effect of effective tillers per plant on yield per plant was observed via panicle weight (-0.061), length- breadth ratio (-0.042), days to 50% flowering (-0.011) and 50% flowering to maturity (-0.002).

Positive indirect effect of plant height on yield per plant was observed via panicle weight (0.048), effective tillers per plant (0.045), grain filling percent (0.010) and 50% flowering to maturity (0.001). Negative indirect contribution was observed via days to 50% flowering (-0.259), panicle length (-0.162), length- breadth ratio (-0.065), 1000 grain weight (-0.060) and grains per panicle (-0.005).

Indirect effect of panicle weight on yield per plant was positive via days to 50% flowering (0.074), length- breadth ratio (0.027), plant height (0.024) and 50% flowering to maturity (0.003). However, contribution was negative via effective tillers per plant (-0.100), 1000 grain weight (-0.073), panicle length (-0.030), grain filling percent (-0.012) and grains per panicle (-0.004).

Positive indirect effect of panicle length on yield per plant was observed via plant height (0.075), panicle weight (0.028), grain filling percent (0.008), 50% flowering to maturity (0.002) and grains per panicle (0.001). However, contribution was negative via days to 50% flowering (-0.124), length- breadth ratio (-0.074), effective tillers per plant (-0.043) and 1000 grain weight (-0.042).

Indirect effect of grains per panicle on yield per plant was positive via panicle weight (0.076), plant height (0.048), panicle length (0.012) and 50% flowering to maturity (0.003). However, contribution was negative via effective tillers per plant (-0.070), 1000 grain weight (-0.044), length- breadth ratio (-0.043), days to 50% flowering (-0.120) and grain filling percent (-0.007).

Indirect effect of grain filling percent on yield per plant was positive via days to 50% flowering (0.286), panicle weight (0.076), panicle length (0.051) and 1000 grain weight (0.002). Negative indirect contribution was observed via effective tillers per plant (-0.037), plant height (-0.030), length- breadth ratio (-0.070), grains per panicle (-0.002) and 50% flowering to maturity (-0.001).

Positive indirect effect of length- breadth ratio on yield per plant was observed via effective tillers per plant (0.078), plant height (0.037) and 50% flowering to maturity (0.006). However, negative indirect contribution was observed via days to 50% flowering (-0.123), panicle length (-0.090), panicle weight (-0.030), 1000 grain weight (-0.017), grains per panicle (-0.002) and grain filling percent (-0.001).

Positive indirect effect of 1000 grain weight on yield per plant was observed via panicle weight (0.155), plant height (0.064), 50% flowering to maturity (0.004) and grain filling percent (0.001). However, negative indirect contribution was observed via days to 50% flowering (-0.136), panicle length (-0.098), effective tillers per plant (-0.067), length-breadth ratio (-0.033) and grains per panicle (-0.005).

4.1.5.3 Residual effect

The value estimate of residual effect was estimated to be 0.3108.

4.1.6 Genetic divergence

The study of genetic divergence of 35 genotypes was done through Mahalanobis D^2 Statistic as described by Rao, 1952. The analysis of variance revealed significant differences among the 35 genotypes for all the characters studied. Utilizing Wilk's criterion to test the significance of differences, the estimated V- statistic was found to be highly significant. Applying Tocher's method, all the 35 genotypes were grouped into eight clusters (Table 6). Cluster I had maximum number of 18 genotypes followed by cluster III with 6 genotypes, Cluster II with 3 genotypes, Cluster IV, V &VI had 2 genotypes each and Cluster VII & VIII with one genotype each.

The estimates of intra and inter- cluster distances has presented in Table 7.The intra- cluster distance ranged from 0.00 (cluster VII & cluster VIII) to 137.33 (cluster VI). Inter- cluster distance was observed to be highest between cluster VII & VIII (935.52) followed by cluster II & VII (776.63) indicating greater diversity between these clusters. Minimum diversity was observed between cluster I & IV (129.11) followed by cluster I & VI (143.91) indicating close relationship between these clusters.

The cluster wise mean values of 11 characters are presented in Table 8.Comparison of cluster means revealed that cluster VII gave exceptionally high values for six characters namely days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, L/B ratio and 1000 grain weight. Cluster mean for panicle weight and grain filling percent was highest for cluster V, panicle length and grains per panicle for cluster VIII and yield per plant for cluster II. The panicle weight, effective tillers per plant and yield per plant contributed maximum towards divergence.

Table: 6. Clustering pattern of 35 genotypes of rice on the basis of genetic divergence

Cluster No.	No. of genotypes	Genotypes included
I	18	Kuki Chaushi, Tevuru(white), Keituo-ulha, Nyapie, Rhineinya, Khezharhi, Ngobanya, Mekrilha(Kepei-u), Thevuru(Kezha-u), Chamben(N.S.Kumelo-u), Tsorenya, Rosholha, Khenou, Kemony Kehnau(white), Kekhnie-LHE-Kenelo-u, Thevurie Tieca, Petkoti, & Aboru
II	3	Ranjit, Bahadur and Piolee
III	6	Wonder rice, Kewhi Vuru, Rulonya, Tsorenya, Kemony Kehnau(white), and Malong
IV	2	Ngoba and Mehuru
V	2	Thevuru(Kelo-u) and Teke
VI	2	Krumiavinya, and N.S.Keniese-u
VII	1	Mekrilha
VIII	1	Mekninya Khol

Table: 7. Average intra and inter- cluster distance

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	118.20	404.87	165.58	129.11	340.17	143.91	277.57	501.20
II		61.31	463.61	294.17	366.84	461.04	776.63	276.61
III			88.94	203.04	189.54	216.16	257.46	421.36
IV				65.01	343.34	164.57	197.94	532.99
V					98.79	465.28	520.02	196.67
VI						137.33	280.86	671.63
VII							0.00	935.52
VIII								0.00

Table: 8. Cluster wise mean values of 11 characters in rice

Cluster No.	No. of cultivars	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers / Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
I	18	109.61	27.92	5.45	137.70	4.04	27.90	110.22	71.90	2.75	26.66	10.90
II	3	84.00	25.55	8.53	102.89	4.08	25.00	98.22	79.17	2.34	22.80	22.16
III	6	106.11	33.61	4.64	142.11	6.94	26.83	117.11	77.30	2.54	28.69	11.94
IV	2	108.83	26.00	9.01	133.83	3.78	25.33	105.83	80.33	3.00	27.04	12.77
V	2	90.50	33.00	4.30	138.83	8.49	26.66	127.16	84.72	3.08	32.60	15.24
VI	2	107.67	32.66	5.10	136.50	2.17	25.33	139.83	76.92	2.61	22.76	14.43
VII	1	117.33	35.67	9.07	187.33	5.47	29.00	154.00	61.87	3.09	33.51	10.50
VIII	1	86.00	20.33	4.07	149.00	8.30	29.67	159.33	79.35	2.27	32.59	17.53
CV		12.35	17.79	35.08	16.40	42.40	6.49	17.91	9.02	11.80	15.14	27.02

4.2 Combining ability & genetic analysis

Data pertaining to the parents and F_1's of 6 x 6 diallel cross (excluding reciprocals) were analyzed according to Griffing (1956) Model I, Method II and Hayman- Jinks method (Jinks & Hayman, 1953; Hayman, 1954 and Jinks, 1954)

4.2.1Analysis of variance

Analysis of variance (Table 9) indicated significant variation among the genotypes for all the characters. On further partitioning, it could be seen that parents, crosses as well as parents versus crosses also showed significant variation for the characters. Thus, not only the parents and the crosses differed among themselves but also the crosses as a whole differed significantly from the parents for all the characters.

4.2.2 Mean performance

A comparison of the mean performances for grain yield per plant and other characters has been presented in Table 10.

For days to 50% flowering, it was observed that on an average the crosses marginally took more number of days to flower than the parents with respective means of 104.20 days and 97.38 days. Among the parents Piolee with 82 days was found to be the earliest in flowering whereas Teke with mean performance of 114 days the latest in flowering. Among the crosses Ranjit x Bahadur (91 days) was found to be the earliest in flowering and Malong x Ranjit (120 days) the latest.

For 50% flowering to maturity on an average the parents marginally took more number of days to mature than the crosses with respective means of 26.88 days and 22.08 days. Among the parents Piolee with 22 days was found to be the earliest in maturing whereas Malong with mean performance of 36 days the latest in maturing. Among the crosses Teke x Bahadur (20.43 days) was found to be the earliest in maturing and Malong x Teke (25.83 days) the latest.

TABLE: 9. ANALYSIS OF VARIANCE FOR DIFFERENT CHARACTERS OF THE GENOTYPES

Sources of Variation	Degree Of Freedom	MEAN SQUARES										
		Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Replication	2	83.539	1.539	2.671	19.634	0.040	3.676	100.492	2.423	0.011	2.090	2.062
Genotype	20	327.696**	41.249**	16.781**	1046.882**	6.763**	7.019**	2797.771**	11.903**	0.288**	27.798**	293.427**
Parent	5	669.12**	78.76**	4.87**	1578.23**	1.83**	13.34*	311.29*	166.97**	0.291**	30.27**	106.28**
Cross	14	186.56**	9.97**	11.71**	83.79**	1.31**	4.94**	1737.23**	92.89**	0.218**	27.14**	305.71**
Parent Vs Cross	1	596.48**	291.60**	147.48**	11873.43**	107.69**	4.48**	29776.29**	2103.33**	1.29	24.69**	525.89**
Error	40	6.973	1.189	0.519	7.184	0.067	1.882	65.325	13.505	0.017	1.671	1.267

* Significant at 5% level of probability
** Significant at 1% level of probability

TABLE: 10. MEAN PERFORMANCE OF THE PARENTS AND CROSSES IN F_1 GENERATION FOR DIFFERENT CHARACTERS

Genotypes	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Parents											
Malong	112.00	36.00	6.27	103.00	3.82	28.17	111.67	65.70	2.74	30.63	11.63
Mehuru	106.33	24.33	5.87	141.33	4.23	25.43	112.33	66.10	2.98	23.36	11.55
Teke	114.00	24.33	7.43	152.00	5.03	30.40	120.00	71.72	2.92	26.26	11.01
Piolee	82.00	22.00	8.03	101.00	3.56	26.07	97.00	84.27	2.25	22.75	21.63
Ranjit	86.00	29.67	9.17	101.00	3.97	24.90	89.67	73.15	2.31	22.73	21.31
Bahadur	84.00	25.00	8.40	106.67	5.60	25.62	108.00	80.09	2.48	22.87	23.55
Crosses											
Malong x Mehuru	110.00	24.33	8.44	81.33	8.36	25.67	157.14	87.36	3.21	17.04	9.96
Malong x Teke	104.67	25.83	12.12	93.00	8.25	26.29	164.80	84.69	2.90	25.80	19.35
Malong x Piolee	108.00	21.47	11.41	85.00	7.92	25.53	139.02	86.35	3.19	17.66	16.60
Malong x Ranjit	120.00	20.83	12.42	81.00	7.62	25.06	120.28	70.72	2.61	20.14	16.94
Malong x Bahadur	108.00	21.17	12.88	90.00	8.26	26.27	158.11	87.07	2.91	22.83	28.19
Mehuru x Teke	100.00	25.77	11.17	86.67	7.10	26.42	152.56	93.43	2.84	23.98	25.10
Mehuru x Piolee	94.00	22.00	12.32	85.00	6.81	25.82	184.96	90.74	3.20	25.71	32.23
Mehuru x Ranjit	106.00	21.98	12.14	96.67	6.64	27.72	169.31	90.13	2.72	23.56	31.37
Mehuru x Bahadur	99.67	20.87	10.33	95.33	7.02	29.67	165.67	84.03	3.15	23.55	29.15
Teke x Piolee	94.33	21.00	10.18	80.67	7.11	24.97	166.67	80.16	3.26	24.90	26.25
Teke x Ranjit	116.00	20.60	12.59	86.00	6.25	25.05	185.25	86.92	2.63	22.01	43.90
Teke x Bahadur	104.67	20.43	12.92	93.00	7.00	27.32	187.50	92.48	2.84	25.94	46.55
Piolee x Ranjit	103.00	22.42	5.95	82.00	6.71	26.09	142.19	85.46	3.19	24.80	23.44
Piolee x Bahadur	103.67	23.40	9.04	86.00	6.72	24.67	116.67	90.30	2.92	26.26	15.19
Ranjit x Bahadur	91.00	23.83	9.80	85.00	7.17	26.04	115.33	84.59	2.38	26.58	23.50
Mean of parents	97.38	26.88	7.52	117.5	4.36	26.76	106.45	73.51	2.61	24.76	16.78
Mean of crosses	104.20	22.40	10.92	87.11	7.26	26.17	155.03	86.29	2.93	23.38	25.84
S.E.(m)	2.15	0.89	0.58	2.18	0.21	1.12	6.59	3.00	0.10	1.05	0.91

For number of effective tillers per plant crosses exhibited increased number compared to parents with respective mean of 10.92 and 7.52. Ranjit exhibited maximum tillers 9.17 among the parents while among the crosses a maximum of 12.92 tillers was recorded for Teke x Bahadur followed by Malong x Bahadur (12.88), Teke x Ranjit (12.59), Mehuru x Piolee (12.32), Malong x Ranjit (12.42), Mehuru x Ranjit (12.14) and Malong x Teke (12.12).

For plant height Teke was observed to be the tallest parent with 152 cm and Ranjit and Piolee were shortest with 101 cm each. Among the crosses Teke x Piolee was found to be shortest (80.67cm) and Mehuru x Ranjit the tallest (96.67cm). The crosses with mean performance of 87.11cm were shorter than parents 117.50cm, respectively.

For panicle weight crosses exhibited increased weight compared to parents with respective mean of 7.26 and 4.36. Bahadur exhibited maximum weight of 5.60gms among the parents while among the crosses Malong x Mehuru 8.36gms followed by Malong x Bahadur 8.26 and Malong x Teke 8.25gms.

For panicle length Teke exhibited the longest panicle (30.40cm) while Ranjit with 24.90cm was shortest among the parents. Among the crosses Mehuru x Bahadur (29.67cm) was the longest followed by Mehuru x Ranjit (27.72), Teke x Bahadur and Malong x Teke (26.29). The crosses with mean performance of 26.17cm were shorter than parents 26.76cm, respectively.

Maximum number of grains per panicle was observed for Teke (120) while Piolee with 97 grains minimum among the parents. Among the crosses Teke x Bahadur with 187.50 grains were maximum followed by Teke x Ranjit (185.25) and Mehuru x Piolee (184.96). Crosse Piolee x Bahadur (116.67) and Ranjit x Bahadur (115.33) were the minimum. Crosses exhibited increased number of grains compared to parents with respective mean of 155.03 and 106.45, respectively.

For grain filling percent Crosses exhibited increased number compared to parents with respective mean of 86.29 and 73.51, respectively. Among the parents maximum filled grains were observed for Piolee (84.27) while Malong with 65.70 minimum. Among the crosses Mehuru x Teke with 94.3% filled grains followed by Teke x Bahadur (92.48), Mehuru x Piolee (90.74) and Mehuru x Ranjit (90.13) were maximum while Malong x Ranjit with 70.72% filled grains minimum.

For length- breadth ratio, among the parents Mehuru 2.98mm was maximum while Piolee with 2.25mm minimum. Among the crosses Teke x Piolee with 3.26mm was maximum while Malong x Ranjit 2.61mm minimum. On an average length- breadth ratio of crosses were more than the parents with respective mean of 2.93 and 2.61.

For 1000- grain weight parents exhibited increased weight compared to crosses with respective mean of 24.76g and 233.38g. Malong exhibited maximum weight of 30.63g among the parents while Ranjit 22.73g minimum. Among the crosses Ranjit x Bahadur with 26.58g maximum while Malong x Ranjit with 20.14g minimum.

For yield per plant crosses exhibited increased yield compared to parents with respective mean of 25.84g and 16.78g. Bahadur exhibited maximum weight of 23.55g among the parents while Teke 11.01g minimum. Among the crosses Teke x Bahadur with 46.55g maximum and Malong x Mehuru 9.96g were minimum.

4.2.3 Analysis of variance for combining ability

Analysis of variance for combining ability (Table 11) revealed the significance of both general combining ability (GCA) and specific combining ability (SCA) for all the characters studied. Mean sum of squares for SCA were higher than that of GCA in general, except for days to 50% flowering for which mean sum of squares for GCA was higher than that of SCA. For 50% flowering to maturity, panicle length, length- breadth ratio and yield per plant GCA and SCA mean sum of squares were almost equal.

Table: 11. Analysis of variance for combining ability for seed yield and its components in rice

Source	df	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
GCA	5	215.76**	14.82**	1.47**	343.56**	0.74**	2.36**	633.20**	52.67**	0.13**	3.77**	100.61**
SCA	15	73.72**	13.39**	6.96**	350.76**	2.75**	2.33**	1032.35**	76.61**	0.08**	11.09**	96.87**
ERROR	40	2.32	0.39	0.17	2.39	0.02	0.62	21.75	4.50	0.01	0.55	0.42

** Significant at 1% level of probability

4.2.3.1. General combining ability effects of the parents

Table 12 presents the general combining ability effects of the parents for all the characters.

For days to 50% flowering, significant positive GCA effect was recorded for Malong (7.30**) followed by Teke (3.99**) and Mehuru (0.82**) while significant negative GCA effect was observed for Piolee (-6.10**) followed by Bahadur (-5.10**) and Ranjit (-0.97**).

Highly significant positive GCA effect for 50% flowering to maturity was observed for the parent Malong (2.51**) followed by Ranjit (0.35**) while significant negative GCA effect was observed for Piolee (-1.44**) followed by Bahadur (-0.65**), Teke (-0.49**) and Mehuru (-0.28**).

In case of effective tillers per plant Teke (0.53**) was the best combiner followed by Bahadur (0.27**). Significant negative GCA effect was observed for Piolee (-0.58**) followed by Mehuru (-0.44**).

For plant height significant positive GCA effect was recorded for Teke (9.10**) followed by Mehuru (7.14**) while significant negative GCA effect was observed for Piolee (-6.36**) followed by Ranjit (-4.61**), Malong (-4.28**) and Bahadur (-0.99*).

Significant positive GCA effect for panicle weight was exhibited by the parent Malong (0.38**) followed by Bahadur (0.29**) and Teke (0.09**). Significant negative GCA effect was observed for Ranjit (-0.34**) followed by Piolee (-0.33**) and Mehuru (-0.08**).

For panicle length significant positive GCA effect was observed for Teke (0.81**) while significant negative GCA effect was observed for Piolee (-0.65**) followed by Ranjit (-0.58*).

Table: 12. General combining ability effects of the Parents for seed yield and its components in rice

Parents/ characters	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Malong	7.36**	2.51**	0.02	-4.28**	0.38**	0.10	-3.32*	-3.86**	0.05**	-0.21	-6.06**
Mehuru	0.82**	-0.28**	-0.44**	7.14**	-0.08**	0.22	8.26**	-0.07	0.15**	-0.74**	-1.49**
Teke	3.99**	-0.49**	0.53**	9.10**	0.09**	0.81**	13.56**	0.33	0.06**	1.09**	2.55**
Poilee	-6.10**	-1.44**	-0.58**	-6.36**	-0.33**	-0.65**	-5.53**	2.88**	0.05**	-0.20	-0.73*
Ranjit	-0.97**	0.35**	0.20	-4.61**	-0.34**	-0.58*	-9.49**	-1.80**	-0.22**	-0.49**	2.37**
Bahadur	-5.10**	-0.65**	0.27*	-0.99*	0.29**	0.10	-3.49**	2.52**	-0.09**	0.55**	3.36**
S.E.(g_i)	0.49	0.20	0.13	0.49	0.04	0.25	1.50	0.68	0.02	0.24	0.20
S.E.(g_i-g_j)	0.76	0.31	0.20	0.77	0.07	0.39	2.33	1.06	0.03	0.37	0.32

* Significant at 5% level of probability

** Significant at 1% level of probability

Significant positive GCA effect for grains per panicle was exhibited by the parent Teke (13.56**) followed by Mehuru (8.26**) while significant negative GCA effect was observed for Ranjit (-9.49**) followed by Piolee (-5.53**), Bahadur (-3.49**) and Malong (-3.32**).

For grain filling percent significant positive GCA effect was observed for Piolee (2.88**) followed by Bahadur (2.52**). Significant negative GCA effect was observed for Malong (-3.86**) followed by Ranjit (-1.80**).

In case of length- breadth ratio Mehuru (0.15**) was the best combiner followed by Teke (0.06**), Malong (0.05**) and Piolee (0.05**). Significant negative GCA effect was observed for Ranjit (-0.22**) followed by Bahadur (-0.09**).

For 1000 grain weight significant positive GCA effect was observed for Teke (1.09**) followed by Bahadur (0.55**) while significant negative GCA effect was observed for Mehuru (-0.74**) followed by Ranjit (-0.49**).

Significant positive GCA effect for yield per plant was exhibited by the parent Bahadur (3.36**) followed by Teke (2.55**) and Ranjit (2.37**) while significant negative GCA effect was observed for Malong (-6.06**) followed by Mehuru (-1.49**) and Piolee (-0.73**).

Out of all the parents Bahadur with GCA effect of 3.36 followed by Teke with 2.37 and Ranjit with 2.37 were the best combiner with regard to yield per plant.

4.2.3.2. Specific combining ability effects

Specific combing ability effects of the crosses are presented in Table 13.

The cross Malong x Teke (-8.93) followed by Mehuru x Teke (-7.06), Teke x Piolee (-5.81), Ranjit x Bahadur (-5.18), Mehuru x Piolee (-5.18) and Mehuru x Piolee (-2.98) was the best combiner for early flowering whereas highest positive sca cffect was exhibited by the cross Piolee x Bahadur (12.61) followed by Malong x Ranjit (11.36),

TABLE: 13. SPECIFIC COMBINING ABILITY OF THE CROSSES

Crosses	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
Malong x Mehuru	-0.43	-1.70**	-1.09**	-17.32**	1.63**	-0.99	10.83**	8.65**	0.17**	-5.79**	-5.74**
Malong x Teke	-8.93**	0.15	1.63**	-7.61**	1.35**	-0.95	12.87**	5.58**	-0.04	1.15	-0.39
Malong x Piolee	4.48**	3.53**	2.02**	-0.15	1.44**	-0.26	6.29	4.69*	0.25**	-5.70**	0.13
Malong x Ranjit	11.36**	5.65**	2.25**	-5.90**	1.15**	-0.80	-8.42*	-6.26**	-0.07	-2.94**	-2.62**
Malong x Bahadur	3.48**	3.99**	2.64**	-0.53	1.16**	-0.27	23.58**	5.77**	0.11*	-1.29*	7.64**
Mehuru x Teke	-7.06**	2.64**	1.13**	-25.36**	0.66**	-0.95	-10.71**	10.53**	-0.20**	-0.15	0.78
Mehuru x Piolee	-2.98*	-0.07	3.40**	-11.57**	0.79**	-0.09	40.71**	5.29**	0.16**	2.87**	11.19**
Mehuru x Ranjit	3.90**	-1.86**	2.43**	-1.65	0.63**	1.73*	29.33**	9.36**	-0.05	1.01	7.22**
Mehuru x Bahadur	1.69	-1.86**	0.55	-6.61**	0.38**	3.01**	20.00**	-1.06	0.25**	-0.04	4.02**
Teke x Piolee	-5.81**	-0.53	0.29	-17.86**	0.92**	-1.53*	17.75**	-5.70**	0.32**	0.24	1.17*
Teke x Ranjit	10.73**	-3.32**	1.92**	-14.28**	0.06	-1.52*	40.04**	5.74**	-0.05	-2.37**	15.72**
Teke x Bahadur	3.52**	-2.32**	2.18**	-10.90**	0.18	0.07	36.04**	6.99**	0.04	0.52	17.38**
Piolee x Ranjit	7.82**	-0.70	-3.62**	-2.82*	0.95**	0.97	16.13**	1.74	0.52**	1.71*	-1.46*
Piolee x Bahadur	12.61**	1.97**	-0.59	-3.45*	0.32*	-1.13	-15.21**	2.26	0.13*	2.13**	-10.70**
Ranjit x Bahadur	-5.18**	0.51	-0.61	-4.20**	0.79**	0.18	-12.58**	1.22	-0.16**	2.73**	-5.49**
S.E.(ij)	1.35	0.55	0.36	1.37	0.13	0.70	4.13	1.88	0.06	0.66	0.57
S.E.(ij-ik)	2.01	0.83	0.54	2.04	0.19	1.04	6.17	2.80	0.10	0.98	0.85
S.E.(ij-kl)	1.86	0.77	0.50	1.89	0.18	0.97	5.71	2.59	0.08	0.91	0.79

* Significant at 5% level of probability
** Significant at 1% level of probability

Teke x Ranjit (10.73), Piolee x Ranjit (7.82), Malong x Piolee (4.48), Mehuru x Ranjit (3.90), Teke x Bahadur (3.52) and Malong x Bahadur (3.48).

The cross Teke x Ranjit exhibited a high negative sea effect of -3.32 for 50% flowering to maturity and was followed by Teke x Bahadur (-2.32), Mehuru x Ranjit (-1.86), Mehuru x Bahadur (-1.86) and Malong x Mehuru (-1.70) where as the cross with high positive sea effects were Malong x Ranjit (5.65), Malong x Bahadur (3.99), Malong x Piolee (3.53), Mehuru x Teke (2.64) and Piolee x Bahadur (1.97).

For number of effective tillers per plant, significant positive sea effects was exhibited by Mehuru x Piolee (3.40) followed by Malong x Bahadur (2.64), Mehuru x Ranjit (2.43), Malong x Ranjit (2.25), Teke x Bahadur (2.18), Malong x Piolee (2.02), Teke x Ranjit (1.92), Malong x Teke (1.63) and Mehuru x Teke (1.13). Significant negative sea effect was observed for cross Piolee x Ranjit (-3.62) and Malong x Mehuru (-1.09).

The cross Mehuru x Teke (-25.36) exhibited a high negative sea effect for plant height followed by Teke x Piolee (-17.86), Malong x Mehuru (-17.32), Teke x Ranjit (-14.28), Mehuru x Piolee (-11.57), Teke x Bahadur (-10.90), Malong x Teke (-7.61), Mehuru x Bahadur (-6.61), Malong x Ranjit (-5.90), Ranjit x Bahadur (-4.20), Piolee x Bahadur (-3.45) and Piolee x Ranjit (-2.82).

The cross Malong x Mehuru (1.63) followed by Malong x Piolee (1.44), Malong x Teke (1.35), Malong x Bahadur (1.16), Malong x Ranjit (1.15), Piolee x Ranjit (0.95), Teke x Piolee (0.92), Mehuru x Piolee (0.79), Ranjit x Bahadur (0.79), Mehuru x Teke (0.66), Mehuru x Ranjit (0.63), Mehuru x Bahadur (0.38) and Piolee x Bahadur (0.32) was considered the best specific combiner with regard to panicle weight.

For panicle length, the highest negative sea effect was exhibited by Teke x Piolee (-1.53) and Teke x Ranjit (-1.52) whereas the cross with high positive sea effects were Mehuru x Bahadur (3.01) and Mehuru x Ranjit (1.73).

The cross Mehuru x Piolee (40.71) followed by Teke x Ranjit (40.04), Teke x Bahadur (36.04), Mehuru x Ranjit (29.33), Malong x Bahadur (23.58), Mehuru x Bahadur (20.00), Teke x Piolee (17.75), Piolee x Ranjit (16.13), Malong x Teke (12.87) and Malong x Mehuru (10.83) were considered the best specific combiner with regard to grains per panicle. High negative sea effect was exhibited by Piolee x Bahadur (-15.21) followed by Ranjit x Bahadur (-12.58), Mehuru x Teke (-10.71) and Malong x Ranjit (-8.42).

For grain filling percent, the cross Mehuru x Teke (10.53) followed by Mehuru x Ranjit (9.36), Malong x Mehuru (8.65), Teke x Bahadur (6.99), Malong x Bahadur (5.77), Teke x Ranjit (5.74), Malong x Teke (5.58), Mehuru x Piolee (5.29) and Malong x Piolee (4.69) were found to exhibit high sca effect. High negative sea effect was observed for Malong x Ranjit (-6.26) and Teke x Piolee (-5.70).

For length- breadth ratio, significant positive sea effect was exhibited by Piolee x Ranjit (0.52) followed by Teke x Piolee (0.32), Mehuru x Bahadur (0.25), Malong x Piolee (0.25), Malong x Mehuru (0.17), Mehuru x Piolee (0.16), Piolee x Bahadur (0.13) and Malong x Bahadur (0.11). High negative sea effect was observed for Mehuru x Teke (-0.20) and Ranjit x Bahadur (-0.16).

For 1000 grain weight, significant positive sea effect was observed for Mehuru x Piolee (2.87) followed by Ranjit x Bahadur (2.73), Piolee x Bahadur (2.13) and Piolee x Ranjit (1.71). High negative sea effect was observed for Malong x Mehuru (-5.79) followed by Malong x Piolee (-5.70), Malong x Ranjit (-2.94), Teke x Ranjit (-2.37) and Malong x Bahadur (-1.29).

The cross Teke x Bahadur with sea effect of 17.38 was considered the best combiner yield per plant followed by Teke x Ranjit (15.72), Mehuru x Piolee (11.19), Malong x Bahadur (7.64), Mehuru x Ranjit (7.22), Mehuru x Bahadur (4.02) and Teke x Piolee (1.17). High negative sea effect was observed for Piolee x Bahadur (-10.70) followed by Malong x Mehuru (-5.74), Ranjit x Bahadur (-5.49), Malong x Ranjit (-2.62) and Piolee x Ranjit (-1.46).

4.2.4. Components of variance for yield and other characters and genetic proportions

The estimates of components of variance as obtained from Vr- Wr statistics are presented in Table 14. The genetic proportions derived from these components are presented in Table 15. For days to 50% flowering, all the components of variation except E were significant revealing the involvement of additive and non- additive gene action in the inheritance of this character. Degree of dominance $(H_1/D)^{½}$ revealed over-dominance for this character. The proportion of $H_2/4\ H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. Number of blocks of dominant genes is estimated by $h^{2/}\ H_2$ ratio which is 0.56. Narrow sense heritability was found to be high (67.90).

All the components of variation except E were significant for days to 50% flowering revealing the involvement of additive and non- additive gene action in the inheritance of this character. Over- dominance was indicated by the proportion $(H_1/D)^{1/2.}$ The value of $H_2/4\ H_1$ was below 0.25 indicating unequal frequencies of positive and negative genes. This was corroborated by the KD/KR value of more than unity indicating more of dominant genes than recessives. The ratio of $h^{2/}\ H_2$ being 1.35 indicated involvement of one or two groups of gene in the control of character. Narrow sense heritability was found to be high (62.21).

For effective tillers per plant, the components (H_1), (H_2) and $(h^{2)}$ were found to be significant indicating that only dominance component of variation was important. Over- dominance was indicated by the proportion $(H_1/D)^{1/2.}$ The proportion of $H_2/4\ H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of

Table: 14. Estimates of genetic components of variance for seed yield and its components in rice

Genetic parameter	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
D	220.72** ±22.51	25.86** ±2.92	1.44 ±1.81	523.68** ±82.57	0.59 ±0.35	3.82** ±1.10	101.99 ±163.29	51.14** ±17.19	0.09** ±0.02	9.53 ±5.37	35.00 ±40.52
H_1	308.85** ±57.15	47.20** ±7.41	23.38** ±4.59	1052.61** ±209.60	7.42** ±0.89	9.51** ±2.79	3056.08** ±414.53	233.72** ±45.51	0.32** ±0.05	51.40** ±13.62	384.80** ±102.87
H_2	225.91** ±51.06	36.14** ±6.62	20.62** ±4.10	862.82** ±187.24	6.57** ±0.79	5.88* ±2.49	2886.50** ±370.31	202.44** ±40.65	0.22** ±0.05	32.96** ±12.17	309.90** ±91.90
h^2	127.57** ±34.36	63.78** ±4.46	31.78** ±2.76	2563.90** ±126.02	23.24** ±0.53	0.62 ±1.68	6447.30** ±249.24	451.89** ±24.36	0.28** ±0.03	5.01 ±8.19	228.17** ±61.85
F	213.82** ±55.00	33.09** ±7.13	3.09 ±4.42	612.75** ±201.71	0.95 ±0.85	6.55* ±2.69	-148.09 ±398.92	58.78 ±43.80	0.11* ±0.05	24.30 ±13.11	35.98 ±99.00
E	2.32 ±8.51	0.40 ±1.10	0.17 ±0.68	2.39 ±31.21	0.02 ±0.13	0.63 ±0.42	21.78 ±61.72	4.50 ±6.78	0.01 ±0.01	0.56 ±2.03	0.42 ±15.32

Table: 15. Proportion of Genetic Components of Variance for 11 characters

Components	Days to 50% Flowering	50% Flowering To Maturity	Effective Tillers Per Plant	Plant Height	Panicle Weight	Panicle Length	Grains Per Panicle	Grain Filling Percent	Length-Breadth Ratio	1000 Grains Weight	Yield Per Plant
$(H_1/D)^{1/2}$	1.18	1.35	4.03	1.42	3.53	1.58	5.47	2.14	1.86	2.32	3.32
$H_2/4H_1$	0.18	0.19	0.22	0.20	0.22	0.15	0.24	0.22	0.18	0.16	0.20
KD/KR	2.38	2.79	1.72	2.40	1.04	3.38	0.76	1.73	1.05	3.43	1.01
h^2/H_2	0.56	1.35	1.54	2.97	3.53	0.10	2.23	2.23	1.27	0.15	0.73
Heritability (ns)	67.90	62.21	6.41	53.81	8.30	41.10	3.00	20.95	28.08	24.53	9.08

dominant genes over recessives. The ratio of h_2/H_2 being 1.54 indicated involvement of one or two groups of gene in the control of character. Heritability in narrow sense was found to be low (6.41).

All the components of variation except E were significant for plant height revealing the involvement of additive and non- additive gene action in the inheritance of this character. Degree of dominance $(H_1/D)^{1/2}$ revealed over- dominance for this character. The proportion of $H_2/4H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. The ratio of h_2/H_2 being 2.97 indicated involvement of two to three groups of gene in the control of character. Heritability estimate (h^2_{ns}) is 53.81% indicating that plant height is highly heritable.

For panicle weight, the components (H_1), (H_2) and (h_2) were found to be significant indicating that only dominance component of variation was important. Degree of dominance $(H_1/D)^{1/2}$ revealed over- dominance for this character. The proportion of $H_2/4H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. The ratio of h_2/H_2 being 3.53 indicated involvement of three to four groups of gene in the control of character. Heritability estimate (h^2_{ns}) was 8.30%.

For panicle length, all the components of variation except h_2 & E were significant revealing the involvement of additive and non- additive gene action in the inheritance of this character. Over- dominance was indicated by the proportion $(H_1/D)^{1/2}$. The proportion of $H_2/4H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. The ratio of h_2/H_2 being 3.38 indicated involvement of three to four groups of gene in the control of character. Heritability estimate ($h2_{ns}$) was 41.10%.

For grains per panicle, the components (H_1), (H_2) and (h_2) were found to be significant indicating that only dominance component of variation was important. Degree of dominance $(H_1/D)^{1/2}$ revealed over- dominance for this character. Since the value of ratio of $H_2/4\ H_1$ is close to 0.25, it seems that the genes with increasing and decreasing effects are symmetrically distributed among the parental lines. The ratio of $h_2/\ H_2$ being 2.23 indicated involvement of two to three groups of gene in the control of character. Heritability estimate ($h2_{ns}$) was 3%.

For grain filling percent, all the components of variation except E were significant revealing the involvement of additive and non- additive gene action in the inheritance of this character. Degree of dominance $(H_1/D)^{1/2}$ revealed over- dominance for this character. The proportion of $H_2/4\ H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. The ratio of $h_2/\ H_2$ being 2.23 indicated involvement of two to three groups of gene in the control of character. Heritability in narrow sense was found to be low (20.95%).

For length- breadth ratio, all the components of variation except E were significant revealing the involvement of additive and non- additive gene action in the inheritance of this character. Over- dominance was indicated by the proportion $(H_1/D)^{1/2}$. The proportion of $H_2/4\ H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. The ratio of $h_2/\ H_2$ being 1.27 indicated involvement of one to two groups of gene in the control of character. Heritability estimate ($h2_{ns}$) was 28.08%.

For 1000 grain weight, the components (H_1), (H_2) and (h_2) were found to be significant indicating that only dominance component of variation was important. Degree of dominance $(H_1/D)^{1/2}$ revealed over- dominance for this character. The proportion of $H_2/4\ H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. The ratio of h_2/H_2 being 0.15 indicated involvement of one gene group in the control of character. Heritability estimate (h^2_{ns}) was 24.53%.

For yield per plant, the components (H_1), (H_2) and (h_2) were found to be significant indicating that only dominance component of variation was important. Over-dominance was indicated by the proportion $(H_1/D)^{1/2.}$ The proportion of $H_2/4H_1$ was less than 0.25 indicating unequal distribution of allelic frequencies and it was also supported by the KD/KR ratio which was greater than unity indicating an excess of dominant genes over recessives. Number of blocks of dominant genes is estimated by h_2/H_2 ratio which is 0.73. Narrow sense heritability was found to be low (9.08).

4.2.5. Graphical analysis

The Vr- Wr graphs for the characters under investigation are depicted in Fig. 1 to 11.

The regression coefficient (b= 1.0766 ± 0. 266) of covariance on the variance for days to 50% flowering did not deviate significantly from unity indicating absence of epistasis. The regression line intercepted the Wr axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

For days to 50% flowering to maturity the regression coefficient (b= 0.7394 ± 0.084) of covariance on the variance deviated significantly from unity indicating presence of epistasis. The regression line intercepted the Wr axis below the origin. The parental points were scattered on the regression line indicating genetic diversity among the parents.

The regression coefficient (b= 0.6102 ± 0.853) of covariance on the variance for effective tillers per plant did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the Wr axis above the

a = -29.15
b = 1.077 ± 0.266$^{N.S.}$

P_1 Malong
P_2Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6Bahadur

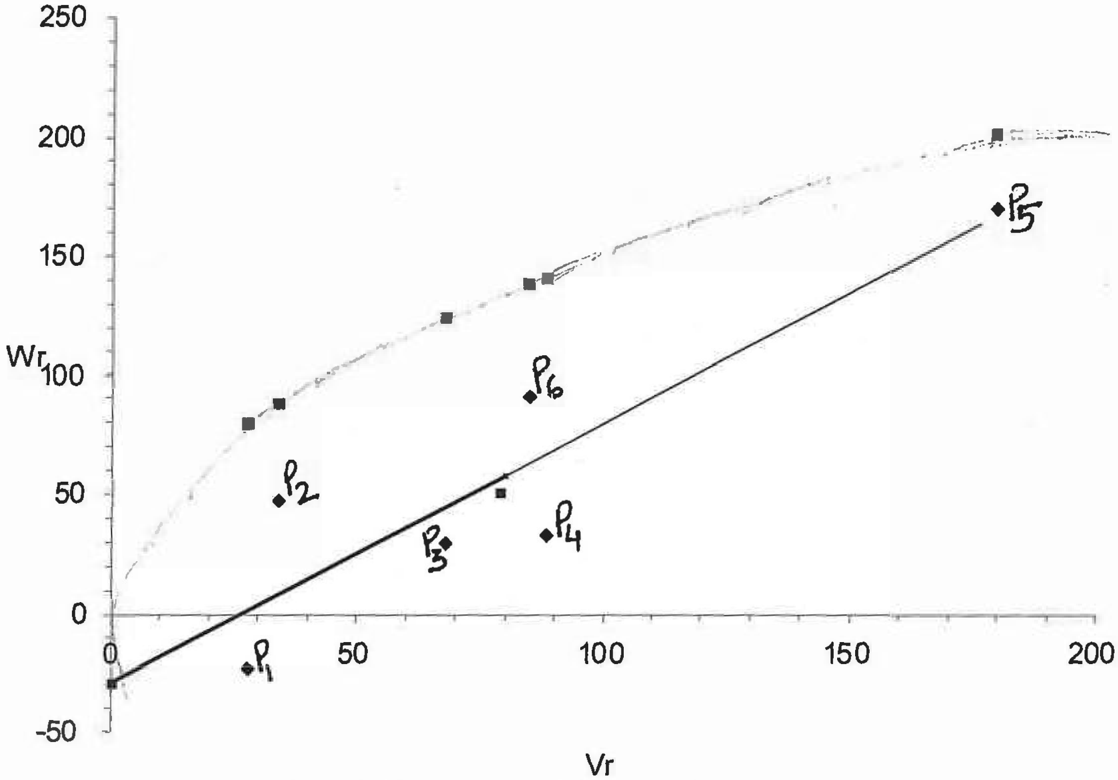

Fig. 1 Days to 50 % flowering

$a = -2.836$
$b = 0.739 \pm 0.08^{*}$

P_1 Malong
P_2Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6Bahadur

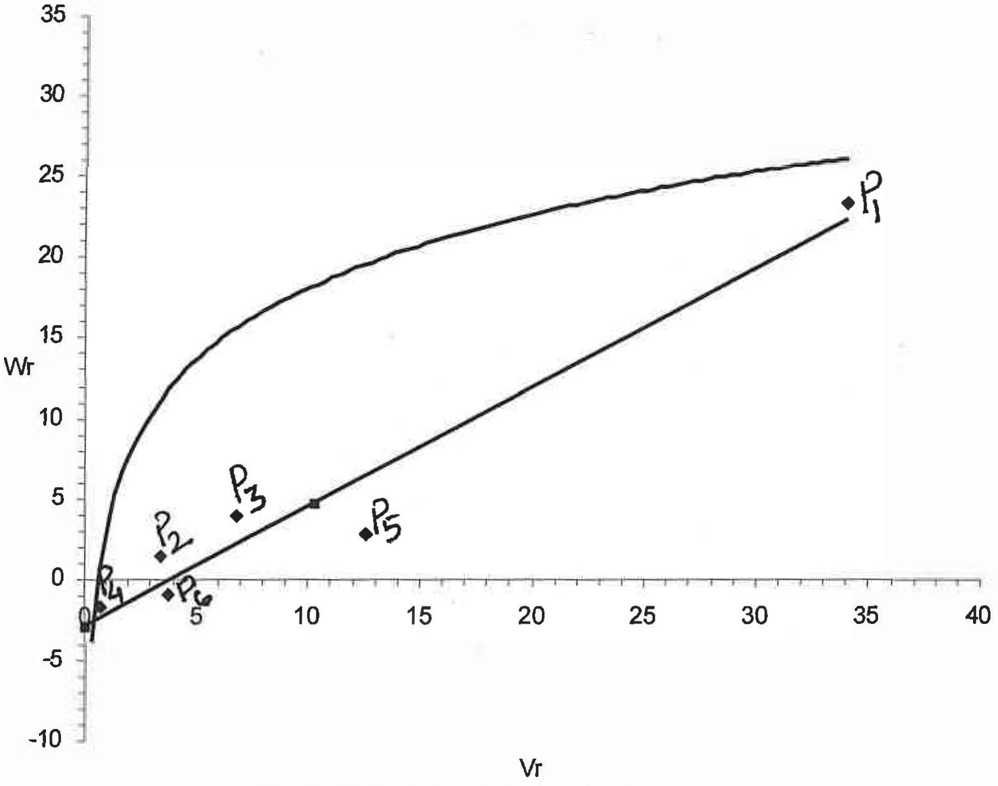

Fig. 2, 50 % flowering to maturity

* Significant

$a = 3.394$
$b = 0.61 \pm 0.853^{N.S.}$

P_1 Malong
P_2 Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6 Bahadur

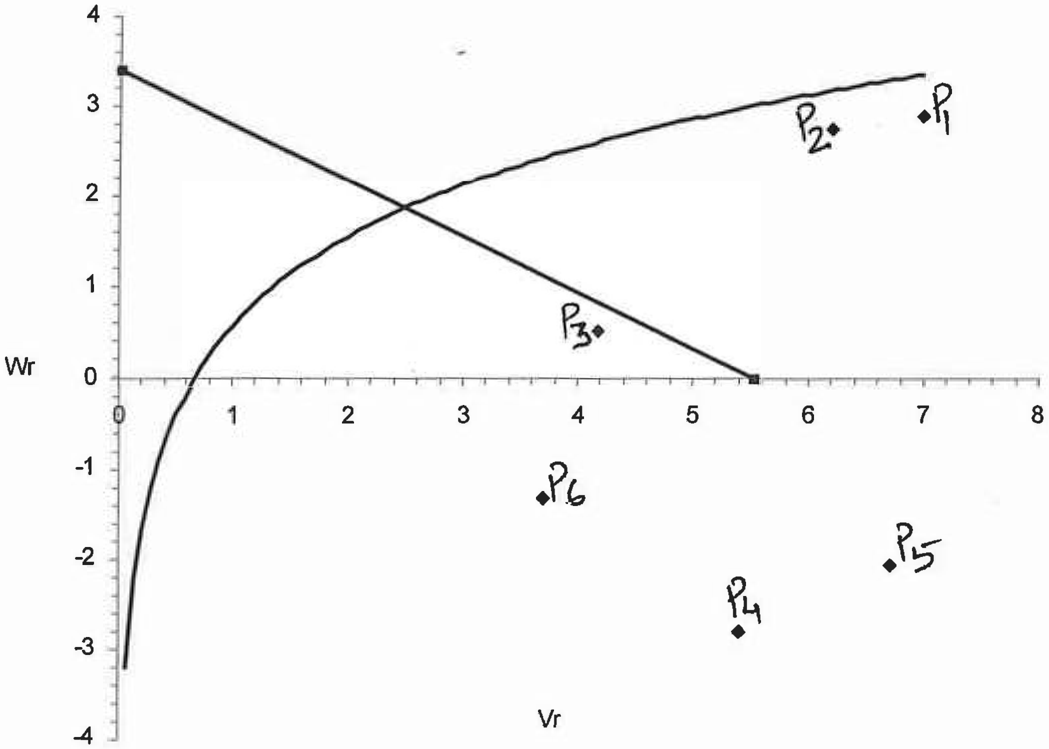

Fig. 3 Effective tillers per plant

origin indicating partial dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

For plant height the regression coefficient (b= 0.6537 ± 0.077) of covariance on the variance deviated significantly from unity indicating presence of epistasis. The regression line intercepted the Wr axis below the origin. The parental points were scattered on the regression line indicating genetic diversity among the parents.

The regression coefficient (b= 0.4738 ± 0.078) of covariance on the variance for panicle weight deviated significantly from unity indicating presence of epistasis. The regression line intercepted the Wr axis below the origin. The parental points were scattered on the regression line indicating genetic diversity among the parents.

For panicle length the regression coefficient (b= 0.7265 ± 0.501) of covariance on the variance did not deviate significantly either from zero or unity indicating absence of epistasis. The regression line intercepted the Wr axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

The regression coefficient (b= 0.5105 ± 0.255) of covariance on the variance for grains per panicle did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the Wr axis above the origin indicating partial dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

For grain filling percent the regression coefficient (b= 0.408 ± 0.161) of covariance on the variance did not deviate significantly either from zero or unity indicating absence of epistasis. The regression line intercepted the Wr axis below the origin indicating over- dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

a = -49.328
b = 0.653 ± 0.077*

P_1 Malong
P_2Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6 Bahadur

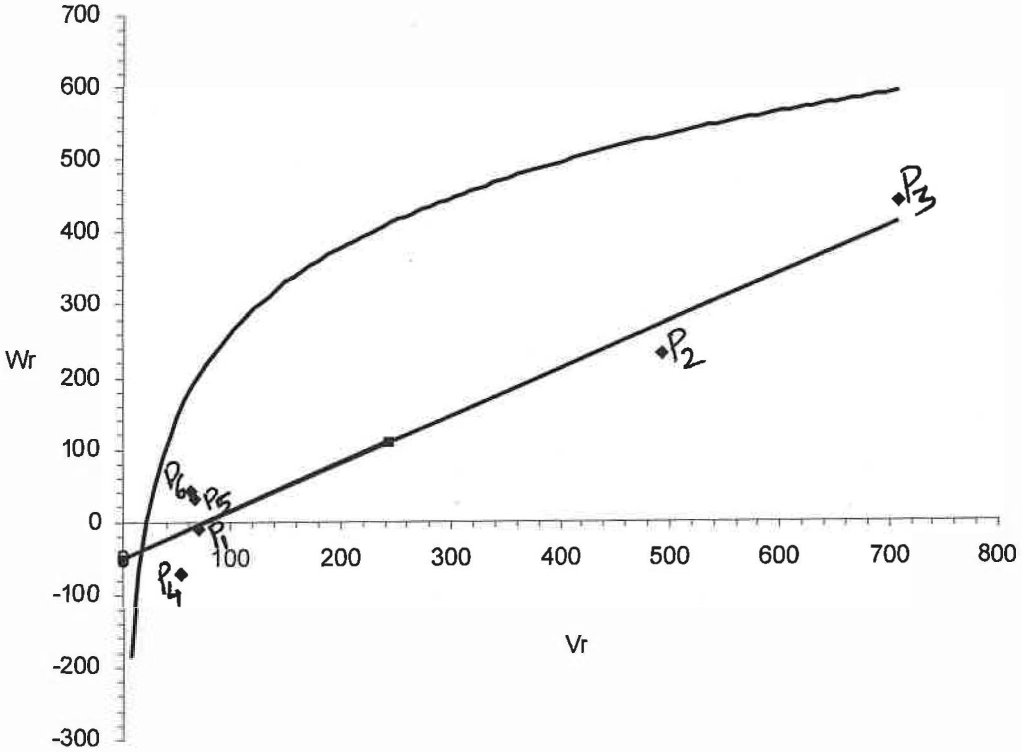

Fig. 4 Plant height

* Significant

a=-0.783
b = 0.474 ± 0.078*

P_1 Malong
P_2Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6 Bahadur

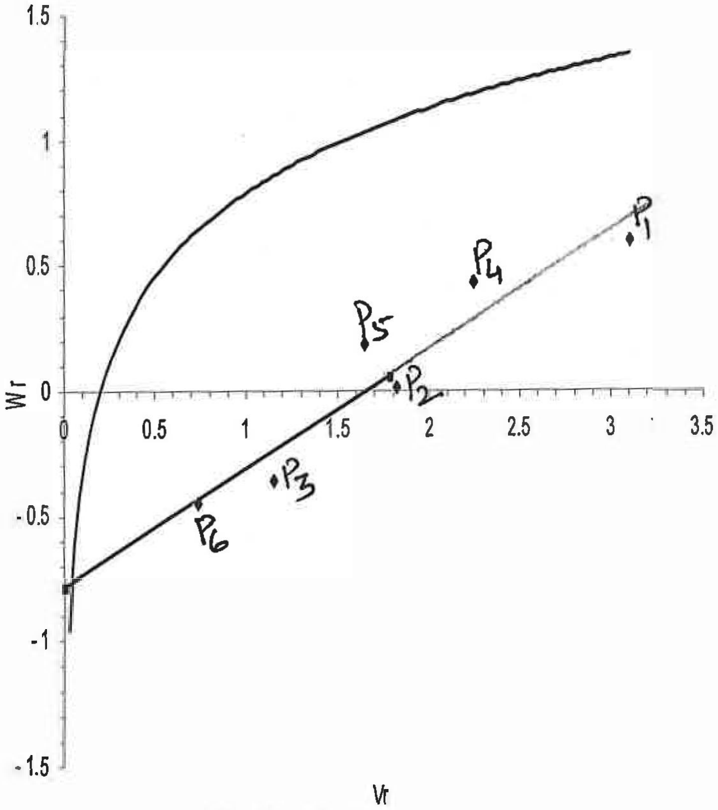

Fig. 5 Panicle weight

* Significant

a = -1.116
b = 0.726 ± 0.501$^{N.S.}$

P_1 Malong
P_2 Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6 Bahadur

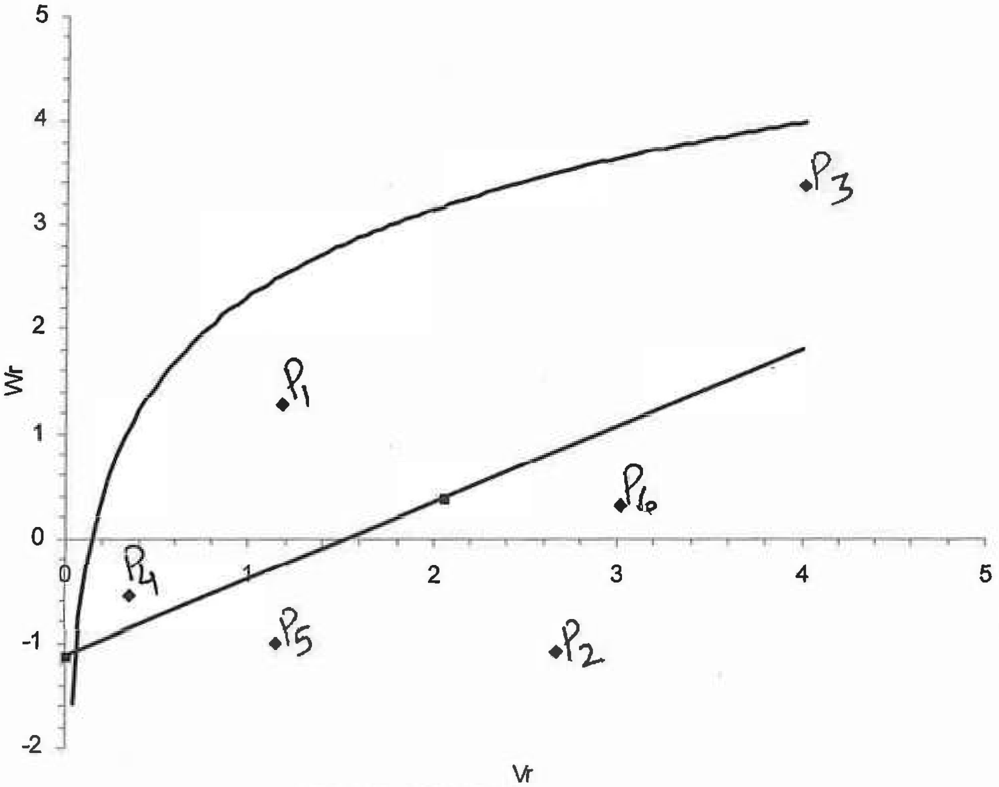

Fig. 6 Panicle length

$a = -336.78$
$b = 0.51 \pm 0.225^{N.S.}$

P_1 Malong
P_2 Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6 Bahadur

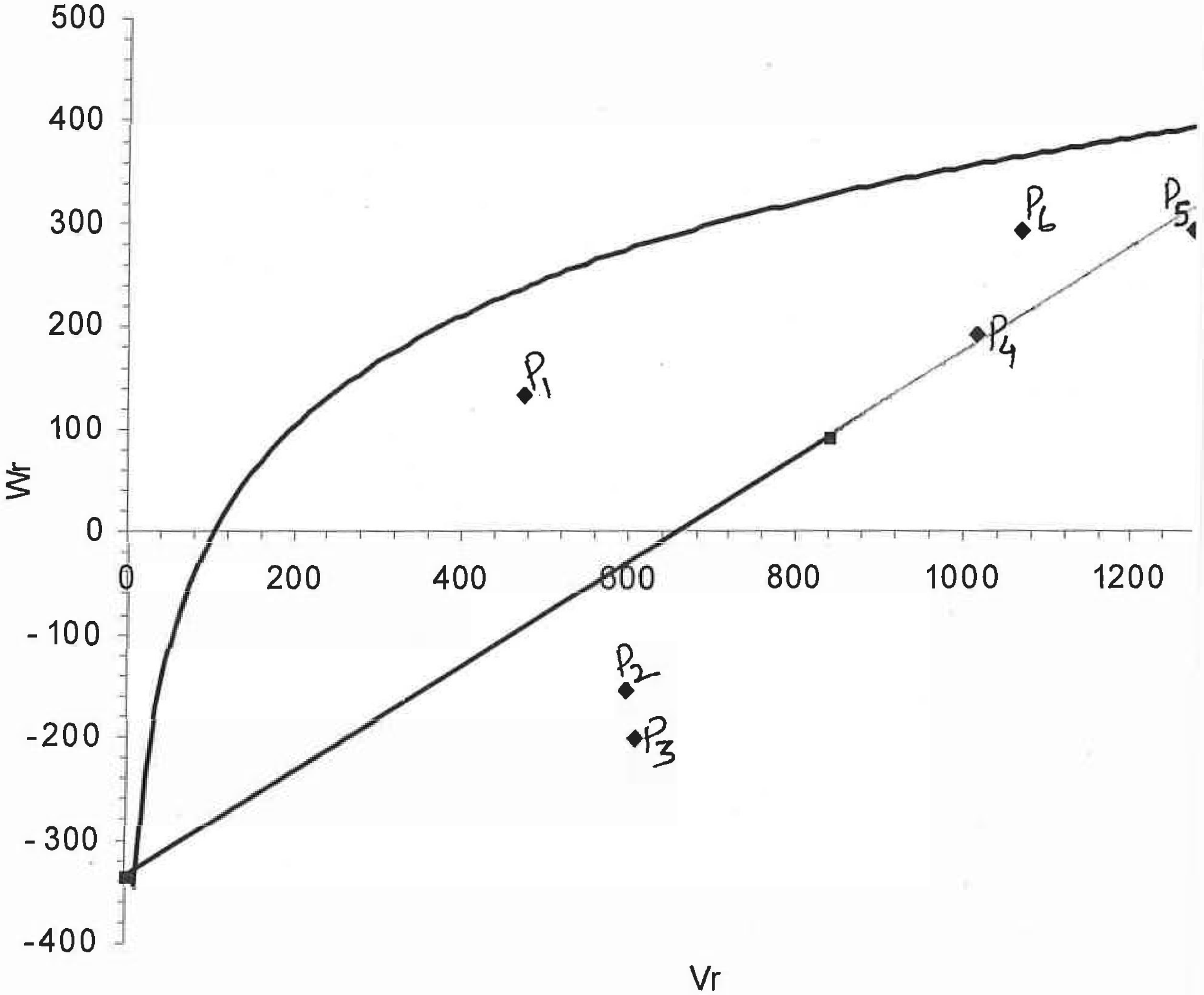

Fig. 7 Grains per panicle

$a = -12.513$
$b = 0.408 \pm 0.161^{N.S.}$

P_1 Malong
P_2 Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6Bahadur

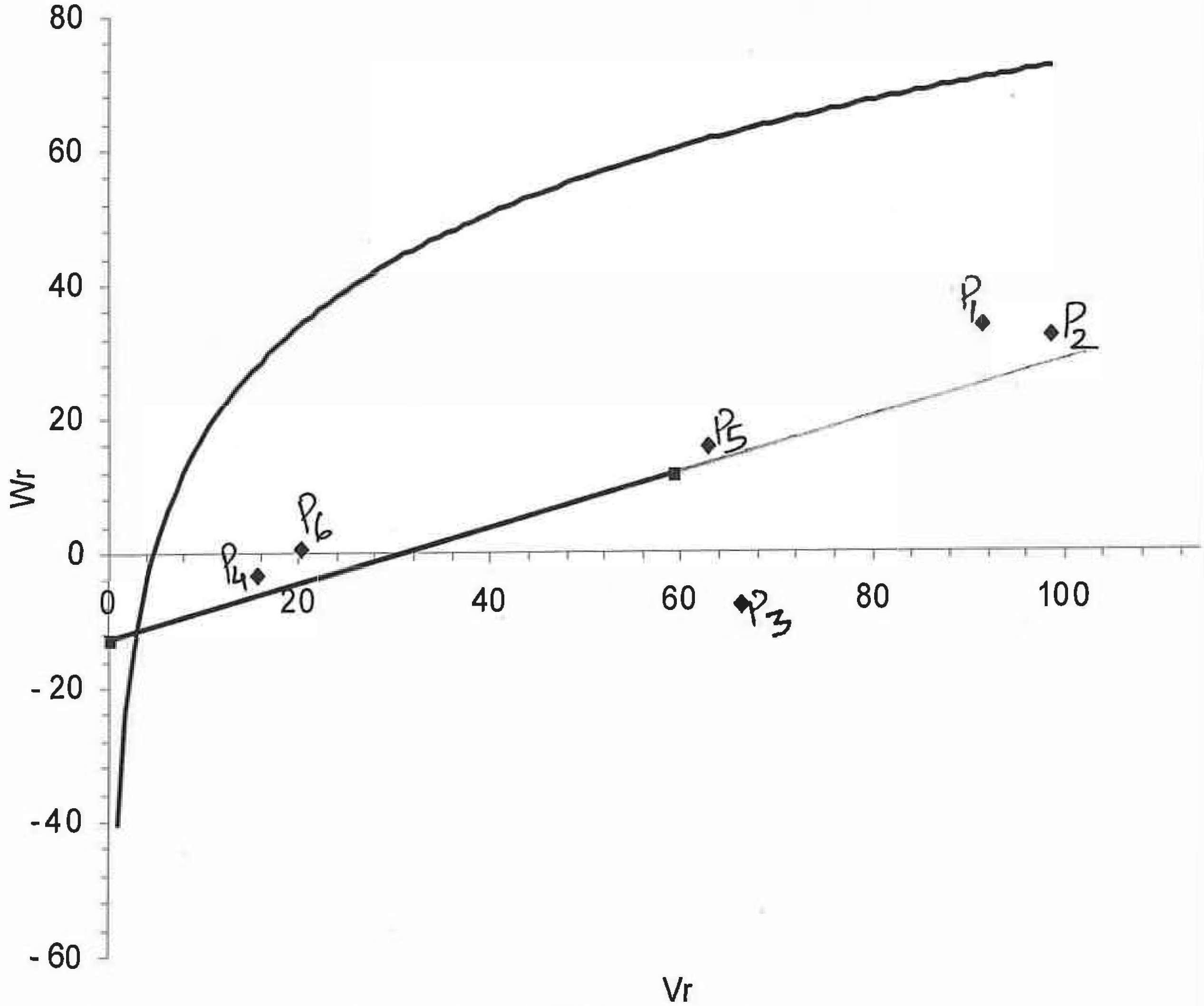

Fig. 8 Grain filling percent

$a = -0.038$
$b = 0.726 \pm 0.29^{N.S.}$

P_1 Malong
P_2 Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6Bahadur

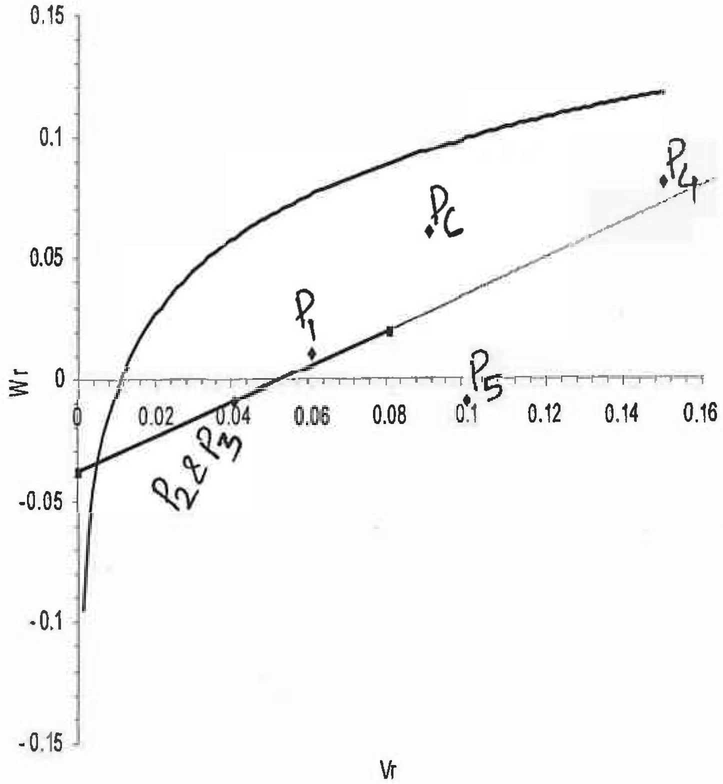

Fig. 9 Length- breadth ratio

a = 7.628
b = 0.676 ± 0.346$^{N.S.}$

P$_1$ Malong
P$_2$ Mehuru
P$_3$ Teke
P$_4$ Piolee
P$_5$ Ranjit
P$_6$ Bahadur

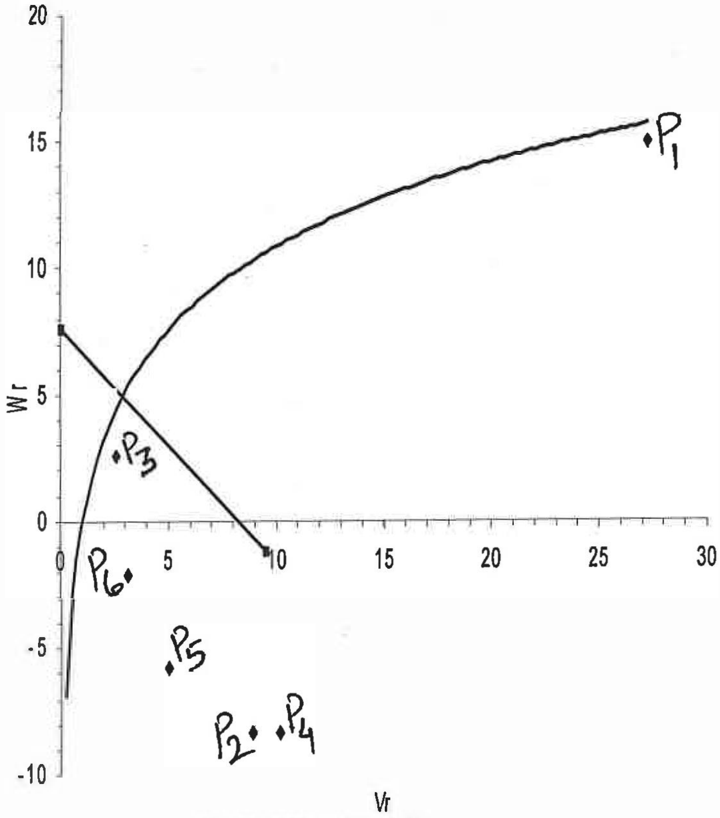

Fig. 10 1000- grain weight

a=-28.38
b = 0.384 ± 0.356$^{N.S.}$

P_1 Malong
P_2 Mehuru
P_3 Teke
P_4 Piolee
P_5 Ranjit
P_6 Bahadur

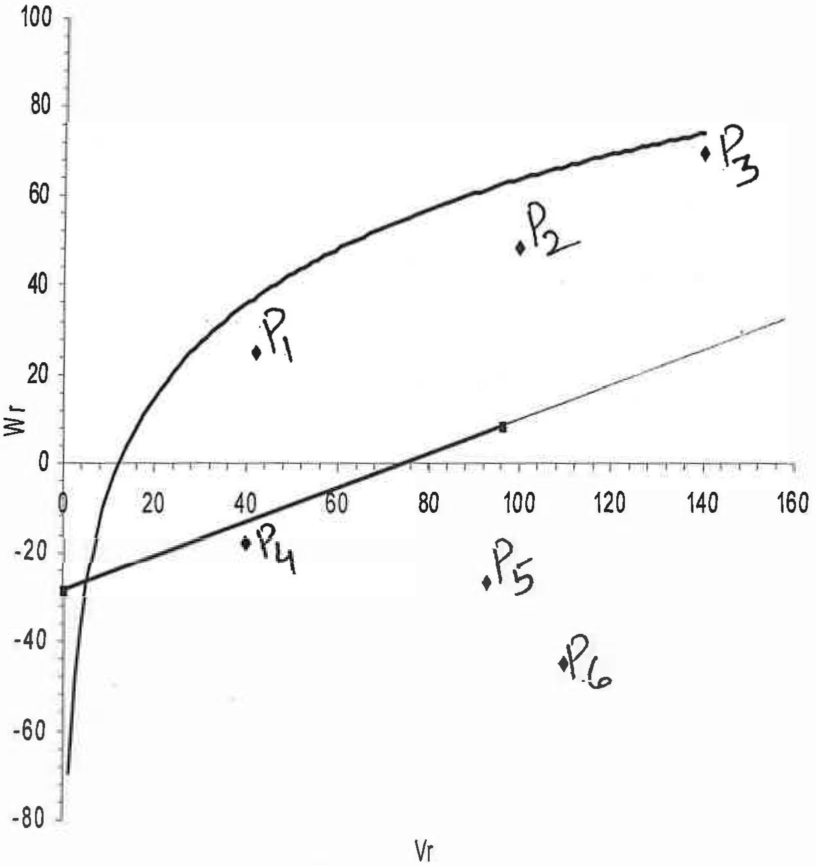

Fig. 11 Yield per plant

The regression coefficient (b= 0.7265 ± 0.292) of covariance on the variance for length- breadth ratio did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the Wr axis below the origin indicating over- dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

The regression coefficient (b= 0.676 ± 0.346) of covariance on the variance for 1000- grain weight did not deviate significantly either from zero or from unity indicating absence of epistasis. The regression line intercepted the Wr axis above the origin indicating partial dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

For yield per plant the regression coefficient (b= 0.3840 ± 0.356) of covariance on the variance did not deviate significantly either from zero or unity indicating absence of epistasis. The regression line intercepted the Wr axis below the origin indicating over-dominance. The parental points were scattered on the regression line indicating genetic diversity among the parents.

4.3 Phenotypic stability

In the present investigation 32 local and three improved genotypes of rice were grown in six environments viz., $E_{1\&2}$ (2003), $E_{3\&4}$ (2004) and $E_{5\&6}$ (2005). In each environment, these genotypes were planted in a Randomized Complete Block Design with three replications. Data were recorded on grain yield per plot in gms.

4.3.1 Analysisof variance

The data was subjected to analysis of variance separately for each individual environment (Table 16). Significant differences were observed among 35 genotypes for yield in each environment indicating considerable variation among genotypes at all the environments.

Table: 16 Analysis of variance for grain yield (gms/ plot) of rice at individual environment

Sources of variation	d.f	MEAN SQUARES					
		E_1	E2	E_3	E_4	E_5	E_6
Replication	2	1731.66	1164.52	2461.66	3094.28	875.23	1388.80
Genotype	34	23944.98**	15545.28**	11227.00**	13723.22**	13111.65**	9347.24**
Error	68	929.46	1027.02	717.54	1166.83	794.11	1245.91

** Significant at 1 % level

4.3.2 Stability analysis

The pooled analysis of variance for genotype- environment interaction and phenotypic stability was carried out following the model of Eberhart and Russell (1966) and is presented in Table 17. The genotypes differed significantly and also the genotype interacted significantly with the additive environmental variation as revealed by significant G x E component. Both linear and non-linear components contributed towards G E interaction as evident from the significance of G x E (linear) and pooled deviation. The stability parameters along with phenotypic indices are presented in Table 18. According to Eberhart & Russell (1966) a variety can be considered as stable if it meets following requirement:

i) High mean over environments (X_i), i.e., a positive phenotypic index
ii) Regression coefficient, b_i equal to 1 and
iii) Deviation mean square (S^2_{di}) approaching zero.

Such a genotype is considered to possess average stability and could be considered for general recommendation.

In the present investigation bi values of all the genotypes did not differ significantly from unity. However, based on high mean and non- significant deviation mean squares, the average stable genotypes were found to be Piolee, Bahadur, Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo, Thevuru (Kelo-u), Kemony Kehnau (white), Teke and Mekrilha (Kepei-u) in that order. However, the first two highest yielders, viz., Piolee and Bahadur are high yielding recommended varieties of Assam and thus amongst the indigenous rice genotypes of Nagaland Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo, Thevuru (Kelo-u), Kemony Kehnau (white), Teke and Mekrilha (Kepei-u) exhibited average stability.

TABLE 17. Analysis of Variance for grain yield of rice

Source	df	SS	MS
Total	209	1075272.48	
Varieties	34	684842.85	20142.43*
Env. + (Varieties X Env.)	175	390429.62	
Environment (linear)	1	90412.80	
Varieties X Env. (linear)	34	38405.46	1129.57*
Pooled Deviation	140	261611.36	1868.65*
Variety 1	4	6460.34	1615.08*
Variety 2	4	7450.00	1862.50*
Variety 3	4	1838.17	459.54
Variety 4	4	1768.01	442.00
Variety 5	4	1417.38	354.34
Variety 6	4	3953.98	988.49*
Variety 7	4	5822.87	1455.71*
Variety 8	4	3322.93	830.73*
Variety 9	4	13168.63	3292.15*
Variety 10	4	16044.49	4011.12*
Variety 11	4	8080.20	2020.05*
Variety 12	4	34481.95	8620.48*
Variety 13	4	9429.72	2357.43*
Variety 14	4	13428.09	3357.02*
Variety 15	4	6959.65	1739.91*
Variety 16	4	9674.98	2418.74*
Variety 17	4	1621.97	405.49
Variety 18	4	6483.42	1620.85*
Variety 19	4	2918.53	729.63
Variety 20	4	2583.62	645.90
Variety 21	4	5838.56	1459.64*
Variety 22	4	9706.55	2426.63*
Variety 23	4	5880.51	1470.12*
Variety 24	4	3186.98	796.74
Variety 25	4	2181.99	545.49
Variety 26	4	22042.48	5510.62*
Variety 27	4	5865.82	1466.45*
Variety 28	4	2901.33	725.33
Variety 29	4	6732.17	1683.04*
Variety 30	4	3089.29	772.32
Variety 31	4	10085.91	2521.47*
Variety 32	4	12179.01	3044.75*
Variety 33	4	11753.73	2938.43*
Variety 34	4	1599.59	399.89
Variety 35	4	1658.34	414.58
Pooled Error	420	140444.44	334.39

Significant at 5% level

Table 18: Stability parameters for grain yield in rice

SN	GENOTYPES	MEAN	Phenotypic indices(Pi)	b_i	S^2di
1	Mekrilha	655.83	2.67	0.33±0.79	1280.69*
2	Ngoba	621.66	-31.50	1.05±0.84	1528.10*
3	Mekninya Khol	716.44	63.28	0.99±0.42	125.15
4	Thevuru(Kelo-u)	691.66	38.50	0.47±0.41	107.61
5	Kuki Chaushi	700.00	46.84	0.29±0.37	19.95
6	Wonder rice	577.50	-75.66	1.19±0.61	654.10*
7	Krumiavinya	663.61	10.45	2.60±0.75	1121.32*
8	Tevuru(white)	599.16	-54.00	1.55±0.56	496.34*
9	Keituo-ulha	756.94	103.78	0.16±1.12	2957.76*
10	Nyapie	543.05	-110.11	2.21±1.55	3676.73*
11	N.S.Keniese-u	597.77	-55.39	2.52±0.88	1685.65*
12	Kewhi Vuru	656.66	3.50	0.81±1.82	8286.09*
13	Rulonya	557.50	-95.66	0.05±0.95	2023.03*
14	Rhineinya	671.38	18.22	0.69±1.14	3022.63*
15	Khezharhi	590.83	-62.33	1.81±0.82	1405.52*
16	Ngobanya	628.33	-24.83	1.13±0.96	2084.35*
17	Mekrilha(Kepei-u)	664.16	1.01	0.28±0.39	71.10
18	Thevuru(Kezha-u)	655.27	2.11	1.01±0.79	1286.46*
19	Chamben(N.S.Kumelo-u)	586.11	-67.05	1.66±0.53	395.24
20	Kencnya Kumui(Red)	597.22	-55.94	2.08±0.50	311.51
21	Tsorenya	530.27	-122.89	0.74±0.75	1125.25*
22	Rosholha	585.00	-68.16	0.70±0.96	2092.24*
23	Khenou	656.94	3.78	1.57±0.75	1135.73*
24	Nyuceimo	695.27	42.11	0.18±0.55	462.35
25	Kemony Kehnau(white)	673.61	20.45	0.40±0.45	211.10
26	Kekhnie-LHE-Kenelo-u	728.61	75.45	0.74±1.46	5176.22*
27	Thevurie Tieca	671.94	18.78	1.05±0.75	1132.06*
28	Petkoti	697.77	44.61	0.37±0.52	390.94
29	Malong	713.61	60.45	0.81±0.65	1348.65*
30	Teke	671.66	18.50	0.93±0.55	437.93
31	Aboru	658.33	5.17	1.32±0.98	2187.08*
32	Mehuru	683.61	30.45	0.65±1.08	2710.36*
33	Ranjit	710.55	57.39	0.56±1.06	2604.04*
34	Bahadur	720.55	67.39	1.05±0.39	65.50
35	Poilee	731.66	78.50	0.90±0.40	80.19

DISCUSSION

5. DISCUSSION

5.1 Genetic variability, correlation & path coefficient

5.1.1 Genetic variability

The development of an effective plant-breeding program depends upon the presence of genetic variability. The efficiency of selection largely depends upon the magnitude of genetic variability present in the plant population. Thus, the success of genetic improvement for any character depends on the nature of variability present in the gene pool for that character. The characters of economic importance are generally quantitative in nature and exhibit considerable degree of interaction with the environment. Therefore, it becomes necessary to obtain information on variability present in the population.

The analysis of variance revealed significant differences among the genotypes for all characters studied, indicating a high degree of variability in the material. The estimates of phenotypic coefficient of variation (PCV) were higher than those of genotypic coefficient of variation (GCV) for all the traits indicating environmental factors influencing the characters. The results are in agreement of earlier reports of Sarawgi *et al.* (2000), Singh *et al.* (2002) and Singh *et al.* (2005).The highest PCV and GCV were recorded for panicle weight followed by effective tillers per plant and yield per plant indicating the presence of ample variation for these traits in the present material. Similar results have also been reported by Khedikar *et al.* (2005) and Das *et al.* (2005).

5.1.2 Heritability & genetic advance

A fair measure of efficiency of selection for any quantitative traits can be derived from the estimates of heritability for the characters under consideration because heritability in broad sense is the ratio of genetic variance to the total variance. But reliability of selection depends not only on heritability but it should also be accompanied by high genetic advance (Johnson *et al.,* 1955). High heritability coupled with high genetic advance shows that a progress can be made through selection. In the present study high estimates of heritability and genetic advance were obtained for panicle weight, effective tillers per plant, days to 50% flowering, 50% flowering to maturity, yield per plant, length- breadth ratio, 1000 grain weight, plant height and grains per panicle. Thus, selection for these traits is likely to accumulate more additive genes leading to further improvement of their performance and these traits may be used as selection criteria in lowland breeding program. Similar observations were reported by Barbora and Hazarika (1998) for plant height, days to 50% flowering, grain weight and grain yield per panicle; Sarawgi *et al.* (2000) for plant height, days to 50% flowering and 100 grain weight.

Moderate heritability with low genetic advance was found in respect of panicle length, indicating non- additive gene action. The heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such trait may not be rewarding. Similar results have also been reported by Barbora and Hazarika (1998) and Sarawgi *et al.* (2000).

5.1.3 Correlation

Yield is a complex character, which is highly variable because of greater influence of environment. It is also influenced directly and indirectly by a set of other characters. It is in this context that the study of the nature and magnitude of association between yield and its component characters are of particular interest and essential prerequisite in a sound-breeding program. Such studies help the breeder to decide the characters to be considered for improvement in overall breeding program. To utilize various quantitative traits in breeding program, inter-relationship between the characters are of immense value (Lerner, 1958). Therefore, in the present study, correlations between eleven characters were studied in all possible combinations at phenotypic and genotypic level. In general, magnitude of genotypic correlation tended to be higher than phenotypic correlations. This suggested a strong genetic association between the traits and the phenotypic expression was suppressed due to environmental influence. Similar observations were reported by Kishore *et al.* (2007).

The grain yield exhibited significant positive correlation with effective tillers per plant indicating relative utility of this trait for selection. Similar results have also been reported by Thakur and Chaubey (1999). Grain yield was also significantly and negatively associated with days to 50 % flowering, panicle length and length- breadth ratio.

1000-grain weight showed significant positive association with plant height, panicle weight, panicle length and grains per panicle. This was in conformity with the findings of Ramakrishnan *et al.* (2006) for plant height and panicle length. Length-breadth ratio showed significant positive association with panicle length and grain filling percent; plant height with grains per panicle, panicle length and days to 50 % flowering. Days to 50 % flowering were negatively and significantly associated with grain filling percent.

5.1.4 Path coefficient

The path analysis revealed that effective tillers per plant had the highest positive direct effect on yield (0.404) followed by panicle weight (0.244) and plant height (0.123). Effective tillers per plant exerted positive direct effect and also exhibited significant positive correlation with yield indicating a true relationship among the traits. This suggests that direct selection for effective tillers per plant would likely be effective in increasing seed yield. This was in agreement with the findings of Sawant (1995) and Kishore (2007). The residual effect estimated were 0.3108 indicating that the traits under study are not sufficient to account for variability and there might be a few more pertinent characters other than those studied in the present investigation and thus solicits inclusion of some more characters. Inclusion of some physiological characters like leaf area index, chlorophyll content, harvest index etc. could be considered important in order to derive a much clear picture of the causal relationship. The present study suggests that while selection, emphasis should be given for effective tillers per plant for improvement in seed yield.

5.2 Genetic divergence

In any crop, germplasm is a valuable source of base population and provides the scope for wider adaptability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F_1 and broad spectrum of variability in subsequent segregation generations (Maurya and Singh, 1997).

The analysis of variance revealed significant differences among the genotypes for all the characters indicating high genetic variability present in the population. Based on the relative magnitude of D^2 values, 35 genotypes were grouped into eight clusters. Cluster I had maximum number of 18 genotypes while cluster VII and VIII had the minimum 1 genotype each. Interestingly the three improved genotypes Ranjit, Bahadur and Piolee belonged to the same cluster i.e. cluster II. The pattern of distribution of genotypes in different clusters indicated that genetic diversity was not related to ecosystem differentiation. This was in agreement with the findings of Rahaman *et al.* (1997) and Shiv Datt and Mani (2003). Many genotypes of close geographic proximity fell in different clusters and vice- versa. Clustering of genotypes from different eco-geographic locations into one cluster could be attributed to the possibility of free exchange of breeding material.

The estimates of intra and inter- cluster distances has presented in Table 2.The intra- cluster distance ranged from 0.00 (cluster VII & cluster VIII) to 137.33 (cluster

VI). The inter- cluster distance was observed to be highest between cluster VII & VIII (935.52) followed by cluster II & VII (776.63) indicating greater diversity between these clusters. Hence the genotypes of cluster VII could be utilized as diverse parent in hybridization program with the genotypes of cluster II & cluster VIII respectively, to achieve greater variability in the segregating generations. Inter- cluster distance was minimum between cluster I & IV (129.11) followed by cluster I & VI (143.91) indicating genotypes belonging to these clusters are relatively closer. Such analysis was meant to avoid selection of parents from genetically closer clusters which may in turn result narrow genetic base and inbreeding depression.

Comparison of cluster means revealed that cluster VII gave exceptionally high values for six characters namely days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, L/B ratio and 1000 grain weight. Cluster mean for panicle weight and grain filling percent was highest for cluster V, panicle length and grains per panicle for cluster VIII and yield per plant for cluster II. The coefficient of variation for different characters indicated that panicle weight, effective tillers per plant and yield per plant contributed maximum towards divergence. This was in agreement with the findings of Roy and Das (2000) for effective tillers per plant; Roy and Das (2000), Shiv Datt and Mani (2003) and Sobita Devi et al (2006) for yield per plant.

5.3 Combining ability & genetic analysis

Crop improvement requires the ability to select higher-performing individuals from a population. Identification of superior individuals requires variation in the population. This is usually overcome by crossing unrelated strains to create variation followed by phenotypic screening. Parental selection for creating genetic variability for crop improvement requires knowledge of the likelihood of improving traits of interest. This likelihood is based on the amount and type of genetic control of the trait. The amount of genetic control is influential because improvement of a trait with very small genetic control relative to environmental influences will be difficult. Several genetic mating designs exist to facilitate dissection of environmental and genetic control underlying quantitative traits in plants. Among the most common mating designs in crop improvement is the 'diallel analysis'.

In self pollinated crops such as rice, wheat etc. diallel analysis is often used for testing the performance of parents in hybrid combinations and also for detecting the nature and magnitude of gene action involved in the expression of quantitative traits. The estimation of general combining ability effects of the crosses helps in choosing the best parents and hybrids. Further the genetic analysis helps in understanding the genetic architecture of the characters under study. In the present investigation attempts were made to study the combining ability involving parents and their F1 progenies (without reciprocals) in a diallel cross and also to elucidate various genetic components following methods of Griffing (1956) and Hayman (1954), respectively.

5.3.1 Analysis of Variance

Sufficient variation was observed among the genotypes for all the characters. On further partitioning of the genotypes, parents and crosses were found to differ significantly among themselves for all the characters except panicle length and grains per panicle. Further, the crosses as a whole were found to differ significantly from the parents with respect to all the characters except length- breadth ratio. These results were indicative of creation of sufficient variation as a result of diallel crossing among the parents.

5.3.2 Mean Performance

An examination of the mean performances for grain yield and other characters revealed higher mean values for the hybrids compared to that of parents except 50% flowering to maturity, plant height and panicle length. This was taken to be an indication of the presence of heterosis for those characters. The crosses Teke x Bahadur and Teke x Ranjit could be considered as the most potential crosses for grain yield per plant. These two crosses were found to be superior for other three to five characters. Teke x Bahadur was superior for five other characters viz., 50% flowering to maturity, effective tillers per plant, panicle length, grains per panicle and grain filling percent while Teke x Ranjit was superior for three other characters viz., flowering to maturity, effective tillers per plant and grains per panicle. These two crosses deserve consideration in breeding program for improvement of yield. Besides these two, other crosses showing superior performance for different characters are Ranjit x Bahadur, Mehuru x Piolee and Teke x Piolee for days to 50% flowering; Teke x Ranjit, Malong x Ranjit and Mehuru x Bahadur for 50% flowering to maturity; Malong x Bahadur, Malong x Ranjit, Mehuru x Piolee, Mehuru x Ranjit and Malong x Teke for effective tillers per plant; Teke x Piolee, Malong x Ranjit, Malong x Mehuru and Piolee x Ranjit for plant height; Malong x Teke, Malong x Bahadur and Malong x Mehuru for panicle weight; Mehuru x Bahadur and Mehuru x Ranjit for panicle length; Mehuru x Piolee for grains per panicle; Mehuru x Teke for grain filling percent; Teke x Piolee, Malong x Mehuru and Mehuru x Piolee for length- breadth ratio; Ranjit x Bahadur and Piolee x Bahadur for 1000 grain weight. It was expected that these crosses would generate some useful segregants in the subsequent generations.

5.3.3 Combining ability analysis

5.3.3.1 GCA and SCA Variances

Combining ability analysis revealed the significance of both general and specific combining ability variances for all the characters. This apparently indicated the presence of both additive and non additive gene action for the characters. However, for characters panicle length, length- breadth ratio, 50% flowering to maturity, panicle weight, yield per plant, effective tillers per plant and plant height the mean squares of gca and sea were more or less equal indicating the importance of both additive and non additive gene action. The characters 1000 grain weight, grain filling percent and grains per panicle were pre-dominantly controlled by additive gene action where as character days to 50%

flowering was pre-dominantly under the control of non- additive gene action. For characters where both additive and non additive gene action were equally important, Comstock *et al.* (1949) suggested the use of reciprocal recurrent selection; for the characters where additive effect forms the principal factor of genetic variance, use of pedigree method may be useful and for the characters where pronounced non additive gene effects along with some additive gene effects were observed, production of hybrids, if commercial seed production is feasible, would be desirable.

Involvement of additive as well as non additive gene action for different characters in rice was reported by Maurya & Singh (1977), Verma *et al.* (1995), Pradhan *et al.* (2006) and Sadhukhan and Chattopadhyay (2006).

5.3.3.2 General Combining Ability Effects

The comparison of general combining ability effects of parents revealed Bahadur to be the best general combiner for yield per plant followed by Teke and Ranjit. The good combining ability of Bahadur for yield per plant could be attributed to its better combining ability for grain filling percent, 1000 grain weight, panicle weight and effective tillers per plant. Teke exhibited high general combining ability effects for the characters days to 50% flowering, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, length- breadth ratio and 1000 grain weight. It was observed by many workers (Maurya & Singh 1977, Verma *et al.* 1995) that a variety with good general combining ability for grain yield was also good combiner for at least some yield attributing characters. Rice genotypes Teke and Bahadur would be ideal for incorporation in a breeding program for developing high yielding variety of rice.

5.3.3.3 Specific Combining Ability Effects

A comparison of specific combining ability effects indicated that the crosses Teke x Bahadur, Teke x Ranjit, Mehuru x Piolee, Malong x Bahdur, Mehuru x Ranjit, Mehuru x Bahadur and Teke x Piolee exhibited significantly high specific combining ability effects for yield per plant. Further, these crosses exhibited significantly high specific combining ability effects for many other characters as well. It could also be seen that except Mehuru x Piolee at least one of the parent was a good general combiner for yield per plant. The crosses which show high specific combining ability effects and in which good general combiner parents involved are expected to produce transgressive segregants which can be identified following simple conventional breeding program. Those crosses which involve good x poor combiners may throw potential segregants if additive genetic system is present in good combiners and fixable epistatic effects in the crosses. Thus, efforts should be made to modify conventional breeding methodologies to capitalize on additive and non- additive genetic effects. As an alternative approach to selfing for a number of generations and selecting after homozygosity is achieved, alternate intermating and selfing would increase span of selection. This would enhance isolation of desirable transgressive segregants in such materials where both general and specific combining ability variances are prevalent. From this viewpoint, the parents Teke, Ranjit and Bahadur and the crosses Malong x Bahadur, Mehuru x Ranjit, Mehuru x Bahadur and Teke x Piolee have considerable potentiality in a breeding program. However, the high specific combining ability effects of the poor x poor combiners can not altogether be neglected since there could be existence of occasional heterosis for specific combining ability effect as exhibited by Mehuru x Piolee for grain yield per plant. This could be due to over- dominance and epistasis. In the present study good x good combiners turned out to be best specific combiners as evident from the crosses Teke x Bahadur and Teke x Ranjit where as cross Ranjit x Bahadur was a poor specific combiner. However, good x poor combiners like Malong x Bahadur, Mehuru x Ranjit, Mehuru x Bahadur and Teke x Piolee were among the best specific combiners. Similar results were also observed for other characters. These observations are in agreement with earlier findings reported by Lavanya (2000), Raju *et al.* (2006), Sadhukhan & Chattopadhyay (2006), Senguttuvel and Bapu (2007).

It may be inferred that high sea effects of crosses involving good x poor combiners might have been as a result of interaction between additive and non- additive components where as high sea effects of crosses involving poor x poor combiners might be attributed to dominance x dominance type of gene action.

5.3.4 Genetic Analysis

5.3.4.1 Genetic Components of Variation

The relative magnitude of dominance components 'H_1 & H_2' were observed to be higher than additive component D for all the characters. For the characters like effective tillers per plant, panicle weight, grains per panicle, 1000 grain weight and yield per plant only dominance components H_1, H_2, & h^2 (except 1000 grain weight) were significant which indicated the involvement of only dominance component of variation in their expression.

All the components D, H and H_2 were significant for the characters days to 50% flowering, 50% flowering to maturity, plant height, panicle length, grain filling percent and length- breadth ratio. This result is in conformity with those of Mehla *et al.* (2000), Pradhan *et al.* (2006) and Raju et al (2006)

As involvement of both additive and non- additive components were observed in the control of yield attributing characters viz., days to 50% flowering, 50% flowering to maturity, plant height, panicle length, grain filling percent and length- breadth ratio, with pre- dominance of non- additive component, simple pedigree selection for these characters will not be effective. In such situations, population improvement program which may bring about the accumulation of fixable gene effects as well as which will maintain considerable variability and heterozygosity for exploiting non- fixable gene effects will prove to be the most effective method (Joshi, 1979).

The value of 'F' was positively significant for days to 50 % flowering, 50% flowering to maturity, plant height, panicle length and length- breadth ratio. This indicates that dominant genes were more frequent in the parents than the recessive genes for these characters.

The estimates of degree of dominance were to be more than unity for all the characters including yield per plant which indicated prevalence of over- dominance.

The proportion of alleles in the parents with positive and negative effects $(H_2/4H_1)$ were below the expected value of 0.25 for all the characters except grains per panicle where it was almost 0.25. This indicated the unequal allelic frequencies for all other characters and equal allelic frequency for grains per panicle.

As indicated by KD/KR, the parents might contain more number of dominant genes than recessives for the characters like days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, panicle weight, panicle length, grain filling percent, and 1000 grain weight whereas recessives might be more than dominants for grains per panicle. These findings corroborated the findings from values of 'F'. The value of KD/KR for the characters length- breadth ratio and yield per plant almost equals to unity which indicates equality of dominance and recessive genes.

The value of h^2/H_2 indicated that one to two gene groups might be involved in the control of days to 50% flowering, 50% flowering to maturity, effective tillers per plant and length- breadth ratio; two to three gene groups for plant height, grains per panicle & grain filling percent and four gene groups for panicle weight. However, the very low values of the parameters for panicle length and 1000 grain weight did not reflect any conclusive inference regarding the number of gene groups controlling these two characters.

The negative correlation between the mean values of the parents 'Yr' and the parental order of the dominance (Wr + Vr) for all the characters except 50% flowering to maturity, plant height, panicle length and 1000 grain weight suggested that the dominant genes were associated with high mean expression. It clearly indicated that early flowering was controlled mostly by recessive genes. The positive correlation for 50% flowering to maturity, plant height, panicle length and 1000 grain weight suggested high mean expression to be associated with more recessive genes. The association of recessive genes with high mean expression is an advantage in breeding program as it might facilitate fixation of the trait in the early generation (Subramanium & Rathinum, 1984).

5.3.5 Graphical Analysis

Graphical analysis of a diallel cross provides useful information on the average degree of dominance, dominance order of the parents and additional information about the relationship among the parents.

The validity of inference drawn from the results of diallel analysis depends on the fulfillment of six assumptions i.e. diploid segregation, homozygous parents, absence of maternal effects, no multiple allelism, no epistatsis and independent distribution of genes among parents. The nature of the crop (diploid segregation) and parents (homozygous) with no reciprocal differences reported fulfilled the first three assumptions. Homogenity of (Wr- Vr) over arrays and non- significant deviation of regression coefficient from unity indicated fulfillment of last three assumptions. The regression of Wr on Vr did not deviate significantly from unity for all the characters except 50% flowering to maturity, plant height and panicle weight. This indicated the absence of epistasis for the other characters and presence of it for the exceptions. Thus, for 50% flowering to maturity, plant height and panicle weight, the present analysis could not reflect any clear cut inference. Kearsey and Jinks (1968) and Daly & Robson (1969) pointed out that in studies of quantitative inheritance complete validity of all the assumptions is unlikely. When a trait exhibits a partial failure of the assumptions, estimates of genetic parameters of that trait are still possible (Hayman, 1954).

The regression line intercepted the Wr axis below the origin for the characters days to 50% flowering, panicle length, grains per panicle, grain filling percent, length-breadth ratio and yield per plant indicating over- dominance, where as interception was above the origin for effective tillers per plant and 1000 grain weight indicating partial dominance for inheritance of these two characters. Contradictory results between graphical analysis and component analysis were observed for effective tillers per plant and 1000 grain weight. Graphical analysis indicated partial dominance for effective tillers per plant and 1000 grain weight where as component analysis indicated over-dominance. Baker (1978) clarified that to assume genes to be distributed independently in the parents of a diallel cross was not a realistic assumption. He further stated that there was a general agreement regarding failure of this assumption often leading to overestimation of the average level of dominance as derived from graphical analysis of Hayman. Coughtrey and Mathur (1970) in their theoretical consideration and the computer simulation of Feyt (1976) showed that Hayman's test for epistasis is reliable only if genes are distributed independently in the parents of diallel. Hayman (1954a) himself pointed out that the estimate of the average degree of dominance may be increased or decreased by lack of independence of genes in the parents. Hence, perturbation of the Wr- Vr graph may be caused by epistasis and / or correlation between genes. The parents were observed to be well scattered on the regression line indicating their diverse genetic nature. Being close to origin parents found to possess most dominant genes were Malong for days to 50% flowering; Mehuru, Teke, Piolee and Bahadur for 50% flowering to maturity; Malong, Piolee, Ranjit & Bahadur for plant height; Teke and Bahadur for panicle weight; Piolee for panicle length; Piolee and Bahadur for grain filling percent; Mehuru and Teke for length- breadth ratio and Teke, Ranlit & Bahadur for 1000 grain weight. Out of these parents Bahadur, Teke and Piolee possess dominant genes for six, four and three characters respectively. Parents located in the middle portion of the graph found to possess more or less equal number of dominant and recessive genes. Those were Mehuru, Teke, Piolee and Bahadur for days to 50%

flowering; Ranjit for 50% flowering to maturity; Teke and Bahadur for effective tillers per plant; Mehuru for plant height; Mehuru, Ranjit and Piolee for panicle weight; Malong, Ranjit, Mehuru and Bahadur for panicle length; Mehuru, Malong and Teke for grains per panicle; Teke and Ranjit for grain filling percent; Malong, Ranjit and Bahadur for length- breadth ratio; Mehuru and Piolee for 1000 grain weight and Malong and Piolee for yield per plant. Parental points furthermost from the origin possess most recessive genes. Those were Ranjit for days to 50% flowering; Malong for 50% flowering to maturity; Malong, Mehuru, Piolee, and Ranjit for effective tillers per plant; Teke for plant height and panicle length; Malong for panicle weight; Piolee, Bahadur and Ranjit for grains per panicle; Malong and Mehuru for grain filling percent; Piolee for length- breadth ratio; Malong for 1000 grain weight and Mehuru, Teke, Ranjit and Bahadur for yield per plant.

5.4 Phenotypic Stability

The analysis of variance for yield in individual and pooled analysis showed highly significant differences among the genotypes and environments for grain yield, indicating the presence of variability among the genotypes as well as the environments under study. The genotype x environment (G x E) interaction was further partitioned into linear and non- linear (pooled deviation) components. Mean squares for both these components were highly significant, indicating that the both predictable and unpredictable components shared G x E interaction. Earlier workers Kumar *et al.* (2005), Shanmuganathan and Ibrahim (2005), Deshpande and Dalvi (2006) and Dushyantha Kumar and Shadakshari (2007) also observed considerable G x E interaction in rice.

Eberhart and Russell (1966) emphasized that both linear (bi) and non- linear (S^2_{di}) components of G x E interaction should be considered in judging the phenotypic stability of a particular genotype. Further, Samuel *et al.*, (1970) suggested that the linear regression could simply be regarded as a measure of response of a particular genotype which depends largely upon a number of environments whereas the deviation from regression line was considered as a measure of stability, genotype with the lowest or non- significant standard deviation being the most stable and vice- versa.

Zubair *et al.*, (2002) suggested that if regression coefficients of the genotypes are not significantly different from 1, the stability of these genotypes should be judged upon other two parameters i.e. mean and deviation from regression (S^2_{di}).

In the present investigation, the regression coefficients of all the varieties were not significantly different from 1, therefore, the stable performance of the varieties in this case is predicted on the basis of other two parameters, i.e. deviation from regression and mean yield over all the environments, which is also reflected in the positive phenotypic indices.

The genotypes Piolee, Bahadur, Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo, Thevuru (Kelo-u), Kemony Kehnau (white), Teke and Mekrilha (Kepei-u) exhibited high mean grain yield as well as non- significant deviation from regression. However, the first two highest yielders, viz., Piolee and Bahadur are high yielding recommended varieties of Assam and thus amongst the indigenous rice genotypes of Nagaland Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo, Thevuru (Kelo-u), Kemony Kehnau (white), Teke and Mekrilha (Kepei-u) exhibited average stability. These genotypes could be considered to possess average stability for grain yield. Such genotypes will perform uniformly over a wide range of environments and are ideal for general recommendation.

5.5 Implications in Plant Breeding

The present investigation generated information which has relevance on initiating low-land rice breeding programme in Nagaland. The landraces of Nagaland studied not only exhibited genetic variation but also were found to be genetically diverse. The clustering pattern revealed scope for identification of genetically diverse genotypes. Amongst them traditional genotype like Teke was also found to be a good general combiner for a number of characters. It also resulted in high specific combining ability effect in crosses with high yielding good general combiners like Bahadur, Ranjit and Piolee. The handling of such populations will be relatively easy through simple conventional breeding approach as they are expected to generate transgressive segregants.

The crosses like Malong x Bahadur, Mehuru x Ranjit and Mehuru x Bahadur which involve good x poor combiners may throw potential segregants if additive genetic system is present in good combiners and fixable epistatic effects in the crosses. For such crosses it will be necessary to modify conventional breeding methodologies to capitalize on additive and non- additive genetic effects. Alternate intermating and selfing would increase span of selection. This would enhance isolation of desirable transgressive segregants in such materials where both general and specific combining ability variances are prevalent.

The population improvement program could be an option to bring about the accumulation of fixable gene effects as well as maintenance of considerable variability and heterozygosity for exploiting non- fixable gene effects for those characters where both additive and non-additive components were revealed in genetic analyses.

Stability in yield is a genetic trait and in the present investigation a number of landraces like Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo Thevuru (Kelo-u), Kemony Kehnau (white) and Teke exhibited average stability. These landraces especially Teke along with high yielding average stable variety Bahadur deserve consideration as potential parents in hybridization programme. These two parents also exhibited good general combining ability effects and their cross exhibited high specific combining ability effect as well.

SUMMARY & CONCLUSION

6. SUMMARY AND CONCLUSION

6.1 Summary

The present investigation on "Biometrical Studies in Lowland Rice (*Oryza sativa* L)" was carried out at the experimental farm of ICAR Research Complex, Jharnapani to estimate (a) nature and extent of genetic variability in the lowland rice landraces (b) genetic diversity present within the population on the basis of morphological and agronomical characteristics (c) combining ability effects and variances of a 6 x 6 diallel cross for different quantitative characters (d) genetic architecture of different quantitative characters through genetic analysis of diallel and (e) phenotypic stability of the landraces in order to identify high yielding phenotypically stable genotypes over variable environments.

For genetic variability and genetic diversity thirty-two local genotypes of rice of Nagaland along with three improved genotypes from Assam were evaluated for days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, grain filling percent, length- breadth ratio, 1000 grains weight and yield per plant. The analysis of variance revealed significant differences among the genotypes for all characters studied, indicating a high degree of variability in the material. The highest PCV and GCV were recorded for panicle weight followed by effective tillers per plant and yield per plant indicating the presence of ample variation for these traits in the present material. In the present study high estimates of heritability and genetic advance were obtained for panicle weight, effective tillers per plant, days to 50% flowering, 50% flowering to maturity, yield per plant, length- breadth ratio, 1000 grain weight, plant height and grains per panicle. Thus, selection for these traits is likely to accumulate more additive genes leading to further improvement of their performance and these traits may be used as selection criteria in lowland breeding program. The grain yield exhibited significant positive correlation with effective tillers per plant indicating relative utility of this trait for selection. Effective tillers per plant exerted positive direct effect and exhibited significant positive correlation with yield indicating a true relationship among the traits.

Based on the relative magnitude of D^2 values, 35 genotypes were grouped into eight clusters. The pattern of distribution of genotypes in different clusters indicated that genetic diversity was not related to ecosystem differentiation. Many genotypes of close geographic proximity fell in different clusters and vice- versa. The inter- cluster distance was observed to be highest between cluster VII & VIII followed by cluster II & VII indicating greater diversity between these clusters. Hence the genotypes of cluster VII could be utilized as diverse parent in hybridization program with the genotypes of cluster II & cluster VIII respectively, to achieve greater variability in the segregating generations. The coefficient of variation for different characters indicated that panicle weight, effective tillers per plant and yield per plant contributed maximum towards divergence.

For genetic studies, six genotypes selected on the basis of phenotypic variability, were crossed in a diallel fashion. Data on days to 50% flowering, 50% flowering to maturity, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, grain filling percent, length- breadth ratio, 1000 grains weight and yield per plant were recorded on ten sampled plants from all the F_1 and their parents. Data were analyzed, firstly following the techniques of analysis of variance; secondly combining ability analysis was performed by using Griffing's technique Model I, Method II and thirdly, genetic analysis was carried out following Hayman's method. Combining ability analysis revealed the significance of both general and specific combining ability variances for all the characters. This apparently indicated the presence of both additive and non additive gene action for the characters. However, for characters panicle length, length- breadth ratio, 50% flowering to maturity, panicle weight, yield per plant, effective tillers per plant and plant height the mean squares of gca and sea were more or less equal indicating the importance of both additive and non additive gene action. The characters 1000 grain weight, grain filling percent and grains per panicle were pre-dominantly controlled by additive gene action where as character days to 50% flowering was pre-dominantly under the control of non- additive gene action. The comparison of general combining ability effects of parents revealed Bahadur to be the best general combiner for yield per plant followed by Teke and Ranjit. The good combining ability of Bahadur for yield per plant could be attributed to its better combining ability for grain filling percent, 1000 grain weight, panicle weight and effective tillers per plant. Teke exhibited high general combining ability effects for the characters days to 50% flowering, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, length-breadth ratio and 1000 grain weight. In the present study good x good combiners like Teke x Bahadur and Teke x Ranjit and good x poor combiners like Malong x Bahadur, Mehuru x Ranjit, Mehuru x Bahadur and Teke x Piolee were among the best specific combiners.

Component analysis indicated importance of both additive and dominance gene action for the characters days to 50% flowering, 50% flowering to maturity, plant height, panicle length, grain filling percent and length- breadth ratio while only the dominance component was important for the characters like effective tillers per plant, panicle weight, grains per panicle, 1000 grain weight and yield per plant. Dominant genes were more frequent in the parents than the recessive genes for the characters days to 50 % flowering, 50% flowering to maturity, plant height, panicle length and length- breadth ratio. Unequal gene frequencies for positive and negative alleles in the parents were observed for all the characters except grains per panicle for which equal gene frequencies were evident. The estimates of degree of dominance were more than unity for all the characters including yield per plant which indicated prevalence of over- dominance. From the graphical approach, over-dominance was evident for days to 50% flowering, 50% flowering to maturity, plant height, panicle weight, panicle length, grains per panicle, grain filling percent, length- breadth ratio, and yield per plant and partial dominance for effective tillers per plant and 1000 grains weight.

For phenotypic stability 32 local along with three improved rice genotypes were grown in six environments. In each environment, these genotypes were planted in Randomized Complete Block Design with three replications. Data were recorded on grain yield per plot in gm. The genotype x environment (G x E) interaction was further partitioned into linear and non- linear (pooled deviation) components. Mean squares for both these components were highly significant, indicating that the both predictable and unpredictable components shared G x E interaction. Amongst the indigenous rice genotypes of Nagaland Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo Thevuru

(Kelo-u), Kemony Kehnau (white), and Teke exhibited average stability and higher grain yield and are ideal for general recommendation.

6.2 Conclusion

The present investigation clearly revealed the presence of extensive genetic variation in the indigenous rice genotypes of Nagaland. These landraces not only exhibited genetic variation but also were found to be genetically diverse as revealed from the results of D^2 analysis. The combining ability studies further indicated the worth of traditional varieties like Teke which not only exhibited high general combining ability effects for the characters days to 50% flowering, effective tillers per plant, plant height, panicle weight, panicle length, grains per panicle, length- breadth ratio and 1000 grain weight but also high specific combining ability effects in crosses with high general combiners like Bahadur, Ranjit and Piolee. Genetic analysis of diallel also indicated relative magnitudes of additive and non additive components of genetic variance and distribution pattern of positive and negative genes in the parents which could help in formulation of breeding programmes directed towards improvement of indigenous landraces of Nagaland. Any programme for development of high yielding rice varieties need to consider incorporation of phenotypic stability so that the developed variety performs uniformly over variable environments. From this point of view indigenous rice varieties like Mekninya Khol, Kuki Chaushi, Petkoti, Nyuceimo Thevuru (Kelo-u), Kemony Kehnau (white) and Teke exhibiting average stability should be considered for inclusion in breeding programme. The genotype Teke as well as Bahadur deserve special consideration as a potential parents in hybridization as both of them not only were good general combiners but also exhibited high specific combining ability effect in cross involving these two parents.

BIBLIOGRAPHY

7. BIBLIOGRAPHY

Acuña, T.L.B., Lafitte, H.R. and Wade, L.J. 2008. Genotype × environment interactions for grain yield of upland rice backcross lines in diverse hydrological environments. Field crop research, 108(2): 117-125.

Al-jibouri, N.A., Miller, P.A. and Robin, H.F. 1958. Genotypic and environmental variances, co-variances in upland cotton of inter-specific origin. Agron. J., 50: 633-637.

Ali, N., Javidfar, F. and Mirza. Y. 2003. Selection of stable rapeseed (Brassica napus L.) genotypes through regression analysis. Pak. J. Bot. 35: 175-183.

Ali, S.S., Jafri, S.J.H., Tasleema-uz-zaman Khan, Aamir Mahmood and Butt, M.A. 2000. Heritability of yield and yield components in rice. Pakistan Journal of Agricultural Research, 16(2): 89-91.

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

Arumugam, M., Rajanna, M.P. and Vidyachandra, B. 2007. Stability of rice genotypes for yield and yield components over extended dates of sowing under Cauvery command area in Karnataka. Oryza, 44(2): 104-107.

Arunachalam, V. 1981. Genetic distance in plant breeding. Indian J. Genet. 41(2): 226-236.

Awasthi, L.P., Mishra, C.H. and Pandey, V.K. 2005. Genetic divergence in Indian aromatic rice. Crop Res. 30(2): 199-201.

Babu, V.R., Kishore, S., Ansari, N.A. and Ravichandaran 2005. Genetic divergence in aromatic rice genotypes. The Andhra agric. J., 52(3&4): 407-410.

Bai, N.R., Devika, R., Regind,A. and Joseph, C.A. 1992. Correlation of yield and yield components in medium duration rice cultivars. Environment and Ecology, **10**: 469-470.

Baker, R.J. 1978. Issues in diallel analysis. Crop Sci., 18: 533-536.

Barbora, T.K. and Hazarika G.N. 1998. Study of genetic variability, heritability and genetic advances for panicle characters in rice. Oryza, **35**: 19-21.

Bhandarkar, S., Verma, R. and Kumar, A. 2002. Genetic variability and correlation analysis in early duration rice. Plant Archives, 2(1):95-98.

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

Bujarbaruah, K.M., Pattanayak, A., Sharma, Y.P., Ngachan, S.V., Dhiman, K.R., Munda, G.C., Azad Thakur, N.S., Satapathy, K.K., Datta, K.K., Prakash, N., Devi, P. and Viswakarma, A.K. 2006. Steps towards optimizing rice production in N. E. India. ICAR complex for NEH Region, Barapani.

Burton, G. W. 1952. Quantitative inheritance in grasses. Proc. 6th Int. Grassland Cong., **1**: 227-83.

Chakraborty, S., Das, P.K., Guha, B., Barman, B. and Sarmah, K.K. 2001. Coheritability, correlation and path analysis of yield components in boro rice. Oryza, **38(3&4)**: 99-101.

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

Chandra, R., Pradhan, S.K., Singh, S., Bose, L.K. and Singh, O.N. 2007. Multivariate Analysis in upland rice genotypes. World Journal of Agricultural Sciences 3(3): 295-300.

Chaturvedi, H.P. and Maurya, D.M. 2005. Genetic divergence analysis in rice (*Oryza sativa* L). Ad. Plant Sci. 18(I): 349-353.

Chauhan, J.S. 1996. Genotypic and Phenotypic correlation between grain yield and other associated characters in very early duration elite breeding cultures of rice. Oryza, 33: 26-30.

Chitra, S., Anand Kumar, C.R. and Vivekanandan, P. 2005. Correlation and path analyses in Assam rice collection (*Oryza sativa* L). The Andhra Agric. J., 52(3&4): 388- 391.

Comstock, R.E.; Robinson, H.F. and Harvey, P.H. 1949. A breeding procedure designed to make maximum use of both general and specific combining ability. Agron. J., 41: 360-364.

Coughtrey, A. and Mather, K. 1970. Interaction and gene association and dispersion in diallel crosses where gene frequencies are unequal. Heredity, 25: 79-88.

Daly, K. and Robson, D.S. 1969. Estimation of genetic parameters from hybrid derivative in Nicotiana. Genetics, Princeton, 62: 201-223.

Darwin, C. 1959. The origin of species by means of natural selection or the preservation of favored races in the struggle for life. Philosophical Library, New York.

Das, L.D.V., Shunmugavalli, N.and Veluswamy, P. 1995. Phenotypic stability in rice. Madras Agricultural Journal. 82(11): 569-571.

Das, R.., Borbora, T.K., Sarma, M.K. and Sarma, N.K. 2005. Genotypic variability for grain yield and flood tolerance in semi deep water rice of Assam. Oryza 42(4): 313-314.

Das, S. and Borah, S.P. 2008. Studies on the genetic components of variabilities for yield attributing and quality characters of some traditional rice varieties of *Nalbari* district of Assam. Indian Journal of Crop Science, 3(1)

De, R.N.; Rao, A.V.S.; Reddy, J.N.and Roy, J.K. 1990. Phenotypic stability in early upland rice. Crop Improvement. 17(2): 182:-183.

De, R.N., Reddy, J.N., Rao, A.V.S. and Mohanty, K.K. 1992. Genetic divergence in early rice under two situations. Indian J. Genet. 52: 225-229.

De, R.N., Reddy, J.N., Rao, A.V.S.; Ramakrishnayya, G. and Pande, K.L. 1992. Stability of rice yield under different lowland situations. Indian J. Genet. Plant Breed.,52(2): 139-143.

Deshpande, V.N. and Dalvi, V.V. 2006. Genotype x Environment interactions in hybrid rice. Oryza 43(4): 318-319.

Dewey, D. R. and Lu, K.H. 1959. Correlation and path coefficient analysis of components of crested wheat grass seed production. Agron. J., **57**: 515-18.

Dhaliwal, T.S. and Sharma, H.L. 1990. Combining ability and maternal effects for agronomic and grain characters in rice. Oryza, 27: 122-128.

Dushyantha Kumar, B.M. and Shadakshari, Y.G. 2007. Stability analysis for grain yield and yield components of red rice in mid lands of hill zone of Karnataka. Environment and Ecology, 25S (1): 207-211.

Eberhart, S.A. and Russell, W.A. 1966. Stability parameters for comparing varieties. Crop Sci., 6: 36-40.

Feyt, H. 1976. Etudecritique de l' analyse des croisements diallels au moyen de la simulation. Ann. Amelior. Plantes 26: 173-193.

Ganesan, K., Manuel, W.W. and Sundaram, T. 1995. Analysis of yield components and yield in rice. Oryza, *32:* 111-112.

Ganesan, K.N. 2001. Direct and indirect effect of yield components on grain yield of rice hybrids. Journal of Ecobiology, 13(1): 29-33.

Gomathinayagam, P., Natrajan, S. and Subramanian, M. 1990. Genetic variability in drought tolerant genotypes of rice. Oryza, 27: 328-330.

Goswami, R.K., Baruah, K.K., Pathak, P.K. and Pathak, A.K. 2000. Evaluation of rice varieties for yield attributes and milling quality. Journal of the Agricultural Science Society of North- East India, 13(1): 1-7.

Goswami, S.B. 2000. Yield potential of direct sown upland traditional rice cultivars in prehumid climate of West Bengal, India. Oryza **37(4)**: 326-330.

Griffing, B. 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian J. Biol. Sci., **9**: 463- 493.

Griffing, B. 1956 a. A generalized treatment of the use of diallel crosses in quantitative inheritance. Heredity, **10**: 31- 50.

Griffing, B. 1956 b. Concept of general and specific combining ability in relation to diallel crossing systems. Australian J. Biol. Sci., **9**: 463- 493.

Griffing, B. and Lindstrom, E.W. 1954. A study of the combining ability of corn hybrids having varying proportions of Corn Belt and non- Corn Belt germplasm. Agron. J., 46: 545-552.

Hari Ramakrishnan, S. H., Anandakumar, C. R., Saravanan, S. and Malini, N. 2006. Association Analysis of Some Yield Traits in Rice (*Oryza sativa L.*) Journal of Applied Sciences Research, 2(7): 402-404.

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

Hawkes, J.G. 1981. Germplasm collection, Preservation and use. In Plant Breeding II, ed. K.J. Frey, Iowa State Univ. Press, Iowa, pp. 57-84.

Hayman, B.I. 1954. The theory of analysis of diallel crosses. Genetics, 39: 789- 809.

Hayman, B.I. 1954a. The theory of analysis of diallel crosses. Genetics, 39: 789- 809.

Hayman, B.I. 1954b. The analysis of variance of a diallel table. Biometrics 10: 235-244.

Huxley, J. 1955. Morphism and evaluation. Heredity, 9: 1-52.

Ibrahim, S.M., Ramalingham, A. and Subramanian, M. 1990. Path analysis of rice grain yield under rain fed low lowland conditions. Intl. Rice Res. Newsletter, **15**: 1-11

Jamadagni, B.M. and Birari, S.P.1990. Phenotypic stability of grain yield in mid-late duration fine grain rice genotypes. *Journal Maharasthra Agricultural University*, 15(2): 235-236.

Jinks, J.L. 1954. The analysis of continuous variation in a diallel cross of Nicotiana rustica varieties. Genetics 39: 767-788.

Jinks, J.L. and Hayman, B.I. 1953. The analysis of diallel crosses. Maize Genetics Coop. Newsletter, 27: 48-54.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. Agron. J., **47**: 314-18.

Joshi, A.B. and Dhawan, N.L.1966. Genetic improvement of yield with special reference to self fertilizing crops. Indian J. Genet., 26: 101-113.

Joshi, A.B. 1979. Breeding methodology for autgamous crops. Indian J. Genet. Plant Breed., 39: 567-578.

Katre, N.B. and Jambhale, N.D. 1996. Combining ability for grain yield and related characters in rice. Oryza, 33: 21-25.

Kearsey, M.J. and Jinks, J. L. 1968. A general method of detecting additive, dominance and epistatic variation for material traits. J. Heredity, 23: 403-410.

Khedikar, V.P., Bharose, A.A., Sharma, D., Khedikar, Y.P. 2003. Studies on genetic parameters in scented rice genotypes. Journal of Soils & Crops, 13(2): 338-342.

Kishore, N.S., Ansari, N.A., Bavu, V.R., Rani, N.S., Rao, L.V.S. and Ravichandran 2007. Correlation and Path analysis in aromatic and non- aromatic rice genotypes. Agricultural Science Digest, 27(2): 122-124.

Kumar, A., Singh, N.K. and Chaudhory, V.K. 2004. Line x Tester analysis for grain yield and related characters in rice. Madras Agric. J. 91 (4-6): 211-214.

Kumar, M., Singh, N.K. and Kumar, A. 2005. Stability of yield in relation to components traits in rice under rainfed low land condition. Madras Agric. J. 92 (4-6): 193-199.

Lavanya, C. and Vijay Kumar, R. 2000. Heterosis and combining ability studies in hybrid rice. Madras Agricultural Journal, 86 (10/12): 630-631.

Lerner, I.M. 1958. The genotype in Mendelian populations. Proc. 9th Intl. Cong. Genet. pp. 124-128.

Lokprakash, R.; Shivashankar, G.; Mahadevappa, M.; Gowda, B.T.S. and Kulkarni, R.S. 1993. Genetic components of variation in rice. Indian J. Genet., 53(1): 4-7.

Mahalanobis P. C. 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci., India (B), 2: 49-55.

Madhavilatha, L. and Suneetha, Y. 2005. Studies on genetic divergence in rice germplasm lines. Madras Agric. J. 92 (1-3): 12-16.

Mahalanobis, P.C. 1928. A statistical study at Chinese head measurement. J. Asiatic Soc. Bengal, 25: 301-377.

Mankesh, K., Singh, N.K. and Kumar, A. 2005. Correlation and path coefficient in rice under rainfed lowland condition. Ann. Pl. Soil Res. 7(1): 95-98.

Manonmani, S. and Fazlullah Khan, A.K. 2004. Relationship between expression of heterosis and parental divergence in rice. Madras Agric. J. 91 (4-6): **202-205.**

Mather, K. and Jinks, J.L. 1982. Biometrical Genetics, 3rd ed. Cambridge University Press. London, N.Y.

Maurya, D.M. & Singh, D.P. 1977. Combining ability in rice for yield and fitness. Indian J. Agric. Sci., 47(**2**); 65-70.

Maurya, D.M. and Singh, D.P. 1977. Genetic divergence in rice. Indian J. Genet., 37(3): 395-402.

Mehla, I.S., Singh. A. and Panwar, D.V.S. 2000. Combining ability studies for yield and its components in rice hybrids involving wild abortive (WA) source of ems line. Agricultural Science Digest, 20(3): 146-149.

Mishra, S.B., Singh, U.K. and Sahu, S.P. 1994. Studies on genetic divergence in fine land races of rice in North Bihar. Annals of Agril. Res., 15: 27-30.

Mohanty, K.K., De, R.N. and Srivastava, D.P. 1995. Mode of gene action for some important characters in rice. Oryza, **32**: 5-9.

Moll, R.N., Sathawana, W.S. and Robinson, H.F. 1962. Heterosis and genetic diversity in varietal crosses of maize. Crop Sci., **2**: 197-198.

Murthy, B.R. and Anand, I.J. 1966. Combining ability and genetic diversity in some varieties of *Linum usitatissimum.* Indian J. Genet., **26**: **21-26**.

Murugan, S. and Ganesan, J. 2006. Combining ability studies in rice. J. Interacad. 10(1): 1-4.

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

Panwar, L.L. and Ali, M. 2007. Correlation and path analysis of yield and yield components in transplanted rice. Oryza, 44(2): 115-120.

Parray, G.A., Shikari, A.B., Ganai, M.A. and Sofi, N.A. 2008. Stability in elite local rice *(Oryza sativa* L.) genotypes under high altitude environments of Kashmir valley. Indian Journal of Crop Science, 3(1)

Patra, S.K., Sarkar, K.K. and Sahu, P. 2001. Genetic variability and correlation study in rice (Oryza sativa L.) for root and shoot characters. Journal of Interacad. 5(1): 25-28.

Pradhan, S.K., Bose, L.K. and Meher, J. 2006. Studies on gene action and combining ability analysis in basmati rice. Journal of Central European agriculture, 7(2): 267-272.

Rahaman, A., Acharya, B., Shukla, S.N. and Pande, K. 1997. Genetic divergence in lowland rice germplasm. Oryza, 34(3): 209-212.

Rahman, M.A., Patwary, A.K. and Miah, A.J. 1981. Combining ability in rice. Indian J. agric Sci., 51(8): 543-546.

Raju, Ch. S., Rao, M.V.B. & Sudarshanam, A. 2006. Heterosis and genetic studies on yield and associated physiological traits in rice *(Oryza sativa* L). Oryza, 43(4): 264-273.

Ram, J., Jain, O.P. and Murty, B.R. 1970. Stability of performance of some varieties and hybrid derivatives in rice under high yielding varieties programme. Indian J. Genet., 30: 187- 198.

Ramalingam, A., Maheswaran, M. and Subramanian, M. 1990. Stability analysis in short duration rice genotypes ((*Oryza sativa* L.). Oryza, 27: 325-327.

Ramakrishnan, Hari S., C.R. Anandakumar, C. R. Saravanan, S. and Malini, N. 2006. Association Analysis of Some Yield Traits in Rice (*Oryza sativa L.*). Journal of Applied Sciences Research, 2(7): 402-404.

Rao C. R. 1952. Advanced statistical methods in biometrical research. John Wiley and Sons Inc., New York.

Reddy, J.N. 1991. Genotype and Environment interaction in a short duration rice (*Oryza sativa* L). Indian Journal of Agricultural Sciences, 61(5): 320-321.

Reddy, J.N. and Choudhary, D. 1991. Stability for grain yield and its components in rice. *Oryza*, 28: 295-299

Reddy, J. N. 2002. Combining ability for grain yield and its components in lowland rice (Oryza sativa L.). Indian Journal of Genetics & Plant Breeding, 62(3): 251-252.

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

Roy, A. and Das, K. 2000. Genetic divergence of hill rice genotypes in Karbi Anglong district of Assam.Oryza, **37(4)**: 319-320.

Sadhukhan, R. and Chattopadhyay, P. 2006. Combining ability of yield and related metric characters in aromatic rice. J. Interacad. 10(4): 451-458.

Samuel, .J.K., Hill, J., Breese, E.L. and Davies, A. 1970. Assessing and predicting environmental response in *Lolium perenne*. J. Agric. Sci., Camb., 75: 1-9.

Saravanan, K., Ramya, B., Kumar, P., Satheesh and Sabesan, T. 2006. Combining ability for yield and quality characters in rice (*Oryza sativa* L) Oryza **43(4)**: 274-277.

Sarawgi, A. K., Rastogi, N. K., Verma, R. and Wade, L. J. 2000. Character association in improved shallow rainfed lowland rices. Oryza **37(4)**: 271-276.

Sarma, M.K. and Bhuyan, J. 2004. Genetic variability and divergence studies in Ahu rices (*Oryza sativa* L.) of Assam. Ad. Plant Sci., 17(I) 323-328.

Sawant, D.S. and Patil, S.L. 1995. Genetic variability and heritability in rice. Ann. Agric.Res. 16(1): 59-61.

Senguttuvel, P. and Bapu, J. R. K. 2007. Combining ability analysis for yield and yield components in rice. Ad. Plant Sci., 20(1): 59-62.

Shanmuganathan, M. and Ibrahim, S.M. 2005. Stability analysis for yield and its components in hybrid rice ('*Oryza sativa* L). Crop Res., **30(1):** 40-45.

Sharma J. R. 1998. Statistical and Biometrical Techniques in Plant Breeding. New Age International Publishers.

Sharma, R.K. and Koranne, K.D. 1995. Line x Tester analysis for yield and yield components in indica x japonica crosses of rice. Oryza, 32: 234- 238.

Sharma, R.K., Koranne, K.D. and Dube, S.D. 1995. Combining ability analysis for yield and yield components in rice. Oryza, 33: 18-20.

Sharma, S.K., Pandey, M.P., Dwivedi, D.K. and Shukla, S.K. 2006. Combining ability and Heterosis among elite bacterial blight resistant lines in rice (*Oryza sativa* L). Oryza **43**(4): 315-317.

Shiv Datt and Mani, S.C. 2003. Genetic divergence in elite genotypes of basmati rice (*Oryza sativa* L). Indian J. Genet., **63(1)**: 73-74.

Shukla, S.K. and Pandey, M.P. 2008. Combining ability and heterosis over environments for yield and yield components in two-line hybrids involving thermosensitive genie male sterile lines in rice (Oryza sativa L.). Plant Breeding, 127(1).

Siddiq, E.A. and Viraktamath, B.C. 2001. Rice in Breeding Field Crops (Ed. V.L.Chopra) pp 82, Oxford & IBH Publishing Co. Pvt. Ltd., New Delhi, India.

Singh, D.P. and Nanda, J.S. 1976. Combining ability and heritability in rice. Indian J. Genet., 36: 10-15.

Singh, J., Dey, K., Singh, S., and Shahi, J.P. 2005. Variability, heritability, genetic advance and genetic divergence in induced mutants of irrigated Basmati rice *(Oryza sativa L).* Oryza 42 (3): 210-213.

Singh, M., Kumar, K. and Singh, R.P. 2007. Study of coefficient of variation, heritability and genetic advance in hybrid rice. Oryza, **44(2):** 160-162.

Singh, M.; Singh, G.; Bhutia, D.T. and Awasthi, R.P. 1995. Genotype x Environment interaction in rice (*Oryza sativa* L). Indian Journal of Agricultural Sciences, 65(11): 832

Singh, N.K., Kumar, A.and Kumar, R. 2007. Combining ability for yield and yield components in rice. Oryza, **44**(2): 156-159.

Singh, N.K.; Sharma, V.K. and Jha, P.B. 1995. Genotype- environment interaction for yield related traits in indica rice. Journal of Research, Birsa Agricultural University, 7(2): 121-125.

Singh, P.K., Mishra, M.N., Hore, D.K. and Panwar, A.S. 2002. Genetic variability in some indigenous lowland rice genotypes of North East India. Indian Journal of Hill Farming **15(1)**: 113-115.

Singh, R.V., Maurya, D.M., Dwivedi, J.L. and Verma, O.P. 2005. Combining ability studies on yield and its components using CMS lines in rice (*Oryza sativa* L). Oryza **42(4)**: 306-309.

Singh, S.P. and Srivastava, M.N. 1982. Combining ability and heterosis in components of grain yield and panicle geometry in rice. Indian J. agric. Sci., 52: 271-277.

Sobita Devi, L., Dass, A., Pandey, M.K. and Kole, C.R. 2006. Depiction of genetic diversity in rice. Crop Res. **32(3)**: 459-461.

Sprague, G.F. and Tatum, L.A. 1942. General vs specific combining ability in single crosses of corn. J. Amer. Soc. Agron. 3: 923-932.

Srivastava, M.N. and Seshu, D.V. 1983. Combining ability for yield and associated characters in rice. Crop Sci., 23: 741-744.

Subramanium, S. and Rathinum, M. 1984. Genetic components of variation in rice. Madras Agric. J. 71(9): 561-565.

Suman, A., **Gouri Shankar V., Subba Rao L. V. and Shreedhar N. 2005.** Variability, heritability and genetic advance in rice (Oryza sativa L.). Crop Res. 30(2): 211-214.

Torres, E. A. and **Isaias O. Geraldi, I. O. 2007.** Partial diallel analysis of agronomic characters in rice (Oryza sativa L.). Genetics and Molecular Biology, 30, 3, 605-613.

Thakur, S.K. and Chaubey, S.K. 1999. Genetic variability and character association in F_2 population in rice. Agricultural Science Digest. 19(3): 187-190.

Vavilov, N.I. **1951**. Origin, variation, immunity and breeding of cultivated plants. Chronia Botanica, Waltham, Mass, USA (Translated from the Russion of Selected Writings).

Verma, O.P. 2003. Diallel analysis in rice (Oryza sativa L.) for physiological traits. Madras Agric. J. 90 (10-12): 637-642.

Verma, Y.S., Singh, H. and Pandey, M.P. 1995. Combining ability for yield and its components in rice. Oryza, 32: 1-5.

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

Zubair, M., Anwar, M., Haqqani, A.M. and Zahid, MA. 2002. Genotype-Environment interaction for grain yield in mash (*Vigna mungo* L. Happer. Asian J. Pl Sci., 1(2): 128-129.

APPENDIX

APPENDIX-A

METEOROLOGICAL – DATA (MAY – OCT.)

PERIOD	TEMPERATURE °C		RELATIVE HUMIDITY (RH)	RAINFALL
2003	Max.	Min.	(%)	(mm)
1/5 – 14/5	28.8	22.12	75.28	8.15
15/5 – 28/5	30.08	24.1	77.78	2.38
29/5 – 11/6	30.47	24.93	74.5	8.70
12/6–26/6	30.04	25.62	79.35	7.32
27/6 – 9/7	29.75	25.44	81.78	3.18
10/7 –23/7	29.78	25.15	82.71	9.32
24/7 – 6/8	27.88	25.58	83.57	3.42
7/8 –20/8	25.88	24.90	86.35	10.23
21/8 –3/9	28.03	24.93	84.28	10.11
3/9– 17/9	25.81	25.78	84.35	4.30
18/9– 1/10	24.91	24.05	84.28	9.02
2/10–15/10	26.04	22.7	85.57	13.90
16/10 – 29/10	23.19	21.92	85.78	1.05

APPENDIX-A

METEOROLOGICAL – DATA (MAY – OCT.)

PERIOD	TEMPERATURE °C		RELATIVE HUMIDITY (RH)	RAINFALL
2004	Max.	Min.	(%)	(mm)
1/5-14/5	31.28	29.65	84.50	0.66
15/5-28/5	29.22	27.22	82.42	4.17
29/5-11/6	31.10	29.32	83.57	5.85
12/6-25/6	30.50	28.07	79.92	8.53
26/6-9/7	31.00	28.80	69.57	11.92
10/7-23/7	28.55	27.00	72.85	10.37
24/7-6/8	31.27	29.54	65.50	17.00
7/8-20/8	31.18	28.84	66.00	9.25
21/8-3/9	31.50	30.28	65.57	3.36
4/9-17/9	29.39	28.37	70.21	11.82
18/9-1/10	30.10	28.61	64.57	11.22
2/10-15/10	28.00	26.44	65.57	10.35
16/10-29/10	28.54	26.46	55.64	0.50

APPENDIX-A

METEOROLOGICAL – DATA (MAY – OCT.)

PERIOD	TEMPERATURE °C		RELATIVE HUMIDITY (RH)	RAINFALL
2005	Max.	Min.	(%)	(mm)
1/5-14/5	28.45	19.62	81.50	3.44
15/5-28/5	27.95	21.71	81.14	9.55
29/5-11/6	31.02	23.80	82.64	0.77
12/6-25/6	30.38	25.69	79.57	9.36
26/6-9/7	31.00	26.07	79.50	10.64
10/7-23/7	29.98	25.32	79.85	3.35
24/7-6/8	30.48	26.07	82.50	8.54
7/8-20/8	30.08	25.62	82.71	21.40
21/8-3/9	30.44	24.60	80.28	1.35
4/9-17/9	31.04	23.22	84028	8.53
18/9-1/10	31.02	23.31	85.14	8.97
2/10-15/10	28.68	21.81	82.28	0.93
16/10-29/10	26.02	20.00	83.64	7.07

BIODATA

1. Name : HANUMAN PRASAD CHATURVEDI

2. Father's Name : Late Jagdamba Prasad Chaturvedi

3. Date of birth : 20-12-1968

4. Educational Qualification : M.Sc.(Ag), NET.

5. Work Experience : Working as Lecturer in Deptt. of Genetics & Plant Breeding, SASRD, Nagaland University since 2.09.2000

6. **Publications**

Papers Published

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

ii) Singh, S. Chaturvedi, H.P. and Singh, K.K. 2005. Variability and character association in Mustard and rapeseed. Nagaland University Research Journal Vol. 3: 21-23.

iii) Chaturvedi, H.P. and Maurya, D.M. 2007. Variability and Character association in various rice ecotypes. In: Composite Farming Practices and Economic Development (Amod Sharma & R.K.Singh eds.) Abhijit Publications, Delhi, pp 108-115.

Papers accepted

iv) Chaturvedi, H.P., Talukdar, P. and Changkija, S. 2009. Genetic Variability in local lowland rice (Oryza sativa L.) germplasm of Nagaland. Nagaland University Research Journal Vol. 6.

v) Chaturvedi, H.P., Talukdar, P. and Changkija, S. 2009. Genetic divergence in lowland rice (*Oryza sativa* L.) genotypes of Nagaland. Nagaland University Research Journal Vol. 6.