STABILITY ANALYSIS FOR GRAIN YIELD AND QUALITY TRAITS IN INDICA RICE (*ORYZA SATIVA* L.) LINES

THESIS

SUBMITTED TO
BIHAR AGRICULTURAL UNIVERSITY
SABOUR - 813210 (BHAGALPUR) BIHAR, INDIA

By
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(Registration Number - D/PBG /19/BAC/2013 -14)

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

DOCTOR OF PHILOSOPHY (AGRICULTURE)
in
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DEPARTMENT OF PLANT BREEDING AND GENETICS
BIHAR AGRICULTURAL COLLEGE, SABOUR
BIHAR AGRICULTURAL UNIVERSITY, SABOUR
BHAGALPUR, BIHAR (INDIA) – 813210

MAY 2018

Dedicated
to
My beloved parents

who Dedicated Their Entire life
for
My success & whose untiring efforts
materialized this Dream.

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It is further certified that the assistance and help or information received during the course of the investigation and preparation of the thesis have been duly acknowledged.

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Place: Sabour

Date: 30/04/18   (**Amit Kumar Mishra**)

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Problem of Research	:	Stability analysis for grain yield and quality traits in indica rice (*Oryza sativa* L.) lines
Research Scholar	:	Amit Kumar Mishra
Registration Number	:	D/PBG/19/BAC/2013-14
Major Advisor	:	Dr. P. K. Singh
Degree Programme	:	Ph.D (Ag.)
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Abstract

The present study was undertaken with the objective to determine the nature and magnitude of genetic variability, heritability and genetic advance, degree of association among yield and quality traits, direct and indirect effects, genetic diversity on the basis of morphological and molecular level, phenotypic stability among 36 advance indica rice lines including 3 checks for 21 yield and quality attributes. The trials were conducted in randomized complete block design (RCBD) with 3 replications and 4 environments (including control and reproductive stage drought stress conditions) during kharif 2014 and kharif 2015. The analysis of variance indicated highly significant differences for the majority of traits studied except few quality traits which indicated the significant differences among these rice lines. In congruence with the previous reports, phenotypic variance (VP) and phenotypic coefficient of variance (PCV) were higher than the genotypic variance (VG) and genotypic coefficient of variance (GCV) subsequently which indicated the influence of environment on the development of the characters. Moderate values (10-20) of GCV and PCV was observed for some traits hence; selection for these traits may be ambiguous if we adopted for its improvement. The higher magnitude of GCV was observed for number of spikelets per panicle, kernel elongation ratio and head rice

recovery while maximum PCV was observed for number of spikelets per panicle, harvest index and number of tillers per plant. High heritability along with higher magnitude of genetic advance as percent of mean was observed for the traits namely; number of spikelets per panicle, head rice recovery and kernel elongation ratio which revealed the preponderance of additive gene action in the inheritance and these traits could be improved through direct selection as GCV is also comparatively high for such traits. Positive or negative significant association with higher positive or negative direct effect were observed for the traits *viz;* plant height, biological yield per plant and harvest index which indicated the effectiveness of these traits for utilization in future rice breeding programmes. Genetic divergence among rice lines showed sufficient amount of genetic diversity hence, crossing among the divergent lines grouped in different clusters would produce superior hybrids and valuable transgressive segregants with higher genetic advance. The molecular diversity also validated the morphological differences among these rice lines and higher PIC values of the markers indicated their utility in explaining the genetic diversity. In case of phenotypic stability on the basis of stability parameters for grain yield per plant, IR 92521-24-5-1-3 was found stable line across all the environments and had maximum grain yield per plant, earliest in days to 50% flowering, better maturity duration, maximum number of spikelets per panicle, good head rice recovery, moderate L/B ratio and it also performed better than all three checks therefore, such line can be recommend to farmers or variety release proposal. Rice line IR 92545-53-4-1-3 was identified for unfavourable or poor environment while IR 92546-17-6-4-3 and IR 92546-17-6-4-4 lines was identified for rich or favourable environment.

Amit Kumar Mishra   **P. K. Singh**

(D/PBG/19/BAC/2013-14)   **(Chairman, Advisory Committee)**

LIST OF ABBREVIATIONS

Abbreviation	Description
%	: Percentage
^{0}C	: Degree Centigrade / Degree Celsius
^{0}E	: Degree East
^{0}N	: Degree North
^{0}S	: Degree South
^{0}W	: Degree West
abs	: Absorption
ANOVA	: Analysis of Variance
bi	: Regression Coefficient
bp	: Base Pair
bs	: Broad Sense
C14, C15	: Control 2014, Control 2015
CD	: Critical Difference
cM	: Centi-Morgan
cm	: Centimeter
CTAB	: Cetyl Trimethyl Ammonium Bromide
CV	: Coefficient of Variation
d.f.	: Degree of Freedom
DNA	: Deoxyribose Nucleic Acid
dNTPs	: Deoxy Nucleoside Triphosphates
dsm^{-1}	: Desi Simon per Meter
DSI	: Drought Susceptibility Index
E1, E2, E3, E4	: Environment (1- 4)
EC	: Electrical Conductivity
ECV	: Environmental Coefficient of Variation
EDTA	: Ethylene Diamine Tetraacetic Acid
EMS	: Error Mean Sum of Squares
Env.	: Environment
ESP	: Error Sum of Products
ESS	: Error Sum of Squares
et al.	: Co-workers
EtBr	: Ethidium Bromide
Fig.	: Figure
g	: Gram
G x E	: Genotype x Environment
GA	: Genetic Advance
GCV	: Genotypic Coefficient of Variation
h^2	: Heritability
IRRI	: International Rice Research Institute
Kbp	: Kilobasepair
kg	: Kilogram
Kg/ha	: Kilogram per Hectare
m	: Meter
M	: Molar
MAS	: Marker Assisted Selection

Max.	:	Maximum
Mg	:	Milligram
Min	:	Minute
Min.	:	Minimum
mM	:	Milimolar
mm	:	Millimeter
MSP (e)	:	Mean Sum of Products due to Error
MSP (t)	:	Mean Sum of Product due to Treatments
MSP	:	Mean Sum of Products
MSP(r)	:	Mean Sum of Products due to Replication
MSS	:	Mean Sum of Squares
N, P, K	:	Nitrogen, Phosphorus, Potassium
NRRI	:	National Rice Research Institute
PCA	:	Principal Component Analysis
PCR	:	Polymerase Chain Reaction
PCV	:	Phenotypic Coefficient of Variation
PIC	:	Polymorphic Information Content
q/ha	:	Quintal per Hectare
RCBD	:	Randomized Complete Block Design
r_g	:	Genotypic Correlation Coefficient
RM	:	Rice Microsatellites
r_p	:	Phenotypic Correlation Coefficient
RPM	:	Revolution per Minute
RSP	:	Replication Sum of Products
RSS	:	Replication Sum of Squares
S14, S15	:	Stress 2014, Stress 2015
S^2di	:	Deviation from Regression
SE (d)	:	Standard Error Difference
Sec.	:	Second
SoV	:	Source of Variation
SP	:	Sum of Products
SS	:	Sum of Squares
SSR	:	Simple Sequence Repeat
STRASA	:	Stress Tolerant Rice for Africa and South Asia
TAE	:	Tris Acetate EDTA
TE	:	Tris EDTA
Tris	:	Tris (hydroxymethyl) Amino Methane
TrSP	:	Treatment Sum of Products
TrSS	:	Treatment Sum of Squares
TSS	:	Total Sum of Squares
u	:	Micron
ug	:	Microgram
ul	:	Microlitre
UPGMA	:	Unweighted Pair Group Method with Arithmetic Mean
UV	:	Ultra Violet
V	:	Volt
VE	:	Environmental Variation
VG	:	Genotypic Variation
VP	:	Phenotypic Variation

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CHAPTER - 1
INTRODUCTION

Introduction:

Rice (*Oryza sativa L.*) belongs to the family *Poaceae* and genus *Oryza* with diploid chromosome no. of 2n = 24. After wheat it is the second most important and staple cereal crop for more than one third of the world population. More than ninety percent of the global rice is cultivated and consumed in Asia where sixty percent of the people on earth live. Rice and its derivatives accounts for 35 to 75% of the calories consumed by more than 3 billion Asians and about 20% of total calories supply worldwide comes from rice because it's the principle sources of nourishment (Anonymous 1, 2004). In India rice covers 43.95 million hectare area with production 106.54 million tones and productivity 2416 Kg/ha (2013 - 14, Anonymous 2. 2014 and Anonymous 3. 2015). In case of Bihar total area of rice 3232314 hectare, production 6802216 million tones and productivity 2104 Kg/ha (2015 - 16, Anonymous 4.). Throughout world, rice occupies 159.17 million hectare area with production 472.16 million tons and productivity 4.42 (Before milling process) metric tons/ha (2015 – 16, Anonymous 5. 2017). Stability to environmental fluctuations is essential for the stabilization of crop production over changed conditions and years because an ideal variety of any crop is one that has higher mean grain yield but a small degree of fluctuation in their performance when grown over dissimilar environmental conditions (Islam *et al*., 2014). An information on genotype x environment interaction leads to successful evaluation to identify stable lines which could be used on farmer's field. Grain yield is a complex polygenic trait which deeply influenced by environmental fluctuations hence, the selection for superior lines based on yield *per se* at a single location in a single year may not be more effective (Shrestha *et. al.,* 2012). Due to physical environmental constraints, all the rice growing environmental conditions were analyzed and have been reported on decline in rice grain production (Roy and Panwar 1994). The main efforts in crop technology, under poor or unfavourable environment should be grain yield stabilization, cost reduction, risk minimization and returns enhancement (Nanda and Tomar 1981). Grain yield is a basic need compared to quality then grain yield stability of performance is one of the most desirable properties of a genotype to be released as a variety for general cultivation. Phenotypic stability is a compound product of genetic yield potential to stress or altered conditions. Breeding lines that can be adapted throughout a reasonable huge geographical area and that show some degree of phenotypic stability over years is a major

challenging task faced by any plant breeders (Mosavi *et al.,* 2012). Quality of rice grain is not always easy to characterize because it depends on the consumers need and the intended end use for the grain. As countries of the globe reaches self-sufficiency in rice grain production then consumers demand for better and enhanced quality rice. Traditionally, the plant breeders have concentrated on breeding for high grain yields and pest resistance, but recently the trend has changed to incorporate preferred important quality characteristics that increase the total economic value of rice grain. The quality preference of rice varies across the world. Amylose content is one of the important chemical properties of rice because it is the indicator of stickiness or non stickiness of cooked rice. Above 25% amylose content in rice gives non sticky cooked rice while most preferable 20 - 25% amylose content in rice gives soft and comparatively sticky cooked rice. The stability of productivity for the characters of economic importance, like yield, is of interest to the plant breeder. The desirable genotypes may show low genotype – environment interaction for agriculturally important characters but, on other hand, may be more flexible for other characters. Such types of genotypes are said to be 'well buffered' as these can maintain their genotypic states in response to the fluctuating environmental conditions. This is also called genetic homeostasis (Lerner, 1954). According to Mather (1943), an adopted lines or population is that one which survives the selection pressure by exhibiting a better performance in survival and production than that of the standard. As the performance of the genotypes may or may not be similar in the different environments and they do interact with the environment as such the knowledge of G x E interaction and stability analysis helps in selecting the stable genotypes. Stability of the genotype, in the predictable and unpredictable environments is another important factor for realising maximum improvement of desired trait. Allard and Bradshow (1964) have classified the different types of predictable and unpredictable environments. Plaisted and Paterson (1959), Finlely and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968) and Freeman and Perkins (1971) have given various parametric models for the evaluation of genotypic and phenotypic stability of a variety. The joint regression analysis of Eberhart and Russell (1966) is widely used for selecting stable, high yielding cultivars. Eberhart and Russell (1966) improved the regression technique suggested by Finley and Wilkinson (1963) by adding another stability parameter (deviation from regression) to describe the performance of genotype over an array of environments. They pointed out that the regression of each cultivar

on environmental index was a function of the required deviation from the regression would provide useful estimates of stability. Genotype x environment interaction provide estimates to identify varieties stable over a wide range of environments and also helps to develop stable, high yielding genotypes through breeding programme. Genetic differences among the lines or genotypes were indicated for the regression of the genotypes on the environmental indices for the different traits with no any evidence of non-additive gene action. Correlation coefficient analysis is a statistical measure which is used to find out the nature, degree and diversion of relationship between two or more variables or association between various characters including grain yield and quality traits. Association analysis measures the mutual relationship between various morphological plant traits & quality traits and determines component traits on which selection can based for improvement of economically important characters. However the extent of relative contribution of a particular character to any dependent component cannot be judge from correlation studies this can be achieved by the path coefficient analysis (Johnson *et al., 1955* and Al - jibouri *et al., 1958).* The component analysis is helpful in partitioning the correlation coefficient at various characters. One of the component being the path coefficient that measure the direct effect of a predictor variable upon its response variable and the second component being the indirect effects of a predictor variable on the response variable through another predictor variable (Dewey and Lu, 1959) with the economically important characters (grain yield) into direct and indirect effects to provide the genuine contribution of an attributes and its influence through other traits. Genetic variability is the differences either in the genetic constitution among individuals of the plant population which grow in fluctuating environments. The existence of genetic variability in base population is essential for resistance to damaging factors and overall improvement of the crop including wider adoptability. Methods for estimation of phenotypic variances (VP), genotypic variance (VG) & environmental variance (VE) suggested by Lush, 1940 and further estimation of phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV) and environmental coefficients of variation (ECV) to calculate the amount of genetic variability was given by Burton, 1952. Heritability estimates along with genetic advance are usually more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et. al.,* 1955). The D^2 technique is based on multivariate analysis

which had been found to be a potent tool in quantifying the degree of divergence in germplasm and provides a measurement of relative contribution of different components on diversity both at intra and inter-cluster level. The rice lines drawn from widely different clusters are likely to produce more heterotic combinations with performance and wide variability may also appear in segregating generations. Moreover, the relative contribution of different yield components to total divergence helps in the identification of selection parameter to be used as criteria for the improvement in the yield. Molecular characterization of genetic diversity has an achievement in evolutionary biology. Information on the basis of genetic diversity within genotypes is essential for rational use of genetic resources. Statistical analysis for genetic divergance quantifies the genetical distance among the selected set of lines and reflects the relative contribution of each trait towards the total divergence. Genetic diversity can be evaluated with morphological traits, seed proteins, isozymes and DNA markers. Conventionally it is estimated by the D^2 analysis and with the help of molecular marker by the UPGMA software. Diversity based on pheonological and a morphological characters generally varies with environmental fluctuation while DNA markers have proved to be powerful tools in assessment of genetic variation. Thus, keeping in view the above facts, the present study was undertaken with thirty six rice genotypes to estimate the nature and magnitude of genetic divergence and to identify divergent stable rice genotypes with superiority in yield, quality and other component characters. This study would help in selection of more divergent parents for crossing programme to develop high yielding rice varieties in future and for identifying the genotypes with good yield potential and stable performance over different environments. Hence, the present investigation will be carried with the following objectives:

Objectives:

1. **To assess the character association among the traits and their direct & indirect effects towards yield.**
2. **To study the morphological and molecular diversity among *indica* rice lines using morphological and microsatellite (SSR) markers.**
3. **To study the stability of rice genotypes for yield and yield attributing traits along with quality traits.**

CHAPTER -2
REVIEW OF LITERATURE

Review of Literature:

The literature relevant to the present study has been reviewed briefly in this chapter under the following heads:

2.1 Genetic variability, Heritability (bs) and Genetic advance

2.2 Correlation coefficient analysis and Path coefficient analysis

2.3 Genetic divergence (D^2 Statistics)

2.4 Molecular diversity (SSR Markers)

2.5 Phenotypic stability or G x E interaction

2.1 Genetic variability, Heritability (bs) and Genetic advance:

Variability refers to the presence of differences among the individuals of plant population. It results due to differences either in the genetic constitution of the individual of a population or in the environment in which they have grown. The existence of variability is essential for resistance to biotic and abiotic factors as well as for wider adoptability. Variability is the most important characteristics and distinct feature of any population. A plant population with higher variability provides greater opportunity for improvement. Hence, it is essential to study and utilize the existing variability in the population. Johanson (1903) gave the basic idea of variability, while developing concept of pure line. Vavilov (1951) ascertained that greater the variability more is the chance of obtaining desirable types and proved it to be the basic fundamental for improvement of crop plant through selection. Variance is the amount of variation present among the members of a population. Fisher (1918) partitioned the total phenotypic variance into genotypic variance and environmental variance. He further divided the genotypic variance in to additive, dominance and epistatic effects. However, it is only the genetic variation which is heritable. Selection is also effective when there is significant amount of genetic variability among the individuals in a population. Hence insight into the magnitude of generic variability present in a population is of paramount importance to plant breeder for staring a breeding programme in any crop including rice. Fisher (1930) first presented the method to separate genotypic and phenotypic effects due to the genotypic and environmental factors. The extent of genotypic variability was presented

by him with appropriate statistical method and the value was expressed as a genotypic coefficient of variation. Lush (1940) suggested the method of estimation of phenotypic, genotypic and environmental variances, which further permits estimation of phenotypic coefficients of variation (PCV), genotypic coefficients of variation (GCV) and environmental coefficients of variation (ECV) (Burton, 1952). Heritability in broad sense refers to the genetic variation in the population in relation to the total observed variance. The efficiency of selection in improving a plant characters depend largely on the extent of transmissibility of the character. The presence of high magnitude of variability in the germplasm of breeding material 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. High transmissibility of a character is due to high genetic variation. Genetic advance refers to improvement of the selected plant over base population. The direct selection parameters like heritability broad sense (Burton and Devane, 1953) and genetic advance as percent of mean (Johnson *et al.*, 1955) are helpful in assessment of transmissibility of characters and role of environment.

Bidhan *et al.* (2001) evaluated 25 medium duration genotypes for eight traits and observed high genotypic and phenotypic variances for grain yield followed by number of filled grains per panicle. They recorded high heritability from 50% (grain yield per hill) to 90% (grain breadth). Genetic advance as percent of mean was highest for number of filled grains per panicle (70.34) followed by grain yield (68.72). Number of filled grains per panicle, 1000 grain weight, kernel length and kernel breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance in rice genotypes.

Da*s et al.* (2001) observed 29 boro rice genotypes and found high heritability with high genetic advance for plant height, number of panicles per plant, harvest index and grain yield per plant. High heritability and moderate to low genetic advance was observed for panicle length, filled grains per panicle and grain weight.

Yadav *et al.* (2002) observed genetic variability heritability and expected genetic advance which were estimated for length of grain, breadth of grain, L/B ratio, kernel elongation, gel consistency, amylase content and gelatinization in rice. The experimental

material included 150 rice germplasm categorized into three groups. *i.e.* long slender, medium slender and short slender. Maximum variability was recorded for test weight in long slender and medium slender groups and for amylase content in medium and short slender groups. Water updake, volume expansion ratio, kernel elongation and gel consistency appeared to be the useful traits in all the groups because high heritability and high genetic gain were recorded for these characters.

Satish *et al.* (2003) studied genetic variability, heritability and genetic advance in 200 scented rice genotypes including one non-scented check, Ratna for grain yield and its nine attributing characters. High GCV and PCV values were found for spikelets/panicle, number of grains/ panicle and grain yield/plant. High heritability along with high genetic advance was observed for number of spikelets/panicle, number of grains/panicle, grain yield/plant.

Singhara *et al.* (2003) evaluated 36 genotypes of rice grown under Kashmir conditions. Wide range of genetic variability was observed for all the characters studied. The PCV and GCV values were larger for number of secondary branches, panicle and grains borne primary branch and low for days to 50% flowering, panicle length, kernel length and kernel breadth. High heritability coupled with high genetic advance were recorded for test weight, grains per panicle and primary branch length indicating greater scope for yield improvement through selection.

Vivek *et al*. (2004) estimated genetic variability for 12 characters in 39 tropical japonica lines. The genotypes showed a wide range of variation for all the characters like grain yield per plant, biological yield per plant, number of tillers per plant and number of panicles per plant had high values of GCV and PCV. High heritability with high genetic advance observed for grain yield per plant, biological yield per plant, harvest index and number of grains per panicle.

Chaudhary *et al.* (2004) studied 54 aromatic rice accessions for genetic variability, heritability and genetic advance for 17 quality and yield traits viz., kernel length, kernel L/B ratio, kernel length after cooking, L/B ratio of cooked rice, elongation ratio, elongation index, alkali spreading value, head rice recovery, milling percentage, panicle

length, number of effective tillers per plant, number of fertile spikelets per panicle, spikelet density, spikelet sterility, biological yield, harvest index and grain yield per plant. GCV, PCV, heritability and genetic advance indicated that selection of genotypes may be carried out for kernel L/B ratio before cooking, L/B ratio of cooked rice and alkali spreading value for quality traits in all the genotypes. All the traits exhibited high heritability coupled with high genetic advance and genetic variability.

Mall *et al*. (2005) evaluated rice genotypes for genetic variation, heritability and genetic advance for yield and its components and suggested that high heritability coupled with high genetic advance observed for plant height, number of tillers per plant, number of panicles per plant, number of spikelet's per panicles and flag leaf length indicated the presence of additive gene action in the expression of these characters and direct selection may be highly effective.

Singh *et al.* (2006) conducted an experiment to study genetic variability in 32 rice genotypes for days to 50% flowering, days to maturity, plant height, number of panicles per plant, biological yield per plant, grain yield per plant and harvest index. A wide range of variation was recorded for all traits. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability and high genetic advance were recorded for plant height, indicating the predominance of additive gene action for this trait.

Karim *et al.* (2007) studied 41 aromatic rice genotypes and observed significant variation. VP was higher than VG for the characters like number of panicles per hill, number of primary branches, number of filled grains per panicle, spikelet sterility (%) and grain yield per hill, which indicating greater influence of the environment for expression of these characters while test weight and days to maturity showed least difference between VP and VG, which indicated additive gene action for expression of the characters. High GCV value was observed for test weight followed by spikelet sterility (%), grain yield per hill and number of filled grains per panicle, whereas days to maturity showed very low GCV. High heritability with high genetic advance as percent of mean (GAPM) was observed for test weight followed by spikelet sterility (%) and number of filled grains per panicle indicated that these characters were under additive

gene control and selection for improvement might be effective. Days to maturity showed high heritability but low genetic advance (GA) (%), which indicated that non additive gene effects were involved for phenotypic expression of this character.

Padmaja *et al.* (2008) recorded considerable amount of genetic variability in 150 rice genotypes for eleven characters. Heritability and genetic advance was recorded high for all the characters except days to 50% flowering and panicle length, which had moderate genetic advance along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Khan *et al.* (2009) conducted study on 25 rice genotypes and found highly significant differences for all the morphological traits under study. They reported low (days to 50% flowering, days to maturity, panicle length, grains per panicle) to moderate difference between VP and VG for the characters studied. They also observed that broad sense heritability was higher for morphological traits and ranged from 67.37 % to 98.24 %.

Nandan *et al.* (2010) observed a trail on rice genotypes and reported that high heritability with high genetic advance as percent of mean for number of effective tillers per plant, panicle weight, 1000 grain weight, kernel length before cooking and seed yield per plant.

Lal and Chauhan (2011) evaluated rice lines and reported high PCV than the corresponding GCV for all the characters studied indicating the influence of environment on the characters. They estimated high GCV for plant height, grains per panicle, L/B ratio, moderate for test weight, days to 50% flowering, grains/plant and days to maturity, whereas low GCV for panicle length. High genetic advance was estimated for plant height, number of panicles per plant, test weight and number of grains per panicle, however moderate for days to 50% flowering.

Seyoum *et al.* (2012) conducted field experiment using 14 rice genotypes and obtained highly significant variation for days to 50% flowering, plant height, panicle length, spikelets per panicle and 1000 grain weight. Higher GCV and PCV showed for days to 50% flowering, plant height, grains per panicle, spikelets per panicle, 1000 grain

weight and grain yield. High to medium estimates of heritability and genetic advance were estimated for plant height, days to 50% flowering, panicles per plant, spikelets per panicle, grains per panicle and thousand grains weight, indicating the role of additive gene action and good scope of selection using their phenotypic performance.

Tuwar *et al.* (2013) studied genetic components of variability of 29 genotypes of rice collected from diverse locations and such analysis revealed that plant height exhibited high estimates of GCV and PCV preceded by number of tillers per plant, effective tillers per plant, number of spikelets per panicle, number of grains per panicle and grain weight per panicle. Heritability was higher for days to 50% flowering followed by days to maturity, plant height and panicle length which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility. High heritability coupled with high genetic advance as per cent of mean was recorded for number of spikelets per panicle, number of grains per panicle and grain weight per panicle. These characters indicate the predominance of additive gene effects in their expression and would respond to selection effectively as they are least influenced by environment.

Karuppaiyan *et al.* (2013) evaluated 27 genotypes of lowland rice under organic conditions for 11 quantitative traits namely days to 50% flowering, days to maturity, plant height, number of tillers per plant, number of productive tillers per plant, panicle length, number of grains/panicle, grain length, grain breadth, L/B ratio and grain yield/ha. Under this study, found significant differences among the genotypes for all the traits studied. Heritability in broad sense was higher for all the traits, highest being recorded for plant height, grain breadth and L/B ratio. Number of tillers per plant, grain yield/ ha and L/B ratio were having high genetic advance coupled with high heritability.

Rai *et al.* (2014) conducted an experiment on 40 genotypes of rice to study variability, heritability and genetic advance and found significant differences among all the characters. High GCV and PCV observed for grain yield per plant and biological yield per plant. High heritability coupled with high genetic advance as percent mean reported for all the characters except days to 50% flowering, days to maturity, number of tillers per plant, number of panicle per plant and plant height.

Rao *et al*. (2014) evaluated 49 rice genotypes and reported existence of significant differences among genotypes for all characters studied in analysis of variance. The magnitude of PCV and GCV was moderate to high for number of grains per panicle, test weight and grain yield. High heritability coupled with high genetic advance as per cent of mean was observed for test weight and grain yield indicating the role of additive gene in expressing these traits.

Sarwar *et al.* (2015) reported significant deviation for all the characters studied and indicated the existence of variation among the genotypes. The PCV values were slightly higher than the respective GCV values for all the characters except unfilled grains per panicle indicating that the characters were less influenced by the environment. Total tillers per plant, effective tillers per plant, filled grains per panicle, unfilled grains per panicle and yield per plant showed high heritability coupled with high genetic advance as percentage of mean which indicated the preponderance of additive gene action. High heritability along with low genetic advance as percentage of mean was found for plant height, days to 50% flowering, panicle length, days to maturity and 1000 grain weight which indicated the non-additive gene action for expression of these characters.

Senapati and Kumar (2015) reported significant differences among 24 genotypes against all the characters studied except panicle weight, grain length, grain breadth and grain L/B ratio. Magnitude of PCV was higher than GCV for all the characters. High PCV and GCV was observed for grain yield per plant, 1000 grain weight, L/B ratio, grain breadth. High heritability coupled with moderate to high genetic advance as percent of mean was recorded for plant height, panicle weight, grain length, grain L/B ratio and 1000 grain weight.

Karim *et al*. (2016) evaluated 25 rice genotypes (local and high yielding varieties) to assess their variability, heritability and genetic advance for yield and yield contributing characters of rice varieties. The analysis of variance indicated the existence of highly significant differences among genotypes for all the characters studied. Laxmi Bilash, Beti, BR22/Kiron, BRRI dhan34, BR25/Nayapajam, Madhu Sail, Nirbhoe, BRRI dhan41, Lati Sail and BR4/Brrisail were found promising in respect of yield and other yield contributing characters. Based upon variability and heritability estimates, it could

be concluded that improvement by direct selection is possible for important traits like days to 50% flowering, weight of grain/panicle, 1000-grain weight, grain yield/plot, grain L/B ratio, plant height and days to maturity.

Chandramohan *et al.* (2016) studied analysis of variance among 44 genotypes of rice which revealed presence of significant variability for all the traits except for number of effective bearing tillers per plant. Higher magnitude of PCV and GCV were recorded for all the characters studied. Additive gene action was predominant for the traits, number of grains per panicle and 1000 grain weight.

Nayak *et al*. (2016) evaluated 25 rice accessions to assess their genetic variability, heritability and genetic advance for grain yield and yield traits. The high estimate of GCV & PCV, heritability and genetic advance were observed for effective tillers per plant, filled grains per panicle, total grains per panicle and grain yield per plant. High heritability with high genetic advance were observed for days to maturity, plant height, filled grain per plant and test weight.

Bhatt *et al.* (2016) studied 8 local rice germplasm during kharif 2015 in RCBD with 3 replications and represented genetic variability for yield and its attributing characters in irrigated condition. Wide range of variation was observed for all the quantitative traits under study indicating enough scope for bringing about improvement in desirable direction for hybridization and study also suggests that there is high contribution of positive and negative genes among the genotypes exhibited higher and lower values for these characters. PCV was highest for grains yield per plant, number of fertile grain per panicle, flag leaf length, L/B ratio and test weight. High heritability values were also recorded for test weight, plant height at maturity and vegetative plant height. Estimate of genetic advance was highest for number of grains per panicle and plant height. Genetic advance as percent of mean was however, highest for number of grains per panicle and grain yield per plant.

Sran *et al.* (2017) observed variability, heritability and genetic advance in rice by evaluating 43 genotypes for yield, yield attributing and quality characters. ANOVA revealed that significant differences for all the characters. Phenotypic variance was slightly higher than the genotypic variance for all the characters indicating the minimal environmental influence on these traits. Among all the characters, high GCV and PCV

were observed for gelatinization temperature followed by grains per panicle and grain yield per plant. Highest heritability was recorded for days to 50 % flowering, plant height, panicle length, spikelets/panicle, grains/panicle, spikelet fertility, 1000-grain weight, grain yield/plant, grain length, grain breadth, L:B ratio, protein content, amylose content, gelatinization temperature and gel consistency which connot that these characters have high genetic variability and transmissibility. In contrast, low genetic advance was obtained for all the characters under study. High heritability with low genetic advance indicated the presence of non-additive gene action.

Sahu *et al.* (2017) studied 71 rice genotypes for genetic variability under irrigated and rainfed conditions. The PCV values were greater than GCV reveal little influence of environment in character expression. Analysis of variance was found to be significant for most of the traits, indicating that there is existence of genetic variability for these traits. High values of heritability along with genetic advance were observed for biological yield and harvest index.

Kalyan *et al.* (2017) studied genetic variability, heritability and genetic advance for 9 characters in 70 genotypes of rice. The analysis of variance revealed that there were highly significant differences for all the characters among the genotypes. The estimates of GCV and PCV were high for all the characters except days to 50% flowering and days to maturity. Heritability and genetic advance were high for all the characters except days to 50% flowering and Days to maturity, which had moderate genetic advance along with high heritability indicating the involvement of additive and non-additive type of gene action respectively in controlling these characters.

2.2 Correlation coefficient analysis and Path coefficient analysis:

Knowledge about association of yield with each other component will be useful in its improvement and correlation studies indicate the magnitude of association between any two characters which form the basis for determining selection index and thereby helping the plant breeder for crop improvement. If the numbers of characters are more, it is essential to measure their contribution with the observed character. It was noticed that association of economically important quantitative characters which are statistically determined by correlation coefficient has been quite helpful as a basis of selection. Various plant breeders tried to explain correlation among different quantitative traits in

India and abroad in different crop plants including rice. The term path coefficient was coined by Sewell Wright (1921) to denote the direct influence of variable (cause) upon another variable (effect) as measured by the standard deviation remaining in the effect after the influence of all other possible paths are eliminated except that of cause. Li (1956) presented a detail account of both basic and applied aspects of path coefficient analysis. The path being free of physical unit is directional and may be greater or less than unit. It is exclusively been used to analyse the real contribution of individual complex component in building up the ultimate complex and product like grain yield. Path coefficient analysis is a standardized partial regression coefficient, which splits the correlation coefficient into measure of direct and indirect effects and also measures the direct and indirect contribution of various independent variables towards the dependent variable. Dewey and Lu (1959) applied the path coefficient technique for the first time in crested wheat grass to establish the importance of fertility, seed size, spikelets per spike and size of plants as determinates of yield despite their association with yield was low in simple correlation analysis and demonstrated the utility or path coefficient analysis in plant selection and since then its applications has been extended to almost every crop.

Nayak *et al.* (2001) performed a trial on rice and observed positive significant correlation between the panicle length and grain yield per plant and reported that number of productive tillers, grains per panicle, 1000 grain weight had positive direct effect on grain yield while days to 50% flowering exhibited positive indirect effect on grain yield through number of grains per panicle.

Madhavilatha *et al.* (2002) reported positive significant correlation between the panicle length, number of grains per panicle and grain yield per plant, and also observed positive significant association of plant height with number of panicles per plant. They estimated high direct effect for number of effective tillers per plant, plant height and harvest index on grain yield per plant. High indirect effect of the different yield components and quality traits were also noticed through plant height and harvest index indicating the need for emphasis on these traits during selection for yield improvement.

Khatun *et al.* (2003) observed 16 aromatic rice varieties for simple correlation based on the mean values obtained to determine the extent and strength of the possible pair of

13 quality characters and reported strong and positive correlation of kernel length, length breath ratio, head rice recovery, gel consistency and expanded volume with different quality characters indicated that these are prime grain quality characters for improvement of genotypes. As reported by Chouhan *et al.* (1987), Deosarkar and Nerkar (1994) and Christopher *et al.* (1999) kernel length exhibited a highly significant positive correlation with L/B ratio in the separate investigations. Sood and siddiqui (1980) showed highly significantly but negative association of kernel breadth with L/B ratio.

Chaudhary and Motiramani (2003) evaluated 54 traditional aromatic rice accessions for association study among 19 grain quality and yield attributes and found that grain yield per plant showed significant positive correlation with effective tillers per plant, spikelet density and biological yield per plant. Path analysis indicated a greater contribution of effective tillers per plant, spikelet density and biological yield per plant towards grain yield.

Patil and Sarawgi (2005) evaluated 128 aromatic rice accessions and found that grain yield had a positive and significant correlation with number of days to 50% flowering, plant height, number of productive tillers per plant, and number of filled grains per panicle at the genetic and phenotypic level. In path analysis 1000-grain weight had the greatest positive direct effect on grain yield, followed by number of productive tillers per plant, number of filled grains per panicle, and number of days to 50% flowering. However, 1000-grain weight had no significant correlation with grain yield per plant due to its negative indirect effect on grain yield per plant through the number of filled grains per panicle and plant height. Thus, direct selection for number of productive tillers per plant, number of filled grains per panicle, and number of days to 50% flowering would likely be effective in increasing grain yield per plant.

De *et al*. (2005) studied correlation and path analysis for ten characters on 14 diverse aromatic rice cultivars and reported that only the number of panicles per hill had a significant ($P<0.01$) positive correlation with grain yield per plant via the indirect effect of kernel length and 1000-grain weight, because its direct effect was very low. High positive direct effect of kernel breadth and protein content on grain yield was evidently nullified by high negative indirect effect of kernel length and plant height, respectively.

Monalisha *et al.* (2006) evaluated 20 low land rice cultivars and reported high positive direct effect with significant positive association of effective tillers per plant and high density grains per panicle with grain yield per plant.

Sandhyakishore *et al*. (2007) studied 70 rice genotypes included aromatic and non-aromatic lines and found that genotypic correlation coefficients were higher than phenotypic correlation coefficients for most of the characters. Character association analysis revealed significantly positive association of grain yield per plant with number of grains per panicle and 1000-grain weight. Path coefficient analysis revealed that 1000-grain weight, number of grains per panicle, productive tillers per plant, days to 50% flowering and plant height had positive direct effects on grain yield, hence due weightage should be given to these characters during selection for future breeding programmes.

Kole *et al.* (2008) evaluated some rice lines and found positive and significant association of grain yield with plant height, number of panicles per plant, straw weight and harvest index at both genotypic and phenotypic level. They also observed that panicle number had the highest positive direct effect followed by grain numbers per panicle, test weight, plant height, days to flowering and straw weight towards grain yield.

Khan *et al.* (2009) conducted a trial on rice genotypes and observed positive significant association of number of grains per panicle with grain yield per plant in rice and also reported that filled grains per panicle had positive direct effect on grain yield per plant.

Satish *et al.* (2009) performed an experiment on rice and reported positive association of grain yield per plant with number of productive tillers per plant, 1000-grain weight, panicle length and number of grains per panicle and had high positive direct effect on grain yield via number of grains per panicle, days to 50 percent flowering, 1000-grain weight and number of productive tillers per plant.

Nandan *et al.* (2010) observed rice genotypes and reported strong positive association of yield with days to 50 % flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility. The number of grains per

panicle had maximum direct effect on grain yield per plant followed by kernel length after cooking (KLAC), days to 50 % flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking (KBAC).

Ekka *et al.* (2011) studied path coefficient analysis in 96 rice accessions of Chhattisgarh and reported that direct selection for days to 50% flowering, 100 seed weight, panicle length, leaf length and milling percentage would be effective for increasing grain yield.

Seyoum *et al.* (2012) studied rice lines and found that grains per panicle had maximum positive direct effect with grain yield which revealed that for increasing rice yield in upland ecology, a genotype should possess more number of grains/panicles, tillers per plant and panicle/plant, high spikelet fertility and large panicle size.

Vanisree *et al.* (2013) evaluated 12 yield and quality traits among 21 rice genotypes and found grain yield per plant exhibited highly significant and positive correlation with days to 50% flowering, plant height, panicle length, productive tillers per plant, panicle density, filled grains per panicle and maximum positive direct effect of plant height, productive tillers per plant, filled grains per panicle, kernel length, kernel breadth on grain yield per plant.

Singh *et al.* (2013) studied some rice genotypes and found positive and significant association was recorded by days to 50% flowering, days to maturity, leaf length, leaf width, filled grains per panicle and total number of grains per panicle among themselves and also with grain yield per plant at genotypic and phenotypic levels. Days to maturity, plant height, number of filled grains per panicle and test weight exhibited positive direct effect at both genotypic and phenotypic levels.

Rai *et al.* (2014) conducted an experiment on 40 genotypes of rice to study path coefficient analysis and concluded that, biological yield per plant and harvest index exhibited maximum positive direct effect on grain yield seems to be primary yield contributing characters and could be relied upon for selection of genotypes to improve genetic yield potential of rice.

Rashid *et al.* (2014) examined 20 diverse rice cultivars for correlation study and found that days to heading, days to maturity, number of productive tillers, 1000-grain

weight had highly significant positive correlation with grain yield per plant whereas, flag leaf area, plant height and panicle length showed highly significant negative correlation with grain yield per plant. Number of grains per panicle was non - significantly positively correlated with grain yield per plant.

Mishra *et al.* (2015) studied interrelationship and cause-effect analysis of grain yield and its component traits using 40 rice accessions. Grain yield per plant was found significant and positively correlated with biological yield per plant, number of fertile tillers per plant, number of spikelet's per panicle, test weight, panicle length and days to maturity at both genotypic and phenotypic level respectively. Phenotypic path analysis revealed that the grain yield per plant had a direct positive effect on biological yield per plant followed by harvest index, number of fertile tiller per plant and days to 50% flowering. Genotypic path revealed that the biological yield per plant was the major contributor of grain yield per plant followed by harvest index, number of fertile tillers per plant, and days to 50% flowering.

Meena *et al.* (2016) studied interrelationship study in 38 rice genotypes. Character association of the yield attributing traits revealed significantly positive association of grain yield per plant with days to 50 per cent flowering followed by number of productive tillers per plant, number of filled grains per panicle, kernel length and kernel breadth. Hence, selection for these traits can improve yield. Path coefficient analysis revealed that number of productive tillers per plant exerted the highest positive direct effect on grain yield followed by number of filled grains per panicle, kernel breath, L/B ratio, days to 50 % flowering, plant height, 1000-grain weight. Among these characters, number of productive tillers per plant possessed both positive association and high direct effects. Therefore, it is suggested that preference should be given to these characters in the selection programme to isolate superior lines with genetic potentiality for higher yield in rice genotypes.

Premkumar *et al.* (2016) studied correlation and path analysis using 43 rice genotypes including thirty hybrids and thirteen parents for grain quality traits on grain yield. The correlation analysis indicated that grain yield was significantly associated with kernel breadth, breadth wise expansion ratio and water uptake at genotypic level. Path-coefficient analysis revealed linear elongation ratio had the highest positive direct

effect on grain yield followed by breadth wise expansion ratio, gel consistency, kernel L/B ratio and alkali spreading value. This study revealed that genetic improvement of grain quality in rice is admissible by selecting characters having high positive correlation and positive direct effect on grain yield.

Priya *et al.* (2017) studied characters association and direct and indirect effect of yield components traits of grain yield in rice for 11 characters *viz.* days to 50% flowering, days to maturity, productive tillers per plant, plant height, panicle length, grains per panicle, test weight, kernel length, kernel breadth, L/B ratio, grain yield per plant and found that productive tillers per plant, number of grains per panicle, test weight, panicle length, days to maturity, kernel breadth, plant height, days to 50% flowering, kernel length posses significant positive association with grain yield per plant at phenotypic level. Path analysis revealed that kernel breadth, L/B ratio, productive tillers per plant, grains per panicle, test weight, days to maturity, days to 50% flowering and plant height showed true relationship with grain yield per plant by establishing significant positive association and highly positive direct effect.

Sahu *et al.* (2017) evaluated 71 rice genotypes for correlation and path analysis under irrigated and rainfed condition and found grain yield was highly significantly and positively correlated with days to 50 % flowering, biological yield, harvest index, panicle length, flag leaf width and second leaf width under irrigated condition, whereas under rainfed condition panicle length and harvest index showed significant and positive correlation with grain yield. Biological yield and harvest index had positive direct effect on grain yield; hence selection of these two traits for grain yield will be effective.

2.3 Genetic divergence (D^2 Statistics):

The expression "divergence in character" was used by Darwin (1859) for the variation in genera and species. Other term "morphism" was used by Huxley (1955) for genetic diversity implying "genetic polymorphism" which means the coexistence of distant genetic forms in population. Early workers regarded the geographical isolation as a reasonable index of genetic diversity (Vavilov, 1926; Joshi and Dhawan, 1966). The varieties, which come from different localities are usually presumed to diverse and are utilized in hybridization programme. However, some workers emphasized that there is no parallelism in geographical distribution and genetic diversity (Maurya and Singh,

1977 and De *et al*., 1992 in rice) advocating that varieties with the same geographical origin could have undergone changes under selection pressure. Thus, for estimation of variation within the germplasm divergence study in the form of classification into different homogenous groups is an important practice. Multivariate analysis based on Mahalanobis-D^2 statistics and canonical variant analysis has been considered as an important tool in quantifying the genetic divergence in different crops (Rao, 1952). A number of scientists (Griffing and Lindstrom 1954, Mall *et. al.* 1962, Arunachalam 1981) have emphasized the importance of genetic diversity in plant breeding for obtaining broad spectrum of desirable variability in segregating generations. Genetic diversity has been suggested to moderate effectiveness in selecting parental lines to produce heterotic high yielding progenies. The available diversity in the germplasm serve as an insurance against unknown future needs. Genetic diversity is one of the important tools to quantity genetic variability in both cross and self pollinated crops (Adhunix Dhaner chas 2003). Precise information on the nature and degree of genetic divergence of the parents is the prerequisite of variety development programme. The quantization of genetic diversity biometrical procedures has made it possible to choose genetically diverge parents for successfully hybridization programme (Anderson 1957 and Rao 1952). It is the common view of the researchers that the more diversity of parents, the greater chance of obtaining high heterosis and broad spectrum of variability in segregating generations. Zaman (2005) studied the diversity in rice using Mahalanabis D^2 analysis and identified three distant and closest pair, and found the character days to 50% flowering exhibition the largest contribution to total divergence. Mahalanabis D^2 determined the distance between any two varieties based on common characters measured on each variety. Contribution of each character towards divergence was calculated taking under consideration of all combinations. Some of the earlier reports on genetic divergence in rice have been reviewed below:

Hegde and Patil (2000) assessed genetic divergence in 40 genotypes of rainfed rice using D^2 statistics. The cultivars fell into 7 clusters and the highest contributing characters to D^2 values were number of spikelets per panicle, photosynthetic rate and 1000-grain weight.

Rather *et al.* (2001) studied genetic divergence in 56 rice cultivars for 12 characters. Genotypes grouped in 6 clusters and grouping of cultivars from various regions into the same cluster indicated that the geographical distribution did not necessarily suggest genetic divergence.

Reddy *et al.* (2002) applied D^2 statistics to 36 lowland rice genotypes and found significant varietal differences were observed for all 13 characters studied. The genotypes were grouped into 12 clusters. Among the different characters, 1000-grain weight, grain length, number of grains per panicle and plant height played a major role in the formation of clusters.

Babu *et al.* (2003) worked out genetic diversity among 33 rice cultivars and grouped them into 10 clusters using Mahalanobis D^2 statistics based on genetic distance. Among the eight different characters, the trait days to 50% flowering contributed maximum towards genetic diversity (51.89%), followed by plant height (22.92%) and panicle length (9.47%).

Chauhan and Singh (2003) studied genetic divergence in 45 elite rainfed upland rice cultivars. Based on divergence, 45 genotypes were grouped into 11 clusters. The D^2 values among the genotypes ranged from 1.69 (between CR 544-1-1 and CR 544-1-6) to 257.8 (between CR 636-7 and Sattari).

Das *et al.* (2004) studied genetic divergence in 50 landraces of rice and reported genotypes were grouped in 10 clusters. Days to 50% flowering, grain yield per plant, kernel length, kernel breadth and 100-kernel weight were identified as potential characters that can be used as parameters while selecting diverse parents in the hybridization programme for yield and quality improvement.

Nayak *et al.* (2004) studied nature and magnitude of genetic divergence among 200 genotypes of scented rice including one non-scented check using Mahalanobis D^2 statistics for 10 quantitative characters. On the basis of D^2 values, the genotypes were grouped into 10 clusters. Grain length and days to 50% flowering played important role in the formation of clusters. Among the different characters, panicle length contributed minimum (0.7%) to total divergence.

Roy *et al.* (2004) evaluated 35 aman rice cultivars for 10 traits (number of panicles per plant, panicle length, number of primary branches per panicle, number of secondary branches per panicle, number of filled grains per panicle, number of unfilled grains per panicle, 1000-grain weight, panicle weight, grain yield per plant and sterility) over 2 environments. The cultivars were grouped into 5 clusters. The greatest genetic divergence was observed between clusters II and IV. As clusters II (Nagra, Khayersali, CRM-30 and Langulmutha) and IV (Randhunipagal) showed the greatest divergence and higher mean values for characters contributing to genetic divergence, the cultivars from both clusters may be used in hybridization programmes to obtain good recombinants.

Bhutia *et al.* (2005) studied 41 high yielding and local genotypes of rice for genetic divergence using Mahalanobis D^2 statistics. The genotypes were grouped into six clusters and Cluster IV showed the maximum genetic distance from cluster VI followed by its distance from cluster V. The desirable yield and quality characteristics were distributed mainly in clusters III, IV and V. The genotypes included in clusters III and IV may be used as parents in hybridization programme to improve yield.

Suman *et al.* (2005) evaluated 114 rice genotypes for 16 quantitative characters to quantify the genetic diversity existing among them. The genotypes fell into 10 clusters. Among the 16 quantitative characters studied, Cluster X had the maximum number of spikelet per panicle. Cluster III exhibited the lowest mean for plant height, days to 50% flowering, panicle length. The genotypes from cluster III and X which had high and low cluster means for majority of the characters, were recommended as parents for hybridization.

Awasthi *et al.* (2005) determine the genetic divergence of 21 Indian aromatic rice genotypes. A total of 21 aromatic rice genotypes were grouped into 6 clusters for different characters. The genotypes of one cluster indicated overall genetic similarity among them. The inter cluster distance ranged from 0.00 for clusters IV, V and VI to 40.21 for cluster III. The inter cluster distance was observed to be highest between clusters II and III, indicating that the genotypes of these 2 clusters were genetically more diverse. The number of grains per panicle, grain yield per plant, days to 50% flowering,

leaf length and leaf width showed high percent contribution towards total genetic divergence.

Sood *et al.* (2005) studied genetic divergence in 43 rice genotypes for 10 yield contributing traits. Genotypes were grouped in 9 clusters and grouping of genotypes in different clusters indicated the existing of significant amount of variability among the genotypes for the traits studied. Cluster IV showed highest intra - cluster distance.

Devi *et al*. (2006) evaluated 54 rice cultivars for genetic diversity and found the genotypes were grouped into 9 clusters. Cluster VI recorded high mean values for plant height (140.33 cm), flag leaf length (48.11 cm) and flag leaf width (2.10 cm). Plant height contributed the most to genetic divergence (40.16%), followed by flag leaf width (20.12%), yield per plant (15.79%).

Mundhe *et al*. (2006) studied genetic diversity of 39 mid-late rice genotypes from India and IRRI, Manila, Philippines. Based on D^2 values, the genotypes were grouped into 7 clusters. Intra-cluster distance was maximum in cluster III followed by cluster II and cluster I. Inter-cluster distance was maximum between cluster V and VII followed by cluster III and V, and cluster II and V. The genotypes from cluster I had better average for plant height, number of spikelet's per panicle, number of filled spikelet's per panicle, 1000 grain weight, yield per plant, kernel breadth and protein content, while cluster V had better average for number of tillers per plant, number of fertile tillers per plant, days to 50% flowering, yield per plant.

Sarkar *et al.* (2006) carried out assessment of genetic divergence among 46 rice genotypes. The genotypes were grouped into seven clusters. Cluster IV showed highest inter-cluster distance from Cluster VI followed by Cluster III and Cluster VII. Highest intra-cluster distance was observed in Cluster V and lowest in Cluster I. The desirable yield and its contributing traits were distributed mainly in Cluster III followed by Cluster VII and Cluster I. The genotypes within Cluster III, VII and I may be used as parents in hybridization program to develop high yielding line.

Chandra *et al*. (2007) assessed genetic divergence among 49 genotypes of non-scented rice including three checks for seven quantitative characters. The significant

varietal difference was observed for all the characters studied on the basis of D^2 values. The genotypes were grouped into 8 clusters. Characters like kernel length, kernel breadth, days to 50% flowering and plant height had more contribution to total divergence.

Sandhyakishore *et al*. (2007) studied genetic divergence for different yield and quality attributing traits in 70 rice genotypes. The genotypes were grouped into 9 different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like water uptake, gel consistency and head rice recovery percentage contributed maximum towards genetic diversity. The maximum inter-cluster distance was recorded between cluster VII and cluster VIII.

Sarawgi and Bisne (2007) studied genetic divergence in 81 scented rice and genotypes were grouped into nine clusters. The genotypes from cluster II having desired mean for characters like hulling %, milling %, head rice recovery and panicle length. Cluster VII had high value for kernel length & L/B ratio and cluster V had low value for days to 50% flowering but highest value for grain yield kilogram per hectare.

Kumar *et al*. (2008) studied genetic divergence among 30 rice genotypes using Mahalanobis D^2 statistic for 12 quantitative traits. These genotypes were grouped into eight clusters. The clustering pattern of genotypes did not follow the geographic origin. The inter-cluster distance was highest between clusters V and VI. This indicates that the genotypes included in these clusters are having broad spectrum of genetic diversity and could be used in hybridization programme and are likely to exhibit high heterosis and possibility of throwing transgressive segregants in subsequent generations.

Sharma *et al.* (2008) studied genetic divergence under irrigated situation using D^2 statistics in a set of 100 aromatic rice genotypes. Genotypes were grouped into nine clusters and it was observed that there was no association between the geographical distribution and genetic diversity. Based on clustering pattern, the maximum genetic distance among genotypes existed between clusters II, VII and IX. The clusters II, VII and IX were ascertained outstanding on the basis of higher cluster means of almost all

component characters. The most divergent clusters have been isolated as VII containing Khao Jao Hawn, Basmati Sufaid-187, KCN-80152, Abor Bora and Hara and cluster IX having Gam Poon. It is expected that the crosses involving the parents from these clusters may exhibit high heterosis for desirable traits as grain yield.

Arivoli *et al.* (2009) reported 23 rice genotypes were grouped into 11 clusters and results revealed the presence of morphological differences between the genotypes. The clusters between V, IX and IV, IX were divergent clusters. Hence, genotypes in clusters IX, IV and V could be crossed among themselves to produce wider segregation among the progenies. Cluster III showed high mean for grain yield per plant. Cluster X showed low mean for earliness. The characters total number of grains per panicle, number of filled grain per panicle and plant height contributed maximum towards total genetic divergence.

Roy *et al.* (2009) evaluated 28 rice genotypes for yield and quality traits to estimate genetic divergence and D^2 values. Genotypes were grouped into four clusters. Members from cluster II recorded higher mean values for number of panicles/plant, panicle weight, length of panicle, grains/panicle, HI, cooked kernel length, cooked kernel L/B ratio, kernel elongation index and seed yield/plant. Cluster III had high values for grains/panicle, brown kernel L/B ratio, 1,000-seed weight and lowest mean value for amylase content While, cluster I possessed the highest values for brown kernel L/B ratio, 1,000-seed weight, cooked kernel L/B ratio and amylase content. Seed yield/plant contributed major portion to the total divergence followed by amylase content, cooked kernel length and 1,000-seed weight in this regard.

Hosan *et al.* (2010) studied 20 rice landraces of Bangladesh to assess the nature and magnitude of genetic divergence among them. Based on 12 traits, the genotypes were grouped into 5 clusters. Parallel relationship between genetic and geographical divergence was not observed. Inter-cluster distances were higher than the intra-cluster distances reflecting wider genetic diversity among the genotypes of different groups. The genotypes under cluster IV showed highest divergence among them as it exhibited highest intra-cluster distance. High level of inter-cluster distance was found between cluster II and V and between cluster I and III. Number of filled grains number/panicle,

number of panicles/plant, biomass index and grain yield contributed considerably towards total divergence.

Vennila *et al.* (2011) evaluated 41 rice genotypes for nine yield and yield attributing characters using Mahalanobis D^2 statistics and grouped all the genotypes into thirteen different clusters. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like number of grains per panicle, plant height, grain length and grain breadth contributed maximum towards genetic diversity.

Sohrabi *et al.* (2012) conducted genetic diversity analysis on 50 accessions of upland rice and clustered into six groups by 12 quantitative traits. Cluster III was the biggest (27 accessions) and cluster VI was the smallest (1 accession) group. Cluster I, II, IV, and V consisted of 6, 10, 2, and 4 members, respectively. The first group had the highest average in comparison with the other five groups considering five traits. Group VI had highest average for four traits.

Chakravorty and Ghosh (2013) studied genetic divergence among 51 landraces of rice using Mahalanobis D^2 analysis. Genotypes were grouped into 11 clusters. Cluster II was found to be the largest comprising of 16 genotypes followed by cluster III (8 genotypes) and cluster I (7 genotypes). Cluster VI and XI had single genotype each. The characters viz., culm diameter, culm length, grain length contributed maximum towards genetic divergence among the genotypes.

Lakshmi *et al.* (2014) studied genetic divergence among 70 genotypes of rice using Mahalanobis D^2 statistics for eleven quantitative characters and found all the characters under study had significant varietal differences. The genotypes were grouped into nine clusters on the basis of D^2 values. Cluster IV was the largest consisting of fourteen genotypes while cluster II had three genotypes. The characters L/B ratio, number of grains per panicle and kernel length contributed maximum towards genetic divergence. Cluster II showed maximum inter cluster distance with cluster IX. Hence the genotypes from these clusters may be used as potential donors for future hybridization programmes.

Sandhya *et al.* (2014) studied 32 elite rice genotypes to identify diverse genotypes using Mahalanobis D^2 statistics and grouped all the genotypes into six clusters. Cluster I and VI was the largest (8 genotypes) followed by cluster IV (6 genotypes). The maximum inter-cluster distance was recorded between clusters V and VI and the maximum intra-cluster distance was found in cluster IV followed by I. The characters like number of number of spikelets per panicle, biological yield per plant, test weight, harvest index and days to 50 percent flowering contributed maximum towards genetic divergence. Hence these characters could be given due importance for selection of genotypes for further crop improvement program.

Rashid *et al.* (2014) examined 20 diverse cultivars of rice and reported cluster analysis revealed that maximum genetic diversity was present between Cluster I and Cluster VI. Minimum genetic diversity was found between Cluster III and Cluster IV. It was concluded that traits like number of productive tillers, number of grains per panicle and 1000-grain weight was useful for direct selection criteria for higher grain yield. Cultivars like IRRI-3, IRRI-4, KSK-133, SR-57, IRRI-5, SRS-64 might be used for rice hybridization and improvement programs for developing new rice varieties.

Sinha *et al.* (2015) studied genetic diversity of 55 rice landraces in lateritic region of West Bengal with the help of 18 agromorphic characters through cluster analysis. Among five clusters, cluster I consist of 50 genotypes, cluster III consist of two and cluster II, cluster IV and V consist only one variety respectively. It was observed that Variety Daharlagra, Neta, Kelesh and Vutmuri were genetically dissimilar than the rest of 51 varieties, these lines may be utilized for selection of parents for production of new improved variety.

Beevi and Venkatesan (2015) studied genetic divergence among 60 rice genotypes and found that all the genotypes were grouped into six clusters. Cluster I was found to be the largest comprising of 50 genotypes followed by cluster II had four genotypes, clusters IV and V had two genotypes each while cluster III and VI are mono-genotypic in nature. The pattern of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters grain yield per plant, number of grains

per panicle and plant height contributed maximum towards genetic divergence among the genotypes. Cluster III recorded highest mean value for grain yield per plant and lowest mean value for days to first flower. The highest inter-cluster distance (D^2 =7925.46) was recorded between clusters III and VI. Selection of genotypes in these clusters which may serve as potential donors for future hybridization programmers to develop potential recombinants with high yield coupled with desirable traits.

Toshimenla *et al.* (2016) obsereved genetic divergence in 74 genotypes of upland rice by using Mahalanobis D^2 statistics for yield and its contributing characters. All the characters showed highly significant differences among genotypes. The genotypes under study were grouped into 15 clusters. In distribution pattern maximum number of genotypes (35) were found in cluster I, followed by cluster II with 12 genotypes, whereas, minimum number of genotype (1) had cluster XV. The inter-cluster distance was greater than intra-cluster distance indicating wide genetic divergence among genotypes. The highest intra-cluster distance was revealed in cluster XIV followed by cluster XIII and cluster XI. The maximum inter-cluster distance was observed between Cluster XIV and XV, followed by Cluster V and XV. The highest cluster mean was observed for yield/plant in cluster VII; however, contributing characters *viz.*, panicle length, panicle weight, filled grains and 100 seed weight were found in cluster XIV. Seed yield/plant was found major contributing character towards the total genetic divergence which may be utilized in selecting genetically diverse parents, especially for exploitation of heterosis.

Chandramohan *et al.* (2016) reported that, In D^2 analysis among 44 genotypes of rice the genotypes were grouped into 11clusters. On the basis of inter cluster distance genotypes from clusters IV and V followed by V and IX could be used as parents for future hybridization programme. Cluster mean analysis revealed the genotypes, JGL 21820 and JGL 21849 could be used in breeding programme for obtaining high yielding super fine grain segregants. Days to 50% flowering and 1000 grain weight manifested highest contribution towards total divergence, thus, these traits could be given due importance for further crop improvement.

Mau *et al.* (2017) studied genetic diversity for red and black upland rice accessions of Indonesia. A total of 26 qualitative and 16 quantitative characters were observed. The

tested rice accessions exhibited substantial differences in most of the observed qualitative and quantitative variables. Cluster analysis employing qualitative variables classified the rice accessions into 4 clusters and 15 sub-clusters. The same analysis using quantitative characters placed the 40 rice accessions into 5 clusters and 8 sub-clusters. Evaluation of agro-morphological characters demonstrated that the rice germplasm under the present study possessed a high genetic diversity.

Allam *et al* (2017) studied 23 basmati rice genotypes for 20 yield and quality attributes using principal component analysis and cluster analysis. PCA identified five principal components with eigen values more than one for four components which contributed 90.40 per cent of the cumulative variance. The genotypes were grouped into six clusters by using cluster analysis. Cluster II was the largest, consisting of six genotypes followed by five genotypes each in clusters III, IV and V, two genotypes each in clusters I and VI. The results indicated that there was some degree of similarity of genotypes clustered together on the basis of their origin. However, the pattern of distribution of some genotypes from different eco-geographical regions was found random, indicating that geographical diversity and genetic diversity were not related. The maximum intra cluster distance was observed for the cluster III. The highest genetic divergence was observed between the clusters IV and III exhibiting wide diversity. Among different traits, plant height, days to 50% flowering, spikelets per panicle, KLAC and amylose content had maximum contribution towards total divergence may be used as selection parameters in segregating generations.

2.4 Molecular Diversity (SSR Markers):

Molecular markers offer a vast scope for improving the effectiveness of conventional plant breeding by carrying out selection of lines not directly on the trait of interest but on molecular markers linked to that particular trait (Mohan *et al*., 1997). A number of molecular marker are now being employed for diversity analysis like Random Amplified Polymorphic DNA (RAPD) (Williams *et al*., 1990), Simple Sequence Repeat(SSR) (Tautz, 1989), Inter Simple Sequence Repeat (ISSR) (Zietkiewicz *et. al*.,

1994) etc. SSRs are among the most commonly used molecular markers. SSR markers are PCR-based markers that are efficient, cost-effective to use, abundant, co-dominant, interspersed throughout the genome. Microsatellite or SSR loci consist of short and tandemly repeated nucleotide motifs, which flanked by conserved sequences (Tautz, 1989). As compared to RAPD markers SSR are multiallelic, generally more informative and are based on heterozygosity values (Powell *et al.* 1996). These molecular markers can detect a significantly higher value or degree of polymorphism in rice lines (Ni *et al.*, 2002, Okoshi *e.t al.*, 2004) which becomes ideal for studies on genetic diversity and intensive genetic mapping as it gives much greater resolution than other types of markers (Cho *et al.*, 2000). In rice genotypes, SSR markers have been efficiently utilized for different purposes including (i) genome mapping (Temnykh *et. al.*, 2000, McCouch *et. al.*, 2002); (ii) for the assessment of the genetic diversity and relatedness among different cultivars including both non-aromatic and aromatic rice (Ravi *et al.*, 2003); (iii) identification of varieties and purity testing of varieties (Joshi and Behera, 2006); (iv) In determination of the genetic relationship between several species or sub-species (Ni *et al.*, 2002). This polymorphism is detected through standard polymerase chain reaction (PCR) technique as variation in the number of repeats among individuals (Weber and May, 1989). Microsatellite framework map has been developed to provide genome wide coverage in rice (Chen *et al.*, 1997) In a study of assessment of genetic diversity, 24 rice cultivars carrying good quality traits were evaluated using 164 SSR markers, a total of 890 alleles were detected by 151 polymorphic markers with an average of 5.89 per locus (Lapitan *et al.*, 2007). Some of the earlier reports molecular diversity in rice has been reviewed below;

Nagaraju *et al.* (2002) studied three rice groups (traditional basmati, evolved basmati and semi dwarf non basmati) using 19 SSR and 12 inter SSR primers. In twenty four rice varieties from the three different groups revealed by a total of 70 SSR alleles and 481 inter-SSR-PCR markers. Minimum genetic diversity was observed among the varieties of traditional basmati (TB) whereas the evolved basmati (EB) varieties showed the highest genetic diversity by both the marker assays.

Ravi *et al.* (2003) studied genetic diversity among 40 cultivated varieties and five wild relatives of rice using 38 SSR and 36 RAPD markers. The total number of 499 alleles was produced among the 45 genotypes (forty cultivated varieties and five wild relatives) with 90% polymorphism. Only one locus viz., RM115 was found monomorphic out of 38 SSR primer pairs which were used,. The average PIC value was 0.578. SSR analysis resulted in a more definitive or clear separation of clusters of the genotypes indicating a higher level of efficiency of those SSR markers.

Priyanka *et al.* (2004) assessed genetic diversity by analyzing SSR markers and prepared a DNA fingerprint database of 24 rice genotypes. A total of 229 alleles were detected at the 50 SSR loci and 49 alleles were present in only one of the 24 cultivars. The size difference between the smallest and largest allele varied from 1 (RM333) to 82 (RM206). Multiple alleles were observed in 13 loci. PIC (Polymorphism information content) values ranged from 0.0 (primer RM 167) to 0.78 (primer RM 170), with an average performance of 0.62 per marker. At 15 of the SSR loci, traditional and cross-bred Basmati rice cultivars amplified a higher number of diverse alleles compared to other rice genotype.

Ram *et al.* (2007) studied molecular genetic diversity among thirty five rice accessions, which included nineteen landraces, nine cultivars and seven wild relatives, by using 19 SSR markers distributed across the rice genome. The mean number of alleles per locus was 4.86, showing 95.2% polymorphism and an average polymorphism information content of 0.707. Microsatellite allelic diversity clearly demarcated the cultivars, wild relatives and landraces into different groups, which is based on cluster analysis. The allelic richness computed for the clusters indicated that molecular genetic diversity was the highest among wild relatives (0.436), followed by landraces (0.356), and the lowest for cultivars.

Ghneim *et al.* (2008) evaluated 11 rice cultivars from Venezuela to assess the genetic diversity using 48 SSR markers. A total of 203 alleles were detected and the number of alleles per marker ranged from 2 to 9 with an average of 4.23. All the genotypes clearly separated by the UPGMA-cluster-analysis based on genetic distance coefficients and revealed that the Venezuelan rice lines are closely related.

Singh *et al.* (2009) evaluated a set of 8 diverse rice genotypes using 201 random SSR loci of different repeat motifs and lengths, representing both genic and intergenic sequences from the 12 rice chromosomes. There was a positive correlation between simple sequence repeat length and average number of alleles per locus but linearity of this relationship was limited to the SSR length range of 10–70 bp. The higher level of polymorphism was observed in the SSR length range of 51–70 bp, beyond which there was stabilization and then decline of polymorphism in SSRs longer than 70 bp. Proportion of polymorphic loci in the various SSR length groups also followed similar pattern with even sharper decline of polymorphism in the highest size range.

Prathyusha *et al.* (2009) evaluated 32 rice genotypes using 11 SSR primers for diversity analysis and found that 7 primers showed distinct polymorphism among genotypes consistently and a total of 33 amplification products were obtained with all the selected 7 primers. The number of alleles varied from 3-7 with a mean of 4.7 and PIC values of 7 primers varied from 0.1986 to 0.3038 with a mean of 0.2625. Cluster analysis based on SSR data revealed that the genotypes MTU-2077 and JGL-1798 were clustered at the two extremes based on their similarity coefficients.

Prabakaran *et al.* (2010) evaluated genetic divergence of 12 rice land races using five SSR markers. A total of 11 alleles were detected in 12 land races and the number of alleles per locus ranged from 2 to 3 with an average of 2.2 per locus. Among the primers used RM 481 identified more number of alleles and average PIC was 0.43. The dendrogram based on SSR marker analysis grouped the 12 rice accession into six clusters, where cluster VI was the largest with three accessions.

Umadevi *et al.* (2010) evaluated 110 rice genotypes for genetic diversity based on quantitative and qualitative using morphological and molecular analysis and found that out of 29 cluster, cluster 3 was largest with 25 genotypes, cluster 4 had 18, cluster 1 had 16, cluster 2 had 14, cluster 6 had 5, cluster 5 and 14 had 4 genotypes each, cluster 15 had 3 while remaining 21 cluster had single genotype each and cluster 25 exhibit the maximum mean value for number of productive tillers per plant and number of secondary branches per panicle. In SSR marker analysis among the 50 primers produce maximum number of alleles. All the IR lines were clustered in cluster 2 (Eleven) and all the RR lines (Six) and ASD lines (six) were clustered in cluster 1 that also confirmed by

molecular study and the highest contribution towards genetic divergence recorded by water uptake, L/B ratio, volume expansion ratio linear elongation and gel consistency and these trait may be use as a selection parameter in segregating generation.

Upadhyay *et al.* (2011) studied 29 rice accessions for genetic diversity using SSR primers. A total 87 alleles were produced with 100% polymorphism. Polymorphic information content value ranged from 0.57 (RM 313) to 0.98 (RM 442 and 163) with average value of 0.78 and average genetic similarity 0.38 was observed. Cluster analysis reveal PCA of rice microsatellites data from 20 pairs separated the 4 early varieties and land races from recently evolved varieties by the 1st and 2nd principal component, which represent 15 and 12.2% diversity in the sample. Out of 29, 14 genotypes produced specific alleles, which can be used as molecular tags for particular genotypes.

Matin *et al.* (2012) studied genetic diversity among 12 deep water rice genotypes of Bangladesh using 18 SSR markers through MAS. Upon PCR amplification the alleles were separated on PAGE system. Initial polymorphism recognition was conducted using 18 SSR primer pairs distributed on 12 rice chromosomes. The chosen microsatellite marker panel consisted of RM1, RM452, RM130, RM252, RM13, RM204, RM11, RM25, RM205, RM244, RM206, and RM463 with one representative from each chromosome. Total 79 alleles were detected with an average of 4.38 alleles per locus. The PIC reflections of allelic diversity frequency among the rice lines, which is ranged from 0.477 to 0.782, with an average value of 0.634. RM 13 was found as the best SSR marker for the identification of genotypes as revealed by PIC values. UPGMA dendrogram revealed 2 different major groups with 4 clusters and the wide range of dissimilarity values (0.14-0.89) which showed a high degree of diversity among the set of cultivars.

Sajib *et al.* (2012) used a total of twenty four SSR markers across twelve elite aromatic rice genotypes for their characterization and discrimination. Among these markers, nine microsatellite markers showed polymorphism. The total number of alleles per locus ranged from 2 alleles (RM510, RM244, and RM277) to 6 alleles (RM 163), with an average of 3.33 alleles across 9 loci obtained in this study. The polymorphic information content values ranged from 0.14 (RM510) to 0.71 (RM163) in all 9 loci with

an average of 0.48. RM163 was found the best marker for the identification of twelve genotypes as revealed by their PIC values. The frequency of most common allele at each locus ranged from 41% (RM163, RM590, and RM413) to 91% (RM510).

Nguyen *et al.* (2012) evaluated genetic diversity in upland rice accessions from Vietnam using 30 SSR markers which reveal the genetic relationship among the varieties. A total of 192 polymorphic bands were detected. The number of alleles per locus ranged from 3 to 12, with an average of 6.4. Cluster analysis based on genetic similarities group in two major groups and further divided in five subgroups. The results suggested that a relatively small number of SSR markers could be used for analysis of genetic diversity in rice germplasm. The upland rice germplasm presents a valuable gene source and sufficient genetic background for future breeding and mapping works on drought tolerance rice in Vietnam.

Meti *et al.* (2013) observed allelic diversity and the relationship among forty eight aromatic rice germplasm with SSR marker. Out of 30 pair of primers, 12 SSR primers showed DNA amplification and polymorphism among 48 rice lines and total 28 bands appeared by using these primers. The number of alleles per locus ranged 1-5 with an average 2.8. Out of 28, 25 bands were polymorphic in nature and remain monomorphic. Result revealed that all the tested primers showed distinct polymorphism among genotypes indicating robust nature of marker. Most of primers showed highest PIC. Phenotypic characteristics are significantly correlated with genotypic characters. Cluster analysis indicates all the genotypes grouped in 2 major clusters and one cluster had 11 and another cluster had 37 genotypes. The larger range of similarity value using SSR primers pair provides greater confidence for the assessment of molecular genetic relationship among the varieties and information from SSR profile helps to identify the specific lines diagnostic marker in all the genotypes. Significant genetic variation at maximum number of loci between varieties indicates rich genetic resources in rice.

Vhora *et al.* (2013) observed the molecular genetic diversity among twenty rice cultivars of non-aromatic, aromatic, and quality traits were studied using twenty five Rice Microsatellite (RM) markers, among which 15 SSR markers were used for analyzing aromatic and non - aromatic rice genotypes. These markers generated higher

level of polymorphism due to which they generated 356 polymorphic reproducible bands with 164 loci. The remaining 10 markers are used for the study of quality traits which shown 222 polymorphic bands with 101 alleles. The dendogram developed for quality traits including aroma showed that the genotypes with common phylogeny and geographical orientation tend to cluster together.

Mukherjee *et al.* (2013) evaluated 21 rice genotypes using 20 SSR markers distributed among 10 chromosomes of rice. These markers exhibited polymorphism and a total of 101 alleles were amplified by 20 markers. An average of 5.05 alleles was produced. Average effective number of alleles was 3.77. Genetic diversity per locus for most of the selected markers was high. The primers RM12921, RM18384, RM23877, RM23744, RM257, RM25181, RM25735 and RM5479 were highly polymorphic. These microsatellites are useful in assessing the genetic diversity of rice. Cluster analysis performed by DARwin V.5.1.153 using un-weighted neighbour joining method clearly separated the genotypes into 3 main clusters with different sub – clusters within a cluster. Promising selections of parents for future hybridization program to generate desirable segregates has been suggested.

Das *et al.* (2013) observed genetic distances among 91 rice accessions from different states of India using 23 previously mapped SSR markers. A total 182 alleles were identified which included 51 rare alleles and 27 null alleles out of 182. The average PIC (Polymorphic Information Content) value was 0.7467 per marker. The non-aromatic landraces from West Bengal was most diverse with 154 alleles and an average PIC value of 0.8005 per marker followed by the aromatic landraces from West Bengal with 118 alleles and an average PIC value of 0.6524 per marker while the landraces from North East ranked third with 113 alleles and an average PIC value of 0.5745 per marker. In the dendrogram distinct clusters consisting of predominantly aromatic landraces and predominantly North East Indian landraces were observed. The non-aromatic landraces from West Bengal were interspersed within these two clusters.

Shahriar *et al.* (2014) studied genetic diversity of 34 advanced rice breeding lines including 4 checks using 3 SSR primers (RM147, RM167 and RM215). All three primers showed polymorphism and 29 alleles were detected among genotypes with an

average of 9.67 alleles per locus. PIC ranged from 0.47 to 0.88 with an average of 0.71. Thirty four genotypes were grouped into 4 major clusters at 0.36 similarity coefficient differentiating the early maturing genotypes from the late maturing types with the help of dendogram.

Sabina *et al.* (2015) analysed 42 genotypes of rice for genetic diversity using 40 SSR primers. Primers generated a total of 250 alleles across these genotypes with a range of 2 - 11 alleles per locus and a mean of 6.89 alleles per locus. The PIC values, measuring allelic diversity and polymorphism ranged from 0.490 (RM2592) on chromosome 1 to 0.806 (RM585) on the chromosome 6, with a mean PIC value of 0.719 per locus. Pair-wise similarity coefficients ranged from 0.10 to 0.89 with the average similarity coefficient around 0.40. Similarity coefficient value revealed presence of good genetic diversity among these genotypes at the molecular level. Clustering pattern revealed grouping of these genotypes into 5 clusters.

Singh *et al.* (2015) evaluated the genetic polymorphism and identification of diverse parents among the 76 rice accessions using SSR markers. The accessions showed significant phenotypic variation for all the characters analyzed. The SSR primers pair were highly polymorphic across all the rice accessions and altogether 79 alleles were detected. The overall PIC value ranged from 0.26 to 0.65 with an average of 2.82 per locus indicting high level of genetic variation. The cluster analysis showed the rice accessions grouped in to two major groups and 14 subgroups. The pair-wise genetic dissimilarity coefficient indicated that the highest dissimilarity was obtained between the cultivar B.3688-TB and IR.67017-1(0.1935) followed by cultivar Badi Kodi and Changhat (0.3333). The markers RM 413, RM 481, RM 206 and RM 20 produced a maximum of four alleles.

Freeg *et al.* (2016) evaluated 41 rice genotypes with different drought tolerance for genetic diversity by using 15 SSR markers. A total of 68 alleles were detected of which 61(89.79%) were polymorphic. The number of alleles detected by a single marker varied from 2 to 8 alleles with an average of 4.71 alleles per locus. The PIC values ranged from 0.07 (RM219) to 0.80 (RM263) with an average of 0.52. Genetic similarity coefficients of pair wise comparisons were estimated on the basis of the polymorphic microsatellite

loci ranged from 0.23 to 0.91 indicating a wide range of genetic variation present among the studied genotypes. It was determined that the primers RM20A, RM302, RM212 and RM286 could be useful for selecting drought tolerant lines through MAS approach.

Krupa *et al.* (2017) studied genetic diversity among 5 rice genotypes using SSR primers. Upon PCR amplification the alleles were separated on Agarose Gel Electrophoresis system and initial polymorphism detection was conducted using 20 SSR primer pairs distributed on five rice chromosomes. A total of 65 alleles were detected with an average of 3.25 alleles per locus. The PIC reflections of alleles diversity frequency among the varieties, which is ranged from 0.215 to 0.791, with an average of 0.493. SSR marker RM 260 was found as the best marker out of 20 markers for the identification of genotypes as revealed by PIC values.

Okello *et al.* (2017) evaluated 48 rice germplasm for genetic diversity using 18 SSR primers in which, each primer showed 100% polymorphism. A total of 275 alleles were generated by 18 primers and each primer produced on an average 15.27 alleles of the size ranging from 172.22 bp to 329.44 bp. Alleles amplified for each primer pair was ranged from 5 to 35. The primer pTA-248 generated a maximum number of alleles (35), while the primer RM-309 produced minimum number of alleles (5). The PIC values of primers ranged from 0.58 (RM-206) to 0.85 (RM-140) with an average PIC value of 0.77. It was also observed that there was no association between % polymorphism and PIC value as primer RM-206 showed minimum PIC value but were 100% polymorphic. RM-140 and RM-122 had higher PIC value, so that were found to be more informative. All the 48 rice genotypes were separated into 2 major clusters.

2.5 Phenotypic stability or G x E interaction:

Rice breeder always target to achieve such genotypes which may gives maximum gain yield over environments and also show consistency in their performance. Stability may be depending on morphological and physiological attributes and allowing others to vary resulting in predictable G x E interaction for specific traits i.e., yield. A plant population which can adjust its phenotypic or genotypic state in response to current environmental fluctuation in their performances, in such a way that it gives higher and stable economic response can be termed as "Well buffered". Maximum varieties when tested under different fluctuating environments differ in their performances under

various environments or agro climatic conditions. Different factors related to environment such as length of the day, photoperiod, sunshine, latitude, altitude, temperature and others play an important role in the selection of a genotype for wider adaptation. It happens only due to the fact that one genotype can flourish well in any particular environment whereas the same genotype does not perform equally well in the other environment. If the influence of the environment can be reduced significantly, then only true expression of the characters true to one genotype can be visualised. G x E interaction has been a challenging issue among the scientists from different departments to identify stable lines. Different methods already developed for determining stability of performances of the advance lines or hybrids. The regression approach was first employed by Finley and Wilkinson (1963) and then its modified by different scientists group including Eberhart and Russell (1966). These are parametric model for identification of stable lines. Eberhart and Russell model (1966) divided in 2 components *viz.* Genotype and Environment + Interaction (E+GxE). Second component divided in 3 components also *viz.* Env. (L), GxE (L) and Pooled deviation. Pooled deviation further divided into sum of square due to individual genotypes. This model measure 3 parameters of stability *viz.* mean yield over location, regression coefficient and deviation from regression. A rice line having higher mean yield over the population mean, non-significant deviation (s^2di) from zero (0) and unit regression coefficient (b=1) with non-significant deviation from one called average stable and better for the all environments, while a rice line with significant b value (b>1* or b<1*) called highly & low stable and better for favorable and unfavorable environments respectively. Some of the earlier reports on phenotypic stability in rice have been reviewed below;

Shantakumar *et al.* (1997) studied 34 genotypes of rice for their phenotypic stability over 3 seasons (Dry, Wet and Winter) during 1990 using Eberhart and Russell model. The results indicated the presence of G x E interaction for all the characters studied. The G x E interaction was attributed by both linear and nonlinear components. None of the genotypes was stable for all the characters studied. KBCP – 1 was found to be most ideal variety for all the environments. The genotypes Mukthi and IR 54 R found to be stable over environments but performance cannot be predictable.

Basavaraja *et al.* (1998) studied 16 rice genotypes under 5 lowland environments (combination for fertilizer and sowing dates) during kharif 1992 indicated a significant G x E interaction for all the traits except grain length. The effect due to the environment (linear) was significant for all the characters except grain breadth and L/B ratio. Variance due to G x E (linear) interaction was significant for plant height, panicle exertion and grain yield. The non – linear component was significant for all the characters. Genotypes IET 9926, IET 5899 and Puttabdatta had average stability (bi = 1). IET 9926 among these three, rated as best due to its high mean yield and desirable plant height. Normal June sowing and July planting with recommended doses of NPK fertilizer were the most favourable environments for maximum yield.

Panwar and Dhaka (1998) studied phenotypic stability for grain yield in 32 rice genotypes grown in 16 different environments. The eight high yielding genotypes were found to be the most stable. Five genotypes were found suitable for rich environments. Two genotypes were found suitable for poor environments.

Lalitha and Sreedhar (2000) observed a significant G x E (linear) interaction for all the characters in rice. The magnitude for non - linear components was found high for L/B ratio and volume expansion ratio while linear component was predominant for amylose content, gel consistency and geltinization temperature. Protein content was found to be stable over environment. The genotype IR 64 showed stable response for four quality characters viz. L/B ratio, protein content, volume expansion ratio and gel consistency while BPT 1235 was found stable over a range of environments for L/B ratio, amylase content and alkali value. The other varieties MTU 7014 (amylase content and alkali value) and MTU 11565 (amylase content and Protein content) also showed stable response to some characters.

Senapati *et al.* (2002) performed G x E interaction in 23 photo-insensitive rice lines with respect to grain yield and number of days before maturity. They evaluated the trial and found a highly significant variation due to genotypes, environments and G x E interaction. Linear regression and pooled deviation equally contributed towards G x E Eberhart and Russell model reveal that PNR 166 was the only genotype for

general/wider adaptation while PNR 519, IET 9978 and IET 1402 possessed specific adaptation for rich, favourable and better environments.

Nayak *et al.* (2003) observed 23 scented rice genotypes for their stable performance with respect to grain yield, straw yields, number of panicles and other yield components. Both the linear and non - linear components of G x E interaction were significant for all the traits studied. These could be explored for improving grain yield in scented rice.

Francis *et al.* (2005) evaluated G x E interaction for grain yield and yield attributing traits in 7 rice cultures and 2 local checks under 3 ecological situation of Kerala and observed significant G x E interaction for many traits. Among the linear and nonlinear components of G x E interaction, linear component was predominant for days to 50% flowering, volume expansion ratio and head rice recovery suggesting variation in the performance of different culture grown over environments could be predicted. Mean Sum Square due to linear environment was also found significant for most of the characters indicating difference between environments and their considerable influence on these characters. Culture C26T (b) was identified stable for grain yield across the environments.

Bughio *et al.* (2005) studied 6 non-aromatic mutants of IR6 and 2 non-aromatic mutants of IR8 along with their parents and the control cultivar Shadab during 2000 and 2001 at nine locations in Sindh, Pakistan to investigate the possible interaction between genotype and environment for grain yield. Combined analysis of variance suggested that the effects of genotype, location, year and their interactions were highly significant. Regression coefficient (*bi*) and deviation from regression (s^2di) showed significant differences among mutants/cultivars. The mutants Sarshar, IR6-25/A and IR6-15/A recorded the highest grain yields among the entries. On the basis of stability parameters, Sarshar showed good adaptation under both favourable and unfavourable environments.

Devi *et al.* (2006) evaluated 10 promising genotypes for stability parameter in respect to grain yield and its components in four environments and found linear components of G x E interaction significant for plant height, days to 50% flowering and grain yield per plot while non linear components was significant for all the characters. Among the genotypes, CAUR-2 and KD-2-7-6-2 showed better grain yield however on

the basis of stability parameters the genotypes RCM-9 and KD-2-7-6 was considered better for grain yield.

Arumagam *et al.* (2007) conducted a trial to study 12 rice genotypes for grain yield and its component characters for sowing dates over six environments. G x E interaction was significant for grain yield along with its component characters viz. Number of productive tillers, panicle length, test weight, harvest index and spikelet fertility % . Stability parameters of genotypes exhibited differential response of some of the genotypes. None of the genotypes used in the study was stable for all the characters while some genotypes were stable for grain yield. Study also also indicated that sowing of long duration varieties could be extended up to July 1st fortnight and that of medium duration varieties up to 2nd fortnight of July instead of June 2nd fortnight and July 1st fortnight respectively without significant reduction in yield.

Panwar *et al.* (2008) observed genotypes x environment interaction for grain yield, its components and grain quality traits in 10 parents and their 45 F1s of scented rice (Oryza sativa L.) under 4 environments created by 4 different dates of transplanting during wet season 2003. Significant G x E interactions was observed for all the eleven characters having homogenous error variance in environments. Among the linear and nonlinear components of G x E interaction, linear component was predominant for most of the characters, suggesting variation in the performance of different genotypes grown over environments could be predicted. Mean squares due to environment (linear) was also found significant for all the characters, indicating differences between environments and their influence on genotypes for expression of these characters. Based on stability parameters and overall mean, genotypes IET 13549 and Pusa Basmati-1 were most stable under different environments, while IET 13846 was suitable for poor environments and the crosses Taroari Basmati x IET 16320, IET 13549 x IET 13846 and Pusa Basmati-1 x IET 13846 were more suitable for favourable environments with respect to these characters.

Sedghi – Azar *et al.* (2008) studied adaptability and stability of grain yield of 10 promising lines and two improved cultivars from 2001 to 2003 in 3 different regions of Mazandaran. Simple and combined analyses of variances indicated significant differences among grain yield of various lines in all regions. Experimental errors

variance was uniform using Bartlet test. Except for effects of year and block × environment (year & location), all effects were significant. Results of grain yield stability analysis indicated significant effects for treatment, environment (linear) and mean squares of deviation from regression. For all lines except line No. 3 there was significant variation for effects of deviation from regression using stability parameters. The highest grain yield was produced by lines No. 7, 8 and 11, showing non - significant differences from each other. Nevertheless, for existence of significant differences among deviation from regression by zero, lines could not be recommended for a particular region. The least amount of regression slope belonged to line No. 1, 2 and 5, which were more suitable than others for unfavorable growth conditions. Overall, line No. 3 indicated the highest adaptation and stability for grain yield under different Mazandaran conditions.

Bhakta and Das (2008) evaluated 26 rice genotypes over 8 environments during wet season 2000 and dry season 2001 for the assessment of yield and yield stability. Pooled analysis of variance for grain yield over environments showed highly significant differences among genotypes, environments and GxE interaction indicating diverse and variable nature of cropping environments. The genotypes were classified into 4 adaptive groups based on regression co-efficient (bi) and deviation from regression (S^2di). Majority of the high yielding genotypes in both mid-early group (Daya, Lalat, Sebati, Konark and ORS 199-5) and medium maturity group (Bhuban, Birupa, Meher, Kharavela and Tapaswini) with high yield potential have either above average (b>1) or below average (b<1) responses. The genotypes Sarathi and IR 36 with low yield potential exhibited average stability with unit regression and S^2di values not significantly different from zero.

Bastia *et al.* (2010) examined 42 early maturing lines of rice for grain yield over four environments and found significance of linear components of variation for grain yield. The genotypes were grouped into 4 classes on the basis of stability performance. 13 genotypes were found to possess high yield and stable performance over environments while 2 genotypes possess higher mean yield but low stability performance indicating their suitability to favourable environments, 4 genotypes had high level of stability but low yield potential indicating their adoptability to

unfavourable environments. Stability of yield performance associated with yield components like effective tiller per square meter and grains per panicle.

Kumar *et al.* (2010) observed genotype (G) x environment (E) interaction and stability for grain yield and some associated traits during 2002-2006 in 8 Halugidda local rice mutants in the hill zone of Karnataka. Significant G x E interaction was observed for all the traits studied. The pooled deviation was significant for the majority of the traits including grain yield and considerable genotypic difference was observed. Both the linear and non-liner components of G x E interaction were significant, but the linear component was more predominant. Based on the stability parameters, rice mutants HSM-23 and HSM-27 showed higher grain yield over the population mean, with regression coefficient near unity and zero deviation from regression. Thus, they were found to be stable and may be recommended for the commercial cultivation in this region/ zone of Karnataka.

Sreedhar *et al.* (2011) conducted a trail to evaluate 60 hybrids and their parents along with 5 checks for stability across 3 different zones of Andhra Pradesh in 2009. G x E interaction was significant due to linear component for panicle length, number of productive tillers per plant, number of filled grains per panicle, test weight and single plant yield indicated significant variability among the experimentation could be predicted. Stability in a single plant yield was due to plasticity and stability in yield components. It is concluded that for yield and its important components, some potential parents were stable and some hybrids better performed for than other hybrid combinations due to having favourable combination of all stability parameters with significantly high mean performance level over promising hybrid checks for yield and its important components across 3 environmental conditions.

Bose *et al.* (2012) evaluated 21 lowland rice genotypes for their stability parameters with respect to grain yield in a five location where pooled analysis of variance reflects existence of genotype x environment interactions and contribution of both linear and non-linear components to genotype x environment interactions and found that Rayda B3, CR 778-95 and CR 661- 236 were suitable for all environments, Sabita and OR 1358-RGA-4 were suitable for better environments and PSR 1209-2-3-2, CR 780-1937,

Ambika, OR 877-ST-4-2, NDR 40055-2-1 and CR 662-2211 were identified for poor environments.

Subudhi *et al.* (2012) evaluated 20 popular rice varieties to study the genotype x environment interaction and stability nature of different yield traits. The characters like plant height, ear bearing tillers (EBT)/hill, panicle length, days to 50% flowering and grain yield were recorded for four different environments and found that the varieties viz. Lalat and Saket- 4 and PR- 113 are stable across the environment for EBT/hill. The variety Daya is stable across the environment for panicle length. IR-72 is stable across the environment for days to 50% flowering. For grain yield, Gouri, IR-8, Jaya and IR-36 exhibited higher yield than population mean with regression coefficient near unity and negligible deviation. Hence these varieties can perform better in all types of environment.

Mall *et al.* (2012) studied 12 selected genotypes in advanced yield trial under vegetative stage, drought stress and irrigated conditions at CRRI, Cuttack for 3 years. Significant genotype x environment interactions were observed for days to maturity, plant height, harvest index and grain yield and having homogenous error variance in environments for these characters. Among the linear and non linear components, G x E interactions was predominant for most of the characters, suggesting variation in the performance of different genotypes grown over environments could be predicted. Based on the stability parameters, the genotypes Vandana and CB 0-13-1 were found to be stable. The top genotypes under stress *viz.* Lalsar and CR 143-2-2 were accepted drought tolerant genotypes.

Rasyad *et al.* (2012) studied G x E interactions and stability in 5 cultivars of rice was evaluated at 3 environments in Indonesia. Traits measured included panicles per plant, number of grains per panicle, filled grain percentage, seed weight and grain yield. A regression coefficient and deviation from regression as proposed by Eberhart and Russel (1966) were used to determine stability of a genotype. There were significant effects of environments on yield and some yield components, except panicle number per plant. The cultivars differed significantly in all yield components and grain yield. Cisokan and IR64 had b value did not significantly ($P < 0.05$) different from 1.0 and had s(d) approaching to zero and were considered as stable for all environments. Kwatik

Putih was considered as unstable genotype and specifically adapted to less favourable environment.

Mosavi *et al.* (2012) investigated 12 rice genotypes for grain yield stability over 3 locations of Iran and found highly significant yield differences among rice genotypes, environment and by environment interaction. Some rice genotypes were adjudged stable when rent yield stability parameters were considered. Danesh showed adaptation to favourable environments while Partov genotype demonstrated insensitivity to environmental conditions, hence it was considered adapted to low yielding environments. A combination of high grain yield potential, stability parameter of regression coefficient of unity and minimum deviation mean squares from regression identified Jelodar as a rice genotype that deserved to be promoted on-farm and for possible release as commercial varieties for the rice growing ecologies in north of Iran.

Koli and Prakash (2012) evaluated 7 aromatic rice varieties for stability of grain yield in RCDB under transplanted condition of Rajasthan. Pooled ANOVA showed highly significant differences among environments (year), genotypes and G x E interaction. Both linear and nonlinear components of G x E interactions were significant showing the importance of both components in the expression of the traits. Based on estimated stability parameters and over all mean performance of grain yield, variety P-1121, P-2511, P-1460 and Pusa Basmati-1 were identified as superior ,which were well adapted to all the environment, stable with above average yielding ability or highest grain yield (45.75, 45.23,43.38 and 41.08 q/ha, respectively) with non-significant bi and s2d values coupled with high sustainability index. This showed that these varieties were better responsive to the favorable environments. Mahi sugandha and Taraori (Checks) was good for low yielding environments (response to poor environment) and contradict with respect to the stability parameters and the sustainability index.

Mahalingam *et al.* (2013) evaluated 40 CMS hybrids of rice in 3 environments to assess the stability of 13 different grain quality traits. ANOVA of Eberhart and Russell revealed that, performance of different hybrids fluctuated significantly from their respective linear path of response to environment. Most of the grain quality parameters showed non-significant mean squares except hulling percentage, milling percentage, head rice recovery, gel consistency and volume expansion ratio, indicating the influence

of G x E interactions on these five grain quality measures. The genotype x environment (linear) interaction component showed significance for hulling, milling percentage, head rice recovery, gel consistency and volume expansion ratio showed the influence of locations on the expression of these parameters. Some hybrids combinations were found to be stable over locations with high mean, around unit regression (bi) and least deviation from regression line (S^2di) for hulling percentage. For gel consistency, some hybrids combination showed below average stability as these hybrids posses greater mean, less than unit regression (bi>1) and non significant deviation from regression (S^2di) and may be suitable for E3 (Environment 3rd).

Padmavathi *et al.* (2013) evaluated 52 hybrid combinations for yield and yield contributing characters over 4 different agro-climatic zones in Andhra Pradesh during dry season 2010-11. 18 promising hybrids from all locations which recorded significant higher yield than check were subjected to analysis for 11 quality characters. The analysis of variance of Eberhart and Russell model indicated the genotypes and environments were significant for all the quality characters except for milling % for genotypes indicating the diversity among the genotypes and environments studied. The G x E interaction was significant only for head rice recovery, water uptake and kernel elongation ratio and non-significant for remaining characters. The high yielding hybrid APMS 9A x MTU II-143-26-2 was stable for head rice recovery and kernel elongation ratio while APMS 10A x MTU 1071 was stable for kernel elongation ratio, alkali spreading value and amylose content.

Chavan *et al.* (2014) examined 20 genotypes of rice at two agro - climatic zone in two seasons of West Bengal. The mean squares due to genotypes, environments and Genotype x environment were found highly significant against all the characters and the linear interaction was significant for all the characters except panicle length and grain number per panicle while non-linear G x E interaction was significant against all the characters and the magnitude of linear variance significantly high against nonlinear variance for panicle number per plant, grain length and 1000 grain weight. BM (Bidhanmoti)-1, BM-14 and BM-17 recorded very high grain yield and stable for grain yield and most of the component characters, genotype BM-6, BM-9 and BM-18 were

also stable for grain yield and for most of the component characters, but they had poor grain yield and below average regression coefficient.

Kumar *et al.* (2014) conducted a trial to identify rice genotypes having high yield potential and stability under water stress conditions among 15 rice genotypes were grown under irrigated and water stress conditions. Drought susceptibility index (DSI) and relative grain yield (RY) were used to illustrate yield stability and yield potential, respectively. Significant variation in drought susceptibility index and relative yield values within genotypes were observed. The DSI values ranged from 0.68 to 1.46 and the mean RY values were 0.85 for irrigated plots and 0.77 for water stressed plots. The rice genotypes IR 83376-BB-24-2, IR 83373-B-B-24-3 IR 84895-B-B-127-CRA-5-1-1 and IR83387-B-B-27-4 showed high yield potential and stability (i.e. DSI<1; and RY>mean RY). These drought tolerant genotypes were also superior in terms of grain yield and higher content of desired physio-morphological traits. These drought tolerant rice genotypes may be adopted in large area in rainfed lowland ecosystem where drought is frequent, particularly at reproductive stage.

Vanave *et al.* (2014) investigated 25 rice varieties / hybrids for their stability in grain yield and straw yield during *kharif* seasons of 2009 - 2011. The highly significant differences among rice genotypes for grain and straw yield over environment and genotype x environment interaction were observed. The genotype Ratnagiri, found stable for straw and grain yield. The genotype Sahyadri 3 (14.276 g) found to perform well under better environmental conditions for straw yield while Ratnagiri 2 (13.541 g) and Panvel 3 (10.410 g) found to perform well under better environmental conditions for grain yield. The genotype Ratnagiri 24 (10.310 g) found to perform well under adverse environmental conditions for straw yield, while genotype Sahyadri 4 (13.510 g) for grain yield. Hence, the genotypes Ratnagiri 1, Sahyadri 3, Ratnagiri 2, Ratnagiri 24 and Sahyadri can be directly used in various breeding programmes for enhancing rice productivity.

Bhatt *et al.* (2015) studied G x E interactions and stability parameter among 48 diverse rice genotypes in four different environments created by presence and absence of inoculation pressure for rice blast disease during wet season 2012 and 2013 to identify stability for grain yield per plant in rice. G x E (linear) and G x E (non-linear) were

found significant for grain yield per plant. The preponderance of linear component noticed would help in predicting the performance of the genotypes across the environments with great precision. 3 genotypes were identified as most promising as it yielded higher than population mean performance coupled with unit regression coefficient and non-significant deviation from regression and therefore they should be recommended for wider cultivation after necessary testing. Some genotypes due to mean value higher than overall mean, bi>1, and non - significant deviation from regression, hence considered as "genotypes with below average stability". Apart from these, one genotype was found with high mean performance than population mean, regression coefficient less than unity and non-significant deviation from regression was regarded as genotype with "above average stability and better adaptability to unfavourable environments".

Singh *et al.* (2016) evaluated 29 genotypes of rice for the stability of yield and yield components under 3 environments. Significant differences among the genotypes and environments for the 12 traits studied, suggested the presence of wide variability. Both the components of G × E interaction were significant, indicating that the major portion of interaction was linear in nature and prediction over the environments could be possible. Significant pooled deviations observed for all the traits, suggested that there is a considerable genotypic differences. Based on the stability parameters, none of the genotype could be identified as stable for higher grain yield over environments but, the genotypes PRR-78, Ketaki, Joha, Swarna Sub-1 and Nagina-22 showed stability for low grain yield in all three environments. Whereas, the genotypes NDR-3026-3-1R, Pusa Basmati-1, IDR-763, Karahani, Kanak Jeer and Pant Dhan-12 for high grain yield per plant were considered as suitable under improved environment.

Paul *et al.* (2016) studied genotype x environment (GxE) interaction for grain yield and some associated traits in 45 rainfed upland rice genotypes under eight different environments in Allahabad (U.P) and Ranchi (Jharkhand) during wet season 2009-10 and 2010-11. The pooled analysis of variance indicated that the mean sum of square due to genotypes for all the traits and G x E interaction for many traits were significant which clearly indicated that the genotypes differ in their adaptability and stability. The significant G x E interaction (linear) of many traits indicated differential response of the

genotype to environmental changes. The pooled deviations were also significant for all the traits studied which suggested that these genotypes differed in their deviation from linearity. Stability parameters (mean, bi and s^2di) of the genotypes estimated separately over eight environments. Considering all the stability parameters, seven genotypes namely BAU 438-6-2, OR 2084-2, BAU 363-96, RR- 410-79-1-B-D2-B , NDR-1054-4-1 , BAU/GVT 435-06 and UPRI-2004-6 were selected as stable and desirable for rainfed upland condition.

Rashmi *et al.* (2017) evaluated 22 advanced rice lines for their stability parameters with respect to yield and its attributes *viz*. Days to 50% flowering, plant height , panicle length, number of tillers per plant and grain yield (kg/ha) in a multi-locational trial at 3 different sites. Pooled ANOVA reflects existence of GxE interactions and it was found that the advanced breeding line JB 15-2 found suitable for all environments. JM 15-4 (Mudigere), JK2 15-7 (Bramhavara) and JK 15-1(Shivamogga) are identified as suitable lines for specific locations**.**

CHAPTER – 3
MATERIALS AND METHODS

Materials and Methods:

3.1.1. Experimental site:

The field experiment conducted during kharif, 2014 and kharif, 2015 at rice section of Bihar Agricultural College (BAU), Sabour, Bhagalpur, Bihar. The experimental plot was well drained loamy soil and good fertility with levelled surface with pH 8.35 & EC 0.150 dsm^{-1} (Control) and pH 8.40 & EC 0.260 dsm^{-1} (Stress).

3.1.2. Weather condition during the crop season:

Bihar Agricultural College, Sabour, Bhagalpur is situated at longitude 87^0 04' 1.6" East and latitude 25^0 14' 11" North at an altitude of 37.19 metre above mean sea level in the heart of vast Indo - Gangatic plains of North India. The data on weather condition for *kharif,* 2014 and 2015 (Table 1 and 2) with respect to maximum and minimum temperature, rainfall and relative humidity were obtained from Agro meteorological observatory unit of BAU, Sabour, Bhagalpur, Bihar. The climates of this place are sub - tropical and slightly sub - humid nature. It is characterized by dry & warm summer, moderate rainfall and dry & cold winter. December and January are usually the coldest month when the mean temperature normally falls as low as 8.4^0C whereas April & May are generally the hottest months having the maximum average temperature of 38^0C (Source: Meteorological observatory unit, BAU, Sabour).

3.1.3. Experimental details including layout:

Design of experiments – Randomized Complete Block Design (RCBD)

Number of genotypes –   36

Number of replications –   3

Number of environment – 4

Number of year – 2 (Kharif 2014 and Kharif 2015)

Number of condition – 2 (Control and Moisture stress)

Location – 1 (Sabour)

Plot size – $4.0 \times 2.0 = 8$ m^2

Spacing – 20×20 cm

Table 3.1 Meteorological observation on standard weekly intervals during the period of experiment (*kharif* 2014)

Month	Standard Weak No.	Temperature		Humidity %		Rain fall
		Max.	Min.	Max.	Min.	(mm)
July 2014	27th week	31.3	24.5	94	81	297.5
	28th week	34.4	26.3	86	72	19.0
	29th week	31.8	26.0	87	78	52.7
	30th week	32.2	24.4	85	74	117.0
	31st week	34.1	24.4	87	71	8.8
Aug 2014	32nd week	32.6	24.8	87	76	23.4
	33rd week	30.4	24.8	93	87	79
	34th week	33.6	25.2	87	78	134.2
	35th week	31.8	24.3	87	75	43.2
Sep 2014	36th week	33.1	25.1	88	71	10.2
	37th week	32.4	24.2	92	81	41.4
	38th week	32.0	23.7	87	81	26.1
	39th week	33.1	22.0	85	73	50.0
Oct 2014	40th week	34.0	23.8	94	65	**Nil**
	41st week	33.3	22.8	82	76	4.2
	42nd week	31.4	18.7	86	64	0.4
	43rd week	31.1	17.4	80	70	**Nil**
	44th week	32.7	16.9	90	61	**Nil**
Nov 2014	45th week	30.8	16.6	86	53	**Nil**
	46th week	29.0	14.3	82	45	**Nil**
	47th week	27.7	12.6	85	46	**Nil**
	48th week	26.6	11.3	90	51	**Nil**

(Source: Agro Meteorological Unit, Bihar Agricultural University, Sabour, Bhagalpur)

Table 3.2 Meteorological observation on standard weekly intervals during the period of experiment (*kharif* 2015)

Month	Standard Weak No.	Temperature		Humidity %		Rain fall
		Max.	Min.	Max.	Min.	(mm)
July 2015	27th week	31.9	24.8	88	77	88.9
	28th week	32	25.6	91	75	41.2
	29th week	31.6	24.8	92	77	110.8
	30th week	33.1	25.4	85	70	30.8
Aug 2015	31st week	32.5	25.1	85	75	26.6
	32nd week	34	26.5	84	68	4.9
	33rd week	32.4	25.5	90	80	117.8
	34th week	29.6	24.9	95	87	200.9
	35th week	32.6	25.8	92	80	25.1
Sep 2015	36th week	32.7	25	80	73	14.8
	37th week	33.5	25.4	86	77	69
	38th week	33	25	92	79	136.1
	39th week	31.7	23.7	88	64	1.8
Oct 2015	40th week	33.8	23.8	86	68	**Nil**
	41st week	32	21.4	86	72	10.2
	42nd week	30.9	20.8	92	70	Nil
	43rd week	30.4	18.3	90	62	Nil
	44th week	29.7	17.7	89	64	**1.2**
Nov 2015	45th week	29.6	15.8	90	62	**Nil**
	46th week	27.5	15.4	90	62	**Nil**
	47th week	28.5	13.4	90	64	**Nil**
	48th week	28.2	14	88	59	**Nil**

(Source: Agro Meteorological Unit, Bihar Agricultural University, Sabour, Bhagalpur)

3.1.4. Experimental Materials:

The experimental materials for the present study consisted of 36 rice genotypes. The present experiment was conducted with a project of IRRI, Philippines STRASA (Stress Tolerant Rice for Africa and South Asia) at Rice section BAC, Sabour during kharif 2014-15 and 2015-16 under Bihar Agricultural University. The detail of genotypes is given in Table 3.3.

3.1.5. Fertilizer application:

The recommended dose of fertilizers @ 100 N: 60 P: 40 K kilogram per hectare was applied. The full dose of P_2O_5 and K_2O and half dose of nitrogen were applied as basal dose at the time of transplanting. The rest of the nitrogen was top dressed in two split doses at the time of maximum tillering stage *i.e.* 27 days after the transplanting and between panicle initiation & boot leaf stage *i.e.* 55 days after transplanting.

3.1.6. Environment:

(a) Irrigation **-** Thin film of water was given at the time of transplanting and 5 cm depth of water was given at the time of maximum tillering stage. Then field was irrigated as and when required up to physiological maturity in control condition.

(b) Stress **-** In case of stress condition before reproductive stage, irrigation was stopped before 15 days to trait like days to initial flowering in each plot. Crop was subjected to significant stress during reproductive stage and stress was measured through instrument.

3.1.7. Inter - cultural operations:

Inter - cultural operations like manual weeding were done in the field three times as per requirements (1st 18 days after transplanting, 2nd 41 days after transplanting and 3rd 54 days after transplanting).

3.2. Observation procedures of entire work:

The morpho-physiological observations during the investigation were recorded on five competitive and randomly selected plants in each replication under all the four environments including two different conditions for all the genotypes and their means were worked out. The

observations were recorded for yield, their components and quality characters of advance rice lines under study.

The present study under four environments was carried out as follows:

1. E1 - Normal irrigated or control condition at Sabour 2014

2. E2 - Moisture stress condition during reproductive Stage at Sabour 2014

3. E3 - Normal irrigated or control condition at Sabour 2015

4. E4 - Moisture stress condition during reproductive Stage at Sabour 2015

3.2.1. Pre and Post harvest yield attributing observations recorded are given below:

1. Days to 50% flowering

2. Plant height (cm)

3. Days to physiological maturity

4. Number of tillers / Plant

5. Number of productive tillers / m^2

6. Panicle length (cm)

7. Number of spikelets / Panicle

8. Grain yield per plant (g)

9. Biological yield per plant (g)

10. Harvest index (%)

11. Grain yield / ha (Kg)

12. Test Weight (g)

3.2.2. Grain quality attributing observations recorded are given below:

1. Hulling (%)

2. Milling (%)

3. Head rice recovery (%)

4. Kernel length (L) before cooking (mm)

5. Kernel breadth (B) before cooking (mm)

6. Kernel L/B ratio before cooking

7. Volume Expansion ratio

8. Amylose content (%)

9. Kernel elongation ratio

The detailed description of the characters studied and techniques adapted to record observations have been furnished below:

(A) Pre and Post harvest yield attributing observations (Morpho-physiological characters):

Plot wise observations recorded in each replication and each environment.

1. Days to 50% flowering:

Days to 50% flowering recorded as the number of days after sowing until time of initiation of flower blooming in the 50% plants of a plot.

2. Plant height (cm):

Plant height was measured in centimetres from the ground level to the tip of the terminal spikelets (excluding awn) of the five randomly selected plants at the time of maturity and average was computed.

3. Days to physiological maturity:

It was expressed as the number of days after seed sowing until the physiological maturity of entire plants in the plot.

4. Number of tillers / Plant:

The total number of tillers of a single plant was counted for the five randomly selected plants and average was computed.

5. Number of productive tillers / m^2:

After putting the iron frame of 1 m^2 area in the middle of each plot and the number of ear bearing tillers in per square metre area was counted as number of productive tillers per square metre.

6. Panicle length (cm):

It was measured in centimeters from the base of panicle to the tip of the terminal spikelets (excluding awn) of the main panicles for the five randomly selected plants and average was computed.

7. Number of spikelets / panicle:

Number of entire spikelets in a panicle was counted for the five randomly selected panicles and average was computed.

8. Grain yield per plant (g):

After threshing and winnowing, the produce was sun dried for 3 to 4 consecutive days up to 14% grain moisture content and with the help of electronic balance, grain-weight of the five randomly selected plants was recorded in grams and average was computed.

9. Biological yield per plant (g):

Sun drying of five randomly selected plants (including grains but excluding roots) was done till the constant weight achieved. Afterwards, the dried plants were weighted in grams on electronic balance and average was computed.

10. Harvest Index (%):

The harvest Index was calculated on single plant basis with the help of following formula.

$$\text{Harvest Index (\%)} = \frac{\text{Economical yield (Grain yield)}}{\text{Biological yield}} \times 100$$

11. Grain yield kilogram per hectare:

After threshing and winnowing the produce was sun dried for 3 to 4 consecutive days up to 14% grain moisture content and with the help of electronic balance grains weight of the entire plot was recorded and it was converted in per hectare area wise in kilograms.

12. Test Weight (g):

Randomly selected 1000 grains was counted from the sun - dried sample and then it was weighted in grams on electronic balance up to two decimal points.

(B) Quality attributing observations:
Sample wise observations will be recorded for each replication & each environment.

1. Hulling %:

A sample of 100 g of paddy was dehusked in a dehusker and then weight of each of the sample was taken and hulling percentage was calculated as per the following formula.

Hulling % = (weight of the dehusked grain / weight of the paddy) x 100

2. Milling %:

Entire dehusked kernels from each of the sample were used for milling by miller, adjusted to obtain standard polished grain. Milling percentage was calculated as follows.

Milling % = (weight of polished kernel / weight of paddy) x 100

3. **Head rice recovery (%):**

The milled rice was graded with different grading cylinder, as per requirement of grain size, after grading, full grains and ¾ size grains are separated from each of the sample from broken grains to quantification and weighted on electronic balance. Head rice recovery was calculated as per following formula:

$$\text{HRR \%} = \frac{\text{Weight of whole polished grain}}{\text{Weight of the paddy}} \times 100$$

4. **Kernel length (L) before cooking (mm):**

Length of kernel was measured from randomly selected 10 unbroken milled rice kernels (From each of the samples) with the help of calliper in millimetre and average was computed.

5. **Kernel breadth (B) before cooking (mm):**

Breadth of kernel was measured from randomly selected 10 unbroken milled rice kernels (From each of the samples) with the help of calliper in millimetre and average was computed.

6. **Kernel L/B ratio before cooking:**

Kernel L/B ratio before cooking was calculated by the formula given below:

$$\text{Kernel L/B ratio} = \frac{\text{Kernel length (L) before cooking (mm)}}{\text{Kernel breadth (B) before cooking (mm)}}$$

Table 3.3 Description of the rice lines used in present investigation.

Entry No.	Designation	Pedigree	Entry No.	Designation	Pedigree
1	CRR 719-1-B (IR 88903-34)	IR 77298-5-6-18/IR05N359	19	IR 92527-6-2-1-4	IR08L119/IR09N516
2	CRR 724-1-B (IR 88889-44)	IR 77298-14-1-2-10/IR05A260	20	IR 92545-53-4-1-3	THADOKKHAM 1/IR 77298-14-1-2-10
3	RP-1-27-7-6-1-2-1	TAICHUNG NATIVE 1/ T 141	21	IR 92545-54-6-1-4	THADOKKHAM 1/IR 77298-14-1-2-10
4	IR 94313:18-4-1-4-1-B	IR 81896-B-B-195/2*IR05F102	22	IR 92546-7-1-1-3	THADOKKHAM 1/IR08L119
5	IR 88287-383-1-B-B-1-1-B	IR 81896-B-B-182/2*SWARNA	23	IR 92546-17-6-4-3	THADOKKHAM 1/IR08L119
6	IR 94391-587-1-2-B	IR 81896-B-B-195/3*IR05F102	24	IR 92546-17-6-4-4	THADOKKHAM 1/IR08L119
7	IR 94314-20-2-1-B	IR 94312:1/SWARNA	25	IR 92546-33-3-1-1	THADOKKHAM 1/IR08L119
8	IR 93339:40-B-18-13-B-B-1	IR 77298-14-1-2-10/SANHUANGZHAN NO 2//IR 45427-2B-2-2B-1-1/NSIC RC 158///IRRI 123/IR 4630-22-2-5-1-3//FEDEARROZ 50/IR07F287	26	IR 92517-1-3-1-1	IRRI 154/IR08L118
9	IR 92521-5-3-1-2	IR08L217/IR08L183	27	IR 92522-45-3-1-4	IR08L183/MTU 1010
10	IR 92521-7-5-1-1	IR08L217/IR08L183	28	IR 92545-23-2-1-1	THADOKKHAM 1/IR 77298-14-1-2-10
11	IR 92521-23-6-1-3	IR08L217/IR08L183	29	IR 92545-24-3-1-1	THADOKKHAM 1/IR 77298-14-1-2-10
12	IR 92521-24-5-1-3	IR08L217/IR08L183	30	IR 92545-40-2-2-3	THADOKKHAM 1/IR 77298-14-1-2-10
13	IR 92522-47-2-1-1	IR08L183/MTU 1010	31	IR 92545-51-1-1-4	THADOKKHAM 1/IR 77298-14-1-2-10
14	IR 92522-47-2-1-4	IR08L183/MTU 1010	32	IR 92546-33-4-2-3	THADOKKHAM 1/IR08L119
15	IR 92522-61-3-1-4	IR08L183/MTU 1010	33	IR 92516-8-3-3-4	IRRI 154/IR08L119
16	IR 92523-35-1-1-1	IR09L347/CNA 10657	34	MTU 1010 (Check)	MTU 2077 (KRISHNAVENI)/IR 64
17	IR 92523-37-1-1-2	IR09L347/CNA 10657	35	IR 64 (Check)	IR 5657-33-2-1/IR 2061-465-1-5-5
18	IR 92527-6-2-1-2	IR08L119/IR09N516	36	LALAT (Check)	OBS 677/IR 2071//VIKRAM/W 1263

7. **Amylose content (%):**

Amylose is defined as the linear fraction of starch and composed of $1 – 4$ glycosidic linked alpha – D glucose unit.

Reagents: 1N NaOH, 1N acetic acid, Ethanol, Iodine solution (1g iodine and 10g KI are dissolved in water and make upto 500 ml)

Procedure: At first take some polished grains of rice and grind it in grinder then take 100 mg powdered sample in a volumetric flask and add 1ml ethanol and shake it after that add 9 ml 1N NaOH and shake again then boil the sample for 10 minutes on hot water bath. Make up the volume upto 100 ml and from whole sample, take only 5 ml extract and add 1 ml 1N acetic acid. Then add 2 ml iodine reagent and keep it under black cloths for 20 minutes. After that, make up the volume upto 100 ml and read absorbance at 620 nm with the help of spectrophotometer then we calculate amylose with standard curve or by the formula given below.

$$\% \text{ Amylose} = \text{abs (Absorption) (at 620 nm)} \times 75 \text{ (Factor)}$$

. Categories: Amylose can be categorized into low, intermediate and high based on the following grouping:

(Categories)	(%)
Waxy	(1-2)
Very low	(2-9)
Low	(10-20)
Intermediate	(20-25)
High	(25-30)

8. **Volume expansion ratio:**

It is the ratio between volumes of cooked sample (V_2) to uncooked sample (V_1)

Procedure: 50 ml water is taken in 100 ml measuring cylinder. 10 gm of uncooked polished rice is added in water and volume of displaced water was noted. The same sample was cooked in other glassware for 20 minutes. After cooking the sample was added in 50 ml water in a measuring cylinder then increased volume of water was noted.

It was calculating by a formula given below:

$$\text{Volume expansion ratio} = V_2 / V_1$$

Where,

V_2 = Volume of cooked sample

V_1 = Volume of uncooked sample

9. Kernel elongation ratio:

It was the ratio of kernel length after cooking to the kernel length before of the average of the 10 kernels from each sample.

3.2.3. Molecular diversity (allelic diversity) analysis through traits linked with simple sequence repeat (SSR) markers:

3.2.3.1. DNA Extraction:

Genomic DNA from leaves of individual genotypes was extracted from 3 week old seedling of 36 genotypes using CTAB method (Doyle and Doyle, 1990). 100 mg leaf tissues were cut into tiny pieces, homogenized and digested with 2 ml DNA extraction buffer [100Mm Tris - Cl (8.0), 1.4M Nacl, 20Mm EDTA(8.0), 2%(w/v) CTAB], a pinch of Polyvinylpyrrolidone and 30µl of mercapthethanol. 750 µl of leaf extracts was placed in waterbath at 65ºC for 45 minutes and was shaked at regular interval. Following incubation, 750 µl solution of chloroform and isoamyl alcohol (24:1) was added, mixed well and centrifuged for 5 minutes at 10,000 rpm. The supernatent was collected and 750 µl of chloroform and isoamyl alcohol (24:1) was again added and was centrifuged for 5 minutes at 10,000 rpm. 750 µl of isopropanol was added to the supernatant, mixed and centrifuged for 10 minutes at 10,000 rpm. Supernatent was discarded leaving a pellet at the bottom of the tube. The DNA pellet was washed with 70% chilled ethanol and air dried. The pellet was dissolved in 15 µl of 10:1 TE buffer (50 mM Tris, 10 mM EDTA). Quality and quantity of DNA sample was examined under visualization of 0.8% Agarose gel in UV spectrophotometer and it was further diluted to a uniform concentration of 50 ng/µl. The extracted DNA samples, along with the diluted samples were stored at -40˚C freezer (REMI quick freezer, model no. NEK2168GK).

3.2.3.2. PCR Amplification through SSR Primers:

Diluted DNA samples were subjected to PCR amplification, using the selected SSR primers in automated thermal cycler (Applied Biosystems model veriti). PCR reaction was carried out in 12µl reaction volume containing 2µl (100ng) of extracted genomic DNA, 1.2µl

10X PCR buffer, 2.5 mM MgCl$_2$, 0.1 mM of dNTPs, 0.83 µM of forward, 0.83 µM of reverse primer and 0.35U of Taq DNA Polymerase. Template DNA was initially denatured at 94ºC for 4 minutes followed by 35 cycles (30 sec denaturation at 94ºC, 40 sec annealing at 55ºC, 40 sec of primer extension at 72ºC) of PCR amplification, and final extension of 72ºC for 10 min followed by hold at 4ºC. On completion of reaction, 2 µl 6X gel loading buffer (Genei) was added to the PCR product. The amplified fragments were separated on 2.5% agarose gel containing ethidium bromide and run for 2 hours in 1X TAE buffer and imaged under gel documentation system.

3.3. Statistical Analysis:

Data recorded on different yield and quality and its contributing characters were compiled and subjected for statistical analysis as mentioned below:

Standard statistical formula was followed for the calculation of;

- Mean performance and range of the genotypes in given environments.
- Analysis of variance (ANOVA) and critical difference for the various characters under different environments.
- Variance and coefficient of variance (VG, VP, VE, GCV, PCV and ECV).
- Heritability (broad sense) of the characters for all the rice lines.
- Genetic advance and genetic gain of the characters for all genotypes.
- Characters association through correlation coefficient analysis.
- Direct and indirect effects on yield and quality through path coefficient analysis.
- Genotype x environment interaction for different characters.
- Phenotypic stability using Eberhart and Russell (1966) model.
- Genetic divergence (D^2 Analysis)
- Molecular diversity analysis (UPGMA method)

3.3.1. Mean performance and Range:

Mean performance:

Mean value for the each genotype over replication were calculated in different environments using the formula given below.

$$\bar{X} = \frac{\sum_{i=1}^{n} X_i}{N}$$

Where, $\sum X_i$ = Summation of all the observations

N = Total number of observations

Range:

Range is the difference between the lowest and highest mean values for each character which were taken in the observation in a sample.

$$R = R_2 - R_1$$

Where,

R_1 = Lowest mean value

R_2 = Highest mean value

3.3.2. Analysis of variance and critical difference:

Analysis of variance (ANOVA):

The total variation was partitioned into 3 components respectively viz., replication, genotype and error according to the method suggested by **Federer (1955)** for RBD (Table 3.4) to test the null hypothesis.

Critical difference:

Critical difference was calculated by the following formula.

$$C.D. = \sqrt{2EMS/r} \text{ x } t_{edf \text{ at } 5\%}$$

Where,

r = Number of replications

EMS = Error mean sum of squares

t_{edf} at 5% = Table value of 't' at error degrees of freedom at 0.05 level of significance

Table 3.4 Analysis of variance and expectation of mean square:

Source of variation	Degree of freedom	Sum of square	Mean sum of square Observed - Expected	F -Value
Replication	(r-1)	$\dfrac{1}{g} \sum_{j} y_j^2 - CF$	$Mr = \sigma_e^2 + \sigma_g^2$	
Genotype	(g-1)	$\dfrac{1}{r} \sum_{i} y_i^2 - CF$	$Mg = \sigma_e^2 + r\sigma_g^2$	$\dfrac{Mg}{Me}$
Error	(r-1) (g-1)	$\sum_{i} \sum_{j} y_{ij}^2 - CF - RRS - GSS$	$Me = \sigma_e^2$	
Total	(rg-1)	$\sum_{i} \sum_{j} y_{ij}^2 - CF$		

$$\text{S. Em.} = \sqrt{Me/r}$$

C.D. = S.EM. x t at 5% (error d. f.)

C. V. = $\sigma / \bar{X}$ x100

Where,

R = Number of replications

g = Number of genotypes

y_j = Total of jth block

y_i = Total of ith genotypes

Mr = Mean sum of square due to replication (block)

Mg = Mean sum of square due to genotypes

σ_e^2 = Error variance

σ_g^2 = Genotypic variance

σ = Standard deviation

$\bar{X}$ = General mean

Test of significance:

If the variance ratio (calculated F) was greater than the tabulated F value at 5% level of significance the difference between the different genotypes in terms of different character was considered to be significant and if it was lower than the tabulated value, it was considered to be non-significant.

3.3.3. Variance and Co-variance:

Variance:

It is defined as the average of the square deviation from the mean on it is the square of the standard deviation; it is an effective measure of variability, which permits partition of variance into various components.

Genotypic variance:

The genotypic variance (VG or $\sigma^2{}_g$) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was

$$VG = \frac{V_t - EMS}{r}$$

Where,

V_t = MSS due to treatment

EMS = Error mean sum of squares

Phenotypic variance:

Phenotypic variance (VP or σ^2_p) denotes the total variance present in a population for particular character and is calculated by following formula.

VP = Genotypic variance (VG) + Error variance (VE)

Environmental or error variance:

The environmental variance (VE or σ^2_e) is the variance due to environmental deviation.

VE = EMS (Error mean sum of square)

Standard deviation:

It is the square root of the variance or square root of the arithmetic mean of square from the population mean. It calculated by the formula given below.

$$SD = \sqrt{\sum X^2 - (\sum X^2)/N / N - 1}$$

Where,

$\sum$, X, X^2 and N = Summation, an observation, square of an observation and number of observation respectively.

Coefficient of variation:

It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage.

$$CV\ (\%) = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

In the present investigation three types of coefficient of variations were estimated *viz.,* phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV). The formulae used to calculate PCV, GCV and ECV were given by Burton (1952).

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$$

$$= \frac{\sqrt{VP}}{\overline{X}} \times 100$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation}}{\text{Grand mean}} \times 100$$

$$= \frac{\sqrt{VG}}{\overline{X}} \times 100$$

$$\text{ECV (\%)} = \frac{\text{Error standard deviation}}{\text{Grand mean}} \times 100$$

$$= \frac{\sqrt{VE}}{\overline{X}} \times 100$$

3.3.4. Heritability (broad sense)

Heritability in broad sense (bs) is the ratio of genotypic variance to the total variance. It is that portion of total variability or phenotypic variability which is heritable and due to the genotype. It was calculated by the formula given by Lush (1949**)** and Burton and Devane (1953).

$$h^2 = \frac{VG}{VP} \times 100$$

Where, VG = genotypic variance

VP = phenotypic variance

3.3.5. Genetic advance and Genetic gain:

Genetic advance:

Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. The estimates of genetic advance were obtained by the formula given by Lush (1949) and Johnson *et al.* (1955).

$$GA = K. \, \sigma_p. \, h^2$$

Where,

K   = Constant selection differential at 5% level intensity (= 2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability in broad sense

Genetic gain:

The genetic gain is the difference between the mean of the progeny of selected individuals (Xp) and the base population (Xo).

$$R = X_p - X_o$$

It can also be predicted using following formula

$$R = i \, \sigma_p \, h^2$$

Where,

i   = standardized selection differential

σ_p = phenotypic standard deviation

h^2 = heritability (broad sense)

3.3.6. Correlation co-efficient:

Correlation coefficient is the mutual association between variables without implying any cause and effect relationship or to find out the relationship of different characters with yield & quality and among themselves also, simple correlation coefficients were computed at genotypic and phenotypic levels between pair of characters adopting following formula given by Panse and Sukhatme (1978).

Simple correlation co-efficient:

$$r \, X_1 . X_2 \quad = \quad \frac{Cov(X_1 . X_2)}{\sqrt{\sigma^2 X_1 . \sigma^2 X_2}}$$

Where,

Cov. ($X_1 \cdot X_2$) = Covariance between characters X_1 and X_2

$\sigma^2 X_1$ = Variance of characters X_1

$\sigma^2 X_1$ = Variance of characters X_2

Test of significance:

To test the significance of correlation coefficient, the estimated values were compared with table values of correlation coefficient prescribed by Fisher and Yates (1938) at (n - 2) treatment degree of freedom at 5% and 1% level of significance of the calculated value of correlation coefficient is greater than tabulated value of considered to be significant and vice-versa.

3.3.7. Path coefficient analysis:

This technique was firstly used by Dewey and Lu. Wright (1921) and Dewey & Lu (1959) suggested that using phenotypic correlation, the direct and indirect effect of yield components upon yield can be worked out by path analysis. Path analysis was worked out by using the estimates of correlation coefficient in all possible combinations among the dependent variables. The path coefficient analysis is simply the standardized partial regression coefficient, which splits the correlation coefficient into the measures of direct and indirect effects of independent variables on the dependent variables. It is the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect. If Y is the effect and X_1 is the cause, the path co-efficient for the path from X_1 to the effect of Y is σ_{X_1} / σ_y. The path co-efficient were obtained by solving a set of linear simultaneous equation of the form indicating the relationship between correlation and path coefficient.

$$r_{yn} = P_{yi} + P_{y2}.r_{2n} + P_{y3}.r_{3n} + ...P_{yn} + r_{yn}$$

Where,

r_{yn} = Correlation between n^{th} characters and yield.

P_{yn} = Direct path coefficient between n^{th} characters and yield.

r_{2n}, r_{3n}, etc = Denotes correlation between 2nd characters, 3rd characters etc.

n = 1, 2, 3............. n various casual characters.

Considering all the simultaneous equations, correlation matrices of the following forms were prepared.

Matrix (A)   Matrix (B)   Matrix (P)

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ . \\ r_{ny} \end{bmatrix}_{n \times 1}$$

$$\begin{pmatrix} 1 & r_{12} & r_{13} & L\,L & r_{1n} \\ r_{21} & 1 & r_{23} & L\,L & r_{2n} \\ M & M & M & & M \\ M & M & M & & M \\ r_{n1} & r_{n2} & r_{n3} & L\,L & 1 \end{pmatrix}_{m\,x\,n}$$

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ . \\ . \\ r_{ny} \end{bmatrix}_{n \times 1}$$

or   A = B, P

$$P = B^{-1} A$$

Where,

$\underline{A}$ = Col. (A_{1y} - r_{ny}), B is corr. Matrix of order n x n

$\underline{P}$ = Col. (P_{1y} – P_{ny})

The indirect effect of a particular character through other characters was worked out by multiplying of direct paths and particular correlation coefficients between those characters, respectively.

Indirect effect of jth trait through i^{th} = $Y_{ij}\,P_{ij}$

Where,

i, j = 1 .... n

$P_{ij} = P_{1y}\,P_{2y}$ ....P_{ny}

The residual factors (Undefined factors), i.e. the variation in yield unaccounted by casual effects under consideration was termed as x. The path value for residual (x) was calculated as follows:

Residual factors P^2 (xy) = $\dfrac{1 - R^2}{\sqrt{1 - \sum_i P_{1y}^2 - 2\sum_{ij} P_{1y}\,P_{iy}\,P_{ij}}}$

Where,

R^2 is the co-efficient of determination and amount of variation in yield also that can be accounted for by the yield component characters.

3.3.8. Genotype – environment interaction:

Analysis of genotype – environment interaction was worked out from the two way table of mean value (Table 3.5.) and ANOVA table will be as follows.

Table 3.5. Analysis of variance for genotype x environment interaction

Source of variation	Degree of freedom	Sum of square	Mean sum of square	F
Genotype (G)	(g-1)	$(1/nr) \sum_i y_i^2 ...... - (y^2 / grn)$	MS_1	
Environment (E)	(n-1)	$(1/gr) \sum_i y_j^2 ...... - (y^2 / grn)$	MS_2	MS_2/MS_4
G x E	(g-1) x (n-1)	$(1/r) \sum_i \sum_j y_{ijk}^2 - y^2 ... / grn$	MS_3	MS_3/MS_4
Pooled error	n (r-1) x (g-1)	$\sum_i S_{ie}^2 /n$	MS_4	

Where,

g　　= Number of genotypes

n　　= Number of environments

S_{ie}^2 /n　= Estimate of error mean square

3.3.9. Phenotypic stability analysis through Eberhart and Russell model (1966):

The phenotypic stability analysis was carried out on the basis of the following mathematical model.

$$Y_{ij} = \mu_i + B_i.I_j + d_{ij}$$

Where,

Y_{ij}　=　Mean performance of the ith genotype in j^{th} environment

μ_i　=　Mean of the ith genotype over all the environments

B_i　=　Regression co- efficient that measure the linear response of ith genotype to several environments

d_{ij} = Deviation from the regression of the ith genotype in the jth environment

I_j = Environmental index, obtained as the mean of all the genotypes at the j environment minus the grand mean

$$I_j = \left(\sum_i Y_{ij} / g \right) - \left(\sum_i \sum_j Y_{ij} / gn \right)$$

With check: $\sum_j I_j = 0$

Phenotypic stability parameters:

All three parameters were determined to describe the stability of a genotype.

(A) Mean performance of a genotype over the environments was calculated as follows:

$$\bar{X} = \sum_j Y_{ij} / n$$

Where,

$\bar{X}$ = Mean of the genotype

n = Number of environments

Y_{ij} = Performance of ith genotype in j^{th} environment

(B) Regresion co – efficient (b_i) which was estimated as follows:

$$b_i = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

Where,

$\sum_j Y_{ij} I_j$ = Sum of products

$\sum_j I_j^2$ = Sum of square

(C) Mean square deviation from linear regression (S^2_{di}) was estimated as:

$$S^2_{d_i} = \frac{\sum_j d_{ij}^2}{n-2} - \frac{s_e^2}{r}$$

Where,

$$\sum_j d_{ij}^2 = \left[\sum_j Y^2_{ij} - \frac{Y_i^2}{g} \right] - \frac{\sum Y_{ij} I_j^2}{\sum_j I_j^2}$$

$\dfrac{S_e^2}{r}$ = The estimate of pooled error i. e. The average of error mean sum of square over all the environments.

Analysis of variance (ANOVA) for stability:

The main features of this analysis is that sum of squares due to genotype x environment (SS₃) is further partitioned into two parts (Table 3.6.).

(A) SS due to G x E (linear) which is in fact S.S. due to regression (SS₄).

(B) SS due to deviation from linearity of response (SS due to pooled deviation) (SS₅).

The pooled deviation has been further partitioned into as many components as the number of genotypes with (n-2) degree of freedom.

Table 3.6 Analysis of variance for phenotypic stability:

Source of Variation	Degree of freedom	Sum of square	MSS	F - value
Total	(ng-1)	$\sum\limits_{j}\sum\limits_{j} Y_{ij}^2 - CF = TSS$		
Genotype	(g-1)	$\dfrac{1}{N}\sum\limits_{j} Y_i^2 - CF = GSS$	MS₁	MS₁/MS₃
Environment	(n-1)	$\dfrac{1}{G}\sum\limits_{j} Y_j^2 - CF = ESS$	MS₂	MS₂/MS₃
G x E	(g-1) (n-1)		MS₃	MS₃/MS₆
Env. (linear)	1	$\dfrac{1}{G}(\sum\limits_{j} Y_j I_j)^2 / \sum\limits_{j} I_j^2$		
G x E (linear)	(g-1)	$\sum \left[(\sum Y_{ij})^2 / \sum r_j^2\right] - Env.(Linear)SS - SS_4$	MS₄	MS₄/MS₅
Pooled deviation	g(n-2)	$\sum\sum \sigma_{ij}^2 = SS_5$	MS₅	
Genotype 1	(n-2)	$\sum\limits_{j} Y_{ij}^2 - \dfrac{(Y_i)^2}{n} - (\sum\limits_{j} Y_{ij} I_j)^2 / \sum\limits_{j} r_j^2$		
.				
.				
.				
.				
Genotype g	(n-2)	$\left[\sum\limits_{j} Y^2_{gi} - \dfrac{Y^2 g}{n}\right] - \sum\limits_{j} Y_{gi} J^2_j / \sum\limits_{j} r^2_j \sum\limits_{i} \sigma^2_{gi}$	MS₆	
Pooled error	n(r-1) (g-1)	$\sum\limits_{i} S_{ie}^2 / n$		

Where,

        g = Number of genotypes

        n = Number of environments

        r = Number of replications

        S^2_{ie} = Estimate of error mean square at each environment

$\sum_{i} S^2_{ie} / n$ = MS for pooled error

Test of significance:

Test of significance were performed given below.

(a) The significance of the difference among genotypes mean was tested using the 'F' test as:

$$F = MS_1/MS_3$$

(b) The significance of difference among environments was tested through the 'F' test as:

$$F = MS_2/MS_3$$

(c) The genotype x environment interaction was tested by the 'F' test as:

$$F = MS_3/MS_6$$

(d) The genetic differences among the genotypes for their regression on the environmental index were tested using the 'F' test as:

$$F = MS_4/MS_5$$

(e) A test of deviation from regression of each genotype was obtained as:

$$F = \frac{(\sum_{i} d^2_{ij}) / (n-2)}{MS_6}$$

3.3.10. Genetic divergence analysis (D^2 statistics):

      To study the genetic divergence among 36 genotypes in the present investigation and to know the fluctuation in clustering pattern of those genotypes, D^2 values were calculated by using D^2 statistics of 21 yield and quality related characters were taken into consideration for this analysis. Following the analysis of variance and co – variance the data was subjected to multivariate analysis, given by Mahalanobis (1928) D^2 statistics. It was calculated according to Rao (1952). Original variable mean were transformed to uncorrelated variables by the pivotal consideration method.

      D^2 values were calculated for multiple pair of combinations, as the sum of differences of the varieties over all transformed variables.

$$D^2 = d_{ij} (X_{i1} - X_{i2}) (X_{j1} - X_{j2})$$

Where,

d_{ij} = Inverse of estimate of variance covariance matrix.

Suppose, if we take 3 characters.

The,

$$D^2 = d_{11} (X_{11} - X_{12})^2 + d_{22} (X_{21} - X_{22})^2 + d_{33} (X_{31} - X_{32})^2 + d_{12} (X_{11} - X_{12}) (X_{21} - X_{22}) + d_{13} (X_{11} - X_{12}) (X_{31} - X_{32}) + d_{23} (X_{21} - X_{22}) (X_{31} - X_{32})$$

To simplify the computational procedure the variables X_1, X_2 and X_3 were transformed to a new set of uncorrelated variables, Y_1, Y_2 and Y_3. Distance D^2 computed by X_1, X_2 and X_3 will be same when computed by Y_1, Y_2 and Y_3.

Hence, the reduced formula would be $D^2 = D^2_1 + D^2_2 + D^2_3$

Now D^2 values which are the sum of square of the differences in transformed uncorrelated values for various characters were calculated and significance of D^2 values were tested treating as X^2 (Chi-square) values at 5% and 1% level of significance.

Formation of group constellation:

The simple device suggested by Tocher (Rao, 1952) was to start with two closely associated treatments and find a third treatment which had the smallest average D^2 from the first two. Similarly, the fourth was chose to have smallest average D^2 of a variety from these already listed appeared to be high then this variety did not fit in with the former varieties and was, therefore, taken outside the former group. The varieties of first cluster were then omitted and rests are treated similarly to form second cluster, third cluster and soon. After formation of clusters on the basis of D^2 values the intra and inter cluster distance were obtained by calculating the average D^2 between any two groups. The square root of the D^2 values represented the distance between and within groups.

Contribution of individual characters towards divergence:

In all the combinations, each character is ranked on the basis of $d_i = Y^j_i - Y^k_i$ values. Rank – I is given to the highest mean difference and Rank – P to the lowest mean difference were P is the total numbers of characters and finally the percent (%) contribution is calculated.

Determination of cluster mean:

The cluster mean for a particular character is the summation of mean values (correlated) of genotypes included in a cluster divided by number of genotypes in the cluster. These values were calculated separately for each cluster and each character.

3.3.11 Molecular diversity analysis (UPGMA method):

Allelic Diversity Analysis:

The frequency of SSR polymorphism was calculated on the basis of presence or absence of common bands where presence was denoted by 1 and absence was denoted by 0. Polymorphism Information Content (PIC) values were calculated by using the given formula.

$$PIC = \frac{1}{n}\sum 2F(1-F)$$

Where,

F = Proportion of a particular allele among the genotypes,

n = No. of alleles generated.

The genetic associations among 36 genotypes of rice were evaluated through Jaccard's similarity coefficient. Dendogram was generated with UPGMA.

CHAPTER – 4
EXPERIMENTAL FINDINGS

Experimental Findings:

The experimental findings on assessment of genetic variability, characters association and their direct and indirect effects, genetic diversity on the basis of morphological as well as molecular level and phenotypic stability analysis using Eberhart and Russell model among thirty six advance indica rice lines (Table 4.0) has been presented in this section. Findings of experiment on the basis of pooled data from the four different environments have been discuss with the help of previous research reports under the following sub - heads:

4.1 Analysis of variance for different characters

4.2 Mean performance of the advance rice lines for different characters

4.3 Estimates of components of variances for different characters

4.4 Heritability (bs) and genetic advance for different characters in rice

4.5 Estimates of correlation coefficient for different characters in rice

4.6 Estimates of path coefficient analysis for different characters in rice

4.7 Genetic divergence analysis among different advance rice lines

4.8 Molecular diversity analysis among rice lines using SSR markers

4.9 Phenotypic stability analysis (Eberhart and Russell model, 1966)

4.1 Analysis of variance for different characters:

The analysis of variance was performed to test the null hypothesis among thirty six advance lines of rice on the basis of pooled data and separate environment wise data from different environments for 21 yield and quality traits. The mean sum of square due to genotypes for the characters namely days to 50% flowering, plant height, days to maturity, number of tillers per plant, number of productive tillers per plant, panicle length, number of spikelets per panicle, grain yield per plant, biological yield per plant, harvest Index, test weight, hulling recovery percentage, milling recovery percentage, head rice recovery, kernel length before cooking, amylose content and grain yield kilogram per hectare were found highly significant (Table 4.1) except some quality characters namely kernel breadth before cooking, kernel L/B ratio before cooking, volume expansion ratio and kernel elongation ratio.

Table 4.0: Important codes, abbreviations and symbols for following activities

Code - 1	Code - 2	Genotypes	Characters	Abbreviations / Symbols
1	A	CRR 719-1-B (IR 88903-34)	DFF	Days to 50% flowering
2	B	CRR 724-1-B (IR 88889-44)	PH	Plant height
3	C	RP-1-27-7-6-1-2-1	DM	Days to maturity
4	D	IR 94313:18-4-1-4-1-B	NT/Pt	Number of tillers per plant
5	E	IR 88287-383-1-B-B-1-1-B	NPT/m^2	Number of productive tillers per meter square
6	F	IR 94391-587-1-2-B	PL	Panicle length
7	G	IR 94314-20-2-1-B	NSP/P	Number of spikelet's per panicle
8	H	IR 93339:40-B-18-13-B-B-1	GY/Pt	Grain yield per plant
9	I	IR 92521-5-3-1-2	BY/Pt	Biological yield per plant
10	J	IR 92521-7-5-1-1	HI	Harvest index
11	K	IR 92521-23-6-1-3	TW	Test weight
12	L	IR 92521-24-5-1-3	HULL. %	Hulling recovery %
13	M	IR 92522-47-2-1-1	MILL. %	Milling recovery %
14	N	IR 92522-47-2-1-4	HRR %	Head rice recovery %
15	O	IR 92522-61-3-1-4	KLBC	Kernel length before cooking
16	P	IR 92523-35-1-1-1	KBBC	Kernel breadth before cooking
17	Q	IR 92523-37-1-1-2	L/B RATIO	Length / Breadth ratio before cooking
18	R	IR 92527-6-2-1-2	AMYLOSE C.	Amylose content
19	S	IR 92527-6-2-1-4	VER	Volume expansion ratio
20	T	IR 92545-53-4-1-3	KER	Kernel elongation ratio
21	U	IR 92545-54-6-1-4	GYKG/Ha	Grain yield kilogram per hectare
22	V	IR 92546-7-1-1-3	*	Significance at 5% level
23	W	IR 92546-17-6-4-3	**	Significance at 1% level
24	X	IR 92546-17-6-4-4		
25	Y	IR 92546-33-3-1-1		
26	Z	IR 92517-1-3-1-1		
27	AA	IR 92522-45-3-1-4		
28	AB	IR 92545-23-2-1-1		
29	AC	IR 92545-24-3-1-1		
30	AD	IR 92545-40-2-2-3		
31	AE	IR 92545-51-1-1-4		
32	AF	IR 92546-33-4-2-3		
33	AG	IR 92516-8-3-3-4		
34	AH	MTU 1010 (Check)		
35	AI	IR 64 (Check)		
36	AJ	LALAT (Check)		

Table 4.1: Analysis of variance for different characters in rice

S.No.	Characters	Mean sum of square		
		Replication (df = 02)	Treatment (df = 35)	Error (df = 385)
1	DFF	9.52	52.00**	14.38
2	PH	11.04	211.46**	39.53
3	DM	1.29	62.01**	17.23
4	NT/Pt	1.56	7.26**	1.92
5	NPT/m^2	100.17	4544.87**	530.46
6	PL	3.53	9.22**	2.16
7	NSP/P	444.44	5822.61**	227.48
8	GY/Pt	0.17	33.64**	7.49
9	BY/Pt	23.54	414.32**	21.27
10	HI	3.74	156.62**	26.32
11	TW	0.53	35.45**	1.76
12	HULL. %	4.44	43.47**	7.42
13	MILL. %	1.10	39.12**	8.32
14	HRR %	1.34	325.31**	5.50
15	KLBC	0.05	1.71**	0.10
16	KBBC	0.00	0.08	0.02
17	L/B RATIO	0.05	0.95	0.08
18	AMYLOSE C.	0.20	16.99**	0.94
19	VER	0.00	0.01	0.00
20	KER	0.00	0.07	0.00
21	GYKG/Ha	9750.21	2185969.75**	127794.41

4.2 Mean performance of the advance rice lines for different characters:

The pooled analyzed data presented in the series of tables (Table 4.2, 4.3, 4.4 and 4.5) showed mean performance and the range of thirty six advanced rice lines for twelve yield and nine quality attributing traits.

4.2.1 Days to 50% flowering:

Mean performance of the lines for the days to 50% flowering ranged from 77.83 to 87.58 days with grand mean of 83.29 days. Genotype CRR 724-1-B (IR 88889-44) (77.83 days) followed by IR 94313:18-4-1-4-1-B (79.17 days), IR 92545-53-4-1-3 (80.33 days) and CRR 719-1-B (IR 88903-34) (80.42 days) found best genotypes with earliest days to 50% flowering out of best check MTU 1010 (81 days) while genotype IR 93339:40-B-18-13-B-B-1 (87.58 days) followed by IR 94314-20-2-1-B (85.92 days) and IR 92546-17-6-4-3 (85.75 days) showed maximum number of days for days to 50% flowering.

4.2.2 Plant height:

Mean performance for the plant height ranged from 93.23 to 108.12 cm with grand mean of 99.76 cm. Genotype IR 92527-6-2-1-4 (93.23 cm) followed by IR 92546-17-6-4-4 (93.54 cm) and IR 94313:18-4-1-4-1-B (94.07 cm) found best genotypes with lowest plant height out of best check IR 64 (97.18 cm) while genotype IR 92521-5-3-1-2 (108.12 cm) followed by IR 92521-23-6-1-3 (187.83 cm) showed maximum plant height.

4.2.3 Days to maturity:

Mean performance for the days to maturity ranged from 110.92 to 120.75 days with grand mean of 115.80 days. Genotype IR 94313:18-4-1-4-1-B (110.92 days) followed by IR 92521-24-5-1-3 (112 days) found best genotypes with lowest number of days to maturity out of best check MTU 1010 (112.25 days) while genotype IR 92521-23-6-1-3 (120.75 days) followed by IR 93339:40-B-18-13-B-B-1 (119 days) and IR 92522-47-2-1-1 (118.67 days) showed highest days to maturity.

4.2.4 Number of tillers per plant:

Mean performance for the number of tillers per plant ranged from 8.67 to 12 with grand mean of 10.81. Genotype IR 88287-383-1-B-B-1-1-B (11.92) followed by RP-1-27-7-6-1-2-1 (11.83) and IR 92522-61-3-1-4 (11.58) found best genotypes with maximum number of tillers per plant out of one of the check IR 64 (10.50) while genotype IR 92521-5-3-1-2 (8.67) followed by IR 92521-23-6-1-3 (9.25) showed lowest number of tillers per plant.

4.2.5 Number of productive tillers per meter square:

Mean performance for the number of productive tillers per meter square ranged from 182.75 to 272.92 with grand mean of 228.75. Genotype IR 92546-7-1-1-3 (272.92) followed by IR 92546-33-3-1-1 (260.83) found best genotypes with maximum number of productive tillers per meter square out of best check IR 64 (260.67) while genotype IR 92521-24-5-1-3 (182.75) followed by IR 92521-5-3-1-2 (195.58) showed minimum number of productive tillers per meter square.

4.2.6 Panicle length:

Mean performance for the panicle length ranged from 24.39 to 28.31 cm with grand mean of 26.06 cm. Genotype IR 93339:40-B-18-13-B-B-1 (27.54 cm) followed by IR 92545-40-2-2-3 (27.41cm) and IR 92522-61-3-1-4 (27.27 cm) found best genotypes with maximum panicle length out of best check IR 64 (26.31 cm) while genotype IR 92522-47-2-1-1 (24.39 cm) followed by IR 92521-24-5-1-3 (24.47 cm) showed lowest panicle length.

4.2.7 Number of spikelets per panicle:

Mean performance for the number of spikelets per panicle ranged from 120.17 to 209.25 with grand mean of 152.45. Genotype IR 92521-7-5-1-1 (209.25) followed by IR 92521-24-5-1-3 (199.50) and IR 92521-5-3-1-2 (196.75) found best genotypes with maximum number of spikelets per panicle out of best check IR 64 (144.50) while genotype IR 92545-54-6-1-4 (120.17) followed by IR 92523-35-1-1-1 (124.08) showed lowest number of spikelets per panicle.

4.2.8 Grain yield per plant:

Mean performance for the grain yields per plant ranged from 24.67 to 31.58 gm with grand mean of 27.62 gm. Genotype IR 94314-20-2-1-B (31.58 gm) followed by IR 92521-24-5-1-3 (30.42 gm) and IR 92523-37-1-1-2 (30.42 gm) found best genotypes with highest grain yields per plant out of best check LALAT (28.17 gm) while genotype IR 92521-7-5-1-1 (24.67 gm) followed by IR 92545-40-2-2-3 (24.67 gm) showed lowest grain yields per plant.

4.2.9 Biological yield per plant:

Mean performance for the biological yields per plant ranged from 56.92 to 76.92 gm with grand mean of 67.46 gm. Genotype IR 92527-6-2-1-4 (76.92 gm) followed by IR

94314-20-2-1-B (75.17 gm) and IR 92521-24-5-1-3 (75.00 gm) found best genotypes with highest biological yields per plant out of best check LALAT (68.50 gm) while genotype IR 92545-23-2-1-1 (56.92 gm) followed by IR 92545-24-3-1-1 (60.08 gm) showed lowest biological yields per plant.

4.2.10 Harvest index:

Mean performance for the harvest index ranged from 34.20 to 47.76 % with grand mean of 41.33 %. Genotype IR 92546-17-6-4-4 (47.76 %) followed by IR 92522-45-3-1-4 (47.47 %) and IR 92545-23-2-1-1 (47.14 %) found best genotypes with maximum harvest index out of best check IR 64 (46.04 %) while genotype IR 92545-40-2-2-3 (34.20 %) followed by IR 92521-7-5-1-1 (35.01 %) showed minimum harvest index.

4.2.11 Test weight (1000 grain weight):

Mean performance for the test weight ranged from 20.47 to 27.96 gm with grand mean of 24.25 gm. Genotype IR 92522-45-3-1-4 (27.96 gm) followed by IR 92545-40-2-2-3 (27.80 gm) and CRR 724-1-B (IR 88889-44) (26.92 gm) found best genotypes with maximum test weight out of best check LALAT (26.58 gm) while genotype IR 92546-33-4-2-3 (20.47 gm) followed by IR 92521-5-3-1-2 (22.00 gm) showed lowest test weight.

4.2.12 Hulling recovery (%):

Mean performance for the hulling recovery ranged from 69.41 to 77.35 % with grand mean of 74.51%. Genotype IR 92545-40-2-2-3 (77.35 %) followed by IR 92545-51-1-1-4 (77.15 %) and IR 92523-35-1-1-1 (76.57 %) found best genotypes with maximum hulling recovery out of best check MTU 1010 (76.42 %) while genotype RP-1-27-7-6-1-2-1 (69.41 %) followed by IR 92527-6-2-1-2 (69.75 %) showed lowest hulling recovery.

4.2.13 Milling recovery (%):

Mean performance for the milling recovery ranged from 56.98 to 65.99 % with grand mean of 62.64 %. Genotype IR 93339:40-B-18-13-B-B-1 (65.99 %) followed by IR 92527-6-2-1-2 (65.93 %) and IR 92522-47-2-1-4 (65.26 %) found best genotypes with maximum milling recovery out of best check IR 64 (63.61 %) while genotype IR 92522-45-3-1-4 (56.98 %) followed by IR 94391-587-1-2-B (59.58 %) showed lowest milling recovery.

4.2.14 Head rice recovery (%):

Mean performance for the head rice recovery ranged from 40.01 to 58.22 % with grand mean of 48.20 %. Genotype IR 92521-5-3-1-2 (58.22 %) followed by IR 92521-7-5-1-1 (56.02 %) and IR 92521-23-6-1-3 (55.92 %) found best genotypes with maximum head rice recovery out of best check IR 64 (55.08 %) while genotype IR 92522-47-2-1-4 (40.01 %) followed by IR 93339:40-B-18-13-B-B-1 (40.12 %) showed lowest head rice recovery.

4.2.15 Kernel length before cooking:

Mean performance for the kernel length before cooking ranged from 6.22 to 7.71 mm with grand mean of 7.05 mm. Genotype IR 92522-47-2-1-4 (7.71 mm) followed by IR 92545-53-4-1-3 (7.63 mm) and IR 94313:18-4-1-4-1-B (7.53 mm) found best genotypes with largest kernel length before cooking out of the best checks IR 64 (7.02 mm) and LALAT (7.02 mm) while genotype IR 92521-23-6-1-3 (6.22 mm) followed by IR 92521-7-5-1-1 (6.26 mm) showed lowest kernel length before cooking.

4.2.16 Kernel breadth before cooking:

Mean performance for the kernel breadth before cooking ranged from 1.92 to 2.23 mm with grand mean of 2.09 mm. Genotype IR 92521-7-5-1-1 (2.23 mm) followed by IR 92523-37-1-1-2 (2.21 mm) found best genotypes with largest kernel breadth before cooking out of the best check LALAT (2.16 mm) while genotype IR 92522-47-2-1-4 (1.92 mm) followed by IR 92545-53-4-1-3 (1.92 mm) showed lowest kernel breadth before cooking.

4.2.17 Kernel L/B ratio before cooking:

Mean performance for the kernel L/B ratio before cooking ranged from 2.81 to 4.02 with grand mean of 3.39. Genotype IR 92522-47-2-1-4 (4.02) followed by IR 92545-53-4-1-3 (4.01) and IR 92527-6-2-1-4 (3.88) found best genotypes with highest kernel L/B ratio before cooking out of the best check MTU 1010 (3.36) while genotype IR 92521-7-5-1-1 (2.81) followed by IR 92521-23-6-1-3 (2.96) showed lowest kernel L/B ratio before cooking.

4.2.18 Amylose content:

Mean performance for the amylose content ranged from 19.25 to 24.62 % with grand mean of 22.13 %. Genotype IR 92546-17-6-4-3 (24.20 %) followed by CRR 719-

1-B (IR 88903-34) (24.16 %) and IR 92546-33-3-1-1 (23.91 %) found best genotypes with highest amylose content out of one of the check IR 64 (22.63 %) while genotype IR 94314-20-2-1-B (19.25 %) followed by IR 92516-8-3-3-4 (20.33) showed lowest amylose content.

4.2.19 Volume expansion ratio:

Mean performance for the volume expansion ratio ranged from 3.32 to 3.45 with grand mean of 3.38. Genotype IR 92521-5-3-1-2 (3.45) followed by IR 92521-7-5-1-1 (3.43) found best genotypes with maximum volume expansion ratio out of the best check IR 64 (3.41) while genotype IR 92546-7-1-1-3 (3.32) followed by IR 92546-17-6-4-3 (3.32) and IR 92545-40-2-2-3 (3.32) showed minimum volume expansion ratio.

4.2.20 Kernel elongation ratio:

Mean performance for the kernel elongation ratio ranged from 1.52 to 1.81 with grand mean of 1.67. Genotype IR 94313:18-4-1-4-1-B (1.81) followed by IR 93339:40-B-18-13-B-B-1 (1.80) and IR 92523-35-1-1-1 (1.78) found best genotypes with maximum kernel elongation ratio out of the best check MTU 1010 (1.74) while genotype IR 92521-5-3-1-2 (1.52) followed by IR 92521-7-5-1-1 (1.53) showed minimum kernel elongation ratio.

4.2.21 Grain yield kilogram per hectare:

Mean performance for the grain yield kilogram per hectare ranged from 3250.00 to 5118.92 kg with grand mean of 4335.71 kg. Genotype IR 92527-6-2-1-2 (5118.92 kg) followed by IR 92527-6-2-1-4 (5079.58 kg) and IR 92546-17-6-4-3 (5078.00 kg) found best genotypes with maximum grain yield kilogram per hectare out of the best check IR 64 (4596.75 kg) while genotype CRR 724-1-B (IR 88889-44) (3250.00 kg) followed by IR 92545-54-6-1-4 (3468.83 kg) showed minimum grain yield kilogram per hectare.

Table 4.2: (a) Mean performance for different quantitative parameters in advance rice lines

S. NO.	Genotypes	DFF	PH	DM	NT/Pt	NPT/m^2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW
1	CRR 719-1-B (IR 88903-34)	80.42	104.29	114.17	9.92	239.50	26.28	137.00	27.33	58.67	46.73	22.63
2	CRR 724-1-B (IR 88889-44)	77.83	98.64	112.42	11.08	197.83	25.43	137.33	27.25	66.75	40.90	26.92
3	RP-1-27-7-6-1-2-1	83.08	104.82	116.25	11.83	223.92	25.48	127.33	26.33	64.17	41.45	22.23
4	IR 94313:18-4-1-4-1-B	79.17	94.07	110.92	11.42	212.08	25.63	127.25	27.00	70.17	38.68	25.14
5	IR 88287-383-1-B-B-1-1-B	82.92	96.92	114.33	11.92	226.58	26.56	176.67	27.75	61.25	45.53	23.50
6	IR 94391-587-1-2-B	82.33	96.48	114.17	10.83	219.17	25.27	138.92	27.50	74.67	37.00	26.24
7	IR 94314-20-2-1-B	85.92	96.35	118.25	10.58	231.67	25.85	135.67	31.58	75.17	42.12	23.72
8	IR 93339:40-B-18-13-B-B-1	87.58	98.15	119.00	10.92	239.08	27.54	144.42	27.75	71.17	39.22	24.38
9	IR 92521-5-3-1-2	81.67	108.12	115.17	8.67	195.58	26.29	196.75	27.25	61.25	44.72	22.00
10	IR 92521-7-5-1-1	82.92	106.40	114.08	11.08	242.25	26.89	209.25	24.67	70.83	35.01	26.75
11	IR 92521-23-6-1-3	83.92	107.83	120.75	9.25	202.25	25.84	172.08	27.00	69.42	38.89	22.47
12	IR 92521-24-5-1-3	81.67	106.00	112.00	9.42	182.75	24.47	199.50	30.42	75.00	40.67	22.42
13	IR 92522-47-2-1-1	83.33	97.11	118.67	10.50	217.50	24.39	165.75	30.33	74.33	41.04	24.29
14	IR 92522-47-2-1-4	82.17	96.63	115.92	11.50	205.00	25.52	130.75	26.50	70.17	37.76	24.24
15	IR 92522-61-3-1-4	84.58	100.40	116.00	11.58	251.67	27.27	160.00	25.75	61.67	42.06	22.71
16	IR 92523-35-1-1-1	81.50	97.90	117.92	11.17	233.50	25.88	124.08	26.00	62.17	42.10	24.70
17	IR 92523-37-1-1-2	85.58	96.14	117.83	11.25	223.75	26.86	167.25	30.42	72.92	41.74	23.95
18	IR 92527-6-2-1-2	84.42	98.40	117.17	11.08	241.67	26.43	133.00	27.50	74.17	37.05	24.86
19	IR 92527-6-2-1-4	85.50	93.23	116.58	11.42	236.92	26.72	139.58	29.58	76.92	38.74	22.99
20	IR 92545-53-4-1-3	80.33	98.00	115.17	11.25	236.92	25.81	136.33	27.67	62.67	44.33	22.98
21	IR 92545-54-6-1-4	83.25	99.50	116.00	10.83	228.83	26.96	120.17	27.00	64.00	42.28	24.88
22	IR 92546-7-1-1-3	85.67	105.23	117.08	10.33	272.92	25.84	165.17	26.42	66.58	39.88	22.69
23	IR 92546-17-6-4-3	85.75	100.78	117.25	11.08	225.75	25.74	155.00	28.42	74.00	38.40	23.53

Table 4.3: (b) Mean performance for different quantitative parameters in advance rice lines

S. NO.	Genotypes	DFF	PH	DM	NT/Pt	NPT/m^2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW
24	IR 92546-17-6-4-4	83.42	93.54	114.50	10.50	213.17	25.59	165.25	28.67	60.17	47.76	23.13
25	IR 92546-33-3-1-1	82.75	97.18	114.08	10.25	260.83	24.82	153.58	26.33	71.92	36.70	23.29
26	IR 92517-1-3-1-1	83.00	95.97	114.25	10.83	248.25	25.90	167.92	29.17	64.67	45.47	25.78
27	IR 92522-45-3-1-4	83.92	96.75	116.58	10.75	237.92	25.74	150.08	29.50	62.42	47.47	27.96
28	IR 92545-23-2-1-1	83.67	103.63	115.83	9.42	219.50	27.15	145.42	26.67	56.92	47.14	23.43
29	IR 92545-24-3-1-1	83.75	101.56	114.42	10.50	229.17	25.25	137.17	26.00	60.08	43.24	26.08
30	IR 92545-40-2-2-3	84.50	104.40	115.50	10.08	230.17	27.41	159.42	24.67	72.83	34.20	27.80
31	IR 92545-51-1-1-4	84.00	99.70	116.92	11.33	214.08	26.61	158.67	27.58	68.92	40.10	24.07
32	IR 92546-33-4-2-3	84.67	97.22	116.33	11.25	255.58	25.51	187.25	30.17	70.67	42.77	20.47
33	IR 92516-8-3-3-4	84.25	95.35	118.00	11.17	227.50	25.37	145.08	26.75	74.00	36.22	25.58
34	MTU 1010 (Check)	81.00	104.02	112.25	12.00	236.67	25.08	141.67	25.25	58.67	43.22	24.52
35	IR 64 (Check)	81.33	97.18	112.83	10.50	260.67	26.31	144.50	27.83	60.75	46.04	24.07
36	LALAT (Check)	86.67	103.56	120.08	11.83	214.42	28.31	133.00	28.17	68.50	41.19	26.58
	Mean	**83.29**	**99.76**	**115.80**	**10.81**	**228.75**	**26.06**	**152.45**	**27.62**	**67.46**	**41.33**	**24.25**
	Lowest Range	77.83	93.23	110.92	8.67	182.75	24.39	120.17	24.67	56.92	34.20	20.47
	Highest Range	87.58	108.12	120.75	12.00	272.92	28.31	209.25	31.58	76.92	47.76	27.96
	CV	4.55	6.30	3.59	12.82	10.07	5.65	9.89	9.91	6.84	12.41	5.46
	CD (5%)	3.04	5.05	3.33	1.11	18.49	1.18	12.11	2.20	3.70	4.12	1.06
	CD (1%)	4.01	6.64	4.39	1.47	24.34	1.55	15.94	2.89	4.87	5.42	1.40
	SE	1.09	1.81	1.20	0.40	6.65	0.42	4.35	0.79	1.33	1.48	0.38
	F - Ratio	3.62	5.35	3.60	3.78	8.57	4.26	25.60	4.49	19.48	5.95	20.19

Table 4.4: (a) Mean performance for different qualitative parameters in advance rice lines

S. NO.	Genotypes	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER	GYKG /HA
1	CRR 719-1-B (IR 88903-34)	76.14	63.23	44.88	7.33	2.10	3.50	24.16	3.33	1.61	3889.17
2	CRR 724-1-B (IR 88889-44)	71.68	63.21	51.31	6.96	2.18	3.20	23.33	3.39	1.62	3250.00
3	RP-1-27-7-6-1-2-1	69.41	62.70	51.77	6.64	2.08	3.21	21.72	3.42	1.64	4584.50
4	IR 94313:18-4-1-4-1-B	74.64	63.36	44.53	7.53	2.11	3.58	22.06	3.40	1.81	3978.75
5	IR 88287-383-1-B-B-1-1-B	72.60	62.89	42.91	7.20	2.00	3.62	22.72	3.37	1.73	3860.75
6	IR 94391-587-1-2-B	76.09	59.58	50.36	7.32	1.99	3.69	21.99	3.36	1.65	4304.00
7	IR 94314-20-2-1-B	73.30	61.28	47.83	7.36	2.14	3.46	19.25	3.38	1.71	4463.92
8	IR 93339:40-B-18-13-B-B-1	71.07	65.99	40.12	7.43	2.07	3.61	21.99	3.36	1.80	4724.83
9	IR 92521-5-3-1-2	74.99	63.22	58.22	7.03	2.18	3.23	21.22	3.45	1.52	3858.33
10	IR 92521-7-5-1-1	74.74	60.92	56.02	6.26	2.23	2.81	20.89	3.43	1.53	4466.92
11	IR 92521-23-6-1-3	73.27	63.41	55.92	6.22	2.11	2.96	21.55	3.39	1.54	4396.83
12	IR 92521-24-5-1-3	74.65	63.29	54.56	6.29	2.13	2.97	21.56	3.39	1.54	3820.83
13	IR 92522-47-2-1-1	76.20	61.16	54.07	6.62	2.09	3.18	23.26	3.40	1.71	4501.92
14	IR 92522-47-2-1-4	75.10	65.26	40.01	7.71	1.92	4.02	23.33	3.42	1.70	3965.08
15	IR 92522-61-3-1-4	74.58	60.62	46.78	7.05	2.18	3.24	22.18	3.39	1.71	4023.00
16	IR 92523-35-1-1-1	76.57	64.00	43.13	7.17	2.08	3.46	21.44	3.41	1.78	4595.58
17	IR 92523-37-1-1-2	76.05	61.63	43.99	7.01	2.21	3.18	20.83	3.42	1.76	4435.92
18	IR 92527-6-2-1-2	69.75	65.93	43.13	7.38	1.95	3.81	21.36	3.42	1.77	5118.92
19	IR 92527-6-2-1-4	74.50	63.75	40.72	7.50	1.94	3.88	22.61	3.37	1.76	5079.58
20	IR 92545-53-4-1-3	75.82	61.67	41.88	7.63	1.92	4.01	22.33	3.42	1.75	4015.92
21	IR 92545-54-6-1-4	75.72	60.58	50.63	6.53	2.18	2.99	20.76	3.41	1.65	3468.83
22	IR 92546-7-1-1-3	73.82	60.72	49.97	7.04	2.03	3.49	23.06	3.32	1.67	4399.42
23	IR 92546-17-6-4-3	75.51	60.53	48.74	7.52	2.05	3.68	24.20	3.32	1.67	5078.00

Table 4.5: (b) Mean performance for different qualitative parameters in advance rice lines

S. NO.	Genotypes	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER	GYKG /HA
24	IR 92546-17-6-4-4	74.04	64.76	52.35	6.68	2.03	3.31	22.70	3.36	1.65	4528.08
25	IR 92546-33-3-1-1	74.45	62.58	49.53	6.75	2.10	3.22	23.91	3.37	1.65	4349.00
26	IR 92517-1-3-1-1	72.22	62.79	44.47	7.28	2.09	3.49	22.44	3.34	1.75	4892.00
27	IR 92522-45-3-1-4	73.74	56.98	42.16	6.79	2.12	3.22	23.72	3.35	1.59	4563.33
28	IR 92545-23-2-1-1	74.88	62.63	55.80	7.29	2.18	3.35	21.14	3.38	1.68	4032.50
29	IR 92545-24-3-1-1	74.33	64.81	47.67	6.82	2.08	3.30	21.10	3.38	1.68	4565.50
30	IR 92545-40-2-2-3	77.35	62.88	43.13	7.18	2.18	3.30	21.34	3.32	1.70	3913.58
31	IR 92545-51-1-1-4	77.15	63.42	49.20	7.16	2.03	3.56	21.37	3.37	1.69	4280.58
32	IR 92546-33-4-2-3	73.75	61.95	42.32	7.05	2.09	3.39	21.62	3.34	1.63	4711.92
33	IR 92516-8-3-3-4	75.94	63.51	48.26	6.96	2.15	3.24	20.33	3.38	1.66	4470.50
34	MTU 1010 (Check)	76.42	63.46	52.47	6.97	2.08	3.36	22.08	3.32	1.74	4502.42
35	IR 64 (Check)	75.43	63.61	55.08	7.02	2.12	3.33	22.63	3.41	1.62	4596.75
36	LALAT (Check)	76.31	62.83	51.38	7.02	2.16	3.26	24.62	3.38	1.65	4398.25
	Mean	**74.51**	**62.64**	**48.20**	**7.05**	**2.09**	**3.39**	**22.13**	**3.38**	**1.67**	**4335.71**
	Lowest Range	69.41	56.98	40.01	6.22	1.92	2.81	19.25	3.32	1.52	3250.00
	Highest Range	77.35	65.99	58.22	7.71	2.23	4.02	24.62	3.45	1.81	5118.92
	CV	3.66	4.60	4.86	4.51	6.72	8.28	4.37	1.55	1.88	8.25
	CD (5%)	2.19	2.31	1.88	0.25	0.11	0.23	0.78	0.04	0.01	286.94
	CD (1%)	2.88	3.05	2.48	0.34	0.15	0.30	1.02	0.06	0.01	377.80
	SE	0.79	0.83	0.68	0.09	0.04	0.08	0.28	0.02	0.00	103.20
	F - Ratio	5.85	4.70	59.19	16.95	4.01	12.01	18.17	5.22	410.04	17.11

4.3 Estimates of components of variances for different characters:

4.3.1 Genotypic and Phenotypic variance (VG and VP):

The estimates of genotypic and phenotypic variance were obtained from different yield and quality traits. Present investigation revealed that the phenotypic variance was higher than the genotypic variance for all the yield and quality attributing traits (Table 4.6) which indicate the environmental influence in the expression of these traits. Both the variances are further significant to study the association among the traits.

An extensive range of variances observed for the traits *viz.,* grain yield kilogram per hectare (VG 175114.61 and VP 299309.03) followed by number of spikelets per panicle (VG 466.26 and VP 693.74), number of productive tillers per meter square (VG 334.53 and VP 864.99), Biological yield per plant (VG 32.75 and VP 54.02), head rice recovery % (VG 26.65 and VP 32.15), plant height (VG 14.33 and VP 53.86) and harvest index (VG 10.86 and VP 37.18).

In case of quality traits, phenotypic and genotypic variances had negligible values with less differences and higher genetic values in comparison to environmental variance for different traits namely; volume expansion ratio had negligible values (VG 0.00 and VP 0.00) followed by kernel elongation ratio (VG 0.01 and VP 0.01), kernel breadth before cooking (VG 0.00 and VP 0.02), L/B ratio (VG 0.07 and VP 0.15) and kernel length before cooking (VG 0.13 and VP 0.23).

4.3.2 Genotypic and Phenotypic coefficient of variance (GCV and PCV):

A wide range of genotypic and phenotypic coefficient of variances was observed for different traits. GCV ranged from 0.92 (volume expansion ratio) to 14.16 (number of spikelets per panicle) while PCV ranged from 1.80 (volume expansion ratio) to 17.28 (number of spikelets per panicle). Phenotypic coefficient of variance (PCV) was higher than the genotypic coefficient of variance (GCV) in all respect for different yield attributing characters along with quality (Table 4.6 and Fig. 4.1). There is good correspondence between the coefficients of variances for different traits under study.

Maximum magnitude of genotypic coefficient of variance (GCV) was observed for traits like number of spikelets per panicle (14.16) followed by kernel elongation ratio (10.99), head rice recovery % (10.71), grain yield kilogram per hectare (9.55), biological yield per plant (8.48) and number of productive tillers per plant (8.00) while maximum

phenotypic coefficient of variance was observed for number of spikelets per panicle (17.28) followed by harvest index (14.75), number of tillers per plant (14.23), number of productive tillers per meter square (12.86), grain yield kilogram per hectare (12.62) and head rice recovery % (11.76).

4.4 Heritability (bs) and genetic advance for different characters in rice:

4.4.1 Heritability (broad sense):

Heritability is the heritable part of phenotypic variance that plays a crucial role to decide the stability and strategy of selection for any particular trait. It also reveals the relative significance of heritability and environment in the expression of a particular trait.

In the present investigation, the estimates of heritability ranged from 18% (days to 50% flowering and days to maturity) to 97% (kernel elongation ratio) and revealed that the different groups of heritability (Table 4.6). Very high heritability (>80%) observed for kernel elongation ratio (97%) and head rice recovery (83%), high heritability (>60%) observed for number of spikelets per panicle (67%) followed by test weight (62%) and biological yield per plant (61%), moderate heritability (40 – 60 %) observed for amylase content (59%) followed by kernel length before cooking (57%), grain yield kilogram per hectare (57%) and kernel L/B ratio (48%), low heritability (<40%) observed for remaining all the traits like number of productive tillers per meter square (39%) followed by harvest index (29%), hulling % (29%), plant height (27%), volume expansion ratio (26%), milling % (24%), grain yield per plant (23%), panicle length (21%), kernel breadth before cooking (20%), number of tillers per plant (19%), days to 50% flowering (18%) and days to maturity (18%).

4.4.2 Genetic advance and Genetic advance as % of mean (Genetic gain):

A character with high heritability may not necessarily give high genetic advance Johnson (1955) reported that high heritability should be accompanied with high genetic advance to turn up at more reliable conclusion. The breeder should be careful in making selection based on heritability as it includes additive and non additive gene actions.

4.4.2.1 Genetic advance:

Genetic advance ranged from 0.03 (Volume expansion ratio) to 645.82 (Grain yield kilogram per hectare) and maximum genetic advance was observed for Grain yield kilogram per hectare (645.82) followed by number of spikelets per panicle (36.47) and

number of productive tillers per meter square (23.43) while minimum genetic advance observed for the characters like volume expansion ratio (0.03) followed by kernel breadth before cooking (0.06) and kernel elongation ratio (0.15) (Table 4.6).

4.4.2.2 Genetic advance as % of mean (Genetic gain):

Genetic advance as % of mean ranged from 0.97 (Volume expansion ratio) to 23.92 (Number of spikelets per panicle) and maximum genetic advance as % of mean was observed for the traits like number of spikelets per panicle (23.92) followed by kernel elongation ratio (22.32) and head rice recovery (20.09) while minimum genetic advance as % of mean observed for the traits like volume expansion ratio (0.97) followed by days to maturity (1.45) and days to 50% flowering (1.85) (Table 4.6).

4.4.3 Heritability along with genetic advance as % of mean (Genetic gain):

Practically, heritability along with genetic advance as % of mean is more useful in crop improvement because both are two complimentary concepts for each-other. In present observation, heritability along with genetic advance as % of mean had been worked out for 12 yield and 9 quality traits. Higher estimate of heritability coupled with high to moderate value of genetic advance as % of mean observed for traits like kernel elongation ratio (97 with 22.32) followed by head rice recovery (83 with 20.09), number of spikelets per panicle (67 with 23.92), test weight (62 with 11.17) and biological yield per plant (61 with 13.61). Moderate heritability with moderate genetic advance as % of mean observed for traits like grain yield kilogram per hectare (57 with 14.90) and kernel L/B ratio (48 with 11.33) (Table 4.6 and Fig. 4.2).

Table 4.6: Estimates of component of variance and genetic parameters for different quantitative and qualitative traits in rice

Characters	VG	VP	GCV	PCV	h^2(bs) in %	GA	GA as % of mean
DFF	3.13	17.52	2.13	5.03	18	1.54	1.85
PH	14.33	53.86	3.79	7.36	27	4.02	4.03
DM	3.73	20.96	1.67	3.95	18	1.68	1.45
NT/Pt	0.45	2.37	6.17	14.23	19	0.60	5.51
NPT/m^2	334.53	864.99	8.00	12.86	39	23.43	10.24
PL	0.59	2.75	2.94	6.37	21	0.73	2.80
NSP/P	466.26	693.74	14.16	17.28	67	36.47	23.92
GY/Pt	2.18	9.67	5.36	11.26	23	1.44	5.23
BY/Pt	32.75	54.02	8.48	10.90	61	9.18	13.61
HI	10.86	37.18	7.97	14.75	29	3.67	8.88
TW	2.81	4.56	6.91	8.81	62	2.71	11.17
HULL. %	3.00	10.43	2.33	4.33	29	1.92	2.57
MILL. %	2.57	10.88	2.56	5.27	24	1.60	2.56
HRR %	26.65	32.15	10.71	11.76	83	9.68	20.09
KLBC	0.13	0.23	5.19	6.88	57	0.57	8.08
KBBC	0.00	0.02	3.36	7.51	20	0.06	3.10
L/B RATIO	0.07	0.15	7.93	11.46	48	0.38	11.33
AMYLOSE C.	1.34	2.27	5.23	6.81	59	1.83	8.26
VER	0.00	0.00	0.92	1.80	26	0.03	0.97
KER	0.01	0.01	10.99	11.15	97	0.15	22.32
GYKG/Ha	175114.61	299309.03	9.55	12.62	57	645.82	14.90

Figure 4.1: Estimates of GCV and PCV for different characters in rice
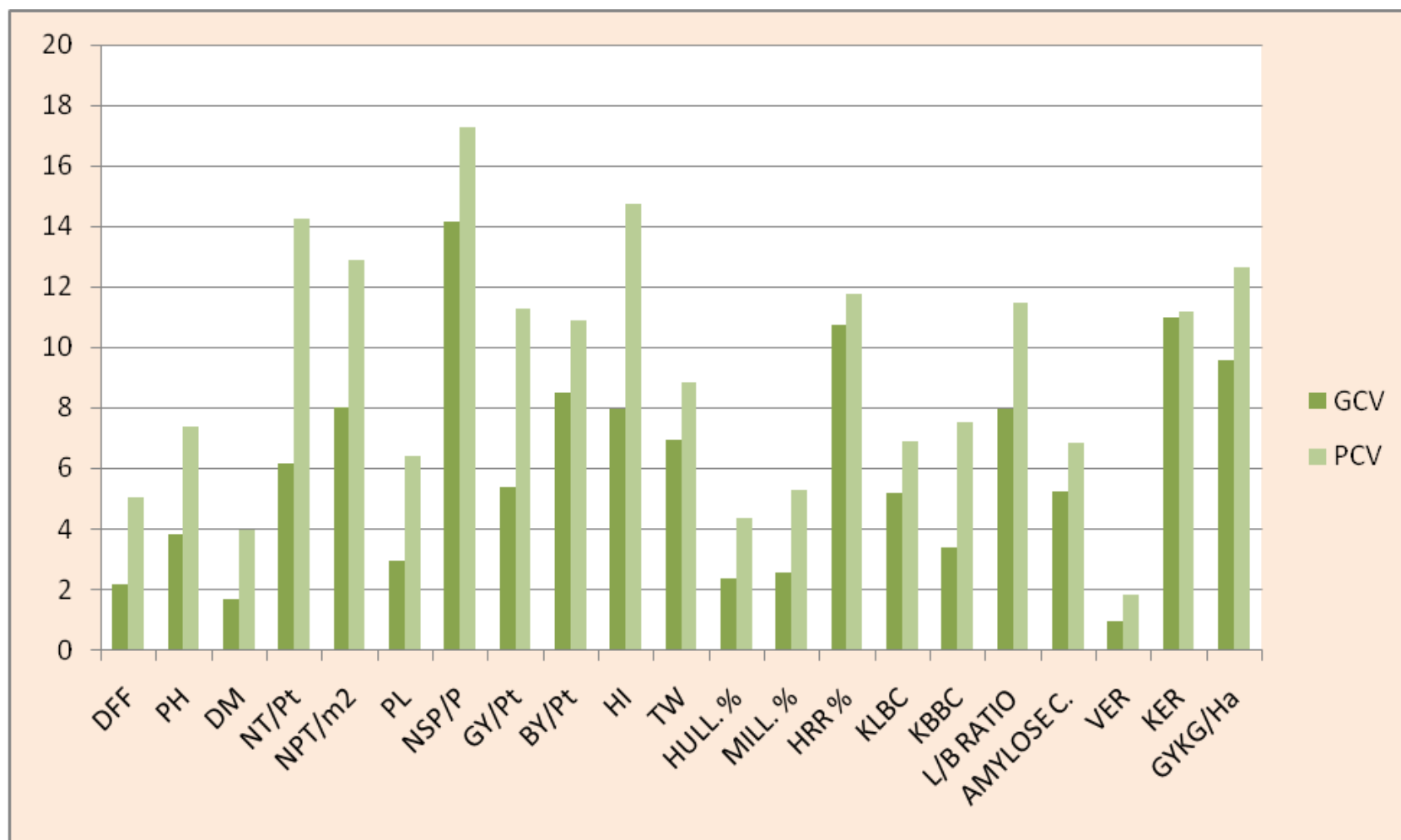
Figure 4.2: Estimates of heritability (bs) and genetic advance for different characters in rice
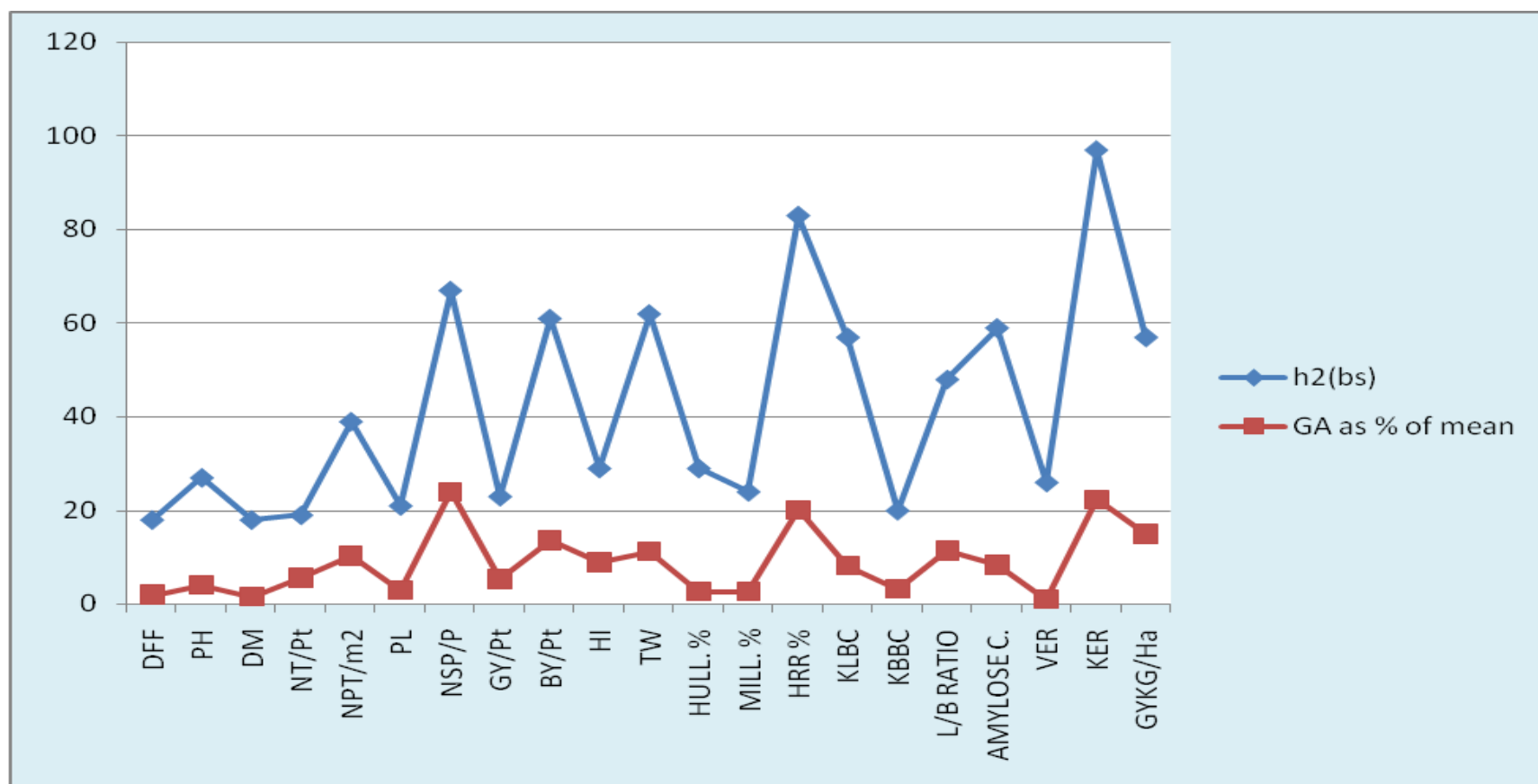
4.5 Estimates of correlation coefficient for different characters in rice:

Association analysis indicates the strength and direction of relationship among variables. A positive value of association reveals that the change of variables in same direction. It measures the mutual relationship among different yield and quality traits and to determine the component traits on which selection may be used for genetic improvement in yield and quality traits. Association studies would provide reliable information when breeder needs to combine higher yield potential with desirable traits with better grain quality traits. In the present investigation both genotypic and phenotypic association of different yield and quality traits and their relationship among themselves are presented in the tables and figures (Table 4.7, 4.8, 4.9 and Fig. 4.3, 4.4) are discussed under following sub-heads;

4.5.1 Phenotypic correlation coefficient:

4.5.1.1 Correlation coefficient of grain yield per plant with other traits:

Grain yield per plant revealed positive and significant association with harvest index (0.654**) having very strong correlation (>0.65).

4.5.1.2 Correlation coefficient among other yield and quality traits:

4.5.1.2.1 Days to 50% flowering:

Days to 50% flowering showed positive and significant association with traits like days to maturity (0.406**) having moderately weak correlation.

4.5.1.2.2 Plant height:

Plant height showed positive and significant correlation with head rice recovery % (0.282*) while negative and significant association with kernel elongation ratio (-0.319*) having very weak and moderately weak association subsequently.

4.5.1.2.3. Number of spikelet's per panicle:

Number of spikelets per panicle showed negative and significant association with kernel length before cooking ((-0.314*) and kernel elongation ratio (-0.414**) having moderately weak association.

4.5.1.2.4. Biological yield per plant:

Biological yield per plant showed negative significant association with harvest index (-0.651**) having very strong correlation.

4.5.1.2.5 Head rice recovery %:

Head rice recovery % showed negative and significant association with kernel length before cooking (-0.448**) followed by kernel L/B ratio (-0.435**) and kernel elongation ratio (-0.594**) having moderately weak to moderately strong association.

4.5.1.2.6 Kernel length before cooking:

Kernel length before cooking revealed that the positive and significant association with kernel L/B ratio (0.737**) followed by kernel elongation ratio (0.496**) having very strong and moderately strong association subsequently.

4.5.1.2.7 Kernel breadth before cooking:

Kernel breadth before cooking revealed that the negative and significant association with kernel L/B ratio (-0.806**) having very strong association.

4.5.1.2.8 Kernel L/B ratio before cooking:

Kernel L/B ratio before cooking revealed the positive and significant association with kernel elongation ratio (0.436**) having moderately weak association.

4.5.2 Genotypic correlation coefficient:

4.5.2.1 Correlation coefficient of grain yield per plant with other traits:

Grain yield per plant revealed positive and significant association with biological yield per plant (0.426**) followed by days to 50% flowering (0.338*) and days to maturity (0.282*) having moderately weak to very weak correlation while negative and significant association with plant height (-0.508**) followed by milling recovery % (-0.283*) and test weight (-0.282*) having moderately strong and very weak association subsequently.

4.5.2.2 Correlation coefficient among other yield and quality traits:

4.5.2.2.1 Days to 50% flowering:

Days to 50% flowering showed positive and significant association with traits like days to maturity (0.906**) followed by panicle length (0.592**), biological yield per plant (0.454**) and number of productive tillers per meter square (0.341*) having very strong, moderately strong and moderately weak association subsequently while negative and significant association with volume expansion ratio (-0.331*) having moderately weak association.

4.5.2.2.2 Plant height:

Plant height showed positive and significant association with head rice recovery % (0.624**) followed by kernel breadth before cooking (0.445**) and number of spikelets per panicle (0.392**) having moderately strong to moderately weak correlation while negative and significant association observed with kernel elongation ratio (-0.637**) followed by number of tillers per plant (-0.568**), kernel L/B ratio (-0.524**) and kernel length before cooking (-0.505**) having moderately strong association.

4.5.2.2.3 Days to maturity:

Days to maturity revealed positive and significant association with panicle length (0.479**) and biological yield per plant (0.357*) having moderately weak correlation.

4.5.2.2.4 Number of tillers per plant:

Number of tillers per plant showed positive and significant association with kernel elongation ratio (0.627**) followed by kernel L/B ratio (0.424**), kernel length before cooking (0.369*) and number of productive tillers per meter square (0.306*) having moderately strong to moderately weak association while negative and significant correlation observed with head rice recovery (-0.565**) followed by number of spikelets per panicle (-0.441**) and kernel breadth before cooking (-0.394**) having moderately strong to moderately weak correlation.

4.5.2.2.5 Number of productive tillers per meter square:

Number of productive tillers per meter square showed positive and significant association with kernel elongation ratio (0.286*) having very weak association while negative and significant association with volume expansion ratio (-0.395**) followed by head rice recovery (-0.336*) having moderately weak correlation.

4.5.2.2.6 Panicle length:

Panicle length showed positive and significant association with kernel breadth before cooking (0.324*) having moderately weak association.

4.5.2.2.7 Number of spikelets per panicle:

Number of spikelets per panicle showed positive and significant association with head rice recovery (0.359*) and kernel breadth before cooking (0.354*) having moderately weak association while negative and significant association with kernel elongation ratio (-0.520**) followed by kernel length before cooking (-0.479**) and

kernel L/B ratio before cooking (-0.465**) having moderately strong to moderately weak correlation.

4.5.2.2.8 Biological yield per plant:

Biological yield per plant showed negative and significant association with harvest index (-0.810**) having very strong association.

4.5.2.2.9 Harvest index:

Harvest index showed negative and significant association with test weight (-0.278*) having very weak correlation.

4.5.2.2.10 Hulling recovery %:

Hulling recovery % showed negative and significant association with milling recovery % (-0.288*) having very weak correlation.

4.5.2.2.11 Milling recovery %:

Milling recovery % showed positive and significant association with kernel elongation ratio (0.323*) and Kernel L/B ratio (0.300*) having moderately weak and very weak correlation while negative and significant association with kernel breadth before cooking (-0.360*) having moderately weak correlation.

4.5.2.2.12 Head rice recovery %:

Head rice recovery % showed positive and significant association with kernel breadth before cooking (0.546**) having moderately strong correlation while negative and significant association with kernel L/B ratio (-0.683**) followed by kernel length before cooking (-0.666**) and kernel elongation ratio (-0.666**) having very strong association.

4.5.2.2.13 Kernel length before cooking:

Kernel length before cooking revealed that positive and significant association with kernel L/B ratio (0.928**) and kernel elongation ratio (0.679**) having very strong correlation while negative and significant correlation with kernel breadth before cooking (-0.608**) having moderately strong correlation.

4.5.2.2.14 Kernel breadth before cooking:

Kernel breadth before cooking showed negative and significant association with kernel L/B ratio (-0.859**) followed by kernel elongation ratio (-0.467**) and amylose content (-0.333*) having very strong and moderately weak correlation subsequently.

4.5.2.2.15 Kernel L/B ratio:

Kernel L/B ratio showed positive and significant association with kernel elongation ratio (0.648**) having near to very strong correlation.

4.5.2.2.16 Amylose content:

Amylose content showed negative and significant association with volume expansion ratio (-0.396**) having moderately weak association.

Table 4.7: (a) Correlation coefficient among different quantitative traits in rice

Characters	r	DFF	PH	DM	NT/Pt	NPT/ m^2	PL	NSP/P	BY/Pt	HI	TW	GY/Pt
DFF	rp rg	**1.000** **1.000**	0.001 -0.024	0.406** 0.906**	0.038 0.093	0.110 0.341*	0.148 0.592**	-0.017 0.145	0.121 0.454**	-0.035 -0.270	-0.021 -0.076	0.078 0.338*
PH	rp rg		**1.000** **1.000**	0.018 0.059	-0.180 -0.568**	-0.090 -0.210	0.081 0.178	0.222 0.392**	-0.109 -0.261	-0.068 -0.061	-0.033 -0.158	-0.200 -0.508**
DM	rp rg			**1.000** **1.000**	-0.006 0.016	-0.016 0.058	0.042 0.479**	-0.106 -0.079	0.128 0.357*	-0.043 -0.222	-0.034 -0.099	0.072 0.282*
NT/Pt	rp rg				**1.000** **1.000**	0.049 0.306*	0.052 0.164	-0.220 -0.441**	0.096 0.074	-0.081 -0.164	0.082 0.235	-0.007 -0.089
NPT/ m^2	rp rg					**1.000** **1.000**	0.027 0.189	-0.043 -0.089	-0.021 -0.142	-0.011 0.045	-0.045 -0.061	-0.035 -0.181
PL	rp rg						**1.000** **1.000**	0.003 -0.085	-0.041 -0.140	0.001 -0.002	0.096 0.199	-0.044 -0.251
NSP/P	rp rg							**1.000** **1.000**	0.078 0.123	-0.011 -0.011	-0.187 -0.263	-0.066 0.178
BY/Pt	rp rg								**1.000** **1.000**	-0.651** -0.810**	0.057 0.097	0.136 0.426**
HI	rp rg									**1.000** **1.000**	-0.148 -0.278*	0.654** 0.184
TW	rp rg										**1.000** **1.000**	-0.144 -0.282*
GY/Pt	**rp** **rg**											**1.000** **1.000**

Table 4.8: (b) Correlation coefficient among different qualitative traits in rice

Characters	r	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER	GY/Pt
HULL %	rp	**1.000**	-0.048	0.072	0.087	0.070	0.006	0.022	-0.045	-0.043	-0.053
	rg	**1.000**	-0.288*	0.127	0.040	0.212	-0.063	0.048	-0.150	-0.061	-0.134
MILL %	rp		**1.000**	-0.045	0.111	-0.062	0.107	-0.036	0.066	0.129	0.038
	rg		**1.000**	-0.131	0.215	-0.360*	0.300*	-0.130	0.214	0.323*	-0.283*
HRR %	rp			**1.000**	-0.448**	0.241	-0.435**	-0.103	0.112	-0.594**	-0.073
	rg			**1.000**	-0.666**	0.546**	-0.683**	-0.111	0.243	-0.666**	-0.153
KLBC	rp				**1.000**	-0.205	0.737**	0.027	-0.085	0.496**	0.014
	rg				**1.000**	-0.608**	0.928**	0.177	-0.180	0.679**	0.078
KBBC	rp					**1.000**	-0.806**	-0.118	-0.038	-0.204	-0.107
	rg					**1.000**	-0.859**	-0.333*	0.176	-0.467**	-0.095
L/B RATIO	rp						**1.000**	0.089	-0.019	0.436**	0.079
	rg						**1.000**	0.255	-0.171	0.648**	0.089
AMYLOSE C.	rp							**1.000**	-0.176	-0.040	0.038
	rg							**1.000**	-0.396**	-0.064	0.010
VER	rp								**1.000**	-0.048	-0.017
	rg								**1.000**	-0.118	-0.032
KER	rp									**1.000**	0.036
	rg									**1.000**	0.058
GY/Pt	rp										**1.000**
	rg										**1.000**

Table 4.9: (c) Correlation coefficient among different yield and quality attributing traits in rice

Characters	r	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER
DFF	rp	-0.032	-0.008	-0.048	0.072	0.022	0.028	-0.118	-0.019	0.080
	rg	-0.117	-0.114	-0.230	0.019	-0.004	0.012	-0.133	-0.331*	0.198
PH	rp	0.030	-0.108	0.282*	-0.143	0.206	-0.227	-0.022	-0.012	-0.319*
	rg	0.048	-0.001	0.624**	-0.505**	0.445**	-0.524**	-0.072	0.042	-0.637**
DM	rp	-0.037	0.050	-0.015	0.075	-0.022	0.057	-0.110	0.051	0.045
	rg	-0.025	-0.092	-0.155	-0.039	-0.027	-0.010	-0.082	0.033	0.114
NT/Pt	rp	-0.082	0.025	-0.200	0.104	-0.109	0.140	0.093	-0.072	0.270
	rg	-0.089	-0.026	-0.565**	0.369*	-0.394**	0.424**	0.165	-0.019	0.627**
NPT/ m²	rp	-0.011	-0.055	-0.179	0.090	0.016	0.045	0.110	-0.090	0.170
	rg	-0.106	-0.250	-0.336*	0.183	-0.142	0.176	0.101	-0.395**	0.286*
PL	rp	0.011	0.027	-0.057	0.137	0.097	0.025	-0.042	0.013	0.089
	rg	0.079	0.072	-0.195	0.244	0.324*	0.024	-0.073	0.116	0.183
NSP/P	rp	0.018	-0.132	0.259	-0.314*	0.112	-0.259	-0.043	-0.045	-0.414**
	rg	0.027	-0.173	0.359*	-0.479**	0.354*	-0.465**	-0.115	-0.039	-0.520**
BY/Pt	rp	0.017	-0.034	0.133	-0.009	-0.073	0.054	-0.065	0.053	0.083
	rg	-0.026	-0.031	-0.180	0.056	-0.117	0.101	-0.140	-0.022	0.098
HI	rp	-0.046	0.064	0.044	0.018	-0.026	0.019	0.075	-0.056	-0.035
	rg	-0.054	-0.158	0.095	0.006	0.059	-0.039	0.165	-0.018	-0.070
TW	rp	0.034	-0.078	-0.060	0.036	0.113	-0.049	0.033	-0.089	0.049
	rg	0.164	-0.183	-0.112	-0.018	0.260	-0.123	0.042	-0.053	0.068

Figure 4.3: Representation of genotypic correlation coefficient among different characters in rice
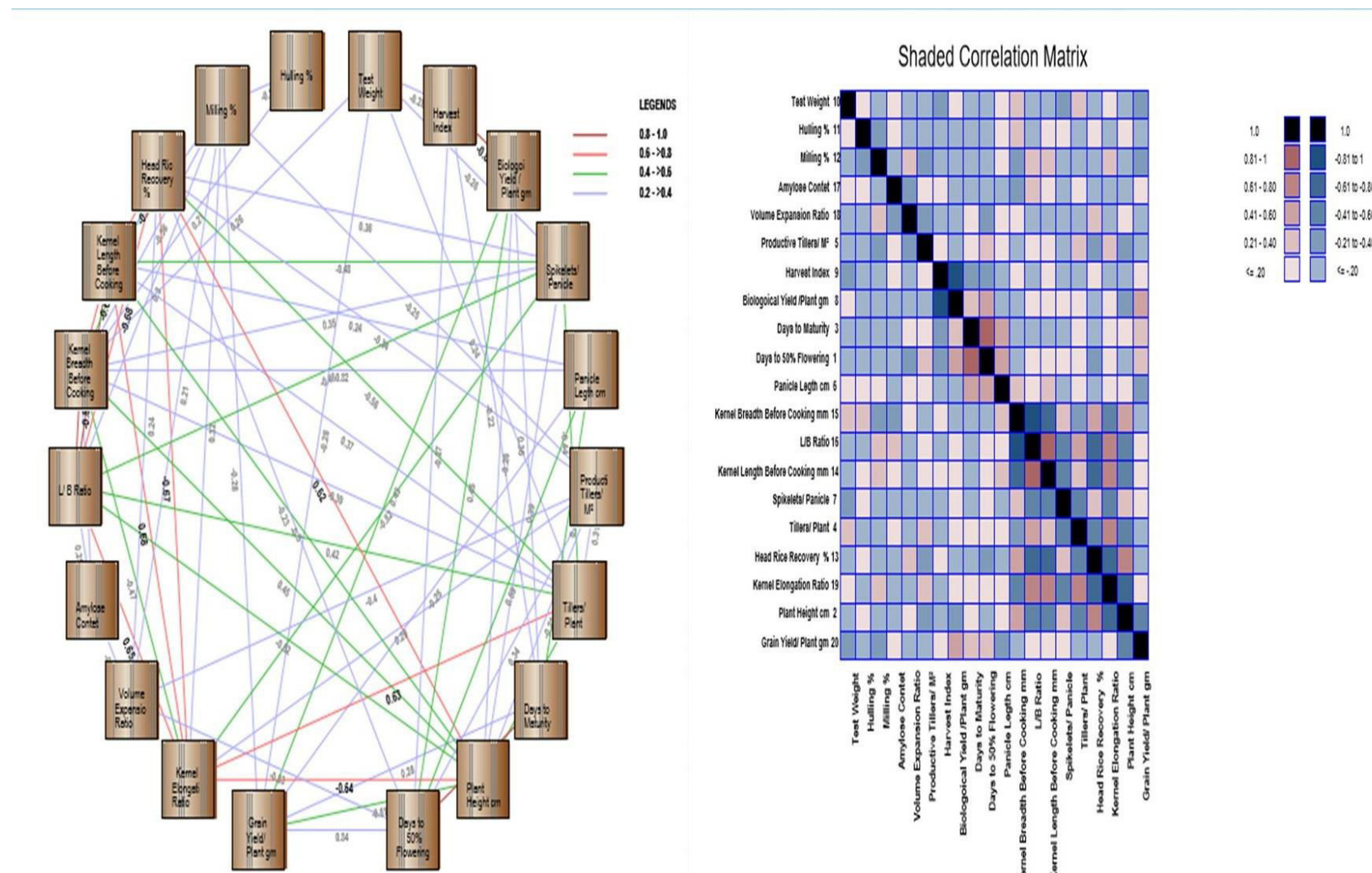
Figure 4.4: Representation of phenotypic correlation coefficient among different characters in rice
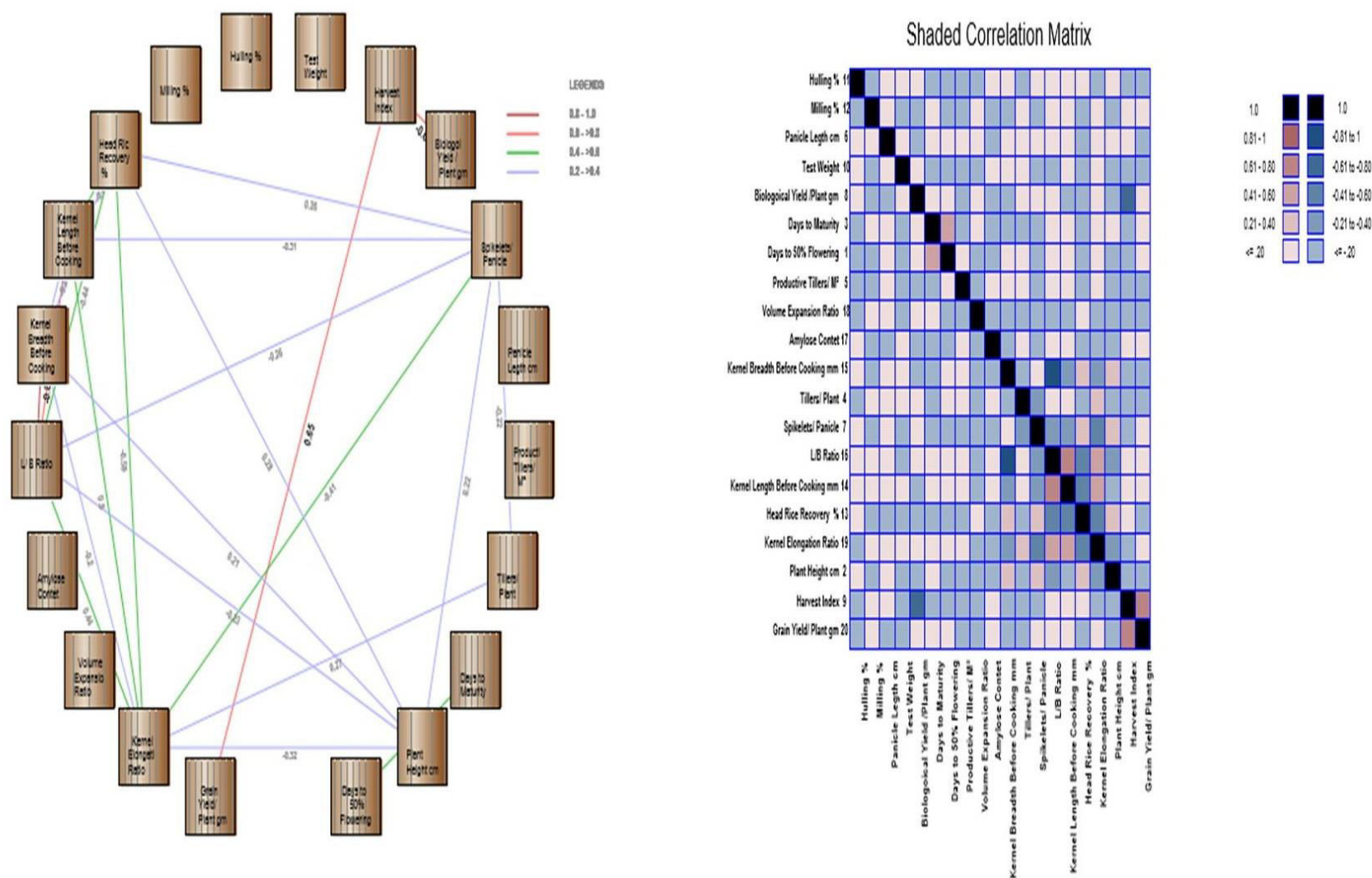
4.6 Estimates of path coefficient analysis for different characters in rice:

Association analysis is unable to provide actual correlation of the traits with each-other, because these attributes are interrelated themselves and influence in considerable amount by each characters. Path coefficient analysis splits the correlation coefficient into the measure of direct and indirect effect or contribution of different independent trait on a dependent trait. In present study, the observed direct and indirect effect on both phenotypic and genotypic level have been that presented in different tables and figures (Table 4.10, 4.11, 4.12, 4.13 and Fig. 4.5, 4.6).

4.6.1 Phenotypic path coefficient analysis:

4.6.1.1 Path coefficient analysis for grain yield per plant:

Grain yield per plant had a highest direct positive effect on harvest index (1.2830) followed by biological yield per plant (0.9683), L/B ratio before cooking (0.0127), kernel breadth before cooking (0.0098), amylose content (0.0071), days to 50% flowering (0.0059), number of spikelets per panicle (0.0056), number of tillers per plant (0.0038), volume expansion ratio (0.0036), days to maturity (0.0030), head rice recovery (0.0026) and kernel elongation ratio (0.0018) while direct negative effect was observed for the traits namely; milling recovery % (-0.0126) followed by hulling recovery % (-0.0102), test weight (-0.0088), plant height (-0.0086), panicle length (-0.0048), kernel length before cooking (-0.0044) and number of productive tillers per plant (-0.0037).

4.6.1.2 Path coefficient analysis for other characters:

4.6.1.2.1 Days to 50% flowering:

Days to 50% flowering had a maximum positive indirect effect on days to maturity (0.0024) followed by panicle length (0.0009) and biological yield per plant (0.0007) while maximum negative indirect effect on amylose content (-0.0007) followed by head rice recovery % (-0.0003).

4.6.1.2.2 Plant height:

Plant height had a maximum positive indirect effect on kernel elongation ratio (0.0027) followed by L/B ratio (0.0019) and number of tillers per plant (0.0015) while maximum negative indirect effect on head rice recovery % (-0.0024) followed by number of spikelets per panicle (-0.0019) and kernel breadth before cooking (-0.0018).

4.6.1.2.3 Days to maturity:

Days to maturity had a maximum positive indirect effect on days to 50% flowering (0.0012) followed by biological yield per plant (0.0004) while maximum negative indirect effect on number of spikelets per panicle (-0.0003) and amylose content (-0.0003).

4.6.1.2.4 Number of tillers per plant:

Number of tillers per plant had a maximum positive indirect effect on kernel elongation ratio (0.0010) followed by L/B ratio (0.0005) while maximum negative indirect effect on number of spikelets per panicle (-0.0008) followed by head rice recovery % (-0.0008) and plant height (-0.0007).

4.6.1.2.5 Number of productive tillers per meter square:

Number of productive tillers per meter square had a maximum positive indirect effect on head rice recovery % (0.0007) followed by plant height (0.0003) and volume expansion ratio (0.0003) while maximum negative indirect effect on kernel elongation ratio (-0.0006) followed by days to 50% flowering (-0.0004) and amylose content (-0.0004)

4.6.1.2.6 Panicle length:

Panicle length had a maximum positive indirect effect on head rice recovery % (0.0003) followed by biological yield per plant (0.0002) and amylose content (0.0002) while maximum negative indirect effect on days to 50% flowering (-0.0007) and kernel length before cooking (-0.0007).

4.6.1.2.7 Number of spikelets per panicle:

Number of spikelets per panicle had a maximum positive indirect effect on head rice recovery % (0.0015) followed by plant height (0.0012) and kernel breadth before cooking (0.0006) while maximum negative indirect effect on kernel elongation ratio (-0.0023) followed by kernel length before cooking (-0.0018) and L/B ratio (-0.0015).

4.6.1.2.8 Biological yield per plant:

Biological yield per plant had a maximum positive indirect effect on days to maturity (0.1238) followed by days to 50% flowering (0.1171) and number of tillers per plant (0.0926) while maximum negative indirect effect on harvest index (-0.6301) and head rice recovery (-0.1283).

4.6.1.2.9 Harvest index:

Harvest index had a maximum positive indirect effect on amylose content (0.0958) followed by milling recovery % (0.0816) and head rice recovery (0.0564) while maximum negative indirect effect on biological yield per plant (-0.8349) and test weight (-0.1905).

4.6.1.2.10 Test weight:

Test weight had a maximum positive indirect effect on number of spikelets per panicle (0.0016) followed by harvest index (0.0013) and volume expansion ratio (0.0008) while maximum negative indirect effect on kernel breadth before cooking (-0.0010) followed by panicle length (-0.0009).

4.6.1.2.11 Hulling recovery %:

Hulling recovery % had a maximum positive indirect effect on number of tillers per plant (0.0008) followed by harvest index (0.0005), milling recovery % (0.0005) and volume expansion ratio (0.0005) while maximum negative indirect effect on kernel length before cooking (-0.0009) followed by head rice recovery (-0.0007) and kernel breadth before cooking (-0.0007).

4.6.1.2.12 Milling recovery %:

Milling recovery % had a maximum positive indirect effect on number of spikelets per panicle (0.0017) followed by plant height (0.0014) and test weight (0.0010) while maximum negative indirect effect on kernel elongation ratio (-0.0016) followed by kernel length before cooking (-0.0014) and L/B ratio before cooking (-0.0013).

4.6.1.2.13 Head rice recovery %:

Head rice recovery % had a maximum positive indirect effect on plant height (0.0007) followed by number of spikelets per panicle (0.0007) and kernel breadth before cooking (0.0006) while maximum negative indirect effect on volume expansion ratio (-0.0015) followed by kernel length before cooking (-0.0012) and L/B ratio (-0.0011).

4.6.1.2.14 Kernel length before cooking:

Kernel length before cooking had a maximum positive indirect effect on head rice recovery (0.0020) followed by number of spikelets per panicle (0.0014) and kernel breadth before cooking (0.0009) while maximum negative indirect effect on L/B ratio (-0.0033) and kernel elongation ratio (-0.0022).

4.6.1.2.15 Kernel breadth before cooking:

Kernel breadth before cooking had a maximum positive indirect effect on head rice recovery (0.0024) and plant height (0.0020) while maximum negative indirect effect on L/B ratio (-0.0079) followed by kernel length before cooking (-0.0020) and kernel elongation ratio (-0.0020).

4.6.1.2.16 Kernel L/B ratio:

L/B ratio had a maximum positive indirect effect on kernel length before cooking (0.0094) followed by kernel elongation ratio (0.0055) and number of tillers per plant (0.0018) while maximum negative indirect effect on kernel breadth before cooking (-0.0102) followed by head rice recovery (-0.0055) and number of spikelets per panicle (-0.0033).

4.6.1.2.17 Amylose content:

Amylose content had a maximum positive indirect effect on number of productive tillers per meter square (0.0008) followed by number of tillers per plant (0.0007) and L/B ratio (0.0006) while maximum negative indirect effect on volume expansion ratio (-0.0012) followed by days to 50% flowering (-0.0008), days to maturity (-0.0008) and kernel breadth before cooking (-0.0008).

4.6.1.2.18 Volume expansion ratio:

Volume expansion ratio had a maximum positive indirect effect on head rice recovery (0.0004) while maximum negative indirect effect on amylose content (-0.0006).

4.6.1.2.19 Kernel elongation ratio:

Kernel elongation ratio had a maximum positive indirect effect on kernel length before cooking (0.0009) followed by L/B ratio (0.0008) and number of tillers per plant (0.0005) while maximum negative indirect effect on head rice recovery (-0.0010) followed by number of spikelets per panicle (-0.0007) and plant height (-0.0006).

4.6.2 Genotypic path coefficient analysis:

4.6.2.1 Path coefficient analysis for grain yield per plant:

Grain yield per plant had a direct positive effect on biological yield per plant (1.1534) followed by harvest index (1.0046), panicle length (0.1208), kernel elongation ratio (0.0895), days to 50% flowering (0.0249), amylose content (0.0197), kernel length before cooking (0.0112) and number of spikelets per panicle (0.0092) while direct

negative effect on plant height (-0.2940) followed by L/B ratio (-0.2378), milling recovery (-0.2241), number of productive tillers per meter square (-0.2205), test weight (-0.1880), kernel breadth before cooking (-0.1616), number of tillers per plant (-0.1329), hulling recovery (-0.0919), volume expansion ratio (-0.0341), head rice recovery (-0.0167) and days to maturity (-0.0116).

4.6.2.2 Path coefficient analysis for other characters:

4.6.2.2.1 Days to 50% flowering:

Days to 50% flowering had a maximum positive indirect effect on days to maturity (0.0226) followed by panicle length (0.0148) and biological yield per plant (0.0113) while maximum negative indirect effect on volume expansion ratio (-0.0083) followed by harvest index (-0.0067) and head rice recovery (-0.0057).

4.6.2.2.2 Plant height:

Plant height has a maximum positive indirect effect on kernel elongation ratio (0.1871) followed by number of tillers per plant (0.1671) and L/B ratio (0.1541) while maximum negative indirect effect on head rice recovery (-0.1836) and kernel breadth before cooking (-0.1310).

4.6.2.2.3 Days to maturity:

Days to maturity had a maximum positive indirect effect on harvest index (0.0026) followed by head rice recovery (0.0018) and test weight (0.0012) while maximum negative indirect effect on days to 50% flowering (-0.0105) and panicle length (-0.0056).

4.6.2.2.4 Number of tillers per plant:

Number of tillers per plant had a maximum positive indirect effect on plant height (0.0756) followed by head rice recovery (0.0751) and number of spikelets per panicle (0.0586) while maximum negative indirect effect on kernel elongation ratio (-0.0833) and L/B ratio (-0.0563).

4.6.2.2.5 Number of productive tillers per meter square:

Number of productive tillers per meter square had a maximum positive indirect effect on volume expansion ratio (0.0872) followed by head rice recovery (0.0742) and milling recovery (0.0552) while maximum negative indirect effect on days to 50% flowering (-0.0752) and number of tillers per plant (-0.0676).

4.6.2.2.6 Panicle length:

Panicle length had a maximum positive indirect effect on days to 50% flowering (0.0715) followed by days to maturity (0.0578) and kernel breadth before cooking (0.0391)   while maximum negative indirect effect on head rice recovery (-0.0236) followed by biological yield per plant (-0.0169).

4.6.2.2.7 Number of spikelets per panicle:

Number of spikelets per panicle had a maximum positive indirect effect on plant height (0.0036) followed by head rice recovery (0.0033) and kernel breadth before cooking (0.0033) while maximum negative indirect effect on kernel elongation ratio (-0.0048) followed by kernel length before cooking (-0.0044) and L/B ratio (-0.0043).

4.6.2.2.8 Biological yield per plant:

Biological yield per plant had a maximum positive indirect effect on days to 50% flowering (0.5240) followed by days to maturity (0.4115) and number of spikelets per panicle (0.1417) while maximum negative indirect effect on harvest index (-0.9339) followed by plant height (-0.3014).

4.6.2.2.9 Harvest index:

Harvest index had a maximum positive indirect effect on amylose content (0.1655) followed by head rice recovery (0.0950) and kernel breadth before cooking (0.0595) while maximum negative indirect effect on biological yield per plant (-0.8135) and test weight (-0.2792).

4.6.2.2.10 Test weight:

Test weight had a maximum positive indirect effect on harvest index (0.0523) followed by number of spikelets per panicle (0.0494) and milling recovery (0.0343) while maximum negative indirect effect on kernel breadth before cooking (-0.0488) followed by number of tillers per plant (-0.0443) and panicle length (-0.0374).

4.6.2.2.11 Hulling recovery %:

Hulling recovery % had a maximum positive indirect effect on milling recovery (0.0265) followed by volume expansion ratio (0.0138) and days to 50% flowering (0.0108) while maximum negative indirect effect on kernel breadth before cooking (-0.0195) and test weight (-0.0150).

4.6.2.2.12 Milling recovery %:

Milling recovery % had a maximum positive indirect effect on kernel breadth before cooking (0.0808) followed by hulling recovery % (0.0646) and number of productive tillers per meter square (0.0561) while maximum negative indirect effect on kernel elongation ratio (-0.0724) followed by L/B ratio (-0.0672) and kernel length before cooking (-0.0482).

4.6.2.2.13 Head rice recovery %:

Head rice recovery % had a maximum positive indirect effect on L/B ratio (0.0114) followed by kernel length before cooking (0.0111) and kernel elongation ratio (0.0111) while maximum negative indirect effect on plant height (-0.0105) and kernel breadth before cooking (-0.0091).

4.6.2.2.14 Kernel length before cooking:

Kernel length before cooking had a maximum positive indirect effect on L/B ratio (0.0104) followed by kernel elongation ratio (0.0076) and number of tillers per plant (0.0041) while maximum negative indirect effect on head rice recovery (-0.0074) followed by kernel breadth before cooking (-0.0068) and plant height (-0.0056).

4.6.2.2.15 Kernel breadth before cooking:

Kernel breadth before cooking had a maximum positive indirect effect on L/B ratio (0.1388) followed by kernel length before cooking (0.0982) and kernel elongation ratio (0.0754) while maximum negative indirect effect on head rice recovery (-0.0883) and plant height (-0.0720).

4.6.2.2.16 kernel L/B ratio:

Kernel L/B ratio before cooking had a maximum positive indirect effect on kernel breadth before cooking (0.2042) followed by head rice recovery (0.1624) and plant height (0.1247) while maximum negative indirect effect on kernel length before cooking (-0.2206) and kernel elongation ratio (-0.1541).

4.6.2.2.17 Amylose content:

Amylose content had a maximum positive indirect effect on L/B ratio (0.0050) followed by kernel length before cooking (0.0035) number of tillers per plant (0.0032) and harvest index (0.0032) while maximum negative indirect effect on volume expansion ratio (-0.0078) and kernel breadth before cooking (-0.0066).

4.6.2.2.18 Volume expansion ratio:

Volume expansion ratio had a maximum positive indirect effect on number of productive tillers per meter square (0.0135) followed by amylose content (0.0135) and days to 50% flowering (0.0113) while maximum negative indirect effect on head rice recovery (-0.0083) followed by milling recovery (-0.0073) and kernel breadth before cooking (-0.0060).

4.6.2.2.19 Kernel elongation ratio:

Kernel elongation ratio had a maximum positive indirect effect on kernel length before cooking (0.0607) followed by L/B ratio (0.0580) and number of tillers per plant (0.0561) while maximum negative indirect effect on head rice recovery (-0.0596) and plant height (-0.0570).

Note: The effect of some independent variables on dependent variables which were not included in present study on dependent variables was called residual effects. Residual effect in present study at phenotypic level was 0.1580 with R^2 value 0.9750 while at genotypic level was 0.1134 with R^2 value 0.9871. Values of residual effects are estimated using direct effects and their simple correlation coefficient. Lenka and Mishra (1973) developed the scales for the estimation of strength of the values. If values of direct or indirect effects are 0.0 to 0.09, 0.10 to 0.19, 0.20 to 0.29, 0.30 to 0.99 and above 1.00 revealed that negligible, low, moderate, high and very high rate subsequently.

Table 4.10: (a) Direct (diagonal) and indirect effects of different component characters attributing to grain yield per plant in rice at phenotypic level

Characters	DFF	PH	DM	NT/Pt	NPT/m^2	PL	NSP/P	BY/Pt	HI	TW
DFF	**0.0059**	0.0000	0.0024	0.0002	0.0006	0.0009	-0.0001	0.0007	-0.0002	-0.0001
PH	0.0000	**-0.0086**	-0.0002	0.0015	0.0008	-0.0007	-0.0019	0.0009	0.0006	0.0003
DM	0.0012	0.0001	**0.0030**	0.0000	0.0000	0.0001	-0.0003	0.0004	-0.0001	-0.0001
NT/Pt	0.0001	-0.0007	0.0000	**0.0038**	0.0002	0.0002	-0.0008	0.0004	-0.0003	0.0003
NPT/ m^2	-0.0004	0.0003	0.0001	-0.0002	**-0.0037**	-0.0001	0.0002	0.0001	0.0000	0.0002
PL	-0.0007	-0.0004	-0.0002	-0.0002	-0.0001	**-0.0048**	0.0000	0.0002	0.0000	-0.0005
NSP/P	-0.0001	0.0012	-0.0006	-0.0012	-0.0002	0.0000	**0.0056**	0.0004	-0.0001	-0.0011
BY/Pt	0.1171	-0.1052	0.1238	0.0926	-0.0203	-0.0402	0.0755	**0.9683**	-0.6301	0.0551
HI	-0.0447	-0.0874	-0.0555	-0.1042	-0.0143	0.0011	-0.0144	-0.8349	**1.2830**	-0.1905
TW	0.0002	0.0003	0.0003	-0.0007	0.0004	-0.0009	0.0016	-0.0005	0.0013	**-0.0088**
HULL. %	0.0003	-0.0003	0.0004	0.0008	0.0001	-0.0001	-0.0002	-0.0002	0.0005	-0.0003
MILL. %	0.0001	0.0014	-0.0006	-0.0003	0.0007	-0.0003	0.0017	0.0004	-0.0008	0.0010
HRR %	-0.0001	0.0007	0.0000	-0.0005	-0.0005	-0.0001	0.0007	-0.0003	0.0001	-0.0002
KLBC	-0.0003	0.0006	-0.0003	-0.0005	-0.0004	-0.0006	0.0014	0.0000	-0.0001	-0.0002
KBBC	0.0002	0.0020	-0.0002	-0.0011	0.0002	0.0010	0.0011	-0.0007	-0.0003	0.0011
L/B RAT.	0.0004	-0.0029	0.0007	0.0018	0.0006	0.0003	-0.0033	0.0007	0.0002	-0.0006
AMY. C.	-0.0008	-0.0002	-0.0008	0.0007	0.0008	-0.0003	-0.0003	-0.0005	0.0005	0.0002
VER	-0.0001	0.0000	0.0002	-0.0003	-0.0003	0.0000	-0.0002	0.0002	-0.0002	-0.0003
KER	0.0001	-0.0006	0.0001	0.0005	0.0003	0.0002	-0.0007	0.0001	-0.0001	0.0001
GY/Pt	**0.0784**	**-0.1996**	**0.0724**	**-0.0074**	**-0.0352**	**-0.0443**	**0.0656**	**0.1358**	**0.6541****	**-0.1445**
R^2 = 0.9750	Residual effect = 0.1580									

Table 4.11: (b) Direct (diagonal) and indirect effects of different component characters attributing to grain yield per plant in rice at phenotypic level

Characters	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RAT.	AMY. C.	VER	KER
DFF	-0.0002	0.0000	-0.0003	0.0004	0.0001	0.0002	-0.0007	-0.0001	0.0005
PH	-0.0003	0.0009	-0.0024	0.0012	-0.0018	0.0019	0.0002	0.0001	0.0027
DM	-0.0001	0.0001	0.0000	0.0002	-0.0001	0.0002	-0.0003	0.0001	0.0001
NT/Pt	-0.0003	0.0001	-0.0008	0.0004	-0.0004	0.0005	0.0003	-0.0003	0.0010
NPT/m^2	0.0000	0.0002	0.0007	-0.0003	-0.0001	-0.0002	-0.0004	0.0003	-0.0006
PL	-0.0001	-0.0001	0.0003	-0.0007	-0.0005	-0.0001	0.0002	-0.0001	-0.0004
NSP/P	0.0001	-0.0007	0.0015	-0.0018	0.0006	-0.0015	-0.0002	-0.0003	-0.0023
BY/Pt	0.0161	-0.0326	-0.1283	-0.0089	-0.0702	0.0524	-0.0625	0.0517	0.0800
HI	-0.0588	0.0816	0.0564	0.0233	-0.0334	0.0244	0.0958	-0.0716	-0.0444
TW	-0.0003	0.0007	0.0005	-0.0003	-0.0010	0.0004	-0.0003	0.0008	-0.0004
HULL. %	**-0.0102**	0.0005	-0.0007	-0.0009	-0.0007	-0.0001	-0.0002	0.0005	0.0004
MILL. %	0.0006	**-0.0126**	0.0006	-0.0014	0.0008	-0.0013	0.0004	-0.0008	-0.0016
HRR %	0.0002	-0.0001	**0.0026**	-0.0012	0.0006	-0.0011	-0.0003	0.0003	-0.0015
KLBC	-0.0004	-0.0005	0.0020	**-0.0044**	0.0009	-0.0033	-0.0001	0.0004	-0.0022
KBBC	0.0007	-0.0006	0.0024	-0.0020	**0.0098**	-0.0079	-0.0012	-0.0004	-0.0020
L/B RAT.	0.0001	0.0014	-0.0055	0.0094	-0.0102	**0.0127**	0.0011	-0.0002	0.0055
AMY. C.	0.0002	-0.0003	-0.0007	0.0002	-0.0008	0.0006	**0.0071**	-0.0012	-0.0003
VER	-0.0002	0.0002	0.0004	-0.0003	-0.0001	-0.0001	-0.0006	**0.0036**	-0.0002
KER	-0.0001	0.0002	-0.0010	0.0009	-0.0004	0.0008	-0.0001	-0.0001	**0.0018**
GY/Pt	**-0.0528**	**0.0384**	**-0.0726**	**0.0138**	**-0.1067**	**0.0786**	**0.0383**	**-0.0173**	**0.0360**
R^2 = 0.9750	Residual effect = 0.1580								

Table 4.12: (a) Direct (diagonal) and indirect effects of different component characters attributing to grain yield per plant in rice at genotypic level

Characters	DFF	PH	DM	NT/Pt	NPT/m^2	PL	NSP/P	BY/Pt	HI	TW
DFF	**0.0249**	-0.0006	0.0226	0.0023	0.0085	0.0148	0.0036	0.0113	-0.0067	-0.0019
PH	0.0070	**-0.2940**	-0.0172	0.1671	0.0617	-0.0524	-0.1151	0.0768	0.0178	0.0464
DM	-0.0105	-0.0007	**-0.0116**	-0.0002	-0.0007	-0.0056	0.0009	-0.0041	0.0026	0.0012
NT/Pt	-0.0124	0.0756	-0.0021	**-0.1329**	-0.0407	-0.0218	0.0586	-0.0098	0.0218	-0.0313
NPT/m^2	-0.0752	0.0463	-0.0127	-0.0676	**-0.2205**	-0.0416	0.0197	0.0312	-0.0098	0.0134
PL	0.0715	0.0215	0.0578	0.0198	0.0228	**0.1208**	-0.0103	-0.0169	-0.0002	0.0240
NSP/P	0.0013	0.0036	-0.0007	-0.0041	-0.0008	-0.0008	**0.0092**	0.0011	-0.0001	-0.0024
BY/Pt	0.5240	-0.3014	0.4115	0.0849	-0.1633	-0.1612	0.1417	**1.1534**	-0.9339	0.1121
HI	-0.2717	-0.0609	-0.2233	-0.1645	0.0448	-0.0016	-0.0106	-0.8135	**1.0046**	-0.2792
TW	0.0143	0.0297	0.0187	-0.0443	0.0114	-0.0374	0.0494	-0.0183	0.0523	**-0.1880**
HULL. %	0.0108	-0.0044	0.0023	0.0082	0.0097	-0.0072	-0.0025	0.0024	0.0049	-0.0150
MILL. %	0.0257	0.0003	0.0205	0.0057	0.0561	-0.0161	0.0388	0.0070	0.0354	0.0409
HRR %	0.0039	-0.0105	0.0026	0.0095	0.0056	0.0033	-0.0060	0.0030	-0.0016	0.0019
KLBC	0.0002	-0.0056	-0.0004	0.0041	0.0020	0.0027	-0.0054	0.0006	0.0001	-0.0002
KBBC	0.0007	-0.0720	0.0044	0.0636	0.0229	-0.0523	-0.0572	0.0189	-0.0096	-0.0420
L/B RAT.	-0.0028	0.1247	0.0023	-0.1008	-0.0419	-0.0057	0.1105	-0.0241	0.0092	0.0292
AMY. C.	-0.0026	-0.0014	-0.0016	0.0032	0.0020	-0.0014	-0.0023	-0.0028	0.0032	0.0008
VER	0.0113	-0.0014	-0.0011	0.0007	0.0135	-0.0040	0.0013	0.0008	0.0006	0.0018
KER	0.0177	-0.0570	0.0102	0.0561	0.0256	0.0164	-0.0465	0.0088	-0.0062	0.0061
GY/Pt	0.3380*	-0.5081**	0.2821*	-0.0890	-0.1812	-0.2512	0.1778	0.4260**	0.1844	-0.2822*
R^2 = 0.9871	Residual effect = 0.1134									

Table 4.13: (b) Direct (diagonal) and indirect effects of different component characters attributing to grain yield per plant in rice at genotypic level

Characters	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RAT.	AMY. C.	VER	KER
DFF	-0.0029	-0.0029	-0.0057	0.0005	-0.0001	0.0003	-0.0033	-0.0083	0.0049
PH	-0.0142	0.0004	-0.1836	0.1484	-0.1310	0.1542	0.0212	-0.0123	0.1871
DM	0.0003	0.0011	0.0018	0.0004	0.0003	0.0001	0.0009	-0.0004	-0.0013
NT/Pt	0.0119	0.0034	0.0751	-0.0490	0.0523	-0.0563	-0.0219	0.0026	-0.0833
NPT/m^2	0.0233	0.0552	0.0742	-0.0402	0.0312	-0.0388	-0.0223	0.0872	-0.0630
PL	0.0095	0.0086	-0.0236	0.0294	0.0391	0.0029	-0.0088	0.0140	0.0221
NSP/P	0.0003	-0.0016	0.0033	-0.0044	0.0033	-0.0043	-0.0011	-0.0004	-0.0048
BY/Pt	-0.0295	-0.0362	-0.2079	0.0651	-0.1349	0.1168	-0.1616	-0.0254	0.1132
HI	-0.0538	-0.1587	0.0950	0.0062	0.0595	-0.0389	0.1655	-0.0183	-0.0699
TW	-0.0308	0.0343	0.0211	0.0034	-0.0488	0.0231	-0.0079	0.0100	-0.0128
HULL. %	**-0.0919**	0.0265	-0.0117	-0.0037	-0.0195	0.0058	-0.0044	0.0138	0.0056
MILL. %	0.0646	**-0.2241**	0.0295	-0.0482	0.0808	-0.0672	0.0292	-0.0479	-0.0724
HRR %	-0.0021	0.0022	**-0.0167**	0.0111	-0.0091	0.0114	0.0019	-0.0041	0.0111
KLBC	0.0004	0.0024	-0.0074	**0.0112**	-0.0068	0.0104	0.0020	-0.0020	0.0076
KBBC	-0.0343	0.0582	-0.0883	0.0982	**-0.1616**	0.1388	0.0539	-0.0284	0.0754
L/B RAT.	0.0149	-0.0713	0.1624	-0.2206	0.2042	**-0.2378**	-0.0606	0.0406	-0.1541
AMY. C.	0.0009	-0.0026	-0.0022	0.0035	-0.0066	0.0050	**0.0197**	-0.0078	-0.0013
VER	0.0051	-0.0073	-0.0083	0.0062	-0.0060	0.0058	0.0135	**-0.0341**	0.0040
KER	-0.0055	0.0289	-0.0596	0.0607	-0.0418	0.0580	-0.0057	-0.0106	**0.0895**
GY/Pt	**-0.1338**	**-0.2835***	**-0.1527**	**0.0780**	**-0.0953**	**0.0891**	**0.0103**	**-0.0317**	**0.0578**
R^2 = 0.9871	Residual effect = 0.1134								

Figure 4.5: Path diagram depicting estimates of phenotypic path for grain yield per plant in rice

Figure 4.6: Path diagram depicting estimates of genotypic path for grain yield per plant in rice
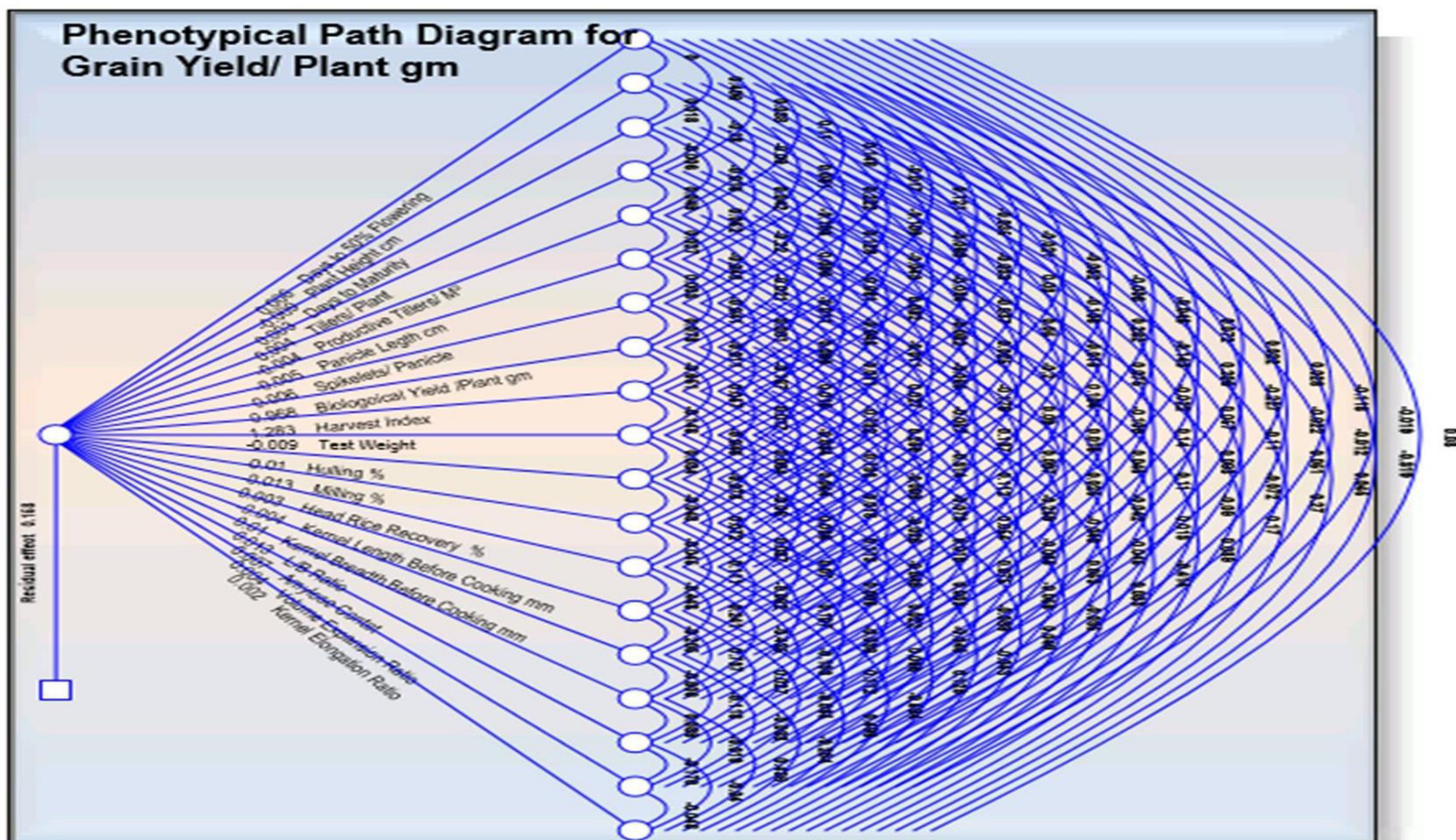
4.7 Genetic divergence analysis among different advance rice lines:

In the genetic divergence study on the basis of pooled performance of genotypes, thirty six advance lines of rice were found to be differed significantly and displayed a marked divergence in respect of twenty one yield and quality attributing characters. The distance analysis among lines of rice has been reported by several geneticists under the assumption that lines within the group are genetically related whereas diverse cultivars are classified into different clusters. In the present study, divergence was assessed by Mahalanobis D^2 statistics with Tocher's method. Limitations of D^2 statistics using Tocher's method are the length and cumbersome computational procedure which restricts its use, moreover cluster constellation is done manually and cluster diagram is arbitrary more so when number of cluster formed is large.

4.7.1 Distribution of advance rice lines in different clusters (Cluster composition):

Based on the performance of lines using relative magnitude of D^2 values, all the thirty six genotypes including checks were grouped into six clusters in such a way that lines within single cluster had smaller D^2 values among themselves than those lines belongs to different clusters. Clusters I, II, III, IV, V and VI contained 12, 17, 04, 1, 1 and 1 lines respectively (Table 4.14 and Fig. 4.7). Among all the clusters, cluster II was found to be largest cluster which consisted maximum number of lines (17 lines) followed by cluster I (12 lines) then cluster III (04 lines) while cluster IV, V and VI was mono-genotypic consisted only single lines.

4.7.2 Intra and inter cluster distances among the different groups:

The intra and inter cluster average distances among six clusters were variable (Table 4.15 and Fig. 4.8). The highest intra-cluster distance was observed for the cluster I (3.512) which was the second largest group with 12 lines followed by cluster II (3.386) that was the largest group with 17 genotypes and cluster III (2.603) was the third largest group with 04 advanced rice lines while cluster IV, V and VI (0.000) had lowest or no intra cluster distance. The inter cluster distances ranged from 3.335 to 36.777 between the clusters IV-V and I-III respectively. The highest inter cluster distance was observed between the clusters I-III (36.777) followed by clusters III-V (26.638), III-IV (24.814)

and clusters I-VI (21.356) while lowest inter cluster distances recorded between the clusters IV-V (3.335) followed by clusters I-IV (4.619) and I-V (4.754).

4.7.3 Cluster mean performance for different yield and quality attributes:

A comparative study of the mean values of different clusters for 21 yield and quality traits has been presented in Table 4.16. Sufficient differences observed in cluster mean values for all the traits studied. The present study revealed that cluster I had highest mean value for the trait kernel elongation ratio (1.754). Cluster II had no highest or lowest values observed for any yield or quality traits and this cluster shows the moderate performance in case of cluster mean for most of the traits. Cluster III showed highest mean value for plant height (107.086), number of spikelets per panicle (194.396) and head rice recovery (56.177) while lowest mean values for days to maturity (115.500), number of tillers per plant (9.604), test weight (23.410), kernel length before cooking (6.450), L/B ratio before cooking (2.992), amylose content (21.305) and kernel elongation ratio (1.533). Cluster IV had highest mean value observed for days to 50% flowering (84.500), panicle length (27.405), biological yield per plant (72.833) hulling recovery % (77.345) and kernel breadth before cooking (2.183) while lowest mean values for days to maturity (115.500), grain yield per plant (24.667), harvest index (34.197) volume expansion ratio (3.322) and grain yield kilogram per hectare (3913.583). Cluster V had highest mean value observed for number of tillers per plant (11.500), milling recovery (65.258), kernel length before cooking (7.708), L/B ratio before cooking (4.018) and volume expansion ratio (3.417) while lowest values for days to 50% flowering (82.167), plant height (96.633), number of productive tillers per meter square (205.000), panicle length (25.522), number of spikelets per panicle (130.750), head rice recovery (40.008) and kernel breadth before cooking (1.925). Cluster VI had highest values observed for the traits like days to maturity (116.583), number of productive tillers per meter square (237.917), grain yield per plant (29.500), harvest index (47.467), test weight (27.958), amylose content (23.716) and grain yield kilogram per hectare (4563.333) while lowest values observed for biological yield per plant (62.417), hulling recovery (73.741) and milling recovery (56.983).

4.7.4 Percent contribution of 21 traits towards divergence in 36 advanced rice lines:

The percent contribution of 21 yield and quality traits towards total genetic divergence is given below (Table 4.17 and Fig. 4.9). Percent contribution is essential for effective selection and choice of parents to get valuable transgressive segregants in F_2 or subsequent generations. Present study revealed that the highest contribution in manifestation of genetic divergence was exhibited by the traits like kernel elongation ratio (71.90) with number of times appearing first in ranking (453) followed by head rice recovery (7.78) with number of times appearing first in ranking (49), biological yield per plant (4.76) with number of times appearing first in ranking (30), amylose content (4.60) with number of times appearing first in ranking (29), test weight (4.13) with number of times appearing first in ranking (26) and grain yield kilogram per hectare (2.22) with number of times appearing first in ranking (14).

Table 4.14: Distribution of 36 advance rice lines among different clusters (cluster composition)

Clusters ↓	Number of Genotypes	Designation of Genotypes
Cluster - I	12	IR 92527-6-2-1-2, IR 92527-6-2-1-4, IR 92517-1-3-1-1, IR 92523-37-1-1-2, IR 92523-35-1-1-1, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3, IR 88287-383-1-B-B-1-1-B, IR 94313:18-4-1-4-1-B, IR 92522-61-3-1-4, MTU 1010 (Check), IR 94314-20-2-1-B
Cluster - II	17	IR 92546-7-1-1-3, IR 92546-33-3-1-1, IR 92546-17-6-4-4, RP-1-27-7-6-1-2-1, IR 64 (Check), IR 94391-587-1-2-B, IR 92516-8-3-3-4, IR 92545-51-1-1-4, IR 92545-24-3-1-1, IR 92545-23-2-1-1, IR 92545-54-6-1-4, LALAT (Check), IR 92546-17-6-4-3, IR 92522-47-2-1-1, CRR 724-1-B (IR 88889-44), CRR 719-1-B (IR 88903-34), IR 92546-33-4-2-3
Cluster - III	4	IR 92521-23-6-1-3, IR 92521-24-5-1-3, IR 92521-5-3-1-2, IR 92521-7-5-1-1
Cluster - IV	1	IR 92545-40-2-2-3
Cluster - V	1	IR 92522-47-2-1-4
Cluster - VI	1	IR 92522-45-3-1-4

Figure 4.7: Dendogram depicting genetic divergence for 36 rice lines
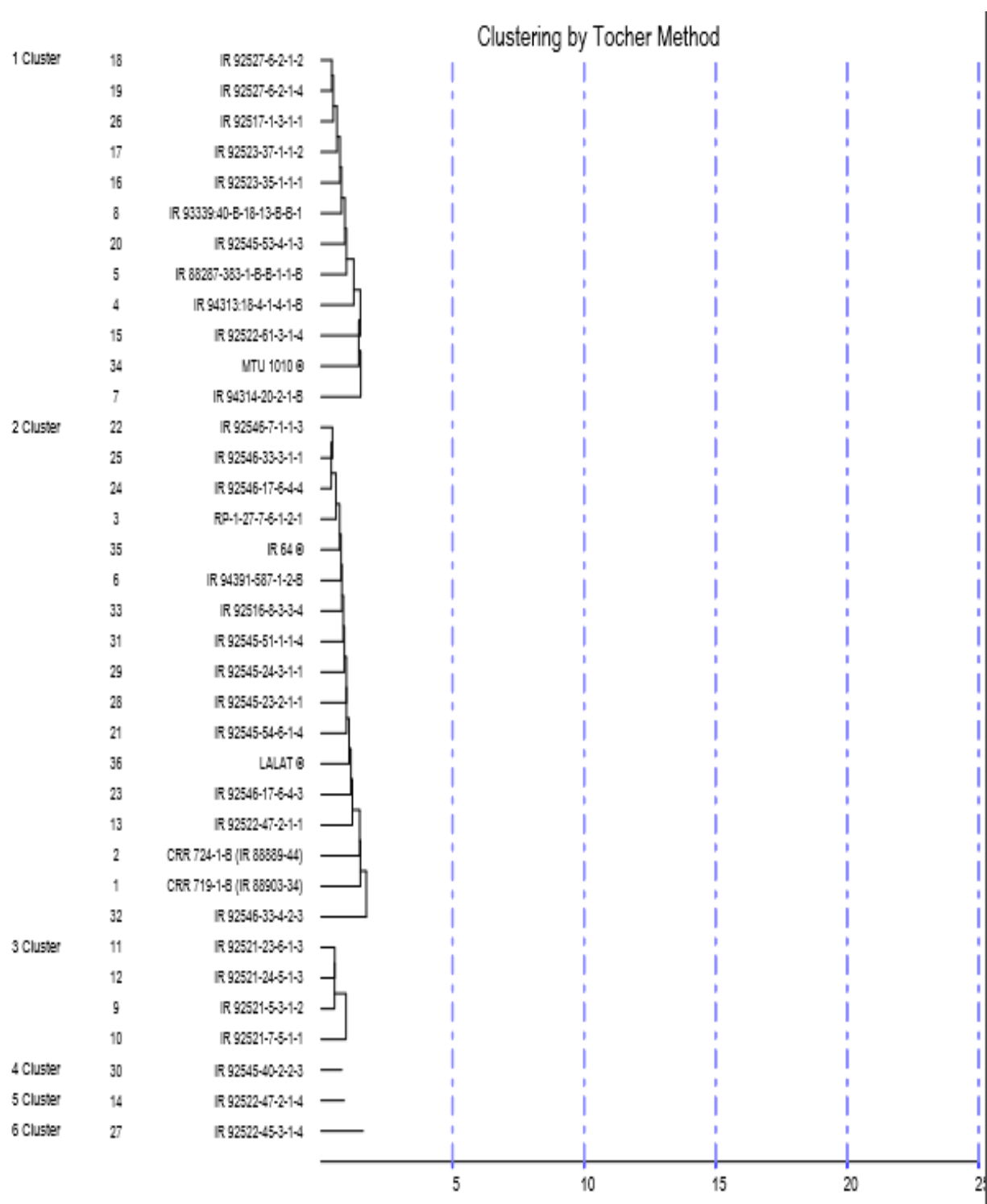
Table 4.15: Average intra and inter cluster distance (value) based on D^2 analysis in rice

Clusters → ↓	Cluster - I	Cluster - II	Cluster - III	Cluster - IV	Cluster - V	Cluster - VI
Cluster - I	**3.512**	10.020	**36.777**	4.619	4.754	**21.356**
Cluster - II		**3.386**	13.753	5.649	5.953	7.449
Cluster - III			**2.603**	**24.814**	**26.638**	10.146
Cluster - IV				**0.000**	3.335	11.736
Cluster - V					**0.000**	12.613
Cluster - VI						**0.000**

Figure 4.8: Representation of cluster distance based on D² analysis in rice (Tocher's method)
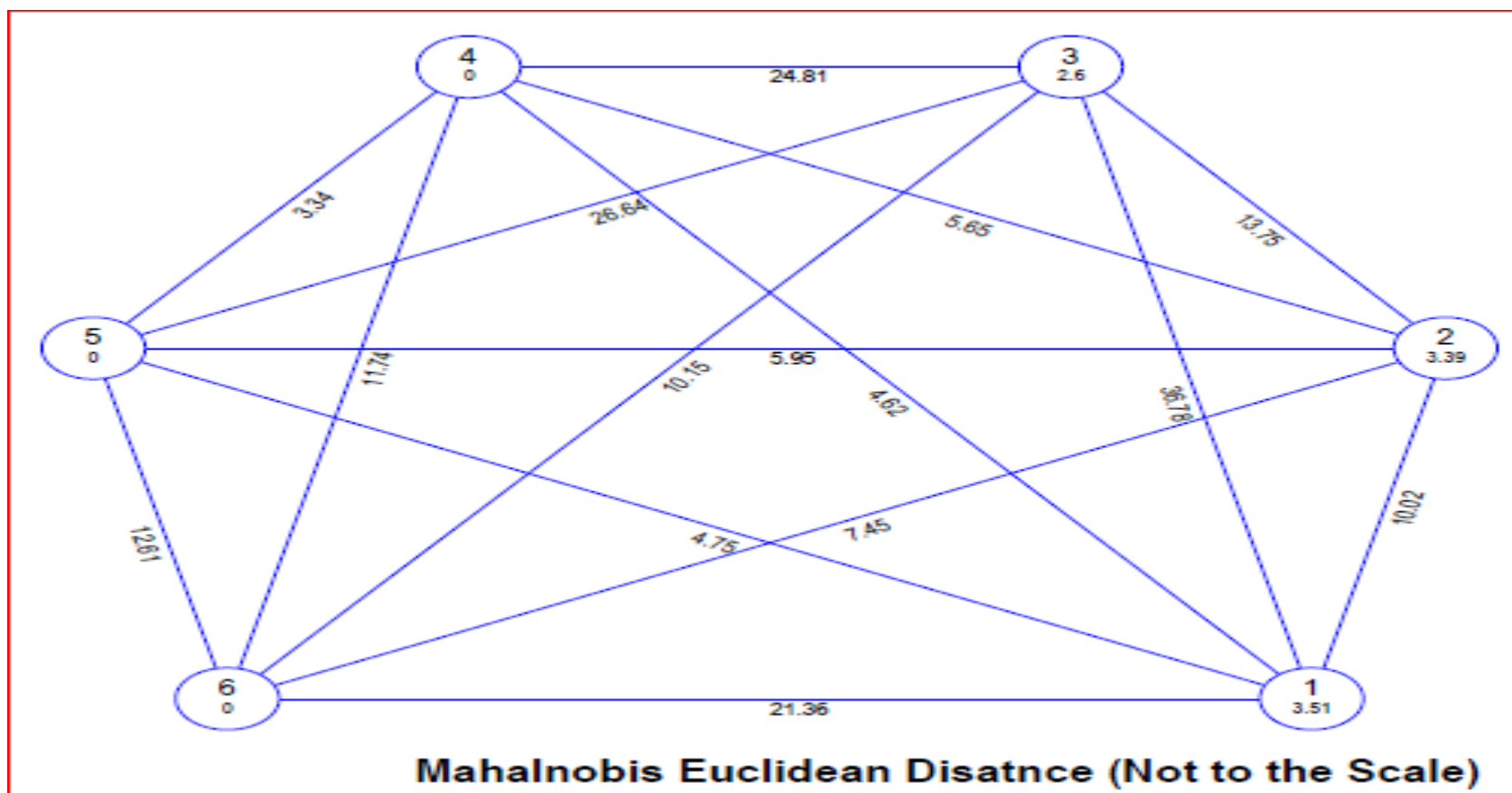
Table 4.16: Cluster mean performance of different characters in rice

Characters	Cluster (I)	Cluster (II)	Cluster (III)	Cluster (IV)	Cluster (V)	Cluster (VI)
DFF	83.458	83.304	82.542	84.500	82.167	83.717
PH	97.462	99.752	107.086	104.396	96.633	96.750
DM	115.806	115.824	115.500	115.500	115.917	116.583
NT/Pt	11.285	10.775	9.604	10.083	11.500	10.750
NPT/m^2	234.896	230.608	205.708	230.167	205.000	237.917
PL	26.293	25.901	25.872	27.405	25.522	25.738
NSP/P	146.153	148.034	194.396	159.417	130.750	150.083
GY/Pt	27.951	27.574	27.333	24.667	26.500	29.500
BY/Pt	67.632	66.770	69.125	72.833	70.167	62.417
HI	41.689	41.696	39.823	34.197	37.758	47.467
TW	24.103	24.125	23.410	27.800	24.242	27.958
HULL. %	73.960	74.755	74.415	77.345	75.102	73.741
MILL. %	63.113	62.460	62.713	62.883	65.258	56.983
HRR %	44.331	50.195	56.177	43.133	40.008	42.158
KLBC	7.292	6.982	6.450	7.175	7.708	6.792
KBBC	2.065	2.097	2.165	2.183	1.925	2.117
L/B RAT.	3.557	3.348	2.992	3.301	4.018	3.222
AMY. C.	21.774	22.464	21.305	21.342	23.332	23.716
VER	3.384	3.372	3.414	3.322	3.417	3.352
KER	1.754	1.645	1.533	1.701	1.697	1.586
GYKG/Ha	4474.299	4318.172	4135.729	3913.583	3965.084	4563.333

Table 4.17: Relative contribution of individual character towards genetic divergence among different advance rice lines

S. No.	Source	Contribution (%)	Times Ranked 1st
1	DFF	0.01	0
2	PH	0.01	0
3	DM	0.16	1
4	NT/Pt	0.01	0
5	NPT/m²	0.48	3
6	PL	0.16	1
7	NSP/P	1.90	12
8	GY/Pt	0.01	0
9	BY/Pt	4.76	30
10	HI	0.01	0
11	TW	4.13	26
12	HULL. %	0.63	4
13	MILL. %	0.01	0
14	HRR %	7.78	49
15	KLBC	1.11	7
16	KBBC	0.16	1
17	L/B RATIO	0.01	0
18	AMYLOSE C.	4.60	29
19	VER	0.01	0
20	KER	71.90	453
21	GYKG/Ha	2.22	14

Figure 4.9: Diagrammatic representation of relative contribution towards genetic divergence of different characters in 36 advance rice lines
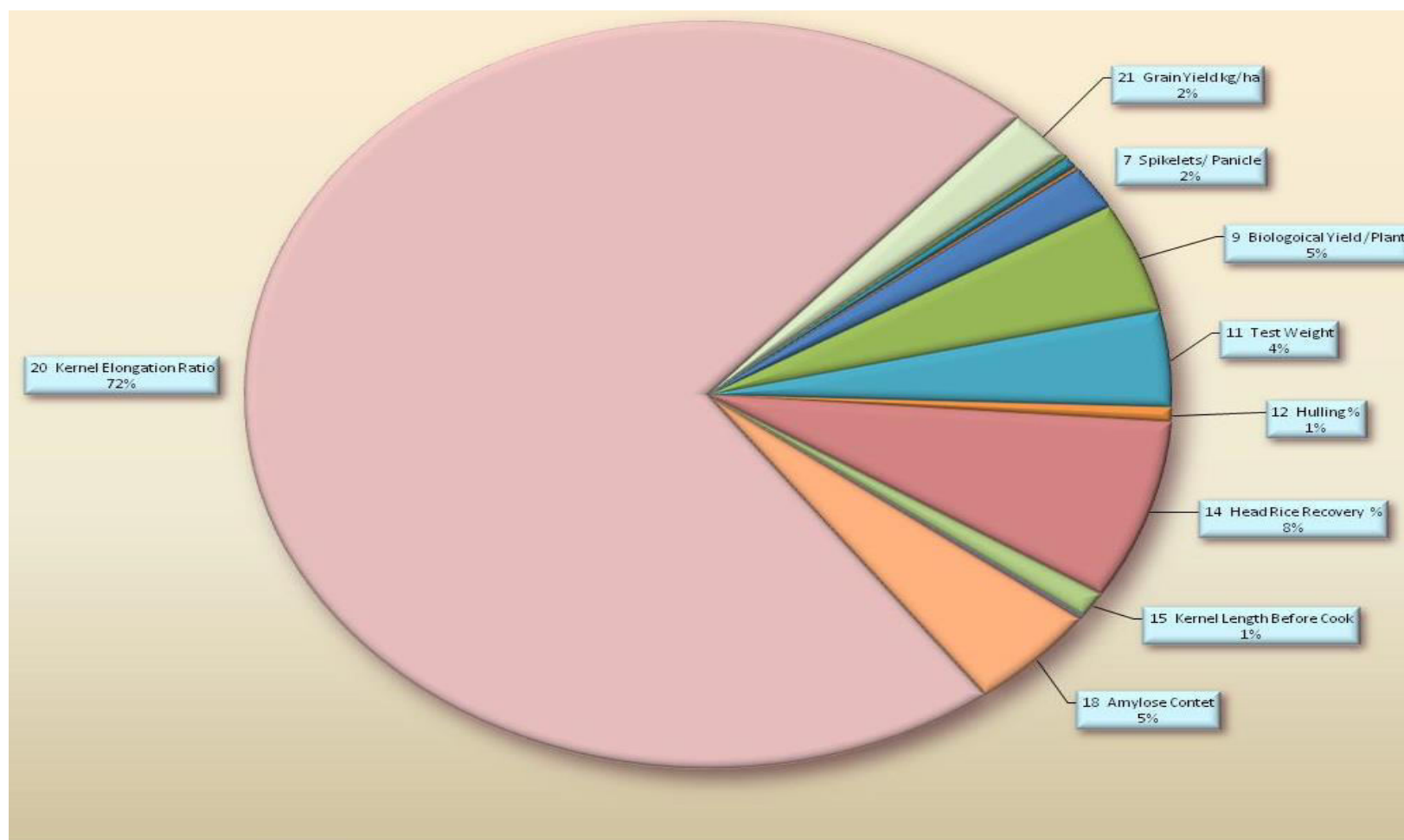
4.8 Molecular diversity analysis among rice lines using SSR markers:

The thirty six advance lines of rice were screened with sixteen simple sequence repeat (SSR) markers. These 16 markers were reported to be linked with yield and quality attributing traits. Amplification profile of 16 SSR markers, allelic diversity of the lines and their relative study of amplification profiles which was resolved on 2% agarose gel are discussed below (Table 4.18, 4.19, 4.20, 4.21, 4.22 and Fig. 4.10, 4.11, 4.12).

4.8.1 Amplification profile and allelic diversity analysis:

4.8.1.1 RM 283:

RM 283 is located on rice linkage group number 1; RM 283 generated three alleles of 156, 166 and 148 base pair. Allele of 156 bp size was found in 24 genotypes which is most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 66.67%. Allele of 166 bp size was found in 10 genotypes with frequency of 27.78%. There is a rare allele of size 148 bp found in 2 genotypes with frequency 5.56%. Polymorphic information content (PIC) value of the RM 283 was 0.317.

4.8.1.2 RM 154:

RM 154 is located on rice linkage group number 2; RM 154 generated four alleles of 190, 167, 203 and 175 base pair (Fig. 4.10). Alleles of 190 bp size and 175 bp size was found to be most frequent among the genotypes and hence considered as the high frequency alleles with a frequency of 30.56% for each. The high frequency alleles were found in 11 different genotypes. Allele of 167 bp size was found in 4 genotypes with frequency of 11.11%. Allele of 203 bp amplification was found in 10 genotypes with frequency of 27.78%. Polymorphic information content (PIC) value of the RM 154 was 0.362.

4.8.1.3 RM 55:

RM 55 is located on rice linkage group number 3; RM 55 generated five alleles of 235, 215, 252, 264 and 289 base pair. Allele of 264 bp size was found to be most frequent

among the genotypes and hence considered as the high frequency allele with a frequency of 30.56%. The high frequency alleles were found in 11 different genotypes. Alleles of 235 bp size, 215 bp size, 252 bp size and 289 bp size was found in 4, 4, 9 and 8 genotypes subsequently with frequency 11.11%, 11.11%, 25% and 22.22%. Polymorphic information content (PIC) value of the RM 55 was 0.308.

4.8.1.4 RM 307:

RM 307 is located on rice linkage group number 4; RM 307 generated three alleles of 143, 134 and 122 base pair. Allele of 134 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 38.89 %. The high frequency allele was found in 14 different genotypes. Allele of 143 bp size was found in 9 genotypes with 25.00% frequency while allele of 122 bp size was found in 13 genotypes with frequency 36.11%. Polymorphic information content (PIC) value of the RM 307 was 0.437.

4.8.1.5 RM 334:

RM 334 is located on rice linkage group number 5; RM 334 generated four alleles of 178, 212, 194 and 224 base pair size. Allele of 194 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 38.89%. The high frequency allele was found in 14 different genotypes. Allele of 178 bp size, 212 bp size and 224 bp size were found in 8, 10 and 4 genotypes subsequently with a frequency of 22.22%, 27.78% and 11.11%. Polymorphic information content (PIC) value of the RM 334 was 0.355.

4.8.1.6 RM 510:

RM 510 is located on rice linkage group number 6; RM 510 generated three alleles of 128, 112 and 95 base pair size. Allele of 112 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 41.67%. The high frequency allele was found in 15 different lines of rice. Allele 128 bp size and 95 bp size was found in 13 and 8 genotypes subsequently with a frequency of 36.11% and 22.22%. PIC value of the marker RM 510 was 0.431.

4.8.1.7 RM 11:

RM 11 is located on rice linkage group number 7; RM 11 generated four different alleles of 130, 146, 166 and 109 base pair size. Allele of 109 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 50.00%. The high frequency allele was found in 18 different rice lines. Allele of 130 bp size and 146 bp size was found in 10 and 6 lines subsequently with a frequency of 27.78% and 16.67%. There is a rare allele 166 bp size was found in 2 rice lines with a frequency of 5.56%. Polymorphic information content (PIC) value of the RM 11 was 0.321.

4.8.1.8 RM 25:

RM 25 is located on rice linkage group number 8; RM 25 generated four alleles of 151, 161, 178 and 134 base pair size (Fig. 4.10). Allele of 161 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 33.33%. The high frequency allele was found in 12 different genotypes. Allele of 151 bp size, 178 bp size and 134 bp size were found in 11, 10 and 3 genotypes subsequently with a frequency of 30.56%, 27.78% and 8.33%. None of the genotypes shows multiple allelism for this particular locus. Polymorphic information content (PIC) value of the marker RM 25 was 0.356.

4.8.1.9 RM 215:

RM 215 is located on rice linkage group number 9; RM 215 generated three alleles of different size such as 155, 149 and 131 base pair. Allele of 149 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 50.00%. The high frequency allele was found in 18 different lines of the set. Allele of 155 bp and allele of 131 bp was found in 12 and 6 rice lines subsequently with a frequency of 33.33% and 16.67%. Polymorphic information content (PIC) value of the RM 215 was 0.407.

4.8.1.10 RM 271:

RM 271 is located on rice linkage group number 10; RM 271 generated four alleles of 105, 119, 84 and 96 base pair. Allele of 105 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 55.56%. The high frequency allele was found in 20 different genotypes. Allele of 119 bp size and allele of 96 bp size was found in 6 and 8 genotypes subsequently with a frequency of 16.67% and 22.22%. There is a rare allele 84 bp size was found in 2 genotypes with a frequency of 5.56%. Polymorphic information content (PIC) value of the RM 271 was 0.306.

4.8.1.11 RM 536:

RM 536 is located on rice linkage group number 11; RM 536 generated four alleles of 235, 252, 227 and 203 base pair size. Allele of 235 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 52.78%. The high frequency allele was found in 19 different rice lines. Allele of 252 bp size, 227 bp size and allele of 203 bp size were found in 6, 8 and 3 lines subsequently with a frequency of 16.67%, 22.22% and 8.33%. None of the genotypes shows multiple allelism for this specific locus. Polymorphic information content (PIC) value of the RM 536 was 0.319.

4.8.1.12 RM 463:

RM 463 is located on rice linkage group number 12; RM 463 generated three alleles of different size such as 193, 187 and 203 base pair. Allele of 187 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 38.89%. The high frequency allele was found in 14 different genotypes of the set. Allele of 193 bp size and 203 bp size was found in 9 and 13 genotypes subsequently with a frequency of 25% and 36.11%. Polymorphic information content (PIC) value of the RM 463 was 0.437.

4.8.1.13 RM 118:

RM 118 is located on rice linkage group number 7; RM 118 generated three alleles of 178, 191 and 166 base pair. Allele of 178 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 50%. The high frequency allele was found in 18 different genotypes. Allele of 191 bp size and 166 bp size was found in 15 and 3 genotypes subsequently with a frequency of 41.67% and 8.33%. PIC value of the marker RM 118 was 0.380.

4.8.1.14 RM 277:

RM 277 is located on rice linkage group number 12; RM 277 generated four alleles of 134, 143, 153 and 123 base pair size. Allele of 143 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of 52.78%. The high frequency allele was found in 19 different genotypes. Allele of 134 bp size, 153 bp size and 123 bp size was found in 4, 8 and 5 genotypes subsequently with a frequency of 11.11%, 22.22% and 13.89%. None of the genotypes shows multiple allelism for RM 277. Polymorphic information content (PIC) value of the RM 277 was 0.320.

4.8.1.15 RM 21:

RM 21 is located on rice linkage group number 11; RM 21 generated four alleles of 170, 138, 157 and 128 base pair size (Fig. 4.10). Allele of 138 bp was found to be most frequent among the rice lines and hence considered as the high frequency allele with a frequency of 36.11%. The high frequency allele was found in 13 rice lines. Allele of 170 bp size, 157 bp size and 128 bp size were found in 8, 8 and 7 lines subsequently with a frequency of 22.22%, 22.22% and 19.44%. Polymorphic information content (PIC) value of the RM 21 was 0.367.

4.8.1.16 RM 484:

RM 484 is located on rice linkage group number 10; RM 484 generated three alleles of 193, 207 and 179 base pair. Allele 193 bp size was found to be most frequent among the genotypes and hence considered as the high frequency allele with a frequency of

66.67%. The high frequency allele was found in 24 different genotypes. Allele of 207 bp size and 179 bp size were found in 8 and 4 genotypes subsequently with a frequency of 22.22% and 11.11%. PIC value of the marker RM 484 was 0.329.

4.8.2 Molecular fingerprinting of the thirty six rice genotypes on the basis of sixteen SSR amplification profiles:

The following figure (Fig. 4.11) depicts the fingerprinting of all the rice genotypes at molecular level on the basis of amplification profile of the thirty six rice genotypes with sixteen simple sequence repeat (SSR) markers as discussed before.

4.8.3 Cluster composition among advance rice lines by UPGMA method using molecular information:

On the basis of amplification profile through sixteen simple sequence repeat (SSR) markers, thirty six advance lines of rice were subjected to cluster analysis using UPGMA technique and the Jaccard's similarity coefficient was calculated (Table 4.21, 4.22 and Fig. 4.12). The thirty six lines of rice were grouped into 2 major groups which further categorised in 6 sub-groups or clusters. Cluster composition of the set of rice lines were fall into 6, 7, 9, 3, 8 and 3 lines respectively from the cluster I - VI. To prepare the cluster composition, the reference point nearest to Nei's distance value 0.33 (Between 0.15 – 0.33) was taken. On the basis of molecular information, dendogram revealed that all the rice lines were distinct from each other except R and S which are similar from each-other in genetic constituents. From above result, it clear that the SSR markers used in this study can be used for future rice molecular diversity analysis purpose. Among six clusters, cluster III contained highest number of coded rice lines (N, O, R, S, T, V, U, P, Q) followed by cluster V (W, X, Y, Z, AA, AB, AC, AD), Cluster II (G, H, I, J, K, L, M), cluster I (A, B, C, D, E, F,C), cluster IV (AH, AJ, AI) and cluster VI had also 3 lines (AE, AF, AG).

A comparative study between the dendrogram obtained from morphological and molecular data revealed that a few rice lines belongs to the same cluster. Different groups of rice lines (A, B, C, and F), (I, J. K and L), (O, P, Q, R, S and T), (W, X, Y, AB and AC) and (AE, AF and AG) comes under same cluster on the basis of morphological and

molecular data and also along with maximum similarity coefficient value. However, in case of inter cluster lines similarity coefficient value was found to be lowest.

4.8.4: Similarity coefficient matrix of advance rice lines based on Jaccard's similarity coefficient analysis

According to Jaccard's similarity coefficient (Table 4.22) least similarity was observed between the coded rice lines G and F (0.00) followed by I and AF (0.00), M and X (0.00) which indicated that almost dissimilar lines from each-other while highest similarity coefficient value observed between the coded rice lines R and S (0.88) followed by T and V (0.78), W and X (0.68).

Table 4.18: Silent features of amplification profile of 36 advance rice lines by 16 SSR markers

S. No.	SSR Markers	C. L.	Primer sequence	A. T. (°C)	E. P. S.	Min. Alleles	Max. Alleles	No. of alleles Generated (58)	PIC Value
1	RM 283	1	gtctacatgtacccttgttggg (F) cggcatgagagtctgtgatg (R)	55	181	130	176	3	0.317
2	RM 154	2	accctctccgcctcgcctcctc (F) ctcctcctcctgcgaccgctcc (R)	61	183	148	230	4	0.362
3	RM 55	3	ccgtcgccgtagtagagaag (F) tcccggttattttaaggcg (R)	55	226	216	247	5	0.308
4	RM 307	4	gtactaccgacctaccgttcac (F) ctgctatgcatgaactgctc (R)	55	174	116	191	3	0.437
5	RM 334	5	gttcagtgttcagtgccacc (F) gactttgatctttggtggacg (R)	55	182	119	207	4	0.355
6	RM 510	6	aaccggattagtttctcgcc (F) gaggacgacgagcagattc (R)	55	122	99	127	3	0.431
7	RM 11	7	tctcctcttccccgatc (F) atagcgggcgaggcttag (R)	55	140	118	151	4	0.321
8	RM 25	8	ggaaagaatgatcttttcatgg (F) ctaccatcaaaaccaatgttc (R)	55	146	121	159	4	0.356
9	RM 215	9	caaaatggagcagcaaga(F) tgagcacctccttctctgtag(R)	55	148	126	161	3	0.407
10	RM 271	10	tcagatctacaattccatcc (F) tcggtgagacctagagagcc (R)	55	101	80	120	4	0.306
11	RM 536	11	tctctcctcttgtttggctc (F) acacaccaacacgaccacac (R)	55	243	223	247	4	0.319
12	RM 277	12	cggtcaaatcatcacctgac (F) caaggcttgcaagggaag (R)	55	124	104	121	4	0.320
13	RM 118	7	ccaatcggagccaccggagagc (F) cacatcctccagcgacgccgag (R)	67	156	149	165	3	0.380
14	RM 463	12	ttcccctccttttatggtgc(F) tgttctcctcagtcactgcg(R)	55	192	147	184	3	0.437
15	RM 21	11	acagtattccgtaggcacgg(F) gctccatgagggtggtagag(R)	55	157	133	201	4	0.367
16	RM 484	10	tctccctcctcaccattgtc (F) tgctgccctctctctctctc (R)	55	299	286	298	3	0.329

**SSR- Simple sequence repeat, A. T. – Annealing temperature, C. L. – Chromosome location,
E. P. S. – Expected product size and P. I. C. – Polymorphic information content (values)**

Table 4.19: (a) Description of amplified alleles using 16 SSR markers

Marker (SSR)	Amplified alleles	Frequency (in Genotypes)	Percentage (%)
RM 283	156	24	66.67
	166	10	27.78
	148	2	5.56
RM 154	190	11	30.56
	167	4	11.11
	203	10	27.78
	175	11	30.56
RM 55	235	4	11.11
	215	4	11.11
	252	9	25.00
	264	11	30.56
	289	8	22.22
RM 307	143	9	25.00
	134	14	38.89
	122	13	36.11
RM 334	178	8	22.22
	212	10	27.78
	194	14	38.89
	224	4	11.11
RM 510	128	13	36.11
	112	15	41.67
	95	8	22.22
RM 11	130	10	27.78
	146	6	16.67
	166	2	5.56
	109	18	50.00
RM 25	151	11	30.56
	161	12	33.33
	178	10	27.78
	134	3	8.33

Table 4.20: (b) Description of amplified alleles using 16 SSR markers

Marker (SSR)	Amplified alleles	Frequency (in genotypes)	Percentage (%)
RM 215	155	12	33.33
	149	18	50.00
	131	6	16.67
RM 271	105	20	55.56
	119	6	16.67
	84	2	5.56
	96	8	22.22
RM 536	235	19	52.78
	252	6	16.67
	227	8	22.22
	203	3	8.33
RM 463	193	9	25.00
	187	14	38.89
	203	13	36.11
RM 118	178	18	50.00
	191	15	41.67
	166	3	8.33
RM 277	134	4	11.11
	143	19	52.78
	153	8	22.22
	123	5	13.89
RM 21	170	8	22.22
	138	13	36.11
	157	8	22.22
	128	7	19.44
RM 484	193	24	66.67
	207	8	22.22
	179	4	11.11

Figure 4.10: Representation of EtBr stained 2.5% agarose gel showing the amplification profile of different SSR markers

S. NO.	Genotypes					
1	CRR 719-1-B (IR 88903-34)	10	IR 92521-7-5-1-1	21	IR 92545-54-6-1-4	
2	CRR 724-1-B (IR 88889-44)	11	IR 92521-23-6-1-3	22	IR 92546-7-1-1-3	31	IR 92545-51-1-1-4
3	RP-1-27-7-6-1-2-1	12	IR 92521-24-5-1-3	23	IR 92546-17-6-4-3	32	IR 92546-33-4-2-3
4	IR 94313:18-4-1-4-1-B	13	IR 92522-47-2-1-1	24	IR 92546-17-6-4-4	33	IR 92516-8-3-3-4
5	IR 88287-383-1-B-B-1-1-B	14	IR 92522-47-2-1-4	25	IR 92546-33-3-1-1	34	MTU 1010 (Check)
6	IR 94391-587-1-2-B	15	IR 92522-61-3-1-4	26	IR 92517-1-3-1-1	35	IR 64 (Check)
7	IR 94314-20-2-1-B	16	IR 92523-35-1-1-1	27	IR 92522-45-3-1-4	36	LALAT (Check)
8	IR 93339:40-B-18-13-B-B-1	17	IR 92523-37-1-1-2	28	IR 92545-23-2-1-1		
9	IR 92521-5-3-1-2	18	IR 92527-6-2-1-2	29	IR 92545-24-3-1-1		
		19	IR 92527-6-2-1-4	30	IR 92545-40-2-2-3		
		20	IR 92545-53-4-1-3				

Figure 4.11: Representation of molecular fingerprinting among thirty six advance rice lines using sixteen SSR markers

Markers	Size of bands	Genotypes (1–36)
RM 283	156	
	166	
	148	
RM 154	190	
	167	
	203	
	175	
RM 55	235	
	215	
	252	
	264	
	289	
RM 307	143	
	134	
	122	
RM 334	178	
	212	
	194	
	224	
RM 510	128	
	112	
	95	
RM 11	130	
	146	
	166	
	109	
RM 25	151	
	161	
	178	
	134	
RM215	155	
	149	
	131	
RM 271	105	
	119	
	84	
	96	
RM 536	235	
	252	
	227	
	203	
RM 463	193	
	187	
	203	
RM 118	178	
	191	
	166	
RM 277	134	
	143	
	153	
	123	
RM 21	170	
	138	
	157	
	128	
RM 484	193	
	207	
	179	

Figure 4.12: Cluster diagram of thirty six advance rice lines by UPGMA technique using molecular information
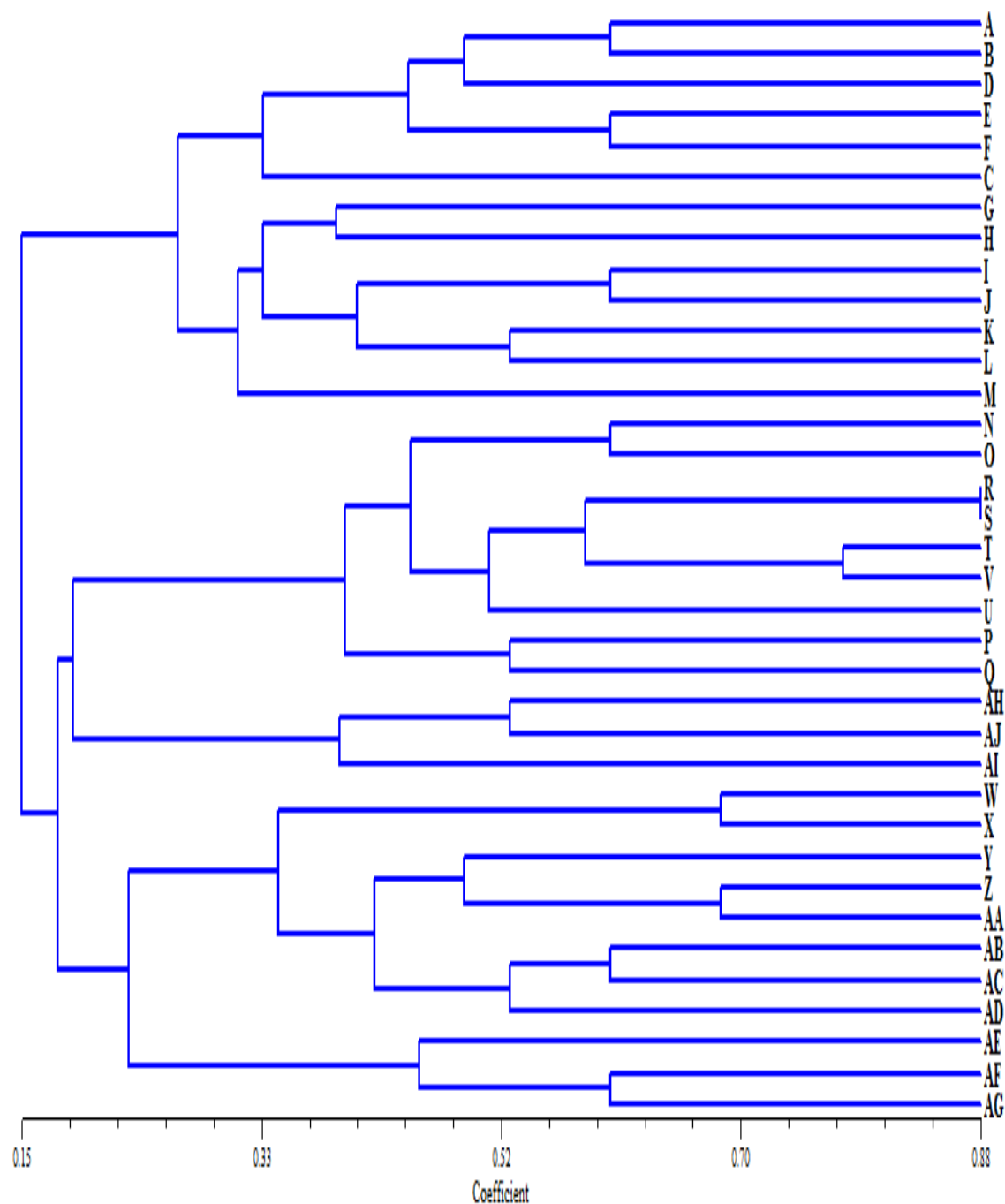
Table 4.21: Clusters composition of thirty six advance rice lines at molecular level

Clusters ↓	Number of Genotypes	Codes of Genotypes
Cluster - I	6	A, B, D, E, F and C
Cluster - II	7	G, H, I, J, K, L and M
Cluster – III	9	N, O, R, S, , T, V, U, P and Q
Cluster – IV	3	AH, AJ and AI
Cluster – V	8	W, X, Y, Z, AA, AB, AC and AD
Cluster - VI	3	AE, AF and AG

Table 4.22 Similarity matrix of 36 advance rice lines based on Jaccard's similarity coefficient

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ
A	1.00																																			
B	0.60	1.00																																		
C	0.33	0.39	1.00																																	
D	0.52	0.45	0.28	1.00																																
E	0.52	0.39	0.33	0.45	1.00																															
F	0.52	0.39	0.28	0.39	0.60	1.00																														
G	0.28	0.28	0.19	0.19	0.23	0.28	1.00																													
H	0.39	0.28	0.28	0.23	0.33	0.39	0.39	1.00																												
I	0.23	0.19	0.19	0.23	0.33	0.33	0.45	0.52	1.00																											
J	0.14	0.10	0.23	0.14	0.19	0.23	0.33	0.28	0.60	1.00																										
K	0.28	0.39	0.45	0.28	0.33	0.39	0.14	0.33	0.33	0.33	1.00																									
L	0.28	0.28	0.33	0.19	0.19	0.23	0.28	0.28	0.45	0.33	0.52	1.00																								
M	0.28	0.23	0.33	0.23	0.33	0.45	0.33	0.28	0.33	0.28	0.28	0.33	1.00																							
N	0.14	0.14	0.14	0.03	0.03	0.10	0.28	0.23	0.23	0.39	0.19	0.45	0.19	1.00																						
O	0.19	0.23	0.23	0.07	0.07	0.14	0.33	0.10	0.14	0.28	0.19	0.45	0.33	0.60	1.00																					
P	0.14	0.28	0.28	0.07	0.10	0.19	0.28	0.23	0.28	0.45	0.28	0.39	0.19	0.45	0.45	1.00																				
Q	0.14	0.23	0.10	0.07	0.07	0.10	0.33	0.14	0.28	0.39	0.19	0.28	0.19	0.39	0.45	0.52	1.00																			
R	0.14	0.19	0.19	0.03	0.07	0.10	0.14	0.07	0.14	0.33	0.23	0.28	0.19	0.39	0.52	0.39	0.45	1.00																		
S	0.14	0.19	0.14	0.03	0.07	0.07	0.14	0.07	0.14	0.28	0.19	0.33	0.14	0.45	0.60	0.45	0.45	0.88	1.00																	
T	0.07	0.19	0.10	0.03	0.07	0.10	0.19	0.14	0.14	0.23	0.28	0.33	0.19	0.45	0.60	0.33	0.39	0.52	0.60	1.00																
U	0.14	0.19	0.14	0.03	0.10	0.10	0.07	0.10	0.07	0.14	0.14	0.14	0.10	0.33	0.33	0.33	0.28	0.52	0.60	0.45	1.00															
V	0.10	0.19	0.07	0.07	0.10	0.10	0.19	0.14	0.14	0.19	0.23	0.23	0.14	0.33	0.45	0.28	0.39	0.60	0.60	0.78	0.45	1.00														
W	0.14	0.14	0.14	0.07	0.10	0.14	0.10	0.23	0.07	0.14	0.19	0.19	0.07	0.23	0.28	0.33	0.23	0.33	0.39	0.39	0.39	0.39	1.00													
X	0.14	0.19	0.14	0.10	0.10	0.10	0.14	0.19	0.07	0.14	0.10	0.14	0.00	0.23	0.19	0.33	0.23	0.28	0.33	0.23	0.33	0.23	0.68	1.00												
Y	0.14	0.19	0.23	0.10	0.10	0.14	0.14	0.28	0.14	0.23	0.28	0.19	0.10	0.28	0.19	0.19	0.19	0.23	0.19	0.23	0.19	0.19	0.39	0.28	1.00											
Z	0.19	0.19	0.28	0.14	0.14	0.19	0.07	0.19	0.07	0.14	0.23	0.14	0.10	0.10	0.14	0.23	0.19	0.28	0.23	0.14	0.28	0.19	0.45	0.33	0.52	1.00										
AA	0.14	0.14	0.23	0.07	0.14	0.19	0.07	0.23	0.07	0.14	0.23	0.10	0.10	0.10	0.14	0.23	0.19	0.28	0.23	0.28	0.39	0.33	0.60	0.39	0.45	0.68	1.00									
AB	0.14	0.14	0.19	0.10	0.14	0.14	0.10	0.28	0.10	0.10	0.19	0.14	0.03	0.14	0.10	0.19	0.10	0.03	0.07	0.19	0.19	0.10	0.33	0.33	0.39	0.39	0.45	1.00								
AC	0.14	0.19	0.28	0.10	0.14	0.14	0.10	0.19	0.07	0.10	0.14	0.10	0.10	0.10	0.14	0.14	0.10	0.19	0.14	0.19	0.19	0.14	0.33	0.39	0.52	0.45	0.45	0.60	1.00							
AD	0.07	0.10	0.19	0.10	0.10	0.10	0.10	0.14	0.14	0.19	0.23	0.10	0.10	0.03	0.10	0.10	0.14	0.14	0.10	0.19	0.19	0.14	0.19	0.14	0.39	0.33	0.39	0.52	0.52	1.00						
AE	0.10	0.19	0.14	0.10	0.19	0.07	0.10	0.10	0.10	0.07	0.10	0.07	0.07	0.07	0.07	0.07	0.10	0.07	0.07	0.14	0.19	0.14	0.10	0.10	0.28	0.23	0.23	0.33	0.39	0.45	1.00					
AF	0.03	0.07	0.10	0.10	0.07	0.03	0.00	0.03	0.00	0.03	0.07	0.03	0.03	0.03	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.07	0.10	0.07	0.19	0.33	0.19	0.23	0.23	0.28	0.45	1.00				
AG	0.03	0.07	0.10	0.07	0.07	0.07	0.03	0.03	0.03	0.10	0.19	0.07	0.10	0.07	0.14	0.03	0.14	0.19	0.14	0.19	0.10	0.19	0.10	0.03	0.28	0.28	0.23	0.23	0.23	0.45	0.45	0.60	1.00			
AH	0.23	0.33	0.23	0.33	0.23	0.23	0.14	0.10	0.03	0.10	0.19	0.10	0.10	0.14	0.23	0.19	0.14	0.19	0.19	0.19	0.19	0.19	0.19	0.19	0.23	0.28	0.23	0.19	0.23	0.19	0.14	0.28	0.19	1.00		
AI	0.33	0.45	0.28	0.33	0.28	0.19	0.28	0.14	0.19	0.14	0.23	0.23	0.14	0.14	0.28	0.19	0.19	0.28	0.28	0.23	0.14	0.28	0.10	0.14	0.19	0.19	0.23	0.19	0.23	0.19	0.23	0.19	0.23	0.45	1.00	
AJ	0.14	0.23	0.10	0.19	0.14	0.14	0.19	0.07	0.03	0.10	0.10	0.07	0.10	0.14	0.19	0.19	0.28	0.14	0.14	0.19	0.07	0.19	0.14	0.19	0.19	0.14	0.14	0.10	0.28	0.23	0.14	0.14	0.28	0.52	0.33	1.00

4.9 Phenotypic stability analysis (Eberhart and Russell model, 1966):

Evaluation of advanced lines under four different environments provided us information on the different stability parameters about the relative performance of the each lines. This types of study help to apportionate the G x E (Genotype x Environment) interaction in different components and furnish the information about the consistency in performance of each individual lines. In present study year x conditions were taken into consideration for creating different environments. Therefore, the individual performances of lines and traits in each environment were combined together for the estimation of stability or G x E interaction.

4.9.1 Analysis of variance of phenotypic stability for different characters:

Pooled analysis of variance for stability based on different yield and quality attributes has been presented in Table 4.23 and 4.24. Replications within the environments were non-significant for all the traits except hulling recovery % on the basis of mean sum square values. The pooled analysis of variance showed that mean sum of square due to genotype (lines) for all the traits under study were highly significant. Highly significant mean sum of square due to environment existed for all traits except for hulling recovery and L/B ratio, where hulling recovery % was significant at 5% level of significance. The mean sum of squares due genotype x environment (G x E) interaction were highly significant for the traits like plant height and hulling recovery. Environment along with interaction (Env. + G x E) for the mean sum of square were found significant and highly significant values except number of tillers per meter square, number of spikelets per panicle, milling recovery, kernel length before cooking, kernel breadth before cooking and L/B ratio before cooking. Mean sum square for environment (linear) were highly significant for all the traits except L/B ratio. In case of linear interaction (G x E linear) only characters like plant height and panicle length are found highly significant except all. Mean sum of square for pooled deviation found highly significant values for all the yield and quality attributing traits except plant height, harvest index and hulling recovery percent.

4.9.2 Environmental indices of different environments for different characters:

Environmental index can provide the basis to identify favourable environments for each character. Maximum positive values among the given environments for any trait

explain the favourable environments for the particular trait in that environment (Table 4.25). Control 2014 (E_1) showed favourable environment for the traits like days to 50% flowering (2.507) followed by number of tillers per plant (1.500), number of productive tillers per meter square (19.750), panicle length (1.637), number of spikelets per panicle (8.873), grain yield per plant (2.597), harvest index (2.496), head rice recovery (1.431), L/B ratio (0.042), kernel elongation ratio (0.009) and grain yield kilogram per hectare (391.442). Stress 2014 (E_2) showed favourable environment for only the trait plant height (3.918). Control 2015 (E_3) found favourable environment for the trait days to maturity (2.750) followed by biological yield per plant (2.539), test weight (0.794), hulling recovery % (1.210), milling recovery % (1.325), kernel length before cooking (0.135), kernel breadth before cooking (0.059) amylose content (0.688) and volume expansion ratio (0.074). Stress 2015 (E_4) did not favour any particular trait out of 21 yield and quality attributing traits.

Table 4.23: (a) Analysis of variance (ANOVA) of phenotypic stability for different traits in rice lines

Source of Variation	Degree of Freedom	DFF	PH	DM	NT/Pt	NPT/m^2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW
Rep. within Env.	8.00	3.12	4.16	0.81	0.62	68.19	0.86	53.28	0.56	3.13	2.59	0.62
Genotypes	35.00	17.33**	70.49**	20.67**	2.42**	1514.96**	3.07**	1940.87**	11.21**	138.11**	52.21**	11.82**
Env.+ (G x E)	108.00	11.85*	36.06**	16.84**	2.37**	700.23	2.99**	250.86	8.07**	18.33*	14.98*	1.87**
Environments	3.00	193.65**	632.58**	305.73**	43.81**	8888.42**	59.26**	2661.57**	160.75**	276.78**	136.41**	26.98**
G x E	105.00	6.66	19.02**	8.59	1.18	466.28	1.38	181.98	3.70	10.95	11.51	1.15
Env. (Lin.)	1.00	580.95**	1897.74**	917.19**	131.43**	26665.27**	177.77**	7984.71**	482.24**	830.34**	409.23**	80.93**
G x E (Lin.)	35.00	4.61	37.63**	8.54	1.33	288.79	2.06**	77.78	2.80	9.64	13.75	1.29
Pooled Dev.	72.00	7.47**	9.44	8.37**	1.07**	539.61**	1.01**	227.58**	4.04**	11.28**	10.11	1.05**
Pooled Error	280.00	4.10	10.99	4.68	0.44	68.27	0.47	36.02	2.05	5.64	7.74	0.37
Total	143.00	13.19	44.48	17.78	2.38	899.64	3.01	664.50	8.84	47.65	24.09	4.30

Table 4.24: (b) Analysis of variance (ANOVA) of phenotypic stability for different traits in rice lines

Source of Variation	Degree of Freedom	HULL %	MILL %	HRR %	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER	GYKG/Ha
Rep. within Env.	8.00	1.65**	0.55	1.80	0.01	0.00	0.01	0.03	0.00	0.00	24173.95
Genotypes	35.00	14.49**	13.04**	108.44**	0.57**	0.03**	0.32**	5.66**	0.00**	0.02**	728656.56**
Env.+ (G x E)	108.00	4.83**	6.76	4.18**	0.10	0.01	0.05	1.71*	0.01**	0.00*	317847.81**
Environments	3.00	62.85*	52.53**	54.36**	0.50**	0.06**	0.04	23.39***	0.24**	0.00**	8034100.50**
G x E	105.00	3.18**	5.45	2.75	0.09	0.01	0.05	1.09	0.00	0.00	97383.46
Env. (Lin.)	1.00	188.54**	157.58**	163.08**	1.51**	0.18**	0.11	70.16**	0.71**	0.01**	24102302.00**
G x E (Lin.)	35.00	5.51	4.68	3.19	0.05	0.01	0.03	0.95	0.00	0.00	111918.20
Pooled Dev.	72.00	1.95	5.68**	2.46**	0.10**	0.01**	0.06**	1.13**	0.00**	0.00**	87612.87**
Pooled Error	280.00	2.21	1.77	1.49	0.01	0.00	0.02	0.02	0.00	0.00	22053.63
Total	143.00	7.20	8.30	29.70	0.21	0.02	0.11	2.68	0.01	0.01	418395.41

Table 4.25: Environmental indices for different characters in rice lines

Characters ↓	Environmental indices			
	C - 2014 (E1)	S - 2014 (E2)	C - 2015 (E3)	S - 2015 (E4)
DFF	2.507	-2.891	1.035	-0.650
PH	3.245	3.918	-2.814	-4.349
DM	1.241	-4.046	2.750	0.056
NT/Pt	1.500	-0.407	0.019	-1.111
NPT/m^2	19.750	-7.639	4.407	-16.519
PL	1.637	0.301	-0.588	-1.350
NSP/P	8.873	-4.544	5.354	-9.683
GY/Pt	2.597	-1.116	0.727	-2.208
BY/Pt	2.206	-2.868	2.539	-1.877
HI	2.496	0.160	-0.438	-2.218
TW	0.697	-0.845	0.794	-0.646
HULL. %	0.921	-1.637	1.210	-0.495
MILL. %	0.567	-1.451	1.325	-0.441
HRR %	1.431	-0.499	0.483	-1.415
KLBC	0.063	-0.112	0.135	-0.085
KBBC	-0.008	-0.030	0.059	-0.022
L/B RATIO	0.042	-0.002	-0.035	-0.005
AMYLOSE C.	0.676	-0.891	0.688	-0.473
VER	0.064	-0.086	0.074	-0.051
KER	0.009	-0.010	0.007	-0.006
GYKG/Ha	391.442	-86.225	328.155	-633.373

4.9.3 Stability parameters for different characters among advance rice lines:

On the basis of good regression coefficient, non-significant deviation from regression and better or moderate mean performance in comparison to population mean, (Table 4.26 to 4.46 and Fig. 4.13 to 4.33) some lines found stable for different environmental conditions except checks. Regression co-efficient (bi) values shows different types of stability level along with non-significant deviations, in which bi score near to one (bi=1) for average stability, more than one (bi>1) for below average stability and less than one (bi<1) for above average stability. Mean performance (m) of each line for each character in comparison to population mean is deciding factor to selection of lines for different types of environment or different stability level.

According to previous reports on phenotypic stability, some researcher strictly follow the standard rule, mean (m) better than population mean, regression coefficient (bi) = 1 or near to 1 and deviation from regression line (s^2di) = 0 or less deviation for wide adaptation while some emphasis lay down on the different criteria *i.e.* (m better than population mean, bi = 1 or above or below and s^2di = non-significant), (m less or moderate or better than population mean, bi = 1 or near to 1, s^2di = 0 or less or non significant for poor or unfavourable environment), (m better than population mean, bi = 1 or near to 1 or above or below and s^2di = significant or non-significant). However in the present investigation for the selection of stable genotypes for different environments followed m better than the population mean, bi = 1 or near to 1 or above or below and s^2di = non-significant.

4.9.3.1 Stability parameter for days to 50% flowering:

In the present study for days to 50% flowering (Table 4.26 and Fig. 4.13), lines CRR 724-1-B (IR 88889-44) (m = 77.833, bi = 1.120, s^2di = -3695), IR 94313:18-4-1-4-1-B (m = 79.167, bi = 1.089, s^2di = 7.743), IR 94314-20-2-1-B (m = 85.917, bi = 1.017, s^2di = -3.372), IR 92521-5-3-1-2 (m = 81.667, bi = 1.002, s^2di = -0.728), IR 92522-47-2-1-1 (m = 83.333, bi = 1.197, s^2di = -2.398), IR 92522-47-2-1-4 (m = 82.167, bi = 0.925, s^2di = 1.755), IR 92546-7-1-1-3 (m = 85.667, bi = 0.836, s^2di = -3.814), IR 92546-17-6-4-3 (m = 85.750, bi = 0.876, s^2di = 8.232), IR 92517-1-3-1-1 (m = 83.000, bi = 0.996, s^2di = -3.969) and IR 92545-40-2-2-3 (m = 84.500, bi = 0.823, s^2di = 1.634) found good performing lines along with population mean (m = 83.289). Among the above good

performing lines, CRR 724-1-B (IR 88889-44), IR 94313:18-4-1-4-1-B, IR 92521-5-3-1-2, IR 92522-47-2-1-4 and IR 92517-1-3-1-1 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.2 Stability parameter for plant height:

In the present study for plant height (Table 4.27 and Fig. 4.14), lines IR 94313:18-4-1-4-1-B (m = 94.071, bi = 1.088, s^2di = 1.261), IR 94391-587-1-2-B (m = 96.479, bi = 0.975, s^2di = 19.377), IR 93339:40-B-18-13-B-B-1 (m = 98.150, bi = 1.121, s^2di = -5.973), IR 92521-5-3-1-2 (m = 108.121, bi = 0.848, s^2di = -4.004), IR 92545-53-4-1-3 (m = 98.000, bi = 0.843, s^2di = -9.985) and IR 92516-8-3-3-4 (m = 95.354, bi = 1.011, s^2di = -10.143) found good performing lines along with population mean (m = 99.763). Among the above good performing lines, IR 94313:18-4-1-4-1-B, IR 94391-587-1-2-B, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3 and IR 92516-8-3-3-4 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.3 Stability parameter for days to maturity:

In the present study for days to maturity (Table 4.28 and Fig. 4.15), lines IR 94314-20-2-1-B (m = 118.250, bi = 1.059, s^2di = -2.263), IR 92521-5-3-1-2 (m = 115.167, bi = 0.803, s^2di = -2.508), IR 92521-7-5-1-1 (m = 114.083, bi = 1.144, s^2di = 2.249), IR 92527-6-2-1-4 (m = 116.583, bi = 1.186, s^2di = -3.009), IR 92546-33-3-1-1 (m = 114.083, bi = 1.041, s^2di = -3.225) and IR 92545-51-1-1-4 (m = 116.917, bi = 0.887, s^2di = -0.551) found good performing lines along with population mean (m = 115.796). Among the above good performing lines, IR 92521-5-3-1-2, IR 92521-7-5-1-1 and IR 92546-33-3-1-1 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.4 Stability parameter for number of tillers per plant:

In the present study for number of tillers per plant (Table 4.29 and Fig. 4.16), lines IR 92521-24-5-1-3 (m = 9.417, bi = 1.097, s^2di = -0.155), IR 92522-61-3-1-4 (m = 11.583, bi = 1.204, s^2di = -0.269), IR 92523-37-1-1-2 (m = 11.250, bi = 0.830, s^2di = 0.007), IR 92546-33-3-1-1 (m = 10.250, bi = 1.204, s^2di = -0.269) and IR 92545-24-3-1-1 (m = 10.500, bi = 0.971, s^2di = 0.560) found good performing lines along with population mean (m = 10.815). Among the above good performing lines, IR 94313:18-4-1-4-1-B, IR

92522-61-3-1-4, IR 92523-37-1-1-2 and IR 92517-1-3-1-1 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.5 Stability parameter for number of productive tillers per meter square:

In the present study for number of productive tillers per meter square (Table 4.30 and Fig. 4.17), lines RP-1-27-7-6-1-2-1 (m = 223.917, bi = 0.864, s^2di = -10.115), IR 94391-587-1-2-B (m = 219.167, bi = 0.877, s^2di = 2.402), IR 92523-35-1-1-1 (m = 233.500, bi = 0.848, s^2di = -44.084), IR 92527-6-2-1-2 (m = 241.667, bi = 0.900, s^2di = -62.860), IR 92546-7-1-1-3 (m = 272.917, bi = 1.185, s^2di = -38.192) and IR 92545-23-2-1-1 (m = 219.500, bi = 1.146, s^2di = -41.538) found good performing lines along with population mean (m = 228.750). Among the above good performing lines, IR 92523-35-1-1-1, IR 92527-6-2-1-2 and IR 92546-7-1-1-3 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.6 Stability parameter for panicle length:

In the present study for panicle length (Table 4.31 and Fig. 4.18), lines CRR 719-1-B (IR 88903-34) (m = 26.248, bi = 1.098, s^2di = 0.498), IR 92522-47-2-1-1 (m = 24.390, bi = 0.968, s^2di = 0.800), IR 92527-6-2-1-2 (m = 26.426, bi = 0.922, s^2di = 0.961), IR 92545-54-6-1-4 (m = 26.958, bi = 1.236, s^2di = 0.185), IR 92546-17-6-4-4 (m = 25.592, bi = 0.929, s^2di = -0.343), IR 92546-33-3-1-1 (m = 24.816, bi = 1.121, s^2di = -0.449), IR 92545-51-1-1-4 (m = 26.616, bi = 1.241, s^2di = 0.113) and IR 92516-8-3-3-4 (m = 25.374, bi = 1.167, s^2di = 0.786) found good performing lines along with population mean (m = 26.055). Among the above good performing lines, CRR 719-1-B (IR 88903-34), IR 92527-6-2-1-2, IR 92545-54-6-1-4 and IR 92545-51-1-1-4 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.7 Stability parameter for number of spikelets per panicle:

In the present study for number of spikelets per panicle (Table 4.32 and Fig. 4.19), lines IR 94313:18-4-1-4-1-B (m = 127.250, bi = 1.139, s^2di = 31.781), IR 92522-61-3-1-4 (m = 160.000, bi = 0.947, s^2di = 23.021), IR 92545-53-4-1-3 (m = 136.333, bi = 0.938, s^2di = 33.535), IR 92546-17-6-4-4 (m = 165.250, bi = 1.141, s^2di = -22.456) and IR 92522-45-3-1-4 (m = 150.083, bi = 0.831, s^2di = 40.444) found good performing lines along with population mean (m = 152.451). Among the above good performing lines, IR

92522-61-3-1-4 and IR 92546-17-6-4-4 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.8 Stability parameter for grain yield per plant:

In the present study for grain yield per plant (Table 4.33 and Fig. 4.20), lines IR 92521-5-3-1-2 (m = 27.250, bi = 0.972, s^2di = 0.707), IR 92521-24-5-1-3 (m = 30.417, bi = 1.016, s^2di = 2.896), IR 92523-35-1-1-1 (m = 26.000, bi = 1.041, s^2di = -1.154), IR 92545-53-4-1-3 (m = 27.667, bi = 0.837, s^2di = 3.189), IR 92546-17-6-4-3 (m = 28.417, bi = 1.130, s^2di = 2.818), IR 92546-17-6-4-4 (m = 28.67, bi = 1.188, s^2di = -0.901) and IR 92516-8-3-3-4 (m = 26.750, bi = 1.067, s2di = 3.852) found good performing lines along with population mean (m = 27.616). Among the above good performing lines, IR 92521-24-5-1-3, IR 92545-53-4-1-3, IR 92546-17-6-4-3 and IR 92546-17-6-4-4 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.9 Stability parameter for biological yield per plant:

In the present study for biological yield per plant (Table 4.34 and Fig. 4.21), lines CRR 719-1-B (IR 88903-34) (m = 58.667, bi =1.094, s^2di = 0.291), CRR 724-1-B (IR 88889-44) (m= 66.750, bi = 1.139, s^2di = -5.038), RP-1-27-7-6-1-2-1 (m = 64.167, bi = 1.088, s^2di = 10.732), IR 92522-47-2-1-4 (m = 70.167, bi = 1.074, s^2di = -3.251) and IR 92523-37-1-1-2 (m = 72.917, bi = 1.116, s^2di = 2.208) found good performing lines along with population mean (m = 67.461). Among the above good performing lines, IR 92522-47-2-1-4 and IR 92523-37-1-1-2 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.10 Stability parameter for harvest index:

In the present study for harvest index (Table 4.35 and Fig. 4.22), lines IR 94313:18-4-1-4-1-B (m = 38.678, bi = -1.054, s^2di = 13.572), IR 92521-5-3-1-2 (m = 44.718, bi =0.980, s^2di = 1.786), IR 92521-24-5-1-3 (40.672, bi = 0.852, s^2di = 13.926), IR 92522-47-2-1-1 (m = 41.038, bi = -1.108, s^2di = -3.322) IR 92523-37-1-1-2 (m = 41.743, bi = 1.195, s^2di = -7.162), IR 92545-54-6-1-4 (m = 42.277, bi = 0.930, s^2di = -6.523), IR 92546-33-3-1-1 (m = 36.699, bi = 0.953, s^2di = -4.567) and IR 92545-24-3-1-1 (m = 43.242, bi = 1.100, s^2di = 7.886) found good performing lines along with population mean (m = 41.328). Among the above good performing lines, IR 92521-5-3-1-2, IR

92523-37-1-1-2, IR 92545-54-6-1-4 and IR 92545-24-3-1-1 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.11 Stability parameter for test weight:

In the present study for test weight (Table 4.36 and Fig. 4.23), lines RP-1-27-7-6-1-2-1 (m = 22.233, bi = 0.937, s^2di = 0.594), IR 94314-20-2-1-B (m = 23.717, bi = 0.852, s^2di = 0.295), IR 92523-35-1-1-1 (m = 24.700, bi = 1.163, s^2di = 0.153), IR 92527-6-2-1-4 (m = 22.992, bi = 1.078, s^2di = 0.332) and IR 92545-24-3-1-1 (m = 26.083, bi = 1.040, s^2di = -0.262) found good performing lines along with population mean (m = 24.250). Among the above good performing lines, IR 92523-35-1-1-1 and IR 92545-24-3-1-1 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.12 Stability parameter for grain yield kilogram per hectare:

In the present study for grain yield kilogram per hectare (Table 4.37 and Fig. 4.24), lines IR 94391-587-1-2-B (m = 4304.000, bi = 0.983, s^2di = 3877.182), IR 94314-20-2-1-B (m = 4463.917, bi = 0.974, s^2di = 4851.137), IR 92522-47-2-1-1 (m = 4501.917, bi = 0.960, s^2di = -1581.477), IR 92522-61-3-1-4 (m = 4023.000, bi = 1.083, s^2di = 7403.377), IR 92545-54-6-1-4 (m = 3468.833, bi = 1.032, s^2di = -3427.673) and IR 92546-7-1-1-3 (m = 4399.417 bi = 0.999, s^2di = 2231.169) found good performing lines along with population mean (m = 4335.706). Among the above good performing lines, IR 94314-20-2-1-B, IR 92522-47-2-1-1 and IR 92546-7-1-1-3 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.13 Stability parameter for hulling recovery %:

In the present study for hulling recovery % (Table 4.38 and Fig. 4.25), lines IR 94313:18-4-1-4-1-B (m = 74.643, bi = 1.289, s^2di = 0.407), IR 92546-33-3-1-1 (m = 74.448, bi = 1.262, s^2di = -0.035), IR 92522-45-3-1-4 (m = 73.741, bi = -0.947, s^2di = -0.549), IR 92546-33-4-2-3 (m = 73.749, bi = 0.798, s^2di = 2.517) and IR 92516-8-3-3-4 (m = 75.937, bi = 0.906, s^2di = -0.853) found good performing lines along with population mean (m = 74.506). Among the above good performing lines, IR 94313:18-4-1-4-1-B and IR 92516-8-3-3-4 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.14 Stability parameter for milling recovery %:

In the present study for milling recovery % (Table 4.39 and Fig. 4.26), lines IR 93339:40-B-18-13-B-B-1 (m = 65.992, bi = 1.097, s^2di = 2.306), IR 92521-5-3-1-2 (m = 63.225, bi = 1.112, s^2di = 1.022), IR 92521-24-5-1-3 (m = 63.292, bi = 1.020, s^2di = -0.903), IR 92546-17-6-4-3 (m = 60.525, bi = -0.909, s^2di = -1.679) and IR 92517-1-3-1-1 (m = 62.792, bi = 0.916, s^2di = 3.161) found good performing lines along with population mean (m = 62.643). Among the above good performing lines, IR 93339:40-B-18-13-B-B-1, IR 92521-5-3-1-2, IR 92521-24-5-1-3 and IR 92517-1-3-1-1 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.15 Stability parameter for head rice recovery %:

In the present study for head rice recovery % (Table 4.40 and Fig. 4.27), lines CRR 724-1-B (IR 88889-44) (m = 51.308, bi = 1.009, s^2di = -1.366), IR 88287-383-1-B-B-1-1-B (m = 42.908, bi = 1.187, s^2di = -0.256), IR 94314-20-2-1-B (m = 47.833, bi = 1.023, s^2di = -0.467), IR 92521-5-3-1-2 (m = 58.217, bi = 1.141, s^2di = -0.156), IR 92546-7-1-1-3 (m = 49.975, bi = 0.844, s^2di = -1.041) and IR 92546-17-6-4-3 (m = 48.742, bi = 1.072, s^2di = -0.004) found good performing lines along with population mean (m = 48.203). Among the above good performing lines, CRR 724-1-B (IR 88889-44), IR 92521-5-3-1-2, IR 92546-7-1-1-3 and IR 92546-17-6-4-3 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.16 Stability parameter for kernel length before cooking:

In the present study for kernel length before cooking (Table 4.41 and Fig. 4.28), lines CRR 724-1-B (IR 88889-44) (m = 6.958, bi = 0.800, s^2di = 0.024), IR 94314-20-2-1-B (m = 7.358, bi = 0.924, s^2di = -0.002) and IR 92521-24-5-1-3 (m = 6.292, bi = 0.987, s^2di = 0.002) found good performing lines along with population mean (m = 7.047). Among the above good performing lines, IR 94314-20-2-1-B and IR 92521-24-5-1-3 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.17 Stability parameter for kernel breadth before cooking:

In the present study for kernel breadth before cooking (Table 4.42 and Fig. 4.29), lines RP-1-27-7-6-1-2-1 (m = 2.075, bi = 0.969, s^2di = 0.000) and IR 92545-54-6-1-4 (m = 2.183, bi = -1.314, s^2di = -0.003) found good performing lines along with population

mean (m = 2.092). Above good performing both lines, RP-1-27-7-6-1-2-1 and IR 92545-54-6-1-4 found best lines for the concerned trait on the basis of stability criteria.

4.9.3.18 Stability parameter for kernel L/B ratio before cooking:

In the present study for kernel L/B ratio before cooking (Table 4.43 and Fig. 4.30), lines IR 92546-33-3-1-1 (m = 3.223, bi = 1.326, s^2di = -0.001), IR 92517-1-3-1-1 (m = 3.493, bi = -1.080, s^2di = 0.020), IR 92522-45-3-1-4 (m = 3.222, bi = 1.295, s^2di = -0.001) and IR 92545-24-3-1-1 (m = 3.303, bi = 1.172, s^2di = 0.029) found good performing lines along with population mean (m = 3.392). Among the above good performing lines, IR 92517-1-3-1-1 and IR 92545-24-3-1-1 found best lines for the concerned trait on the basis of stability criteria.

4.9.3.19 Stability parameter for amylose content:

In the present study for amylose content (Table 4.44 and Fig. 4.31), only line IR 92546-33-4-2-3 (m = 21.618, bi = 0.879, s^2di = 0.015) found good performing or best genotypes for the concerned trait on the basis of stability criteria with population mean (m = 22.133). Above mentioned best performing line have lowest performance in comparison to population mean but regression co-efficient and deviation from regression was good.

4.9.3.20 Stability parameter for volume expansion ratio:

In the present study for volume expansion ratio (Table 4.45 and Fig. 4.32), lines IR 92521-5-3-1-2 (m = 3.452, bi = 1.079, s2di = 0.001), IR 92521-23-6-1-3 (m = 3.387, bi = 1.117, s2di = 0.001), IR 92522-47-2-1-4 (m = 3.417, bi = 1.102, s2di = 0.000), IR 92546-33-3-1-1 (m = 3.366, bi = 1.106, s2di = 0.000) and IR 92522-45-3-1-4 (m = 3.352, bi = 1.112, s2di = 0.000) found good performing lines along with population mean (m = 3.380). Among the above good performing lines, IR 92521-5-3-1-2, IR 92521-23-6-1-3 and IR 92522-47-2-1-4 found best genotypes for the concerned trait on the basis of stability criteria.

4.9.3.21 Stability parameter for kernel elongation ratio:

In the present study for kernel elongation ratio (Table 4.46 and Fig. 4.33), only line IR 92522-47-2-1-1 (m = 1.706, bi = 1.169, s^2di = 0.000) found good performing or best genotypes for the concerned trait on the basis of stability criteria with population mean (m = 1.674).

Table 4.26: Stability parameters for days to 50% flowering

S.No.	Genotypes	Days to 50% Flowering		
		m	**bi**	**s²di**
1	CRR 719-1-B (IR 88903-34)	80.417	1.242	-3.032
2	CRR 724-1-B (IR 88889-44)	77.833	1.120	-3.695
3	RP-1-27-7-6-1-2-1	83.083	1.383	-3.788
4	IR 94313:18-4-1-4-1-B	79.167	1.089	7.743
5	IR 88287-383-1-B-B-1-1-B	82.917	0.331	22.977**
6	IR 94391-587-1-2-B	82.333	0.800	9.769*
7	IR 94314-20-2-1-B	85.917	1.017	-3.372
8	IR 93339:40-B-18-13-B-B-1	87.583	0.306	-3.672
9	IR 92521-5-3-1-2	81.667	1.002	-0.728
10	IR 92521-7-5-1-1	82.917	0.751	1.092
11	IR 92521-23-6-1-3	83.917	-0.135	39.604**
12	IR 92521-24-5-1-3	81.667	1.242	-2.857
13	IR 92522-47-2-1-1	83.333	1.197	-2.398
14	IR 92522-47-2-1-4	82.167	0.925	1.755
15	IR 92522-61-3-1-4	84.583	1.281	25.834**
16	IR 92523-35-1-1-1	81.500	0.473	-3.929
17	IR 92523-37-1-1-2	85.583	1.765*	1.732
18	IR 92527-6-2-1-2	84.417	1.407	-3.121
19	IR 92527-6-2-1-4	85.500	1.404	4.746
20	IR 92545-53-4-1-3	80.333	1.344	-1.869
21	IR 92545-54-6-1-4	83.250	1.538	-3.232
22	IR 92546-7-1-1-3	85.667	0.836	-3.814
23	IR 92546-17-6-4-3	85.750	0.876	8.232
24	IR 92546-17-6-4-4	83.417	1.426	8.344*
25	IR 92546-33-3-1-1	82.750	1.311	-0.459
26	IR 92517-1-3-1-1	83.000	0.996	-3.969
27	IR 92522-45-3-1-4	83.917	1.175	-2.503
28	IR 92545-23-2-1-1	83.667	1.770*	7.656
29	IR 92545-24-3-1-1	83.750	1.672*	9.529*
30	IR 92545-40-2-2-3	84.500	0.823	1.634
31	IR 92545-51-1-1-4	84.000	1.480	14.139*
32	IR 92546-33-4-2-3	84.667	0.520	-2.136
33	IR 92516-8-3-3-4	84.250	-0.834	9.921*
34	MTU 1010 (Check)	81.000	1.248	-1.528
35	IR 64 (Check)	81.333	0.774	0.537
36	LALAT (Check)	86.667	0.443	-2.874
	Population Mean	**83.289**		

Figure 4.13: Representation of stability on the basis of regression coefficient and deviation from regression for days to 50% flowering
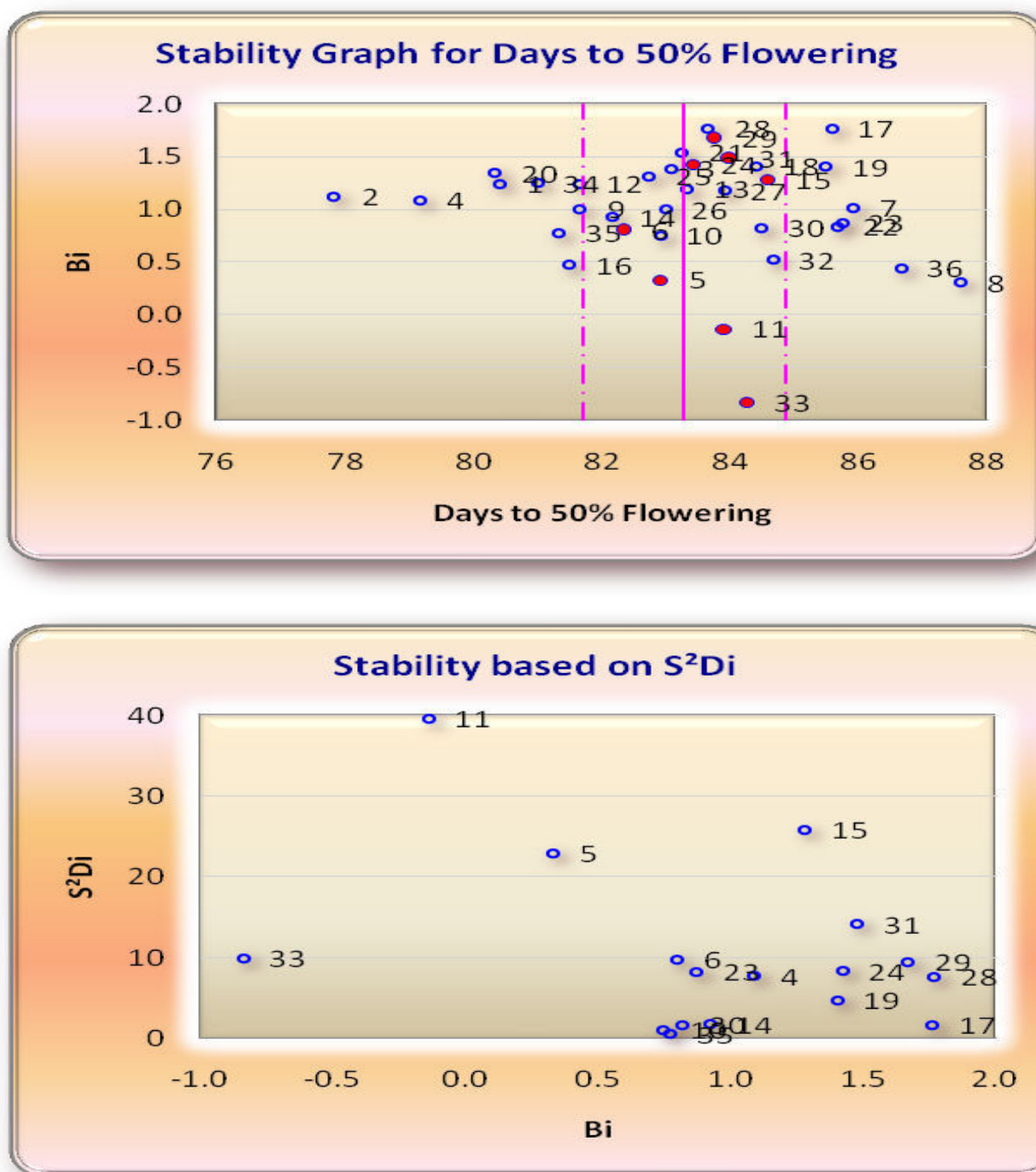
Table 4.27: Stability parameters for plant height

S.No.	Genotypes	Plant Height (cm)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	104.287	-0.359	12.970
2	CRR 724-1-B (IR 88889-44)	98.642	0.625	7.669
3	RP-1-27-7-6-1-2-1	104.825	0.714	-2.648
4	IR 94313:18-4-1-4-1-B	94.071	1.088	1.261
5	IR 88287-383-1-B-B-1-1-B	96.917	1.322	-0.673
6	IR 94391-587-1-2-B	96.479	0.975	19.377
7	IR 94314-20-2-1-B	96.354	2.665**	17.057
8	IR 93339:40-B-18-13-B-B-1	98.150	1.121	-5.973
9	IR 92521-5-3-1-2	108.121	0.848	-4.004
10	IR 92521-7-5-1-1	106.396	2.722**	-4.869
11	IR 92521-23-6-1-3	107.833	0.559	-6.460
12	IR 92521-24-5-1-3	105.996	0.222	0.642
13	IR 92522-47-2-1-1	97.108	1.500	23.453*
14	IR 92522-47-2-1-4	96.633	0.551	-2.911
15	IR 92522-61-3-1-4	100.404	0.200	-4.259
16	IR 92523-35-1-1-1	97.896	2.569**	7.450
17	IR 92523-37-1-1-2	96.137	-0.120	0.629
18	IR 92527-6-2-1-2	98.396	2.183**	-6.617
19	IR 92527-6-2-1-4	93.233	1.829*	-8.674
20	IR 92545-53-4-1-3	98.000	0.843	-9.985
21	IR 92545-54-6-1-4	99.504	2.427**	20.347
22	IR 92546-7-1-1-3	105.233	0.745	-7.827
23	IR 92546-17-6-4-3	100.779	-0.066	-9.732
24	IR 92546-17-6-4-4	93.542	0.260	-3.052
25	IR 92546-33-3-1-1	97.183	0.586	-9.950
26	IR 92517-1-3-1-1	95.971	1.295	-9.981
27	IR 92522-45-3-1-4	96.750	1.284	-4.766
28	IR 92545-23-2-1-1	103.625	0.335	-8.959
29	IR 92545-24-3-1-1	101.563	2.000**	-7.360
30	IR 92545-40-2-2-3	104.396	-0.167	-3.347
31	IR 92545-51-1-1-4	99.704	0.586	-10.487
32	IR 92546-33-4-2-3	97.221	2.168**	-7.595
33	IR 92516-8-3-3-4	95.354	1.011	-10.143
34	MTU 1010 (Check)	104.017	0.696	2.103
35	IR 64 (Check)	97.179	0.327	-8.444
36	LALAT (Check)	103.563	0.456	-3.113
	Population Mean	**99.763**		

Figure 4.14: Representation of stability on the basis of regression coefficient and deviation from regression for plant height
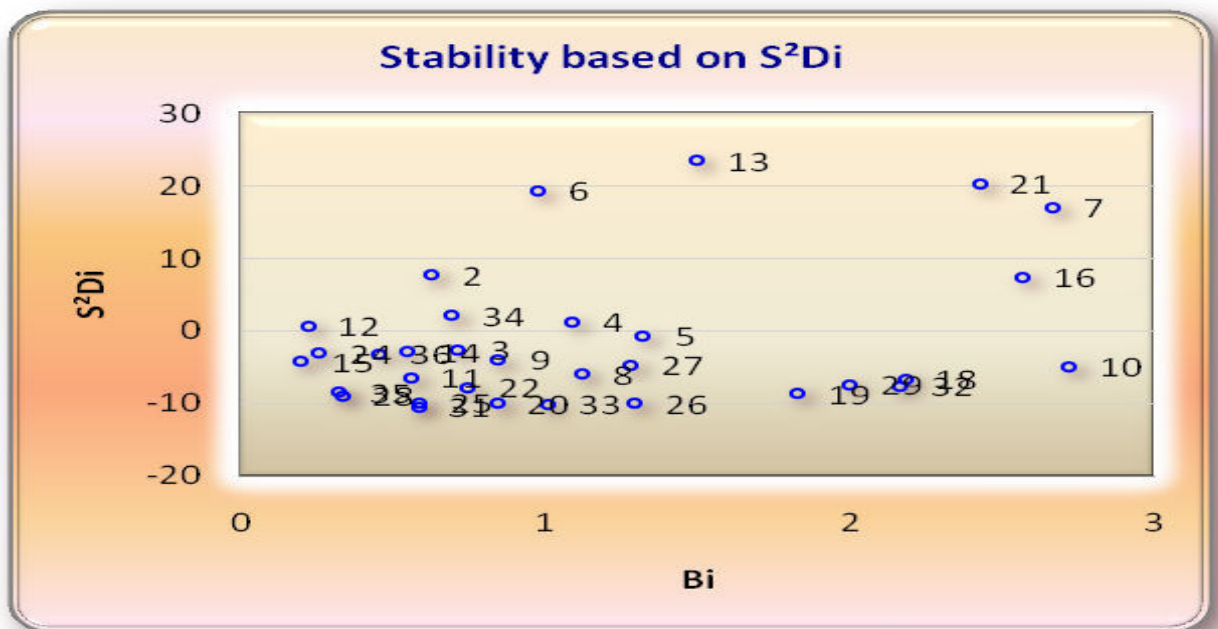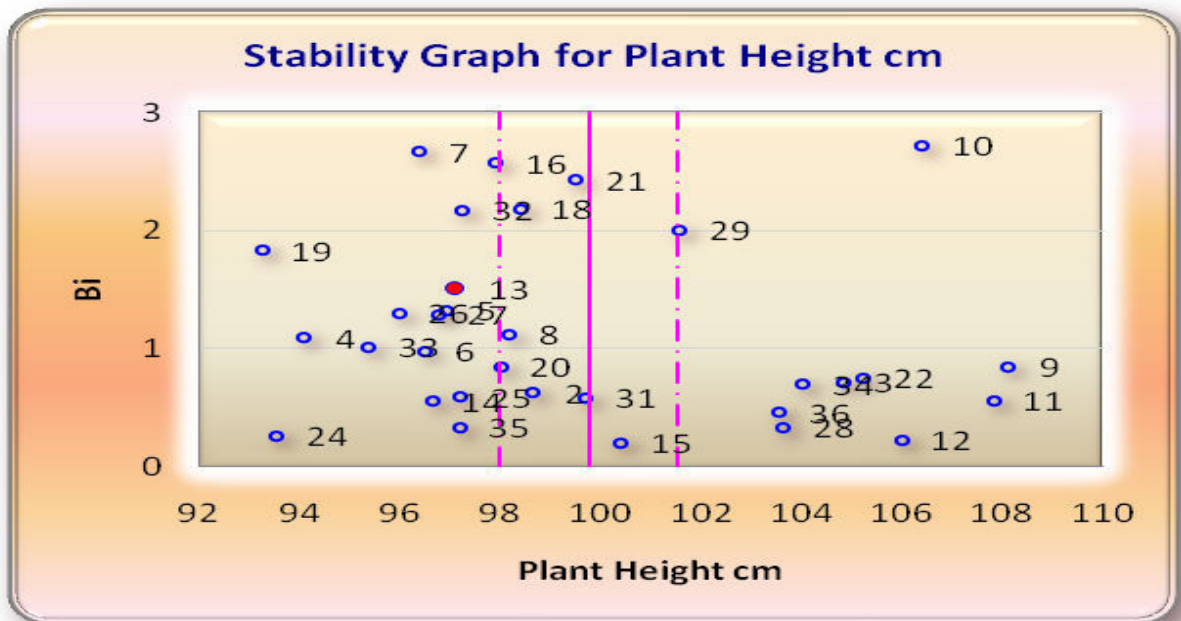
Table 4.28: Stability parameters for days to maturity

S.No.	Genotypes	Days to Maturity		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	114.167	1.586	-0.133
2	CRR 724-1-B (IR 88889-44)	112.417	1.678*	1.399
3	RP-1-27-7-6-1-2-1	116.250	1.294	4.818
4	IR 94313:18-4-1-4-1-B	110.917	0.294	10.033*
5	IR 88287-383-1-B-B-1-1-B	114.333	-0.830	18.988**
6	IR 94391-587-1-2-B	114.167	1.393	20.223**
7	IR 94314-20-2-1-B	118.250	1.059	-2.263
8	IR 93339:40-B-18-13-B-B-1	119.000	0.519	-2.784
9	IR 92521-5-3-1-2	115.167	0.803	-2.508
10	IR 92521-7-5-1-1	114.083	1.144	2.249
11	IR 92521-23-6-1-3	120.750	0.363	10.570*
12	IR 92521-24-5-1-3	112.000	0.899	14.345*
13	IR 92522-47-2-1-1	118.667	1.444	-0.800
14	IR 92522-47-2-1-4	115.917	1.354	-1.562
15	IR 92522-61-3-1-4	116.000	1.594	6.517
16	IR 92523-35-1-1-1	117.917	1.586	2.110
17	IR 92523-37-1-1-2	117.833	1.725*	9.153
18	IR 92527-6-2-1-2	117.167	1.519	-0.111
19	IR 92527-6-2-1-4	116.583	1.186	-3.009
20	IR 92545-53-4-1-3	115.167	1.687*	-2.532
21	IR 92545-54-6-1-4	116.000	1.513	-3.956
22	IR 92546-7-1-1-3	117.083	0.318	-4.374
23	IR 92546-17-6-4-3	117.250	1.234	0.726
24	IR 92546-17-6-4-4	114.500	1.330	-3.926
25	IR 92546-33-3-1-1	114.083	1.041	-3.225
26	IR 92517-1-3-1-1	114.250	0.744	0.523
27	IR 92522-45-3-1-4	116.583	0.753	-2.750
28	IR 92545-23-2-1-1	115.833	0.792	23.274**
29	IR 92545-24-3-1-1	114.417	1.554	10.495*
30	IR 92545-40-2-2-3	115.500	0.527	14.726*
31	IR 92545-51-1-1-4	116.917	0.887	-0.551
32	IR 92546-33-4-2-3	116.333	0.002	7.763
33	IR 92516-8-3-3-4	118.000	0.058	14.832*
34	MTU 1010 (Check)	112.250	1.433	-3.372
35	IR 64 (Check)	112.833	0.654	2.040
36	LALAT (Check)	120.083	0.863	-0.019
	Population Mean	**115.796**		

Figure 4.15: Representation of stability on the basis of regression coefficient and deviation from regression for days to maturity
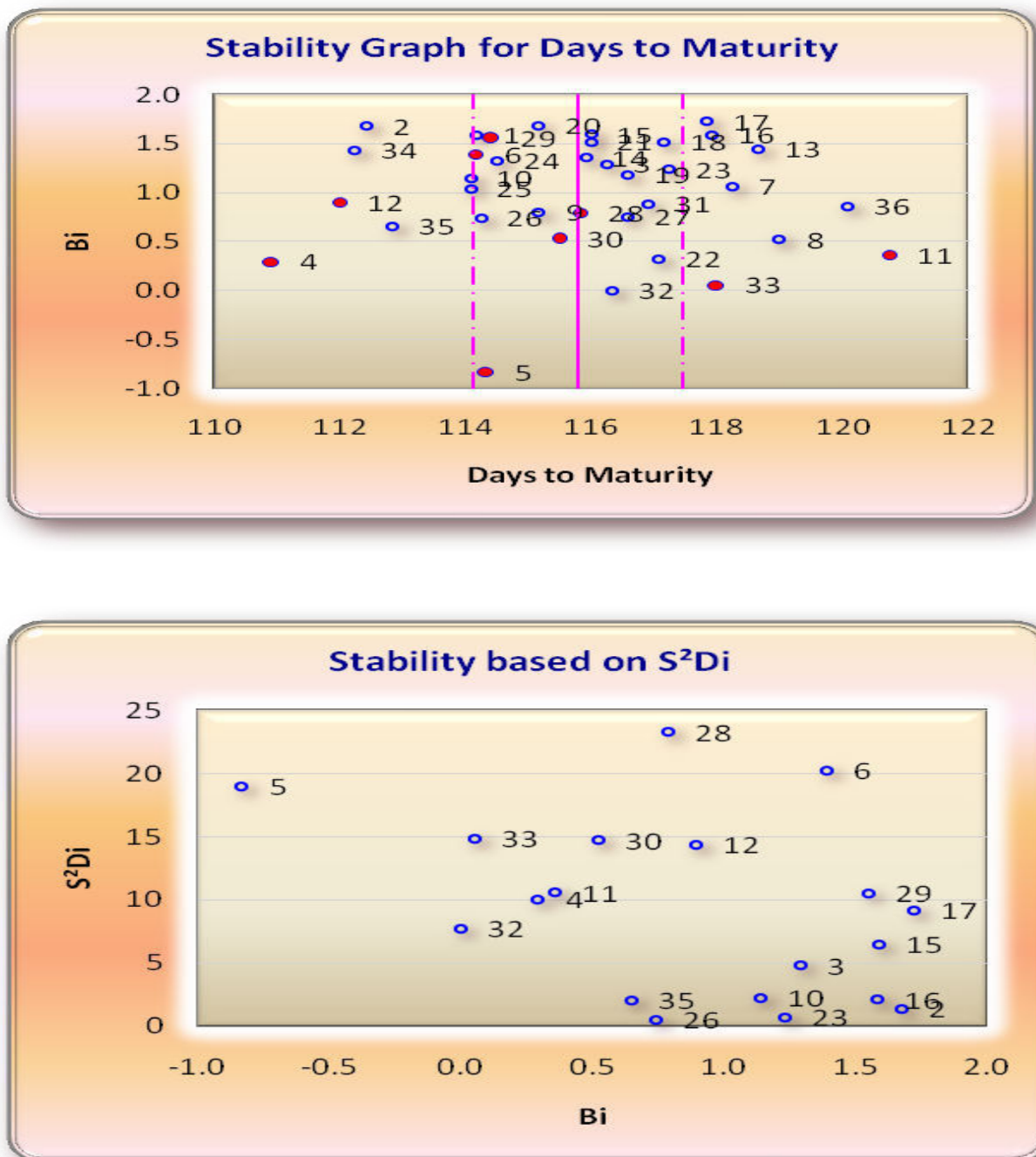
Table 4.29: Stability parameters for number of tillers per plant

S.No.	Genotypes	Number of tillers per plant		
		m	**bi**	**s²di**
1	CRR 719-1-B (IR 88903-34)	9.917	0.198	-0.139
2	CRR 724-1-B (IR 88889-44)	11.083	0.428	0.820
3	RP-1-27-7-6-1-2-1	11.833	0.100	1.372*
4	IR 94313:18-4-1-4-1-B	11.417	1.271	0.092
5	IR 88287-383-1-B-B-1-1-B	11.917	1.248	1.201*
6	IR 94391-587-1-2-B	10.833	1.119	2.770**
7	IR 94314-20-2-1-B	10.583	0.539	1.290*
8	IR 93339:40-B-18-13-B-B-1	10.917	0.514	-0.439
9	IR 92521-5-3-1-2	8.667	0.774	6.907**
10	IR 92521-7-5-1-1	11.083	1.324	2.066**
11	IR 92521-23-6-1-3	9.250	2.820**	2.413**
12	IR 92521-24-5-1-3	9.417	1.097	-0.155
13	IR 92522-47-2-1-1	10.500	1.904*	0.219
14	IR 92522-47-2-1-4	11.500	0.654	-0.280
15	IR 92522-61-3-1-4	11.583	1.204	-0.269
16	IR 92523-35-1-1-1	11.167	0.583	0.103
17	IR 92523-37-1-1-2	11.250	0.830	0.007
18	IR 92527-6-2-1-2	11.083	0.582	-0.130
19	IR 92527-6-2-1-4	11.417	0.692	-0.163
20	IR 92545-53-4-1-3	11.250	1.339	-0.341
21	IR 92545-54-6-1-4	10.833	1.151	2.970**
22	IR 92546-7-1-1-3	10.333	0.637	0.260
23	IR 92546-17-6-4-3	11.083	1.451	1.424*
24	IR 92546-17-6-4-4	10.500	1.299	-0.243
25	IR 92546-33-3-1-1	10.250	1.204	-0.269
26	IR 92517-1-3-1-1	10.833	0.776	0.069
27	IR 92522-45-3-1-4	10.750	1.677*	-0.425
28	IR 92545-23-2-1-1	9.417	0.330	0.400
29	IR 92545-24-3-1-1	10.500	0.971	0.560
30	IR 92545-40-2-2-3	10.083	-0.122	1.238*
31	IR 92545-51-1-1-4	11.333	1.882*	-0.352
32	IR 92546-33-4-2-3	11.250	0.649	-0.393
33	IR 92516-8-3-3-4	11.167	0.654	-0.280
34	MTU 1010 (Check)	12.000	1.359	0.406
35	IR 64 (Check)	10.500	2.188**	-0.236
36	LALAT (Check)	11.833	0.673	0.230
	Population Mean	**10.815**		

Figure 4.16: Representation of stability on the basis of regression coefficient and deviation from regression for number of tillers per plant
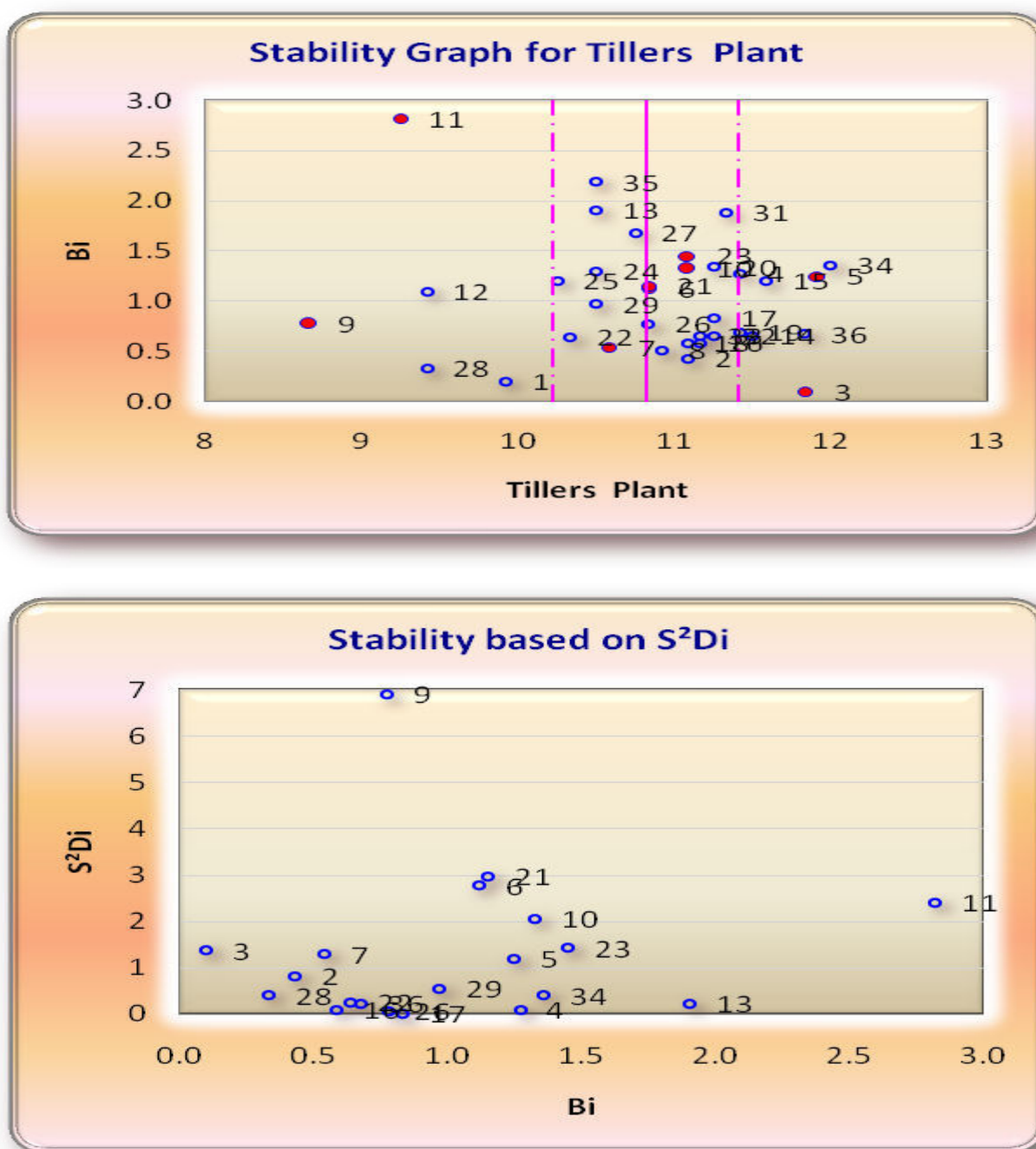
Table 4.30: Stability parameters for number of productive tillers / M^2

S.No.	Genotypes	Number of productive tillers/ m²		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	239.500	2.083**	270.208**
2	CRR 724-1-B (IR 88889-44)	197.833	1.503	57.369
3	RP-1-27-7-6-1-2-1	223.917	0.864	-10.115
4	IR 94313:18-4-1-4-1-B	212.083	1.117	3700.078**
5	IR 88287-383-1-B-B-1-1-B	226.583	0.512	78.109
6	IR 94391-587-1-2-B	219.167	0.877	2.402
7	IR 94314-20-2-1-B	231.667	1.694*	525.623**
8	IR 93339:40-B-18-13-B-B-1	239.083	0.927	220.032*
9	IR 92521-5-3-1-2	195.583	1.332	-60.078
10	IR 92521-7-5-1-1	242.250	0.506	274.894**
11	IR 92521-23-6-1-3	202.250	2.119**	1380.963**
12	IR 92521-24-5-1-3	182.750	1.892*	2791.691**
13	IR 92522-47-2-1-1	217.500	0.808	170.488*
14	IR 92522-47-2-1-4	205.000	0.079	-56.688
15	IR 92522-61-3-1-4	251.667	1.851*	23.268
16	IR 92523-35-1-1-1	233.500	0.848	-44.084
17	IR 92523-37-1-1-2	223.750	0.386	-43.468
18	IR 92527-6-2-1-2	241.667	0.900	-62.860
19	IR 92527-6-2-1-4	236.917	0.924	175.084*
20	IR 92545-53-4-1-3	236.917	1.200	925.263**
21	IR 92545-54-6-1-4	228.833	0.307	-45.657
22	IR 92546-7-1-1-3	272.917	1.185	-38.192
23	IR 92546-17-6-4-3	225.750	1.265	95.346
24	IR 92546-17-6-4-4	213.167	1.393	1270.750**
25	IR 92546-33-3-1-1	260.833	1.146	772.197**
26	IR 92517-1-3-1-1	248.250	-0.970	2227.910**
27	IR 92522-45-3-1-4	237.917	0.975	765.293**
28	IR 92545-23-2-1-1	219.500	1.146	-41.538
29	IR 92545-24-3-1-1	229.167	1.145	439.641**
30	IR 92545-40-2-2-3	230.167	1.747*	517.044**
31	IR 92545-51-1-1-4	214.083	0.344	-5.741
32	IR 92546-33-4-2-3	255.583	1.615	250.333*
33	IR 92516-8-3-3-4	227.500	0.259	29.754
34	MTU 1010 (Check)	236.667	0.487	258.557**
35	IR 64 (Check)	260.667	0.831	178.509*
36	LALAT (Check)	214.417	0.702	-24.298
	Population Mean	**228.750**		

Figure 4.17: Representation of stability on the basis of regression coefficient and deviation from regression for number of productive tillers / M^2
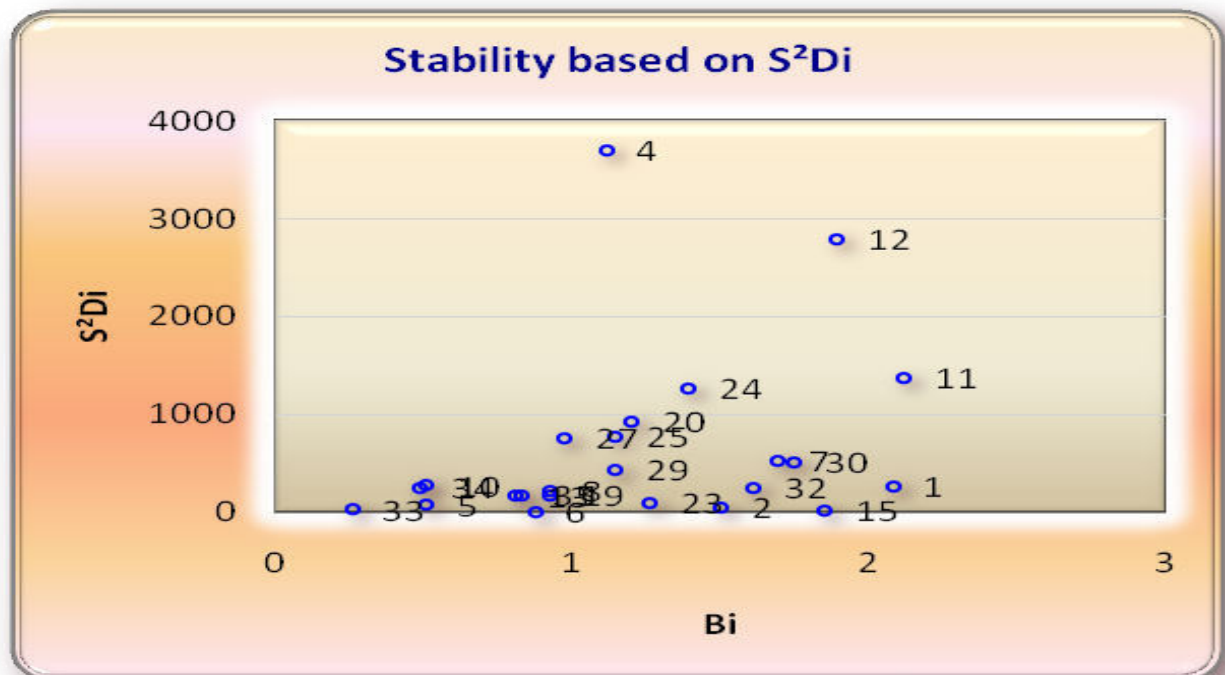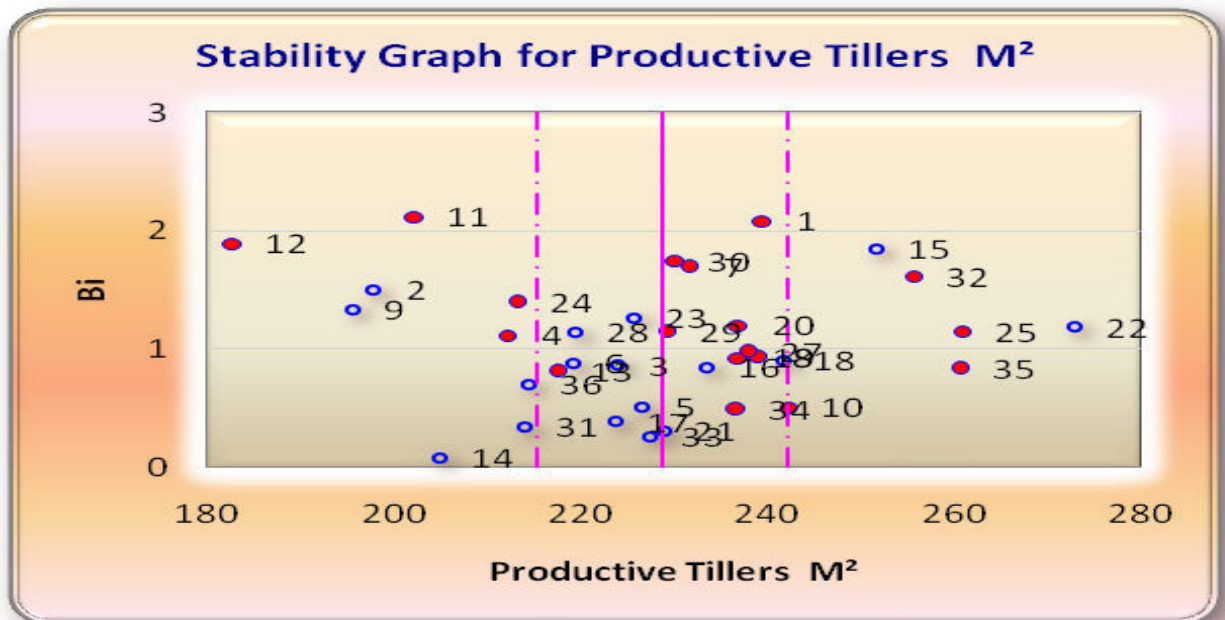
Table 4.31: Stability parameters for panicle length

S.No.	Genotypes	Panicle length (cm)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	26.284	1.098	0.498
2	CRR 724-1-B (IR 88889-44)	25.430	1.737*	-0.343
3	RP-1-27-7-6-1-2-1	25.483	1.768*	-0.155
4	IR 94313:18-4-1-4-1-B	25.625	2.056**	0.010
5	IR 88287-383-1-B-B-1-1-B	26.563	-0.068	0.381
6	IR 94391-587-1-2-B	25.271	0.018	-0.053
7	IR 94314-20-2-1-B	25.846	1.164	8.363**
8	IR 93339:40-B-18-13-B-B-1	27.544	0.260	0.751
9	IR 92521-5-3-1-2	26.292	0.296	0.885
10	IR 92521-7-5-1-1	26.888	1.763*	0.095
11	IR 92521-23-6-1-3	25.840	1.366	0.157
12	IR 92521-24-5-1-3	24.466	0.696	1.503*
13	IR 92522-47-2-1-1	24.390	0.968	0.800
14	IR 92522-47-2-1-4	25.522	1.844*	0.100
15	IR 92522-61-3-1-4	27.269	0.541	-0.175
16	IR 92523-35-1-1-1	25.876	0.608	-0.450
17	IR 92523-37-1-1-2	26.861	0.060	1.160*
18	IR 92527-6-2-1-2	26.426	0.922	0.961
19	IR 92527-6-2-1-4	26.715	0.317	-0.180
20	IR 92545-53-4-1-3	25.812	1.433	1.423*
21	IR 92545-54-6-1-4	26.958	1.236	0.185
22	IR 92546-7-1-1-3	25.842	1.563	-0.320
23	IR 92546-17-6-4-3	25.735	1.546	0.486
24	IR 92546-17-6-4-4	25.592	0.929	-0.343
25	IR 92546-33-3-1-1	24.816	1.121	-0.449
26	IR 92517-1-3-1-1	25.903	0.212	-0.455
27	IR 92522-45-3-1-4	25.738	1.906*	-0.477
28	IR 92545-23-2-1-1	27.146	1.879*	2.411**
29	IR 92545-24-3-1-1	25.254	2.038**	-0.345
30	IR 92545-40-2-2-3	27.405	0.460	-0.124
31	IR 92545-51-1-1-4	26.613	1.241	0.113
32	IR 92546-33-4-2-3	25.515	0.580	1.086*
33	IR 92516-8-3-3-4	25.374	1.167	0.786
34	MTU 1010 (Check)	25.079	0.727	-0.334
35	IR 64 (Check)	26.313	0.127	0.984*
36	LALAT (Check)	28.305	0.420	0.066
	Population Mean	**26.055**		

Figure 4.18: Representation of stability on the basis of regression coefficient and deviation from regression for panicle length
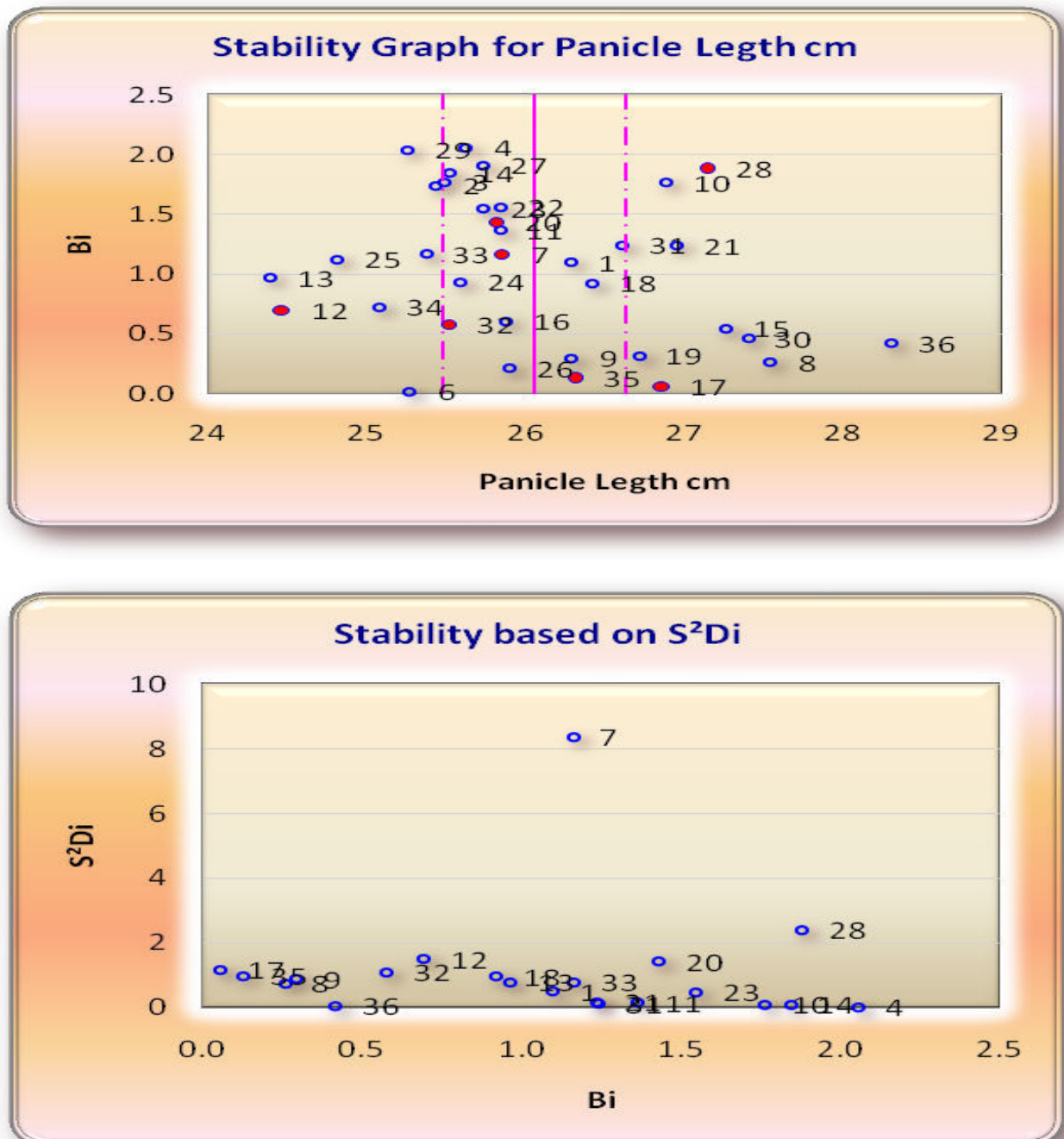
Table 4.32: Stability parameters for number of spikelets per panicle

S.No.	Genotypes	Number of spikelets / Panicle		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	137.000	0.686	112.096*
2	CRR 724-1-B (IR 88889-44)	137.333	1.386	25.028
3	RP-1-27-7-6-1-2-1	127.333	0.503	124.537*
4	IR 94313:18-4-1-4-1-B	127.250	1.139	31.781
5	IR 88287-383-1-B-B-1-1-B	176.667	2.222**	846.846**
6	IR 94391-587-1-2-B	138.917	0.317	100.649*
7	IR 94314-20-2-1-B	135.667	1.437	317.630**
8	IR 93339:40-B-18-13-B-B-1	144.417	0.322	36.840
9	IR 92521-5-3-1-2	196.750	1.403	715.515**
10	IR 92521-7-5-1-1	209.250	2.678**	935.541**
11	IR 92521-23-6-1-3	172.083	0.848	238.822**
12	IR 92521-24-5-1-3	199.500	0.085	372.194**
13	IR 92522-47-2-1-1	165.750	0.433	224.825**
14	IR 92522-47-2-1-4	130.750	0.794	81.661*
15	IR 92522-61-3-1-4	160.000	0.947	23.021
16	IR 92523-35-1-1-1	124.083	1.473	36.077
17	IR 92523-37-1-1-2	167.250	0.236	1.012
18	IR 92527-6-2-1-2	133.000	0.334	111.700*
19	IR 92527-6-2-1-4	139.583	1.024	439.460**
20	IR 92545-53-4-1-3	136.333	0.938	33.535
21	IR 92545-54-6-1-4	120.167	0.738	356.113**
22	IR 92546-7-1-1-3	165.167	1.220	226.650**
23	IR 92546-17-6-4-3	155.000	1.221	304.628**
24	IR 92546-17-6-4-4	165.250	1.141	-22.456
25	IR 92546-33-3-1-1	153.583	1.681*	81.788*
26	IR 92517-1-3-1-1	167.917	1.462	302.625**
27	IR 92522-45-3-1-4	150.083	0.831	40.444
28	IR 92545-23-2-1-1	145.417	0.633	13.743
29	IR 92545-24-3-1-1	137.167	0.955	91.670*
30	IR 92545-40-2-2-3	159.417	0.226	33.905
31	IR 92545-51-1-1-4	158.667	0.338	320.053**
32	IR 92546-33-4-2-3	187.250	2.033**	69.906
33	IR 92516-8-3-3-4	145.083	1.608	-17.608
34	MTU 1010 (Check)	141.667	0.976	285.722**
35	IR 64 (Check)	144.500	1.140	16.368
36	LALAT (Check)	133.000	0.592	-33.320
	Population Mean	**152.451**		

Figure 4.19: **Representation of stability on the basis of regression coefficient and deviation from regression for number of spikelets per panicle**
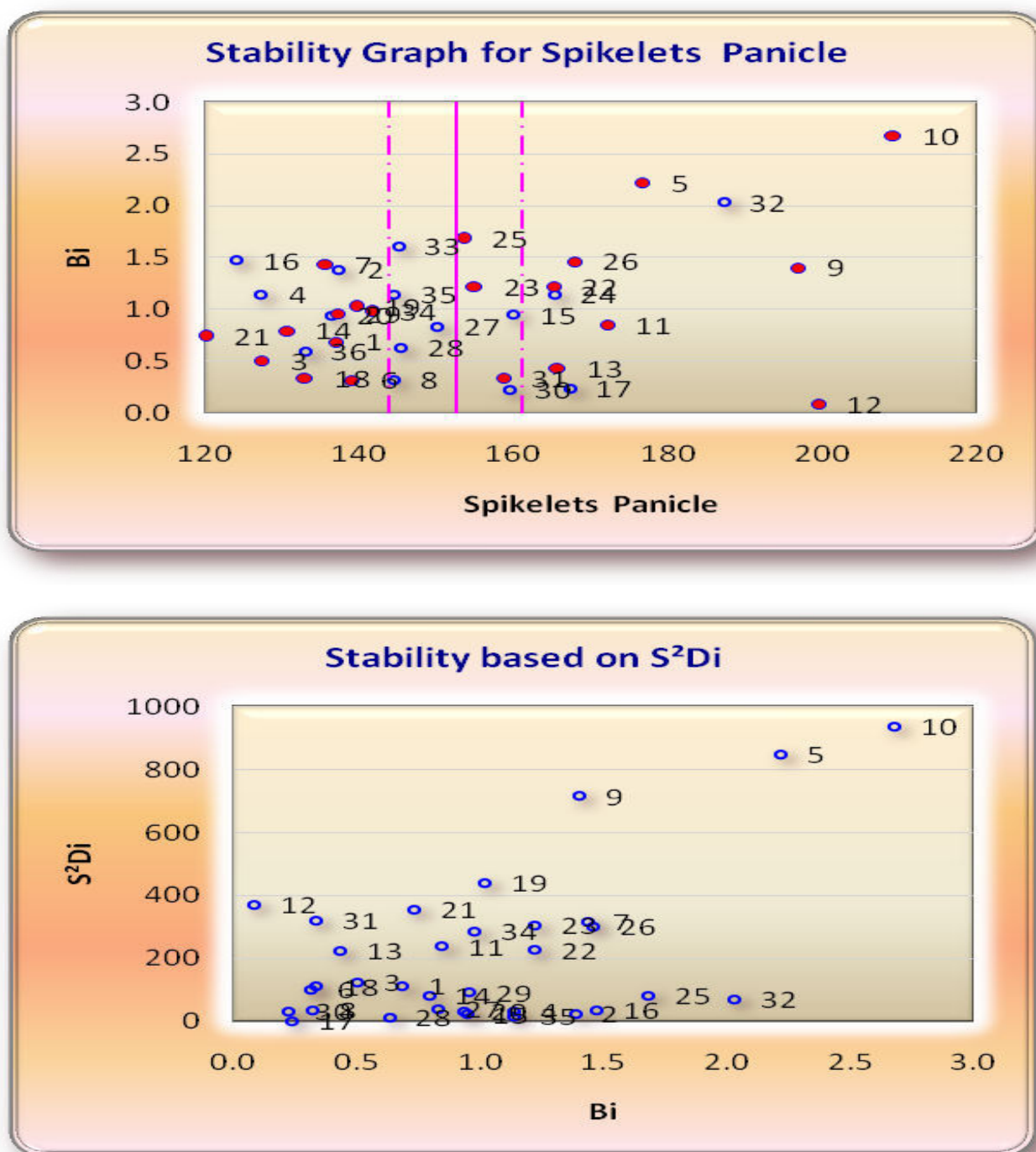
Table 4.33: Stability parameters for grain yield per plant

S.No.	Genotypes	Grain yield/ Plant (g)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	27.333	1.604	0.762
2	CRR 724-1-B (IR 88889-44)	27.250	0.598	-1.917
3	RP-1-27-7-6-1-2-1	26.333	1.656*	5.625*
4	IR 94313:18-4-1-4-1-B	27.000	0.553	1.281
5	IR 88287-383-1-B-B-1-1-B	27.750	1.566	1.067
6	IR 94391-587-1-2-B	27.500	1.415	-1.477
7	IR 94314-20-2-1-B	31.583	1.433	0.066
8	IR 93339:40-B-18-13-B-B-1	27.750	0.375	-0.795
9	IR 92521-5-3-1-2	27.250	0.972	0.707
10	IR 92521-7-5-1-1	24.667	0.530	1.893
11	IR 92521-23-6-1-3	27.000	1.501	1.015
12	IR 92521-24-5-1-3	30.417	1.016	2.896
13	IR 92522-47-2-1-1	30.333	0.314	2.225
14	IR 92522-47-2-1-4	26.500	2.008**	0.947
15	IR 92522-61-3-1-4	25.750	0.559	1.720
16	IR 92523-35-1-1-1	26.000	1.041	-1.154
17	IR 92523-37-1-1-2	30.417	1.538	-0.909
18	IR 92527-6-2-1-2	27.500	1.077	9.395**
19	IR 92527-6-2-1-4	29.583	1.003	9.524**
20	IR 92545-53-4-1-3	27.667	0.837	3.189
21	IR 92545-54-6-1-4	27.000	0.708	-0.802
22	IR 92546-7-1-1-3	26.417	0.692	7.270*
23	IR 92546-17-6-4-3	28.417	1.130	2.818
24	IR 92546-17-6-4-4	28.667	1.188	-0.901
25	IR 92546-33-3-1-1	26.333	1.362	0.350
26	IR 92517-1-3-1-1	29.167	1.362	-1.923
27	IR 92522-45-3-1-4	29.500	0.229	9.256**
28	IR 92545-23-2-1-1	26.667	0.811	2.593
29	IR 92545-24-3-1-1	26.000	1.183	6.954*
30	IR 92545-40-2-2-3	24.667	-0.017	2.661
31	IR 92545-51-1-1-4	27.583	1.480	7.149*
32	IR 92546-33-4-2-3	30.167	0.697	1.018
33	IR 92516-8-3-3-4	26.750	1.067	3.852
34	MTU 1010 (Check)	25.250	0.727	-0.720
35	IR 64 (Check)	27.833	0.827	-1.089
36	LALAT (Check)	28.167	0.956	-1.297
	Population Mean	**27.616**		

Figure 4.20: Representation of stability on the basis of regression coefficient and deviation from regression for grain yield per plant
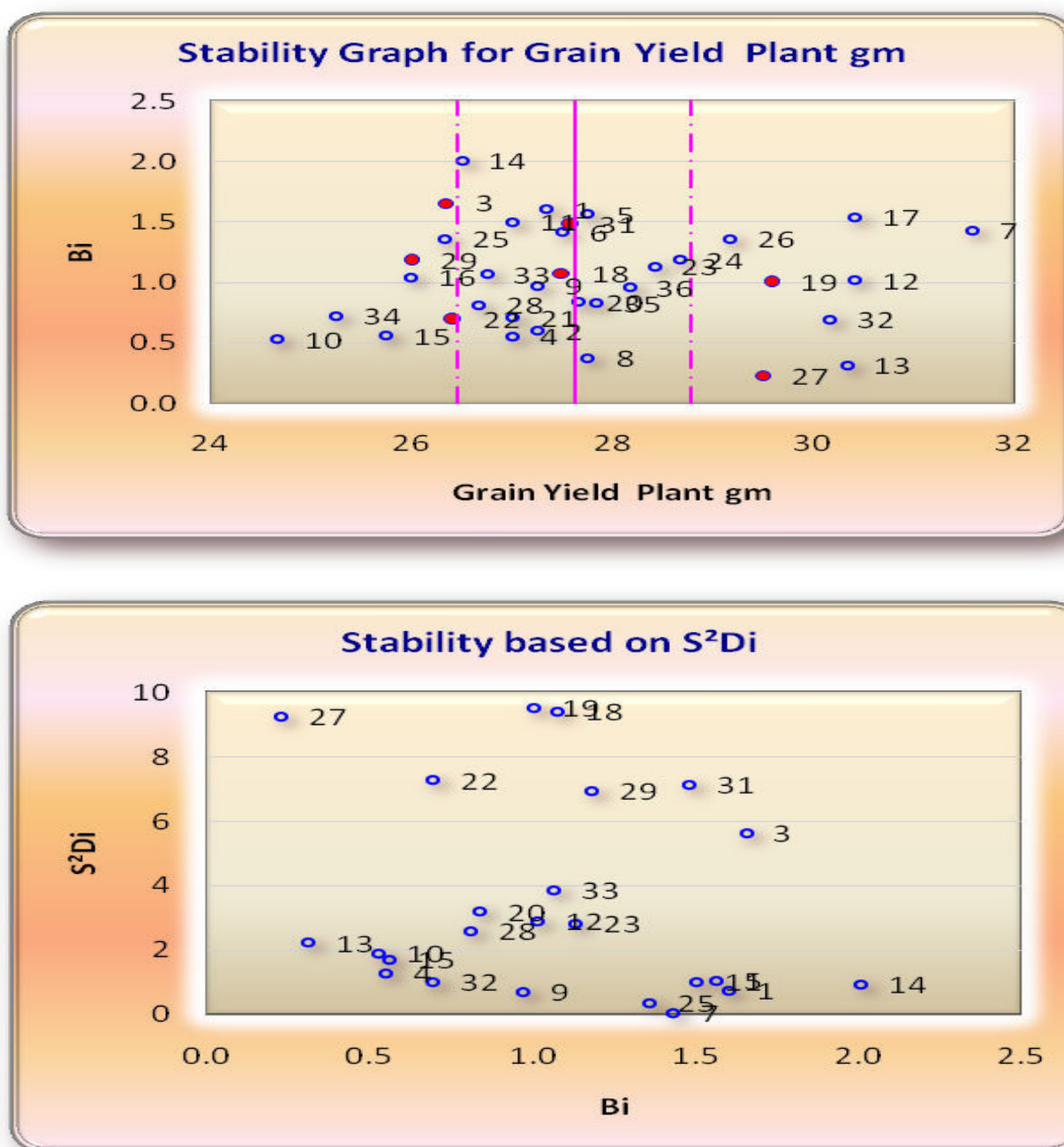
Table 4.34: Stability parameters for biological yield per plant

| S.No.	Genotypes	Biological yield/ Plant (g)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	58.667	1.094	0.291
2	CRR 724-1-B (IR 88889-44)	66.750	1.139	-5.038
3	RP-1-27-7-6-1-2-1	64.167	1.088	10.732
4	IR 94313:18-4-1-4-1-B	70.167	0.350	33.074**
5	IR 88287-383-1-B-B-1-1-B	61.250	0.730	0.990
6	IR 94391-587-1-2-B	74.667	0.965	12.033*
7	IR 94314-20-2-1-B	75.167	1.684*	18.325*
8	IR 93339:40-B-18-13-B-B-1	71.167	1.868*	7.810
9	IR 92521-5-3-1-2	61.250	1.515	-5.227
10	IR 92521-7-5-1-1	70.833	1.260	6.399
11	IR 92521-23-6-1-3	69.417	0.810	17.676*
12	IR 92521-24-5-1-3	75.000	-0.422	4.037
13	IR 92522-47-2-1-1	74.333	1.975**	-3.314
14	IR 92522-47-2-1-4	70.167	1.074	-3.251
15	IR 92522-61-3-1-4	61.667	1.511	1.555
16	IR 92523-35-1-1-1	62.167	-0.193	2.277
17	IR 92523-37-1-1-2	72.917	1.116	2.208
18	IR 92527-6-2-1-2	74.167	2.255**	-2.713
19	IR 92527-6-2-1-4	76.917	1.935*	-2.245
20	IR 92545-53-4-1-3	62.667	0.676	2.271
21	IR 92545-54-6-1-4	64.000	0.741	0.199
22	IR 92546-7-1-1-3	66.583	0.596	4.702
23	IR 92546-17-6-4-3	74.000	1.512	15.180*
24	IR 92546-17-6-4-4	60.167	-0.038	-4.866
25	IR 92546-33-3-1-1	71.917	1.679*	12.846*
26	IR 92517-1-3-1-1	64.667	0.733	22.338**
27	IR 92522-45-3-1-4	62.417	1.622	26.584**
28	IR 92545-23-2-1-1	56.917	0.223	-4.328
29	IR 92545-24-3-1-1	60.083	1.306	4.691
30	IR 92545-40-2-2-3	72.833	1.586	1.049
31	IR 92545-51-1-1-4	68.917	0.497	-0.494
32	IR 92546-33-4-2-3	70.667	0.601	13.260*
33	IR 92516-8-3-3-4	74.000	0.092	26.552**
34	MTU 1010 (Check)	58.667	0.837	-4.659
35	IR 64 (Check)	60.750	1.241	-4.288
36	LALAT (Check)	68.500	0.343	-1.097
	Population Mean	**67.461**		

Figure 4.21: Representation of stability on the basis of regression coefficient and deviation from regression for biological yield per plant
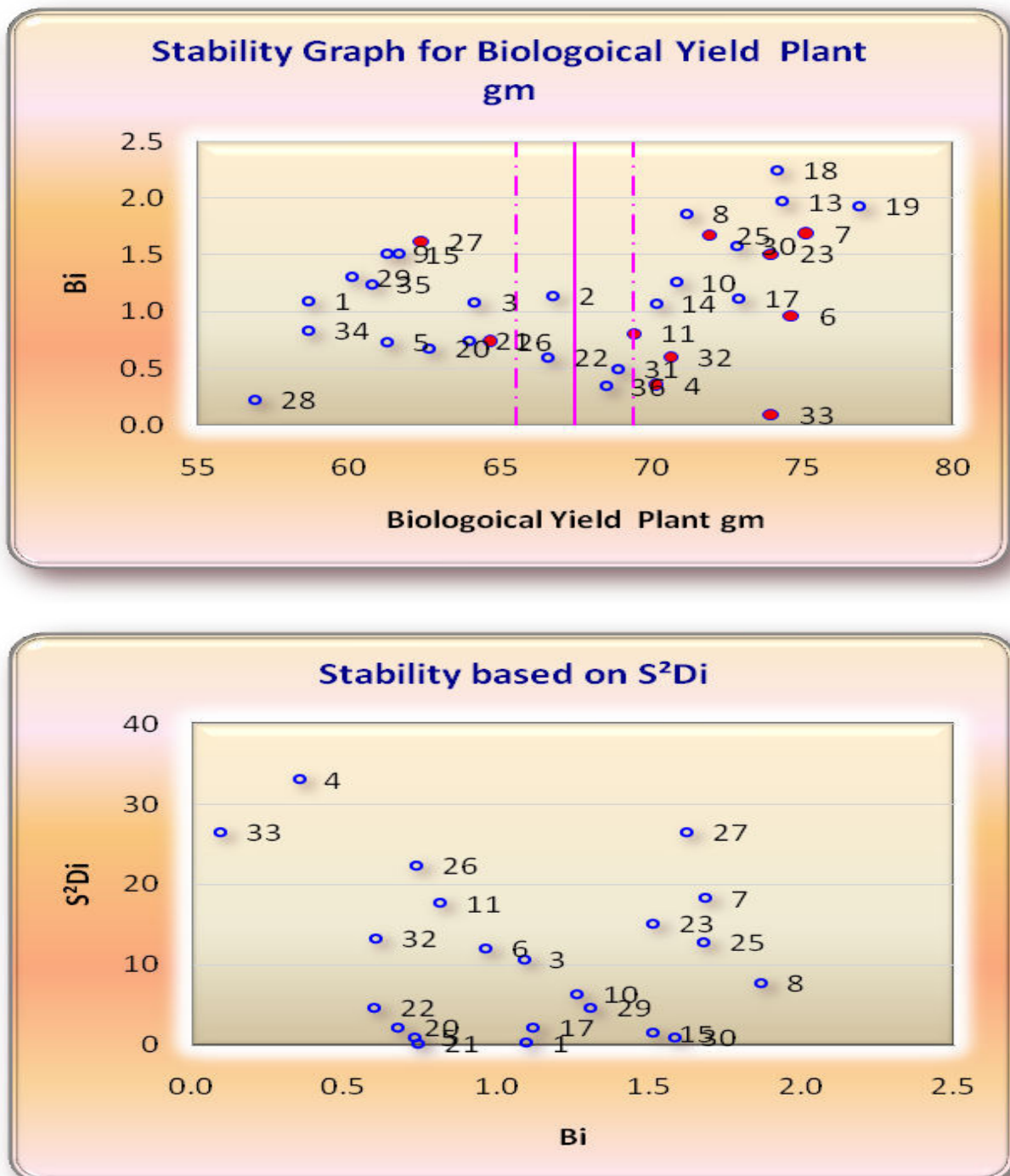
Table 4.35: Stability parameters for harvest index

S.No.	Genotypes	Harvest index (%)		
		m	**bi**	**s²di**
1	CRR 719-1-B (IR 88903-34)	46.730	1.491	-1.560
2	CRR 724-1-B (IR 88889-44)	40.895	0.263	-6.478
3	RP-1-27-7-6-1-2-1	41.453	3.750**	9.595
4	IR 94313:18-4-1-4-1-B	38.678	-1.054	13.572
5	IR 88287-383-1-B-B-1-1-B	45.533	2.509**	-4.775
6	IR 94391-587-1-2-B	36.998	1.993**	-3.933
7	IR 94314-20-2-1-B	42.123	-0.083	-2.357
8	IR 93339:40-B-18-13-B-B-1	39.225	0.231	-1.160
9	IR 92521-5-3-1-2	44.718	0.980	1.786
10	IR 92521-7-5-1-1	35.014	0.606	-3.021
11	IR 92521-23-6-1-3	38.887	0.347	15.809*
12	IR 92521-24-5-1-3	40.672	0.852	13.926
13	IR 92522-47-2-1-1	41.038	-1.108	-3.322
14	IR 92522-47-2-1-4	37.758	2.670**	-5.391
15	IR 92522-61-3-1-4	42.059	0.225	6.136
16	IR 92523-35-1-1-1	42.097	1.247	0.365
17	IR 92523-37-1-1-2	41.743	1.195	-7.162
18	IR 92527-6-2-1-2	37.047	0.023	-2.589
19	IR 92527-6-2-1-4	38.741	1.743*	26.367*
20	IR 92545-53-4-1-3	44.329	-0.235	10.453
21	IR 92545-54-6-1-4	42.277	0.930	-6.523
22	IR 92546-7-1-1-3	39.879	2.293**	14.090
23	IR 92546-17-6-4-3	38.403	0.526	-2.418
24	IR 92546-17-6-4-4	47.759	2.038**	-4.811
25	IR 92546-33-3-1-1	36.699	0.953	-4.567
26	IR 92517-1-3-1-1	45.472	2.815**	-6.576
27	IR 92522-45-3-1-4	47.467	-0.080	-6.264
28	IR 92545-23-2-1-1	47.140	0.616	18.824*
29	IR 92545-24-3-1-1	43.242	1.100	7.886
30	IR 92545-40-2-2-3	34.197	0.367	19.903*
31	IR 92545-51-1-1-4	40.097	2.297**	1.899
32	IR 92546-33-4-2-3	42.773	-0.696	5.278
33	IR 92516-8-3-3-4	36.217	1.731*	3.080
34	MTU 1010 (Check)	43.217	1.147	-2.952
35	IR 64 (Check)	46.038	1.133	-0.168
36	LALAT (Check)	41.190	1.185	-2.724
	Population Mean	**41.328**		

Figure 4.22: Representation of stability on the basis of regression coefficient and deviation from regression for harvest index (%)
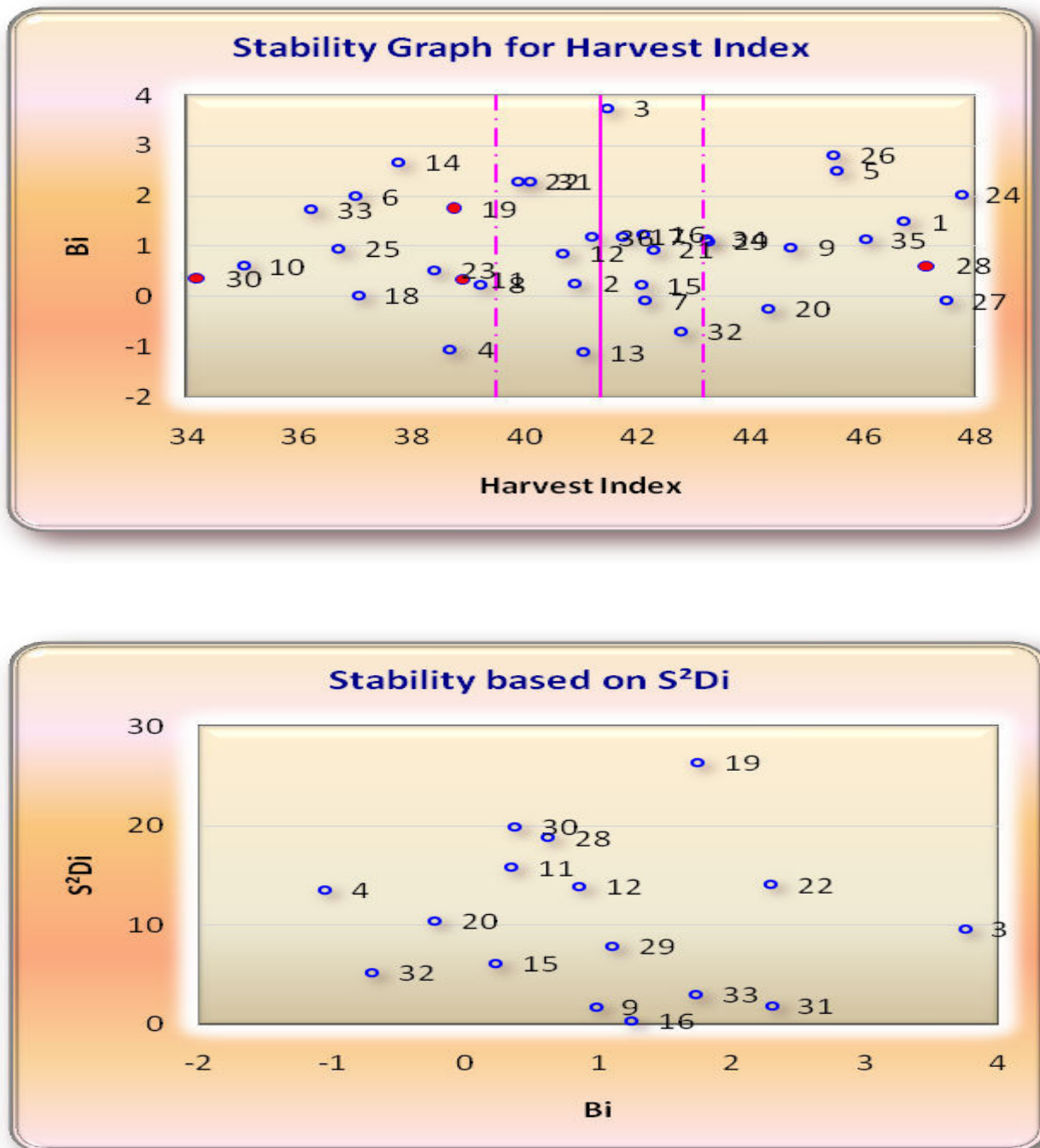
Table 4.36: Stability parameters for test weight (1000 grain weight)

| S.No.	Genotypes	Test weight (g)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	22.633	0.590	0.858*
2	CRR 724-1-B (IR 88889-44)	26.917	0.963	2.812**
3	RP-1-27-7-6-1-2-1	22.233	0.937	0.594
4	IR 94313:18-4-1-4-1-B	25.142	0.022	0.132
5	IR 88287-383-1-B-B-1-1-B	23.500	1.783*	1.332*
6	IR 94391-587-1-2-B	26.242	1.298	1.760**
7	IR 94314-20-2-1-B	23.717	0.852	0.295
8	IR 93339:40-B-18-13-B-B-1	24.375	0.219	1.981**
9	IR 92521-5-3-1-2	22.000	-0.079	1.218*
10	IR 92521-7-5-1-1	26.750	1.539	0.983*
11	IR 92521-23-6-1-3	22.467	1.647	0.345
12	IR 92521-24-5-1-3	22.425	0.349	0.458
13	IR 92522-47-2-1-1	24.292	2.443**	0.310
14	IR 92522-47-2-1-4	24.242	-0.196	-0.297
15	IR 92522-61-3-1-4	22.708	-0.441	1.351*
16	IR 92523-35-1-1-1	24.700	1.163	0.153
17	IR 92523-37-1-1-2	23.950	1.571	0.564
18	IR 92527-6-2-1-2	24.858	0.899	2.794**
19	IR 92527-6-2-1-4	22.992	1.078	0.332
20	IR 92545-53-4-1-3	22.983	1.303	0.005
21	IR 92545-54-6-1-4	24.875	2.614**	-0.001
22	IR 92546-7-1-1-3	22.692	0.610	0.052
23	IR 92546-17-6-4-3	23.533	1.953*	1.607**
24	IR 92546-17-6-4-4	23.125	0.695	0.884*
25	IR 92546-33-3-1-1	23.292	0.115	-0.250
26	IR 92517-1-3-1-1	25.783	0.620	-0.103
27	IR 92522-45-3-1-4	27.958	0.415	-0.166
28	IR 92545-23-2-1-1	23.433	0.367	0.478
29	IR 92545-24-3-1-1	26.083	1.040	-0.262
30	IR 92545-40-2-2-3	27.800	1.412	0.052
31	IR 92545-51-1-1-4	24.067	1.512	1.179*
32	IR 92546-33-4-2-3	20.467	1.921*	0.652
33	IR 92516-8-3-3-4	25.583	2.525**	0.118
34	MTU 1010 (Check)	24.525	0.731	2.084**
35	IR 64 (Check)	24.067	0.534	-0.107
36	LALAT (Check)	26.583	0.997	-0.229
	Population Mean	**24.250**		

Figure 4.23: Representation of stability on the basis of regression coefficient and deviation from regression for test weight
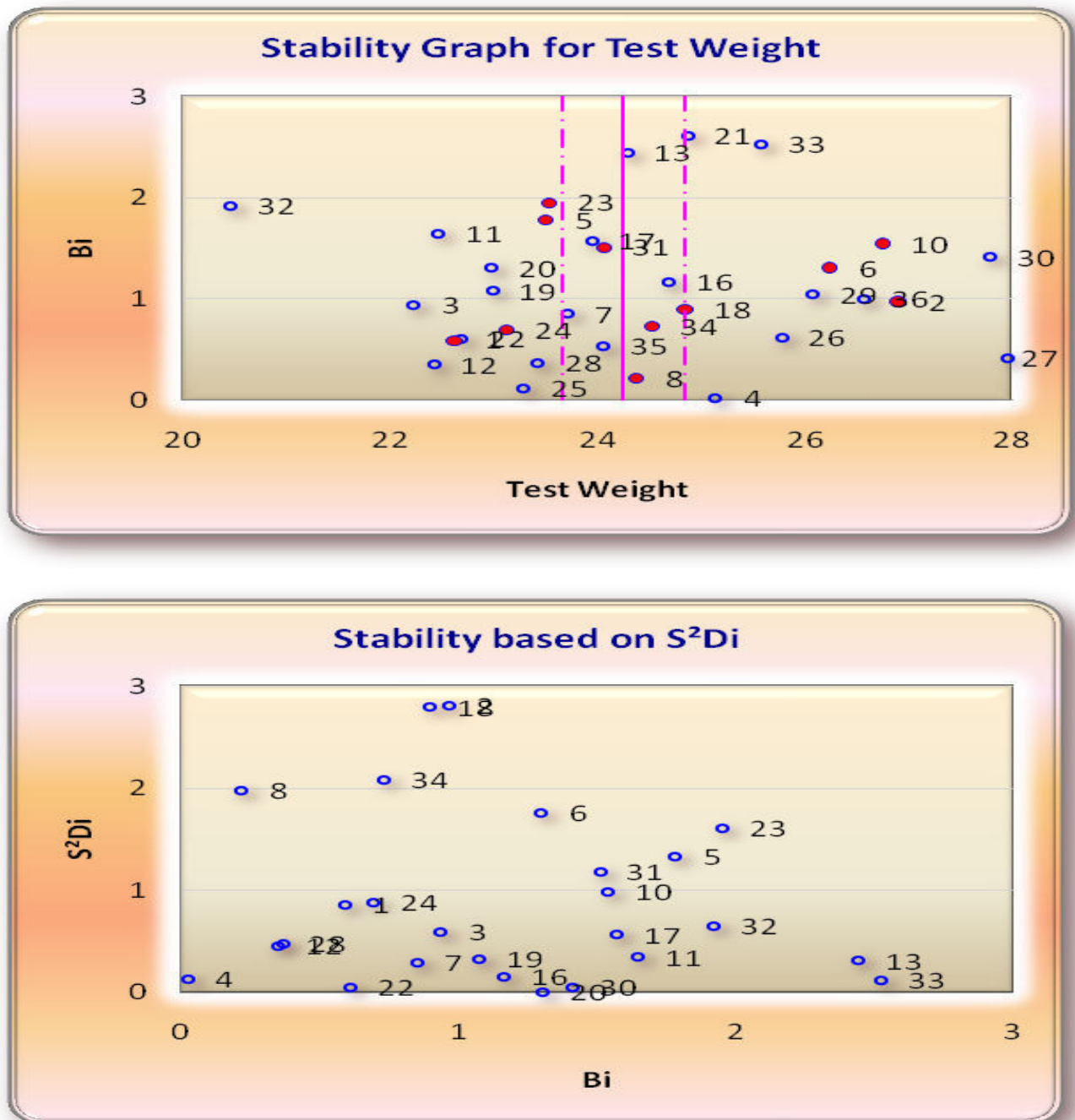
Table 4.37: Stability parameters for grain yield kilogram per hectare

| S.No.	Genotypes	Grain yield kilogram per hectare (Kg)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	3889.167	1.261	80282.734*
2	CRR 724-1-B (IR 88889-44)	3250.000	0.318	26511.250
3	RP-1-27-7-6-1-2-1	4584.500	1.735*	64362.230*
4	IR 94313:18-4-1-4-1-B	3978.750	1.716*	114787.109**
5	IR 88287-383-1-B-B-1-1-B	3860.750	0.952	423882.125**
6	IR 94391-587-1-2-B	4304.000	0.983	3877.182
7	IR 94314-20-2-1-B	4463.917	0.974	4851.137
8	IR 93339:40-B-18-13-B-B-1	4724.833	0.790	31780.047
9	IR 92521-5-3-1-2	3858.333	0.937	189263.641**
10	IR 92521-7-5-1-1	4466.917	0.835	8999.906
11	IR 92521-23-6-1-3	4396.833	1.376	63115.875*
12	IR 92521-24-5-1-3	3820.833	1.007	151298.672**
13	IR 92522-47-2-1-1	4501.917	0.960	-15881.473
14	IR 92522-47-2-1-4	3965.083	0.742	-6043.270
15	IR 92522-61-3-1-4	4023.000	1.083	7403.377
16	IR 92523-35-1-1-1	4595.583	1.113	298029.750**
17	IR 92523-37-1-1-2	4435.917	0.595	91185.930**
18	IR 92527-6-2-1-2	5118.917	1.472	281507.500**
19	IR 92527-6-2-1-4	5079.583	0.857	-10505.412
20	IR 92545-53-4-1-3	4015.917	0.081	-9033.049
21	IR 92545-54-6-1-4	3468.833	1.032	-3427.673
22	IR 92546-7-1-1-3	4399.417	0.999	2231.169
23	IR 92546-17-6-4-3	5078.000	1.296	79484.406*
24	IR 92546-17-6-4-4	4528.083	1.259	6365.671
25	IR 92546-33-3-1-1	4349.000	0.551	-13241.322
26	IR 92517-1-3-1-1	4892.000	0.480	58154.754*
27	IR 92522-45-3-1-4	4563.333	1.203	-3590.106
28	IR 92545-23-2-1-1	4032.500	0.723	-8053.892
29	IR 92545-24-3-1-1	4565.500	0.428	148895.688**
30	IR 92545-40-2-2-3	3913.583	0.821	54052.152*
31	IR 92545-51-1-1-4	4280.583	0.888	138656.531**
32	IR 92546-33-4-2-3	4711.917	1.313	-18452.934
33	IR 92516-8-3-3-4	4470.500	2.046**	84550.750**
34	MTU 1010 (Check)	4502.417	1.173	-13956.492
35	IR 64 (Check)	4596.750	1.429	46441.156*
36	LALAT (Check)	4398.250	0.571	226.936
	Population Mean	**4335.706**		

Figure 4.24: Representation of stability on the basis of regression coefficient and deviation from regression for grain yield kilogram / Ha
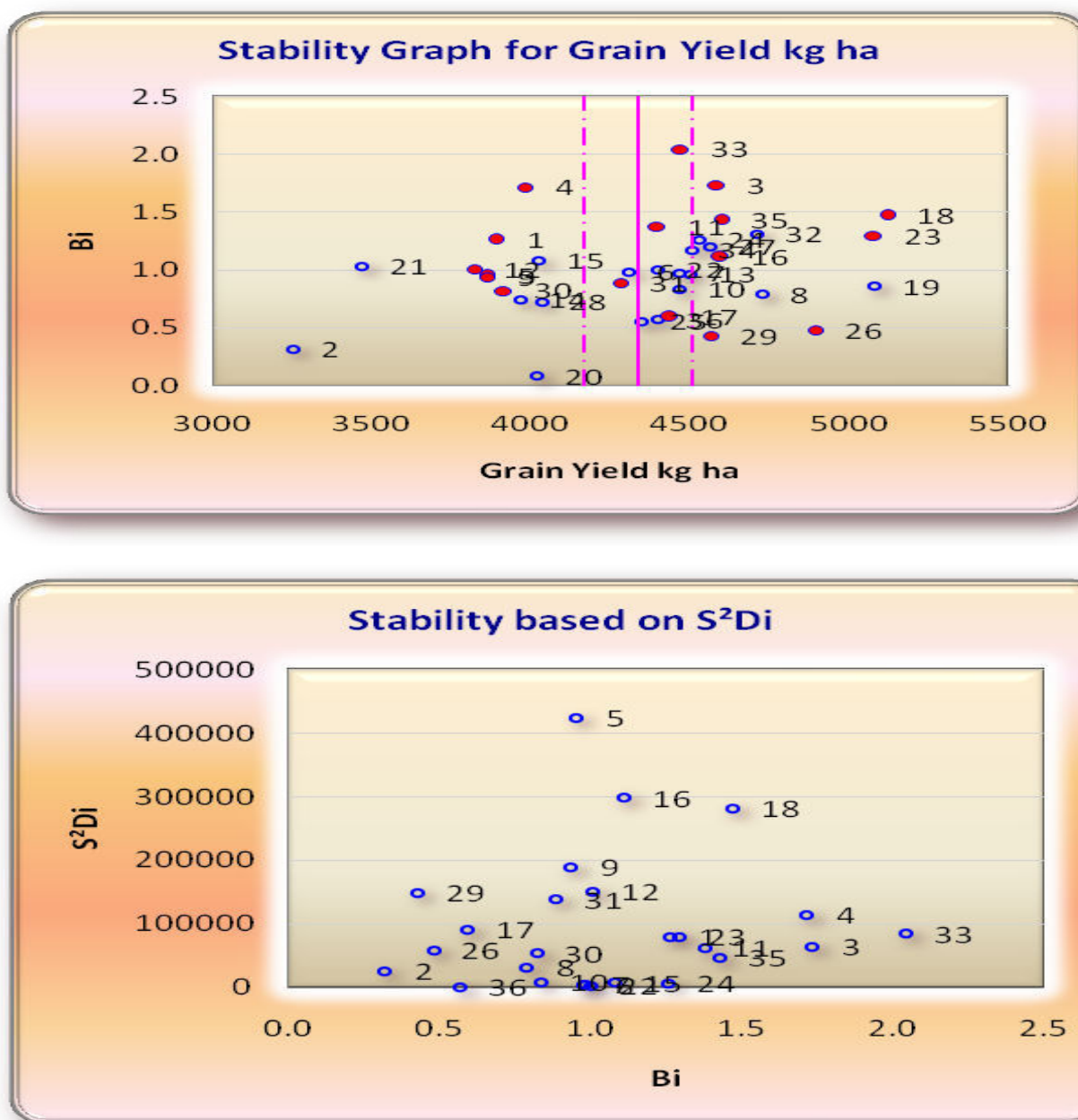
Table 4.38: Stability parameters for hulling recovery

| S.No.	Genotypes	Hulling recovery (%)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	76.142	2.176**	-0.822
2	CRR 724-1-B (IR 88889-44)	71.675	1.961*	-1.243
3	RP-1-27-7-6-1-2-1	69.407	-0.671	-1.846
4	IR 94313:18-4-1-4-1-B	74.643	1.289	0.407
5	IR 88287-383-1-B-B-1-1-B	72.598	2.979**	-0.096
6	IR 94391-587-1-2-B	76.088	1.356	-1.904
7	IR 94314-20-2-1-B	73.301	0.150	0.384
8	IR 93339:40-B-18-13-B-B-1	71.071	2.450**	-0.880
9	IR 92521-5-3-1-2	74.991	2.384**	-0.726
10	IR 92521-7-5-1-1	74.744	0.386	-1.642
11	IR 92521-23-6-1-3	73.274	-1.763*	-0.686
12	IR 92521-24-5-1-3	74.649	0.462	-2.134
13	IR 92522-47-2-1-1	76.202	1.478	1.524
14	IR 92522-47-2-1-4	75.102	0.514	-1.550
15	IR 92522-61-3-1-4	74.577	1.436	0.831
16	IR 92523-35-1-1-1	76.573	1.770*	-1.912
17	IR 92523-37-1-1-2	76.046	0.266	-0.826
18	IR 92527-6-2-1-2	69.745	-0.145	2.184
19	IR 92527-6-2-1-4	74.497	2.215**	-1.950
20	IR 92545-53-4-1-3	75.825	0.206	-0.766
21	IR 92545-54-6-1-4	75.720	1.873*	2.102
22	IR 92546-7-1-1-3	73.819	1.582	-2.010
23	IR 92546-17-6-4-3	75.511	0.652	2.654
24	IR 92546-17-6-4-4	74.045	0.645	5.745*
25	IR 92546-33-3-1-1	74.448	1.262	-0.035
26	IR 92517-1-3-1-1	72.223	1.334	0.404
27	IR 92522-45-3-1-4	73.741	-0.947	-0.549
28	IR 92545-23-2-1-1	74.882	0.433	-2.169
29	IR 92545-24-3-1-1	74.327	0.319	-1.544
30	IR 92545-40-2-2-3	77.345	1.721*	-1.090
31	IR 92545-51-1-1-4	77.147	-0.235	1.155
32	IR 92546-33-4-2-3	73.749	0.798	2.517
33	IR 92516-8-3-3-4	75.937	0.906	-0.853
34	MTU 1010 (Check)	76.418	1.269	-1.664
35	IR 64 (Check)	75.433	1.707*	0.054
36	LALAT (Check)	76.306	1.783*	0.165
	Population Mean	**74.506**		

Figure 4.25: Representation of stability on the basis of regression coefficient and deviation from regression for hulling recovery (%)
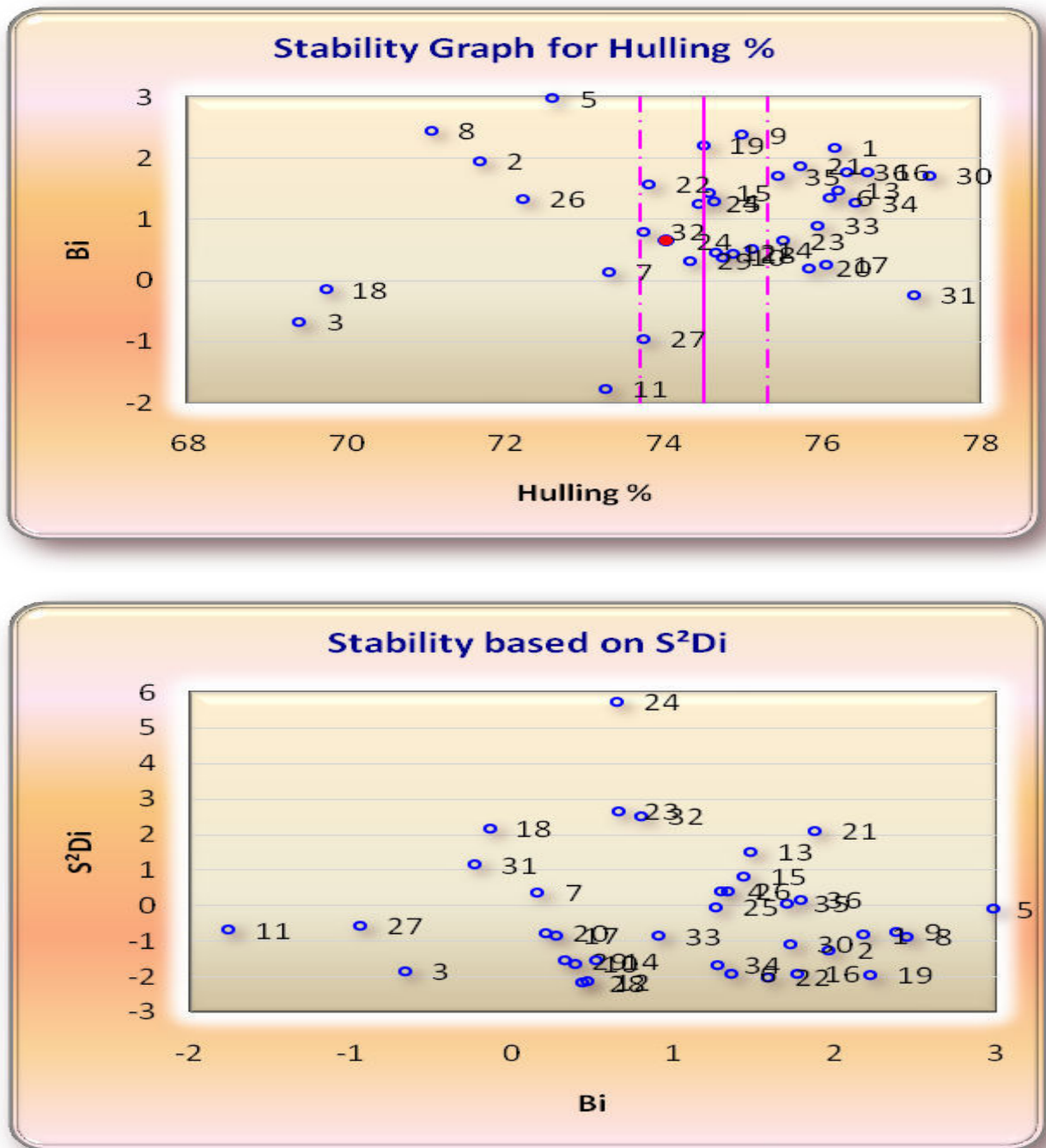
Table 4.39: Stability parameters for milling recovery

| S.No.	Genotypes	Milling recovery (%)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	63.233	1.389	-1.377
2	CRR 724-1-B (IR 88889-44)	63.208	1.207	2.926
3	RP-1-27-7-6-1-2-1	62.700	0.591	2.100
4	IR 94313:18-4-1-4-1-B	63.358	2.285**	3.728*
5	IR 88287-383-1-B-B-1-1-B	62.892	-1.129	12.286**
6	IR 94391-587-1-2-B	59.583	1.707*	1.279
7	IR 94314-20-2-1-B	61.275	-0.912	6.274*
8	IR 93339:40-B-18-13-B-B-1	65.992	1.097	2.306
9	IR 92521-5-3-1-2	63.225	1.112	1.022
10	IR 92521-7-5-1-1	60.925	3.534**	2.023
11	IR 92521-23-6-1-3	63.408	0.347	10.777**
12	IR 92521-24-5-1-3	63.292	1.020	-0.903
13	IR 92522-47-2-1-1	61.158	-0.567	10.349**
14	IR 92522-47-2-1-4	65.258	1.487	3.610*
15	IR 92522-61-3-1-4	60.617	-0.551	1.899
16	IR 92523-35-1-1-1	64.000	2.727**	-0.147
17	IR 92523-37-1-1-2	61.625	0.084	3.843*
18	IR 92527-6-2-1-2	65.925	1.842*	2.933
19	IR 92527-6-2-1-4	63.750	2.061**	0.571
20	IR 92545-53-4-1-3	61.667	0.934	9.905**
21	IR 92545-54-6-1-4	60.583	1.371	2.067
22	IR 92546-7-1-1-3	60.725	1.385	0.790
23	IR 92546-17-6-4-3	60.525	-0.909	-1.679
24	IR 92546-17-6-4-4	64.758	-0.130	9.382**
25	IR 92546-33-3-1-1	62.583	0.936	4.487*
26	IR 92517-1-3-1-1	62.792	0.916	3.161
27	IR 92522-45-3-1-4	56.983	1.676*	19.350**
28	IR 92545-23-2-1-1	62.633	0.498	24.328**
29	IR 92545-24-3-1-1	64.808	0.727	-0.208
30	IR 92545-40-2-2-3	62.883	1.792*	-1.570
31	IR 92545-51-1-1-4	63.417	0.924	7.461**
32	IR 92546-33-4-2-3	61.950	0.737	1.814
33	IR 92516-8-3-3-4	63.508	2.310**	0.026
34	MTU 1010 (Check)	63.458	0.557	-1.136
35	IR 64 (Check)	63.608	1.476	-1.632
36	LALAT (Check)	62.833	1.466	-0.041
	Population Mean	**62.643**		

Figure 4.26: Representation of stability on the basis of regression coefficient and deviation from regression for milling recovery (%)
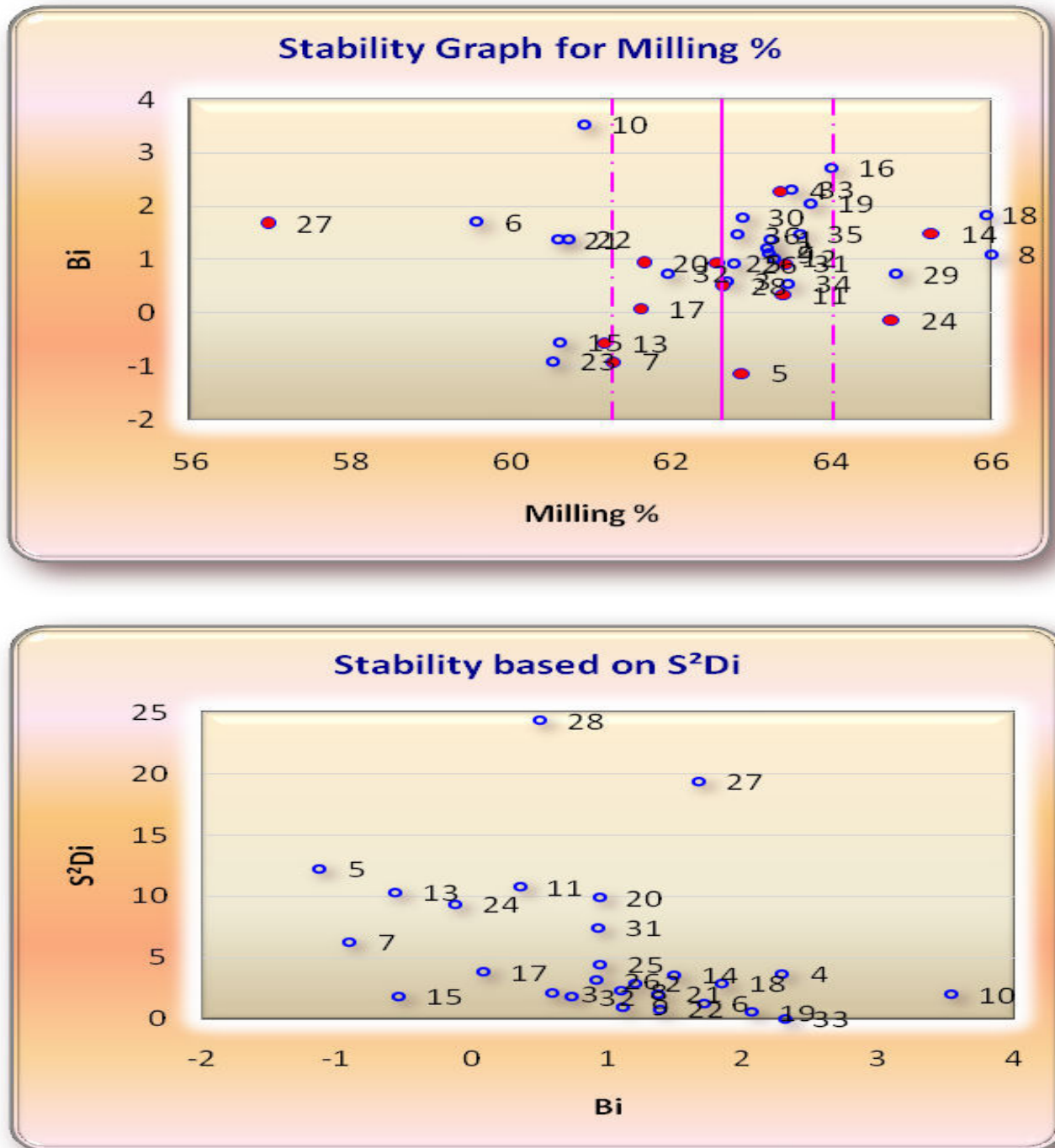
Table 4.40: Stability parameters for head rice recovery

| S.No.	Genotypes	Head rice recovery (%)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	44.883	0.741	1.580
2	CRR 724-1-B (IR 88889-44)	51.308	1.009	-1.366
3	RP-1-27-7-6-1-2-1	51.767	0.332	0.807
4	IR 94313:18-4-1-4-1-B	44.533	0.272	-0.355
5	IR 88287-383-1-B-B-1-1-B	42.908	1.187	-0.256
6	IR 94391-587-1-2-B	50.358	1.284	-0.547
7	IR 94314-20-2-1-B	47.833	1.023	-0.467
8	IR 93339:40-B-18-13-B-B-1	40.117	0.046	0.302
9	IR 92521-5-3-1-2	58.217	1.141	-0.156
10	IR 92521-7-5-1-1	56.017	2.213**	-0.306
11	IR 92521-23-6-1-3	55.917	2.160**	0.822
12	IR 92521-24-5-1-3	54.558	3.036**	5.083*
13	IR 92522-47-2-1-1	54.067	1.331	1.109
14	IR 92522-47-2-1-4	40.008	-0.712	-1.196
15	IR 92522-61-3-1-4	46.783	0.541	1.042
16	IR 92523-35-1-1-1	43.125	0.202	1.153
17	IR 92523-37-1-1-2	43.992	0.660	4.283*
18	IR 92527-6-2-1-2	43.125	0.267	7.326**
19	IR 92527-6-2-1-4	40.717	0.230	-0.666
20	IR 92545-53-4-1-3	41.883	0.003	-0.829
21	IR 92545-54-6-1-4	50.633	1.198	1.436
22	IR 92546-7-1-1-3	49.975	0.844	-1.041
23	IR 92546-17-6-4-3	48.742	1.072	-0.004
24	IR 92546-17-6-4-4	52.350	0.363	1.000
25	IR 92546-33-3-1-1	49.533	0.755	-1.047
26	IR 92517-1-3-1-1	44.475	1.614	-0.750
27	IR 92522-45-3-1-4	42.158	2.319**	2.651
28	IR 92545-23-2-1-1	55.800	2.203**	3.093*
29	IR 92545-24-3-1-1	47.667	0.261	4.979*
30	IR 92545-40-2-2-3	43.133	-0.207	0.961
31	IR 92545-51-1-1-4	49.200	2.135**	3.511*
32	IR 92546-33-4-2-3	42.317	1.573	-0.664
33	IR 92516-8-3-3-4	48.258	1.739*	0.914
34	MTU 1010 (Check)	52.475	0.985	1.995
35	IR 64 (Check)	55.083	1.862*	-1.074
36	LALAT (Check)	51.375	0.317	1.398
	Population Mean	**48.203**		

Figure 4.27: Representation of stability on the basis of regression coefficient and deviation from regression for head rice recovery (%)
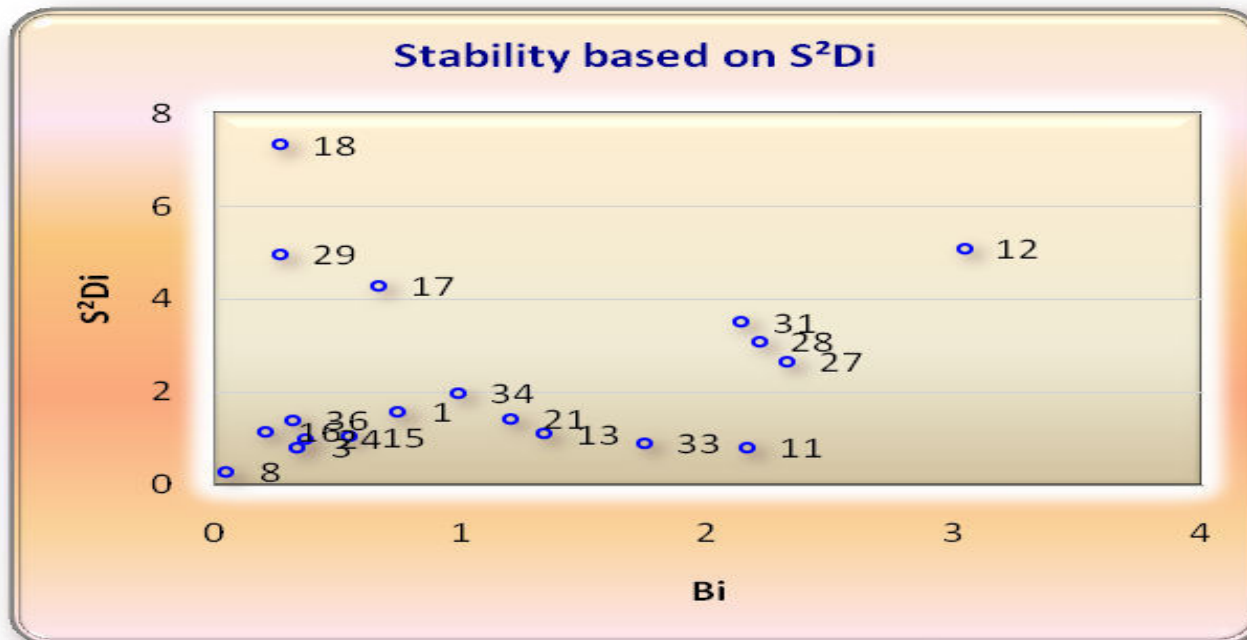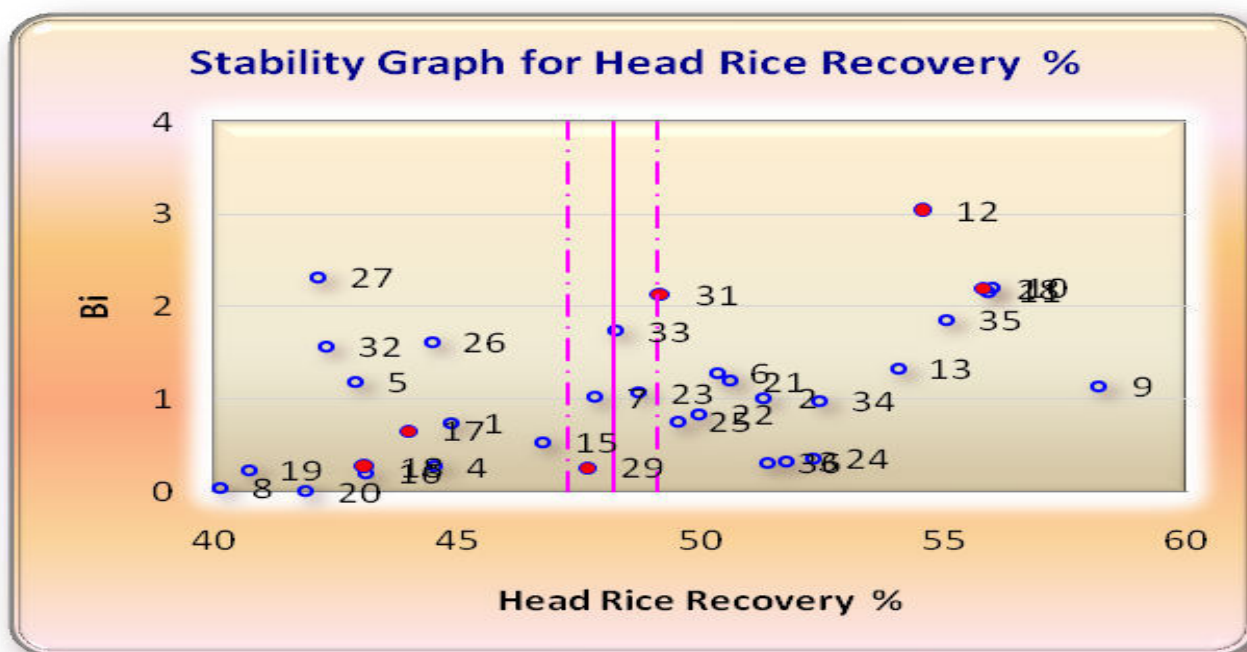
Table 4.41: Stability parameters for kernel length before cooking

| S.No.	Genotypes	Kernel length before cooking (mm)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	7.333	2.404**	0.089**
2	CRR 724-1-B (IR 88889-44)	6.958	0.800	0.024
3	RP-1-27-7-6-1-2-1	6.642	-0.620	0.043*
4	IR 94313:18-4-1-4-1-B	7.525	1.073	0.160**
5	IR 88287-383-1-B-B-1-1-B	7.200	0.758	0.063**
6	IR 94391-587-1-2-B	7.317	0.505	0.033*
7	IR 94314-20-2-1-B	7.358	0.924	-0.002
8	IR 93339:40-B-18-13-B-B-1	7.425	1.430	0.064**
9	IR 92521-5-3-1-2	7.033	0.828	0.244**
10	IR 92521-7-5-1-1	6.258	-0.760	0.023
11	IR 92521-23-6-1-3	6.217	0.665	0.025
12	IR 92521-24-5-1-3	6.292	0.987	0.002
13	IR 92522-47-2-1-1	6.617	1.887*	0.017
14	IR 92522-47-2-1-4	7.708	2.678**	0.041*
15	IR 92522-61-3-1-4	7.050	1.818*	0.013
16	IR 92523-35-1-1-1	7.167	3.357**	0.253**
17	IR 92523-37-1-1-2	7.008	3.362**	0.196**
18	IR 92527-6-2-1-2	7.375	1.657*	-0.009
19	IR 92527-6-2-1-4	7.500	2.155**	-0.012
20	IR 92545-53-4-1-3	7.633	1.307	0.010
21	IR 92545-54-6-1-4	6.525	0.725	0.294**
22	IR 92546-7-1-1-3	7.042	-1.581	0.023
23	IR 92546-17-6-4-3	7.517	0.721	0.076**
24	IR 92546-17-6-4-4	6.683	1.654*	0.007
25	IR 92546-33-3-1-1	6.750	-0.690	0.054**
26	IR 92517-1-3-1-1	7.283	0.211	0.000
27	IR 92522-45-3-1-4	6.792	1.333	-0.001
28	IR 92545-23-2-1-1	7.292	0.802	0.688**
29	IR 92545-24-3-1-1	6.825	1.858*	0.038*
30	IR 92545-40-2-2-3	7.175	0.062	0.052**
31	IR 92545-51-1-1-4	7.158	-1.164	0.049**
32	IR 92546-33-4-2-3	7.050	0.904	0.429**
33	IR 92516-8-3-3-4	6.958	0.819	0.122**
34	MTU 1010 (Check)	6.975	0.470	0.086**
35	IR 64 (Check)	7.017	0.952	0.011
36	LALAT (Check)	7.017	1.707*	0.042*
	Population Mean	**7.047**		

Figure 4.28: Representation of stability on the basis of regression coefficient and deviation from regression for kernel length before cooking
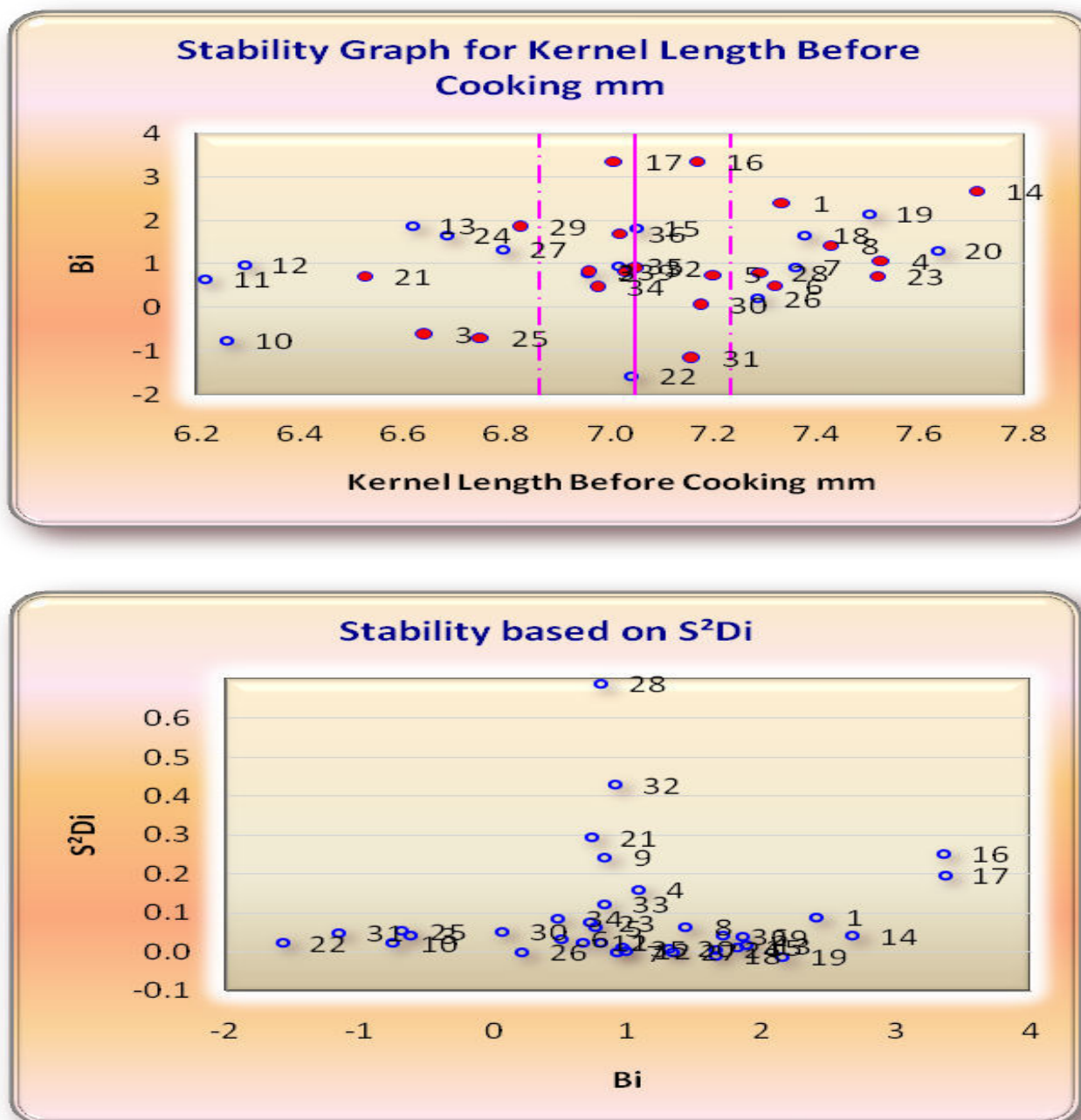
Table 4.42: Stability parameters for kernel breadth before cooking

| S.No.	Genotypes	Kernel breadth before cooking (mm)		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	2.100	3.422**	-0.003
2	CRR 724-1-B (IR 88889-44)	2.183	2.108**	-0.004
3	RP-1-27-7-6-1-2-1	2.075	0.969	0.000
4	IR 94313:18-4-1-4-1-B	2.108	2.368**	0.001
5	IR 88287-383-1-B-B-1-1-B	2.000	2.250**	-0.003
6	IR 94391-587-1-2-B	1.992	-1.498	0.015*
7	IR 94314-20-2-1-B	2.142	2.330**	0.021**
8	IR 93339:40-B-18-13-B-B-1	2.067	-0.435	0.019**
9	IR 92521-5-3-1-2	2.183	0.501	0.001
10	IR 92521-7-5-1-1	2.233	2.344**	0.001
11	IR 92521-23-6-1-3	2.108	-2.755**	-0.002
12	IR 92521-24-5-1-3	2.133	-1.626	0.003
13	IR 92522-47-2-1-1	2.092	1.942*	0.001
14	IR 92522-47-2-1-4	1.925	2.850**	0.007
15	IR 92522-61-3-1-4	2.183	1.768*	-0.001
16	IR 92523-35-1-1-1	2.083	-0.520	0.006
17	IR 92523-37-1-1-2	2.208	1.933*	0.010*
18	IR 92527-6-2-1-2	1.950	0.123	0.028**
19	IR 92527-6-2-1-4	1.942	2.028**	0.004
20	IR 92545-53-4-1-3	1.917	0.614	0.001
21	IR 92545-54-6-1-4	2.183	-1.314	-0.003
22	IR 92546-7-1-1-3	2.033	2.609**	-0.002
23	IR 92546-17-6-4-3	2.050	1.144	0.031**
24	IR 92546-17-6-4-4	2.033	1.494	0.033**
25	IR 92546-33-3-1-1	2.100	0.284	0.021**
26	IR 92517-1-3-1-1	2.092	0.581	0.006
27	IR 92522-45-3-1-4	2.117	2.391**	0.004
28	IR 92545-23-2-1-1	2.183	1.616	0.000
29	IR 92545-24-3-1-1	2.075	0.421	0.017*
30	IR 92545-40-2-2-3	2.183	2.410**	0.004
31	IR 92545-51-1-1-4	2.033	-1.645	0.027**
32	IR 92546-33-4-2-3	2.092	0.468	0.003
33	IR 92516-8-3-3-4	2.150	0.161	0.007
34	MTU 1010 (Check)	2.083	3.526**	-0.001
35	IR 64 (Check)	2.117	2.108**	-0.004
36	LALAT (Check)	2.158	-0.969	0.000
	Population Mean	**2.092**		

Figure 4.29: Representation of stability on the basis of regression coefficient and deviation from regression for kernel breadth before cooking
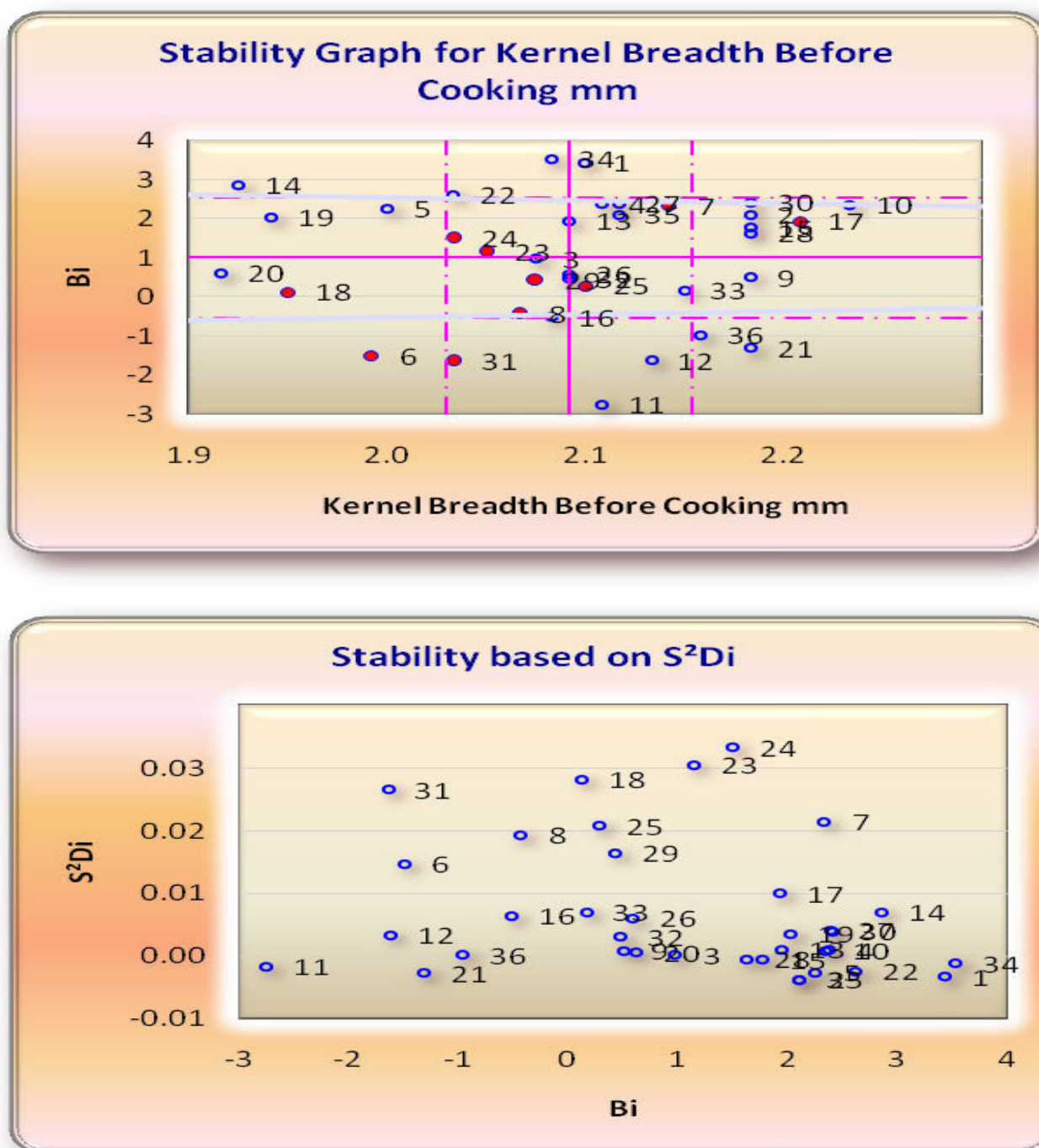
Table 4.43: Stability parameters for kernel L/B ratio before cooking

| S.No.	Genotypes	Kernel L/B ratio before cooking		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	3.503	3.616**	-0.003
2	CRR 724-1-B (IR 88889-44)	3.196	-0.600	-0.001
3	RP-1-27-7-6-1-2-1	3.214	3.791**	0.030
4	IR 94313:18-4-1-4-1-B	3.576	2.325**	0.005
5	IR 88287-383-1-B-B-1-1-B	3.615	4.144**	-0.003
6	IR 94391-587-1-2-B	3.693	-4.918**	0.044*
7	IR 94314-20-2-1-B	3.457	1.813*	0.055*
8	IR 93339:40-B-18-13-B-B-1	3.608	-0.370	0.035
9	IR 92521-5-3-1-2	3.227	-1.455	0.035
10	IR 92521-7-5-1-1	2.813	2.533**	0.041*
11	IR 92521-23-6-1-3	2.960	-2.408**	0.031
12	IR 92521-24-5-1-3	2.967	-4.544**	0.016
13	IR 92522-47-2-1-1	3.180	2.182**	-0.007
14	IR 92522-47-2-1-4	4.018	2.031**	0.005
15	IR 92522-61-3-1-4	3.236	1.763*	-0.014
16	IR 92523-35-1-1-1	3.457	-3.680**	0.124**
17	IR 92523-37-1-1-2	3.180	4.092**	0.019
18	IR 92527-6-2-1-2	3.814	7.680**	0.078**
19	IR 92527-6-2-1-4	3.877	4.684**	0.004
20	IR 92545-53-4-1-3	4.013	4.318**	0.018
21	IR 92545-54-6-1-4	2.995	1.483	0.021
22	IR 92546-7-1-1-3	3.485	2.746**	0.053*
23	IR 92546-17-6-4-3	3.684	2.611**	0.019
24	IR 92546-17-6-4-4	3.313	-0.315	0.116**
25	IR 92546-33-3-1-1	3.223	1.326	-0.001
26	IR 92517-1-3-1-1	3.493	-1.080	0.020
27	IR 92522-45-3-1-4	3.222	1.295	-0.001
28	IR 92545-23-2-1-1	3.350	3.962**	0.202**
29	IR 92545-24-3-1-1	3.303	1.172	0.029
30	IR 92545-40-2-2-3	3.301	-2.771**	0.040*
31	IR 92545-51-1-1-4	3.557	-7.027**	0.124**
32	IR 92546-33-4-2-3	3.386	7.075**	0.114**
33	IR 92516-8-3-3-4	3.244	-0.711	0.063*
34	MTU 1010 (Check)	3.363	3.783**	0.013
35	IR 64 (Check)	3.326	-0.662	-0.006
36	LALAT (Check)	3.263	-3.884**	0.035
	Population Mean	**3.392**		

Figure 4.30: Representation of stability on the basis of regression coefficient and deviation from regression for kernel L/B ratio before cooking
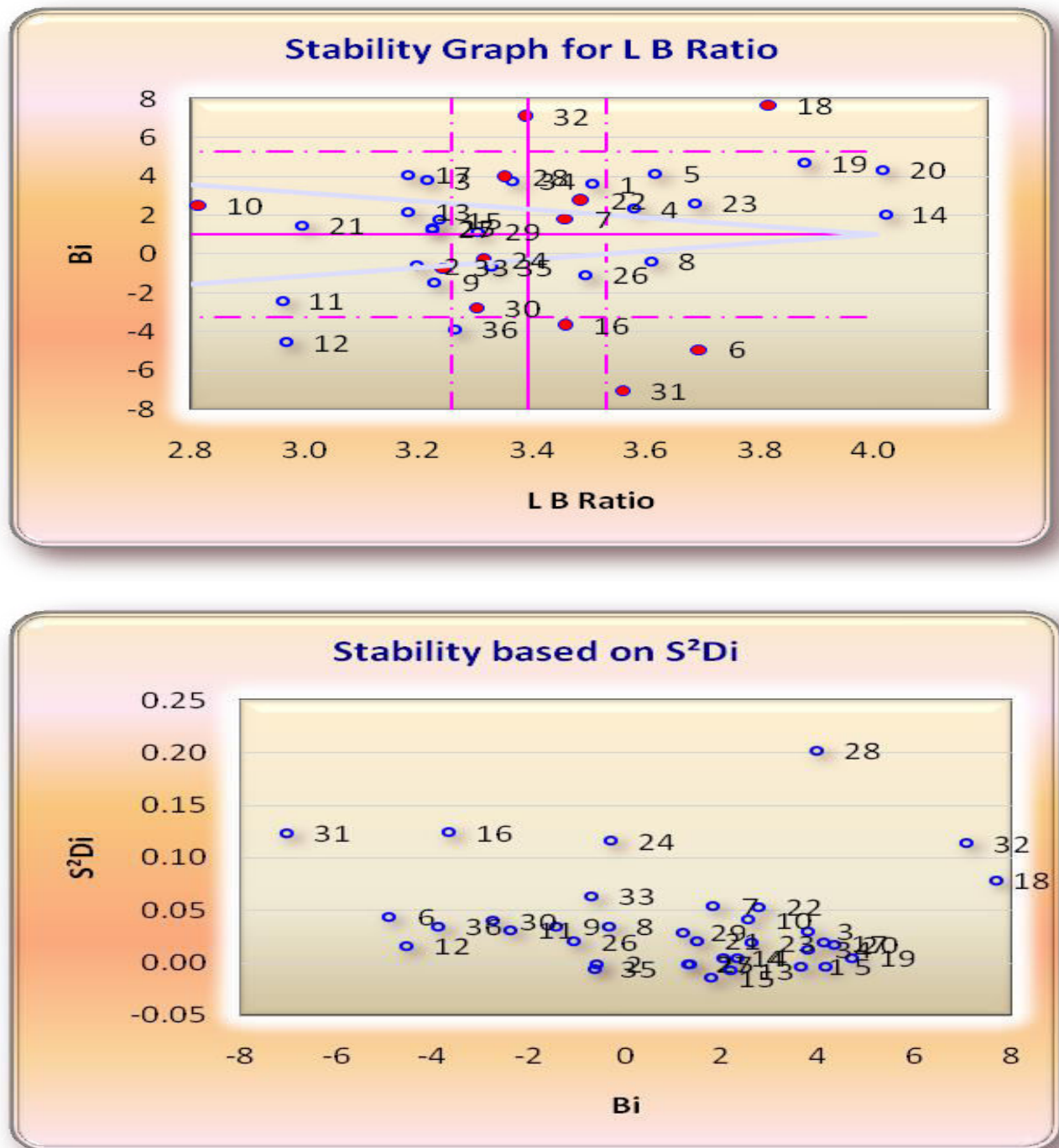
Table 4.44: Stability parameters for amylose content

| S.No.	Genotypes	Amylose content		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	24.156	0.738	1.517**
2	CRR 724-1-B (IR 88889-44)	23.326	0.804	2.125**
3	RP-1-27-7-6-1-2-1	21.718	0.562	0.911**
4	IR 94313:18-4-1-4-1-B	22.058	0.736	2.137**
5	IR 88287-383-1-B-B-1-1-B	22.718	1.300	4.804**
6	IR 94391-587-1-2-B	21.987	1.810*	3.772**
7	IR 94314-20-2-1-B	19.246	0.133	1.440**
8	IR 93339:40-B-18-13-B-B-1	21.989	1.407	3.125**
9	IR 92521-5-3-1-2	21.215	0.813	1.717**
10	IR 92521-7-5-1-1	20.894	0.543	0.081**
11	IR 92521-23-6-1-3	21.548	0.602	0.284**
12	IR 92521-24-5-1-3	21.563	0.620	0.353**
13	IR 92522-47-2-1-1	23.255	1.764*	2.156**
14	IR 92522-47-2-1-4	23.332	0.528	0.197**
15	IR 92522-61-3-1-4	22.182	2.485**	0.606**
16	IR 92523-35-1-1-1	21.438	-0.460	0.962**
17	IR 92523-37-1-1-2	20.834	0.901	0.318**
18	IR 92527-6-2-1-2	21.356	1.569	0.801**
19	IR 92527-6-2-1-4	22.615	0.540	0.091**
20	IR 92545-53-4-1-3	22.328	-0.172	1.455**
21	IR 92545-54-6-1-4	20.757	2.041**	0.177**
22	IR 92546-7-1-1-3	23.061	1.878*	2.617**
23	IR 92546-17-6-4-3	24.204	1.243	0.351**
24	IR 92546-17-6-4-4	22.702	1.431	1.481**
25	IR 92546-33-3-1-1	23.911	1.805*	0.260**
26	IR 92517-1-3-1-1	22.439	1.185	0.163**
27	IR 92522-45-3-1-4	23.716	1.776*	2.599**
28	IR 92545-23-2-1-1	21.144	0.823	0.713**
29	IR 92545-24-3-1-1	21.101	0.061	0.288**
30	IR 92545-40-2-2-3	21.342	0.206	0.114**
31	IR 92545-51-1-1-4	21.373	0.183	0.371**
32	IR 92546-33-4-2-3	21.618	0.879	0.015
33	IR 92516-8-3-3-4	20.327	2.258**	1.079**
34	MTU 1010 (Check)	22.082	0.719	0.047*
35	IR 64 (Check)	22.631	0.876	0.631**
36	LALAT (Check)	24.624	1.414	0.176**
	Population Mean	**22.133**		

Figure 4.31: Representation of stability on the basis of regression coefficient and deviation from regression for amylose content
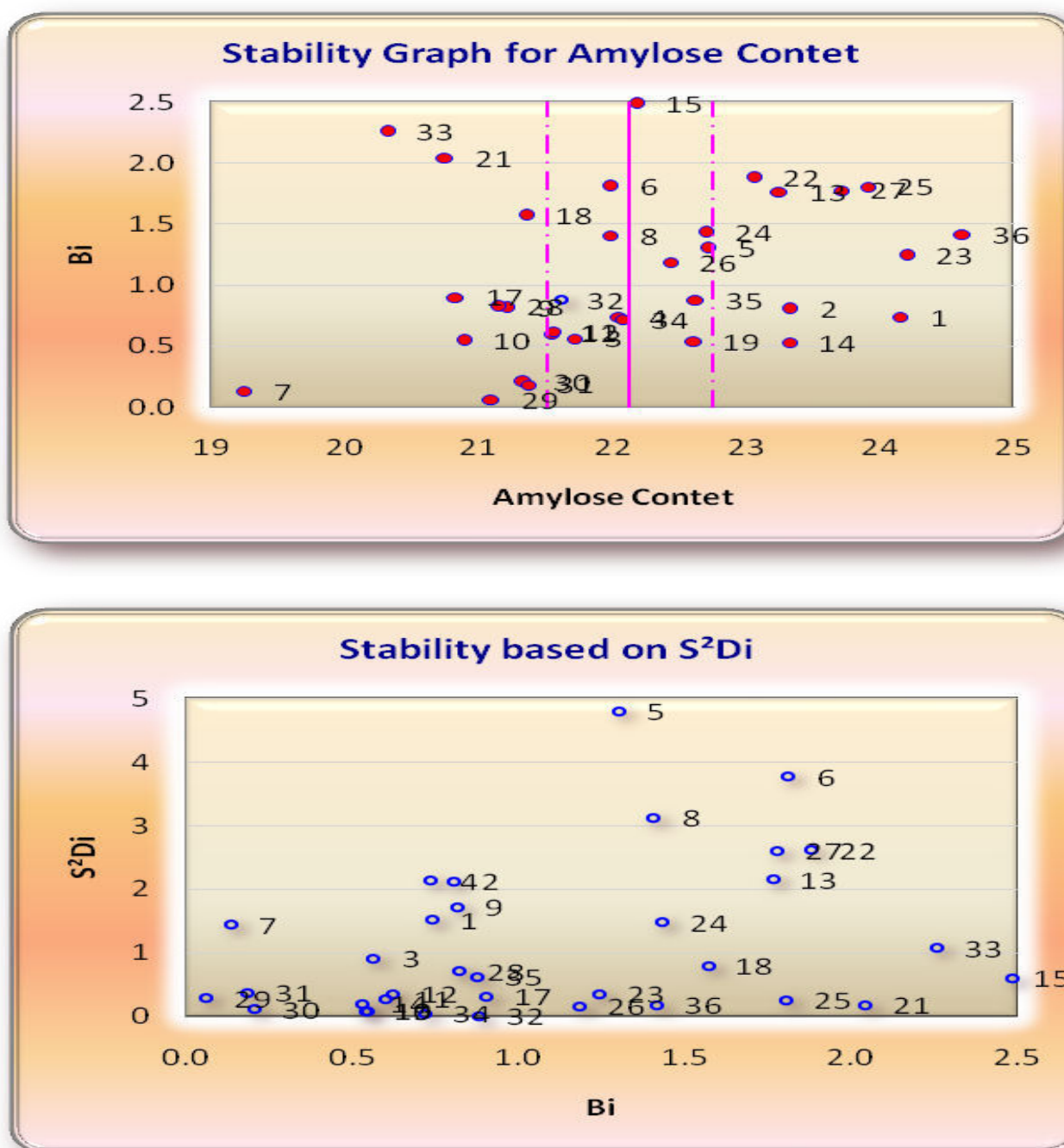
Table 4.45: Stability parameters for volume expansion ratio

| S.No.	Genotypes	Volume expansion ratio		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	3.333	1.560	0.001*
2	CRR 724-1-B (IR 88889-44)	3.387	1.175	0.002**
3	RP-1-27-7-6-1-2-1	3.422	0.413	0.002**
4	IR 94313:18-4-1-4-1-B	3.400	0.794	0.004**
5	IR 88287-383-1-B-B-1-1-B	3.367	0.839	0.000
6	IR 94391-587-1-2-B	3.358	0.988	0.001**
7	IR 94314-20-2-1-B	3.383	0.755	0.001
8	IR 93339:40-B-18-13-B-B-1	3.359	1.232	0.000
9	IR 92521-5-3-1-2	3.452	1.079	0.001
10	IR 92521-7-5-1-1	3.428	0.720	0.001
11	IR 92521-23-6-1-3	3.387	1.117	0.001
12	IR 92521-24-5-1-3	3.388	0.626	0.000
13	IR 92522-47-2-1-1	3.397	1.188	0.003**
14	IR 92522-47-2-1-4	3.417	1.102	0.000
15	IR 92522-61-3-1-4	3.388	1.762*	0.001*
16	IR 92523-35-1-1-1	3.408	1.505	0.000
17	IR 92523-37-1-1-2	3.422	1.314	0.003**
18	IR 92527-6-2-1-2	3.424	1.604	0.003**
19	IR 92527-6-2-1-4	3.374	0.568	0.006**
20	IR 92545-53-4-1-3	3.418	1.150	0.000
21	IR 92545-54-6-1-4	3.414	0.864	0.008**
22	IR 92546-7-1-1-3	3.320	1.328	0.001
23	IR 92546-17-6-4-3	3.321	1.328	0.001*
24	IR 92546-17-6-4-4	3.357	1.361	0.000
25	IR 92546-33-3-1-1	3.366	1.106	0.000
26	IR 92517-1-3-1-1	3.343	1.317	0.000
27	IR 92522-45-3-1-4	3.352	1.112	0.000
28	IR 92545-23-2-1-1	3.381	1.031	0.007**
29	IR 92545-24-3-1-1	3.383	0.741	0.005**
30	IR 92545-40-2-2-3	3.322	1.182	0.001
31	IR 92545-51-1-1-4	3.373	1.000	0.003**
32	IR 92546-33-4-2-3	3.336	0.641	0.004**
33	IR 92516-8-3-3-4	3.375	0.567	0.001
34	MTU 1010 (Check)	3.322	0.178	0.000
35	IR 64 (Check)	3.414	0.450	0.000
36	LALAT (Check)	3.383	0.307	0.000
	Population Mean	**3.380**		

Figure 4.32: Representation of stability on the basis of regression coefficient and deviation from regression for volume expansion ratio
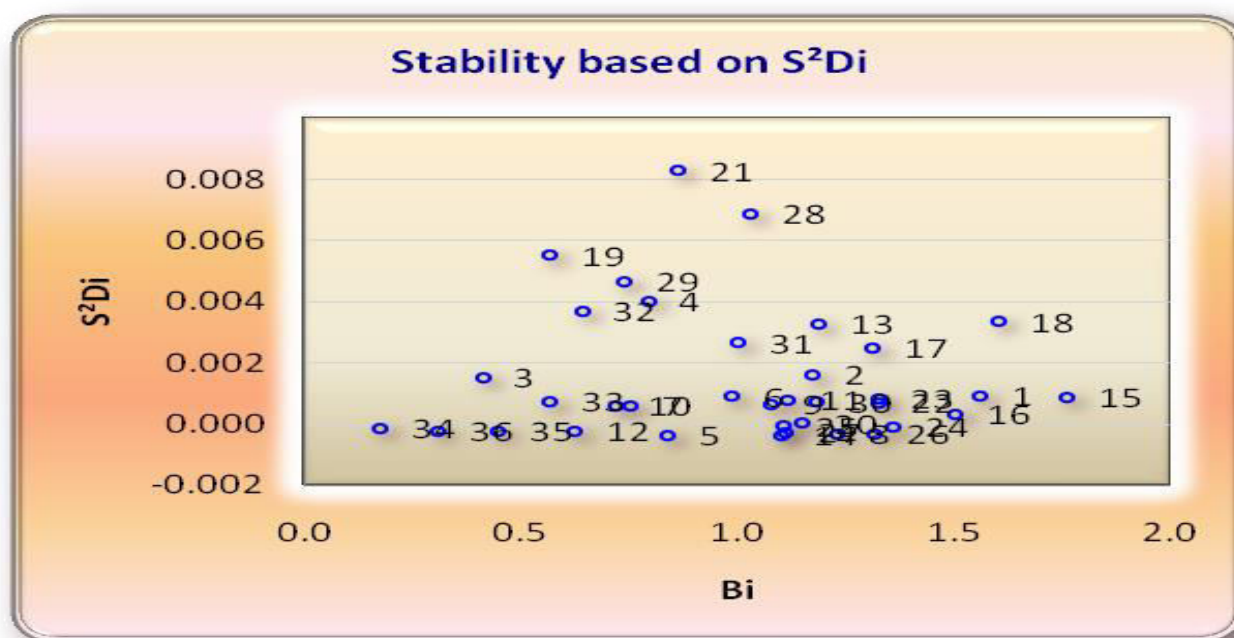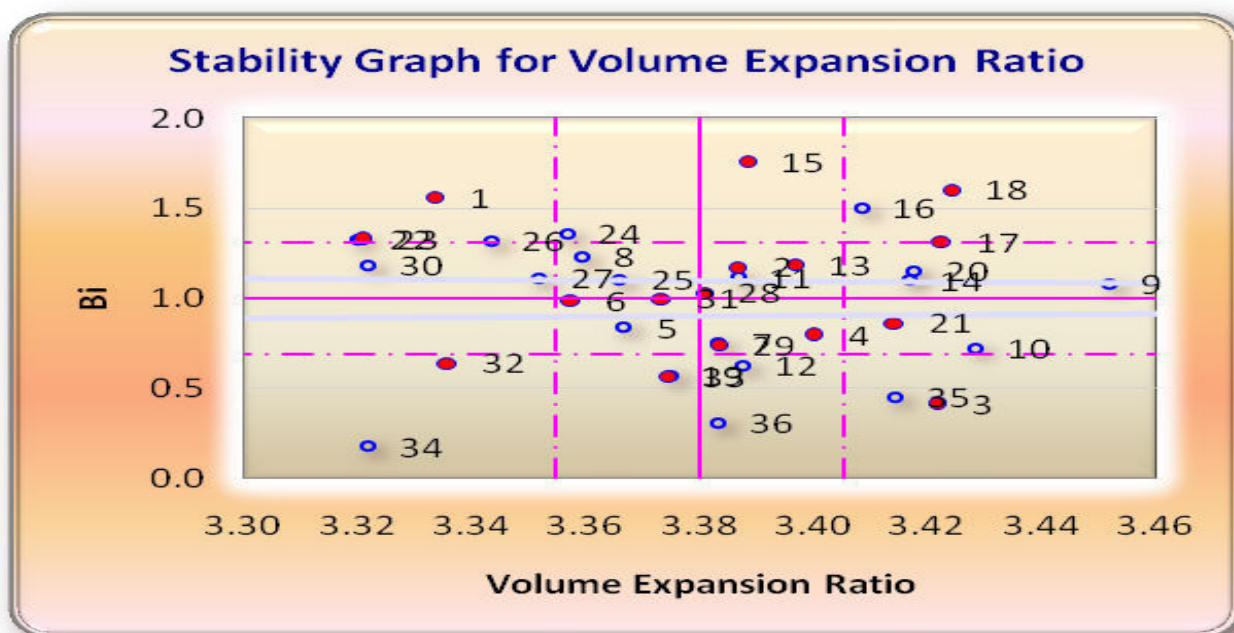
Table 4.46: Stability parameters for kernel elongation ratio

| S.No.	Genotypes	Kernel elongation ratio		
		m	bi	s²di
1	CRR 719-1-B (IR 88903-34)	1.611	1.273	0.000**
2	CRR 724-1-B (IR 88889-44)	1.615	1.602	0.000**
3	RP-1-27-7-6-1-2-1	1.645	2.132**	0.000**
4	IR 94313:18-4-1-4-1-B	1.807	1.642	0.000
5	IR 88287-383-1-B-B-1-1-B	1.729	1.494	0.000**
6	IR 94391-587-1-2-B	1.646	1.711*	0.000**
7	IR 94314-20-2-1-B	1.714	0.042	0.001**
8	IR 93339:40-B-18-13-B-B-1	1.800	-0.365	0.000**
9	IR 92521-5-3-1-2	1.524	1.304	0.000**
10	IR 92521-7-5-1-1	1.526	1.480	0.000**
11	IR 92521-23-6-1-3	1.541	1.404	0.000*
12	IR 92521-24-5-1-3	1.543	0.063	0.000**
13	IR 92522-47-2-1-1	1.706	1.169	0.000
14	IR 92522-47-2-1-4	1.697	1.281	0.000**
15	IR 92522-61-3-1-4	1.709	0.636	0.000**
16	IR 92523-35-1-1-1	1.775	-0.620	0.000
17	IR 92523-37-1-1-2	1.756	1.627	0.000**
18	IR 92527-6-2-1-2	1.766	2.057**	0.000*
19	IR 92527-6-2-1-4	1.756	0.013	0.000**
20	IR 92545-53-4-1-3	1.748	0.621	0.000**
21	IR 92545-54-6-1-4	1.654	2.427**	0.000**
22	IR 92546-7-1-1-3	1.674	0.413	0.001**
23	IR 92546-17-6-4-3	1.672	1.037	0.000**
24	IR 92546-17-6-4-4	1.652	1.316	0.000**
25	IR 92546-33-3-1-1	1.647	0.726	0.000*
26	IR 92517-1-3-1-1	1.748	-0.377	0.000**
27	IR 92522-45-3-1-4	1.586	0.251	0.000**
28	IR 92545-23-2-1-1	1.679	2.209**	0.001**
29	IR 92545-24-3-1-1	1.677	1.874*	0.001**
30	IR 92545-40-2-2-3	1.701	-0.340	0.000**
31	IR 92545-51-1-1-4	1.687	1.056	0.001**
32	IR 92546-33-4-2-3	1.635	1.446	0.000**
33	IR 92516-8-3-3-4	1.655	0.951	0.000**
34	MTU 1010 (Check)	1.736	0.769	0.000
35	IR 64 (Check)	1.617	1.340	0.000**
36	LALAT (Check)	1.646	0.332	0.000**
	Population Mean	**1.674**		

Figure 4.33: Representation of stability on the basis of regression coefficient and deviation from regression for kernel elongation ratio
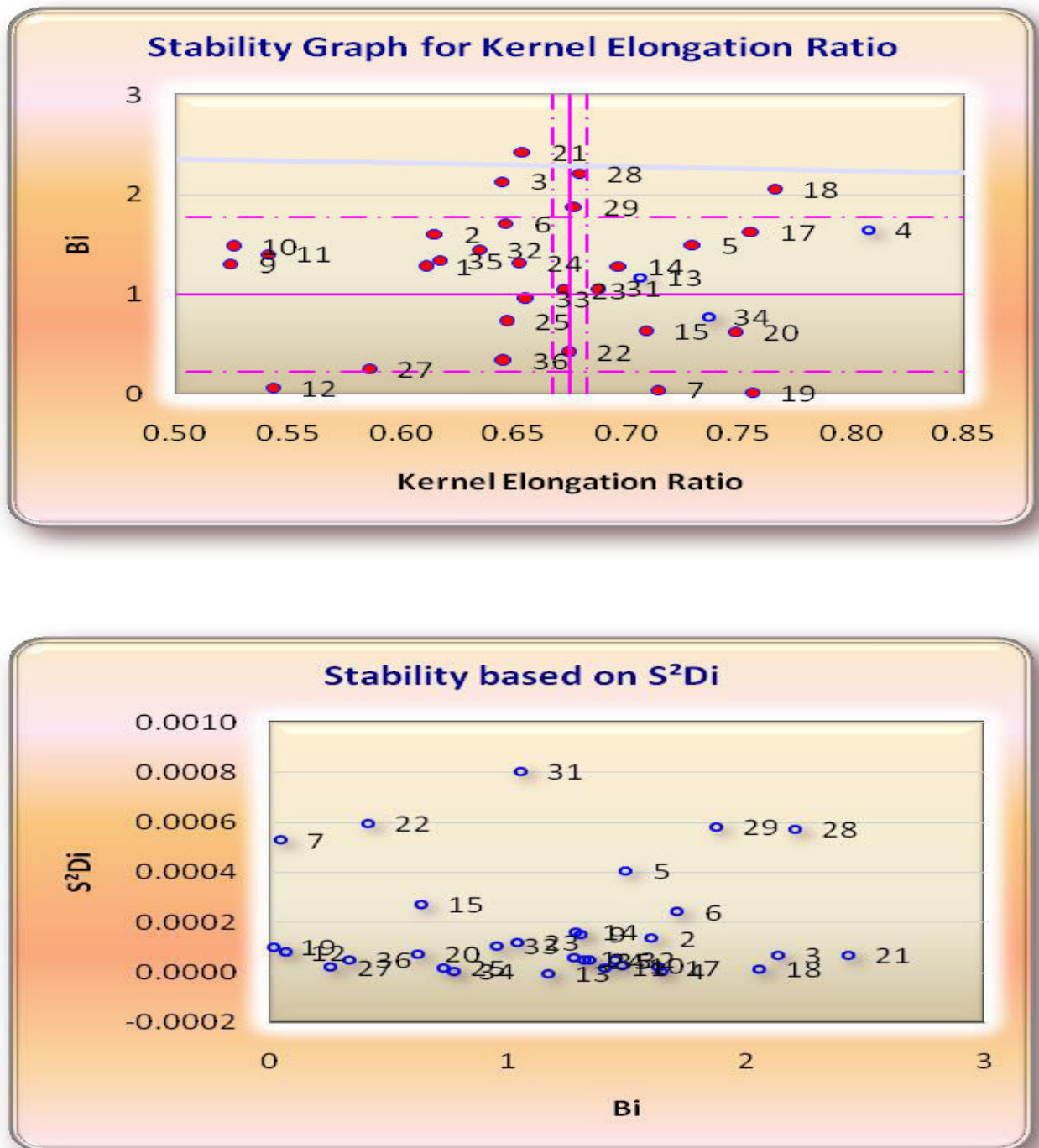
CHAPTER – 5
DISCUSSION

Discussion:

Rice (*Oryza sativa* L.) is one of the major cereal crop and staple food crop for 2/3rd of the world population, particularly in South East Asia. India is dominating country in rice production after china with different ecosystem. The world population is expected to reach 8 billion by 2030 and production of rice must increase by 50% in order to meet the growing demand or in other word; to feed the world population (Khus and Brar 2002). It is an excellent entry point to mobilize national as well as international resources to achieve specific goals. Rice is a cultural identity along with global unity, therefore, during the international year of rice (2004); a slogan "Rice is Life" came under the consideration (Anonymous 1, 2004). In present experiment, trails were conducted under medium irrigated land which is the flood prone region surrounded by the Ganga basin. Average rain fall in this sub-tropical region is 1200 mm that's mostly precipitated during middle of June to middle of October. Overall climate of this region suited to rice cultivation along with average productivity medium to high. Among abiotic stress, drought stress is a major constraint of rice cultivation, so that we need to varieties perform well in irrigated as well as drought condition. As a rice breeder, we need high yielding lines along with better quality which may exhibit the narrow range of fluctuation and to get rice lines having more buffering capacity. Thirty six elite advance rice lines from STRASA (Stress Tolerant Rice for Africa and South Asia) project were taken for the present investigation. These materials were grown under four environments including two year (kharif 2014 and kharif 2015) and two conditions (Control and Reproductive stage drought Stress). Twelve quantitative and nine qualitative traits were studied under different environments to identify stable lines for good yield with quality.

Discussions on the experimental findings are as under following sub - heads;

5.1 Analysis of variance (ANOVA) for different characters

5.2 Mean performance of elite advance rice lines for different yield and quality characters

5.3 Estimates of components of variances for different characters

5.4 Estimates of heritability (bs) and genetic advance for different characters

5.5 Estimates of correlation coefficient among different characters

5.6 Estimates of path coefficient analysis for different characters

5.7 Genetic divergence analysis among rice lines (D^2 statistics with Tocher's Method)

5.8 Molecular diversity analysis among thirty six elite rice lines using SSR markers

5.9 Phenotypic stability analysis (Eberhart and Russell model, 1966) of thirty six elite rice lines for twenty one characters

5.1 Analysis of variance (ANOVA) for different characters:

Analysis of variance separates the total variation into different types of components and estimates entire component of variance. In present experiment, ANOVA was carried out with three replications in randomized complete block design (RCBD). Under study, maximum characters were highly significant except some quality traits which revealed that the significant differences for different traits between or within elite advance rice lines. However the quality traits and some other data were found non-significant due to minimum differences between replications and among lines. Pooled ANOVA shown that the elite rice lines were posses' inherent genetic variances among themselves with respect to the traits studied. This indicates ample scope of improvement and selection in rice lines for different yield and quality attributing traits.

Similar findings of analysis of variance for yield and quality traits was reported by earlier workers like Singh *et al.* (2012), Jayasudha and Sharma (2010), Devi *et al.* (2017), Singh *et al.* (2014), Singh *et al.* (2013), Neha and Lal (2012), Rai *et al.* (2014) and Sahu *et al.* (2017).

5.2 Mean performance of elite advance rice lines for different yield and quality characters:

The better performing genotypes among the set of thirty six elite advance rice lines may be accredited to the possible gathering of favorable genes which is the reservoir of genetic variability for different yield and quality attributing traits of indica rice resulting naturally synthesized variants. Mean performance of the different yield along with quality traits will be discussed below;

5.2.1 Days to 50% flowering:

Rice lines CRR 724-1-B (IR 88889-44) followed by IR 94313:18-4-1-4-1-B, IR 92545-53-4-1-3 and CRR 719-1-B (IR 88903-34) found earliest days to 50% flowering in comparison to grand mean and all three check MTU 1010, IR 64 and Lalat. Breeder always needed earliest days to 50% flowering, therefore these lines (above mentioned)

can be selected as earliest days to 50% flowering lines for further rice improvement out of thirty six rice lines.

5.2.2 Plant height:

Among elite rice lines, lines IR 92527-6-2-1-4 followed by IR 92546-17-6-4-4 and IR 94313:18-4-1-4-1-B identified as better genotypes in case of semi-dwarf nature with lowest plant height in comparison to grand mean and out of all three checks namely; MTU 1010, IR 64 and Lalat. Lowest plant height is desirable in rice due to lodging stress; therefore these three lines above mentioned may be selected for any breeding programme out of thirty six rice lines.

5.2.3 Days to maturity:

Genotype IR 94313:18-4-1-4-1-B followed by IR 92521-24-5-1-3 observed best genotypes with earliest days to maturity in comparison to grand mean and all three checks MTU 1010, IR 64 and Lalat. Generally minimum days are desirable to days to physiological maturity due to different agronomic causes, therefore both genotypes (above mentioned) having earliest days to maturity can be beneficial for any breeding activities.

5.2.4 Number of tillers per plant:

Among advance lines, IR 88287-383-1-B-B-1-1-B found best line in comparison to grand mean and two checks IR 64 & Lalat followed by RP-1-27-7-6-1-2-1 observed better or at par than grand mean and checks IR 64 and Lalat. IR 92522-61-3-1-4 identified good performing line with maximum number of tillers per plant than single check IR 64. Maximum number of tillers per plant is essential or desirable characters in rice then we can prefer above mentioned lines according to their mean performance for further improvement.

5.2.5 Number of productive tillers per meter square:

Elite rice lines, IR 92546-7-1-1-3 followed by IR 92546-33-3-1-1 identified as better lines with highest number of productive tillers per meter square in comparison to grand mean and out of all three checks. Maximum number of ear bearing tillers in per meter square area is essential for quantum jump in case of rice production, therefore; out of thirty six lines, above mentioned both lines is good to selection for concerned trait.

5.2.6 Panicle length:

   Lines IR 93339:40-B-18-13-B-B-1 followed by IR 92545-40-2-2-3 and IR 92522-61-3-1-4 found best lines with maximum panicle length in comparison to grand mean and two checks out of three; MTU 1010 & IR 64. Maximum length of panicles is a desirable feature of yield attributing traits, therefore selection of these lines (IR 93339:40-B-18-13-B-B-1, IR 92545-40-2-2-3 and IR 92522-61-3-1-4) is effective for such trait out of set of thirty six lines.

5.2.7 Number of spikelets per panicle:

   Rice genotypes, IR 92521-7-5-1-1 followed by IR 92521-24-5-1-3 and IR 92521-5-3-1-2 observed as better genotypes with maximum number of spikelets per panicle in comparison to grand mean and all three checks namely; MTU 1010, IR 64 and Lalat. Number of spikelets per panicle directly gives more contribution in total production of grain yield, that's why selection of above mentioned genotypes is advantageous to enhance grain yield.

5.2.8 Grain yield per plant:

   Among thirty advance rice lines, IR 94314-20-2-1-B followed by IR 92521-24-5-1-3 and IR 92523-37-1-1-2 identified as better performing lines for highest grain yields per plant in comparison to grand mean and different checks MTU 1010, IR 64 and Lalat. Grain yield per plant is a central key trait among all yield attributing traits, therefore all three lines out of thirty six are best lines to start any breeding programme.

5.2.9 Biological yield per plant:

   Genotype IR 92527-6-2-1-4 followed by IR 94314-20-2-1-B and IR 92521-24-5-1-3 found best genotypes with highest biological yields per plant in comparison to grand mean and checks MTU 1010, IR 64 and Lalat. This trait is also a major yield attributing trait to enhance grain as well as straw yield, so that IR 92527-6-2-1-4, IR 94314-20-2-1-B, IR 92521-24-5-1-3 lines are good for selection for such trait.

5.2.10 Harvest index:

   Rice lines IR 92546-17-6-4-4 followed by IR 92522-45-3-1-4 and IR 92545-23-2-1-1 identified as best lines along with maximum harvest index in comparison to grand mean and all the checks namely; MTU 1010, IR 64 and Lalat. Harvest index (%) play a crucial

role in the selection of specific lines, therefore all three lines which is mentioned above is good for effective selection out of thirty six lines.

5.2.11 Test weight (1000 grain weight):

Among thirty six elite rice lines, IR 92522-45-3-1-4 followed by IR 92545-40-2-2-3 and CRR 724-1-B (IR 88889-44) found best genotypes with maximum test weight in comparison to grand mean of the set of lines and all three checks MTU 1010, IR 64 and Lalat. Test weight is a one of the major selection criteria to initiate any breeding programme with any types of genetic stocks of rice, therefore above mentioned lines is good for selection for such trait.

5.2.12 Hulling recovery (%):

Rice genotypes IR 92545-40-2-2-3 followed by IR 92545-51-1-1-4 and IR 92523-35-1-1-1 found superior genotypes with maximum hulling recovery in comparison to grand mean and all three checks namely; MTU 1010, IR 64 and Lalat. This trait is initially important quality attributing trait for selection, that's why selection of these lines for such quality trait is profitable.

5.2.13 Milling recovery (%):

Among thirty six indica rice lines, IR 93339:40-B-18-13-B-B-1 followed by IR 92527-6-2-1-2 and IR 92522-47-2-1-4 identified as best lines with maximum milling recovery in comparison to grand mean of the trait and checks MTU 1010, IR 64 and Lalat. Maximum recovery of polished rice is beneficial quality trait in rice; therefore all these three lines have better milling recovery and may be select for further improvement of this trait.

5.2.14 Head rice recovery (%):

Rice lines IR 92521-5-3-1-2 followed by IR 92521-7-5-1-1 and IR 92521-23-6-1-3 found better lines along with maximum head rice recovery than grand mean of the trait and checks (MTU 1010, IR 64 and Lalat) out of thirty six lines. HRR is one of the major quality criteria when we go for the selection of lines having better quality, therefore these lines fulfilled the criteria of such trait with good head rice recovery.

5.2.15 Kernel length before cooking:

Rice genotype IR 92522-47-2-1-4 followed by IR 92545-53-4-1-3 and IR 94313:18-4-1-4-1-B identified as best genotypes with largest kernel length before cooking than

grand mean and checks. Longest or largest kernel length is a desirable feature of quality rice, that's why the identified lines out of thirty six lines, can be select for this trait.

5.2.16 Kernel breadth before cooking:

Among advance lines, IR 92521-7-5-1-1 followed by IR 92523-37-1-1-2 found super lines with maximum kernel breadth before cooking than grand mean and checks namely; MTU 1010, IR 64 and Lalat. Kernel breadth before cooking is a one of the quality trait and average kernel breadth is good for this trait, therefore above mentioned both the lines is desirable for the selection of such character.

5.2.17 Kernel L/B ratio before cooking:

Rice lines IR 92522-47-2-1-4 followed by IR 92545-53-4-1-3 and IR 92527-6-2-1-4 found better lines with highest kernel L/B ratio before cooking in comparison to grand mean of the character and all three checks namely; MTU 1010, IR 64 and Lalat out of the set of thirty six lines. Kernel L/B ratio before cooking is also a major criteria in the judgment of rice quality for selection, therefore these lines may be select for their further activities.

5.2.18 Amylose content:

Genotype IR 92546-17-6-4-3 followed by CRR 719-1-B (IR 88903-34) and IR 92546-33-3-1-1 identified as best genotypes with highest amylose content (21-25 good for cooking quality) than grand mean and checks. All three genotypes (Above mentioned) had intermediate or perfect amylose which is good for cooking quality, that's why selection of such lines can be advantageous for this quality character.

5.2.19 Volume expansion ratio:

Elite rice lines IR 92521-5-3-1-2 and IR 92521-7-5-1-1 found better lines with maximum volume expansion ratio out of thirty six lines in comparison to grand mean of the trait and checks namely; MTU 1010, IR 64 and Lalat. Both the lines can be go for selection because these lines have perfect VER according to current need for this trait.

5.2.20 Kernel elongation ratio:

Among thirty six advance lines of rice, IR 94313:18-4-1-4-1-B followed by IR 93339:40-B-18-13-B-B-1 and IR 92523-35-1-1-1 observed superior lines with maximum kernel elongation ratio than grand mean and cheks. KER is a one of the important eating

quality traits, so we can select all three lines (Above mentioned) for such trait having better kernel elongation.

5.2.21 **Grain yield kilogram per hectare:**

Genotype IR 92527-6-2-1-2 followed by IR 92527-6-2-1-4 and IR 92546-17-6-4-3 found best genotypes with maximum grain yield kilogram per hectare out of the set of thirty six advance lines in comparison to grand mean of this trait and all three checks MTU 1010, IR 64 and Lalat. This trait is also a central point among yield attributing characters. Maximum grain yield per plant is a most desirable feature of any breeding programme, hence high yielding lines as mentioned above can be used in future rice breeding activities to enhance production easily.

Similar results for mean performances of different traits using different sets of genotypes were also obtained by Subudhi and Dikshit (2009), Konate *et al.* (2016), Tandekar and Koshta (2014), Vanaja and Babu (2006), Toshimenla and Changkija (2013) and Sarma *et al*. (2015).

5.3 Estimates of components of variances for different characters:

The amount of total variation of the population is calculated and expressed as the variance, if values are articulated as deviation from its population mean then variance is just the mean of the squared values. ANOVA permits the estimates of genotypic and phenotypic coefficient of variation (Burton 1952). The genotypic and phenotypic coefficient of variance value of 10 or 10-20 or above 20 is considered as low, moderate and high GCV and PCV subsequently (Sivasubramanian and Madhavamenon, 1973). Different types of variances and coefficient of variances under study are discussed below.

5.3.1 **Phenotypic and genotypic variances:**

In present investigation, phenotypic variances was higher than the genotypic variances for all the yield along with quality attributing traits, hence both the variances (Genotypic and Phenotypic) are sufficiently significant to study the interrelationship among the yield and quality traits. Less difference in the estimate of both the variances with higher genotypic value in comparison to environmental variances for all the traits revealed that the variability present among the advance rice lines were mainly due genetic cause. Some yield attributing traits namely; number of spikelets per panicle, biological yield per plant, test weight along with quality traits namely; head rice

recovery, kernel length before cooking, L/B ratio, amylose content, volume expansion ratio and kernel elongation ratio had less differences in both the variances in comparison to other traits, so variability for these traits are heritable and minimum influence of the environment than other traits. Genotypic estimates of genetic variability being more advantageous in the amount of role of the genotypes to the expression of a specific trait and also give valuable hint to compare variability. Selection of these traits (Above mentioned) having less environmental influence is valuable for rice breeding activities.

Similar findings for genotypic and phenotypic variance of some traits were reported by earlier researchers Karim *et al.* (2016), Neha and Lal (2012), Bitew (2016) and Konate *et al.* (2016).

5.3.2 Phenotypic and genotypic coefficient of variance:

The genetic coefficient of variability is an important and valuable parameter to calculate the range and genetic variability for a particular trait. Genetic coefficient of variability also grants a mean for the comparison of genetic variability for different yield and quality attributing traits. Under study, phenotypic coefficient of variance also higher in magnitude than genotypic coefficient of variance for all the yield and quality characters shows that the environmental influence on the manifestation of these characters. There was better correspondence between both the coefficients of variance for different traits studied. According to values of the present investigation, some traits had less or more differences between genotypic and phenotypic coefficients of variance which revealed that the traits had less or more environmental influence on the expression of phenotype of the particular trait due to either additive or non additive gene action. Moderate values (10-20) of GCV observed for characters namely; number of spikelets per panicle, head rice recovery and kernel elongation ratio while in case of PCV some traits posses moderate values viz; number of tillers per plant, number of productive tillers per meter square, number of spikelets per panicle, grain yield per plant, biological yield per plant, harvest index, head rice recovery, L/B ratio, kernel elongation ratio and grain yield kilogram per hectare, therefore; selection for these traits may be ambiguous if we adopted for its improvement. The estimates of genotypic and phenotypic coefficient of variance were low (<10) for some traits, that's why selection for those traits offers very little scope for its genetic enhancement.

This finding of genotypic and phenotypic coefficient of variance for some traits is accordance with the findings of Ahmad *et al.* (2010), Singh *et al.* (2014), Veeresha *et al.* (2014), Devi *et. al.* (2017), Savitha and Kumari (2016) and Kachanur *et al.* (2009).

5.4 Estimates of heritability (bs) and genetic advance for different characters:

Heritability specify the fraction of the total genetic variability and helpful in selection of elite lines from the source population due to genetic cause. Heritability along with genetic advance as per cent of mean gives information to get genetic gain under selection. Heritability values <30, 30-60 and >60 shows low, moderate and high heritability subsequently while in case of genetic advance as per cent of mean <10, 10-20 and >20 reveals low, moderate and high genetic advance as per cent of mean subsequently. Selection of elite lines always may be effective when either heritability along with genetic advance as per cent of mean both will be high or at least genetic advance will be high. Heritability plays a significant role in deciding the stability and approach for the selection of a particular trait. The heritability in permutation with intensity of selection and quantity of genetic variability present in the source population influences the genetic gain to be obtained from the selection. Heritability and genetic advance under study will be discussed below.

5.4.1 Heritability (broad sense):

In current experiment, high heritability values of the characters namely; number of spikelets per panicle, biological yield per plant, test weight (1000 grain weight), head rice recovery and kernel elongation ratio revealed that the environmental influence is less in the expression of these traits and improvement of these traits could be possible through simple selection method. High heritability also indicated that the main role of additive gene action in the inheritance of these characters. Moderate values of heritability for some traits *viz;* number of productive tillers per meter square, kernel length before cooking, L/B ratio, amylose content and grain yield kilogram per hectare can be effective when genetic advance as per cent of the mean will be high because heritability alone does not show any proposal about the quantity of genetic progress for the selection of best lines from the source population.

Similar findings for heritability (bs) of different yield attributing traits along with quality reported by Mini and Mohanan (2009), Sahu *et al.* (2017), Mohanty *et al.* (2012) and Singh *et al.* (2014).

5.4.2 Genetic advance and genetic advance as per cent of mean (Genetic gain):

Higher genetic advance under study, observed for the traits namely number of productive tillers per meter square, number of spikelets per panicle and grain yield kilogram per hectare which helps in the prediction of genetic gain that could be obtained in further generations, .if appropriate selection is made for improving the specific trait under consideration.

Approximately same results of genetic advance for some traits reported by Babu *et. al.* (2012), Naha and Lal (2012), Vanisree *et. al.* (2013), Mohanty *et al.* (2012) and Konate *et al.* (2016).

Due to additive genetic effect, higher genetic advance as per cent of mean observed for the traits *viz;* number of spikelets per panicle, head rice recovery and kernel elongation ratio, hence selection would be effective for those traits and lower heritability is doesn't matter in this case.

Similar findings of genetic advance as % of mean for different some traits observed by Singh *et al.* (2014), Abarshahr *et al.* (2011), Sahu *et al.* (2017), Singh *et al.* (2012) and Savitha and Kumari (2016).

5.4.3 Heritability along with genetic advance as % of mean (Genetic gain):

Under study, number of spikelets per panicle, head rice recovery and kernel elongation ratio had higher heritability coupled with higher estimate of genetic advance as per cent of mean which reveals the preponderance of additive gene action for such traits and these traits could be improved through direct selection because genotypic coefficient of variance is also sufficiently high for these traits. High heritability or low heritability being exhibited was due to favourable or unfavourable influence of the environment rather than rice genotypes. High heritability or moderate heritability along with moderate genetic advance as per cent of mean observed for the traits namely; number of tillers per plant, number of productive tillers per meter square, biological yield per plant, harvest index, test weight, kernel length before cooking, L/B ratio, amylose content and grain yield kilogram per hectare. Such types of characters could be included

in the rice breeding programme as composite traits. Moderate heritability along with moderate genetic advance for some traits under present investigation shows that the intermediate expression of both dominance and additive gene effect. High heritability in association with moderate genetic advance reveals the presence of both non additive and additive genetic effect in the inheritance of the traits. In the prediction of genetic gain under selection, estimates of heritability along with genetic advance are more useful (Sinha *et al.* 2004; Johnson *et al.* 1955). If non additive gene action governs the characters then it may give high heritability along with low genetic advance (Panse, 1957). Here no any traits found having high heritability associated with low genetic advance and low GCV which controls by the dominance and epistatic effects. Under study, low heritability along with low genetic advance as per cent of mean observed for some characters and these characters were predominantly govern by the non additive gene action. Those traits posses high heritability with moderate to low genetic advance as per cent of mean and governed by non additive gene action, improvement in such traits may be possible through recombination breeding.

Similar findings (h^2 with genetic advance as % of mean) for different characters were obtained by Rao *et al.* (2014), Subbaiah *et al.* (2011), Bhatia *et al.* (2012), Ovung *et al*. (2012), Neha and Lal (2012), Singh *et al.* (2014), Yadav *et al.* (2010), Sahu *et al.* (2017), Bitew (2016), Devi *et al.* 2017, Rai *et al.* (2014), Vanaja and Babu (2006), and Singh *et al.* (2013).

5.5 Estimates of correlation coefficient among different characters:

Association analysis deals the mutual relationship among different yield and quality traits and determines the constituent traits on which selection can be relied upon for genetic enhancement of yield as well as quality traits. Positive and negative correlations are results of coupling and repulsion phase of linkage of genes which controls two different traits subsequently. Positive and negative correlation is also an indicator of increase and decrease between both the characters in the same direction and opposite direction subsequently. Positive association between desirable traits of rice is favourable to rice breeder because it helps in simultaneous improvement of both the traits. Nature of association can often be changed by selection and hybridization. Under association, a trait has low heritability and another has high with high association value

with the former trait is chosen to make effective selection, thus genetic enhancement is achieved using indirect selection through component traits along with higher heritability. Phenotypic association includes genotypic and environmental effects, that's why it's differ under changed environmental conditions. Genotypic association among the traits may be either due to pleiotropic action or linkage or both but major genetic reason of genotypic association is pleiotropic effect having manifold effect of a gene (Falconer, 1989). If positive or negative association between two characters remains same in parental and segregating population that means correlation is due to pleiotropic effect while it's become changed in segregating population reveals that such type of association is due to linkage only. Either pleiotropy or linkage involves two wanted or one wanted and another unwanted trait. Genotypic association is stable association, so such association is important for rice breeder for genetic enhancement of yield as well as quality of rice. On the basis of experimental findings, interrelationship among yield and quality attributing traits at both genotypic and phenotypic level; will be discuss under following sub- heads;

5.5.1 Phenotypic correlation coefficient:

In present observation, grain yield per plant have strong positive and significant association with harvest index has low heritability along with low genetic advance. Phenotypic correlation value is higher than the genotypic correlation for such association which reveals that association between these traits is not only due to genetic cause but also due to favourable interference of the environment.

Days to 50% flowering have positive and significant association with days to maturity. Plant height has positive and significant correlation with head rice recovery. Kernel length before cooking has positive and significant association with kernel L/B ratio and kernel elongation ratio. Kernel L/B ratio before cooking have positive and significant association with kernel elongation ratio at phenotypic level exposed that increase in one character will be reason of increase in another character for each positive and significant association vice versa.

Plant height had also negative and significant association with kernel elongation ratio. Number of spikelets per panicle has negative and significant association with kernel length before cooking and kernel elongation ratio. Biological yield per plant have

negative significant association with harvest index. Head rice recovery has negative and significant association with kernel length before cooking, kernel L/B ratio and kernel elongation ratio. Kernel breadth before cooking have negative and significant association with kernel L/B ratio at phenotypic level exposed that increase in one character will be reason of decrease in another character for each negative and significant association vice versa.

5.5.2 Genotypic correlation coefficient:

Values of genotypic association are higher than the phenotypic association in reference to maximum association among the traits reveals that the strong correlation among the traits genetically, but the actual phenotypic values is lessened by the significant interference of environment.

Grain yield per plant has positive and significant association with biological yield per plant, days to 50% flowering and days to maturity while negative and significant association with plant height, milling recovery and test weight at genotypic level, therefore correlation among these traits are high and true due to genetic cause. For better yield and quality, selection of such traits would be effective for further improvement. Biological yield per plant and test weight have higher heritability along with moderate genetic advance and positive and significant association with grain yield per plant, hence selection based on these traits may be more advantageous than other traits having positive and significant association with grain yield per plant.

Days to 50% flowering had positive and significant association with days to maturity, panicle length, biological yield per plant and number of productive tillers per meter square. Plant height had positive and significant association with head rice recovery, kernel breadth before cooking and number of spikelets per panicle. Days to maturity had positive and significant association with panicle length and biological yield per plant. Number of tillers per plant had positive and significant association with kernel elongation ratio, kernel L/B ratio, kernel length before cooking and number of productive tillers per meter square. Number of productive tillers per meter square had positive and significant association with kernel elongation ratio. Panicle length had positive and significant association with kernel breadth before cooking. Number of spikelets per panicle has positive and significant association with head rice recovery and kernel

breadth before cooking. Milling recovery had positive and significant association with kernel elongation ratio and Kernel L/B ratio. Head rice recovery had positive and significant association with kernel breadth before cooking. Kernel length before cooking has positive and significant association with kernel L/B ratio and kernel elongation ratio. Kernel L/B ratio has positive and significant association with kernel elongation ratio at genotypic level shows that, increase in one character will be reason of increase in another character for each positive and significant association vice versa. Selection of such traits having positive and significant genotypic association among each-other may be profitable in further rice breeding activities.

Days to 50% flowering had negative and significant association with volume expansion ratio. Plant height had negative and significant association with kernel elongation ratio, number of tillers per plant, kernel L/B ratio and kernel length before cooking. Number of tillers per plant has negative and significant correlation with head rice recovery, number of spikelets per panicle and kernel breadth before cooking. Number of productive tillers per meter square has negative and significant association with volume expansion ratio and head rice recovery. Number of spikelets per panicle had negative and significant association with kernel elongation ratio, kernel length before cooking and kernel L/B ratio before cooking. Biological yield per plant has negative and significant association with harvest index. Harvest index has negative and significant association with test weight. Hulling recovery has negative and significant association with milling recovery. Milling recovery had negative and significant association with kernel breadth before cooking. Head rice recovery has negative and significant association with kernel L/B ratio, kernel length before cooking and kernel elongation ratio. Except in environment 1 (C-14) both the genotypic and phenotypic correlation between milling percentage and head rice recovery in all environments were negatively correlated. The correlation coefficient between milling percentage and head rice recovery in environment 1 (C-14) was positive and non significant. The negative correlation between milling percentage and head rice recovery might be due to higher broken grains after milling of the samples. Kernel length before cooking has negative and significant correlation with kernel breadth before cooking. Kernel breadth before cooking has negative and significant association with kernel L/B ratio, kernel elongation ratio and

amylose content. Amylose content has negative and significant association with volume expansion ratio at genotypic level reveled that increase in one character will be reason of decrease in another character for each negative and significant association vice versa, same as in case of phenotypic level. Sometimes significant negative genotypic association also gives valuable results according to need; hence selection of such traits having significant negative genotypic association can be gainful for any rice breeding activities.

Values of genotypic association are higher than phenotypic due to the modified or masking effect of given environment on the traits (Singh, 1980). Under study, characters were positively and significantly correlated with each other having higher value, designated as interdependent characters. Approximately fifty per cent grain quality traits had non-significant and slightly positive association with grain yield per plant which is indicated that improvement of such material employed under study. Genotypic association is essential in assessment of the possibility of simultaneous improvement of several characters or a single complex character on the theory of correlated response to selection.

Similar findings report of significant positive or negative association among different yield and quality attributing traits on genotypic and phenotypic level were reported by Jyothula and Nitu Singh (2010), Krishna Veni and Shobha Rani (2007), Krishna Naik *et al.* (2005), Malini *et al.* (2011), Mehetre *et al.* (1994), Lanceras *et al.* (2004), Abarshahr *et al.* (2011), Nandan *et al.* (2010), Premkumar *et al.* (2016), Sarika Mathure *et al.* (2010), Manonmani *et al.* (2010), Yadav *et al.* (2010), Singh *et al.* (2014), Umadevi *et al* (2009), Mishra *et al.* (2015), Sahu *et. al.* (2017), Singh *et al.* (2013), vanisree *et al.* (2013), Hardari and Hittalmani (2017), Satheeshkumar and Saravanan (2012), Bhatia *et al.* (2012), Jayasudha and Sharma (2010), Rai *et al.* (2014), Kumari Neha and Lal (2012) and Vinoth *et al.* (2016).

5.6 Estimates of path coefficient analysis for different characters:

Association among the traits does not provide the actual graph of the degree of association among the traits, so to find out the actual effect of a specific trait on grain yield, we go for path coefficient analysis (Dewey and Lu, 1959). Path coefficient analysis is a standard fractional regression coefficient which separates the strength of association

into the determination of direct and indirect effect. It shows that association of the traits with grain yield is due to their direct effect on grain yield or is a result of their indirect effect via other component traits. Association among the traits at phenotypic and genotypic level under study is used for the estimation of phenotypic and genotypic path. Under study, path diagram can be explained in provisions of cause & effect relationship of different traits and utility of this diagram is that a set of simultaneous equations can be written straightly from the diagram and solution obtained from these equations gives valuable information on direct and indirect inputs of these casual factors to the effect. According to Lenka and Mishra (1973), values of direct and indirect contribution of the traits is 0.00 – 0.09, 0.10 – 0.19, 0.20 - 0.29, 0.30 – 1.00 and >1.00 for the negligible, low, moderate, high and very high effect subsequently. Residual effect dealings the part of other possible independent variables which were not included under study on dependent variables. Minimum combination of association and heritability values are needed for indirect selection to be more efficient than direct selection of grain yield. R^2 is determinates of results for direct and indirect contribution of traits. The achievement of any breeding plan depends upon the information, how those components had direct or indirect influence on grain yield in a particular environment or across the different environments. Findings of the path coefficient analysis will be discussed under following sub-heads;

5.6.1 Phenotypic path coefficient analysis:

Grain yield per plant had a direct positive effect on harvest index, biological yield per plant, L/B ratio before cooking, kernel breadth before cooking, amylose content, days to 50% flowering, number of spikelets per panicle, number of tillers per plant, volume expansion ratio, days to maturity, head rice recovery and kernel elongation ratio while direct negative effect for milling recovery, hulling recovery, test weight, plant height, panicle length, kernel length before cooking and number of productive tillers per plant. Under study, positive and significant association between grain yield and characters having very high positive direct effect such as harvest index, it reveals actual relationship between them at phenotypic level. Biological yield per plant have moderate values of variances, coefficient of variances, genetic advance, higher value of heritability and weak positive association with grain yield per plant then higher positive direct effect on grain

yield per plant gives recommendation of this trait, therefore direct selection for such traits will be rewarding for the enhancement of grain yield and quality.

Days to 50% flowering had a maximum positive indirect effect on days to maturity, panicle length and biological yield per plant. Plant height had a maximum positive indirect effect on kernel elongation ratio, L/B ratio and number of tillers per plant. Days to maturity had a maximum positive indirect effect on days to 50% flowering and biological yield per plant. Number of tillers per plant had a maximum positive indirect effect on kernel elongation ratio and L/B ratio. Number of productive tillers per meter square had a maximum positive indirect effect on head rice recovery, plant height and volume expansion ratio. Panicle length had a maximum positive indirect effect on head rice recovery, biological yield per plant and amylose content. Number of spikelets per panicle had a maximum positive indirect effect on head rice recovery, plant height and kernel breadth before cooking. Biological yield per plant had a maximum positive indirect effect on days to maturity, days to 50% flowering and number of tillers per plant. Harvest index had a maximum positive indirect effect on amylose content, milling recovery and head rice recovery. Test weight had a maximum positive indirect effect on number of spikelets per panicle, harvest index and volume expansion ratio. Hulling recovery had a maximum positive indirect effect on number of tillers per plant, harvest index, milling recovery and volume expansion ratio. Milling recovery had a maximum positive indirect effect on number of spikelets per panicle, plant height and test weight. Head rice recovery had a maximum positive indirect effect on plant height, number of spikelets per panicle and kernel breadth before cooking. Kernel length before cooking had a maximum positive indirect effect on head rice recovery, number of spikelets per panicle and kernel breadth before cooking. Kernel breadth before cooking had a maximum positive indirect effect on head rice recovery and plant height. L/B ratio had a maximum positive indirect effect on kernel length before cooking, kernel elongation ratio and number of tillers per plant. Amylose content had a maximum positive indirect effect on number of productive tillers per meter square, number of tillers per plant and L/B ratio. Volume expansion ratio had a maximum positive indirect effect on head rice recovery. Kernel elongation ratio had a maximum positive indirect effect on kernel length before cooking L/B ratio and number of tillers per plant. In present experiment, highest

positive direct effect of harvest index on grain yield per plant is the result of the positive indirect contribution of some yield and quality traits namely; panicle length, milling recovery, head rice recovery, kernel length before cooking, L/B ratio and amylose content. After harvest index, biological yield per plant posses highest positive direct effect on grain yield per plant which is also the result of positive indirect contribution of some yield and quality traits namely; days to 50% flowering, days to maturity, number of tillers per plant, number of spikelets per panicle, test weight, hulling recovery, L/B ratio, volume expansion ratio and kernel elongation ratio. These positive indirect contributions among different traits are beneficial for the strength of selection.

Days to 50% flowering had a maximum negative indirect effect on amylose content and head rice recovery. Plant height had a maximum negative indirect effect on head rice recovery, number of spikelets per panicle and kernel breadth before cooking. Days to maturity had a maximum negative indirect effect on number of spikelets per panicle and amylose content. Number of tillers per plant had a maximum negative indirect effect on number of spikelets per panicle, head rice recovery and plant height. Number of productive tillers per meter square had a maximum negative indirect effect on kernel elongation ratio, days to 50% flowering and amylose content. Panicle length had a maximum negative indirect effect on days to 50% flowering and kernel length before cooking. Number of spikelets per panicle had a maximum negative indirect effect on kernel elongation ratio, kernel length before cooking and L/B ratio. Biological yield per plant had a maximum negative indirect effect on harvest index and head rice recovery. Harvest index had a maximum negative indirect effect on biological yield per plant and test weight. Test weight had a maximum negative indirect effect on kernel breadth before cooking and panicle length. Hulling recovery had a maximum negative indirect effect on kernel length before cooking, head rice recovery and kernel breadth before cooking. Milling recovery had a maximum negative indirect effect on kernel elongation ratio, kernel length before cooking and L/B ratio before cooking. Head rice recovery had a maximum negative indirect effect on volume expansion ratio, kernel length before cooking and L/B ratio. Kernel length before cooking had a maximum negative indirect effect on L/B ratio and kernel elongation ratio. Kernel breadth before cooking had a maximum negative indirect effect on L/B ratio, kernel length before cooking and kernel

elongation ratio. L/B ratio had a maximum negative indirect effect on kernel breadth before cooking, head rice recovery and number of spikelets per panicle. Amylose content had a maximum negative indirect effect on volume expansion ratio, days to 50% flowering, days to maturity and kernel breadth before cooking. Volume expansion ratio had a maximum negative indirect effect on amylose content. Kernel elongation ratio had a maximum negative indirect effect on head rice recovery, number of spikelets per panicle and plant height. Same as positive indirect contribution, higher positive direct effect of biological yield per plant and harvest index on grain yield per plant is the result of some traits having indirect contribution for both traits. Harvest index had maximum positive direct effect on grain yield which is the result of some traits having negative indirect contribution namely; days to 50% flowering, plant height, days to maturity, number of tillers per plant, number of productive tillers per meter square, number of spikelets per panicle, biological yield per plant, test weight, hulling recovery, kernel breadth before cooking, volume expansion ratio and kernel elongation ratio while biological yield per plant had maximum positive direct effect on grain yield after harvest index which is the result of some traits having negative indirect contribution namely; plant height, number of productive tillers per meter square, panicle length, harvest index, milling recovery, head rice recovery, kernel length before cooking, kernel breadth before cooking and amylose content at phenotypic level. Sometimes, these negative indirect contributions are also useful for selection of better lines for any specific trait.

5.6.2 Genotypic path coefficient analysis:

At genotypic level, grain yield per plant had a direct positive effect on biological yield per plant, harvest index, panicle length, kernel elongation ratio, days to 50% flowering, amylose content, kernel length before cooking and number of spikelets per panicle while direct negative effect on plant height, L/B ratio, milling recovery, number of productive tillers per meter square, test weight, kernel breadth before cooking, number of tillers per plant, hulling recovery, volume expansion ratio, head rice recovery and days to maturity. In present investigation, association between grain yield and a character such as biological yield per plant is due to higher positive direct effect and moderate components of variances, higher heritability with moderate genetic advance as per cent of mean while in case of harvest index, it posses higher positive direct effect with weak

positive association with grain yield per plant, hence it shows that actual relationship between them and direct selection for such traits will be rewarding for the augmentation of grain yield and quality.

Days to 50% flowering had a maximum positive indirect effect on days to maturity, panicle length and biological yield per plant. Plant height had a maximum positive indirect effect on kernel elongation ratio, number of tillers per plant and L/B ratio. Days to maturity had a maximum positive indirect effect on harvest index, head rice recovery and test weight. Number of tillers per plant had a maximum positive indirect effect on plant height head rice recovery and number of spikelets per panicle. Number of productive tillers per meter square had a maximum positive indirect effect on volume expansion ratio, head rice recovery and milling recovery. Panicle length had a maximum positive indirect effect on days to 50% flowering, days to maturity and kernel breadth before cooking. Number of spikelets per panicle had a maximum positive indirect effect on plant height, head rice recovery and kernel breadth before cooking. Biological yield per plant had a maximum positive indirect effect on days to 50% flowering, days to maturity and number of spikelets per panicle. Harvest index had a maximum positive indirect effect on amylose content, head rice recovery and kernel breadth before cooking. Test weight had a maximum positive indirect effect on harvest index, number of spikelets per panicle and milling recovery. Hulling recovery had a maximum positive indirect effect on milling recovery, volume expansion ratio and days to 50% flowering. Milling recovery had a maximum positive indirect effect on kernel breadth before cooking, hulling recovery and number of productive tillers per meter square. Head rice recovery had a maximum positive indirect effect on L/B ratio kernel length before cooking and kernel elongation ratio. Kernel length before cooking had a maximum positive indirect effect on L/B ratio, kernel elongation ratio and number of tillers per plant. Kernel breadth before cooking had a maximum positive indirect effect on L/B ratio, kernel length before cooking and kernel elongation ratio. Kernel L/B ratio before cooking had a maximum positive indirect effect on kernel breadth before cooking, head rice recovery and plant height. Amylose content had a maximum positive indirect effect on L/B ratio, kernel length before cooking, number of tillers per plant and harvest index. Volume expansion ratio had a maximum positive indirect effect on number of productive tillers per meter

square, amylose content and days to 50% flowering. Kernel elongation ratio had a maximum positive indirect effect on kernel length before cooking, L/B ratio and number of tillers per plant at genotypic level. Under study, highest positive direct effect of biological yield per plant on grain yield per plant is the result of the positive indirect contribution of some yield and quality attributing traits *viz*; days to 50% flowering, days to maturity, number of tillers per plant, number of spikelets per panicle, test weight, kernel length before cooking, L/B ratio and kernel elongation ratio. After biological yield per plant, harvest index posses highest positive direct effect on grain yield per plant which is also the result of positive indirect contribution of some yield and quality traits *viz*; number of productive tillers per meter square, head rice recovery, kernel length before cooking, kernel breadth before cooking and amylose content. These maximum positive indirect contributions among the traits on genotypic level are advantageous for the strength of selection based on grain yield per plant.

Days to 50% flowering had a maximum negative indirect effect on volume expansion ratio, harvest index and head rice recovery. Plant height had a maximum negative indirect effect on head rice recovery and kernel breadth before cooking. Days to maturity had a maximum negative indirect effect on days to 50% flowering and panicle length. Number of tillers per plant had a maximum negative indirect effect on kernel elongation ratio and L/B ratio. Number of productive tillers per meter square had a maximum negative indirect effect on days to 50% flowering and number of tillers per plant. Panicle length had a maximum negative indirect effect on head rice recovery and biological yield per plant. Number of spikelets per panicle had a maximum negative indirect effect on kernel elongation ratio, kernel length before cooking and L/B ratio. Biological yield per plant had a maximum negative indirect effect on harvest index and plant height. Harvest index had a maximum negative indirect effect on biological yield per plant and test weight. Test weight had a maximum negative indirect effect on kernel breadth before cooking, number of tillers per plant and panicle length. Hulling recovery had a maximum negative indirect effect on kernel breadth before cooking and test weight. Milling recovery had a maximum negative indirect effect on kernel elongation ratio, L/B ratio and kernel length before cooking. Head rice recovery had a maximum negative indirect effect on plant height and kernel breadth before cooking. Kernel length before

cooking had a maximum negative indirect effect on head rice recovery, kernel breadth before cooking and plant height. Kernel breadth before cooking had a maximum negative indirect effect on head rice recovery and plant height. Kernel L/B ratio before cooking had a maximum negative indirect effect on kernel length before cooking and kernel elongation ratio. Amylose content had a maximum negative indirect effect on volume expansion ratio and kernel breadth before cooking. Volume expansion ratio had a maximum negative indirect effect on head rice recovery, milling recovery and kernel breadth before cooking. Kernel elongation ratio had a maximum negative indirect effect on head rice recovery and plant height. Same as positive indirect contribution at genotypic level, higher positive direct effect of biological yield per plant on grain yield per plant is the result of some traits having indirect contribution for such trait *viz*. plant height, number of productive tillers per meter square, panicle length, harvest index, hulling recovery, milling recovery, head rice recovery, kernel breadth before cooking, amylose content and volume expansion ratio while harvest index had maximum positive direct effect on grain yield after biological yield per plant which is the result of some traits having negative indirect contribution *viz*; days to 50% flowering, plant height, days to maturity, number of tillers per plant, panicle length, number of spikelets per panicle, biological yield per plant, test weight, hulling recovery, milling recovery, L/B ratio, volume expansion ratio and kernel elongation ratio. In some cases, these maximum negative indirect contributions among different traits at genotypic level are also useful for selection of superior lines for the particular traits.

In present study, some associations between the traits such as plant height, days to maturity and test weight is majorly due to the indirect contribution of the traits through another component traits, indirect selection through the same trait will be live for the improvement of rice lines. Residual effects are less at genotypic and phenotypic level reveals that, maximum attributes are covered for the estimation of path coefficient analysis except some that means traits studied in this experiment which is sufficient to explain genetic variability. The genetic construction of grain yield per plant is based on the overall net effect produced by different yield and quality components interacting with each-other. Some traits have positive direct effect but could not contribute towards grain yield due to preponderance of negative indirect contribution of other traits under study.

On the basis of overall description, selection of rice lines for the traits biological yield per plant and harvest index would be effective at genotypic or phenotypic level.

Similar results of genotypic and phenotypic path coefficient for different traits reported by Yadav *et al.* (2010), Jayasudha, S. and Sharma (2010), P. satheeshkumar and K. Sarvanan (2012), Sahu *et al.* (2017), Rao *et al* (2014), Rai *et al* (2014), Vanisree *et al.* (2013), Devi *et al.* (2017), Ekka *et al.* (2011), Mishra *et al.* (2015), Priya *et al.* (2017) and Premkumar *et al* (2016).

5.7 Genetic divergence analysis among rice lines (D^2 statistics with Tocher's Method):

Genetic divergence is essential for the selection of superior parents to exploit maximum heterosis in hybrid rice. For the measurement of genetic divergence, D^2 statistics is an effective technique than other. Genetic divergence arises due to different factors such as geographical partition, genetic barriers to cross ability and various evolutionary patterns. Replicated and multi-seasonal data were used in present investigation to estimate genetic divergence which gives more reliable consequences of D^2 statistics.

In the present investigation, all the thirty six lines of rice grouped into six clusters. Among the clusters, cluster II had maximum genotypes followed by cluster I than cluster III and remaining clusters are mono-genotypic reveals that the presence of sufficient amount of genetic diversity on the basis of clustering pattern.

Cluster I had maximum intra cluster distance followed by Clusters II and III suggested that genetic diversity available among the lines belongs to these clusters and crossing between the genotypes of the cluster I gives good segregants with higher genetic advance while maximum inter cluster distance observed between cluster I and III followed by clusters III and V then clusters III and IV revels wider diversity between these clusters. Genotypes between the clusters I and III may be used in hybridization programme for the improvement of set of the thirty six lines while minimum inter clusters distance observed between cluster IV and V followed by clusters I and IV then clusters I and V indicated that close relationship between the genotypes of these clusters and these genotypes may not be used in crossing scheme. Crossing between the genotypes belongs to the cluster I and III or genotypes within the cluster I can be gives

more valuable segregants having maximum inter and intra cluster distance subsequently. Those lines grouped in same clusters have less divergence in comparison to those placed among various clusters. To get valuable heterosis, we will select only one or two lines from the clusters having maximum genetic distance such as cluster I and III along with other important features. Pattern of clustering group constellation proved that the existence of sufficient amount of divergence. The clustering pattern of the 36 advanced lines revealed that the clustering of lines did not follow any particular pattern with respect to their origin. Distribution of lines also indicated that the lines originated from different place were grouped in same cluster and lines of same place scattered in different clusters that means cluster were not formed according to origin. Therefore the kind of genetic divergence found among the lines belonging to same origin might be due to differences in stability or adaptation, selection procedure, selection pressure and environmental fluctuations or conditions.

The genetic diversity was also supported by the considerable amount of variation among the cluster means for different traits. On the basis of comparative study of clusters mean values for different traits, observable differences available in cluster mean values. Cluster I had highest mean value for kernel elongation ratio. Cluster III showed highest mean value for plant height, number of spikelets per panicle and head rice recovery. Cluster IV had highest mean value for days to 50% flowering, panicle length, biological yield per plant, hulling recovery and kernel breadth before cooking. Cluster V had highest mean value observed for number of tillers per plant, milling recovery, kernel length before cooking, L/B ratio before cooking and volume expansion ratio. Cluster VI had highest values observed for the traits like days to maturity, number of productive tillers per meter square, grain yield per plant, harvest index, test weight, amylose content and grain yield kilogram per hectare indicated the selection of lines grouped in cluster VI, V, IV (All three are mono-genotypic) because these clusters showed maximum cluster mean values in sequence for most of the traits. Cluster III and I had more inter-cluster genetic distance but lowest cluster mean for majority of the traits. Mono-genotypic clusters (VI, V and IV) have single genotypes for each cluster but these lines are more valuable on the basis of cluster mean because they posses highest cluster means for maximum characters. Under study rice lines IR 92521-23-6-1-3, IR 92521-24-5-1-3, IR

92521-5-3-1-2, IR 92521-7-5-1-1, IR 92545-40-2-2-3, IR 92522-47-2-1-4 and IR 92522-45-3-1-4 are better lines out of thirty six in reference to cluster mean performance for most of the traits. Genotypic lines with higher cluster mean values may be directly used for alteration or may be used as a parent in any future rice breeding programme.

In present study with different twenty one yield and quality traits, higher input in the manifestation of genetic divergence was exhibited by kernel elongation ratio, head rice recovery, biological yield per plant, amylose content, test weight and grain yield kilogram per hectare shows that these characters plays an important role in total genetic divergence among the set of thirty six advance rice lines and also we may go for direct selection of these traits for diversity purpose. For the selection of parents on the basis of D^2 values, these relative contribution or input of each trait comes under the consideration. Above mentioned six traits having maximum contribution on genetic divergence are valuable in respect to the varieties under consideration and they have proved more practical to study genetic divergence among them.

If we initiate any crossing programme that should be operate between the elite lines belongs to the more divergent clusters and those clusters are separated by the maximum inter-cluster distance. Selection of any specific line for crossing should have highest cluster means for various traits in the selected clusters along with maximum relative percent contribution of such traits in total divergence. Greater genetic distance between the clusters provides wider genetic divergence between their genotypic lines. However, while considering genetic divergence among the parents to be included in crossing programme, parents with higher yielding ability and wider genetic divergence are likely to be yield superior segregants within a very short period (Roy and Panwar, 1993). Highly divergent lines also produce broad spectrum of variability in segregating generations enables further improvement and facilitate success of rice breeding. Distant cross helps to produce valuable transgressive segregants with higher magnitude of heterosis.

Similar findings of non-correspondence on geographic origin with genetic divergence were reported by Beevi and Venkatesan (2015), Shanmugasundaram *et al. (*2000), Ovung *et al.* (2012), Qamar *et al.* (2012), Nayak *et al. (*2004), Bisht *et al.* (2007),

Sarawgi and Rastogi (2000), Allam *et al.* (2017), Ekka *et al.* (2012), Parikh *et al.,* (2011), Garg *et al.* (2011), Islam *et al.* (2014), Karuppaiyan *et al.* (2013) Sinha and Mishra (2015), Sandhyakishore *et al.* (2007), Patil *et al.* (2005), Sinha *et al.* (1991), Rajesh *et al.* (2010), Ubarhande *et al.* (2009) and Kandamoorthy and Govindarasu (2005).

5.8 Molecular diversity analysis among thirty six elite rice lines using SSR markers:

Molecular marker techniques facilitate the identification of rice lines and estimate genetic variations available among them. These techniques are considered to detect the presence and absence of specific DNA sequence or combination of a particular sequence which uniquely identify the rice lines. These techniques based upon either polymerase chain reaction or nucleic acid hybridizations. Plant DNA analysis permits the direct assessment of variations in rice lines because evaluation of phenotype cannot be a trustworthy measurement of genetic differences due to environmental influence on genetic expression. Within one and half decades, number of molecular markers assays available for the genetic diversity analysis which differing in principle, in applications, in cost, in time requirement and in amount as well as type of polymorphism detection. Genetic diversity recognized by using random SSR markers which are essentially derived from the functionally non-coding regions of the genome might not illustrate the 'functional' diversity, that's why it's important to use markers which could unravel the diversity in functionally related coding regions of the genome to identify the variability among rice lines.

Simple sequence repeat (SSR) markers were used for the assessment of genetic diversity using thirty six elite rice lines under study. SSR is the most commonly used marker for the assessment of genetic diversity in rice, that's why I'm choosing this marker for the same.

In present study, using 16 SSR markers to analyze the genetic diversity of 36 advance rice lines, we found 58 alleles with a mean of 3.62 alleles. The numbers of allele per locus ranged from 3 to 5 and most of the markers revealed 3 or 4 alleles indicated that the significant differences available in allelic diversity among number of SSR loci in elite lines. To assess the polymorphic level, PIC value for each marker was used; that means

PIC values demonstrating the allelic diversity and their frequency among the rice lines varied from one locus to another. The average PIC value for the markers was 0.360 with the range of 0.306 (RM 271) to 0.437 (RM 307 and RM 463) which infers that yet a few more markers that wrap the entire genome were to be used to validate the genetic diversity existing in the set of thirty six rice lines to the maximum extant. These markers are not highly polymorphic but have sufficient informative polymorphism to assess genetic diversity of 36 elite rice lines. Among six clusters on the basis of SSR markers, cluster III have highest number of lines followed by cluster V, Cluster II, cluster I, cluster IV and cluster VI. A comparison between both the dendrogram obtained from morphological and molecular level revealed the different groups of rice lines comes under same cluster along with maximum similarity coefficient value which gives confirmatory result for those lines having same clusters but in case of inter cluster lines, similarity coefficient value is lowest, therefore crossing between the lines belongs to different clusters having minimum similarity will be beneficial to get effective transgressive segregants in F$_2$ or subsequent generations. The genotypes lying in cluster II (AH, AJ and AI) on the basis of phenotypic clustering also fall in the same cluster that is cluster IV while clustering at molecular level. However the genotypes A, B, D, E, F and C lying together in cluster I at molecular level are falling under clusters I and II at phenotypic level. Similar is the case of genotypes lying in clusters III, IV V and VI at molecular level when compared with phenotypic clustering. Above information, shows that the geographical distribution and the source of rice lines played an important role in clustering along with the similarity coefficient and differences in their adaptation, selection pressure, selection criteria and conditions of environment (Bose and Pradhan, 2005 and Singh *et al.* 2008). The similarity index values varied from 0.00 to 0.78 and least similarity was observed between G and F, I and AF & M and X which indicated that almost dissimilar lines from each-other, entire results of similarity coefficient reveals that the presence of wider range of diversity among the lines which provides ample scope of selection of true parents that would be gave superior hybrids or segregants in next generations.

Approximately similar findings using SSR markers with different types of genetic stocks reported by earlier workers Prathyusha *et al.* (2009), Venkatesan and Bhatt (2015),

Sajib *et al.* (2012), Shahriar *et al.* (2014), Upadhyay *et al.* (2011), Singh *et al.* (2015), Freeg *et al.* (2016), Zhang *et al.* (2010), Krupa *et al.* (2017), Matin *et al.* (2012) and Seetharam *et al.* (2009).

5.9 Phenotypic stability analysis (Eberhart and Russell model, 1966) of thirty six elite rice lines for twenty one characters:

The phenotypic reaction in changing environmental conditions is not similar for each rice lines; the effect of variation in phenotype fully depends upon the environment. The interaction in the consequence of genetic and non-genetic on improvement is called G x E interaction which is the chief consequence to the rice breeder in the procedure of evolution of superior varieties. The objective of any rice breeding programme is to develop rice lines that can withstand under unpredictable transient environmental fluctuations. Biological concept of phenotypic stability is referred to the stable performance of a line over an extensive range of environments and such idea of phenotypic stability is in conformity with the concept of homeostatis generally used in genetics. An adopted rice lines is simply one which survives the selection process of the breeder that is one which performs better than the standard adopted varieties under comparison. Regression analysis is verified that an important technique for assessing the reaction of various rice lines under fluctuating environmental conditions for phenotypic stability. Eberhart and Russell partitioning the G x E interaction of each rice genotypes into slope of regression line and deviation from the regression line for the estimation of phenotypic stability. Analysis of phenotypic stability parameter is simple and it requires less area to conduct the experiment with better precisions, that's why chosen this model for stability analysis. Productivity of rice lines is the function of its adaptation, while the later is a negotiation of fitness and flexibility. In fact phenotypic stability may depends on some physiological and morphological traits and allowing other to vary ensuing in predictable genotype x environment interaction for the final trait say grain yield. The stability of rice lines always remains a matter of grand concern to the rice breeders; rice lines have to interact with the given environment in respect to its component characters, which have yet to be planned as per requirement of the rice lines. Rice breeders requirement, in common is to identify average stable lines of rice which could perform better under average environmental conditions. Regression of each rice lines on

environmental index is a function of required period from the regression and would thus give useful estimate of stability. I will discuss about the findings of phenotypic stability under following sub-heads;

5.9.1 Analysis of variance (ANOVA) of phenotypic stability for different characters:

In present investigation, thirty six lines of rice were undertaken to study phenotypic stability under four different environments to select the lines showing the stable performance over the environments and having lowest genotype x environment interaction.

Analysis of variance indicated that the highly significant differences existed among the 36 rice lines for all the yield and quality traits indicated that these lines sufficiently differed in respect to all the traits and presence of genetic variability. Mean sum of square due to environments were also significant for all the traits except L/B ratio shows that considerable difference among all the environments under study. Genotype x environment interaction was highly significant for plant height and hulling recovery reveals that the differential response of rice lines for these traits under various environmental conditions. Environment (linear) had highly significant mean sum of square for all the yield and quality attributing traits except L/B ratio shows that the existence of variation among the environments tested. Linear component of G x E interaction was significant for plant height and panicle length and non significant for remaining traits reveals that significant differences among the rice lines for linear response of environments and also indicating the importance of regression coefficient and deviation from regression in determination of phenotypic stability for these characters and absence of genetic differences among the lines for regression on environmental indices and thus the further prediction of lines would be difficult for the traits which are non-significant for G x E (linear). Pooled deviation under ANOVA table were highly significant for all the characters except plant height, harvest index and hulling recovery indicated that performance of various lines fluctuated considerably in respect to their phenotypic stability for respective traits. Environment + interaction was also significant at 5% or 1% level of significance for all the characters except number of productive tillers per meter square, number of spikelets per panicle, milling recovery, kernel length before cooking, kernel breadth before cooking and L/B ratio reveals that differential

response of environment on the phenotypic expression of rice lines for these traits which were significant.

5.9.2 Environmental indices of different environments for yield and quality attributes:

Environmental index under phenotypic stability can offer the basis for identifying the favourable environments of the rice lines for the expression of greatest potential of these lines. Control 2014 (E_1) reveals the favourable and suitable environment for days to 50% flowering, number of tillers per plant, number of productive tillers per meter square, panicle length, number of spikelets per panicle, grain yield per plant, harvest index, head rice recovery, L/B ratio, kernel elongation ratio and grain yield kilogram per hectare. Stress 2014 (E_2) showed favourable environment for only the trait plant height. Control 2015 (E_3) found favourable environment for the trait days to maturity, biological yield per plant, test weight, hulling recovery, milling recovery, kernel length before cooking, kernel breadth before cooking, amylose content and volume expansion ratio while Stress 2015 (E_4) does not favour any particular trait out of twenty one. Highest positive value among the four environments for each trait indicated that, this environment is favourable and suitable for the specific trait and higher potential for such particular trait would be achieve under this environment while negative values for any trait in any particular given environment indicates as a poor environment for such specific trait. Above results across the environments indicated that almost all the traits except plant height favours environment 1 (E_1) or environment 2 (E_2) which are the control or normal irrigated conditions of Kharif 2014 and 2015 while no more characters except plant height favours the reproductive drought stress environment (E_2 and E_4) in Kharif 2014 and Kharif 2015 that means these traits are suitable to give maximum yield potential along with better quality under normally irrigated conditions.

These results of ANOVA for phenotypic stability and environmental indices for different traits are in agreement to earlier worker Rashmi *et al.* (2017), Vijaya Lakshmi *et al.* (2014), Chavan *et al.* (2014), Gopinath and Reddy (2005), Singh *et al.* (2016), Mahapatra and Das (1999), Arumugam *et al.* (2007), Francis *et al.* (2005), Majumder and Borthakur (1996), Bastia *et al.* (2010), Devi *et al.* (2006) and Bose *et al.* (2012).

5.9.3 Stability parameters for different traits among advanced rice lines:

Stable rice lines for the different yield attributing traits along with quality were selected on the basis of perfect balance among mean value in comparison to population mean, regression coefficient and deviation from regression line. On the basis of detailed experimental findings (already given in previous chapter) it will be discuss, how those rice lines selected for phenotypic stability across the all environments or in a particular environment in reference to any yield and quality attributes. Parametric phenotypic stability for different traits will be discussed under following sub-heads;

5.9.3.1 Stability parameter for days to 50% flowering:

Under study, among good performing lines CRR 724-1-B (IR 88889-44), IR 94313:18-4-1-4-1-B, IR 92521-5-3-1-2, IR 92522-47-2-1-4 and IR 92517-1-3-1-1 found best lines for days to 50% flowering on the basis of stability criteria in which CRR 724-1-B (IR 88889-44) posses earliest days to 50% flowering than population mean along with below average stability and non significant deviation from regression line hence, such line suitable for favourable environmental conditions while remaining advance rice lines also possed earliest days to 50% flowering than population mean along with near to average stability and non significant deviation for regression line, hence these lines are widely adopted lines for such trait.

5.9.3.2 Stability parameter for plant height:

In the present study for plant height, among the good performing lines IR 94313:18-4-1-4-1-B, IR 94391-587-1-2-B, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3 and IR 92516-8-3-3-4 found best lines for the concerned trait on the basis of stability criteria in which IR 93339:40-B-18-13-B-B-1 shows semi - dwarf nature of plant height than population mean along with below average stability and non significant deviation from regression line hence, such line perform better in favourable environments while IR 92545-53-4-1-3 had also semi – dwarf nature of plant height than population mean along with above average stability and non significant deviation from regression line hence, this line will perform better in poor environment. Remaining all the lines have short stature of plant height than population mean along with regression coefficient values near to

average stability and non significant deviation from regression line hence, these lines are widely adopted across the environments for such trait.

5.9.3.3 Stability parameter for days to maturity:

In the present experiment for days to maturity, among the good performing lines IR 92521-5-3-1-2, IR 92521-7-5-1-1 and IR 92546-33-3-1-1 found best rice lines for days to maturity on the basis of stability criteria in which IR 92521-5-3-1-2 indicated earliest days to maturity than population mean along with above average stability and non significant deviation from regression line hence, such lines recommended for poor environment while IR 92521-7-5-1-1 also shows earliest days to maturity than population mean along with below average stability and non significant deviation from regression line hence, such lines recommended for better environment. Advance rice line IR 92546-33-3-1-1 had earliest days to maturity in comparison to population mean with performance of regression coefficient near to average stability and non significant deviation from regression line hence, these lines are widely adopted across the all environments for this trait.

5.9.3.4 Stability parameter for number of tillers per plant:

Under present study for number of tillers per plant, among the good performing lines IR 94313:18-4-1-4-1-B, IR 92522-61-3-1-4, IR 92523-37-1-1-2 and IR 92517-1-3-1-1 found best lines for the concerned trait on the basis of stability criteria in which IR 94313:18-4-1-4-1-B and IR 92522-61-3-1-4 indicated higher number of tillers per plant than population mean along with below average stability and non significant deviation from regression line, that's why both genotypes recommended for favourable environment while IR 92523-37-1-1-2 and IR 92517-1-3-1-1 also shows maximum number of tillers per plant than population mean along with above average stability and non significant deviation from regression line hence, both the genotypes recommended foe unfavourable environments. No one genotype found with wider adoptability along with higher mean value for this trait.

5.9.3.5 Stability parameter for number of productive tillers per meter square:

Under study, among the good performing lines IR 92523-35-1-1-1, IR 92527-6-2-1-2 and IR 92546-7-1-1-3 found best genotypes for number of productive tillers per meter square on the basis of stability criteria in which IR 92523-35-1-1-1 and IR 92527-6-2-1-2

reveals maximum number of productive tillers per meter square than population mean along with above average stability and non significant deviation from regression line therefore, these two lines suitable for unfavourable or poor environment while IR 92546-7-1-1-3 have also maximum number of productive tillers per meter square than population mean along with below average stability and non significant deviation from regression line so, this line perform better in favourable environments. No one lines found widely stable with higher mean value for such trait.

5.9.3.6 Stability parameter for panicle length:

In present investigation for panicle length, among good performing lines CRR 719-1-B (IR 88903-34), IR 92527-6-2-1-2, IR 92545-54-6-1-4 and IR 92545-51-1-1-4 found best genotypes for the concerned trait on the basis of stability criteria in which CRR 719-1-B (IR 88903-34) and IR 92527-6-2-1-2 posses higher panicle length in comparison to population mean along with near to average stability and non significant deviation from population mean hence, both the lines have wider stability across the all environments for this particular trait while IR 92545-54-6-1-4 and IR 92545-51-1-1-4 had also higher panicle length than population mean along with below average stability and non significant deviation from regression line, that's why these genotypes recommended for favourable environments for such trait.

5.9.3.7 Stability parameter for number of spikelets per panicle:

In present investigation, among the good performing lines IR 92522-61-3-1-4 and IR 92546-17-6-4-4 identified as best genotypes for number of spikelets per panicle on the basis of stability criteria in which IR 92522-61-3-1-4 had maximum number of spikelets per panicle than population mean along with near to average stability and non significant deviation from regression line hence, such genotype recommended for number of spikelets per panicle across the all environments while another genotype IR 92546-17-6-4-4 posses maximum number of spikelets per panicle than population mean along with below average stability and non significant deviation from regression line hence, this lines suitable for number of spikelets per panicle under rich environment.

5.9.3.8 Stability parameter for grain yield per plant:

Under study, among the good performing lines IR 92521-24-5-1-3, IR 92545-53-4-1-3, IR 92546-17-6-4-3 and IR 92546-17-6-4-4 found best rice lines for grain yield per

plant on the basis of stability criteria in which IR 92521-24-5-1-3 had maximum grain yield per plant than population mean along with near to average stability and non significant deviation from regression line hence, such genotype recommend to farmers having wider stability across the environments for grain yield per plant while IR 92545-53-4-1-3 had also maximum grain yield per plant in comparison to population mean along with above average stability and non significant deviation from regression line so, this genotype suitable for unfavourable or poor environment. Genotypes IR 92546-17-6-4-3 and IR 92546-17-6-4-4 had greater grain yield per plant than population mean value along with below average stability and non significant deviation from regression line hence, both the genotypes suitable for favourable or rich environment for grain yield per plant.

5.9.3.9 Stability parameter for biological yield per plant:

Under present study, among the good performing lines IR 92522-47-2-1-4 and IR 92523-37-1-1-2 found best rice lines out of thirty six for the concerned trait on the basis of stability criteria in which line IR 92522-47-2-1-4 posses higher biological yield than population mean along with near to average stability and non significant deviation from regression line that's why this line recommend to wider stability across the environment for such trait while IR 92523-37-1-1-2 had also maximum biological yield than population mean along with below average stability and non significant deviation from regression line hence, this genotype suitable for rich environment for such particular trait.

5.9.3.10 Stability parameter for harvest index:

In present investigation for harvest index, among the good performing lines IR 92521-5-3-1-2, IR 92523-37-1-1-2, IR 92545-54-6-1-4 and IR 92545-24-3-1-1 found best rice lines for the concerned trait on the basis of stability criteria in which IR 92521-5-3-1-2 and IR 92545-54-6-1-4 had maximum value of harvest index than population mean along with near to average stability and non significant deviation from regression line hence, both the lines are widely adoptable across all the environments for harvest index while IR 92523-37-1-1-2 and IR 92545-24-3-1-1 posses maximum value of harvest index in comparison to population mean along with below average stability and non significant deviation hence, both lines are suitable for favourable environment for harvest index.

5.9.3.11 Stability parameter for test weight:

Under study, among the good performing lines IR 92523-35-1-1-1 and IR 92545-24-3-1-1 found best lines for the test weight on the basis of stability criteria in which IR 92523-35-1-1-1 had maximum value of test weight than population mean along with below average stability and non significant deviation from regression line therefore, this genotypes suitable for the cultivation under favourable environment for such trait while another genotype IR 92545-24-3-1-1 had also maximum value of test weight than population mean along with near to average stability and non significant deviation from regression line hence, such genotype is widely adoptable genotypes for test weight.

5.9.3.12 Stability parameter for grain yield kilogram per hectare:

In the present study, among the good performing lines IR 94314-20-2-1-B, IR 92522-47-2-1-1 and IR 92546-7-1-1-3 found best genotypes for grain yield kilogram per hectare on the basis of stability criteria in which all the elite rice lines (Above mentioned) posses higher grain yield kilogram per hectare than population mean along with near to average stability and non significant deviation from regression line hence, all the rice genotypes having wider stability across the all types of environments for such trait recommended to farmers.

5.9.3.13 Stability parameter for hulling recovery %:

In present investigation for hulling recovery, among the good performing lines, IR 94313:18-4-1-4-1-B and IR 92516-8-3-3-4 found best lines for the concerned trait on the basis of stability criteria in which IR 94313:18-4-1-4-1-B had maximum hulling recovery in comparison to population mean along with below average stability and non significant deviation from regression line hence, this rice line suitable for rich environment for hulling recovery while IR 92516-8-3-3-4 had also maximum hulling recovery than population mean along with near to average stability and non significant deviation from regression line therefore, such genotype widely adopted to all the environments for hulling recovery.

5.9.3.14 Stability parameter for milling recovery %:

In present experiment for milling recovery, among the good performing lines, IR 93339:40-B-18-13-B-B-1, IR 92521-5-3-1-2, IR 92521-24-5-1-3 and IR 92517-1-3-1-1 found best genotypes for milling recovery on the basis of stability criteria in which IR

92521-5-3-1-2 had maximum milling recovery than population mean along with below average stability and non significant deviation from regression line that's why this line suitable for favourable environment for milling recovery while remaining all genotypes (Above mentioned) also posses maximum milling recovery than population mean along with near to average stability and non significant deviation from regression line hence, these lines are widely stable across the all environments for milling recovery.

5.9.3.15 Stability parameter for head rice recovery %:

In the present study for head rice recovery, among the good performing lines, CRR 724-1-B (IR 88889-44), IR 92521-5-3-1-2, IR 92546-7-1-1-3 and IR 92546-17-6-4-3 found best lines of rice for the concerned trait on the basis of stability criteria in which IR 92521-5-3-1-2 line posses higher head rice recovery than population mean along with below average stability and non significant deviation from regression line hence, this genotype suitable under rich environment for head rice recovery while IR 92546-7-1-1-3 also posses maximum head rice recovery than population mean along with above average stability and non significant deviation from regression line that's why such genotype perform better in poor or unfavourable environment for head rice recovery. Rice lines CRR 724-1-B (IR 88889-44) and IR 92546-17-6-4-3 had higher head rice recovery in comparison to population mean value along with near to average stability and non significant deviation from regression line reveals that both the genotype perform well under all types of environments or wider stability for such trait.

5.9.3.16 Stability parameter for kernel length before cooking:

Under study, among the good performing lines, IR 94314-20-2-1-B and IR 92521-24-5-1-3 identified as best lines for the concerned trait on the basis of stability parameters. Genotype IR 94314-20-2-1-B had better kernel length before cooking than population mean along with near to average stability and non significant deviation from regression line hence, this genotype recommend to across the all environments that means it posses wider stability for kernel length before cooking while IR 92521-24-5-1-3 posses lowest kernel length before cooking than population mean along with near to average stability and non significant deviation from regression line hence, such line suitable under rich or favourable environments for kernel length before cooking.

5.9.3.17 Stability parameter for kernel breadth before cooking:

In present investigation, among the good performing lines, IR 92545-54-6-1-4 and RP-1-27-7-6-1-2-1 found best genotypes for kernel breadth before cooking on the basis of stability parameters. Elite rice line IR 92545-54-6-1-4 had maximum kernel breadth before cooking than population mean along with above average stability (due to negative bi score above one) and non significant deviation from regression line hence, such genotype well adopted under poor or unfavourable environment for kernel breadth before cooking while RP-1-27-7-6-1-2-1 posses lowest mean value than population mean but having value near to average stability and non significant deviation from regression line that's why such genotype stable across the all environments for kernel breadth before cooking.

4.9.3.18 Stability parameter for kernel L/B ratio before cooking:

Under the present investigation for kernel L/B ratio before cooking, among the good performing lines, IR 92517-1-3-1-1 and IR 92545-24-3-1-1 found best lines for the concerned trait on the basis of stability parameters in which IR 92517-1-3-1-1 had maximum L/B ratio before cooking in comparison to population mean along with near to average stability (due to negative value of regression coefficient) and non significant deviation from regression line hence, this line suitable for poor or unfavourable environment for such trait while IR 92545-24-3-1-1 posses lowest L/B ratio than population mean but having below average stability and non significant deviation from regression line therefore, this genotype suitable for the cultivation under favourable or rich environment for L/B ratio before cooking.

5.9.3.19 Stability parameter for amylose content:

Under study for amylose content, among all the good performing lines only IR 92546-33-4-2-3 had lowest mean performance for such trait in comparison to population mean along with above average stability and non significant deviation from regression line hence, this line suitable for amylase content under poor or unfavorable environment.

5.9.3.20 Stability parameter for volume expansion ratio:

In the present study for volume expansion ratio, among the good performing lines IR 92521-5-3-1-2, IR 92521-23-6-1-3 and IR 92522-47-2-1-4 identified as best genotypes for the concerned trait on the basis of stability parameter in which IR 92521-23-6-1-3 and

IR 92522-47-2-1-4 had better volume expansion ratio than population mean along with below average stability and non significant deviation from regression line hence, these lines suitable for favourable environment for such trait while IR 92521-5-3-1-2 had also better volume expansion ratio than population mean along with near to average stability and non significant deviation from regression line therefore, this line widely adoptable for volume expansion ratio.

4.9.3.21 Stability parameter for kernel elongation ratio:

Under present study for kernel elongation ratio, only line IR 92522-47-2-1-1 found good performing line for the concerned trait on the basis of stability parameter having better kernel elongation ratio than population mean along with below average stability and non significant deviation from regression line hence, this line suitable under rich environment for such trait.

Out of thirty six lines, IR 92521-24-5-1-3 had maximum grain yield per plant, earliest days to 50% flowering, better maturity duration, better number of spikelets per panicle, good head rice recovery and moderate L/B ratio than population mean. This genotype also perform better than the all three checks (MTU 1010, IR 64 and Lalat) for grain yield per plant therefore, such genotype recommend to farmers or variety release proposal having wider stability across the all types of environments for grain yield per plant.

IR 92545-53-4-1-3 had also maximum grain yield per plant, earliest days to 50% flowering, better maturity duration, maximum number of tillers per plant, maximum productive tillers per meter square, good harvest index and better L/B ratio in comparison to population mean. This elite rice line had better performance than check MTU 1010 out of three checks for grain yield per plant so, this genotype recommended for unfavourable or poor environment for grain yield per plant.

Genotypes IR 92546-17-6-4-3 and IR 92546-17-6-4-4 had greater grain yield per plant, better maturity duration, number of tillers per plant, number of spikelets per panicle, harvest index, head rice recovery and L/B ratio than population mean value. Both the genotypes perform better than all three checks (MTU 1010, IR 64 and Lalat) for grain yield per plant hence, both the genotypes suitable for favourable or rich environment.

Above mentioned genotypes would be performing better in their respective environments.

The findings of stability parameters are in confirmation of earlier workers (They used different types of rice germplasm and hybrids) Paul *et al.* (2016), Rashmi *et al.* (2017), Bhatt *et al.* (2015), Singh *et al.* (2016), Vijaya Lakshmi *et al.* (2014), Panwar *et al.* (2008), Padmavathi *et al.* (2013), Parmar *et al.* (2016), Sreedhar *et al.* (2011), Patil *et al.* (2013), Ramezanil and Torabil (2011), Kumar *et al.* (2010), Subudhi *et al.* (2012), Mall *et al.* (2012), Mahalingam *et al.* (2013), Chavan *et al.* (2014), Devi *et al.* (2006), Bastia *et al.* (2010), Majumdar and Borthakur (1996), Francis *et al.* (2005), Arumugam *et al.* (2007), Mahapatra and Das (1999) and Gopinath and Reddy (2005).

CHAPTER – 6
SUMMARY AND CONCLUSIONS

Summary and Conclusion:

6.1 Summary of the research work:

The present experiment entitled; "stability analysis for grain yield and quality traits in indica rice (*Oryza sativa* L.) lines" was undertaken with thirty six elite advance rice lines from STRASA project. These rice lines were grown at experimental plots of rice section, Bihar Agricultural University Sabour during kharif 2014 and kharif 2015 under control and reproductive drought stress condition. Objectives of the experiment ware to study genetic variability, heritability, genetic advance, interrelationship of the characters, genetic diversity at morphological as well as molecular level and phenotypic stability among 36 elite rice lines with 21 yield and yield attributing traits along with quality traits. Pooled data from all the four environments were used for different statistical analysis through various methods given by the different statisticians or scientists. Randomized complete block design (RCBD) was adopted for the experiment with three replications in each trail. The rice lines were raised in plot size 4 x 2 = 8m^2 with spacing 20 x 20 cm. Observations were recorded for twenty one yield and quality attributing characters viz., days to 50% flowering, plant height (cm), days to maturity, number of tillers per plant, number of productive tillers / meter^2, panicle length (cm), number of spikelet's per panicle, grain yield per plant (g), biological yield per plant (g), harvest index (%), test weight (g), hulling (%), milling (%), head rice recovery (%), kernel length before cooking (mm), kernel breadth before cooking (mm), L/B ratio, amylose content, volume expansion ratio, kernel elongation ratio and grain yield kilogram per hectare. The experimental plot was well drained loamy soil and good fertility with levelled surface along with pH 8.35 & EC 0.150 dsm^{-1} (For control condition) and pH 8.40 & EC 0.260 dsm^{-1} (For stress condition). Area of the research plots were situated at longitude 87^0 04' 1.6" East and latitude 25^0 14' 11" North at an altitude of 37.19 metre above mean sea level in the heart of vast Indo - Gangatic plains of North India. Sub - tropical and slightly sub - humid nature of the climate appears in this place which is characterized by dry and warm summer, moderate rainfall, dry and cold winter. December and January are usually the coldest month when the mean temperature normally falls as low as 8.4^{0}C whereas April and May are generally the hottest months having the maximum average

temperature of 38^0C. The recommended dose of fertilizers @ 100 N: 60 P: 40 K kilogram per hectare was applied according to detailed procedure. Inter - cultural operations like manual weeding were done in the field at three times as per requirements. Thin film of water was given at the time of transplanting and 5 cm depth of water was given at the time of maximum tillering stage. In control condition, field was irrigated when required up to physiological maturity while in case of stress condition before reproductive stage; irrigation was stopped before 15 days to initiation of first flower in each plot. Crop was subjected to significant stress during reproductive stage and stress was measured through the instrument. All the recommended agronomic practices were applied to raise a healthy crop. Brief summary in reference to outcome of research are given below;

The mean sum of square due to rice lines for the maximum characters were found highly significant except some quality characters revealed that the significant differences are present for different traits between elite advance rice lines.

For days to 50% flowering, rice lines CRR 724-1-B (IR 88889-44), IR 94313:18-4-1-4-1-B, IR 92545-53-4-1-3 and CRR 719-1-B (IR 88903-34) found best lines with earliest days to 50% flowering out of best check MTU 1010. For plant height, rice lines IR 92527-6-2-1-4, IR 92546-17-6-4-4 and IR 94313:18-4-1-4-1-B found best lines with lowest plant height out of best check IR 64. For days to maturity, rice lines IR 94313:18-4-1-4-1-B, IR 92521-24-5-1-3 found best lines with lowest number of days to maturity out of best check MTU 1010. For number of tillers per plant, rice lines IR 88287-383-1-B-B-1-1-B, RP-1-27-7-6-1-2-1 and IR 92522-61-3-1-4 found best lines with maximum number of tillers per plant out of one of the check IR 64. For number of productive tillers per meter square, rice lines IR 92546-7-1-1-3 and IR 92546-33-3-1-1 found best lines with maximum number of productive tillers per meter square out of best check IR 64. For panicle length, rice lines IR 93339:40-B-18-13-B-B-1, IR 92545-40-2-2-3 and IR 92522-61-3-1-4 found best lines with maximum panicle length out of best check IR 64. For number of spikelets per panicle, rice lines IR 92521-7-5-1-1, IR 92521-24-5-1-3 and IR 92521-5-3-1-2 found best lines with maximum number of spikelets per panicle out of best check IR 64. For grain yields per plant, rice lines IR 94314-20-2-1-B, IR 92521-24-5-1-3 and IR 92523-37-1-1-2 found best lines with highest grain yields per plant out of best check Lalat. For biological yields per plant, rice lines IR 92527-6-2-1-4, IR 94314-

20-2-1-B and IR 92521-24-5-1-3 found best lines with highest biological yields per plant out of best check Lalat. For harvest index, rice lines IR 92546-17-6-4-4, IR 92522-45-3-1-4 and IR 92545-23-2-1-1 found best lines with maximum harvest index out of best check IR 64. For test weight, rice lines IR 92522-45-3-1-4, IR 92545-40-2-2-3 and CRR 724-1-B (IR 88889-44) found best lines with maximum test weight out of best check Lalat. For hulling recovery, rice lines IR 92545-40-2-2-3, IR 92545-51-1-1-4 and IR 92523-35-1-1-1 found best lines with maximum hulling recovery out of best check MTU 1010. For milling recovery, rice lines IR 93339:40-B-18-13-B-B-1, IR 92527-6-2-1-2 and IR 92522-47-2-1-4 found best lines with maximum milling recovery out of best check IR 64. For head rice recovery, rice lines IR 92521-5-3-1-2, IR 92521-7-5-1-1 and IR 92521-23-6-1-3 found best lines with maximum head rice recovery out of best check IR 64. For kernel length before cooking, rice lines IR 92522-47-2-1-4, IR 92545-53-4-1-3 and IR 94313:18-4-1-4-1-B found best lines with largest kernel length before cooking out of the best checks IR 64 and Lalat. For kernel breadth before cooking, rice lines IR 92521-7-5-1-1 and IR 92523-37-1-1-2 found best lines with largest kernel breadth before cooking out of the best check Lalat. For kernel L/B ratio before cooking, rice lines IR 92522-47-2-1-4, IR 92545-53-4-1-3 and IR 92527-6-2-1-4 found best lines with highest kernel L/B ratio before cooking out of the best check MTU 1010. For amylose content, rice lines IR 92546-17-6-4-3, CRR 719-1-B (IR 88903-34) and IR 92546-33-3-1-1 found best lines with highest amylose content out of one of the check IR 64. For volume expansion ratio, rice lines IR 92521-5-3-1-2 and IR 92521-7-5-1-1 found best lines with maximum volume expansion ratio out of the best check IR 64. For Kernel elongation ratio, rice lines IR 94313:18-4-1-4-1-B, IR 93339:40-B-18-13-B-B-1 and IR 92523-35-1-1-1 found best lines with maximum kernel elongation ratio out of the best check MTU 1010. For grain yield kilogram per hectare, rice lines IR 92527-6-2-1-2, IR 92527-6-2-1-4 and IR 92546-17-6-4-3 found best lines with maximum grain yield kilogram per hectare out of the best check IR 64. Above mentioned these rice lines are desirable for different traits hence, these elite rice lines would be effective to start any rice breeding activities for further rice improvement.

VP and PCV were higher than the VG and GCV for all the component traits shows that the environmental influence on the manifestation of these traits. Maximum VG and

VP were observed for grain yield kilogram per hectare, number of spikelets per panicle and number of productive tillers per meter square. Maximum GCV observed for number of spikelets per panicle, kernel elongation ratio and head rice recovery while maximum PCV observed for number of spikelets per panicle, harvest index, number of tillers per plant. Moderate values (10-20) of GCV and PCV observed for some traits hence; selection for these traits may be ambiguous if we adopted for its improvement.

Higher heritability observed for kernel elongation ratio and head rice recovery, number of spikelets per panicle, test weight and biological yield per plant revealed that the environmental influence is less in the expression of these traits and improvement of these traits could be possible through simple selection method due to additive gene action. Maximum genetic advance observed for grain yield kilogram per hectare, number of spikelets per panicle and number of productive tillers per meter square which helps in the prediction of genetic gain that could be obtained in further generations. Maximum genetic advance as % of mean observed for number of spikelets per panicle, kernel elongation ratio and head rice recovery hence, selection would be effective for these traits. Higher estimate of heritability coupled with higher value of genetic advance as % of mean observed for traits like kernel elongation ratio, head rice recovery and number of spikelets per panicle which revealed that the preponderance of additive gene action in the inheritance of these traits and these traits could be improved through direct selection because GCV is also comparatively high for these traits.

At phenotypic level, grain yield per plant revealed positive and significant association with harvest index has low heritability along with low genetic advance. Phenotypic correlation is higher than the genotypic correlation for harvest index which revealed that the association between these traits is not only due to genetic cause but also due to favourable interference of the environment. At genotypic level, grain yield per plant revealed positive and significant association with biological yield per plant, days to 50% flowering and days to maturity while negative and significant association with plant height, milling recovery and test weight therefore, correlation among these traits are high and true due to genetic cause. For better yield and quality, selection of such traits would be effective for further improvement. Genotypic association are higher than the phenotypic association in reference to maximum association among the traits revealed that

the strong correlation among the traits genetically, but the actual phenotypic values is lessened by the significant interference of environment.

At phenotypic and genotypic level, grain yield per plant had a maximum and considerable positive direct positive effect of harvest index and biological yield per plant. Positive and significant association between grain yield per plant with harvest index and biological yield per plant revealed that the actual relationship between them and provides recommendation for these traits therefore, direct selection for such traits will be rewarding for the enhancement of grain yield and quality. Under study, different positive indirect contribution via different traits is also available hence; those traits are beneficial for the strength of selection.

On the basis of genetic divergence, all the thirty six rice lines were grouped into six clusters. Clusters I, II, III, IV, V and VI contains 12, 17, 04, 1, 1 and 1 lines respectively reveals that the presence of sufficient amount of genetic diversity. The highest intra-cluster distance was observed for the cluster I followed by II and III suggested that genetic diversity available among the lines belongs to these clusters. The highest inter cluster distance was observed between the clusters I-III followed by III-V and III-VI revealed that the wider diversity present between these clusters. Crossing between the rice lines within cluster I and between the clusters I and III would produce good segregants with higher genetic advance for the improvement of these lines. Cluster I had highest mean value for single trait, cluster II had no higher mean values for any trait, cluster III showed highest mean value for three traits, cluster IV had highest mean value for five traits, cluster V had highest mean value for five traits and cluster VI had highest mean values for seven traits indicated that the selection of lines grouped in cluster VI, V, IV having highest cluster mean values in sequence for most of the traits. Highest contribution in the manifestation of genetic divergence ware exhibited by kernel elongation ratio, head rice recovery, biological yield per plant, amylose content and test weight revealed that these traits plays an important role in total genetic divergence among rice lines and also we may go for direct selection of these traits for diversity purpose.

Under molecular genetic diversity, 16 SSR markers (RM series) analyze the genetic diversity of 36 advance rice lines. Totally 58 alleles produced during investigation with a mean of 3.62 alleles indicated that the significant differences available in allelic diversity

among number of SSR loci in elite rice lines. The average PIC value for the markers was 0.360 with the range of 0.306 (RM 271) to 0.437 (RM 307 and RM 463) which infers that yet a few more markers that wrap the entire genome were to be used to validate the genetic diversity existing in the set of thirty six rice lines to the maximum extant. These markers are not highly polymorphic but have sufficient informative polymorphism to assess genetic diversity. Among the clusters, cluster III have highest number of lines (9) followed by cluster V (8), Cluster II (7), cluster I (6), cluster IV (3) and cluster VI (3). Dendrogram obtained from both level revealed that, different groups of rice lines comes under same cluster along with maximum similarity coefficient value which provides confirmatory result for those lines had same clusters but in case of inter cluster lines, similarity coefficient value is lowest, therefore crossing between these lines having minimum similarity will be beneficial to get effective transgressive segregants. Least similarity ware observed between G and F, I and AF, M and X which indicated that these lines are almost dissimilar from each-other. Entire results of similarity coefficient revealed that the presence of wider range of diversity among the lines which provides ample scope of selection of true parents that would be gave superior hybrids or segregants in next generations.

The ANOVA for stability analysis through Eberhart and Russell model (1966) showed that MSS due to genotype for all the traits were found highly significant and indicated that these lines are sufficiently differ in respect to all the traits. Highly significant and significant MSS due to environment existed for all traits except L/B ratio shows that considerable difference among all the environments under study. MSS due to G x E interaction were highly significant for the traits; plant height and hulling recovery reveals that the differential response of rice lines for these traits under various environmental conditions. MSS for environment (linear) were highly significant for all the traits except L/B ratio shows that the existence of variation among the environments tested. In case of G x E interaction (linear), only plant height and panicle length are found highly significant except all the traits reveals that significant differences among the genotypes for linear response of environments. and also indicating the importance of regression coefficient and deviation from regression in determination of phenotypic stability for these characters and absence of genetic differences among the lines for

regression on environmental indices and thus the further prediction of lines would be difficult for the traits which are non-significant. MSS for the pooled deviation are highly significant for all the traits except plant height, harvest index and hulling recovery indicated that performance of various lines fluctuated considerably in respect to their phenotypic stability for the respective traits. Control 2014 and 2015 (E_1 and E_3) revealed that the favourable environment for all the traits except plant height. Stress 2014 and 2015 (E_2 and E_4) showed favourable environment for only the trait plant height. Above results revealed that almost all the traits except plant height favours control or normal irrigated conditions while only plant height favours the reproductive drought stress environment that means these traits are suitable to produce maximum yield potential along with better quality under normally irrigated conditions. In case of days to 50% flowering, rice genotype CRR 724-1-B (IR 88889-44) found suitable for favorable environment while IR 94313:18-4-1-4-1-B, IR 92521-5-3-1-2, IR 92522-47-2-1-4 and IR 92517-1-3-1-1 for all types of environment. For plant height, IR 93339:40-B-18-13-B-B-1 found suitable for rich environment, IR 92545-53-4-1-3 suitable for poor environment and IR 94313:18-4-1-4-1-B, IR 94391-587-1-2-B, and IR 92516-8-3-3-4 for wider adaptation across all the environment. For days to maturity, line IR 92521-5-3-1-2 suitable for poor environment, IR 92521-7-5-1-1 for better environment and IR 92546-33-3-1-1 for all types of environment. For number of tillers per plant, IR 94313:18-4-1-4-1-B and IR 92522-61-3-1-4 suitable for favourable environment, IR 92523-37-1-1-2 and IR 92517-1-3-1-1 for unfavourable environment. For number of productive tillers per meter square, IR 92523-35-1-1-1 and IR 92527-6-2-1-2 lines supported unfavorable environment while IR 92546-7-1-1-3 for favourable environment. For panicle length, CRR 719-1-B (IR 88903-34) and IR 92527-6-2-1-2 found best widely adoptable line across all the environments while IR 92545-54-6-1-4 and IR 92545-51-1-1-4 recommended for favourable environment. For number of spikelets per panicle, IR 92522-61-3-1-4 is widely adoptable genotype while IR 92546-17-6-4-4 suitable for rich environment. For grain yield per plant, IR 92521-24-5-1-3 is widely adopted genotype across all the environments, IR 92545-53-4-1-3 for unfavourable environment, IR 92546-17-6-4-3 and IR 92546-17-6-4-4 for rich or favourable environment. For biological yield per plant, rice line IR 92522-47-2-1-4 recommended for wider stability while IR 92523-

37-1-1-2 suitable for rich environment. For harvest index, IR 92521-5-3-1-2 and IR 92545-54-6-1-4 suitable across all the environments while IR 92523-37-1-1-2 and IR 92545-24-3-1-1 desirable for favourable environment. For test weight, rice line IR 92523-35-1-1-1 suitable under favourable environment while IR 92545-24-3-1-1 suitable across the all environment. For grain yield kilogram per hectare, lines IR 94314-20-2-1-B, IR 92522-47-2-1-1 and IR 92546-7-1-1-3 widely stable lines across all the environments. For hulling recovery, IR 94313:18-4-1-4-1-B line suitable for rich or favourable environment while IR 92516-8-3-3-4 widely adopted across different environment. For milling recovery, IR 92521-5-3-1-2 suitable for favourable environment while IR 93339:40-B-18-13-B-B-1, IR 92521-24-5-1-3 and IR 92517-1-3-1-1 widely stable across all the environments. For head rice recovery, line IR 92521-5-3-1-2 suitable for rich environment, IR 92546-7-1-1-3 suitable for poor environment, CRR 724-1-B (IR 88889-44) and IR 92546-17-6-4-3 recommended for all types of environments. For kernel length before cooking, IR 94314-20-2-1-B and IR 92521-24-5-1-3 lines widely stable across all the environments. For kernel breadth before cooking, IR 92545-54-6-1-4 line suitable under unfavourable environment while RP-1-27-7-6-1-2-1 widely stable across all the environments. For kernel L/B ratio, IR 92517-1-3-1-1 suitable for poor environment while IR 92545-24-3-1-1 for favourable environment. For amylose content, only IR 92546-33-4-2-3 line suitable under poor environmental conditions. For volume expansion ratio, IR 92521-23-6-1-3 and IR 92522-47-2-1-4 lines suitable for rich environment while IR 92521-5-3-1-2 line widely adoptable for all types of environments. For kernel elongation ratio, only IR 92522-47-2-1-1 line suitable under favourable environment. These rice lines were identified for different traits on the basis of stability parameters. Rice line IR 92521-24-5-1-3 had maximum grain yield per plant, earliest days to 50% flowering, better maturity duration, better number of spikelets per panicle, good head rice recovery and moderate L/B ratio and also performed better than all three checks therefore, such line can be recommend to farmers or variety release proposal having wider stability across all the environments for grain yield per plant.

6.2 Conclusion:

Intrinsically in reference to spirit of the research it may be concluded that, there is adequate amount of genetic variability present in the elite genetic stock used under investigation. Some genotypes performed better in their strength for different traits out of check varieties. Improvement of this set of rice lines may be possible through the improvement of some traits *viz;* number of spikelets per panicle, head rice recovery, kernel elongation ratio, biological yield per plant and harvest index having higher heritability along with higher genetic advance and better interrelationship strength. Sufficient amount of genetic diversity available among the advance rice lines and validated by the morphological and molecular estimation to get valuable transgressive segregants under study. Based on the stability parameters, rice line IR 92521-24-5-1-3, IR 92523-35-1-1-1, IR 92521-5-3-1-2 and IR 92516-8-3-3-4 found widely stable line across all the environments, line IR 92545-53-4-1-3, IR 92545-23-2-1-1, IR 92545-54-6-1-4 and IR 92546-33-4-2-3 identified better lines for unfavourable or poor environment while lines IR 92546-17-6-4-3, IR 92546-17-6-4-4, IR 92546-33-3-1-1 and IR 92517-1-3-1-1 observed best lines for favourable or rich environment in reference to grain yield per plant and important quality attributes on the basis of either at par or superior performance from the best check.

FUTURE SCOPE OF RESEARCH
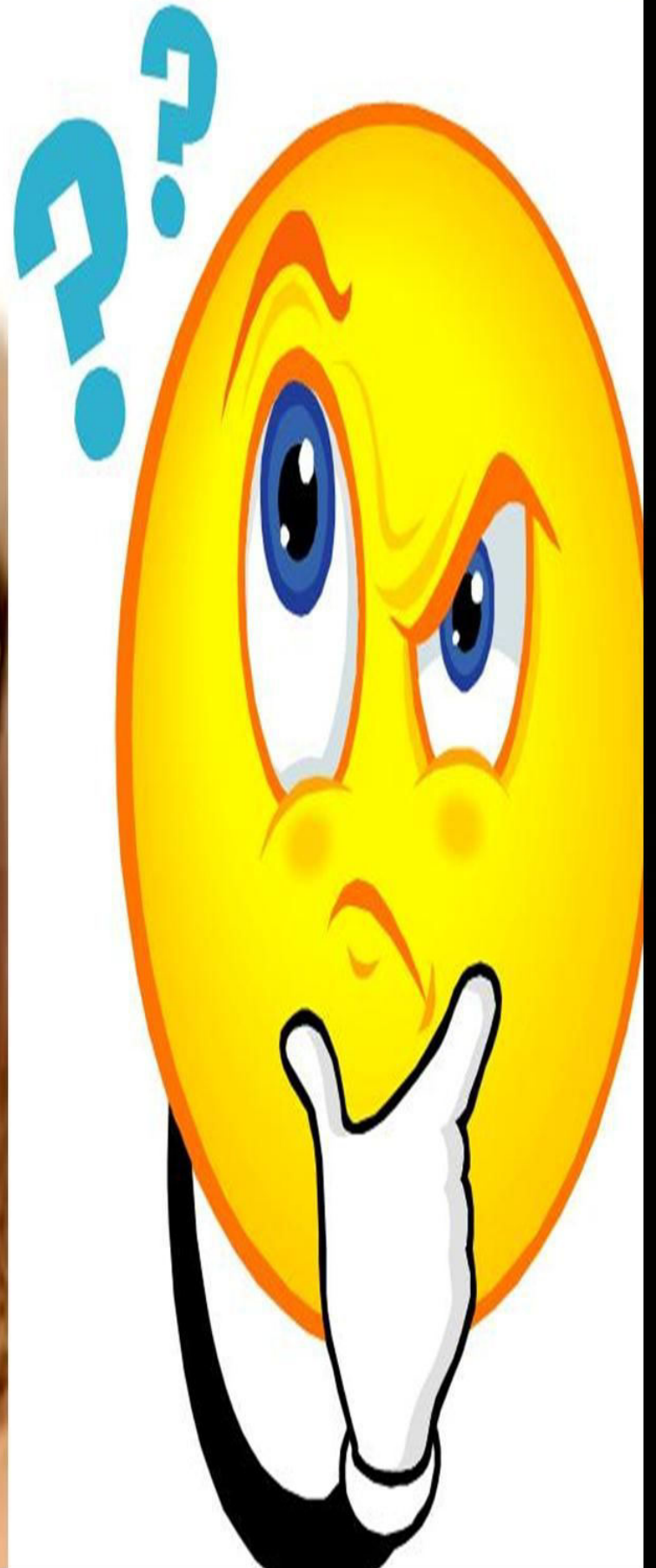
Future scope of research: 244

- ❖ The set of rice lines used in present investigation which have sufficient amount of genetic variability hence, these lines may be used in future rice breeding activities.

- ❖ On the basis of pooled mean performances, the superior lines identified for the each particular trait may be effective in the improvement of rice for such specific trait.

- ❖ Higher heritability (broad sense) along with higher estimates of genetic advance as percent of mean was observed for the traits *viz;* number of spikelets per panicle, head rice recovery and kernel elongation ratio therefore, these traits may be responsive in selection procedure.

- ❖ Desirable positive or negative significant associations with considerable positive or negative direct effects observed for the traits *viz;* biological yield per plant, harvest index and plant height that's why these traits may be used in effective rice breeding scheme because having better interrelationship with grain yield per plant.

- ❖ Genetic diversity on the basis of morphological trait and molecular markers indicated the presence of genetic diversity among the rice lines and there is a scope to get superior hybrids or transgressive segregants after crossing among these lines.

- ❖ On the basis of phenotypic stability parameter, the rice line IR 92521-24-5-1-3 was to be found best for the grain yield per plant and it was widely stable across all the environments under study hence, this line may be released for commercial cultivation after the conducting of multi-location trail.

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APPENDIX

Appendix 1: Analysis of variance for different traits in rice (C – 14)

S.No.	Characters	Mean sum of square		
		Replication (df = 02)	Treatment (df = 35)	Error (df = 70)
1	DFF	29.62	19.34**	10.33
2	PH	2.99	72.12**	30.48
3	DM	0.06	23.50**	13.22
4	NT/Pt	2.26	4.99**	1.40
5	NPT/m²	47.19	1713.02**	243.10
6	PL	6.57	5.03**	2.62
7	NSP/P	212.01	1693.34**	104.70
8	GY/Pt	3.73	17.20**	6.92
9	BY/Pt	3.69	148.34**	17.95
10	HI	5.06	66.94**	25.52
11	TW	2.52	12.13**	1.10
12	HULL. %	0.09	21.10**	5.24
13	MILL. %	0.43	33.84**	5.41
14	HRR %	7.15	112.32**	4.54
15	KLBC	0.01	0.59	0.04
16	KBBC	0.00	0.05	0.01
17	L/B RATIO	0.01	0.38	0.04
18	AMYLOSE C.	0.04	7.37**	0.07
19	VER	0.00	0.01	0.00
20	KER	0.00	0.02	0.00
21	GYKG/Ha	2626.93	731962.19**	56136.46

Appendix 2: Analysis of variance for different traits in rice (C – 15)

S.No.	Characters	Mean sum of square		
		Replication (df = 02)	Treatment (df = 35)	Error (df = 70)
1	DFF	1.23	35.86**	10.92
2	PH	20.89	136.64**	38.43
3	DM	6.56	56.21**	15.80
4	NT/Pt	3.69	4.28**	1.54
5	NPT/m²	360.40	2658.43**	159.24
6	PL	1.75	6.89**	0.88
7	NSP/P	221.08	2274.08**	94.54
8	GY/Pt	1.40	19.17**	5.21
9	BY/Pt	14.58	134.82**	16.43
10	HI	11.89	67.30**	17.67
11	TW	0.90	11.48**	0.81
12	HULL. %	15.49	21.43**	5.64
13	MILL. %	1.97	17.66**	4.17
14	HRR %	5.40	85.35**	3.96
15	KLBC	0.02	0.63	0.02
16	KBBC	0.00	0.05	0.01
17	L/B RATIO	0.03	0.27	0.04
18	AMYLOSE C.	0.14	6.79**	0.05
19	VER	0.00	0.01	0.00
20	KER	0.00	0.02	0.00
21	GYKG/Ha	33331.03	1007811.56**	94086.98

Appendix 3: Analysis of variance for different traits in rice (S – 14)

S.No.	Characters	Mean sum of square		
		Replication (df = 02)	Treatment (df = 35)	Error (df = 70)
1	DFF	4.01	33.81**	15.78
2	PH	16.74	82.38**	34.10
3	DM	2.11	39.36**	14.43
4	NT/Pt	0.45	4.12**	1.27
5	NPT/m²	107.11	2333.50**	250.28
6	PL	0.04	3.87**	1.52
7	NSP/P	183.62	1957.36**	113.80
8	GY/Pt	0.08	14.24**	6.12
9	BY/Pt	13.12	125.20**	15.54
10	HI	2.71	65.87**	26.21
11	TW	3.95	13.61**	1.32
12	HULL. %	3.18	17.80**	8.89
13	MILL. %	4.02	23.44**	6.60
14	HRR %	1.37	82.60**	5.05
15	KLBC	0.03	0.57	0.06
16	KBBC	0.01	0.05	0.02
17	L/B RATIO	0.02	0.37	0.07
18	AMYLOSE C.	0.02	6.60**	0.05
19	VER	0.00	0.01	0.00
20	KER	0.00	0.02	0.00
21	GYKG/Ha	59155.90	574481.00**	49652.34

Appendix 4: Analysis of variance for different traits in rice (S – 15)

S.No.	Characters	Mean sum of square		
		Replication (df = 02)	Treatment (df = 35)	Error (df = 70)
1	DFF	2.53	22.90**	12.12
2	PH	9.27	91.46**	28.44
3	DM	0.95	20.24**	12.68
4	NT/Pt	1.01	4.51**	1.04
5	NPT/m²	303.62	2036.43**	166.64
6	PL	2.00	5.85**	0.67
7	NSP/P	22.70	1535.65**	119.17
8	GY/Pt	1.45	16.36**	6.29
9	BY/Pt	6.19	104.50**	17.78
10	HI	11.40	60.13**	23.54
11	TW	0.04	8.56**	1.26
12	HULL. %	1.05	11.73**	6.77
13	MILL. %	0.14	13.25**	5.03
14	HRR %	7.65	69.80**	4.31
15	KLBC	0.04	0.71	0.04
16	KBBC	0.04	0.05	0.01
17	L/B RATIO	0.11	0.37	0.06
18	AMYLOSE C.	0.12	6.04**	0.05
19	VER	0.00	0.01	0.00
20	KER	0.00	0.01	0.00
21	GYKG/Ha	194973.53	748166.13**	64767.85

Appendix 5: Comparative analysis of variance (ANOVA) for different traits in rice

Characters ↓	Treatment Mean sum of square (df = 35)				
	CONTROL 14 (E1)	**STRESS 14 (E2)**	**CONTROL 15 (E3)**	**STRESS 15 (E4)**	**POOLED**
DFF	19.34**	33.81**	35.86**	22.90**	52**
PH	72.12**	82.4**	136.64**	91.46**	211.5**
DM	23.5**	39.4**	56.21**	20.24**	62.01**
NT/Pt	5**	4.12**	4.28**	4.51**	7.26**
NPT/Pt	1713.02**	2333.50**	2658.43**	2036.44**	4545**
PL	5.03**	3.87**	6.89**	5.9**	9.22**
NSP/P	1693.34**	1957.36**	2274.08**	1535.65**	5822.61**
GY/Pt	17.20**	14.24**	19.17**	16.36**	33.64**
BY/Pt	148.34**	125.20**	134.82**	104.50**	414.32**
HI	66.94**	65.9**	67.30**	60.13**	156.62**
TW	12.13**	13.62**	11.48**	8.56**	35.45**
HULL. %	21.1**	17.8**	21.43**	11.73**	43.47**
MILL. %	33.84**	23.44**	17.66**	13.25**	39.12**
HRR %	112.32**	82.6**	85.35**	69.8**	325.31**
KLBC	0.59	0.57	0.64	0.71	1.71**
KBBC	0.05	0.05	0.05	0.05	0.08
L/B RATIO	0.38	0.37	0.27	0.37	1.00
AMYLOSE C.	7.37**	6.60**	6.79**	6.05**	17.00**
VER	0.01	0.01	0.01	0.01	0.01
KER	0.02	0.02	0.02	0.01	0.07
GYKG/Ha	731962.2**	574481.00**	1007811.56**	748166.13**	2185969.75**

Appendix 6: Estimates of component of variance and genetic parameters for different characters in rice (C – 14)

Characters	VG	VP	GCV	PCV	h^2(bs) in %	GA	GA as % of mean
DFF	2.00	13.34	2.02	4.26	23	1.69	1.97
PH	13.88	44.36	3.62	6.47	31	4.29	4.17
DM	3.43	16.64	1.58	3.49	21	1.73	1.48
NT/Pt	1.20	2.60	8.88	13.09	46	1.53	12.41
NPT/m^2	489.97	733.07	8.91	10.90	67	37.28	15.00
PL	0.80	3.43	3.24	6.69	23	0.89	3.23
NSP/P	529.55	634.24	14.26	15.61	83	43.32	26.85
GY/Pt	3.43	10.35	6.13	10.65	33	2.19	7.26
BY/Pt	43.46	61.42	9.46	11.25	71	11.42	16.40
HI	13.81	39.33	8.48	14.31	35	4.54	10.35
TW	3.68	4.77	7.69	8.76	77	3.47	13.90
HULL. %	5.29	10.52	3.05	4.30	50	3.36	4.45
MILL. %	9.48	14.88	4.87	6.10	64	5.06	8.01
HRR %	35.93	40.47	12.08	12.82	89	11.63	23.44
KLBC	0.18	0.22	6.05	6.64	83	0.81	11.35
KBBC	0.01	0.02	5.18	7.23	51	0.16	7.65
L/B RATIO	0.11	0.16	9.75	11.52	72	0.58	16.99
AMYLOSE C.	2.43	2.51	6.84	6.94	97	3.17	13.88
VER	0.00	0.00	1.15	1.59	52	0.06	1.72
KER	0.01	0.01	10.71	10.73	100	0.15	22.04
GYKG/Ha	225275.25	281411.72	10.04	11.22	80	874.80	18.51

Appendix 7: Estimates of component of variance and genetic parameters for different characters in rice (C – 15)

Characters	VG	VP	GCV	PCV	h^2(bs) in %	GA	GA as % of mean
DFF	8.31	19.23	3.42	5.20	43	3.91	4.63
PH	32.60	71.43	5.89	8.72	46	7.95	8.20
DM	13.47	29.27	3.10	4.56	46	5.13	4.33
NT/Pt	0.91	2.45	8.81	14.46	37	1.20	11.06
NPT/m^2	833.06	992.30	12.38	13.51	84	54.48	23.97
PL	2.00	2.88	5.56	6.67	69	2.43	9.54
NSP/P	726.51	821.05	17.08	18.16	88	52.23	33.10
GY/Pt	4.65	9.86	7.61	11.08	47	3.05	10.77
BY/Pt	39.46	55.89	8.97	10.68	71	10.87	15.53
HI	16.54	34.22	9.95	14.31	48	5.83	14.25
TW	3.56	4.37	7.53	8.35	81	3.50	13.99
HULL. %	5.26	10.90	3.03	4.36	48	3.28	4.34
MILL. %	4.50	8.66	3.32	4.60	52	3.15	4.92
HRR %	27.13	31.09	10.70	11.45	87	10.02	20.59
KLBC	0.20	0.23	6.30	6.62	91	0.89	12.34
KBBC	0.01	0.02	5.12	7.32	49	0.16	7.39
L/B RATIO	0.07	0.12	8.15	10.22	64	0.45	13.38
AMYLOSE C.	2.25	2.30	6.57	6.65	98	3.05	13.37
VER	0.00	0.00	1.21	1.59	58	0.07	1.91
KER	0.01	0.01	10.71	10.73	100	0.15	22.04
GYKG/Ha	304574.84	398661.84	11.83	13.54	76	993.71	21.31

Appendix 8: Estimates of component of variance and genetic parameters for different characters in rice (S – 14)

Characters	VG	VP	GCV	PCV	h^2(bs) in %	GA	GA as % of mean
DFF	6.01	21.79	3.05	5.81	28	2.65	3.30
PH	16.09	50.19	3.87	6.83	32	4.68	4.51
DM	8.31	22.74	2.58	4.27	37	3.59	3.21
NT/Pt	0.95	2.22	9.35	14.32	43	1.31	12.59
NPT/m^2	694.41	944.69	11.92	13.90	74	46.54	21.05
PL	0.78	2.31	3.36	5.76	34	1.06	4.03
NSP/P	614.52	728.32	16.76	18.25	84	46.91	31.71
GY/Pt	2.71	8.83	6.21	11.21	31	1.88	7.08
BY/Pt	36.55	52.09	9.36	11.17	70	10.43	16.15
HI	13.22	39.43	8.76	15.14	34	4.34	10.45
TW	4.10	5.42	8.65	9.94	76	3.63	15.50
HULL. %	2.97	11.86	2.36	4.73	25	1.78	2.44
MILL. %	5.61	12.21	3.87	5.71	46	3.31	5.41
HRR %	25.85	30.90	10.66	11.65	84	9.58	20.08
KLBC	0.17	0.23	5.94	6.92	74	0.73	10.50
KBBC	0.01	0.03	4.82	7.88	37	0.13	6.07
L/B RATIO	0.10	0.17	9.35	12.13	59	0.50	14.84
AMYLOSE C.	2.18	2.24	6.96	7.04	98	3.01	14.15
VER	0.00	0.00	1.57	1.87	70	0.09	2.71
KER	0.01	0.01	11.86	11.88	100	0.16	24.38
GYKG/Ha	174942.89	224595.23	9.84	11.15	78	760.44	17.89

Appendix 9: Estimates of component of variance and genetic parameters for different characters in rice (S – 15)

Characters	VG	VP	GCV	PCV	h^2(bs) in %	GA	GA as % of mean
DFF	3.59	15.71	2.29	4.80	23	1.87	2.26
PH	21.01	49.44	4.80	7.37	42	6.15	6.45
DM	2.52	15.20	1.37	3.36	17	1.33	1.15
NT/Pt	1.16	2.20	11.09	15.27	53	1.61	16.58
NPT/m²	623.27	789.90	11.76	13.24	79	45.68	21.52
PL	1.73	2.39	5.32	6.26	72	2.30	9.31
NSP/P	472.16	591.33	15.22	17.03	80	40.00	28.02
GY/Pt	3.36	9.65	7.21	12.33	35	2.23	8.76
BY/Pt	28.91	46.68	8.20	10.42	62	8.72	13.29
HI	12.20	35.74	8.93	15.29	34	4.20	10.75
TW	2.43	3.69	6.61	8.14	66	2.61	11.05
HULL. %	1.65	8.42	1.74	3.92	20	1.17	1.59
MILL. %	2.74	7.77	2.66	4.48	35	2.02	3.25
HRR %	21.83	26.14	9.99	10.93	84	8.80	18.80
KLBC	0.22	0.26	6.78	7.33	86	0.90	12.92
KBBC	0.01	0.02	4.87	7.63	41	0.13	6.40
L/B RATIO	0.11	0.16	9.58	11.86	65	0.54	15.93
AMYLOSE C.	2.00	2.05	6.53	6.61	98	2.88	13.27
VER	0.00	0.01	1.88	2.15	77	0.11	3.39
KER	0.01	0.01	11.27	11.29	100	0.15	23.18
GYKG/Ha	227799.44	292567.28	12.89	14.61	78	867.57	23.43

Appendix 10: Comparative mean performance of days to 50% flowering in advance rice lines

Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
Days to 50% flowering					
CRR 719-1-B (IR 88903-34)	82.67	76.33	82.67	80.00	80.42
CRR 724-1-B (IR 88889-44)	80.33	74.67	79.67	76.67	77.83
RP-1-27-7-6-1-2-1	87.00	79.33	84.00	82.00	83.08
IR 94313:18-4-1-4-1-B	84.00	76.00	76.33	80.33	79.17
IR 88287-383-1-B-B-1-1-B	88.00	85.00	79.33	79.33	82.92
IR 94391-587-1-2-B	82.33	80.33	87.33	79.33	82.33
IR 94314-20-2-1-B	89.00	83.00	86.00	85.67	85.92
IR 93339:40-B-18-13-B-B-1	88.33	87.00	88.33	86.67	87.58
IR 92521-5-3-1-2	85.67	79.33	80.67	81.00	81.67
IR 92521-7-5-1-1	83.33	80.67	86.33	81.33	82.92
IR 92521-23-6-1-3	88.33	88.67	80.67	78.00	83.92
IR 92521-24-5-1-3	85.00	77.67	82.00	82.00	81.67
IR 92522-47-2-1-1	86.67	80.67	85.00	81.00	83.33
IR 92522-47-2-1-4	86.33	80.00	80.33	82.00	82.17
IR 92522-61-3-1-4	83.33	77.67	90.00	87.33	84.58
IR 92523-35-1-1-1	83.00	80.33	81.67	81.00	81.50
IR 92523-37-1-1-2	90.00	81.67	89.00	81.67	85.58
IR 92527-6-2-1-2	87.33	80.33	87.00	83.00	84.42
IR 92527-6-2-1-4	86.67	80.67	90.33	84.33	85.50
IR 92545-53-4-1-3	83.00	76.67	83.33	78.33	80.33
IR 92545-54-6-1-4	86.33	78.33	85.67	82.67	83.25
IR 92546-7-1-1-3	87.33	83.00	87.00	85.33	85.67
IR 92546-17-6-4-3	85.00	81.33	89.67	87.00	85.75
IR 92546-17-6-4-4	84.00	77.67	88.33	83.67	83.42
IR 92546-33-3-1-1	85.00	77.67	84.33	84.00	82.75
IR 92517-1-3-1-1	85.67	80.33	84.00	82.00	83.00
IR 92522-45-3-1-4	87.33	81.33	85.33	81.67	83.92
IR 92545-23-2-1-1	91.00	80.00	82.00	81.67	83.67
IR 92545-24-3-1-1	85.00	76.67	88.00	85.33	83.75
IR 92545-40-2-2-3	86.67	81.00	83.67	86.67	84.50
IR 92545-51-1-1-4	91.33	81.67	81.33	81.67	84.00
IR 92546-33-4-2-3	85.67	82.33	84.67	86.00	84.67
IR 92516-8-3-3-4	85.33	88.33	79.67	83.67	84.25
MTU 1010 (Check)	83.00	76.33	83.00	81.67	81.00
IR 64 (Check)	82.33	77.67	82.00	83.33	81.33
LALAT (Check)	87.33	84.67	87.00	87.67	86.67
Mean	**85.80**	**80.40**	**84.32**	**82.64**	**83.29**
C.V.	3.75	4.94	3.92	4.21	4.20
F ratio	1.87	2.14	3.28	1.89	2.30
S.E.	1.86	2.29	1.91	2.01	2.02
C.D. 5%	5.24	6.47	5.38	5.67	5.69
C.D. 1%	6.95	8.59	7.14	7.53	7.55

Appendix 11: Comparative mean performance of plant height in advance rice lines

Plant height (cm)				
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	107.30	98.58	107.77	103.50	104.29
CRR 724-1-B (IR 88889-44)	96.27	104.83	98.50	94.97	98.64
RP-1-27-7-6-1-2-1	104.47	109.75	104.58	100.50	104.83
IR 94313:18-4-1-4-1-B	94.28	101.58	89.92	90.50	94.07
IR 88287-383-1-B-B-1-1-B	103.62	99.50	95.25	89.30	96.92
IR 94391-587-1-2-B	101.00	100.17	87.75	97.00	96.48
IR 94314-20-2-1-B	104.08	108.67	83.33	89.33	96.35
IR 93339:40-B-18-13-B-B-1	103.77	101.00	93.50	94.33	98.15
IR 92521-5-3-1-2	108.23	113.67	106.83	103.75	108.12
IR 92521-7-5-1-1	117.00	115.83	96.58	96.17	106.40
IR 92521-23-6-1-3	109.77	109.50	108.50	103.57	107.83
IR 92521-24-5-1-3	107.90	105.17	108.67	102.25	106.00
IR 92522-47-2-1-1	97.13	106.58	97.47	87.25	97.11
IR 92522-47-2-1-4	95.50	101.33	95.87	93.83	96.63
IR 92522-61-3-1-4	102.67	99.33	101.83	97.78	100.40
IR 92523-35-1-1-1	106.50	108.58	86.00	90.50	97.90
IR 92523-37-1-1-2	98.30	92.92	98.67	94.67	96.14
IR 92527-6-2-1-2	106.00	106.08	94.33	87.17	98.40
IR 92527-6-2-1-4	99.20	100.67	86.50	86.57	93.23
IR 92545-53-4-1-3	101.67	100.50	95.33	94.50	98.00
IR 92545-54-6-1-4	110.27	107.42	87.00	93.33	99.50
IR 92546-7-1-1-3	106.18	109.67	102.25	102.83	105.23
IR 92546-17-6-4-3	101.50	99.58	101.40	100.63	100.78
IR 92546-17-6-4-4	96.17	93.42	90.17	94.42	93.54
IR 92546-33-3-1-1	99.23	99.17	96.50	93.83	97.18
IR 92517-1-3-1-1	99.30	101.75	92.83	90.00	95.97
IR 92522-45-3-1-4	101.83	100.50	95.50	89.17	96.75
IR 92545-23-2-1-1	103.97	105.83	101.53	103.17	103.63
IR 92545-24-3-1-1	109.67	107.75	96.83	92.00	101.56
IR 92545-40-2-2-3	106.33	101.25	106.00	104.00	104.40
IR 92545-51-1-1-4	101.15	102.33	98.50	96.83	99.70
IR 92546-33-4-2-3	105.97	104.33	90.08	88.50	97.22
IR 92516-8-3-3-4	97.83	100.08	92.33	91.17	95.35
MTU 1010 (Check)	102.53	110.00	103.03	100.50	104.02
IR 64 (Check)	99.47	97.17	97.17	94.92	97.18
LALAT (Check)	102.25	108.00	101.83	102.17	103.56
Mean	**103.01**	**103.68**	**96.95**	**95.41**	**99.76**
C.V.	5.36	5.63	6.43	5.59	5.75
F ratio	2.37	2.42	3.52	3.22	2.88
S.E.	3.19	3.37	3.60	3.08	3.31
C.D. 5%	8.99	9.51	10.15	8.68	9.33
C.D. 1%	11.94	12.62	13.47	11.53	12.39

Appendix 12: Comparative mean performance of days to physiological maturity in advance rice lines

Days to physiological maturity					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	113.67	108.00	120.00	115.00	114.17
CRR 724-1-B (IR 88889-44)	111.67	105.67	118.33	114.00	112.42
RP-1-27-7-6-1-2-1	114.33	111.00	121.33	118.33	116.25
IR 94313:18-4-1-4-1-B	115.33	108.67	108.33	111.33	110.92
IR 88287-383-1-B-B-1-1-B	119.00	117.33	109.00	112.00	114.33
IR 94391-587-1-2-B	112.67	110.67	122.67	110.67	114.17
IR 94314-20-2-1-B	119.33	114.67	122.33	116.67	118.25
IR 93339:40-B-18-13-B-B-1	118.33	117.33	121.67	118.67	119.00
IR 92521-5-3-1-2	114.67	112.33	118.67	115.00	115.17
IR 92521-7-5-1-1	113.00	110.33	119.67	113.33	114.08
IR 92521-23-6-1-3	119.00	121.00	125.33	117.67	120.75
IR 92521-24-5-1-3	116.67	106.67	110.33	114.33	112.00
IR 92522-47-2-1-1	118.33	112.67	123.33	120.33	118.67
IR 92522-47-2-1-4	115.67	110.33	120.33	117.33	115.92
IR 92522-61-3-1-4	114.67	109.00	121.00	119.33	116.00
IR 92523-35-1-1-1	117.33	112.33	124.67	117.33	117.92
IR 92523-37-1-1-2	123.33	111.67	122.33	114.00	117.83
IR 92527-6-2-1-2	118.67	112.00	123.00	115.00	117.17
IR 92527-6-2-1-4	117.33	112.33	121.00	115.67	116.58
IR 92545-53-4-1-3	115.67	108.67	121.00	115.33	115.17
IR 92545-54-6-1-4	118.67	110.00	120.00	115.33	116.00
IR 92546-7-1-1-3	117.33	116.00	118.33	116.67	117.08
IR 92546-17-6-4-3	116.33	112.00	121.33	119.33	117.25
IR 92546-17-6-4-4	115.33	109.00	118.33	115.33	114.50
IR 92546-33-3-1-1	115.67	109.33	116.00	115.33	114.08
IR 92517-1-3-1-1	117.33	111.67	116.00	112.00	114.25
IR 92522-45-3-1-4	118.33	114.00	119.00	115.00	116.58
IR 92545-23-2-1-1	123.00	112.00	114.33	114.00	115.83
IR 92545-24-3-1-1	117.00	106.33	115.67	118.67	114.42
IR 92545-40-2-2-3	117.33	111.33	113.33	120.00	115.50
IR 92545-51-1-1-4	120.00	113.67	119.00	115.00	116.92
IR 92546-33-4-2-3	119.33	115.00	113.00	118.00	116.33
IR 92516-8-3-3-4	122.67	118.33	117.00	114.00	118.00
MTU 1010 (Check)	113.67	106.00	115.67	113.67	112.25
IR 64 (Check)	114.00	109.00	112.67	115.67	112.83
LALAT (Check)	118.67	116.67	123.67	121.33	120.08
Mean	**117.04**	**111.75**	**118.55**	**115.85**	**115.80**
C.V.	3.11	3.40	3.35	3.07	3.23
F ratio	1.78	2.73	3.56	1.60	2.41
S.E.	2.10	2.19	2.30	2.06	2.16
C.D. 5%	5.92	6.19	6.47	5.80	6.09
C.D. 1%	7.86	8.21	8.59	7.70	8.09

Appendix 13: Comparative mean performance of number of tillers per plant in advance rice lines

Number of tillers per plant					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	10.33	10.33	9.33	9.67	9.92
CRR 724-1-B (IR 88889-44)	11.67	9.67	12.00	11.00	11.08
RP-1-27-7-6-1-2-1	12.67	11.67	10.33	12.67	11.83
IR 94313:18-4-1-4-1-B	13.67	10.33	11.00	10.67	11.42
IR 88287-383-1-B-B-1-1-B	14.00	12.67	10.67	10.33	11.92
IR 94391-587-1-2-B	13.00	8.33	11.00	11.00	10.83
IR 94314-20-2-1-B	12.00	10.67	9.00	10.67	10.58
IR 93339:40-B-18-13-B-B-1	11.67	10.67	11.00	10.33	10.92
IR 92521-5-3-1-2	8.67	7.33	12.00	6.67	8.67
IR 92521-7-5-1-1	13.33	8.67	11.67	10.67	11.08
IR 92521-23-6-1-3	14.00	9.33	7.33	6.33	9.25
IR 92521-24-5-1-3	11.33	8.67	9.00	8.67	9.42
IR 92522-47-2-1-1	13.33	10.67	10.00	8.00	10.50
IR 92522-47-2-1-4	12.33	11.00	12.00	10.67	11.50
IR 92522-61-3-1-4	13.33	10.67	12.00	10.33	11.58
IR 92523-35-1-1-1	11.67	11.00	12.00	10.00	11.17
IR 92523-37-1-1-2	12.33	10.33	12.00	10.33	11.25
IR 92527-6-2-1-2	11.67	11.00	11.67	10.00	11.08
IR 92527-6-2-1-4	12.33	10.67	12.00	10.67	11.42
IR 92545-53-4-1-3	13.33	10.33	11.33	10.00	11.25
IR 92545-54-6-1-4	12.00	9.00	13.00	9.33	10.83
IR 92546-7-1-1-3	11.33	11.00	9.67	9.33	10.33
IR 92546-17-6-4-3	13.33	12.00	10.00	9.00	11.08
IR 92546-17-6-4-4	12.67	10.00	10.00	9.33	10.50
IR 92546-33-3-1-1	12.00	9.33	10.67	9.00	10.25
IR 92517-1-3-1-1	12.00	11.33	10.33	9.67	10.83
IR 92522-45-3-1-4	13.33	10.00	10.67	9.00	10.75
IR 92545-23-2-1-1	9.67	10.33	9.33	8.33	9.42
IR 92545-24-3-1-1	11.67	9.33	11.67	9.33	10.50
IR 92545-40-2-2-3	9.67	11.67	9.67	9.33	10.08
IR 92545-51-1-1-4	14.00	10.67	11.67	9.00	11.33
IR 92546-33-4-2-3	12.33	11.00	11.00	10.67	11.25
IR 92516-8-3-3-4	12.00	10.67	11.67	10.33	11.17
MTU 1010 (Check)	13.67	12.33	12.33	9.67	12.00
IR 64 (Check)	14.00	9.67	10.00	8.33	10.50
LALAT (Check)	13.00	12.33	11.00	11.00	11.83
Mean	**12.31**	**10.41**	**10.83**	**9.70**	**10.81**
C.V.	9.62	10.84	11.46	10.50	10.60
F ratio	3.56	3.23	2.77	4.35	3.48
S.E.	0.68	0.65	0.72	0.59	0.66
C.D. 5%	1.93	1.84	2.02	1.66	1.86
C.D. 1%	2.56	2.44	2.68	2.20	2.47

Appendix 14: Comparative mean performance of number of productive tillers per meter square in advance rice lines

Number of productive tillers per meter square					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	292.33	227.67	226.67	211.33	239.50
CRR 724-1-B (IR 88889-44)	228.33	199.00	197.67	166.33	197.83
RP-1-27-7-6-1-2-1	237.67	211.33	236.00	210.67	223.92
IR 94313:18-4-1-4-1-B	218.33	141.67	270.67	217.67	212.08
IR 88287-383-1-B-B-1-1-B	244.33	225.67	214.33	222.00	226.58
IR 94391-587-1-2-B	232.67	220.33	226.33	197.33	219.17
IR 94314-20-2-1-B	281.33	218.00	211.33	216.00	231.67
IR 93339:40-B-18-13-B-B-1	256.33	251.67	236.67	211.67	239.08
IR 92521-5-3-1-2	220.00	186.33	204.33	171.67	195.58
IR 92521-7-5-1-1	240.00	244.00	263.33	221.67	242.25
IR 92521-23-6-1-3	255.67	222.67	176.00	154.67	202.25
IR 92521-24-5-1-3	228.00	226.67	152.67	123.67	182.75
IR 92522-47-2-1-1	233.00	193.67	229.33	214.00	217.50
IR 92522-47-2-1-4	204.33	205.67	208.67	201.33	205.00
IR 92522-61-3-1-4	282.00	241.33	269.00	214.33	251.67
IR 92523-35-1-1-1	253.33	228.33	231.33	221.00	233.50
IR 92523-37-1-1-2	234.67	221.00	219.67	219.67	223.75
IR 92527-6-2-1-2	261.00	234.67	243.00	228.00	241.67
IR 92527-6-2-1-4	262.00	242.00	224.00	219.67	236.92
IR 92545-53-4-1-3	246.00	204.67	277.33	219.67	236.92
IR 92545-54-6-1-4	235.00	221.00	232.33	227.00	228.83
IR 92546-7-1-1-3	292.67	265.00	284.00	250.00	272.92
IR 92546-17-6-4-3	244.33	207.67	246.00	205.00	225.75
IR 92546-17-6-4-4	246.00	160.33	228.00	218.33	213.17
IR 92546-33-3-1-1	281.33	285.67	255.33	221.00	260.83
IR 92517-1-3-1-1	213.00	211.33	290.67	278.00	248.25
IR 92522-45-3-1-4	240.67	216.67	276.67	217.67	237.92
IR 92545-23-2-1-1	245.33	212.33	218.33	202.00	219.50
IR 92545-24-3-1-1	261.00	239.00	210.33	206.33	229.17
IR 92545-40-2-2-3	280.67	209.33	213.33	217.33	230.17
IR 92545-51-1-1-4	224.67	217.00	206.67	208.00	214.08
IR 92546-33-4-2-3	292.67	260.67	246.33	222.67	255.58
IR 92516-8-3-3-4	227.67	219.00	240.00	223.33	227.50
MTU 1010 (Check)	241.33	215.00	255.00	235.33	236.67
IR 64 (Check)	278.33	272.00	254.67	237.67	260.67
LALAT (Check)	230.00	201.67	217.67	208.33	214.42
Mean	**248.50**	**221.11**	**233.16**	**212.23**	**228.75**
C.V.	6.27	7.15	5.41	6.08	6.23
F ratio	7.05	9.32	16.69	12.22	11.32
S.E.	9.00	9.13	7.29	7.45	8.22
C.D. 5%	25.39	25.76	20.55	21.02	23.18
C.D. 1%	33.71	34.20	27.28	27.91	30.78

Appendix 15: Comparative mean performance of panicle length in advance rice lines

Panicle length (cm)					
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	28.67	25.42	25.94	25.11	26.28
CRR 724-1-B (IR 88889-44)	28.50	25.50	24.50	23.22	25.43
RP-1-27-7-6-1-2-1	28.73	25.50	24.17	23.53	25.48
IR 94313:18-4-1-4-1-B	28.75	26.33	25.17	22.25	25.63
IR 88287-383-1-B-B-1-1-B	26.25	26.42	27.67	25.92	26.56
IR 94391-587-1-2-B	25.42	25.42	24.50	25.75	25.27
IR 94314-20-2-1-B	26.42	29.58	23.05	24.33	25.85
IR 93339:40-B-18-13-B-B-1	28.33	26.50	28.40	26.94	27.54
IR 92521-5-3-1-2	26.83	25.67	27.45	25.22	26.29
IR 92521-7-5-1-1	30.17	27.00	25.22	25.17	26.89
IR 92521-23-6-1-3	28.08	26.67	24.11	24.50	25.84
IR 92521-24-5-1-3	24.83	25.58	25.12	22.33	24.47
IR 92522-47-2-1-1	25.25	25.83	24.17	22.31	24.39
IR 92522-47-2-1-4	28.08	27.00	24.23	22.78	25.52
IR 92522-61-3-1-4	28.30	26.92	27.50	26.36	27.27
IR 92523-35-1-1-1	26.95	26.00	25.33	25.22	25.88
IR 92523-37-1-1-2	27.25	25.75	28.13	26.31	26.86
IR 92527-6-2-1-2	28.62	25.25	26.36	25.48	26.43
IR 92527-6-2-1-4	27.42	26.25	27.03	26.17	26.71
IR 92545-53-4-1-3	28.33	26.67	23.36	24.89	25.81
IR 92545-54-6-1-4	29.08	27.58	25.28	25.89	26.96
IR 92546-7-1-1-3	28.42	26.50	24.45	24.00	25.84
IR 92546-17-6-4-3	28.25	26.75	23.69	24.25	25.73
IR 92546-17-6-4-4	27.33	25.42	25.17	24.45	25.59
IR 92546-33-3-1-1	26.68	25.00	24.36	23.22	24.82
IR 92517-1-3-1-1	26.17	26.17	25.67	25.61	25.90
IR 92522-45-3-1-4	28.82	26.42	24.55	23.17	25.74
IR 92545-23-2-1-1	29.87	29.17	24.28	25.27	27.15
IR 92545-24-3-1-1	28.35	26.25	24.17	22.25	25.25
IR 92545-40-2-2-3	28.53	26.83	27.20	27.05	27.41
IR 92545-51-1-1-4	28.82	27.08	25.00	25.55	26.61
IR 92546-33-4-2-3	26.75	24.58	26.45	24.28	25.52
IR 92516-8-3-3-4	28.00	24.42	24.72	24.36	25.37
MTU 1010 (Check)	26.08	25.75	24.40	24.08	25.08
IR 64 (Check)	26.00	26.75	27.42	25.08	26.31
LALAT (Check)	28.58	28.92	28.61	27.11	28.31
Mean	**27.69**	**26.36**	**25.47**	**24.71**	**26.06**
C.V.	5.85	4.68	3.68	3.30	4.38
F ratio	1.92	2.54	7.83	8.78	5.27
S.E.	0.94	0.71	0.54	0.47	0.66
C.D. 5%	2.64	2.01	1.53	1.33	1.88
C.D. 1%	3.50	2.67	2.03	1.76	2.49

Appendix 16: Comparative mean performance of number of spikelets per panicle in advance rice lines

Number of spikelet's per panicle					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	146.67	146.33	132.00	123.00	137.00
CRR 724-1-B (IR 88889-44)	154.00	123.33	142.00	130.00	137.33
RP-1-27-7-6-1-2-1	138.33	135.67	118.33	117.00	127.33
IR 94313:18-4-1-4-1-B	142.67	114.67	129.33	122.33	127.25
IR 88287-383-1-B-B-1-1-B	184.67	138.33	212.67	171.00	176.67
IR 94391-587-1-2-B	141.00	124.33	146.00	144.33	138.92
IR 94314-20-2-1-B	157.00	146.00	127.00	112.67	135.67
IR 93339:40-B-18-13-B-B-1	140.00	141.33	155.67	140.67	144.42
IR 92521-5-3-1-2	217.33	218.33	184.67	166.67	196.75
IR 92521-7-5-1-1	236.33	231.67	207.67	161.33	209.25
IR 92521-23-6-1-3	177.33	150.00	185.67	175.33	172.08
IR 92521-24-5-1-3	194.00	178.67	214.67	210.67	199.50
IR 92522-47-2-1-1	156.67	158.00	186.00	162.33	165.75
IR 92522-47-2-1-4	134.67	116.00	142.67	129.67	130.75
IR 92522-61-3-1-4	162.00	153.67	173.67	150.67	160.00
IR 92523-35-1-1-1	143.67	111.33	126.00	115.33	124.08
IR 92523-37-1-1-2	164.33	164.33	175.33	165.00	167.25
IR 92527-6-2-1-2	143.33	140.33	122.67	125.67	133.00
IR 92527-6-2-1-4	150.33	159.33	134.67	114.00	139.58
IR 92545-53-4-1-3	148.00	123.00	140.33	134.00	136.33
IR 92545-54-6-1-4	136.00	134.33	106.67	103.67	120.17
IR 92546-7-1-1-3	168.00	145.67	186.33	160.67	165.17
IR 92546-17-6-4-3	170.67	168.67	149.00	131.67	155.00
IR 92546-17-6-4-4	172.33	162.33	174.33	152.00	165.25
IR 92546-33-3-1-1	175.67	153.00	151.33	134.33	153.58
IR 92517-1-3-1-1	174.67	143.00	189.67	164.33	167.92
IR 92522-45-3-1-4	157.00	156.33	151.67	135.33	150.08
IR 92545-23-2-1-1	157.33	141.67	141.33	141.33	145.42
IR 92545-24-3-1-1	147.00	145.33	136.33	120.00	137.17
IR 92545-40-2-2-3	154.00	160.67	169.00	154.00	159.42
IR 92545-51-1-1-4	157.00	137.33	173.00	167.33	158.67
IR 92546-33-4-2-3	213.67	181.33	186.67	167.33	187.25
IR 92516-8-3-3-4	162.67	134.67	150.67	132.33	145.08
MTU 1010 (Check)	142.67	120.67	162.00	141.33	141.67
IR 64 (Check)	150.00	134.33	158.00	135.67	144.50
LALAT (Check)	136.67	130.67	138.00	126.67	133.00
Mean	**161.32**	**147.91**	**157.81**	**142.77**	**152.45**
C.V.	6.34	7.21	6.16	7.65	6.84
F ratio	16.17	17.20	24.05	12.89	17.58
S.E.	5.91	6.16	5.61	6.30	6.00
C.D. 5%	16.66	17.37	15.83	17.78	16.91
C.D. 1%	22.12	23.06	21.02	23.60	22.45

Appendix 17: Comparative mean performance of grain yield per plant in advance rice lines

Grain yield per plant (g)					
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	32.67	25.33	26.67	24.67	27.33
CRR 724-1-B (IR 88889-44)	29.00	26.67	27.33	26.00	27.25
RP-1-27-7-6-1-2-1	31.33	27.33	25.33	21.33	26.33
IR 94313:18-4-1-4-1-B	28.33	24.33	28.33	27.00	27.00
IR 88287-383-1-B-B-1-1-B	32.67	27.33	27.00	24.00	27.75
IR 94391-587-1-2-B	30.67	26.00	29.33	24.00	27.50
IR 94314-20-2-1-B	34.33	29.67	34.33	28.00	31.58
IR 93339:40-B-18-13-B-B-1	28.00	27.00	29.33	26.67	27.75
IR 92521-5-3-1-2	29.00	27.67	28.67	23.67	27.25
IR 92521-7-5-1-1	24.67	24.00	27.33	22.67	24.67
IR 92521-23-6-1-3	31.00	23.33	28.67	25.00	27.00
IR 92521-24-5-1-3	34.33	27.67	29.67	30.00	30.42
IR 92522-47-2-1-1	31.00	27.67	31.67	31.00	30.33
IR 92522-47-2-1-4	32.67	25.33	26.00	22.00	26.50
IR 92522-61-3-1-4	27.00	27.33	25.67	23.00	25.75
IR 92523-35-1-1-1	29.33	25.00	25.67	24.00	26.00
IR 92523-37-1-1-2	35.00	29.33	30.33	27.00	30.42
IR 92527-6-2-1-2	29.67	22.67	30.67	27.00	27.50
IR 92527-6-2-1-4	33.00	32.00	27.67	25.67	29.58
IR 92545-53-4-1-3	29.33	24.33	30.00	27.00	27.67
IR 92545-54-6-1-4	28.33	25.33	28.67	25.67	27.00
IR 92546-7-1-1-3	29.67	28.00	23.67	24.33	26.42
IR 92546-17-6-4-3	31.33	29.67	28.33	24.33	28.42
IR 92546-17-6-4-4	32.33	28.00	28.33	26.00	28.67
IR 92546-33-3-1-1	30.33	26.33	26.00	22.67	26.33
IR 92517-1-3-1-1	32.67	27.33	30.33	26.33	29.17
IR 92522-45-3-1-4	29.00	26.00	32.67	30.33	29.50
IR 92545-23-2-1-1	28.67	23.33	28.33	26.33	26.67
IR 92545-24-3-1-1	27.33	23.00	30.33	23.33	26.00
IR 92545-40-2-2-3	25.67	26.33	22.33	24.33	24.67
IR 92545-51-1-1-4	31.67	29.33	27.00	22.33	27.58
IR 92546-33-4-2-3	31.00	28.33	32.67	28.67	30.17
IR 92516-8-3-3-4	29.00	23.00	29.33	25.67	26.75
MTU 1010 (Check)	27.33	25.67	25.00	23.00	25.25
IR 64 (Check)	30.00	28.00	28.00	25.33	27.83
LALAT (Check)	30.33	26.33	29.67	26.33	28.17
Mean	**30.21**	**26.50**	**28.34**	**25.41**	**27.62**
C.V.	8.71	9.34	8.05	9.87	8.99
F ratio	2.49	2.33	3.68	2.60	2.77
S.E.	1.52	1.43	1.32	1.45	1.43
C.D. 5%	4.28	4.03	3.72	4.08	4.03
C.D. 1%	5.69	5.35	4.93	5.42	5.35

Appendix 18: Comparative mean performance of biological yield per plant in advance rice lines

Biological yield per plant (g)				
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	63.00	57.00	60.00	54.67	58.67
CRR 724-1-B (IR 88889-44)	70.00	63.67	69.00	64.33	66.75
RP-1-27-7-6-1-2-1	63.67	58.33	69.00	65.67	64.17
IR 94313:18-4-1-4-1-B	74.33	74.00	69.00	63.33	70.17
IR 88287-383-1-B-B-1-1-B	64.33	57.33	61.33	62.00	61.25
IR 94391-587-1-2-B	75.33	68.33	77.67	77.33	74.67
IR 94314-20-2-1-B	82.33	73.67	77.00	67.67	75.17
IR 93339:40-B-18-13-B-B-1	71.67	64.67	79.00	69.33	71.17
IR 92521-5-3-1-2	64.00	57.00	65.67	58.33	61.25
IR 92521-7-5-1-1	70.67	65.33	76.33	71.00	70.83
IR 92521-23-6-1-3	74.67	70.33	69.00	63.67	69.42
IR 92521-24-5-1-3	75.67	78.67	73.00	72.67	75.00
IR 92522-47-2-1-1	78.67	70.00	79.67	69.00	74.33
IR 92522-47-2-1-4	72.00	68.33	73.67	66.67	70.17
IR 92522-61-3-1-4	64.67	59.67	66.33	56.00	61.67
IR 92523-35-1-1-1	63.67	64.67	60.33	60.00	62.17
IR 92523-37-1-1-2	77.67	71.33	74.00	68.67	72.92
IR 92527-6-2-1-2	78.33	66.33	80.33	71.67	74.17
IR 92527-6-2-1-4	79.67	70.33	83.00	74.67	76.92
IR 92545-53-4-1-3	67.00	60.33	61.67	61.67	62.67
IR 92545-54-6-1-4	64.33	60.00	66.67	65.00	64.00
IR 92546-7-1-1-3	65.67	62.67	69.67	68.33	66.58
IR 92546-17-6-4-3	81.33	72.00	74.67	68.00	74.00
IR 92546-17-6-4-4	60.33	61.00	60.00	59.33	60.17
IR 92546-33-3-1-1	80.00	68.00	72.33	67.33	71.92
IR 92517-1-3-1-1	63.67	58.33	68.00	68.67	64.67
IR 92522-45-3-1-4	62.33	53.67	69.00	64.67	62.42
IR 92545-23-2-1-1	56.67	57.00	58.33	55.67	56.92
IR 92545-24-3-1-1	61.67	53.67	64.00	61.00	60.08
IR 92545-40-2-2-3	73.67	68.33	79.33	70.00	72.83
IR 92545-51-1-1-4	72.33	67.33	68.00	68.00	68.92
IR 92546-33-4-2-3	75.67	71.33	69.33	66.33	70.67
IR 92516-8-3-3-4	69.67	70.33	77.67	78.33	74.00
MTU 1010 (Check)	59.67	56.67	61.67	56.67	58.67
IR 64 (Check)	62.33	57.33	65.00	58.33	60.75
LALAT (Check)	67.33	68.33	71.33	67.00	68.50
Mean	**69.67**	**64.59**	**70.00**	**65.58**	**67.46**
C.V.	6.08	6.10	5.79	6.43	6.10
F ratio	8.26	8.06	8.21	5.88	7.60
S.E.	2.45	2.28	2.34	2.43	2.37
C.D. 5%	6.90	6.42	6.60	6.87	6.70
C.D. 1%	9.16	8.52	8.76	9.12	8.89

Appendix 19: Comparative mean performance of harvest index in advance rice lines

Harvest index (%)				
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	52.01	44.91	44.70	45.30	46.73
CRR 724-1-B (IR 88889-44)	41.47	41.93	39.68	40.51	40.90
RP-1-27-7-6-1-2-1	49.41	46.95	36.98	32.47	41.45
IR 94313:18-4-1-4-1-B	38.16	32.88	41.07	42.60	38.68
IR 88287-383-1-B-B-1-1-B	50.88	47.95	44.16	39.14	45.53
IR 94391-587-1-2-B	40.89	38.10	37.93	31.06	37.00
IR 94314-20-2-1-B	41.80	40.37	44.78	41.54	42.12
IR 93339:40-B-18-13-B-B-1	39.06	42.18	37.18	38.47	39.23
IR 92521-5-3-1-2	45.47	48.52	43.91	40.97	44.72
IR 92521-7-5-1-1	35.17	36.95	35.89	32.05	35.01
IR 92521-23-6-1-3	41.62	33.11	41.59	39.23	38.89
IR 92521-24-5-1-3	45.44	35.36	40.59	41.30	40.67
IR 92522-47-2-1-1	39.52	39.64	39.85	45.14	41.04
IR 92522-47-2-1-4	45.33	37.27	35.42	33.02	37.76
IR 92522-61-3-1-4	41.76	46.18	38.79	41.51	42.06
IR 92523-35-1-1-1	46.49	38.85	42.76	40.29	42.10
IR 92523-37-1-1-2	45.14	41.24	41.05	39.54	41.74
IR 92527-6-2-1-2	38.04	34.33	38.19	37.63	37.05
IR 92527-6-2-1-4	41.50	45.64	33.34	34.48	38.74
IR 92545-53-4-1-3	43.95	40.48	48.98	43.91	44.33
IR 92545-54-6-1-4	44.26	42.16	43.12	39.57	42.28
IR 92546-7-1-1-3	45.17	44.68	34.09	35.57	39.88
IR 92546-17-6-4-3	38.44	41.18	37.97	36.03	38.40
IR 92546-17-6-4-4	53.67	46.05	47.41	43.91	47.76
IR 92546-33-3-1-1	38.09	38.90	36.15	33.65	36.70
IR 92517-1-3-1-1	51.86	46.91	44.62	38.50	45.47
IR 92522-45-3-1-4	46.61	48.81	47.43	47.02	47.47
IR 92545-23-2-1-1	51.12	40.95	48.81	47.68	47.14
IR 92545-24-3-1-1	44.52	42.85	47.41	38.19	43.24
IR 92545-40-2-2-3	35.10	38.63	28.23	34.83	34.20
IR 92545-51-1-1-4	43.92	43.73	39.78	32.95	40.10
IR 92546-33-4-2-3	40.95	39.81	47.13	43.21	42.77
IR 92516-8-3-3-4	41.60	32.66	37.76	32.84	36.22
MTU 1010 (Check)	45.77	45.59	40.62	40.89	43.22
IR 64 (Check)	48.34	49.12	43.06	43.63	46.04
LALAT (Check)	45.15	38.68	41.62	39.31	41.19
Mean	**43.82**	**41.49**	**40.89**	**39.11**	**41.33**
C.V.	11.53	12.34	10.28	12.41	11.64
F ratio	2.62	2.51	3.81	2.55	2.87
S.E.	2.92	2.96	2.43	2.80	2.78
C.D. 5%	8.23	8.34	6.85	7.90	7.83
C.D. 1%	10.92	11.07	9.09	10.49	10.39

Appendix 20: Comparative mean performance of test weight in advance rice lines

Genotypes	Test weight (g)				
	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	23.00	21.10	23.00	23.43	22.63
CRR 724-1-B (IR 88889-44)	28.57	27.53	26.97	24.60	26.92
RP-1-27-7-6-1-2-1	23.47	20.70	22.33	22.43	22.23
IR 94313:18-4-1-4-1-B	25.27	24.47	24.97	25.87	25.14
IR 88287-383-1-B-B-1-1-B	24.20	20.87	25.27	23.67	23.50
IR 94391-587-1-2-B	28.03	26.27	26.60	24.07	26.24
IR 94314-20-2-1-B	24.33	22.23	24.27	24.03	23.72
IR 93339:40-B-18-13-B-B-1	25.57	23.13	23.43	25.37	24.38
IR 92521-5-3-1-2	21.57	20.93	22.13	23.37	22.00
IR 92521-7-5-1-1	28.43	26.40	27.53	24.63	26.75
IR 92521-23-6-1-3	23.63	21.87	23.87	20.50	22.47
IR 92521-24-5-1-3	22.87	22.97	22.63	21.23	22.43
IR 92522-47-2-1-1	26.00	23.00	26.33	21.83	24.29
IR 92522-47-2-1-4	24.23	24.17	23.93	24.63	24.24
IR 92522-61-3-1-4	22.53	21.87	22.07	24.37	22.71
IR 92523-35-1-1-1	24.93	23.27	26.10	24.50	24.70
IR 92523-37-1-1-2	24.53	21.83	25.57	23.87	23.95
IR 92527-6-2-1-2	25.23	25.73	26.03	22.43	24.86
IR 92527-6-2-1-4	24.53	21.77	23.07	22.60	22.99
IR 92545-53-4-1-3	24.10	22.43	23.90	21.50	22.98
IR 92545-54-6-1-4	26.80	23.23	26.93	22.53	24.87
IR 92546-7-1-1-3	23.73	21.93	22.57	22.53	22.69
IR 92546-17-6-4-3	23.63	21.20	26.17	23.13	23.53
IR 92546-17-6-4-4	22.70	21.87	24.43	23.50	23.13
IR 92546-33-3-1-1	23.60	22.93	23.13	23.50	23.29
IR 92517-1-3-1-1	26.37	25.73	26.20	24.83	25.78
IR 92522-45-3-1-4	28.33	28.03	28.27	27.20	27.96
IR 92545-23-2-1-1	24.50	23.60	23.03	22.60	23.43
IR 92545-24-3-1-1	26.57	25.43	27.17	25.17	26.08
IR 92545-40-2-2-3	28.97	27.20	28.83	26.20	27.80
IR 92545-51-1-1-4	24.93	23.93	25.60	21.80	24.07
IR 92546-33-4-2-3	20.90	19.30	22.90	18.77	20.47
IR 92516-8-3-3-4	26.80	23.00	28.03	24.50	25.58
MTU 1010 (Check)	23.50	23.40	26.47	24.73	24.53
IR 64 (Check)	24.50	23.13	24.37	24.27	24.07
LALAT (Check)	27.23	26.10	27.47	25.53	26.58
Mean	**24.95**	**23.40**	**25.04**	**23.60**	**24.25**
C.V.	4.20	4.91	3.60	4.76	4.37
F ratio	11.07	10.32	14.11	6.79	10.58
S.E.	0.60	0.66	0.52	0.65	0.61
C.D. 5%	1.70	1.87	1.47	1.83	1.72
C.D. 1%	2.26	2.48	1.95	2.43	2.28

Appendix 21: Comparative mean performance of grain yield kilogram per hectare in advance rice lines

Grain yield kilogram per hectare					
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	4112.67	3677.00	4650.00	3117.00	3889.17
CRR 724-1-B (IR 88889-44)	3373.00	2969.33	3500.00	3157.67	3250.00
RP-1-27-7-6-1-2-1	5356.33	4721.33	4892.00	3368.33	4584.50
IR 94313:18-4-1-4-1-B	4568.00	4278.00	4375.00	2694.00	3978.75
IR 88287-383-1-B-B-1-1-B	4701.00	4159.00	3458.33	3124.67	3860.75
IR 94391-587-1-2-B	4545.33	4183.33	4800.00	3687.33	4304.00
IR 94314-20-2-1-B	4918.00	4522.33	4625.00	3790.33	4463.92
IR 93339:40-B-18-13-B-B-1	4809.67	4829.00	5125.00	4135.67	4724.83
IR 92521-5-3-1-2	4594.67	3962.00	3666.67	3210.00	3858.33
IR 92521-7-5-1-1	4705.33	4252.00	4916.67	3993.67	4466.92
IR 92521-23-6-1-3	4765.00	4068.00	5150.00	3604.33	4396.83
IR 92521-24-5-1-3	4567.00	3868.33	3700.00	3148.00	3820.83
IR 92522-47-2-1-1	4943.00	4341.00	4791.67	3932.00	4501.92
IR 92522-47-2-1-4	4210.00	3782.00	4325.00	3543.33	3965.08
IR 92522-61-3-1-4	4369.00	3782.33	4545.33	3395.33	4023.00
IR 92523-35-1-1-1	5205.33	5054.00	4460.00	3663.00	4595.58
IR 92523-37-1-1-2	4653.00	4003.67	4865.00	4222.00	4435.92
IR 92527-6-2-1-2	5595.33	4406.00	6041.67	4432.67	5118.92
IR 92527-6-2-1-4	5305.33	5040.00	5458.33	4514.67	5079.58
IR 92545-53-4-1-3	3951.67	3971.00	4166.67	3974.33	4015.92
IR 92545-54-6-1-4	3951.33	3479.67	3666.67	2777.67	3468.83
IR 92546-7-1-1-3	4737.33	4164.33	4868.67	3827.33	4399.42
IR 92546-17-6-4-3	5819.33	4621.67	5450.00	4421.00	5078.00
IR 92546-17-6-4-4	4904.33	4607.33	4958.33	3642.33	4528.08
IR 92546-33-3-1-1	4581.33	4188.33	4576.67	4049.67	4349.00
IR 92517-1-3-1-1	5137.33	4509.00	5182.67	4739.00	4892.00
IR 92522-45-3-1-4	5100.67	4571.67	4823.33	3757.67	4563.33
IR 92545-23-2-1-1	4194.33	4014.67	4373.33	3547.67	4032.50
IR 92545-24-3-1-1	4666.67	4084.00	5030.00	4481.33	4565.50
IR 92545-40-2-2-3	4191.33	4173.33	4041.67	3248.00	3913.58
IR 92545-51-1-1-4	4520.00	3800.33	4917.00	3885.00	4280.58
IR 92546-33-4-2-3	5179.00	4571.33	5208.33	3889.00	4711.92
IR 92516-8-3-3-4	5316.33	4649.33	4891.67	3024.67	4470.50
MTU 1010 (Check)	4915.67	4509.00	4875.00	3710.00	4502.42
IR 64 (Check)	4970.33	4761.33	5100.00	3555.33	4596.75
LALAT (Check)	4743.33	4406.33	4423.33	4020.00	4398.25
Mean	**4727.15**	**4249.48**	**4663.86**	**3702.33**	**4335.71**
C.V.	5.01	5.24	6.58	6.87	5.93
F ratio	13.04	11.57	10.71	11.55	11.72
S.E.	136.79	128.65	177.09	146.93	147.37
C.D. 5%	385.83	362.87	499.51	414.43	415.66
C.D. 1%	512.25	481.76	663.17	550.22	551.85

Appendix 22: Comparative mean performance of hulling recovery in advance rice lines

Hulling recovery (%)				
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	78.12	73.38	79.33	73.73	76.14
CRR 724-1-B (IR 88889-44)	72.45	68.26	74.77	71.23	71.68
RP-1-27-7-6-1-2-1	69.29	70.79	68.37	69.17	69.41
IR 94313:18-4-1-4-1-B	74.33	73.00	77.77	73.48	74.64
IR 88287-383-1-B-B-1-1-B	76.90	67.97	75.08	70.45	72.60
IR 94391-587-1-2-B	77.74	74.17	77.60	74.85	76.09
IR 94314-20-2-1-B	71.71	73.06	74.92	73.51	73.30
IR 93339:40-B-18-13-B-B-1	74.41	66.75	72.92	70.20	71.07
IR 92521-5-3-1-2	78.14	70.58	76.74	74.50	74.99
IR 92521-7-5-1-1	74.36	73.86	75.66	75.10	74.74
IR 92521-23-6-1-3	72.37	75.49	70.10	75.14	73.27
IR 92521-24-5-1-3	74.81	73.85	75.40	74.54	74.65
IR 92522-47-2-1-1	77.92	72.50	76.83	77.55	76.20
IR 92522-47-2-1-4	74.81	73.95	76.15	75.50	75.10
IR 92522-61-3-1-4	74.44	72.89	77.97	73.01	74.58
IR 92523-35-1-1-1	78.73	73.86	78.40	75.30	76.57
IR 92523-37-1-1-2	76.37	74.81	75.77	77.23	76.05
IR 92527-6-2-1-2	70.02	68.59	68.30	72.07	69.75
IR 92527-6-2-1-4	76.00	70.86	77.61	73.52	74.50
IR 92545-53-4-1-3	74.88	75.82	77.23	75.37	75.82
IR 92545-54-6-1-4	79.27	73.61	77.11	72.89	75.72
IR 92546-7-1-1-3	75.19	70.93	75.61	73.55	73.82
IR 92546-17-6-4-3	77.81	73.49	74.25	76.49	75.51
IR 92546-17-6-4-4	71.59	72.92	77.31	74.36	74.05
IR 92546-33-3-1-1	74.35	72.92	77.38	73.13	74.45
IR 92517-1-3-1-1	74.62	69.29	72.37	72.62	72.22
IR 92522-45-3-1-4	71.83	74.64	73.02	75.48	73.74
IR 92545-23-2-1-1	75.22	74.06	75.38	74.86	74.88
IR 92545-24-3-1-1	73.75	73.71	75.38	74.47	74.33
IR 92545-40-2-2-3	80.03	74.78	78.68	75.88	77.34
IR 92545-51-1-1-4	76.85	78.78	77.77	75.19	77.15
IR 92546-33-4-2-3	75.68	73.81	74.64	70.88	73.75
IR 92516-8-3-3-4	77.80	74.06	75.92	75.97	75.94
MTU 1010 (Check)	77.34	73.85	77.83	76.65	76.42
IR 64 (Check)	77.37	73.67	77.89	72.81	75.43
LALAT (Check)	78.89	74.32	78.31	73.71	76.31
Mean	**75.43**	**72.87**	**75.72**	**74.01**	**74.51**
C.V.	3.03	4.09	3.14	3.51	3.44
F ratio	4.03	2.00	3.80	1.73	2.89
S.E.	1.32	1.72	1.37	1.50	1.48
C.D. 5%	3.73	4.86	3.87	4.24	4.17
C.D. 1%	4.95	6.45	5.13	5.62	5.54

Appendix 23: Comparative mean performance of milling recovery in advance rice lines

Milling recovery (%)				
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	63.37	61.13	65.40	63.03	63.23
CRR 724-1-B (IR 88889-44)	61.87	62.57	66.60	61.80	63.21
RP-1-27-7-6-1-2-1	64.73	62.63	62.97	60.47	62.70
IR 94313:18-4-1-4-1-B	64.27	58.40	65.67	65.10	63.36
IR 88287-383-1-B-B-1-1-B	64.80	66.50	61.07	59.20	62.89
IR 94391-587-1-2-B	62.57	57.00	60.63	58.13	59.58
IR 94314-20-2-1-B	57.47	62.87	62.10	62.67	61.27
IR 93339:40-B-18-13-B-B-1	68.23	63.20	65.83	66.70	65.99
IR 92521-5-3-1-2	64.33	60.40	63.73	64.43	63.23
IR 92521-7-5-1-1	62.20	54.53	65.30	61.67	60.93
IR 92521-23-6-1-3	66.83	64.20	62.77	59.83	63.41
IR 92521-24-5-1-3	62.90	62.17	65.40	62.70	63.29
IR 92522-47-2-1-1	56.90	61.77	62.53	63.43	61.16
IR 92522-47-2-1-4	66.00	61.43	66.33	67.27	65.26
IR 92522-61-3-1-4	62.13	60.47	58.30	61.57	60.62
IR 92523-35-1-1-1	64.10	60.03	68.43	63.43	64.00
IR 92523-37-1-1-2	59.43	62.70	63.70	60.67	61.63
IR 92527-6-2-1-2	67.97	64.60	68.57	62.57	65.92
IR 92527-6-2-1-4	63.43	60.30	67.07	64.20	63.75
IR 92545-53-4-1-3	58.30	60.20	65.07	63.10	61.67
IR 92545-54-6-1-4	60.40	57.40	62.27	62.27	60.58
IR 92546-7-1-1-3	60.67	57.77	62.50	61.97	60.73
IR 92546-17-6-4-3	59.90	61.70	59.30	61.20	60.53
IR 92546-17-6-4-4	68.40	65.30	62.67	62.67	64.76
IR 92546-33-3-1-1	65.43	62.10	63.00	59.80	62.58
IR 92517-1-3-1-1	65.40	60.33	62.17	63.27	62.79
IR 92522-45-3-1-4	53.53	53.07	60.87	60.47	56.98
IR 92545-23-2-1-1	67.70	63.67	61.57	57.60	62.63
IR 92545-24-3-1-1	64.03	64.37	66.80	64.03	64.81
IR 92545-40-2-2-3	63.70	60.57	65.53	61.73	62.88
IR 92545-51-1-1-4	66.77	63.13	63.63	60.13	63.42
IR 92546-33-4-2-3	60.47	61.73	64.50	61.10	61.95
IR 92516-8-3-3-4	63.90	59.47	66.70	63.97	63.51
MTU 1010 (Check)	64.67	62.50	63.60	63.07	63.46
IR 64 (Check)	64.30	61.27	65.53	63.33	63.61
LALAT (Check)	64.47	61.43	64.73	60.70	62.83
Mean	**63.21**	**61.19**	**63.97**	**62.20**	**62.64**
C.V.	3.68	4.20	3.19	3.61	3.67
F ratio	6.26	3.55	4.24	2.63	4.17
S.E.	1.34	1.48	1.18	1.30	1.32
C.D. 5%	3.79	4.18	3.32	3.65	3.74
C.D. 1%	5.03	5.55	4.41	4.85	4.96

Appendix 24: Comparative mean performance of head rice recovery in advance rice lines

Head rice recovery (%)					
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	45.47	42.77	46.80	44.50	44.88
CRR 724-1-B (IR 88889-44)	52.60	51.20	51.83	49.60	51.31
RP-1-27-7-6-1-2-1	51.60	50.33	53.50	51.63	51.77
IR 94313:18-4-1-4-1-B	45.17	45.50	43.77	43.70	44.53
IR 88287-383-1-B-B-1-1-B	45.03	43.30	42.37	40.93	42.91
IR 94391-587-1-2-B	52.03	50.87	50.67	47.87	50.36
IR 94314-20-2-1-B	48.70	48.27	48.77	45.60	47.83
IR 93339:40-B-18-13-B-B-1	39.47	41.43	40.57	39.00	40.12
IR 92521-5-3-1-2	60.27	58.70	57.63	56.27	58.22
IR 92521-7-5-1-1	60.00	54.97	55.83	53.27	56.02
IR 92521-23-6-1-3	58.20	56.37	57.43	51.67	55.92
IR 92521-24-5-1-3	58.43	56.07	55.27	48.47	54.56
IR 92522-47-2-1-1	57.20	53.33	52.90	52.83	54.07
IR 92522-47-2-1-4	38.57	40.50	40.23	40.73	40.01
IR 92522-61-3-1-4	46.77	48.17	47.43	44.77	46.78
IR 92523-35-1-1-1	42.17	43.63	44.80	41.90	43.12
IR 92523-37-1-1-2	44.67	41.00	46.00	44.30	43.99
IR 92527-6-2-1-2	43.80	39.50	44.50	44.70	43.13
IR 92527-6-2-1-4	40.67	39.83	41.77	40.60	40.72
IR 92545-53-4-1-3	42.50	41.47	41.17	42.40	41.88
IR 92545-54-6-1-4	52.17	48.13	52.40	49.83	50.63
IR 92546-7-1-1-3	50.67	49.60	51.13	48.50	49.97
IR 92546-17-6-4-3	50.47	46.77	49.67	48.07	48.74
IR 92546-17-6-4-4	53.53	50.43	52.37	53.07	52.35
IR 92546-33-3-1-1	50.73	48.37	50.10	48.93	49.53
IR 92517-1-3-1-1	47.43	43.70	44.27	42.50	44.48
IR 92522-45-3-1-4	45.53	43.33	42.07	37.70	42.16
IR 92545-23-2-1-1	60.13	56.07	54.43	52.57	55.80
IR 92545-24-3-1-1	47.00	45.37	50.40	47.90	47.67
IR 92545-40-2-2-3	43.37	44.70	41.53	42.93	43.13
IR 92545-51-1-1-4	52.93	50.30	48.17	45.40	49.20
IR 92546-33-4-2-3	45.17	41.90	42.00	40.20	42.32
IR 92516-8-3-3-4	51.47	48.60	47.43	45.53	48.26
MTU 1010 (Check)	53.53	50.00	54.43	51.93	52.48
IR 64 (Check)	57.93	53.40	56.07	52.93	55.08
LALAT (Check)	51.43	49.47	52.97	51.63	51.38
Mean	**49.63**	**47.70**	**48.69**	**46.79**	**48.20**
C.V.	4.29	4.71	4.09	4.44	4.38
F ratio	24.75	16.36	21.57	16.20	19.72
S.E.	1.23	1.30	1.15	1.20	1.22
C.D. 5%	3.47	3.66	3.24	3.38	3.44
C.D. 1%	4.61	4.86	4.30	4.49	4.56

Appendix 25: Comparative mean performance of kernel length before cooking in advance rice lines

Kernel length before cooking (mm)					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	7.47	6.77	7.63	7.47	7.33
CRR 724-1-B (IR 88889-44)	6.83	7.00	7.20	6.80	6.96
RP-1-27-7-6-1-2-1	6.77	6.87	6.47	6.47	6.64
IR 94313:18-4-1-4-1-B	7.30	7.13	7.83	7.83	7.53
IR 88287-383-1-B-B-1-1-B	7.43	7.30	7.20	6.87	7.20
IR 94391-587-1-2-B	7.50	7.40	7.30	7.07	7.32
IR 94314-20-2-1-B	7.30	7.30	7.57	7.27	7.36
IR 93339:40-B-18-13-B-B-1	7.83	7.23	7.40	7.23	7.43
IR 92521-5-3-1-2	6.70	6.63	7.37	7.43	7.03
IR 92521-7-5-1-1	6.37	6.20	6.03	6.43	6.26
IR 92521-23-6-1-3	6.43	6.23	6.20	6.00	6.22
IR 92521-24-5-1-3	6.23	6.13	6.50	6.30	6.29
IR 92522-47-2-1-1	6.93	6.37	6.73	6.43	6.62
IR 92522-47-2-1-4	8.13	7.43	7.90	7.37	7.71
IR 92522-61-3-1-4	7.00	6.80	7.40	7.00	7.05
IR 92523-35-1-1-1	7.47	6.30	7.50	7.40	7.17
IR 92523-37-1-1-2	7.23	6.20	7.40	7.20	7.01
IR 92527-6-2-1-2	7.47	7.13	7.60	7.30	7.38
IR 92527-6-2-1-4	7.67	7.23	7.77	7.33	7.50
IR 92545-53-4-1-3	7.80	7.60	7.77	7.37	7.63
IR 92545-54-6-1-4	6.97	6.80	6.40	5.93	6.53
IR 92546-7-1-1-3	6.73	7.20	6.97	7.27	7.04
IR 92546-17-6-4-3	7.27	7.33	7.80	7.67	7.52
IR 92546-17-6-4-4	6.67	6.60	7.00	6.47	6.68
IR 92546-33-3-1-1	6.43	6.77	6.83	6.97	6.75
IR 92517-1-3-1-1	7.17	7.27	7.40	7.30	7.28
IR 92522-45-3-1-4	6.80	6.73	7.03	6.60	6.79
IR 92545-23-2-1-1	7.67	7.90	7.27	6.33	7.29
IR 92545-24-3-1-1	7.20	6.60	6.90	6.60	6.82
IR 92545-40-2-2-3	6.90	7.13	7.37	7.30	7.18
IR 92545-51-1-1-4	6.87	7.17	7.13	7.47	7.16
IR 92546-33-4-2-3	7.50	7.43	6.97	6.30	7.05
IR 92516-8-3-3-4	7.17	7.17	7.00	6.50	6.96
MTU 1010 (Check)	6.87	6.67	7.10	7.27	6.97
IR 64 (Check)	6.90	6.93	7.27	6.97	7.02
LALAT (Check)	6.97	6.67	7.33	7.10	7.02
Mean	**7.11**	**6.93**	**7.18**	**6.96**	**7.05**
C.V.	2.73	3.55	2.04	2.79	2.78
F ratio	15.68	9.40	29.72	18.72	18.38
S.E.	0.11	0.14	0.08	0.11	0.11
C.D. 5%	0.32	0.40	0.24	0.32	0.32
C.D. 1%	0.42	0.53	0.32	0.42	0.42

Appendix 26: Comparative mean performance of kernel breadth before cooking in advance rice lines

Kernel breadth before cooking (mm)				
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	2.07	1.97	2.30	2.07	2.10
CRR 724-1-B (IR 88889-44)	2.20	2.10	2.30	2.13	2.18
RP-1-27-7-6-1-2-1	2.03	2.00	2.13	2.13	2.07
IR 94313:18-4-1-4-1-B	2.00	2.07	2.27	2.10	2.11
IR 88287-383-1-B-B-1-1-B	2.00	1.97	2.13	1.90	2.00
IR 94391-587-1-2-B	2.13	1.90	1.87	2.07	1.99
IR 94314-20-2-1-B	2.10	2.23	2.30	1.93	2.14
IR 93339:40-B-18-13-B-B-1	2.17	2.17	2.03	1.90	2.07
IR 92521-5-3-1-2	2.10	2.23	2.23	2.17	2.18
IR 92521-7-5-1-1	2.27	2.20	2.37	2.10	2.23
IR 92521-23-6-1-3	2.17	2.13	1.93	2.20	2.11
IR 92521-24-5-1-3	2.20	2.23	2.03	2.07	2.13
IR 92522-47-2-1-1	2.13	2.07	2.20	1.97	2.09
IR 92522-47-2-1-4	2.03	1.80	2.07	1.80	1.92
IR 92522-61-3-1-4	2.10	2.13	2.30	2.20	2.18
IR 92523-35-1-1-1	2.20	2.10	2.03	2.00	2.08
IR 92523-37-1-1-2	2.10	2.10	2.33	2.30	2.21
IR 92527-6-2-1-2	1.73	2.00	2.00	2.07	1.95
IR 92527-6-2-1-4	1.87	1.83	2.07	2.00	1.94
IR 92545-53-4-1-3	1.83	1.90	1.97	1.97	1.92
IR 92545-54-6-1-4	2.23	2.23	2.10	2.17	2.18
IR 92546-7-1-1-3	1.97	2.00	2.20	1.97	2.03
IR 92546-17-6-4-3	1.90	1.93	2.13	2.23	2.05
IR 92546-17-6-4-4	2.03	1.80	2.10	2.20	2.03
IR 92546-33-3-1-1	1.97	2.03	2.13	2.27	2.10
IR 92517-1-3-1-1	2.10	2.17	2.13	1.97	2.09
IR 92522-45-3-1-4	2.10	2.13	2.27	1.97	2.12
IR 92545-23-2-1-1	2.20	2.07	2.27	2.20	2.18
IR 92545-24-3-1-1	2.13	2.17	2.10	1.90	2.07
IR 92545-40-2-2-3	2.27	2.03	2.30	2.13	2.18
IR 92545-51-1-1-4	2.13	2.20	1.93	1.87	2.03
IR 92546-33-4-2-3	2.00	2.07	2.13	2.17	2.09
IR 92516-8-3-3-4	2.23	2.03	2.13	2.20	2.15
MTU 1010 (Check)	2.00	1.97	2.30	2.07	2.08
IR 64 (Check)	2.13	2.03	2.23	2.07	2.12
LALAT (Check)	2.20	2.23	2.10	2.10	2.16
Mean	**2.08**	**2.06**	**2.15**	**2.07**	**2.09**
C.V.	5.04	6.23	5.23	5.88	5.59
F ratio	4.17	2.79	3.88	3.06	3.48
S.E.	0.06	0.07	0.06	0.07	0.07
C.D. 5%	0.17	0.21	0.18	0.20	0.19
C.D. 1%	0.23	0.28	0.24	0.26	0.25

Appendix 27: Comparative mean performance of kernel L / B ratio in advance rice lines

Kernel L / B ratio					
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	3.62	3.44	3.32	3.63	3.50
CRR 724-1-B (IR 88889-44)	3.11	3.35	3.13	3.19	3.20
RP-1-27-7-6-1-2-1	3.33	3.46	3.03	3.03	3.21
IR 94313:18-4-1-4-1-B	3.66	3.45	3.46	3.74	3.58
IR 88287-383-1-B-B-1-1-B	3.73	3.73	3.38	3.62	3.62
IR 94391-587-1-2-B	3.51	3.90	3.93	3.43	3.69
IR 94314-20-2-1-B	3.48	3.29	3.29	3.77	3.46
IR 93339:40-B-18-13-B-B-1	3.62	3.36	3.64	3.81	3.61
IR 92521-5-3-1-2	3.19	2.98	3.30	3.44	3.23
IR 92521-7-5-1-1	2.81	2.82	2.55	3.07	2.81
IR 92521-23-6-1-3	2.97	2.92	3.21	2.74	2.96
IR 92521-24-5-1-3	2.84	2.75	3.21	3.06	2.97
IR 92522-47-2-1-1	3.25	3.12	3.06	3.29	3.18
IR 92522-47-2-1-4	4.02	4.13	3.82	4.10	4.02
IR 92522-61-3-1-4	3.34	3.19	3.22	3.19	3.24
IR 92523-35-1-1-1	3.40	3.01	3.70	3.71	3.46
IR 92523-37-1-1-2	3.45	2.96	3.17	3.14	3.18
IR 92527-6-2-1-2	4.31	3.59	3.81	3.55	3.81
IR 92527-6-2-1-4	4.11	3.95	3.78	3.67	3.88
IR 92545-53-4-1-3	4.26	4.06	3.97	3.76	4.01
IR 92545-54-6-1-4	3.12	3.05	3.05	2.75	3.00
IR 92546-7-1-1-3	3.46	3.61	3.17	3.71	3.49
IR 92546-17-6-4-3	3.84	3.79	3.67	3.44	3.68
IR 92546-17-6-4-4	3.29	3.68	3.34	2.95	3.31
IR 92546-33-3-1-1	3.29	3.33	3.20	3.07	3.22
IR 92517-1-3-1-1	3.42	3.36	3.47	3.73	3.49
IR 92522-45-3-1-4	3.24	3.16	3.11	3.37	3.22
IR 92545-23-2-1-1	3.49	3.82	3.21	2.88	3.35
IR 92545-24-3-1-1	3.38	3.06	3.29	3.48	3.30
IR 92545-40-2-2-3	3.05	3.53	3.20	3.42	3.30
IR 92545-51-1-1-4	3.23	3.26	3.73	4.01	3.56
IR 92546-33-4-2-3	3.76	3.60	3.27	2.92	3.39
IR 92516-8-3-3-4	3.21	3.52	3.29	2.96	3.24
MTU 1010 (Check)	3.44	3.39	3.10	3.53	3.36
IR 64 (Check)	3.24	3.43	3.26	3.38	3.33
LALAT (Check)	3.17	2.99	3.49	3.39	3.26
Mean	**3.43**	**3.39**	**3.36**	**3.39**	**3.39**
C.V.	6.14	7.74	6.17	6.99	6.76
F ratio	8.56	5.38	6.23	6.63	6.70
S.E.	0.12	0.15	0.12	0.14	0.13
C.D. 5%	0.34	0.43	0.34	0.39	0.37
C.D. 1%	0.46	0.57	0.45	0.51	0.50

Appendix 28: Comparative mean performance of amylose content in advance rice lines

Amylose content (%)					
Genotypes	**Control 2014**	**Stress 2014**	**Control 2015**	**Stress 2015**	**Mean**
CRR 719-1-B (IR 88903-34)	25.23	24.47	24.44	22.48	24.16
CRR 724-1-B (IR 88889-44)	23.46	23.72	24.68	21.44	23.33
RP-1-27-7-6-1-2-1	22.36	20.49	21.58	22.44	21.72
IR 94313:18-4-1-4-1-B	21.93	20.24	22.76	23.30	22.06
IR 88287-383-1-B-B-1-1-B	22.65	19.82	23.92	24.48	22.72
IR 94391-587-1-2-B	24.71	19.51	21.43	22.29	21.99
IR 94314-20-2-1-B	20.35	18.68	18.18	19.78	19.25
IR 93339:40-B-18-13-B-B-1	24.65	21.38	21.49	20.43	21.99
IR 92521-5-3-1-2	21.34	21.47	22.54	19.51	21.21
IR 92521-7-5-1-1	21.14	20.64	21.47	20.33	20.89
IR 92521-23-6-1-3	21.42	21.07	22.52	21.18	21.55
IR 92521-24-5-1-3	21.39	20.79	22.50	21.57	21.56
IR 92522-47-2-1-1	23.85	20.51	24.64	24.03	23.26
IR 92522-47-2-1-4	23.38	22.54	23.88	23.53	23.33
IR 92522-61-3-1-4	23.14	19.61	24.48	21.50	22.18
IR 92523-35-1-1-1	21.89	22.46	20.59	20.81	21.44
IR 92523-37-1-1-2	21.36	20.49	21.70	19.78	20.83
IR 92527-6-2-1-2	22.52	20.71	22.61	19.59	21.36
IR 92527-6-2-1-4	22.64	22.09	23.30	22.43	22.61
IR 92545-53-4-1-3	21.52	21.58	22.57	23.64	22.33
IR 92545-54-6-1-4	21.70	18.80	22.54	19.98	20.76
IR 92546-7-1-1-3	25.43	22.50	23.66	20.64	23.06
IR 92546-17-6-4-3	25.13	23.60	25.16	22.93	24.20
IR 92546-17-6-4-4	24.89	21.76	22.60	21.56	22.70
IR 92546-33-3-1-1	25.61	22.55	24.77	22.71	23.91
IR 92517-1-3-1-1	22.89	21.55	23.66	21.65	22.44
IR 92522-45-3-1-4	24.46	20.81	24.91	24.68	23.72
IR 92545-23-2-1-1	20.85	20.47	22.57	20.69	21.14
IR 92545-24-3-1-1	20.66	21.23	21.68	20.83	21.10
IR 92545-40-2-2-3	21.51	21.46	21.56	20.83	21.34
IR 92545-51-1-1-4	21.63	21.73	21.55	20.58	21.37
IR 92546-33-4-2-3	22.10	20.70	22.29	21.39	21.62
IR 92516-8-3-3-4	21.86	17.46	21.57	20.43	20.33
MTU 1010 (Check)	22.57	21.65	22.65	21.45	22.08
IR 64 (Check)	23.08	22.48	23.61	21.36	22.63
LALAT (Check)	25.82	23.70	25.48	23.50	24.62
Mean	**22.81**	**21.24**	**22.82**	**21.66**	**22.13**
C.V.	1.19	1.10	1.02	1.04	1.09
F ratio	99.76	121.67	126.38	118.79	116.65
S.E.	0.16	0.13	0.13	0.13	0.14
C.D. 5%	0.44	0.38	0.38	0.37	0.39
C.D. 1%	0.59	0.50	0.50	0.49	0.52

Appendix 29: Comparative mean performance of volume expansion ratio in advance rice lines

Volume expansion ratio					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	3.43	3.23	3.46	3.21	3.33
CRR 724-1-B (IR 88889-44)	3.47	3.32	3.47	3.28	3.39
RP-1-27-7-6-1-2-1	3.42	3.42	3.48	3.36	3.42
IR 94313:18-4-1-4-1-B	3.47	3.39	3.45	3.29	3.40
IR 88287-383-1-B-B-1-1-B	3.43	3.30	3.42	3.32	3.37
IR 94391-587-1-2-B	3.42	3.30	3.44	3.27	3.36
IR 94314-20-2-1-B	3.42	3.34	3.46	3.31	3.38
IR 93339:40-B-18-13-B-B-1	3.44	3.25	3.44	3.30	3.36
IR 92521-5-3-1-2	3.50	3.33	3.54	3.43	3.45
IR 92521-7-5-1-1	3.50	3.35	3.45	3.41	3.43
IR 92521-23-6-1-3	3.44	3.32	3.49	3.30	3.39
IR 92521-24-5-1-3	3.42	3.34	3.44	3.34	3.39
IR 92522-47-2-1-1	3.41	3.30	3.54	3.33	3.40
IR 92522-47-2-1-4	3.49	3.33	3.50	3.35	3.42
IR 92522-61-3-1-4	3.53	3.25	3.49	3.27	3.39
IR 92523-35-1-1-1	3.52	3.26	3.50	3.35	3.41
IR 92523-37-1-1-2	3.53	3.35	3.51	3.30	3.42
IR 92527-6-2-1-2	3.51	3.23	3.54	3.41	3.42
IR 92527-6-2-1-4	3.39	3.26	3.42	3.43	3.37
IR 92545-53-4-1-3	3.48	3.33	3.52	3.34	3.42
IR 92545-54-6-1-4	3.45	3.26	3.47	3.47	3.41
IR 92546-7-1-1-3	3.37	3.22	3.45	3.24	3.32
IR 92546-17-6-4-3	3.41	3.24	3.42	3.21	3.32
IR 92546-17-6-4-4	3.43	3.23	3.47	3.30	3.36
IR 92546-33-3-1-1	3.45	3.26	3.43	3.32	3.37
IR 92517-1-3-1-1	3.43	3.22	3.43	3.28	3.34
IR 92522-45-3-1-4	3.42	3.25	3.44	3.31	3.35
IR 92545-23-2-1-1	3.47	3.22	3.41	3.41	3.38
IR 92545-24-3-1-1	3.41	3.26	3.44	3.42	3.38
IR 92545-40-2-2-3	3.43	3.24	3.39	3.24	3.32
IR 92545-51-1-1-4	3.42	3.24	3.45	3.38	3.37
IR 92546-33-4-2-3	3.40	3.33	3.38	3.23	3.34
IR 92516-8-3-3-4	3.43	3.35	3.40	3.31	3.38
MTU 1010 (Check)	3.32	3.29	3.34	3.33	3.32
IR 64 (Check)	3.45	3.38	3.44	3.38	3.41
LALAT (Check)	3.42	3.36	3.39	3.37	3.38
Mean	**3.44**	**3.29**	**3.45**	**3.33**	**3.38**
C.V.	1.10	1.02	1.02	1.03	1.04
F ratio	4.31	8.11	5.20	10.89	7.13
S.E.	0.02	0.02	0.02	0.02	0.02
C.D. 5%	0.06	0.05	0.06	0.06	0.06
C.D. 1%	0.08	0.07	0.08	0.07	0.08

Appendix 30: Comparative mean performance of kernel elongation ratio in advance rice lines

Kernel elongation ratio					
Genotypes	Control 2014	Stress 2014	Control 2015	Stress 2015	Mean
CRR 719-1-B (IR 88903-34)	1.62	1.59	1.62	1.61	1.61
CRR 724-1-B (IR 88889-44)	1.62	1.59	1.63	1.61	1.61
RP-1-27-7-6-1-2-1	1.67	1.62	1.65	1.63	1.64
IR 94313:18-4-1-4-1-B	1.82	1.79	1.82	1.79	1.81
IR 88287-383-1-B-B-1-1-B	1.75	1.70	1.73	1.74	1.73
IR 94391-587-1-2-B	1.68	1.63	1.64	1.64	1.65
IR 94314-20-2-1-B	1.72	1.73	1.72	1.69	1.71
IR 93339:40-B-18-13-B-B-1	1.80	1.82	1.80	1.78	1.80
IR 92521-5-3-1-2	1.54	1.52	1.53	1.50	1.52
IR 92521-7-5-1-1	1.54	1.51	1.53	1.51	1.53
IR 92521-23-6-1-3	1.55	1.52	1.56	1.53	1.54
IR 92521-24-5-1-3	1.54	1.55	1.55	1.53	1.54
IR 92522-47-2-1-1	1.72	1.70	1.72	1.70	1.71
IR 92522-47-2-1-4	1.72	1.69	1.70	1.68	1.70
IR 92522-61-3-1-4	1.72	1.72	1.71	1.69	1.71
IR 92523-35-1-1-1	1.77	1.78	1.77	1.78	1.78
IR 92523-37-1-1-2	1.77	1.73	1.76	1.75	1.76
IR 92527-6-2-1-2	1.78	1.74	1.78	1.76	1.77
IR 92527-6-2-1-4	1.75	1.76	1.76	1.75	1.76
IR 92545-53-4-1-3	1.76	1.75	1.75	1.74	1.75
IR 92545-54-6-1-4	1.68	1.62	1.67	1.65	1.65
IR 92546-7-1-1-3	1.69	1.69	1.68	1.64	1.67
IR 92546-17-6-4-3	1.69	1.66	1.67	1.67	1.67
IR 92546-17-6-4-4	1.66	1.63	1.67	1.65	1.65
IR 92546-33-3-1-1	1.65	1.64	1.65	1.65	1.65
IR 92517-1-3-1-1	1.75	1.76	1.74	1.75	1.75
IR 92522-45-3-1-4	1.58	1.58	1.59	1.58	1.59
IR 92545-23-2-1-1	1.69	1.63	1.70	1.69	1.68
IR 92545-24-3-1-1	1.69	1.64	1.69	1.69	1.68
IR 92545-40-2-2-3	1.69	1.72	1.70	1.69	1.70
IR 92545-51-1-1-4	1.69	1.65	1.70	1.71	1.69
IR 92546-33-4-2-3	1.65	1.61	1.64	1.63	1.63
IR 92516-8-3-3-4	1.65	1.64	1.67	1.65	1.66
MTU 1010 (Check)	1.74	1.73	1.74	1.73	1.74
IR 64 (Check)	1.62	1.60	1.63	1.61	1.62
LALAT (Check)	1.65	1.65	1.65	1.64	1.65
Mean	**1.68**	**1.66**	**1.68**	**1.67**	**1.67**
C.V.	0.55	0.67	0.55	0.68	0.61
F ratio	1155.80	935.06	1123.25	820.99	1008.77
S.E.	0.00	0.00	0.00	0.00	0.00
C.D. 5%	0.01	0.01	0.01	0.01	0.01
C.D. 1%	0.01	0.01	0.01	0.01	0.01

Appendix 31: Estimates of micronutrient content in polished rice grain

Genotypes	Zn (PPM)	Fe (PPM)	Cu (PPM)	Mn (PPM)
CRR 719-1-B (IR 88903-34)	0.18	1.56	0.1	0.13
CRR 724-1-B (IR 88889-44)	0.12	1.23	0.05	0.09
RP-1-27-7-6-1-2-1	0.2	1.79	0.09	0.1
IR 94313:18-4-1-4-1-B	0.15	2.12	0.06	0.09
IR 88287-383-1-B-B-1-1-B	0.29	1.45	0.09	0.08
IR 94391-587-1-2-B	0.19	2.05	0.09	0.1
IR 94314-20-2-1-B	0.14	1.73	0.08	0.17
IR 93339:40-B-18-13-B-B-1	0.2	1.39	0.07	0.09
IR 92521-5-3-1-2	0.22	2.03	0.09	0.13
IR 92521-7-5-1-1	0.2	1.94	0.09	0.12
IR 92521-23-6-1-3	0.19	1.99	0.08	0.13
IR 92521-24-5-1-3	0.21	2.01	0.09	0.13
IR 92522-47-2-1-1	0.17	1.62	0.08	0.09
IR 92522-47-2-1-4	0.16	1.59	0.09	0.09
IR 92522-61-3-1-4	0.17	1.61	0.08	0.1
IR 92523-35-1-1-1	0.2	1.9	0.09	0.11
IR 92523-37-1-1-2	0.19	1.92	0.08	0.1
IR 92527-6-2-1-2	0.26	1.82	0.09	0.11
IR 92527-6-2-1-4	0.28	1.79	0.08	0.1
IR 92545-53-4-1-3	0.25	1.73	0.07	0.11
IR 92545-54-6-1-4	0.27	1.84	0.05	0.13
IR 92546-7-1-1-3	0.09	1.17	0.08	0.1
IR 92546-17-6-4-3	0.11	1.24	0.1	0.11
IR 92546-17-6-4-4	0.1	1.23	0.09	0.11
IR 92546-33-3-1-1	0.09	1.21	0.09	0.09
IR 92517-1-3-1-1	0.24	2.04	0.09	0.1
IR 92522-45-3-1-4	0.18	0.61	0.09	0.09
IR 92545-23-2-1-1	0.30	2.5	0.11	0.12
IR 92545-24-3-1-1	0.4	2.01	0.09	0.13
IR 92545-40-2-2-3	0.31	2.04	0.1	0.13
IR 92545-51-1-1-4	0.32	2.05	0.09	0.13
IR 92546-33-4-2-3	0.12	1.06	0.09	0.19
IR 92516-8-3-3-4	0.26	1.28	0.1	0.1
MTU 1010 (Check)	0.24	1.89	0.09	0.1
IR 64 (Check)	0.22	2.13	0.09	0.09
LALAT (Check)	0.21	1.73	0.08	0.1

Appendix 32: Skelton of pooled analysis of variance (ANOVA)

ANOVA for days to 50% flowering

SoV	df	SS	MSS	F- Ratio	Probability	
Replicate	2	19.0324	9.5162	0.6616	0.5166	
Locations	1	15.9468	15.9468	1.7164	0.1909	
Environments	1	1354.6875	1354.6875	145.8078	0.0000	**
Loc * Env	1	372.2245	372.2245	40.0633	0.0000	**
Interactions	6	55.7455	9.2909	0.6460	0.6934	
Overall Sum	11	1817.6366	165.2397	11.4889	0.0000	**
Treatments	35	1819.9143	51.9976	3.6153	0.0000	**
Error	385	5537.2803	14.3825			

ANOVA for plant height (cm)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	22.0882	11.0441	0.2794	0.7564	
Locations	1	5541.6265	5541.6265	427.9214	0.0000	**
Environments	1	20.0855	20.0855	1.5510	0.2137	
Loc * Env	1	131.5063	131.5063	10.1548	0.0016	**
Interactions	6	77.7006	12.9501	0.3276	0.9224	
Overall Sum	11	5793.0073	526.6370	13.3227	0.0000	**
Treatments	35	7401.0356	211.4582	5.3494	0.0000	**
Error	385	15218.7529	39.5292			

ANOVA for days to maturity

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	2.5880	1.2940	0.0751	0.9277	
Locations	1	850.0833	850.0833	303.5858	0.0000	**
Environments	1	1720.0093	1720.0093	614.2578	0.0000	**
Loc * Env	1	181.4815	181.4815	64.8115	0.0000	**
Interactions	6	16.8009	2.8001	0.1625	0.9864	
Overall Sum	11	2770.9629	251.9057	14.6173	0.0000	**
Treatments	35	2170.2407	62.0069	3.5981	0.0000	**
Error	385	6634.8706	17.2334			

ANOVA for number of tillers per plant

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	3.1296	1.5648	0.8143	0.4437	
Locations	1	128.9259	128.9259	66.0950	0.0000	**
Environments	1	249.0370	249.0370	127.6710	0.0000	**
Loc * Env	1	16.3333	16.3333	8.3734	0.0040	**
Interactions	6	11.7037	1.9506	1.0150	0.4150	
Overall Sum	11	409.1296	37.1936	19.3541	0.0000	**
Treatments	35	254.1852	7.2624	3.7791	0.0000	**
Error	385	739.8704	1.9217			

ANOVA for number of productive tillers per meter square

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	200.3472	100.1736	0.1888	0.8280	
Locations	1	15841.3330	15841.3330	66.1758	0.0000	**
Environments	1	63026.6758	63026.6758	263.2884	0.0000	**
Loc * Env	1	1127.7875	1127.7875	4.7112	0.0306	*
Interactions	6	1436.2960	239.3827	0.4513	0.8440	
Overall Sum	11	81632.4453	7421.1313	13.9901	0.0000	**
Treatments	35	159070.5000	4544.8716	8.5678	0.0000	**
Error	385	204226.0625	530.4573			

ANOVA for panicle length (cm)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	7.0679	3.5339	1.6334	0.1966	
Locations	1	405.6738	405.6738	178.4309	0.0000	**
Environments	1	118.7238	118.7238	52.2193	0.0000	**
Loc * Env	1	8.9068	8.9068	3.9175	0.0485	*
Interactions	6	13.6414	2.2736	1.0509	0.3919	
Overall Sum	11	554.0135	50.3649	23.2790	0.0000	**
Treatments	35	322.7246	9.2207	4.2619	0.0000	**
Error	385	832.9604	2.1635			

ANOVA for number of spikelets per panicle

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	888.8750	444.4375	1.9538	0.1431	
Locations	1	2023.6689	2023.6689	31.1366	0.0000	**
Environments	1	21859.5586	21859.5586	336.3361	0.0000	**
Loc * Env	1	70.8905	70.8905	1.0907	0.2970	
Interactions	6	389.9592	64.9932	0.2857	0.9436	
Overall Sum	11	25232.9512	2293.9048	10.0841	0.0000	**
Treatments	35	203791.2344	5822.6064	25.5964	0.0000	**
Error	385	87578.7969	227.4774			

ANOVA for grain yield per plant (g)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.3380	0.1690	0.0226	0.9777	
Locations	1	237.0370	237.0370	109.4405	0.0000	**
Environments	1	1193.3427	1193.3427	550.9688	0.0000	**
Loc * Env	1	16.3333	16.3333	7.5411	0.0063	**
Interactions	6	12.9954	2.1659	0.2891	0.9420	
Overall Sum	11	1460.0463	132.7315	17.7142	0.0000	**
Treatments	35	1177.3796	33.6394	4.4895	0.0000	**
Error	385	2884.7871	7.4930			

ANOVA for biological yield per plant (g)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	47.0880	23.5440	1.1070	0.3316	
Locations	1	47.3356	47.3356	10.1083	0.0016	**
Environments	1	2432.0022	2432.0022	519.3412	0.0000	**
Loc * Env	1	11.6691	11.6691	2.4919	0.1153	
Interactions	6	28.0972	4.6829	0.2202	0.9702	
Overall Sum	11	2566.1921	233.2902	10.9692	0.0000	**
Treatments	35	14501.0811	414.3166	19.4810	0.0000	**
Error	385	8188.0581	21.2677			

ANOVA for harvest index (%)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	7.4725	3.7362	0.1420	0.8677	
Locations	1	761.8789	761.8789	83.6379	0.0000	**
Environments	1	457.4852	457.4852	50.2220	0.0000	**
Loc * Env	1	8.3278	8.3278	0.9142	0.3396	
Interactions	6	54.6555	9.1093	0.3461	0.9120	
Overall Sum	11	1289.8198	117.2563	4.4553	0.0000	**
Treatments	35	5481.5713	156.6163	5.9508	0.0000	**
Error	385	10132.6289	26.3185			

ANOVA for test weight (g)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	1.0745	0.5372	0.3059	0.7366	
Locations	1	2.3556	2.3556	1.0264	0.3116	
Environments	1	240.1584	240.1584	104.6487	0.0000	**
Loc * Env	1	0.2852	0.2852	0.1243	0.7246	
Interactions	6	13.7694	2.2949	1.3069	0.2529	
Overall Sum	11	257.6430	23.4221	13.3381	0.0000	**
Treatments	35	1240.7659	35.4505	20.1879	0.0000	**
Error	385	676.0712	1.7560			

ANOVA for grain yield kilogram per hectare

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	19500.4219	9750.2109	0.0763	0.9266	
Locations	1	10061040.0000	10061040.0000	107.6671	0.0000	**
Environments	1	55924576.0000	55924576.0000	598.4706	0.0000	**
Loc * Env	1	6321284.0000	6321284.0000	67.6465	0.0000	**
Interactions	6	560674.9375	93445.8203	0.7312	0.6247	
Overall Sum	11	72887072.0000	6626097.5000	51.8497	0.0000	**
Treatments	35	76508936.0000	2185969.7500	17.1054	0.0000	**
Error	385	49200848.0000	127794.4063			

ANOVA for hulling recovery (%)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	8.8708	4.4354	0.5974	0.5507	
Locations	1	55.2838	55.2838	10.7918	0.0011	**
Environments	1	490.7096	490.7096	95.7898	0.0000	**
Loc * Env	1	19.6352	19.6352	3.8329	0.0510	
Interactions	6	30.7366	5.1228	0.6900	0.6578	
Overall Sum	11	605.2360	55.0215	7.4113	0.0000	**
Treatments	35	1521.3208	43.4663	5.8549	0.0000	**
Error	385	2858.2188	7.4239			

ANOVA for milling recovery (%)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	2.2114	1.1057	0.1329	0.8756	
Locations	1	84.3584	84.3584	46.4537	0.0000	**
Environments	1	386.6567	386.6567	212.9207	0.0000	**
Loc * Env	1	1.7252	1.7252	0.9500	0.3303	
Interactions	6	10.8958	1.8160	0.2183	0.9708	
Overall Sum	11	485.8475	44.1680	5.3106	0.0000	**
Treatments	35	1369.3486	39.1242	4.7042	0.0000	**
Error	385	3202.0020	8.3169			

ANOVA for head rice recovery (%)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	2.6846	1.3423	0.2442	0.7834	
Locations	1	93.8002	93.8002	13.9080	0.0002	**
Environments	1	395.4095	395.4095	58.6286	0.0000	**
Loc * Env	1	0.0283	0.0283	0.0042	0.9483	
Interactions	6	40.4659	6.7443	1.2271	0.2914	
Overall Sum	11	532.3887	48.3990	8.8056	0.0000	**
Treatments	35	11386.0000	325.3143	59.1872	0.0000	**
Error	385	2116.0989	5.4964			

ANOVA for kernel length before cooking (mm)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.0950	0.0475	0.4711	0.6247	
Locations	1	0.2650	0.2650	12.8352	0.0004	**
Environments	1	4.2206	4.2206	204.4050	0.0000	**
Loc * Env	1	0.0556	0.0556	2.6917	0.1017	
Interactions	6	0.1239	0.0206	0.2048	0.9752	
Overall Sum	11	4.7601	0.4327	4.2919	0.0000	**
Treatments	35	59.7973	1.7085	16.9452	0.0000	**
Error	385	38.8174	0.1008			

ANOVA for kernel breadth before cooking (mm)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.0091	0.0045	0.2297	0.7949	
Locations	1	0.1519	0.1519	8.3686	0.0040	**
Environments	1	0.2852	0.2852	15.7156	0.0001	**
Loc * Env	1	0.0919	0.0919	5.0625	0.0250	*
Interactions	6	0.1089	0.0181	0.9187	0.4813	
Overall Sum	11	0.6469	0.0588	2.9771	0.0008	**
Treatments	35	2.7691	0.0791	4.0050	0.0000	**
Error	385	7.6056	0.0198			

ANOVA for kernel L/B ratio

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.0971	0.0486	0.6160	0.5406	
Locations	1	0.1716	0.1716	4.5988	0.0326	*
Environments	1	0.0062	0.0062	0.1648	0.6850	
Loc * Env	1	0.1500	0.1500	4.0200	0.0457	*
Interactions	6	0.2239	0.0373	0.4732	0.8282	
Overall Sum	11	0.6488	0.0590	0.7480	0.6920	
Treatments	35	33.1320	0.9466	12.0057	0.0000	**
Error	385	30.3566	0.0788			

ANOVA for amylose content (%)

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.3991	0.1996	0.2134	0.8080	
Locations	1	4.9816	4.9816	124.2240	0.0000	**
Environments	1	201.0509	201.0509	5013.5625	0.0000	**
Loc * Env	1	4.4550	4.4550	111.0945	0.0000	**
Interactions	6	0.2406	0.0401	0.0429	0.9997	
Overall Sum	11	211.1272	19.1934	20.5202	0.0000	**
Treatments	35	594.6879	16.9911	18.1657	0.0000	**
Error	385	360.1055	0.9353			

ANOVA for volume expansion ratio

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.0035	0.0017	0.6298	0.5333	
Locations	1	0.0558	0.0558	56.5751	0.0000	**
Environments	1	2.0460	2.0460	2074.2073	0.0000	**
Loc * Env	1	0.0165	0.0165	16.7296	0.0001	**
Interactions	6	0.0059	0.0010	0.3584	0.9049	
Overall Sum	11	2.1277	0.1934	70.2765	0.0000	**
Treatments	35	0.5031	0.0144	5.2227	0.0000	**
Error	385	1.0597	0.0028			

ANOVA for kernel elongation ratio

SoV	df	SS	MSS	F - Ratio	Probability	
Replicate	2	0.0001	0.0001	0.3339	0.7163	
Locations	1	0.0001	0.0001	38.9228	0.0000	**
Environments	1	0.0303	0.0303	8767.3164	0.0000	**
Loc * Env	1	0.0010	0.0010	285.7561	0.0000	**
Interactions	6	0.0000	0.0000	0.0214	1.0000	
Overall Sum	11	0.0315	0.0029	17.7731	0.0000	**
Treatments	35	2.3148	0.0661	410.0350	0.0000	**
Error	385	0.0621	0.0002			

Appendix 33: Genotypic correlation coefficient among different traits (Control 2014)

Character	DFF	PH	DM	NT/Pt	NPT/M2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL. %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	0.18	0.64	-0.09	-0.11	0.17	0.01	0.42	0.34	-0.05	-0.13	-0.21	0.11	-0.06	0.16	0.03	0.07	-0.33	-0.13	0.24	0.38
PH	0.18	1.00	-0.14	-0.33	0.39	0.78	0.55	-0.41	-0.29	0.03	0.00	0.02	-0.02	0.35	-0.37	0.39	-0.40	-0.47	0.00	-0.57	0.03
DM	0.64	-0.14	1.00	-0.02	0.10	0.25	-0.04	0.41	0.18	0.08	-0.12	0.16	-0.02	-0.14	0.29	0.33	0.00	-0.46	0.13	0.36	0.37
NT/Pt	-0.09	-0.33	-0.02	1.00	-0.16	-0.23	-0.13	0.22	0.17	-0.05	0.07	-0.16	-0.12	-0.02	-0.08	-0.27	0.09	0.16	-0.21	0.17	0.30
NPT/M2	-0.11	0.39	0.10	-0.16	1.00	0.00	0.05	-0.10	0.05	-0.11	-0.30	-0.09	-0.12	-0.19	-0.01	-0.27	0.15	0.15	-0.23	-0.02	0.08
PL	0.17	0.78	0.25	-0.23	0.00	1.00	-0.19	0.11	-0.20	-0.57	0.43	-0.34	0.18	-0.17	0.14	0.09	0.07	-0.11	0.48	-0.03	-0.37
NSP/P	0.01	0.55	-0.04	-0.13	0.05	-0.19	1.00	-0.02	0.09	-0.11	-0.29	-0.02	-0.09	0.45	-0.47	0.11	-0.35	-0.22	0.10	-0.57	0.10
GY/Pt	0.42	-0.41	0.41	0.22	-0.10	0.11	-0.02	1.00	0.50	0.15	-0.58	-0.14	-0.12	-0.15	0.15	-0.36	0.27	0.15	-0.18	0.09	0.32
BY/Pt	0.34	-0.29	0.18	0.17	0.05	-0.20	0.09	0.50	1.00	-0.78	-0.01	-0.10	-0.22	-0.20	0.05	-0.28	0.21	0.00	0.04	0.13	0.25
HI	-0.05	0.03	0.08	-0.05	-0.11	-0.57	-0.11	0.15	-0.78	1.00	-0.41	-0.01	0.18	0.13	0.06	0.04	-0.03	0.12	-0.16	-0.07	-0.03
TW	-0.13	0.00	-0.12	0.07	-0.30	0.43	-0.29	-0.58	-0.01	-0.41	1.00	0.15	-0.21	-0.05	-0.04	0.59	-0.33	0.02	0.03	0.01	-0.21
HULL. %	-0.21	0.02	0.16	-0.16	-0.09	-0.34	-0.02	-0.14	-0.10	-0.01	0.15	1.00	-0.11	0.05	0.13	0.47	-0.18	0.09	-0.10	0.03	-0.19
MILL. %	0.11	-0.02	-0.02	-0.12	-0.12	0.18	-0.09	-0.12	-0.22	0.18	-0.21	-0.11	1.00	0.06	0.07	0.00	0.04	0.01	0.13	0.12	0.05
HRR %	-0.06	0.35	-0.14	-0.02	-0.19	-0.17	0.45	-0.15	-0.20	0.13	-0.05	0.05	0.06	1.00	-0.73	0.47	-0.73	-0.13	-0.10	-0.68	-0.07
KLBC	0.16	-0.37	0.29	-0.08	-0.01	0.14	-0.47	0.15	0.05	0.06	-0.04	0.13	0.07	-0.73	1.00	-0.38	0.83	-0.01	0.20	0.69	0.00
KBBC	0.03	0.39	0.33	-0.27	-0.27	0.09	0.11	-0.36	-0.28	0.04	0.59	0.47	0.00	0.47	-0.38	1.00	-0.82	-0.26	0.17	-0.48	-0.44
L/B Ratio	0.07	-0.40	0.00	0.09	0.15	0.07	-0.35	0.27	0.21	-0.03	-0.33	-0.18	0.04	-0.73	0.83	-0.82	1.00	0.12	0.05	0.69	0.25
AMY. C.	-0.33	-0.47	-0.46	0.16	0.15	-0.11	-0.22	0.15	0.00	0.12	0.02	0.09	0.01	-0.13	-0.01	-0.26	0.12	1.00	-0.29	-0.02	0.10
VER	-0.13	0.00	0.13	-0.21	-0.23	0.48	0.10	-0.18	0.04	-0.16	0.03	-0.10	0.13	-0.10	0.20	0.17	0.05	-0.29	1.00	0.08	-0.27
KER	0.24	-0.57	0.36	0.17	-0.02	-0.03	-0.57	0.09	0.13	-0.07	0.01	0.03	0.12	-0.68	0.69	-0.48	0.69	-0.02	0.08	1.00	0.15
GYKG/Ha	0.38	0.03	0.37	0.30	0.08	-0.37	0.10	0.32	0.25	-0.03	-0.21	-0.19	0.05	-0.07	0.00	-0.44	0.25	0.10	-0.27	0.15	1.00

Appendix 34: Phenotypic correlation coefficient among different traits (Control 2014)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	0.01	0.44	-0.09	-0.01	0.20	-0.04	0.23	0.06	0.12	-0.03	-0.02	0.09	-0.02	0.06	0.01	0.04	-0.16	-0.02	0.11	0.04
PH	0.01	1.00	0.03	-0.22	0.24	-0.03	0.29	-0.32	-0.04	-0.21	-0.01	0.06	0.01	0.17	-0.22	0.15	-0.22	-0.25	0.06	-0.32	-0.05
DM	0.44	0.03	1.00	-0.15	-0.11	0.03	0.00	0.18	0.13	0.03	0.07	0.06	-0.03	-0.10	0.18	-0.04	0.13	-0.21	-0.05	0.16	0.15
NT/Pt	-0.09	-0.22	-0.15	1.00	-0.14	-0.04	-0.08	-0.01	0.09	-0.10	0.03	-0.14	-0.20	0.00	-0.08	-0.11	0.03	0.12	-0.13	0.11	0.18
NPT/m2	-0.01	0.24	-0.11	-0.14	1.00	0.04	0.07	-0.11	0.09	-0.15	-0.25	0.03	-0.08	-0.15	-0.01	-0.11	0.06	0.13	-0.07	-0.02	0.08
PL	0.20	-0.03	0.03	-0.04	0.04	1.00	-0.09	-0.14	-0.26	0.10	0.18	-0.10	0.06	-0.07	0.05	0.06	0.01	-0.04	0.13	-0.01	-0.11
NSP/P	-0.04	0.29	0.00	-0.08	0.07	-0.09	1.00	-0.03	0.12	-0.12	-0.23	-0.02	-0.07	0.40	-0.43	0.10	-0.31	-0.20	0.09	-0.52	0.12
GY/Pt	0.23	-0.32	0.18	-0.01	-0.11	-0.14	-0.03	1.00	0.19	0.60	-0.26	-0.11	-0.01	-0.08	0.15	-0.21	0.22	0.06	-0.08	0.04	0.07
BY/Pt	0.06	-0.04	0.13	0.09	0.09	-0.26	0.12	0.19	1.00	-0.67	0.07	0.01	-0.19	-0.14	0.04	-0.19	0.17	0.02	0.00	0.11	0.18
HI	0.12	-0.21	0.03	-0.10	-0.15	0.10	-0.12	0.60	-0.67	1.00	-0.24	-0.09	0.18	0.07	0.08	-0.01	0.04	0.04	-0.08	-0.05	-0.08
TW	-0.03	-0.01	0.07	0.03	-0.25	0.18	-0.23	-0.26	0.07	-0.24	1.00	0.06	-0.13	-0.04	-0.04	0.29	-0.20	0.01	0.00	0.01	-0.18
HULL %	-0.02	0.06	0.06	-0.14	0.03	-0.10	-0.02	-0.11	0.01	-0.09	0.06	1.00	-0.07	0.03	0.11	0.17	-0.06	0.05	-0.12	0.02	-0.11
MILL. %	0.09	0.01	-0.03	-0.20	-0.08	0.06	-0.07	-0.01	-0.19	0.18	-0.13	-0.07	1.00	0.06	0.06	0.01	0.03	-0.03	0.10	0.09	-0.02
HRR %	-0.02	0.17	-0.10	0.00	-0.15	-0.07	0.40	-0.08	-0.14	0.07	-0.04	0.03	0.06	1.00	-0.61	0.31	-0.56	-0.12	-0.10	-0.64	-0.05
KLBC	0.06	-0.22	0.18	-0.08	-0.01	0.05	-0.43	0.15	0.04	0.08	-0.04	0.11	0.06	-0.61	1.00	-0.28	0.76	0.00	0.08	0.63	0.01
KBBC	0.01	0.15	-0.04	-0.11	-0.11	0.06	0.10	-0.21	-0.19	-0.01	0.29	0.17	0.01	0.31	-0.28	1.00	-0.83	-0.18	0.01	-0.34	-0.25
L/B Ratio	0.04	-0.22	0.13	0.03	0.06	0.01	-0.31	0.22	0.17	0.04	-0.20	-0.06	0.03	-0.56	0.76	-0.83	1.00	0.10	0.05	0.58	0.16
AMY. C.	-0.16	-0.25	-0.21	0.12	0.13	-0.04	-0.20	0.06	0.02	0.04	0.01	0.05	-0.03	-0.12	0.00	-0.18	0.10	1.00	-0.23	-0.02	0.10
VER	-0.02	0.06	-0.05	-0.13	-0.07	0.13	0.09	-0.08	0.00	-0.08	0.00	-0.12	0.10	-0.10	0.08	0.01	0.05	-0.23	1.00	0.06	-0.23
KER	0.11	-0.32	0.16	0.11	-0.02	-0.01	-0.52	0.04	0.11	-0.05	0.01	0.02	0.09	-0.64	0.63	-0.34	0.58	-0.02	0.06	1.00	0.14
GYKG/Ha	0.04	-0.05	0.15	0.18	0.08	-0.11	0.12	0.07	0.18	-0.08	-0.18	-0.11	-0.02	-0.05	0.01	-0.25	0.16	0.10	-0.23	0.14	1.00

Appendix 35: Genotypic correlation coefficient among different traits (Control 2015)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	-0.24	0.64	0.26	0.25	0.23	-0.08	0.26	0.46	-0.20	0.00	-0.06	-0.28	-0.06	0.01	-0.04	0.05	0.02	0.00	0.13	0.67
PH	-0.24	1.00	-0.05	-0.62	-0.34	0.12	0.43	-0.57	-0.19	-0.28	-0.28	-0.10	-0.16	0.50	-0.27	0.31	-0.42	0.42	0.08	-0.55	-0.20
DM	0.64	-0.05	1.00	0.11	-0.03	-0.12	-0.39	0.20	0.31	-0.14	0.09	-0.26	-0.13	0.06	0.02	-0.36	0.27	-0.10	0.62	0.01	0.42
NT/Pt	0.26	-0.62	0.11	1.00	0.30	0.30	-0.32	-0.21	-0.02	-0.17	0.32	0.46	0.37	-0.32	0.24	-0.01	0.24	0.01	0.12	0.38	-0.15
NPT/m2	0.25	-0.34	-0.03	0.30	1.00	-0.04	-0.11	-0.06	-0.10	0.05	0.08	0.04	-0.22	-0.31	0.20	0.29	-0.01	0.22	-0.11	0.33	0.37
PL	0.23	0.12	-0.12	0.30	-0.04	1.00	0.23	-0.17	0.10	-0.21	-0.07	0.22	0.20	-0.23	0.21	0.17	0.05	0.16	-0.07	0.15	-0.06
NSP/P	-0.08	0.43	-0.39	-0.32	-0.11	0.23	1.00	-0.09	0.00	-0.08	-0.12	0.00	-0.32	0.19	-0.39	0.14	-0.38	0.12	-0.08	-0.36	-0.13
GY/Pt	0.26	-0.57	0.20	-0.21	-0.06	-0.17	-0.09	1.00	0.24	0.50	0.13	-0.39	-0.06	-0.08	0.03	-0.12	0.10	-0.18	0.21	-0.04	0.26
BY/Pt	0.46	-0.19	0.31	-0.02	-0.10	0.10	0.00	0.24	1.00	-0.72	0.24	-0.24	0.20	-0.21	0.02	-0.13	0.11	-0.13	0.03	0.09	0.36
HI	-0.20	-0.28	-0.14	-0.17	0.05	-0.21	-0.08	0.50	-0.72	1.00	-0.12	-0.05	-0.19	0.09	0.03	0.02	-0.01	-0.03	0.12	-0.09	-0.14
TW	0.00	-0.28	0.09	0.32	0.08	-0.07	-0.12	0.13	0.24	-0.12	1.00	0.09	0.18	-0.09	-0.09	0.09	-0.10	-0.01	-0.23	0.06	0.01
HULL %	-0.06	-0.10	-0.26	0.46	0.04	0.22	0.00	-0.39	-0.24	-0.05	0.09	1.00	-0.01	-0.04	0.30	0.27	0.09	0.12	-0.26	0.06	-0.41
MILL. %	-0.28	-0.16	-0.13	0.37	-0.22	0.20	-0.32	-0.06	0.20	-0.19	0.18	-0.01	1.00	-0.24	0.15	-0.20	0.25	-0.28	0.08	0.21	0.09
HRR %	-0.06	0.50	0.06	-0.32	-0.31	-0.23	0.19	-0.08	-0.21	0.09	-0.09	-0.04	-0.24	1.00	-0.63	0.15	-0.59	0.01	0.07	-0.64	-0.13
KLBC	0.01	-0.27	0.02	0.24	0.20	0.21	-0.39	0.03	0.02	0.03	-0.09	0.30	0.15	-0.63	1.00	0.02	0.76	0.10	0.04	0.60	0.08
KBBC	-0.04	0.31	-0.36	-0.01	0.29	0.17	0.14	-0.12	-0.13	0.02	0.09	0.27	-0.20	0.15	0.02	1.00	-0.63	0.14	-0.15	-0.08	-0.21
L/B Ratio	0.05	-0.42	0.27	0.24	-0.01	0.05	-0.38	0.10	0.11	-0.01	-0.10	0.09	0.25	-0.59	0.76	-0.63	1.00	-0.02	0.13	0.52	0.21
AMY. C.	0.02	0.42	-0.10	0.01	0.22	0.16	0.12	-0.18	-0.13	-0.03	-0.01	0.12	-0.28	0.01	0.10	0.14	-0.02	1.00	-0.05	-0.15	-0.08
VER	0.00	0.08	0.62	0.12	-0.11	-0.07	-0.08	0.21	0.03	0.12	-0.23	-0.26	0.08	0.07	0.04	-0.15	0.13	-0.05	1.00	0.01	-0.10
KER	0.13	-0.55	0.01	0.38	0.33	0.15	-0.36	-0.04	0.09	-0.09	0.06	0.06	0.21	-0.64	0.60	-0.08	0.52	-0.15	0.01	1.00	0.23
GYKG/Ha	0.67	-0.20	0.42	-0.15	0.37	-0.06	-0.13	0.26	0.36	-0.14	0.01	-0.41	0.09	-0.13	0.08	-0.21	0.21	-0.08	-0.10	0.23	1.00

Appendix 36: Phenotypic correlation coefficient among different traits (Control 2015)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	-0.10	0.31	-0.02	0.17	0.14	-0.05	0.08	0.20	-0.08	0.00	-0.06	-0.24	-0.05	0.04	-0.02	0.05	0.03	0.00	0.10	0.32
PH	-0.10	1.00	-0.12	-0.17	-0.22	0.06	0.28	-0.23	-0.18	-0.03	-0.13	-0.10	-0.10	0.33	-0.21	0.11	-0.23	0.28	-0.05	-0.37	-0.15
DM	0.31	-0.12	1.00	0.07	-0.06	-0.07	-0.26	0.08	0.23	-0.10	0.00	-0.13	0.07	0.08	0.03	-0.18	0.17	-0.06	0.33	0.01	0.26
NT/Pt	-0.02	-0.17	0.07	1.00	0.17	0.18	-0.22	0.01	0.05	-0.03	0.20	0.07	0.18	-0.17	0.15	0.05	0.07	0.00	0.06	0.23	-0.06
NPT/m2	0.17	-0.22	-0.06	0.17	1.00	-0.04	-0.09	-0.03	-0.06	0.01	0.06	0.00	-0.18	-0.26	0.15	0.19	-0.03	0.22	-0.07	0.30	0.31
PL	0.14	0.06	-0.07	0.18	-0.04	1.00	0.20	-0.01	0.09	-0.08	-0.04	0.10	0.09	-0.16	0.17	0.10	0.03	0.13	-0.06	0.13	-0.01
NSP/P	-0.05	0.28	-0.26	-0.22	-0.09	0.20	1.00	0.03	0.02	0.00	-0.09	0.00	-0.19	0.15	-0.35	0.06	-0.27	0.11	-0.08	-0.34	-0.08
GY/Pt	0.08	-0.23	0.08	0.01	-0.03	-0.01	0.03	1.00	0.13	0.66	0.08	-0.19	-0.06	-0.04	-0.01	-0.12	0.08	-0.13	0.10	-0.03	0.18
BY/Pt	0.20	-0.18	0.23	0.05	-0.06	0.09	0.02	0.13	1.00	-0.65	0.18	-0.19	0.14	-0.19	0.02	-0.08	0.08	-0.11	0.01	0.08	0.30
HI	-0.08	-0.03	-0.10	-0.03	0.01	-0.08	0.00	0.66	-0.65	1.00	-0.07	0.02	-0.14	0.09	-0.01	-0.04	0.02	-0.03	0.06	-0.07	-0.09
TW	0.00	-0.13	0.00	0.20	0.06	-0.04	-0.09	0.08	0.18	-0.07	1.00	0.07	0.09	-0.08	-0.08	0.07	-0.09	-0.03	-0.24	0.05	0.01
HULL %	-0.06	-0.10	-0.13	0.07	0.00	0.10	0.00	-0.19	-0.19	0.02	0.07	1.00	0.07	0.01	0.23	0.15	0.05	0.07	-0.18	0.05	-0.35
MILL. %	-0.24	-0.10	0.07	0.18	-0.18	0.09	-0.19	-0.06	0.14	-0.14	0.09	0.07	1.00	-0.17	0.14	-0.06	0.14	-0.19	0.09	0.15	0.06
HRR %	-0.05	0.33	0.08	-0.17	-0.26	-0.16	0.15	-0.04	-0.19	0.09	-0.08	0.01	-0.17	1.00	-0.56	0.10	-0.44	0.01	0.05	-0.60	-0.08
KLBC	0.04	-0.21	0.03	0.15	0.15	0.17	-0.35	-0.01	0.02	-0.01	-0.08	0.23	0.14	-0.56	1.00	0.00	0.66	0.10	0.03	0.58	0.06
KBBC	-0.02	0.11	-0.18	0.05	0.19	0.10	0.06	-0.12	-0.08	-0.04	0.07	0.15	-0.06	0.10	0.00	1.00	-0.75	0.09	-0.10	-0.07	-0.18
L/B Ratio	0.05	-0.23	0.17	0.07	-0.03	0.03	-0.27	0.08	0.08	0.02	-0.09	0.05	0.14	-0.44	0.66	-0.75	1.00	-0.02	0.11	0.42	0.18
AMY. C.	0.03	0.28	-0.06	0.00	0.22	0.13	0.11	-0.13	-0.11	-0.03	-0.03	0.07	-0.19	0.01	0.10	0.09	-0.02	1.00	-0.03	-0.15	-0.05
VER	0.00	-0.05	0.33	0.06	-0.07	-0.06	-0.08	0.10	0.01	0.06	-0.24	-0.18	0.09	0.05	0.03	-0.10	0.11	-0.03	1.00	0.01	-0.03
KER	0.10	-0.37	0.01	0.23	0.30	0.13	-0.34	-0.03	0.08	-0.07	0.05	0.05	0.15	-0.60	0.58	-0.07	0.42	-0.15	0.01	1.00	0.20
GYKG/Ha	0.32	-0.15	0.26	-0.06	0.31	-0.01	-0.08	0.18	0.30	-0.09	0.01	-0.35	0.06	-0.08	0.06	-0.18	0.18	-0.05	-0.03	0.20	1.00

Appendix 37: Genotypic correlation coefficient among different traits (Stress 2014)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	0.08	0.58	0.46	0.32	0.28	0.12	-0.02	0.54	-0.59	-0.19	-0.07	0.04	-0.03	0.06	0.25	-0.10	-0.41	0.00	0.06	0.47
PH	0.08	1.00	0.14	-0.20	0.07	0.29	0.34	-0.47	-0.11	-0.22	0.13	-0.23	-0.17	0.61	-0.29	0.59	-0.48	-0.08	0.28	-0.38	0.00
DM	0.58	0.14	1.00	0.49	0.20	0.16	0.09	0.07	0.32	-0.31	-0.26	-0.04	0.00	-0.04	0.15	0.20	-0.02	-0.31	-0.02	0.05	0.46
NT/Pt	0.46	-0.20	0.49	1.00	-0.06	0.39	-0.52	0.31	0.00	0.20	-0.15	-0.21	0.46	-0.57	0.44	-0.40	0.47	0.18	-0.17	0.69	0.44
NPT/m2	0.32	0.07	0.20	-0.06	1.00	-0.13	0.15	0.08	-0.07	0.12	-0.13	-0.17	-0.06	-0.14	0.00	0.14	-0.09	0.07	-0.17	-0.08	0.16
PL	0.28	0.29	0.16	0.39	-0.13	1.00	-0.11	0.00	-0.08	0.05	0.16	0.35	-0.07	0.17	0.28	0.58	-0.11	-0.04	-0.03	0.14	-0.11
NSP/P	0.12	0.34	0.09	-0.52	0.15	-0.11	1.00	0.33	0.10	0.13	-0.19	-0.04	-0.21	0.35	-0.41	0.36	-0.44	-0.06	0.02	-0.53	0.03
GY/Pt	-0.02	-0.47	0.07	0.31	0.08	0.00	0.33	1.00	0.40	0.24	-0.50	-0.31	0.08	-0.13	0.04	-0.11	0.08	0.25	-0.01	0.20	0.33
BY/Pt	0.54	-0.11	0.32	0.00	-0.07	-0.08	0.10	0.40	1.00	-0.79	-0.12	0.24	0.06	-0.02	-0.06	0.04	-0.05	-0.13	0.32	0.14	0.11
HI	-0.59	-0.22	-0.31	0.20	0.12	0.05	0.13	0.24	-0.79	1.00	-0.22	-0.48	-0.03	-0.04	0.05	-0.10	0.07	0.30	-0.31	-0.04	0.12
TW	-0.19	0.13	-0.26	-0.15	-0.13	0.16	-0.19	-0.50	-0.12	-0.22	1.00	0.10	-0.47	-0.02	-0.03	0.24	-0.15	0.07	-0.14	-0.02	-0.20
HULL %	-0.07	-0.23	-0.04	-0.21	-0.17	0.35	-0.04	-0.31	0.24	-0.48	0.10	1.00	-0.34	0.22	-0.28	0.20	-0.27	-0.06	0.11	-0.37	-0.13
MILL. %	0.04	-0.17	0.00	0.46	-0.06	-0.07	-0.21	0.08	0.06	-0.03	-0.47	-0.34	1.00	-0.04	0.08	-0.25	0.18	0.15	-0.07	0.19	-0.05
HRR %	-0.03	0.61	-0.04	-0.57	-0.14	0.17	0.35	-0.13	-0.02	-0.04	-0.02	0.22	-0.04	1.00	-0.36	0.46	-0.48	-0.10	0.27	-0.69	-0.22
KLBC	0.06	-0.29	0.15	0.44	0.00	0.28	-0.41	0.04	-0.06	0.05	-0.03	-0.28	0.08	-0.36	1.00	-0.47	0.87	-0.08	-0.22	0.37	0.02
KBBC	0.25	0.59	0.20	-0.40	0.14	0.58	0.36	-0.11	0.04	-0.10	0.24	0.20	-0.25	0.46	-0.47	1.00	-0.84	-0.26	0.17	-0.30	-0.22
L/B Ratio	-0.10	-0.48	-0.02	0.47	-0.09	-0.11	-0.44	0.08	-0.05	0.07	-0.15	-0.27	0.18	-0.48	0.87	-0.84	1.00	0.09	-0.21	0.39	0.11
AMY. C.	-0.41	-0.08	-0.31	0.18	0.07	-0.04	-0.06	0.25	-0.13	0.30	0.07	-0.06	0.15	-0.10	-0.08	-0.26	0.09	1.00	-0.25	-0.06	-0.08
VER	0.00	0.28	-0.02	-0.17	-0.17	-0.03	0.02	-0.01	0.32	-0.31	-0.14	0.11	-0.07	0.27	-0.22	0.17	-0.21	-0.25	1.00	-0.23	0.03
KER	0.06	-0.38	0.05	0.69	-0.08	0.14	-0.53	0.20	0.14	-0.04	-0.02	-0.37	0.19	-0.69	0.37	-0.30	0.39	-0.06	-0.23	1.00	0.37
GYKG/Ha	0.47	0.00	0.46	0.44	0.16	-0.11	0.03	0.33	0.11	0.12	-0.20	-0.13	-0.05	-0.22	0.02	-0.22	0.11	-0.08	0.03	0.37	1.00

Appendix 38: Phenotypic correlation coefficient among different traits (Stress 2014)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	0.07	0.56	0.11	0.07	0.07	0.06	0.05	0.10	-0.05	-0.11	-0.03	0.10	-0.04	0.10	0.11	-0.03	-0.22	0.02	0.03	0.28
PH	0.07	1.00	0.08	-0.14	0.00	0.20	0.17	-0.16	-0.03	-0.10	0.07	0.03	-0.16	0.33	-0.19	0.40	-0.37	-0.07	0.09	-0.22	-0.09
DM	0.56	0.08	1.00	0.07	0.08	0.19	0.02	0.04	0.12	-0.06	-0.17	-0.08	0.10	-0.04	0.12	0.12	-0.02	-0.20	-0.01	0.04	0.25
NT/Pt	0.11	-0.14	0.07	1.00	-0.03	-0.02	-0.31	0.06	0.01	0.04	-0.07	-0.09	0.19	-0.39	0.20	-0.20	0.24	0.14	-0.10	0.44	0.25
NPT/m2	0.07	0.00	0.08	-0.03	1.00	-0.08	0.12	0.10	-0.07	0.12	-0.18	-0.01	-0.01	-0.09	0.00	0.05	-0.04	0.06	-0.16	-0.08	0.12
PL	0.07	0.20	0.19	-0.02	-0.08	1.00	-0.10	0.07	0.01	0.03	0.17	0.13	0.03	0.15	0.18	0.14	0.02	-0.02	-0.06	0.08	-0.06
NSP/P	0.06	0.17	0.02	-0.31	0.12	-0.10	1.00	0.15	0.08	0.05	-0.15	0.03	-0.13	0.32	-0.27	0.23	-0.30	-0.05	0.02	-0.48	-0.01
GY/Pt	0.05	-0.16	0.04	0.06	0.10	0.07	0.15	1.00	0.10	0.66	-0.29	0.00	0.11	-0.01	0.06	-0.05	0.07	0.12	-0.02	0.11	0.09
BY/Pt	0.10	-0.03	0.12	0.01	-0.07	0.01	0.08	0.10	1.00	-0.67	-0.02	0.16	0.01	0.00	-0.08	0.03	-0.06	-0.12	0.24	0.12	0.04
HI	-0.05	-0.10	-0.06	0.04	0.12	0.03	0.05	0.66	-0.67	1.00	-0.20	-0.12	0.07	0.00	0.09	-0.04	0.08	0.16	-0.17	-0.02	0.03
TW	-0.11	0.07	-0.17	-0.07	-0.18	0.17	-0.15	-0.29	-0.02	-0.20	1.00	0.00	-0.28	0.01	-0.03	0.17	-0.12	0.05	-0.10	-0.01	-0.13
HULL %	-0.03	0.03	-0.08	-0.09	-0.01	0.13	0.03	0.00	0.16	-0.12	0.00	1.00	-0.15	0.17	-0.06	-0.03	-0.01	-0.04	0.11	-0.18	-0.09
MILL. %	0.10	-0.16	0.10	0.19	-0.01	0.03	-0.13	0.11	0.01	0.07	-0.28	-0.15	1.00	-0.01	0.05	-0.05	0.06	0.09	-0.04	0.12	-0.01
HRR %	-0.04	0.33	-0.04	-0.39	-0.09	0.15	0.32	-0.01	0.00	0.00	0.01	0.17	-0.01	1.00	-0.29	0.27	-0.34	-0.09	0.21	-0.63	-0.23
KLBC	0.10	-0.19	0.12	0.20	0.00	0.18	-0.27	0.06	-0.08	0.09	-0.03	-0.06	0.05	-0.29	1.00	-0.31	0.77	-0.06	-0.17	0.33	0.06
KBBC	0.11	0.40	0.12	-0.20	0.05	0.14	0.23	-0.05	0.03	-0.04	0.17	-0.03	-0.05	0.27	-0.31	1.00	-0.84	-0.19	0.09	-0.18	-0.19
L/B Ratio	-0.03	-0.37	-0.02	0.24	-0.04	0.02	-0.30	0.07	-0.06	0.08	-0.12	-0.01	0.06	-0.34	0.77	-0.84	1.00	0.10	-0.15	0.30	0.15
AMY. C.	-0.22	-0.07	-0.20	0.14	0.06	-0.02	-0.05	0.12	-0.12	0.16	0.05	-0.04	0.09	-0.09	-0.06	-0.19	0.10	1.00	-0.21	-0.06	-0.07
VER	0.02	0.09	-0.01	-0.10	-0.16	-0.06	0.02	-0.02	0.24	-0.17	-0.10	0.11	-0.04	0.21	-0.17	0.09	-0.15	-0.21	1.00	-0.19	0.03
KER	0.03	-0.22	0.04	0.44	-0.08	0.08	-0.48	0.11	0.12	-0.02	-0.01	-0.18	0.12	-0.63	0.33	-0.18	0.30	-0.06	-0.19	1.00	0.33
GYKG/Ha	0.28	-0.09	0.25	0.25	0.12	-0.06	-0.01	0.09	0.04	0.03	-0.13	-0.09	-0.01	-0.23	0.06	-0.19	0.15	-0.07	0.03	0.33	1.00

Appendix 39: Genotypic correlation coefficient among different traits (Stress 2015)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	0.00	0.43	0.14	0.43	0.36	-0.26	0.00	0.22	-0.22	0.24	-0.27	0.43	-0.18	0.15	0.21	-0.02	-0.28	-0.13	0.21	0.46
PH	0.00	1.00	0.21	-0.40	-0.48	0.20	0.41	-0.73	-0.37	-0.21	-0.04	0.13	-0.34	0.66	-0.03	0.53	-0.30	-0.20	-0.21	-0.58	-0.39
DM	0.43	0.21	1.00	-0.10	-0.23	0.09	-0.15	0.07	-0.17	0.12	-0.19	-0.04	0.35	0.12	-0.15	-0.13	-0.04	0.08	-0.04	-0.05	0.36
NT/Pt	0.14	-0.40	-0.10	1.00	0.36	0.12	-0.53	-0.25	0.32	-0.49	0.27	-0.82	0.11	-0.44	0.20	-0.09	0.18	0.18	-0.13	0.41	0.01
NPT/m2	0.43	-0.48	-0.23	0.36	1.00	0.31	-0.35	-0.11	0.00	-0.07	0.27	-0.13	0.12	-0.29	0.32	-0.22	0.34	0.01	-0.07	0.55	0.37
PL	0.36	0.20	0.09	0.12	0.31	1.00	-0.01	-0.29	0.05	-0.22	0.13	-0.20	-0.29	-0.17	0.22	0.16	0.07	-0.33	0.06	0.22	0.12
NSP/P	-0.26	0.41	-0.15	-0.53	-0.35	-0.01	1.00	0.25	0.13	0.07	-0.37	0.28	-0.31	0.11	-0.23	0.08	-0.20	-0.06	-0.25	-0.36	0.01
GY/Pt	0.00	-0.73	0.07	-0.25	-0.11	-0.29	0.25	1.00	0.28	0.49	-0.20	0.10	-0.01	-0.24	-0.33	0.03	-0.26	0.19	-0.19	0.05	0.10
BY/Pt	0.22	-0.37	-0.17	0.32	0.00	0.05	0.13	0.28	1.00	-0.70	-0.08	0.03	0.05	-0.24	-0.05	-0.10	0.02	-0.07	-0.05	0.01	0.31
HI	-0.22	-0.21	0.12	-0.49	-0.07	-0.22	0.07	0.49	-0.70	1.00	-0.07	0.09	-0.10	0.04	-0.21	0.16	-0.23	0.21	-0.11	0.03	-0.22
TW	0.24	-0.04	-0.19	0.27	0.27	0.13	-0.37	-0.20	-0.08	-0.07	1.00	0.28	0.36	-0.18	0.39	-0.22	0.37	0.13	-0.06	0.20	-0.06
HULL %	-0.27	0.13	-0.04	-0.82	-0.13	-0.20	0.28	0.10	0.03	0.09	0.28	1.00	0.04	0.30	0.14	0.26	-0.04	0.04	-0.03	-0.07	0.16
MILL. %	0.43	-0.34	0.35	0.11	0.12	-0.29	-0.31	-0.01	0.05	-0.10	0.36	0.04	1.00	-0.33	0.46	-0.69	0.69	-0.11	0.12	0.30	-0.01
HRR %	-0.18	0.66	0.12	-0.44	-0.29	-0.17	0.11	-0.24	-0.24	0.04	-0.18	0.30	-0.33	1.00	-0.36	0.56	-0.56	-0.26	0.33	-0.55	-0.17
KLBC	0.15	-0.03	-0.15	0.20	0.32	0.22	-0.23	-0.33	-0.05	-0.21	0.39	0.14	0.46	-0.36	1.00	-0.32	0.86	0.09	-0.28	0.51	0.22
KBBC	0.21	0.53	-0.13	-0.09	-0.22	0.16	0.08	0.03	-0.10	0.16	-0.22	0.26	-0.69	0.56	-0.32	1.00	-0.76	-0.32	-0.18	-0.37	-0.25
L/B Ratio	-0.02	-0.30	-0.04	0.18	0.34	0.07	-0.20	-0.26	0.02	-0.23	0.37	-0.04	0.69	-0.56	0.86	-0.76	1.00	0.22	-0.10	0.55	0.29
AMY. C.	-0.28	-0.20	0.08	0.18	0.01	-0.33	-0.06	0.19	-0.07	0.21	0.13	0.04	-0.11	-0.26	0.09	-0.32	0.22	1.00	-0.27	0.08	-0.04
VER	-0.13	-0.21	-0.04	-0.13	-0.07	0.06	-0.25	-0.19	-0.05	-0.11	-0.06	-0.03	0.12	0.33	-0.28	-0.18	-0.10	-0.27	1.00	-0.06	0.05
KER	0.21	-0.58	-0.05	0.41	0.55	0.22	-0.36	0.05	0.01	0.03	0.20	-0.07	0.30	-0.55	0.51	-0.37	0.55	0.08	-0.06	1.00	0.29
GYKG/Ha	0.46	-0.39	0.36	0.01	0.37	0.12	0.01	0.10	0.31	-0.22	-0.06	0.16	-0.01	-0.17	0.22	-0.25	0.29	-0.04	0.05	0.29	1.00

Appendix 40: Phenotypic correlation coefficient among different traits (Stress 2015)

Character	DFF	PH	DM	NT/Pt	NPT/m2	PL	NSP/P	GY/Pt	BY/Pt	HI	TW	HULL %	MILL. %	HRR %	KLBC	KBBC	L/B Ratio	AMY. C.	VER	KER	GYKG/Ha
DFF	1.00	0.03	0.29	0.14	0.19	0.21	-0.05	-0.03	0.11	-0.11	0.09	-0.01	-0.02	-0.08	0.09	-0.01	0.06	-0.12	-0.07	0.10	0.24
PH	0.03	1.00	0.16	-0.20	-0.32	0.12	0.14	-0.09	-0.18	0.06	-0.07	0.18	-0.22	0.31	0.04	0.17	-0.09	-0.13	-0.12	-0.37	-0.15
DM	0.29	0.16	1.00	-0.06	0.01	0.05	-0.14	-0.02	-0.02	-0.02	-0.02	0.06	0.06	-0.02	-0.02	0.04	-0.04	0.03	-0.09	-0.02	0.13
NT/Pt	0.14	-0.20	-0.06	1.00	0.20	0.09	-0.29	-0.09	0.24	-0.24	0.19	-0.19	0.00	-0.30	0.16	-0.18	0.22	0.12	-0.11	0.29	0.04
NPT/m2	0.19	-0.32	0.01	0.20	1.00	0.21	-0.29	-0.11	-0.04	-0.05	0.23	-0.07	0.07	-0.23	0.22	-0.10	0.20	0.02	-0.06	0.48	0.30
PL	0.21	0.12	0.05	0.09	0.21	1.00	-0.02	-0.07	0.04	-0.07	0.07	-0.09	-0.11	-0.13	0.16	0.10	0.04	-0.27	0.03	0.18	0.18
NSP/P	-0.05	0.14	-0.14	-0.29	-0.29	-0.02	1.00	0.12	0.09	0.02	-0.32	0.08	-0.16	0.15	-0.22	0.05	-0.17	-0.05	-0.18	-0.32	-0.03
GY/Pt	-0.03	-0.09	-0.02	-0.09	-0.11	-0.07	0.12	1.00	0.11	0.71	-0.09	0.10	0.11	-0.16	-0.13	-0.05	-0.05	0.11	-0.05	0.02	0.01
BY/Pt	0.11	-0.18	-0.02	0.24	-0.04	0.04	0.09	0.11	1.00	-0.61	0.00	0.09	-0.03	-0.20	-0.02	-0.04	0.03	-0.06	-0.03	0.01	0.19
HI	-0.11	0.06	-0.02	-0.24	-0.05	-0.07	0.02	0.71	-0.61	1.00	-0.06	0.03	0.09	0.01	-0.09	-0.01	-0.07	0.12	-0.02	0.00	-0.14
TW	0.09	-0.07	-0.02	0.19	0.23	0.07	-0.32	-0.09	0.00	-0.06	1.00	0.00	0.13	-0.16	0.30	-0.11	0.24	0.12	-0.04	0.16	-0.05
HULL %	-0.01	0.18	0.06	-0.19	-0.07	-0.09	0.08	0.10	0.09	0.03	0.00	1.00	0.00	0.07	0.09	-0.01	0.07	0.00	-0.02	-0.03	0.08
MILL. %	-0.02	-0.22	0.06	0.00	0.07	-0.11	-0.16	0.11	-0.03	0.09	0.13	0.00	1.00	-0.13	0.22	-0.18	0.25	-0.05	0.13	0.17	0.02
HRR %	-0.08	0.31	-0.02	-0.30	-0.23	-0.13	0.15	-0.16	-0.20	0.01	-0.16	0.07	-0.13	1.00	-0.32	0.29	-0.39	-0.23	0.28	-0.50	-0.14
KLBC	0.09	0.04	-0.02	0.16	0.22	0.16	-0.22	-0.13	-0.02	-0.09	0.30	0.09	0.22	-0.32	1.00	-0.23	0.76	0.07	-0.21	0.47	0.19
KBBC	-0.01	0.17	0.04	-0.18	-0.10	0.10	0.05	-0.05	-0.04	-0.01	-0.11	-0.01	-0.18	0.29	-0.23	1.00	-0.81	-0.19	-0.14	-0.24	-0.14
L/B Ratio	0.06	-0.09	-0.04	0.22	0.20	0.04	-0.17	-0.05	0.03	-0.07	0.24	0.07	0.25	-0.39	0.76	-0.81	1.00	0.16	-0.04	0.45	0.21
AMY. C.	-0.12	-0.13	0.03	0.12	0.02	-0.27	-0.05	0.11	-0.06	0.12	0.12	0.00	-0.05	-0.23	0.07	-0.19	0.16	1.00	-0.23	0.08	-0.03
VER	-0.07	-0.12	-0.09	-0.11	-0.06	0.03	-0.18	-0.05	-0.03	-0.02	-0.04	-0.02	0.13	0.28	-0.21	-0.14	-0.04	-0.23	1.00	-0.05	0.06
KER	0.10	-0.37	-0.02	0.29	0.48	0.18	-0.32	0.02	0.01	0.00	0.16	-0.03	0.17	-0.50	0.47	-0.24	0.45	0.08	-0.05	1.00	0.26
GYKG/Ha	0.24	-0.15	0.13	0.04	0.30	0.18	-0.03	0.01	0.19	-0.14	-0.05	0.08	0.02	-0.14	0.19	-0.14	0.21	-0.03	0.06	0.26	1.00

RESEARCH ALBUM

1. Seed sowing, Nursery and Transplanting

2. Transplanting and Transplanted field

3. Overview of field and Research scholar

4. Standard checks and Stress condition

5. During field observations

6. Molecular, Micronutrients and Quality related work

7. Preparations for Postharvest observations

8. During Quality Observations

9. At NRRI, With Major Advisor and Research Field View

10. During Molecular, Quality and Field Work

11. Quality, Micronutrients and Harvesting

12. Quality work and Molecular

(General BIO-DATA)

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Place: Sabour   …………………………...

Date: 02/05/18   **(Amit Kumar Mishra)**

SELF ATTESTATION

This is to certify that, I have personally worked on the thesis entitled **"Stability analysis for grain yield and quality traits in indica rice (*Oryza sativa* L.) lines".** The data mentioned in this Ph.D. thesis were obtained during unfeigned work done and were collected from the field and laboratory during my experiment. Any other information in this thesis, which have been collected or borrowed from outside agency, has been duly acknowledged.

Place: Sabour   **…………………….**

Date: …………   **(Amit Kumar Mishra)**

BIOGRAPHICAL SKETCH

Amit Kumar Mishra was born on August 3rd, 1986 in Siliguri Town, District Darjeeling (WB) while his native place is Village Sisotar in District Ballia (UP). He belongs to Indian Hindu Brahmins family. His parents, Mr. Kalipad Mishra (Businessman) & Mrs. Sushila Mishra (Housewife) and only sister Miss Shweta Mishra (MA in Political Science, BHU). Initial education of Amit was done in Siliguri in Hindi medium schools from Nursery to 8th standard & he was a good student during this period. After that his family shifted to his native place and his education (10th and 10+2 both in science stream) continued from Gandhi Inter College, Sikandarpur from UP Board. After that he moved to Agricultural Sciences due to his interest and done B.Sc. (Ag.) from SMMTD Post Graduate College, Ballia through Veer Bahadur Singh Purvanchal University, Jaunpur and M. Sc. (Ag) from Sam Higginbottom University of Agriculture, Technology and Sciences, Naini (Allahabad) in main campus. He was an average student during this period (9th to M. Sc. Ag.) and scored 1st class marks in all four standards. His carrier objectives are to serve agriculture through academic and research. Amit is a very friendly personality. He is very optimistic and always thinks about human beings, agricultural sciences and its philosophies. His message to everyone is that "Hard labour is only investment that never failed"......!!!

PUBLICATIONS

FULL LENGTH ARTICLE   **OPEN ACCESS**
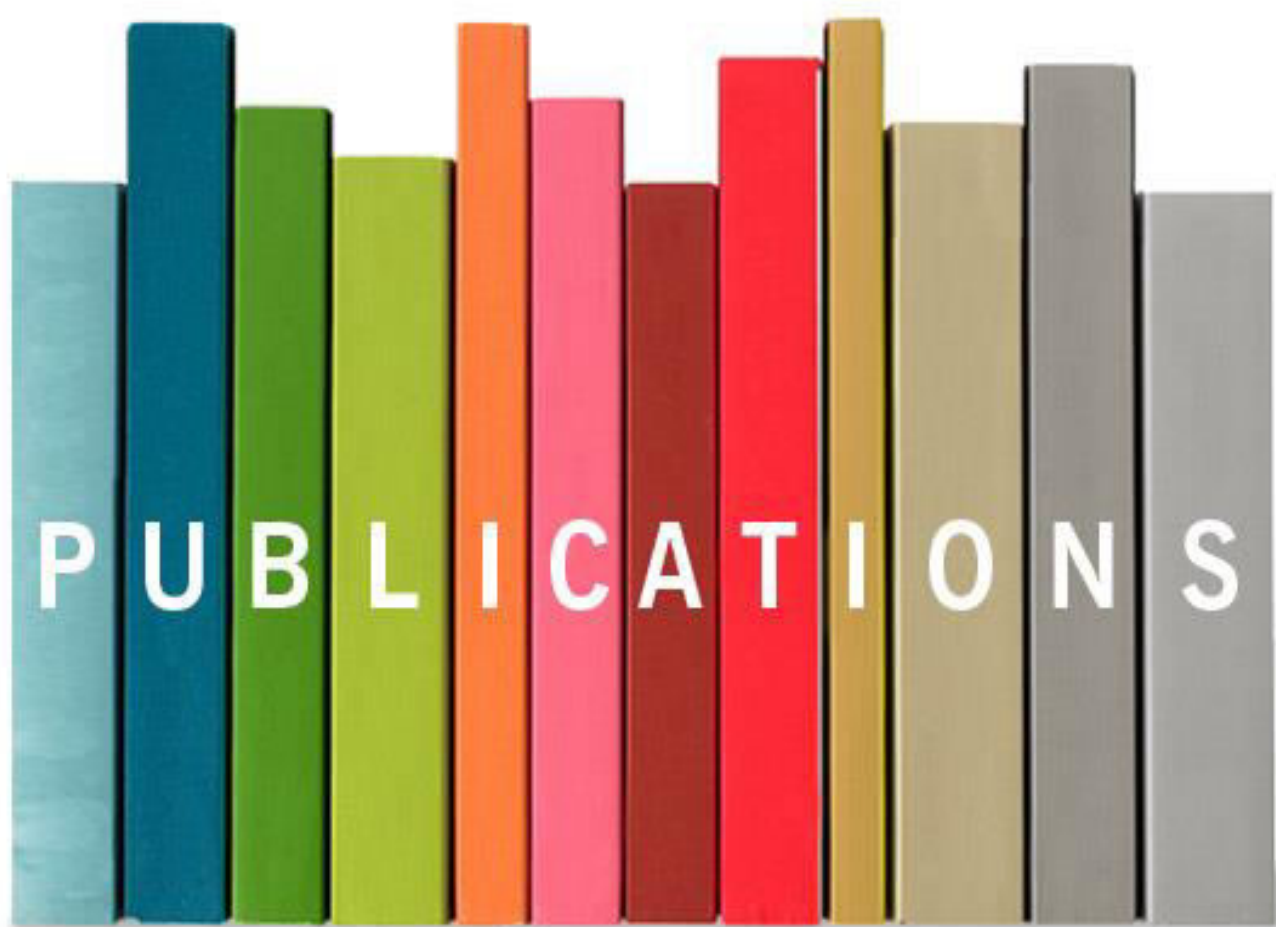
Genetic variability in advance indica rice (*Oryza sativa* L.) lines for yield and quality attributes

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ABSTRACT
The present study performed to estimate genetic variability in 36 lines of rice during Kharif - 2014 (control / irrigated condition) with three replications in RCBD fashion for 21 yield and quality traits. Analysis of variance (ANOVA) exhibited presence of significant differences between genotypes for all the parameters except some quality parameters; indicate ample scope of selection from experimental material. All the VP and PCV values are higher than the VG and GCV values in respect to such yield and quality attributes. Minimum differences between GCV and PCV indicate less interference of environment. The yield and quality characters are varying in sense of heritability (bs) and exhibited low, moderate, high and very high heritability groups. The characters, number of spikelet's per panicle, head rice recovery % and kernel elongation ratio had high broad sense heritability coupled with high genetic advance as % of mean showed preponderance of additive gene expression in these characters and that can be use in future improvement of such materials for such specific traits.
Key words: Genetic Variability, Rice, Yield, Quality, Heritability and Genetic advance.

INTRODUCTION

Rice is one of the important cereal crops of the world particularly in South - East Asian countries. Among the rice growing countries in the world, India occupied largest area under rice crop and attained second position next to China in case of production. Rice is a major staple food for half of the world population and population is increasing in alarming rate so its urgent need to produce high yielding varieties with better quality, which requires sufficient amount of genetic variability in breeding stocks of rice. Grain yield is a highly environmental influenced complex character, hence direct selection is less effective and ultimately limited success achieve in grain yield improvement. Rice quality is another important consideration of rice after grain yield. Knowledge about genetic variability is needed to develop any variety having higher yield and quality. Variations present in the set of advance lines are heritable or not is illustrated by the knowledge of genetic variability. The heritable component is important to estimate actual magnitude of variation for future rice improvement program. Range of variability present in different attributes indicated by the GCV (Genotypic coefficient of variance) while role of environment influence on rice lines indicated with the help of PCV (Phenotypic coefficient of variance). Heritability estimation is a essential criteria during selection and rice improvement because it's indicate the transmissibility of characters into next or subsequent generations. Heritability along with genetic advance gives reliable information about genetic gain under selection for successful improvement program. Present study is designed to assess the genetic variability, broad sense heritability and genetic advance of yield and quality attributes in 36 rice genotypes.

MATERIALS AND METHODS

The experiment conducted at rice section (Bihar Agricultural University) Sabour. This site situated at longitude 87^0 04' 1.6" East, latitude 25^0 14' 11" North and altitude 37.19 meter above mean sea level in the heart of vast Indo - gangatic plains of North India. The experimental plot has well drained loamy soil and good fertility with leveled surface with pH 8.35 & EC 0.150 ds/m. Thirty six advance rice lines planted

in three replications in randomized complete block design (RCBD) in kharif 2014 under control condition. Plot size of the experiment was 4 × 2 = 8 m^2 and Spacing 20×20 cm. Data were recorded on five randomly selected plants from each plot for each lines for the characters named days to 50% flowering, plant height (cm), days to physiological maturity, number of tillers / plant, number of productive tillers / plant, panicle length (cm), number of spikelet's / panicle, grain yield per plant (g), biological yield per plant (g), harvest Index (%), test weight (g), grain yield kilogram / ha (Kg), hulling %, milling %, head rice recovery (%), kernel length before cooking (mm), kernel breadth before cooking (mm), kernel L/B ratio before cooking, amylose content (%), volume expansion ratio and kernel elongation ratio. The coefficient of variation was calculated as per Burton 1952, heritability calculated by the formula given by Lush 1949 and Burton and Devane 1953 and genetic advance by Lush, 1949 and Johnson *et al.* 1955. Obtained mean data were analyzed with the help of software at Khetan graphics, Hyderabad.

RESULTS AND DISCUSSION

In the findings of the experimental trail, the analysis of variance (Table 1) showed highly significant (1% level of significance) differences among the advance lines for the maximum yield and quality traits except kernel length before cooking (0.59), kernel breadth before cooking (0.05), kernel L/B ratio (0.38), volume expansion ratio (0.01) and kernel elongation ratio (0.02), that indicate the presence of a considerable amount of genetic variability among the lines. Phenotypic variance and phenotypic coefficient of variance is higher than the genotypic variance and genotypic coefficient of variance (Table 2) for all the characters which is the result of influence of the environmental factors on these traits. The maximum phenotypic and genotypic variation was obtained from Grain yield kilogram / hectare (VG 225275.25 and VP 281411.72) followed by Number of spikelet's / Panicle (VG 529.55 and VP 634.24) and Number of productive tillers / meter^2 (VG 489.97 and VP 733.07). Present findings supported by Das *et al.,*[1], Singh *et al.*, [2], Dutt *et al.*, [3] who also observed significant variability for yield and quality attributes in rice. The genotypic coefficient of variation provides a measure to compare the genetic variability present in various quantitative traits. The highest genotypic and phenotypic coefficient of variation was recorded for Number of spikelet's / Panicle (GCV 14.26 and PCV 15.61) followed by Head rice recovery % (GCV 12.08 and PCV 12.82) and Kernel elongation ratio (GCV 10.71 and PCV 10.73). The higher values of GCV and PCV evidently indicated a high degree of variability in these quantitative characters and suggest the possibility of yield improvement through selection of these traits. Mostly higher magnitude of PCV than GCV indicates interaction of environment and genotype. Similar findings were reported by Kundu *et al.*, [4], Rema Bai *et al.,* [5], Devi *et al.*, [6], Prajapati *et al.*, [7] and Anandrao *et al.*, [8. Highest magnitude of heritability recorded for Kernel elongation ratio (100%) followed by Amylose content (97%) and Head rice recovery % (89%). The results indicated that high estimates of heritability with less difference between PCV and GCV for these characters like Number of spikelet's / Panicle, Kernel elongation ratio, Head rice recovery %, and Grain yield kilogram / hectare could mean that the characters are mainly controlled by the genetic factor and selection based on these characters will be rewarding. These results are in accordance with Hussian *et al.* [9], T. Vanaja and Luckins C. Babu [10]. Highest magnitude of Genetic advance as % of mean exhibited by Number of spikelet's / Panicle (26.85) followed by Head rice recovery % (23.44) and Kernel elongation ratio (22.04) These finding is supported by findings of Prajapati *et al.*, [7]. Estimation of heritability and genetic advance not effective separately while high heritability coupled with moderate to high genetic advance as % of mean reflects additive nature of gene action and selection becomes effective for those traits, In the present study high heritability coupled with higher value of genetic advance as percentage of means was observed for Number of spikelet's / Panicle (83% and 26.85) followed by Head rice recovery % (89% and 23.44) and Kernel elongation ratio (100% and 22.04). Similar findings reported by Prajapati *et al.*, [7] The magnitude of variation among advance breeding lines was reflected by the values of mean, range, coefficient of variation, critical differences and other important parameters (Table 3a and 3b) showed that the actual behavior of the concerned lines under given environment for effective selection and fitness of the experiment. Values of coefficient of variation for all the traits are good according to the nature of the characters showed that experiment was conducted very well and range for the each character had sufficient differences and it's also exhibited variability and genetic worth in the set of genetic materials for particular traits. Other parameter from the table 3a and 3b also exhibited fitness of the conduction of experiment.

Table 1: Analysis of variance for yield and quality traits in rice.

S.No.	Characters	Mean sum of square		
		Replication (df = 02)	Treatment (df = 35)	Error (df = 70)
1	DFF	29.62	19.34**	10.33
2	PH	2.99	72.12**	30.48
3	DM	0.06	23.50**	13.22
4	NT/Pt	2.26	4.99**	1.40
5	NPT/m²	47.19	1713.02**	243.10
6	PL	6.57	5.03**	2.62
7	NSP/P	212.01	1693.34**	104.70
8	GY/Pt	3.73	17.20**	6.92
9	BY/Pt	3.69	148.34**	17.95
10	HI	5.06	66.94**	25.52
11	TW	2.52	12.13**	1.10
12	HULL. %	0.09	21.10**	5.24
13	MILL. %	0.43	33.84**	5.41
14	HRR %	7.15	112.32**	4.54
15	KLBC	0.01	0.59	0.04
16	KBBC	0.00	0.05	0.01
17	L/B RATIO	0.01	0.38	0.04
18	AMY. C.	0.04	7.37**	0.07
19	VER	0.00	0.01	0.00
20	KER	0.00	0.02	0.00
21	GYKG/Ha	2626.93	731962.19**	56136.46

Abbreviations: DFF – Days to 50% flowering, PH – Plant height, DM – Days to maturity, NT/Pt – Number of tillers / Plant, NPT/m² – Number of productive tillers / meter² , PL – Panicle length, NSP/P – Number of spikelet's / Panicle, GY/Pt – Grain yield / Plant, BY/Pt – Biological yield / Plant, HI – Harvest index, TW – Test weight, HULL. % - Hulling %, MILL. % - Milling %, HRR % - Head rice recovery %, KLBC – Kernel length before cooking, KBBC - Kernel breadth before cooking, L/B RATIO – Length / Breadth ratio, AMY. C. – Amylose content, VER – Volume expansion ratio, KER – Kernel elongation ratio, GYKG/Ha – Grain yield kilogram / hectare.

Table 2: Component of genetic parameters for yield and quality attributes in rice.

Characters	VG	VP	GCV	PCV	h²(bs) in %	GA	GA as % of mean
DFF	2.00	13.34	2.02	4.26	23	1.69	1.97
PH	13.88	44.36	3.62	6.47	31	4.29	4.17
DM	3.43	16.64	1.58	3.49	21	1.73	1.48
NT/Pt	1.20	2.60	8.88	13.09	46	1.53	12.41
NPT/m²	489.97	733.07	8.91	10.90	67	37.28	15.00
PL	0.80	3.43	3.24	6.69	23	0.89	3.23
NSP/P	529.55	634.24	14.26	15.61	83	43.32	26.85
GY/Pt	3.43	10.35	6.13	10.65	33	2.19	7.26
BY/Pt	43.46	61.42	9.46	11.25	71	11.42	16.40
HI	13.81	39.33	8.48	14.31	35	4.54	10.35
TW	3.68	4.77	7.69	8.76	77	3.47	13.90
HULL. %	5.29	10.52	3.05	4.30	50	3.36	4.45
MILL. %	9.48	14.88	4.87	6.10	64	5.06	8.01
HRR %	35.93	40.47	12.08	12.82	89	11.63	23.44
KLBC	0.18	0.22	6.05	6.64	83	0.81	11.35
KBBC	0.01	0.02	5.18	7.23	51	0.16	7.65
L/B RATIO	0.11	0.16	9.75	11.52	72	0.58	16.99
AMY. C.	2.43	2.51	6.84	6.94	97	3.17	13.88
VER	0.00	0.00	1.15	1.59	52	0.06	1.72
KER	0.01	0.01	10.71	10.73	100	0.15	22.04
GYKG/Ha	225275.25	281411.72	10.04	11.22	80	874.80	18.51

Table 3 (a): Mean performance and various parameters for different yield attributes in rice.

Characters	DFF	PH (cm)	DM	NT/Pt	NPT/Pt	PL (cm)	NSP/Pa	GY/Pt (g)	BY/Pt (g)	HI	TW (g)
Lowest Range	80.33	94.28	111.67	8.67	204.33	24.83	134.67	24.67	56.67	35.10	20.90
Highest Range	91.33	117.00	123.33	14.00	292.67	30.17	236.33	35.00	82.33	53.67	28.97
Mean	85.80	103.01	117.04	12.31	248.50	27.69	161.32	30.21	69.67	43.82	24.95
CV	3.75	5.36	3.11	9.62	6.27	5.85	6.34	8.71	6.08	11.53	4.20
CD (5%)	5.24	8.99	5.92	1.93	25.39	2.64	16.66	4.28	6.90	8.23	1.70
CD (1%)	6.95	11.94	7.86	2.56	33.71	3.50	22.12	5.69	9.16	10.92	2.26
F Ratio	1.87	2.37	1.78	3.56	7.05	1.92	16.17	2.49	8.26	2.62	11.07
SE	1.86	3.19	2.10	0.68	9.00	0.94	5.91	1.52	2.45	2.92	0.60

Table 3 (b): Mean performance and various parameters for different quality and a yield attributes in rice.

.Characters	HULL %	MILL %	HRR %	KLBC (mm)	KBBC (mm)	L/B RATIO	AMY. C.	VER	KER	GYKG/Ha
Lowest Range	69.29	53.53	38.57	6.23	1.73	2.81	20.35	3.32	0.54	3373.00
Highest Range	80.03	68.40	60.27	8.13	2.27	4.31	25.82	3.53	0.82	5819.33
Mean	75.43	63.21	49.63	7.11	2.08	3.43	22.81	3.44	0.68	4727.15
CV	3.03	3.68	4.29	2.73	5.04	6.14	1.19	1.10	0.55	5.01
CD (5%)	3.73	3.79	3.47	0.32	0.17	0.34	0.44	0.06	0.01	385.83
CD (1%)	4.95	5.03	4.61	0.42	0.23	0.46	0.59	0.08	0.01	512.25
F Ratio	4.03	6.26	24.75	15.68	4.17	8.56	99.76	4.31	1155.80	13.04
SE	1.32	1.34	1.23	0.11	0.06	0.12	0.16	0.02	0.00	136.79

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Original Research Article

Genetic Divergence Study in Advance Indica Rice (*Oryza sativa* L.) Lines for Yield and Quality Attributes

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A B S T R A C T

Keywords

Rice, genetic diversity, D2 statistics, grain yield, grain quality

An experiment was conducted during Kharif 2014 and 2015 with two different conditions (Control and Reproductive stress) at research farm of Bihar Agricultural University, Sabour (Bhagalpur) to study the existing genetic diversity in thirty six advance rice lines through Mahalanobis D^2 statistics for grain yield and quality traits. Based on the D^2 analysis, the genotypes were grouped into six clusters revealed the presence of considerable amount of genetic diversity in the material with each other for different yield and quality traits. The inter-cluster distances were higher than intra-cluster distances indicating wider genetic diversity among the genotypes of different clusters. The intra-cluster distances were lower in all the cases reflecting homogeneity of the genotypes within the clusters. The cluster II contained the highest number of genotypes (17) followed by cluster I (12), cluster III (4) and the clusters IV, V and VI are mono-genotypic. The highest intra-cluster distance was noticed for the cluster I followed by cluster II, cluster III and nil distance for clusters IV, V and VI. The highest inter-cluster distance was observed between cluster I and III, followed by cluster III and V, cluster III and IV and the lowest between cluster IV and V. The above results indicate that these genotypes have maximum genetic diversity and useful for developing a large number of segregants through crossing program by using maximum diverse genotypes. Cluster VI showed highest mean value for grain yield per plant, grain yield kilogram per hectare, 1000-grain weight, harvest index, number of spikelet's per panicle, number of productive tillers/m², amylose content and days to maturity. Cluster V showed highest mean value for number of tillers/plant, milling%, kernel length before cooking, L/B ratio and volume expansion ratio. The crosses between the genotypes/parents of cluster VI and cluster V would exhibit high heterosis as well as higher level of yield potential. Therefore, more emphasis should be given for selection of the genotypes from clusters VI and V for future breeding program. Among the twenty one traits studied, maximum contribution was made by Kernel elongation ratio (71.90%) followed by biological yield per plant (4.76%), amylase content (4.60%) and 1000-grain eight (4.13%). Therefore, these characters may be given importance during hybridization program.

Introduction

Rice is the principal food crop and a primary food source for more than one third of the world's population. The population growth in most of the Asian countries, except China, continues to be around 2% per year. Hence it is very pertinent to critically

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consider whether the rice production can be further increased to keep pace with population growth. In order to meet the food requirement of growing population, development of high yielding varieties is essential. The success of any breeding program depends on the selection of parents for hybridization. The parents involved in the development of varieties should be divergent. The germplasm provides immense scope for wider variability. Diversity analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra and inter cluster levels (Murty and Arunachalam, 1966; Ram and Panwar, 1970). Information on nature and degree of genetic divergence would help the plant breeder in choosing the right parents for the breeding program (Vivekanandan and Subramaniam, 1993). It also permits to select the genetically diverged parents which can produce new recombinants with desirable traits when they are crossed together. Keeping this in view, the present study was undertaken to assess the genetic diversity of promising rice genotypes using Mahalanobis D^2 statistics.

Materials and Methods

Thirty six advance lines of rice consisting genotypes of IRRI were raised at field experimentation centre, Bihar Agricultural University, Sabour (Bhagalpur), Bihar during Kharif, 2014 and 2015 with control and reproductive stress condition to identify diverse genotypes. The experiment was laid out in randomized complete block design with three replications. The genotypes were raised in plot size 4 x 2 = 8m^2. Row to row and plant to plant spacing was maintained at 20 x 20 cm. The recommended agronomic practices were followed. They were

evaluated for twenty one yield and quality attributing characters viz., days to 50% flowering, plant height (cm), days to maturity, number of tillers per plant, number of productive tillers / meter[2,] panicle length (cm), number of spikelet's per panicle, grain yield per plant (g), biological yield per plant (g), harvest index (%), 1000-grain weight (g), hulling (%), milling (%), head rice recovery (%), kernel length before cooking (mm), kernel breadth before cooking(mm), L/B ratio, amylose content, volume expansion ratio, kernel elongation ratio, grain yield per plot (kg/ha). Five random plants per replication per genotype were tagged for recording observations for above mentioned characters except days to 50% flowering, days to maturity and grain yield kilogram per hectare which were recorded on plot basis. The genetic distance between the genotypes was worked out using Mahalanobis D^2 analysis (1936) and grouping of varieties into clusters was done following the Tocher's method as detailed by Rao, (1952).

Results and Discussion

Analysis of variance showed significant differences for all the twenty one characters studied among the genotypes. Based on D^2 values, 36 genotypes were grouped into 6 clusters (Table – 1 and Figure - 1) in such a way that the genotypes within a cluster had a small or low D^2 values than those of in between the characters. Among the different clusters cluster II had maximum number of genotypes (17 genotypes) followed by cluster I (12 genotypes), cluster III (4 genotypes) while, cluster IV, V and VI are mono-genotypic. The pattern of group constellation proved the existence of significant amount of variability. The overall composition of the clustering pattern showed that genotypes collected from the same geographic origin were distributed in

different clusters. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Shanmugasundaram, *et al.,* 2000 and Nayak, *et al.,* 2004. The inter-cluster distance is higher than intra-cluster, indicating wide genetic diversity among the genotypes. The highest inter - cluster distance varied from 3.335 to 36.777. The highest inter-cluster distance was observed between cluster I and III (36.777) (Table - 2 and Fig - 2) followed by cluster III and V (26.638), cluster III and IV (24.814) and cluster I and VI (21.356). On the other hand minimum distance was observed between cluster IV and V (3.335), indicating close relationship between these clusters would not provide any good result. The greater the distance between clusters wider the genetic diversity between the genotypes. Highly divergent genotype would produce a broad spectrum of variability in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants or higher magnitude of heterosis. This would be useful in rice breeding program to evolve miracle varieties with high yield potential along with better quality traits. Highly divergent genotypes deem to produce wide variability that may help further selection for genetic improvement (Rahaman *et al.,* 1997). Hybrid developed from the genotypes within the limit of compatibility of those clusters may manifest high heterosis or desirable transgressive segregants, which would be beneficial for genetic improvement. Dey *et al.,* (2011) also suggested the use of divergent genotypes for development of lines with high yielding potential and better adaptability. Hybridization between genetically divergent parents to generate high heterotic segregants reported promising (Roy and Panwar, 1993;

Vivekanandan and Subramaniam1993; Sharma *et al.,* 1997) and a similar finding was of Sarawgi and Rastogi (2000), Nayak *et al.,* (2004) and Parikh *et al.,* (2011). The maximum intra cluster distance was observed for cluster I (3.512) followed by cluster II (3.386) and cluster III (2.603) (Table – 2 and Figure - 2). Maximum intra-cluster distance was observed among the genotypes, viz., IR 92527-6-2-1-2, IR 92527-6-2-1-4, IR 92517-1-3-1-1, IR 92523-37-1-1-2, IR 92523-35-1-1-1, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3, IR 88287-383-1-B-B-1-1-B, IR 94313:18-4-1-4-1-B, IR 92522-61-3-1-4, MTU 1010, IR 94314-20-2-1-B in cluster I, indicating existence of wide genetic divergence among the constituent genotypes in it. High degree of divergence among the genotypes within a cluster would produce more segregating breeding materials and selection within such cluster might be executed based on maximum mean value for the desirable characters. It was reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding material for achieving maximum genetic advance (Bose and Pradhan, 2005). The minimum intra-cluster distance was observed in cluster IV, V and VI (0.000) indicating homogeneous nature of the genotypes with no deviation between the genotypes, therefore selection will be ineffective. Similar findings were also reported by Rajesh *et al.,* 2010 and Nayak *et al.,* (2004). A perusal of results on cluster means (Table - 3) revealed that the cluster VI showed highest mean value for grain yield/plant, grain yield/plot (Kg/ha), 1000-grain weight, harvest index, number of spikelet's per panicle, number of productive tillers/m2, amylose content and days to maturity. Cluster V showed highest mean value for number of tillers/plant, milling%, kernel length before cooking, L/B ratio and volume expansion ratio.

Table.1 Distribution of 36 advance rice lines in various clusters

Clusters ↓	Number of Genotypes	Name of Genotypes
Cluster I	12	IR 92527-6-2-1-2, IR 92527-6-2-1-4, IR 92517-1-3-1-1, IR 92523-37-1-1-2, IR 92523-35-1-1-1, IR 93339:40-B-18-13-B-B-1, IR 92545-53-4-1-3, IR 88287-383-1-B-B-1-1-B, IR 94313:18-4-1-4-1-B, IR 92522-61-3-1-4, MTU 1010, IR 94314-20-2-1-B
Cluster II	17	IR 92546-7-1-1-3, IR 92546-33-3-1-1, IR 92546-17-6-4-4, RP-1-27-7-6-1-2-1, IR 64,IR 94391-587-1-2-B, IR 92516-8-3-3-4, IR 92545-51-1-1-4, IR 92545-24-3-1-1, IR 92545-23-2-1-1, IR 92545-54-6-1-4, LALAT, IR 92546-17-6-4-3, IR 92522-47-2-1-1, CRR 724-1-B (IR 88889-44), CRR 719-1-B (IR 88903-34), IR 92546-33-4-2-3
Cluster III	4	IR 92521-23-6-1-3, IR 92521-24-5-1-3, IR 92521-5-3-1-2, IR 92521-7-5-1-1
Cluster IV	1	IR 92545-40-2-2-3
Cluster V	1	IR 92522-47-2-1-4
Cluster VI	1	IR 92522-45-3-1-4

Table.2 Average intra and inter cluster distance among six clusters for thirty six advanced lines of rice

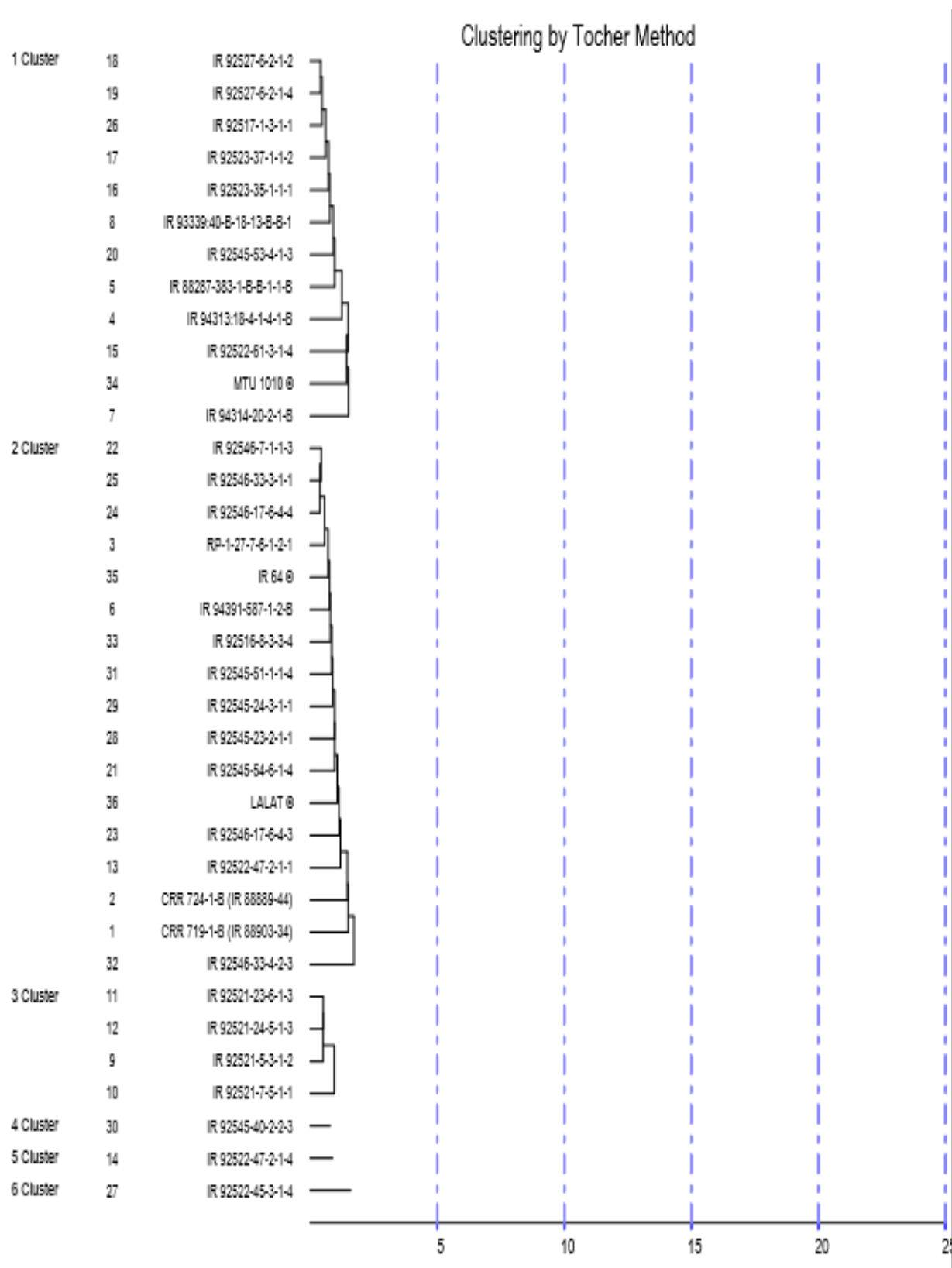| Clusters → ↓	Cluster - I	Cluster - II	Cluster - III	Cluster - IV	Cluster - V	Cluster – VI
Cluster – I	**3.512**	10.020	**36.777**	4.619	4.754	**21.356**
Cluster – II		**3.386**	13.753	5.649	5.953	7.449
Cluster – III			**2.603**	**24.814**	**26.638**	10.146
Cluster – IV				**0.000**	3.335	11.736
Cluster – V					**0.000**	12.613
Cluster – VI						**0.000**

Table.3 Mean values of clusters for different characters towards genetic divergence in thirty six advance rice lines

| Characters	Cluster (I)	Cluster (II)	Cluster (III)	Cluster (IV)	Cluster (V)	Cluster (VI)
Days to 50% flowering	83.458	83.304	82.542	84.500	82.167	83.717
Plant height (cm)	97.462	99.752	107.086	104.396	96.633	96.750
Days to maturity	115.806	115.824	115.500	115.300	115.917	116.583
No. of tillers per plant	11.285	10.775	9.604	10.083	11.500	10.750
No. of productive tillers/m^2	234.896	230.608	205.708	230.167	205.000	237.917
Panicle length (cm)	26.293	25.901	25.872	27.405	25.522	25.738
No. of spikelets per panicle	146.153	148.034	194.396	159.417	130.750	150.083
Grain yield per plant (g)	27.951	27.574	27.333	24.667	26.500	29.500
Biological yield per plant	67.632	66.770	69.125	72.833	70.167	62.417
Harvest index (%)	41.689	41.696	39.823	34.197	37.758	47.467
1000-grain weight (g)	24.103	24.125	23.410	27.800	24.242	27.958
Hulling (%)	73.960	74.755	74.415	77.345	75.102	73.741
Milling (%)	63.113	62.460	62.713	62.883	65.258	56.983
Head rice recovery (%)	44.331	50.195	56.177	43.133	40.008	42.158
Kernel Length before cooking	7.292	6.982	6.450	7.175	7.708	6.792
Kernel Breadth before cooking	2.065	2.097	2.165	2.183	1.925	2.117
L/B ratio	3.557	3.348	2.992	3.301	4.018	3.222
Amylose content	21.774	22.464	21.305	21.342	23.332	23.716
Volume expansion ratio	3.384	3.372	3.414	3.322	3.417	3.352
Kernel elongation ratio	0.754	0.645	0.533	0.701	0.697	0.586
Grain yield/plot (Kg/ha)	4474.299	4318.172	4135.729	3913.583	3965.084	4563.333

Table.4 Contribution of different yield and quality traits towards genetic divergence of 36 advance rice lines

| S. No.	Source	Contribution %	Times Ranked 1st
1	Days to 50% flowering	0.01	0
2	Plant height (cm)	0.01	0
3	Days to maturity	0.16	1
4	No. of tillers per plant	0.01	0
5	No. of productive tillers/m^2	0.48	3
6	Panicle length (cm)	0.16	1
7	No. of spikelets per panicle	1.90	12
8	Grain yield per plant (g)	0.01	0
9	Biological yield per plant	4.76	30
10	Harvest index (%)	0.01	0
11	1000-grain weight (g)	4.13	26
12	Hulling (%)	0.63	4
13	Milling (%)	0.01	0
14	Head rice recovery (%)	7.78	49
15	Kernel Length before cooking	1.11	7
16	Kernel Breadth before cooking	0.16	1
17	L/B ratio	0.01	0
18	Amylose content	4.60	29
19	Volume expansion rate	0.01	0
20	Kernel elongation ratio	71.90	453
21	Grain yield/plot (Kg/ha)	2.22	14

Fig.1 Distribution of 36 advance rice lines in various clusters

Fig.2 Average intra and inter cluster distance among six clusters for thirty six advanced lines of rice

Mahalnobis Euclidean Disatnce (Not to the Scale)
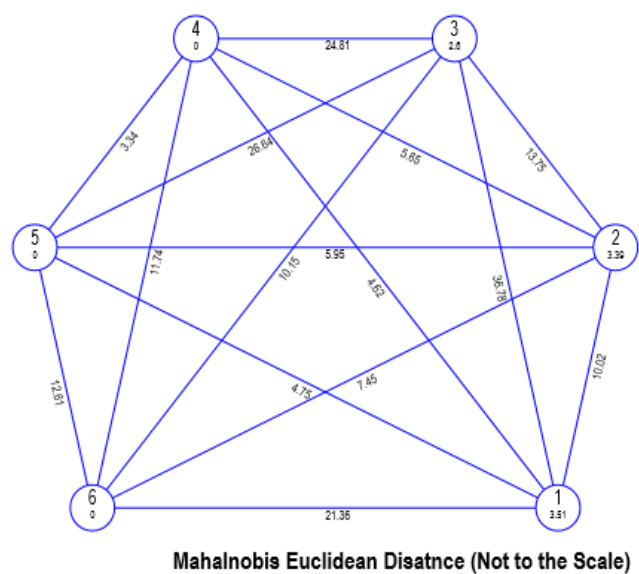
Fig.3 Contribution of different yield and quality traits towards genetic divergence of 36 advance rice lines
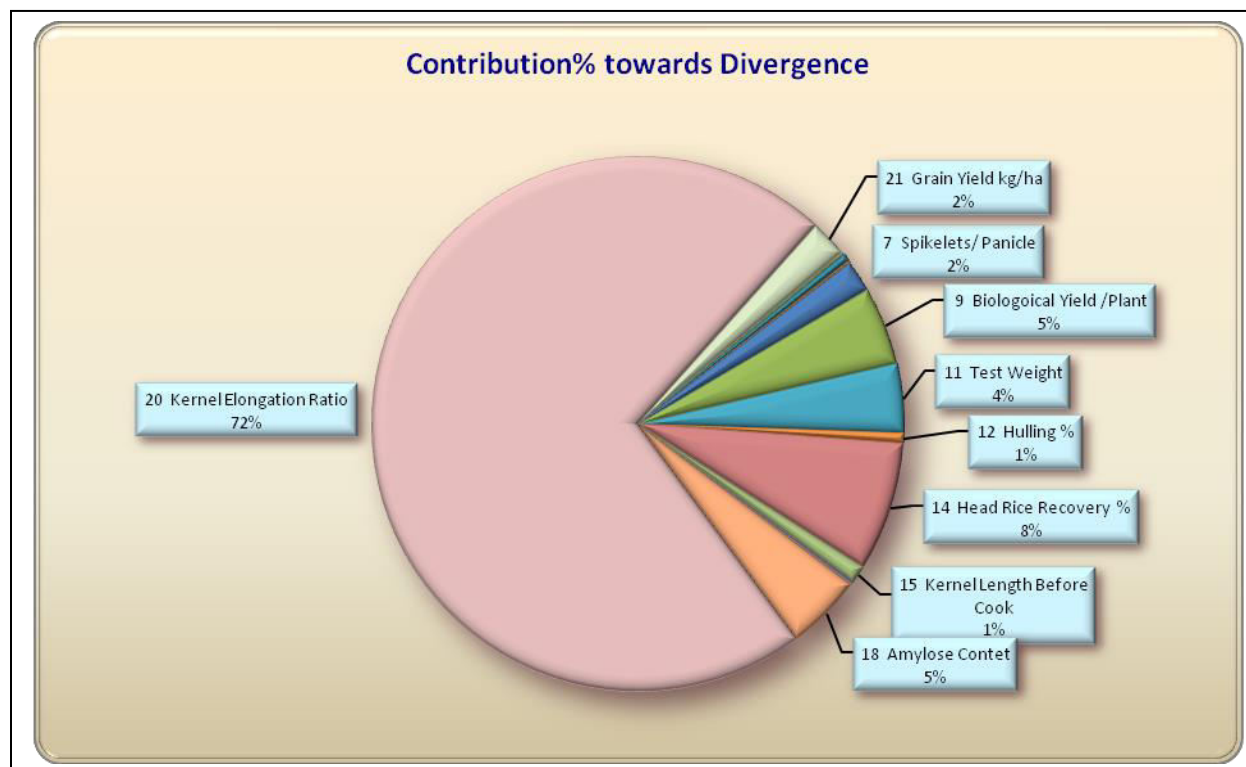
Cluster IV showed highest mean value for days to 50% flowering with better panicle length, biological yield per plant, hulling% and kernel breadth before cooking. Cluster III showed highest mean value for plant height with head rice recovery%. While cluster I showed highest mean value for kernel elongation ratio. The results suggest that intercrossing of genotypes from different cluster showing good mean performance may help in obtaining high yield. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining better heterosis and give broad spectrum of variability in segregating generation. The better genotypes can be selected for most of characters on the basis of mean performance in the cluster. The promising genotypes for grain yield per plant, grain yield per plot (Kg/ha), 1000-grain weight, harvest index, number of spikelet's per panicle, number of productive tillers/m^2, amylase content and number of tillers per plant, milling (%), kernel length before cooking, L/B ratio and volume expansion rate were identified from cluster VI and V on the basis of mean values which could be utilized for hybridization program for the development of high yielding genotypes.

The utility of D^2 analysis, which is a potent tool to quantify the extent of divergence in biological populations at genetic level, is further enhanced by its applicability to estimate the relative contribution of the various plant characters to genetic divergence. The present study revealed that out of twenty one traits studied, maximum contribution was made by Kernel elongation ratio (71.90%) (Table – 4 and Figure 3) followed by biological yield per plant (4.76%), amylose content (4.60%) and 1000-grain eight (4.13%). Therefore, these characters may be given importance during hybridization program.

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Inter - relationship study among advance indica rice (*Oryza sativa* L.) lines for yield and quality attributes

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Abstract
An experiment was conducted in RCBD during Kharif, 2014 and 2015 at Rice section BAU, Sabour to study inter-relationship for different yield and quality attributing traits among 36 rice lines. In the present study, genotypic correlation was higher in magnitude than phenotypic correlations. This indicated that there was strong inherent association among the traits and therefore, the selection based on phenotypic traits could be effective in achieving the genotypic gain for different attributes. Grain yield per plant had significant positive correlation with biological yield per plant, days to 50% flowering and days to maturity at genotypic level, indicating the importance of the characters for yield improvement. Harvest index showed significant and positive phenotypic correlation with grain yield per plant. The kernel elongation ratio showed significant and positive association with kernel length before cooking and L/B ratio at genotypic and phenotypic level. The milling% had significant positive correlation with kernel elongation ratio and significant and negative association with head rice recovery%. In path coefficient analysis at genotypic level, highest direct positive effect observed for biological yield per plant followed by harvest index, panicle length, kernel elongation ratio, days to 50% flowering and amylose content. Biological yield per plant, days to 50% flowering and days to maturity showed positive and significant correlation with grain yield on genotypic level while, only biological yield per plant reflected highest direct positive effect on genotypic level, therefore selection will be effective for this trait. At phenotypic level, harvest index showed highest direct positive effect having positive and highly significant correlation with grain yield per plant. Biological yield per plant, harvest index, panicle length, days to 50% flowering, days to maturity, kernel length before cooking, amylose content and kernel elongation ratio may be considered for genetic improvement of rice. Information about associations and their cause effect can be well utilized as an indicator for effective selection strategies to improve the grain yield along with grain quality. Hence it may be possible to combine grain yield and quality by specific breeding programme like bi-parental mating. This will break the linkage between unrelated traits and leads to more recombinants.

Keywords: Rice, Correlation - coefficient, Path – coefficient, Yield and Quality

Introduction
Rice (*Oryza Sativa* L.) is the most important staple food crop of the developing countries. 90% of the people of south-east Asia consume rice as staple food. The population growth in most of the Asian countries, except China, continues to be around 2% per year. Hence, it is very pertinent to critically consider whether the rice production can be further increased to keep pace with population growth with the current green revolution technologies, it is estimated that by 2020 at least 115-120 million tonnes of milled rice is to be produced in India to maintain the present level of self-sufficiency. Production of rice in India is low with respect to its demand and there is continuous need of varieties having high genetic potential in terms of yield and quality. To feed the ever-increasing population of the world, annual rice production must increase from the present 460 million tonnes to 760 million tonnes by 2020. Most of the characters of interest to breeders are complex and are the result of the interaction of a number of components. Grain yield is the ultimate criteria which a plant breeder always keep in mind while developing new variety with high yield potential. However, while carrying out selection for a highly variable character like grain yield; straight selection may not be always efficient, since it is a polygenic character largely influenced by environment? Grain yield and grain quality trait of rice is a complex character which is directly (or) indirectly related with each-other. Association analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in different traits. Breeding strategy in rice mainly depends upon the degree of associated characters as well as its magnitude and nature of variation (Zahid *et al.*, 2006; Prasad *et al.*, 2001) [24, 16]. Selection for yield via highly correlated characters becomes easy if the

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contribution of different characters to yield is quantified using path coefficient analysis (Dewey and Lu, 1959) [3]. Path coefficient analysis partitions into direct and indirect matrix presenting correlation in a more meaningful way (Mohsin *et al.*, 2009) [14]. Hence, the present investigation was carried out with the objective to study the inter - relationship among yield and quality characters which will be useful in formulating selection criteria for high yielding genotypes along with better quality in rice improvement.

Materials and Methods
The present study was carried out by using 36 advance lines of rice. The experiment was conducted at field experimentation centre, Bihar Agricultural University, Sabour (Bhagalpur), Bihar during Kharif, 2014 and 2015 in four environments including control and reproductive drought stress condition. Pooled data from all four environments were used for inter – relationship studies. Randomized complete block design (RCBD) was adopted for the experiment with three replications. The genotypes were raised in plot size 4 x 2 = 8m^2 with spacing 20 x 20 cm. The recommended agronomic practices were followed to raise a healthy crop. Observations were record for 21 yield and quality attributing characters viz., days to 50% flowering, plant height (cm), days to maturity, number of tillers per plant, number of productive tillers / meter^2, panicle length (cm), number of spikelet's per panicle, grain yield per plant (g), biological yield per plant (g), harvest index (%), test weight (g), hulling (%), milling (%), head rice recovery (%), kernel length before cooking (mm), kernel breadth before cooking (mm), L/B ratio, amylose content, volume expansion ratio, kernel elongation ratio and grain yield per plot (kg/ha). Five randomly selected plants per replication per genotype were tagged for recording observations except days to 50% flowering, days to maturity and grain yield per plot (kg/ha) which were recorded on plot basis. Observations on grain characteristics *viz.,* kernel length, kernel breadth, kernel L/B ratio were recorded from 10 randomly selected kernels. Required quantities (100 g) of harvested seeds were used to record the hulling percentage, which were properly cleaned before starting the experiment. Hulling% was calculated by dividing weight of the dehusked grain and weight of the paddy then multiplying by 100. Likewise, milling per cent was estimated by dehusking entire kernels by miller to obtain 7% polished rice and value was obtained through dividing weight of polished kernel and weight of paddy then multiplying with 100. Similarly, head rice recovery percent was obtained by dividing weight of whole perfect (not broken) polished grain and weight of the paddy thereafter, multiplying with 100. For kernel length and breadth measurement, Vernier calipers were used. L/B ratio was estimated by the proportion of Kernel length (L) before cooking (mm) and Kernel breadth (B) before cooking (mm). Amylose content was estimated by the iodine colorimetric procedure, whereas, volume expansion ratio was recorded by the difference between volumes of cooked sample and uncooked sample, then dividing by volume of uncooked sample. Kernel elongation ratio was estimated by the difference between length of cooked and uncooked rice. Correlation coefficient was computed as per the procedure outlined by Panse and Sukhatme (1978). Path coefficient analysis was done as per the method suggested by Dewey and Lu (1959) [3].

Results and Discussion
The estimates of genotypic correlation coefficients are essential in evaluating the possibility of simultaneous improvement of many characters or improvement of a single complex trait on the assumption of correlated response to selection. In the present study, genotypic correlation were higher in magnitude than phenotypic correlations which indicated that there was strong inherent association among the traits and therefore, the selection based on phenotypic traits could be effective in achieving the genotypic gain for different attributes. Grain yield per plant had significant positive correlation with biological yield per plant (rg 0.426** and rp 0.136), days to 50% flowering (rg 0.338* and rp 0.078) and days to maturity (rg 0.282* and rp 0.072) indicating the importance of the characters for yield improvement while, the plant height (rg -0.508** and rp -0.200), test weight (rg -0.282* and rp -0.144) and milling% (rg -0.283* and rp 0.038) showed significant and negative correlation with grain yield per plant at genotypic level (Table 1 and 2). Harvest index (rg 0.184 and rp 0.654**) showed significant and positive phenotypic correlation with grain yield per plant (Table 1). These results were in agreement with the earlier findings of Jyothula and Nitu Singh (2010) [6] and Krishna Veni and Shobha Rani (2007) [8]. A significant negative association was observed between amylose content and kernel breadth before cooking, (Table 2) similar findings reported by Krishna Naik *et al.* (2005) [7] and Malini *et al.* (2011) [10]. These associations can be well utilized as an indicator to affect selection strategies to improve the grain yield along with grain quality. Knowledge on interrelationship between grain yield and grain quality traits revealed the intensity and direction of association with each-other. This could facilitate effective selection for simultaneous improvement of one (or) more yield contributing traits and grain quality characters. Panicle length (rg 0.592** and rp 0.148) and biological yield per plant (rg 0.454** and rp 0.121) showed significant positive association with days to 50% flowering while, panicle length also showed positive significant association with kernel breadth before cooking (rg 0.324* and rp 0.097) at genotypic level (Table 1 and 3). Number of productive tillers/m^2 was found significantly and positively correlated with number of tillers per plant (rg 0.306* and rp 0.049), days to 50% flowering (rg 0.341* and rp 0.110) and kernel elongation ratio (rg 0.286* and rp 0.170) on genotypic level while significant and negative correlation with head rice recovery% (rg -0.336* and rp -0.179) and volume expansion ratio (rg -0.395** and rp -0.090) at genotypic level, (Table 1 and 3) these results were consistent with findings of Mehetre *et al.* (1994), Lanceras *et al.* (2004) [9] and Abarshahr *et al.* (2011) [1]. Significant and positive correlation between yield and other traits showed that each factor leads to changes in these traits will change correlation coefficients. Significant positive association of number of spikelets per panicle with plant height (rg 0.392** and rp 0.222), head rice recovery% (rg 0.0359* and rp 0.259) and kernel breadth before cooking (rg 0.354* and rp 0.112) while significantly and negatively correlated with number of tillers per plant (rg -0.441** and rp -0.220), kernel length before cooking (rg -0.479** and rp -0.314*), L/B ratio (rg -0.465** and rp -0.259) and kernel elongation ratio (rg -0.520** and rp -0.414**) at genotypic and phenotypic level (Table 1 and 3). The results were supported by the earlier findings of Nandan *et al.* (2010) [15] and Premkumar *et al.* (2016) [17]. A significant and positive genotypic and phenotypic correlation of days to 50% flowering was observed with days to maturity (rg 0.906** and rp 0.406**) (Table 1). The kernel elongation ratio showed significant and positive association with kernel length before

cooking (rg 0.679** and rp 0.496**) and L/B ratio (rg 0.648** and rp 0.436**) at genotypic and phenotypic level (Table 2). The milling% had significant positive correlation with kernel elongation ratio (rg 0.323* and rp 0.129) and negative significant association with head rice recovery% (rg -0.666** and rp -0.594**) at both level, (Table 2) Similar findings reported by Nandan *et al.* (2010) [15] and Sarika Mathure *et al.* (2010). Volume expansion ratio had significant negative association with amylose content (rg -0.396** and rp -0.176) while, amylose content showed significant negative association with kernel breadth before cooking (rg -0.333* and rp 0.118) at genotypic level (Table 2). L/B ratio recorded significant positive association with kernel length before cooking (rg 0.928** and rp 0.737**) and significant negative association with head rice recovery% (rg -0.683** and rp -0.435**) and kernel breadth before cooking (rg -0.859** and rp -0.806**) at genotypic and phenotypic level, respectively (Table 2). At genotypic and phenotypic level, kernel length before cooking showed significant positive association with head rice recovery% (rg -0.666** and rp -0.448**) (Table 2) which is an consonance with Manonmani *et al.* (2010) [11] and Premkumar *et al.* (2016) [17]. Milling% had significant negative association with hulling% (rg -0.288* and rp -0.048) at genotypic level (Table 2). Plant height was found significantly positively correlated with head rice recovery% (rg 0.624** and rp 0.282*) and kernel breadth before cooking (0.445** and rp 0.206) while significant negative association with kernel length before cooking (rg -0.505** and rp -0.143), L/B ratio (rg -0.524** and -0.227) and kernel elongation ratio (rg -0.637** and rp -0.319*) at both level (Table 3). Number of tillers per plant had significant positive association with kernel length before cooking (rg 0.369* and rp 0.104), L/B ratio (rg 0.424** and rp 0.140) and kernel elongation ratio (rg 0.627** and rp 0.270) while, significant negative association with head rice recovery% (rg -0.565** and rp -0.200), kernel breadth before cooking (rg -0.394** and rp -0.109) at genotypic level (Table 3). According to above mentioned results, among all traits had significant positive or negative correlations with each - other. In some cases, significant negative correlation becomes beneficial while in maximum time significant positive association becomes prefer for effective selection which depends upon the traits and their intensity of association. The genotypic and phenotypic correlation was partitioned into the direct and indirect effects and provided the actual information on the contribution of traits and thus forms the basis for selection to improve quality and grain yield. The highest direct positive effect was exhibited by biological yield per plant (1.1534) followed by harvest index (1.0046), panicle length (0.1208), kernel elongation ratio (0.0895) on genotypic level (Table 4a and 4b) while highest positive direct effect on phenotypic level observed for harvest index (1.2830) (Table 5a), this result is in accordance with the result of Jayasudha, S. and Sharma (2010) [5], P. satheeshkumar and K. Sarvanan (2012) [22], Sahu *et al.* (2017) [20], Rao *et al* (2014) [19], Rai *et al* (2014) [18], Vanisree *et al.* (2013) [23], Devi *et al.* (2017) [2] and Ekka *et al.* (2011) [4]. On genotypic level, direct effect of biological yield per plant was the result of indirect contribution of five quantitative and three qualitative traits namely, days to 50% flowering (0.5240), days to maturity (0.4115), no. of spikelets

per panicle (0.1417), L/B ratio (0.1168), kernel elongation ratio (0.1132), test weight (0.1121), number of tillers per plant (0.0849) and kernel length before cooking (0.0651) (Table 4a and 4b) this result is in accordance with findings of Mishra *et al.* (2015), while rest of the eleven traits showed negative direction of its indirect effect to biological yield per plant. However, harvest index reflected its effect via a single quantitative character that is number of productive tillers per metre square (0.0448) (Table 4a) and has nullifying effect of the other metric traits whereas, four qualitative traits also contributed indirectly viz. amylose content (0.1655), head rice recovery (0.0950), kernel breadth before cooking (0.0595) and kernel length before cooking (0.0062) (Table 4b) has been supported by the result of Jayasudha, S. and Sharma (2010) [5]. In case of Panicle length, days to 50% flowering (0.0715), days to maturity (0.0578), test weight (0.0240), number of productive tillers per meter square (0.0228), plant height (0.0215) and number of tillers per plant (0.0198) contributed indirectly along with kernel breadth before cooking (0.0391), volume expansion ratio (0.0140), kernel length before cooking (0.0294) and kernel elongation ratio (0.0221) (Table 4a and 4b). In spite of this, L/B ratio, milling% and hulling% also contributed appreciably to panicle length (Table 4b), this is in confirmation with similar findings for some characters of Rao *et al* (2014) [19], P. Satheeshkumar and K. Sarvanan (2012) [22]. Likewise kernel elongation ratio has gain major indirect contribution by kernel length before cooking, L/B ratio (0.580), number of tillers per plant (0.0561), number of productive tillers per meter square (0.0256) and milling% (0.0289) (Table 4a and 4b). Four traits showed minor contribution and rest did not contributed with its negative effects. Major indirect contribution to days to 50% flowering was shown by days to maturity (0.226) and panicle length (0.0148) (Table 4a). A very little contribution of seven traits was shown indirectly in case of amylose content. Kernel length before cooking and number of spikelets per panicle itself contributed very less through direct effect hence role of its indirect contributor was negligible. On phenotypic level, highest direct effect of harvest index was the result of indirect contribution of only one quantitative and five qualitative traits namely, panicle length (0.0011), amylose content (0.0958) followed by milling% (0.0816), head rice recovery% (0.0564), L/B ratio (0.0244) and kernel length before cooking (0.0233) while rest of the characters showed negative direction of its indirect effect to harvest index (Table 5a and 5b). Biological yield per plant showed the highest direct effect after harvest index on phenotypic level, which is the result of indirect contribution of some yield and quality attributing traits namely: days to maturity (0.1238) followed by days to 50% flowering (0.1171), number of tillers per plant (0.0926), number of spikelets per panicle (0.0755), test weight (0.0551) and some quality traits namely; kernel elongation ratio (0.800) followed by L/B ratio (0.0524), volume expansion ratio (0.0517), hulling% (0.0161) (Table 5a and 5b). According to above findings about path analysis, biological yield per plant and harvest index had maximum positive direct effects with positive indirect contributions of different traits on genotypic and phenotypic level, therefore; such traits may be beneficial for effective selection.

Table 1: Phenotypic and genotypic correlation – coefficient among different yield and yield attributing traits in rice

Characters	r	DFF	PH	DM	NT/Pt	NPT/ m²	PL	NSP/P	BY/Pt	HI	TW	GY/Pt
DFF	rp	1.000	0.001	0.406**	0.038	0.110	0.148	-0.017	0.121	-0.035	-0.021	0.078
	rg	1.000	-0.024	0.906**	0.093	0.341*	0.592**	0.145	0.454**	-0.270	-0.076	0.338*
PH	rp		1.000	0.018	-0.180	-0.090	0.081	0.222	-0.109	-0.068	-0.033	-0.200
	rg		1.000	0.059	-0.568**	-0.210	0.178	0.392**	-0.261	-0.061	-0.158	-0.508**
DM	rp			1.000	-0.006	-0.016	0.042	-0.106	0.128	-0.043	-0.034	0.072
	rg			1.000	0.016	0.058	0.479**	-0.079	0.357*	-0.222	-0.099	0.282*
NT/Pt	rp				1.000	0.049	0.052	-0.220	0.096	-0.081	0.082	-0.007
	rg				1.000	0.306*	0.164	-0.441**	0.074	-0.164	0.235	-0.089
NPT/ m²	rp					1.000	0.027	-0.043	-0.021	-0.011	-0.045	-0.035
	rg					1.000	0.189	-0.089	-0.142	0.045	-0.061	-0.181
PL	rp						1.000	0.003	-0.041	0.001	0.096	-0.044
	rg						1.000	-0.085	-0.140	-0.002	0.199	-0.251
NSP/P	rp							1.000	0.078	-0.011	-0.187	-0.066
	rg							1.000	0.123	-0.011	-0.263	0.178
BY/Pt	rp								1.000	-0.651**	0.057	0.136
	rg								1.000	-0.810**	0.097	0.426**
HI	rp									1.000	-0.148	0.654**
	rg									1.000	-0.278*	0.184
TW	rp										1.000	-0.144
	rg										1.000	-0.282*
GY/Pt	rp											1.000
	rg											1.000

Note: Significance at 5% and 1% level, indicated by * and **

Table 2: Phenotypic and genotypic correlation – coefficient among different quality and quality attributing traits in rice

Characters	r	HULL%	MILL%	HRR%	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER	GY/Pt
HULL%	rp	1.000	-0.048	0.072	0.087	0.070	0.006	0.022	-0.045	-0.043	-0.053
	rg	1.000	-0.288*	0.127	0.040	0.212	-0.063	0.048	-0.150	-0.061	-0.134
MILL%	rp		1.000	-0.045	0.111	-0.062	0.107	-0.036	0.066	0.129	0.038
	rg		1.000	-0.131	0.215	-0.360*	0.300*	-0.130	0.214	0.323*	-0.283*
HRR%	rp			1.000	-0.448**	0.241	-0.435**	-0.103	0.112	-0.594**	-0.073
	rg			1.000	-0.666**	0.546**	-0.683**	-0.111	0.243	-0.666**	-0.153
KLBC	rp				1.000	-0.205	0.737**	0.027	-0.085	0.496**	0.014
	rg				1.000	-0.608**	0.928**	0.177	-0.180	0.679**	0.078
KBBC	rp					1.000	-0.806**	-0.118	-0.038	-0.204	-0.107
	rg					1.000	-0.859**	-0.333*	0.176	-0.467**	-0.095
L/B RATIO	rp						1.000	0.089	-0.019	0.436**	0.079
	rg						1.000	0.255	-0.171	0.648**	0.089
AMYLOSE C.	rp							1.000	-0.176	-0.040	0.038
	rg							1.000	-0.396**	-0.064	0.010
VER	rp								1.000	-0.048	-0.017
	rg								1.000	-0.118	-0.032
KER	rp									1.000	0.036
	rg									1.000	0.058
GY/Pt	rp										1.000
	rg										1.000

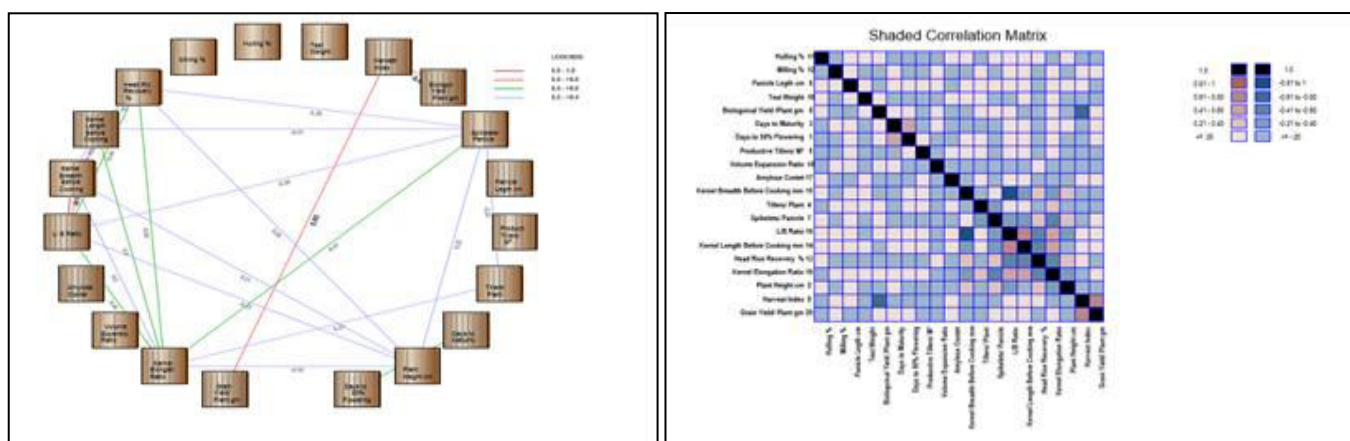*Note:* Significance at 5% and 1% level, indicated by * and **

Table 3: Phenotypic and genotypic correlation – coefficient among different yield and quality attributing traits in rice

Characters	r	HULL%	MILL%	HRR%	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER
DFF	rp	-0.032	-0.008	-0.048	0.072	0.022	0.028	-0.118	-0.019	0.080
	rg	-0.117	-0.114	-0.230	0.019	-0.004	0.012	-0.133	-0.331*	0.198
PH	rp	0.030	-0.108	0.282*	-0.143	0.206	-0.227	-0.022	-0.012	-0.319*
	rg	0.048	-0.001	0.624**	-0.505**	0.445**	-0.524**	-0.072	0.042	-0.637**
DM	rp	-0.037	0.050	-0.015	0.075	-0.022	0.057	-0.110	0.051	0.045
	rg	-0.025	-0.092	-0.155	-0.039	-0.027	-0.010	-0.082	0.033	0.114
NT/Pt	rp	-0.082	0.025	-0.200	0.104	-0.109	0.140	0.093	-0.072	0.270
	rg	-0.089	-0.026	-0.565**	0.369*	-0.394**	0.424**	0.165	-0.019	0.627**
NPT/ m²	rp	-0.011	-0.055	-0.179	0.090	0.016	0.045	0.110	-0.090	0.170
	rg	-0.106	-0.250	-0.336*	0.183	-0.142	0.176	0.101	-0.395**	0.286*
PL	rp	0.011	0.027	-0.057	0.137	0.097	0.025	-0.042	0.013	0.089
	rg	0.079	0.072	-0.195	0.244	0.324*	0.024	-0.073	0.116	0.183
NSP/P	rp	0.018	-0.132	0.259	-0.314*	0.112	-0.259	-0.043	-0.045	-0.414**
	rg	0.027	-0.173	0.359*	-0.479**	0.354*	-0.465**	-0.115	-0.039	-0.520**
BY/Pt	rp	0.017	-0.034	0.133	-0.009	-0.073	0.054	-0.065	0.053	0.083
	rg	-0.026	-0.031	-0.180	0.056	-0.117	0.101	-0.140	-0.022	0.098
HI	rp	-0.046	0.064	0.044	0.018	-0.026	0.019	0.075	-0.056	-0.035
	rg	-0.054	-0.158	0.095	0.006	0.059	-0.039	0.165	-0.018	-0.070
TW	rp	0.034	-0.078	-0.060	0.036	0.113	-0.049	0.033	-0.089	0.049
	rg	0.164	-0.183	-0.112	-0.018	0.260	-0.123	0.042	-0.053	0.068

Note: Significance at 5% and 1% level, indicated by * and **
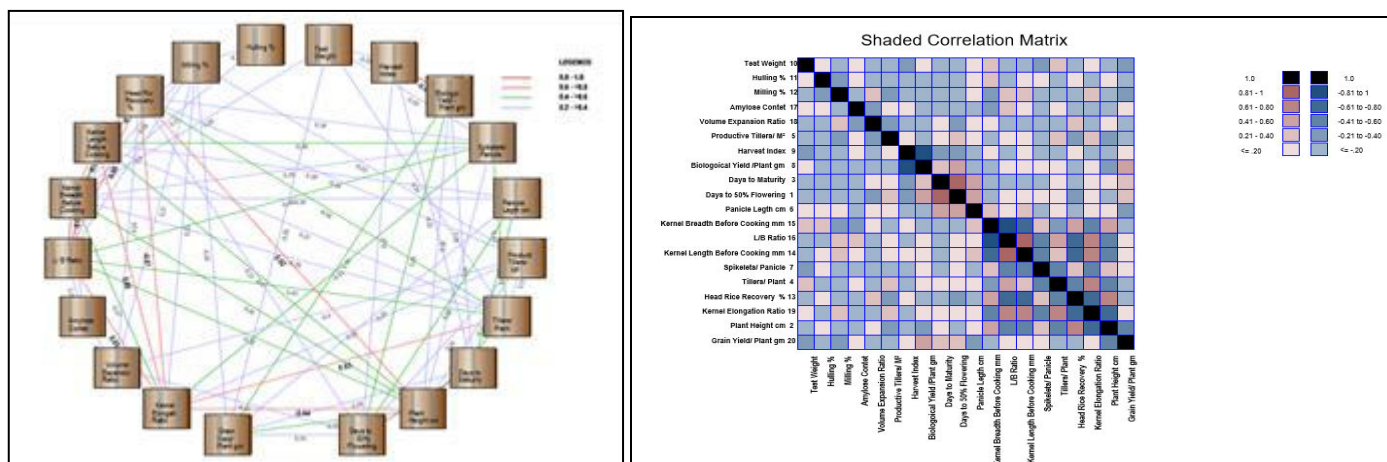
Diagram 1: Genotypic correlation – coefficient among different yield and quality attributing traits in rice

Diagram 2: Phenotypic correlation – coefficient among different yield and quality attributing traits in rice

Table 4 (a): Direct (diagonal) and indirect effect of components traits attributing yield and quality in rice lines at genotypic level

Characters	DFF	PH	DM	NT/Pt	NPT/m²	PL	NSP/P	BY/Pt	HI	TW
DFF	0.0249	-0.0006	0.0226	0.0023	0.0085	0.0148	0.0036	0.0113	-0.0067	-0.0019
PH	0.0070	-0.2940	-0.0172	0.1671	0.0617	-0.0524	-0.1151	0.0768	0.0178	0.0464
DM	-0.0105	-0.0007	-0.0116	-0.0002	-0.0007	-0.0056	0.0009	-0.0041	0.0026	0.0012
NT/Pt	-0.0124	0.0756	-0.0021	-0.1329	-0.0407	-0.0218	0.0586	-0.0098	0.0218	-0.0313
NPT/m²	-0.0752	0.0463	-0.0127	-0.0676	-0.2205	-0.0416	0.0197	0.0312	-0.0098	0.0134
PL	0.0715	0.0215	0.0578	0.0198	0.0228	0.1208	-0.0103	-0.0169	-0.0002	0.0240
NSP/P	0.0013	0.0036	-0.0007	-0.0041	-0.0008	-0.0008	0.0092	0.0011	-0.0001	-0.0024
BY/Pt	0.5240	-0.3014	0.4115	0.0849	-0.1633	-0.1612	0.1417	1.1534	-0.9339	0.1121
HI	-0.2717	-0.0609	-0.2233	-0.1645	0.0448	-0.0016	-0.0106	-0.8135	1.0046	-0.2792
TW	0.0143	0.0297	0.0187	-0.0443	0.0114	-0.0374	0.0494	-0.0183	0.0523	-0.1880
HULL.%	0.0108	-0.0044	0.0023	0.0082	0.0097	-0.0072	-0.0025	0.0024	0.0049	-0.0150
MILL.%	0.0257	0.0003	0.0205	0.0057	0.0561	-0.0161	0.0388	0.0070	0.0354	0.0409
HRR%	0.0039	-0.0105	0.0026	0.0095	0.0056	0.0033	-0.0060	0.0030	-0.0016	0.0019
KLBC	0.0002	-0.0056	-0.0004	0.0041	0.0020	0.0027	-0.0054	0.0006	0.0001	-0.0002
KBBC	0.0007	-0.0720	0.0044	0.0636	0.0229	-0.0523	-0.0572	0.0189	-0.0096	-0.0420
L/B RATIO	-0.0028	0.1247	0.0023	-0.1008	-0.0419	-0.0057	0.1105	-0.0241	0.0092	0.0292
AMYLOSE C.	-0.0026	-0.0014	-0.0016	0.0032	0.0020	-0.0014	-0.0023	-0.0028	0.0032	0.0008
VER	0.0113	-0.0014	-0.0011	0.0007	0.0135	-0.0040	0.0013	0.0008	0.0006	0.0018
KER	0.0177	-0.0570	0.0102	0.0561	0.0256	0.0164	-0.0465	0.0088	-0.0062	0.0061
GY/Pt	0.3380*	-0.5081**	0.2821*	-0.0890	-0.1812	-0.2512	0.1778	0.4260**	0.1844	-0.2822*
R² = 0.9871	Residual effect = 0.1134									

Table 4 (b): Direct (diagonal) and indirect effect of components traits attributing yield and quality in rice lines at genotypic level

Characters	HULL%	MILL%	HRR%	KLBC	KBBC	L/B RATIO	AMYLOSE C.	VER	KER
DFF	-0.0029	-0.0029	-0.0057	0.0005	-0.0001	0.0003	-0.0033	-0.0083	0.0049
PH	-0.0142	0.0004	-0.1836	0.1484	-0.1310	0.1542	0.0212	-0.0123	0.1871
DM	0.0003	0.0011	0.0018	0.0004	0.0003	0.0001	0.0009	-0.0004	-0.0013
NT/Pt	0.0119	0.0034	0.0751	-0.0490	0.0523	-0.0563	-0.0219	0.0026	-0.0833
NPT/m²	0.0233	0.0552	0.0742	-0.0402	0.0312	-0.0388	-0.0223	0.0872	-0.0630
PL	0.0095	0.0086	-0.0236	0.0294	0.0391	0.0029	-0.0088	0.0140	0.0221
NSP/P	0.0003	-0.0016	0.0033	-0.0044	0.0033	-0.0043	-0.0011	-0.0004	-0.0048
BY/Pt	-0.0295	-0.0362	-0.2079	0.0651	-0.1349	0.1168	-0.1616	-0.0254	0.1132
HI	-0.0538	-0.1587	0.0950	0.0062	0.0595	-0.0389	0.1655	-0.0183	-0.0699
TW	-0.0308	0.0343	0.0211	0.0034	-0.0488	0.0231	-0.0079	0.0100	-0.0128
HULL.%	-0.0919	0.0265	-0.0117	-0.0037	-0.0195	0.0058	-0.0044	0.0138	0.0056
MILL.%	0.0646	-0.2241	0.0295	-0.0482	0.0808	-0.0672	0.0292	-0.0479	-0.0724
HRR%	-0.0021	0.0022	-0.0167	0.0111	-0.0091	0.0114	0.0019	-0.0041	0.0111
KLBC	0.0004	0.0024	-0.0074	0.0112	-0.0068	0.0104	0.0020	-0.0020	0.0076
KBBC	-0.0343	0.0582	-0.0883	0.0982	-0.1616	0.1388	0.0539	-0.0284	0.0754
L/B RATIO	0.0149	-0.0713	0.1624	-0.2206	0.2042	-0.2378	-0.0606	0.0406	-0.1541
AMYLOSE C.	0.0009	-0.0026	-0.0022	0.0035	-0.0066	0.0050	0.0197	-0.0078	-0.0013
VER	0.0051	-0.0073	-0.0083	0.0062	-0.0060	0.0058	0.0135	-0.0341	0.0040
KER	-0.0055	0.0289	-0.0596	0.0607	-0.0418	0.0580	-0.0057	-0.0106	0.0895
GY/Pt	-0.1338	-0.2835*	-0.1527	0.0780	-0.0953	0.0891	0.0103	-0.0317	0.0578
R^2 = 0.9871					Residual effect = 0.1134				

Table 5 (a): Direct (diagonal) and indirect effect of components traits attributing yield and quality in rice lines at phenotypic level

Characters	DFF	PH	DM	NT/Pt	NPT/m²	PL	NSP/P	BY/Pt	HI	TW
DFF	0.0059	0.0000	0.0024	0.0002	0.0006	0.0009	-0.0001	0.0007	-0.0002	-0.0001
PH	0.0000	-0.0086	-0.0002	0.0015	0.0008	-0.0007	-0.0019	0.0009	0.0006	0.0003
DM	0.0012	0.0001	0.0030	0.0000	0.0000	0.0001	-0.0003	0.0004	-0.0001	-0.0001
NT/Pt	0.0001	-0.0007	0.0000	0.0038	0.0002	0.0002	-0.0008	0.0004	-0.0003	0.0003
NPT/ m²	-0.0004	0.0003	0.0001	-0.0002	-0.0037	-0.0001	0.0002	0.0001	0.0000	0.0002
PL	-0.0007	-0.0004	-0.0002	-0.0002	-0.0001	-0.0048	0.0000	0.0002	0.0000	-0.0005
NSP/P	-0.0001	0.0012	-0.0006	-0.0012	-0.0002	0.0000	0.0056	0.0004	-0.0001	-0.0011
BY/Pt	0.1171	-0.1052	0.1238	0.0926	-0.0203	-0.0402	0.0755	0.9683	-0.6301	0.0551
HI	-0.0447	-0.0874	-0.0555	-0.1042	-0.0143	0.0011	-0.0144	-0.8349	1.2830	-0.1905
TW	0.0002	0.0003	0.0003	-0.0007	0.0004	-0.0009	0.0016	-0.0005	0.0013	-0.0088
HULL.%	0.0003	-0.0003	0.0004	0.0008	0.0001	-0.0001	-0.0002	-0.0002	0.0005	-0.0003
MILL.%	0.0001	0.0014	-0.0006	-0.0003	0.0007	-0.0003	0.0017	0.0004	-0.0008	0.0010
HRR%	-0.0001	0.0007	0.0000	-0.0005	-0.0005	-0.0001	0.0007	-0.0003	0.0001	-0.0002
KLBC	-0.0003	0.0006	-0.0003	-0.0005	-0.0004	-0.0006	0.0014	0.0000	-0.0001	-0.0002
KBBC	0.0002	0.0020	-0.0002	-0.0011	0.0002	0.0010	0.0011	-0.0007	-0.0003	0.0011
L/B RATIO	0.0004	-0.0029	0.0007	0.0018	0.0006	0.0003	-0.0033	0.0007	0.0002	-0.0006
AMYLOSE C.	-0.0008	-0.0002	-0.0008	0.0007	0.0008	-0.0003	-0.0003	-0.0005	0.0005	0.0002
VER	-0.0001	0.0000	0.0002	-0.0003	-0.0003	0.0000	-0.0002	0.0002	-0.0002	-0.0003
KER	0.0001	-0.0006	0.0001	0.0005	0.0003	0.0002	-0.0007	0.0001	-0.0001	0.0001
GY/Pt	0.0784	-0.1996	0.0724	-0.0074	-0.0352	-0.0443	0.0656	0.1358	0.6541**	-0.1445
R^2 = 0.9750					Residual effect = 0.1580					

Table 5 (b): Direct (diagonal) and indirect effect of components traits attributing yield and quality in rice lines at phenotypic level

Characters	Hull%	Mill%	Hrr%	Klbc	Kbbc	L/B Ratio	Amylose C.	Ver	Ker
DFF	-0.0002	0.0000	-0.0003	0.0004	0.0001	0.0002	-0.0007	-0.0001	0.0005
PH	-0.0003	0.0009	-0.0024	0.0012	-0.0018	0.0019	0.0002	0.0001	0.0027
DM	-0.0001	0.0001	0.0000	0.0002	-0.0001	0.0002	-0.0003	0.0001	0.0001
NT/Pt	-0.0003	0.0001	-0.0008	0.0004	-0.0004	0.0005	0.0003	-0.0003	0.0010
NPT/m²	0.0000	0.0002	0.0007	-0.0003	-0.0001	-0.0002	-0.0004	0.0003	-0.0006
PL	-0.0001	-0.0001	0.0003	-0.0007	-0.0005	-0.0001	0.0002	-0.0001	-0.0004
NSP/P	0.0001	-0.0007	0.0015	-0.0018	0.0006	-0.0015	-0.0002	-0.0003	-0.0023
BY/Pt	0.0161	-0.0326	-0.1283	-0.0089	-0.0702	0.0524	-0.0625	0.0517	0.0800
HI	-0.0588	0.0816	0.0564	0.0233	-0.0334	0.0244	0.0958	-0.0716	-0.0444
TW	-0.0003	0.0007	0.0005	-0.0003	-0.0010	0.0004	-0.0003	0.0008	-0.0004
HULL.%	-0.0102	0.0005	-0.0007	-0.0009	-0.0007	-0.0001	-0.0002	0.0005	0.0004
MILL.%	0.0006	-0.0126	0.0006	-0.0014	0.0008	-0.0013	0.0004	-0.0008	-0.0016
HRR%	0.0002	-0.0001	0.0026	-0.0012	0.0006	-0.0011	-0.0003	0.0003	-0.0015
KLBC	-0.0004	-0.0005	0.0020	-0.0044	0.0009	-0.0033	-0.0001	0.0004	-0.0022
KBBC	0.0007	-0.0006	0.0024	-0.0020	0.0098	-0.0079	-0.0012	-0.0004	-0.0020
L/B RATIO	0.0001	0.0014	-0.0055	0.0094	-0.0102	0.0127	0.0011	-0.0002	0.0055
AMYLOSE C.	0.0002	-0.0003	-0.0007	0.0002	-0.0008	0.0006	0.0071	-0.0012	-0.0003
VER	-0.0002	0.0002	0.0004	-0.0003	-0.0001	-0.0001	-0.0006	0.0036	-0.0002
KER	-0.0001	0.0002	-0.0010	0.0009	-0.0004	0.0008	-0.0001	-0.0001	0.0018
GY/Pt	-0.0528	0.0384	-0.0726	0.0138	-0.1067	0.0786	0.0383	-0.0173	0.0360
R^2 = 0.9750					Residual effect = 0.1580				
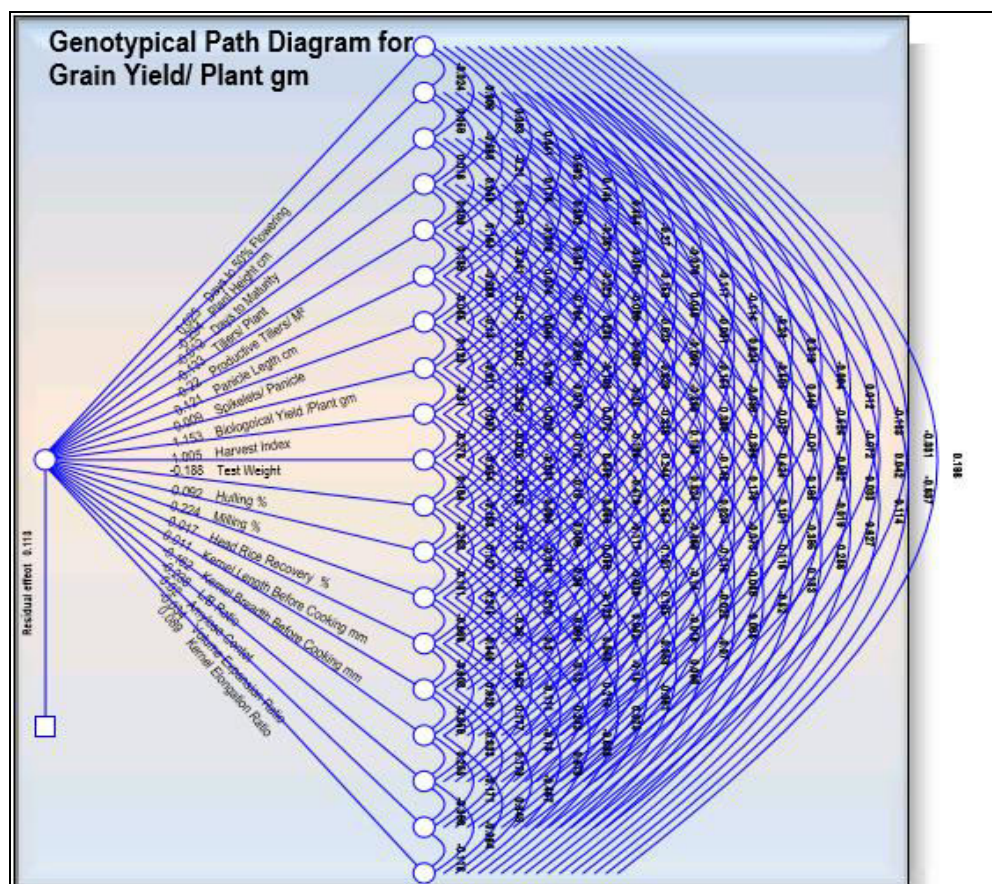
Diagram 1: Direct (diagonal) and indirect effect of components traits attributing yield and quality in rice lines at genotypic level
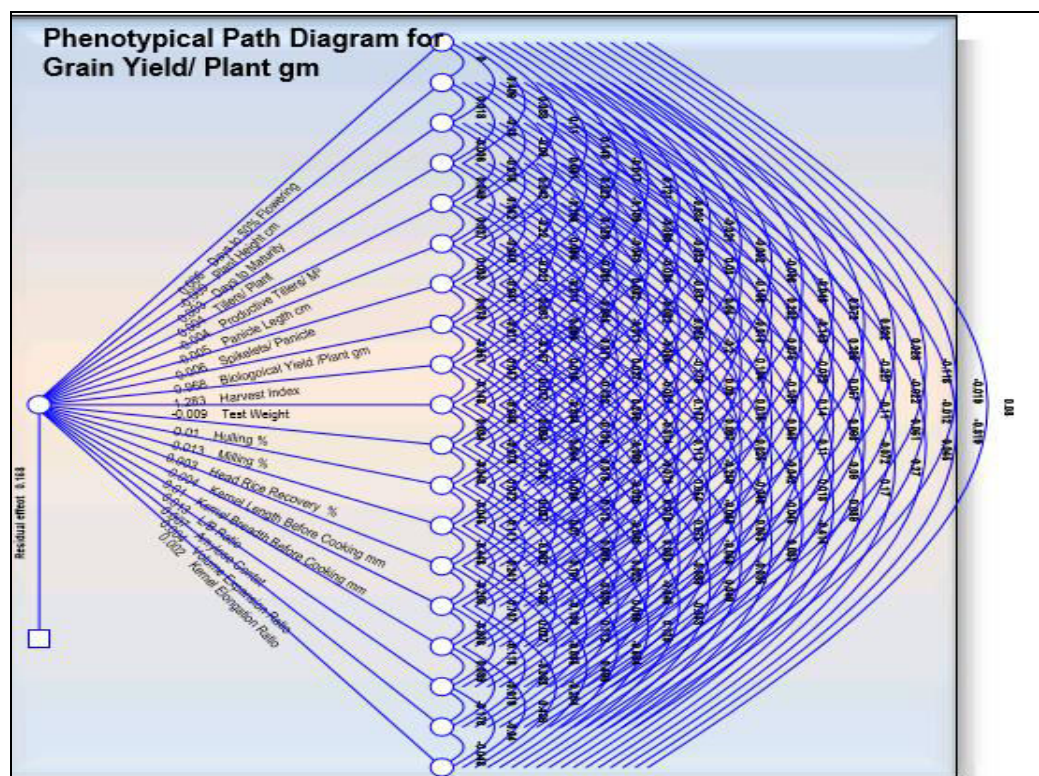
Diagram 2: Direct (diagonal) and indirect effect of components traits attributing yield and quality in rice lines at phenotypic level

Conclusion

So keeping in view of the above results, it may be concluded that such inter – relationship among the different traits *viz.,* biological yield per plant, days to 50% flowering and days to maturity, harvest index, plant height, kernel elongation ratio, kernel length before cooking, kernel L/B ratio, milling%, kernel breadth before cooking, amylose content and head rice recovery can be used as an indicator for effective selection strategies for genetic improvement of grain yield along with grain quality in rice. Hence it may be possible to combine improved grain yield along with better quality by specific breeding methods like bi-parental mating, which will break the linkage between unrelated traits and leads to more desirable recombinants.

Abbreviations: DFF – Days to 50% flowering, PH – Plant height, DM – Days to maturity, NT/Pt – Number of tillers / Plant, NPT/m^2 – Number of productive tillers / meter^2, PL – Panicle length, NSP/P – Number of spikelet's / Panicle, GY/Pt – Grain yield / Plant, BY/Pt – Biological yield / Plant, HI – Harvest index, TW – Test weight, HULL.% - Hulling%, MILL.% - Milling%, HRR% - Head rice recovery%, KLBC – Kernel length before cooking, KBBC - Kernel breadth before cooking, L/B RATIO – Length / Breadth ratio, AMY. C. – Amylose content, VER – Volume expansion ratio, KER – Kernel elongation ratio, r – Correlation, rg and rp - Genotypic and Phenotypic correlation.

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