GENETIC ANALYSIS AND HAPLOTYPING FOR EARLINESS AND YIELD TRAITS IN RICE (*Oryza sativa* L.) USING SSR MARKERS

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B. Sc. (Ag.)

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(GENETICS AND PLANT BREEDING)

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BY

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B. Sc. (Ag.)

THESIS SUBMITTED TO THE PROFESSOR JAYASHANKAR TELANGANA STATE AGRICULTURAL UNIVERSITY IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF

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(GENETICS AND PLANT BREEDING)

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2016

DECLARATION

I, **J. SWAPNA,** hereby declare that the thesis entitled **"GENETIC ANALYSIS AND HAPLOTYPING FOR EARLINESS AND YIELD TRAITS IN RICE (*Oryza sativa* L.) USING SSR MARKERS''** submitted to the **Professor Jayashankar Telangana State Agricultural University** for the degree of **Master of Science in Agriculture** is the result of the original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Date: **(J. SWAPNA)**

Place: Hyderabad **I.D. No. RAM/14-47**

CERTIFICATE

Ms. J. SWAPNA has satisfactorily prosecuted the course of research and that the thesis entitled **"GENETIC ANALYSIS AND HAPLOTYPING FOR EARLINESS AND YIELD TRAITS IN RICE (*Oryza sativa* L.) USING SSR MARKERS''** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by her for a degree of any university.

Date: **Dr. V. GOURI SHANKAR**

Place: Hyderabad **Chairperson**

CERTIFICATE

This is to certify that the thesis entitled **"GENETIC ANALYSIS AND HAPLOTYPING FOR EARLINESS AND YIELD TRAITS IN RICE (*Oryza sativa* L.) USING SSR MARKERS''** submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture of the Professor Jayashankar Telangana State Agricultural University, Hyderabad is a record of the bonafide original research work carried out by **Ms. J. SWAPNA** under our guidance and supervision. The subject of the thesis has been approved by the student's Advisory Committee.

No part of the thesis has been submitted by the student for any other degree or diploma. The published part and all assistance received during the course of the investigations have been duly acknowledged by the author of the thesis.

Dr. V. GOURI SHANKAR

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Date:

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
ANOVA	:	Analysis of variance
C.D.	:	Critical difference
C.V.	:	Coefficient of variation
d.f.	:	degrees of freedom
GA	:	Genetic Advance
GAM	:	Genetic Advance as percent of mean
GCV	:	Genotypic Co-efficient of Variation
PCV	:	Phenotypic Co-efficient of Variation
h^2	:	Heritability in broad sense
MSS	:	Mean Sum of Squares
TMSS	:	Treatment Mean Sum of Squares
EMSS	:	Error Mean Sum of Squares
RBD	:	Randomized Block Design
r	:	Correlation Co-efficient
SE	:	Standard Error
SEd	:	Standard Error of difference
SEm	:	Standard Error of mean
cm	:	Centimeter
g	:	gram
kg	:	kilogram
ton/ha	:	Tonnes per hectare
No.	:	Number
/	:	Per
et al.	:	and others
Fig	:	Figure
i.e.	:	that is
Viz.	:	Namely
AMMI	:	Additive Main effects and Multiplicative Interaction model
GGE	:	Genotype effect and Genotype x Environment effect
GxE	:	Genotype x Environment interaction
PCA	:	Principal component analysis

IPCA : Interaction principal component axis
SS% : Sum of squares percentage
QTL : Quantitative Trait Loci
PIC : Polymorphic Information Content
MAS : Marker Assisted Selection
DNA : Deoxy Ribo Nucleic Acid
SSR : Simple Sequence Repeats
RM : Rice Microsatellite
PCR : Polymerase Chain Reaction
CTAB : Cetyl Trimethyl Ammonium Bromide
EDTA : Ethylene Diamine Tetra Acetic Acid
TRIS : Tris (Hydroxyl Methyl) Amino Methane
PVP : Polyvinyl Pyrrolidine
TBE : Tris Boric acid EDTA
UV : Ultraviolet
dNTP : Deoxynucleotide Triphosphate
Taq : *Thermus aquaticus*
cM : Centi Morgan
bp : Base pairs
µl : Micro Litres
µM : Micro Molar
mM : Milli Molar
ml : Milli Liter
ng : Nano Grams
S.No : Serial Number
UPGMA : Unweighted Pair Group Method with Arithmetic Averages Algorithm
DFF : Days to 50 % flowering
DM : Days to maturity
PH : Plant height
TN : Number of tillers per plant
PTN : Number of productive tillers per plant
PL : Panicle length
PW : Panicle weight

FG	: Number of filled grains per panicle
UFG	: Number of unfilled grains per panicle
TG	: Number of total grains per panicle
SF	: Spikelet fertility
SP	: Sterility percentage
TGW	: Thousand grain weight
SPY	: Single plant yield
BM	: Biomass per plant
BY	: Biological yield per plant
HI	: Harvest index
PP	: Per day productivity

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ABSTRACT

The present investigation was undertaken for screening of early lines and the study the stability of early lines for yield and also to study genotyping and haplotyping for earliness using SSR markers in rice.

Fifty eight lines along with one check Prasanna (early line) were evaluated during *Rabi* 2014-15, *Kharif* 2015 and *Rabi* 2015-16 to estimate the genetic variability parameters among the genotypes for yield, and the extent of association between yield and its component characters including direct and indirect effects. The experiment was laid out in a Randomized Complete Block Design with three replications at Indian Institute of Rice Research, Hyderabad, Rajendranagar, during three seasons.

Analysis of variance indicated the existence of significant genotypic differences among the genotypes for yield, its components for all the characters during three seasons.

A perusal of genetic variability parameters revealed that high variability, high heritability coupled with high genetic advance as percent of mean was observed for number of total tillers per plant, number of productive tillers per plant, biomass per plant, biological yield per plant and per day productivity across all the three seasons, which indicate preponderance of additive gene action, hence these traits could be used for selection in crop improvement.

Combined analysis of variance for the data showed significant genotype, environment and genotype x environment interaction, indicating the presence of variability among the genotypes and environments. The significant genotype x environment interaction effect showed that the genotypes responded differently to the variation in environmental (seasonal fluctuations) conditions.

The SS% explained that most of the traits were contributed mainly by genotype, followed by environment, and their interaction. As per AMMI biplot analysis the season *Kharif,* 2015 is the best suited environment for potential expression of single plant grain yield and other yield related traits.

Results of stability analysis revealed that, among early and mid early lines the genotypes Tellahamsa, SM776, SM4371, 27 K, SM686, 258 S and SM219 were identified as the best stable genotypes across all the three seasons for single plant grain yield and other traits, hence suitable for wider environments.

The character association studies revealed that single plant grain yield had significant positive association with days to maturity, number of total tillers per plant, number of productive tillers per plant, panicle length, panicle weight, spikelet fertility, thousand grain weight, biomass per plant, biological yield per plant, harvest index and per day productivity indicating that this characters are very important for yield improvement and simultaneous selection of these characters will ultimately result in high yield.

Path coefficient analysis revealed that number of filled grains per panicle exerted the highest positive direct effect on single plant grain yield followed by biological yield per plant, per day productivity, days to 50% flowering, thousand grain weight and plant height indicating that the selection for this characters is likely to bring about an overall improvement in single plant grain yield directly.

In conclusion, character association and path analysis indicated that thousand grain weight, biological yield per plant and per day productivity displayed significant positive correlation as well as positive direct effect on single plant grain yield. The positive direct effect of these traits on yield resulted in strong genetic correlation. Hence, these traits were considered as important attributes in formulating selection criterion for achieving desired targets.

Among the 57 SSR markers used in the present study 42 SSR markers were polymorphic which produced a total of 99 alleles among the 84 rice genotypes with an average of 2.35 alleles per locus. The number of alleles generated by microsatellite markers ranged from 2 to 5 alleles of which RM1369 marker produced the highest numbers of alleles per locus followed by RM163. The PIC values ranged from 0.511 to 0.939 with an average of 0.745 per locus. High PIC value indicates that the SSR markers used in present study are informative and the best markers in differentiating of rice genotypes for heading date in diversity studies.

The dendrogram generated using UPGMA cluster analysis grouped 84 genotypes into ten major clusters. The clusters, cluster Ia, cluster III and cluster VII are having mixture of lines from early to late duration genotypes. Cluster I b, cluster II and cluster X are having mid early, tall genotypes. Cluster IV and IX are having mid early, medium tall genotypes with medium thousand grain weight. Cluster V has early genotypes with medium panicle length. Cluster VI has late duration, medium tall genotypes. Cluster VIII a is having early, tall genotypes. Cluster VIII b is having early, medium tall genotypes. Haplotype analysis of the genotypes for earliness linked genes showed that wild introgression lines from *O. nivara* are having more allelic diversity than *O. sativa* cultivars and these introgression lines can be exploited for identification of new genes / QTLs linked to heading date.

INTRODUCTION

Chapter I

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the world's major staple food crops and a model cereal species. Developing countries account for 95% of global rice production. Asia alone produces 90% of world rice, with China and India accounting for over half of the world's output. It is a primary source of carbohydrates for more than half of the world population. Global rice acreage is about 158.8 million hectares (Statista, 2015-16) and per capita rice consumption is about 57.5 kg per year. Global rice production is about 749.8 million tonnes (FAO, 2015). Among the rice growing countries in the world, India has the largest area under rice crop of about 38.35 million hectares (Indiastat, 2015-16) and ranks second in production with 103.61 million tonnes (Indiastat, 2015-16) next to China with 207.44 million tonnes paddy production. Rice contributes 42 percent of total food grain production and 45 per cent of total cereal production in India. In Telangana rice acreage, productivity and production is about 13.67 lakh hectares, 31.62 quintals per hectare and 43.22 lakh tonnes respectively.

The world population is predicted to grow from 6.9 billion in 2010 to 8.3 billion in 2030 and to 9.1 billion in 2050. It is estimated that the demand for rice will be 121.2 million tonnes by the year 2030, 129.6 million tonnes by the year 2040 and 137.3 million tonnes by the year 2050 (FAO, 2006). However, due to urbanization, industrialization and popularization of other crops there may be a decline of rice area by 6-7 million hectares by 2050. About 55 per cent of the rice area is under irrigated ecosystem in India. Unlike other cereal crops *viz..,* wheat, maize, sorghum *etc.,* Rice requires more water per unit grain production. It is estimated that by 2050, about 22 per cent of the geographic area and 17 per cent of the population will be under absolute water scarcity.

The combined effects of escalating population and declining water scarcity, decrease in arable land, deteriorating resources, the constant battle against new emerging pathogens and pests and possible adverse effects from climate change associated events such as rise in temperatures, altered patterns of precipitation, and possibly increased frequency of drought and floods, will depress yield and increase production risks with serious implications for meeting the food production targets per unit area as well as unit time.

Earliness is the emerging key agronomic character which provides greater adaptability to varieties to fit into different ecosystems, in different cropping seasons. It helps in escape of crop from various pests and diseases attack and reduce crop loss. It minimizes the utilization of water during the growing season and cut down the cost of cultivation by limited use of inputs and can be used for another crop. It addresses problems encountered due to unseasonal rains and cyclones during harvesting period. Under existing scenario, in order to sustain the rice production and to meet the future demands, growing early high yielding varieties will enhance the rice productivity, resource and input use efficiency and profitability per unit area and per unit time.

Though more than 900 rice varieties have been released in India, many of them have been out of cultivation within a few years due to inconsistent performance in diverse environments and only few varieties with stable performance continue to be under cultivation even after 15 - 20 years of release (Bose *et al.,* 2014a). Yield and heading date are complex characters, dependent on a number of other characters and highly influenced by many genetic factors as well as environmental fluctuation. For obtaining expected yield potential, it is necessary to identify the stable genotypes suitable for wide range of environments. Stability of a cultivar refers to its consistency in performance across environments and is affected by the presence of genotype and environment interaction (Sharma *et al.,* 1987). Wider adaptability and stability are prime considerations in formulating efficient breeding programme.

The success of crop improvement and production activities can be enhanced with scientific information generated form genotype-environment interactions. GxE interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments and also to help plant breeders in selecting varieties (Dewi *et al.*, 2014). Since, GxE interaction is naturally multivariate, the Additive Main effects and Multiplicative Interaction (AMMI) model offers appropriate statistical analysis of yield trials a well known GxE interaction effects (Zobel *et al.*, 1998).

The Additive Main Effects and Multiplicative Interaction (AMMI) model has found more use recently since it incorporates both the classical additive main effects model for GxE interaction and the multiplicative components into an integrated least square analysis and thus becomes more effective in selection of stable genotypes (McLaren and Chaudhary *et al.,* 1994). It not only gives estimate of total GxE interaction effect of each genotype but also partitions it into interaction effects due to individual environments (Zobel *et al*., 1988). In present study, we will select stable early genotypes and genotypes with wider adaptability for grain yield using stability analysis. So that selected genotypes can be suggested for hybridization in further breeding programme and develop early genotypes with high yield as early genotypes are mostly low yielding due to less photosynthetic duration.

Identified genetic variations based on DNA polymorphism are abundant and independent of environmental factor. DNA markers that differentiate genotype are more reliable and convenient than physiological or morphological characters in the identification and characterization of genetic variation (Zeng *et al.,* 2004). Among various PCR based markers, SSR markers are more popular in rice because they are highly informative, mostly mono locus, co-dominant and cost effective (Chambers and Avoy, 2000). A haplotype is a collection of specific alleles (particular DNA sequences) in a cluster of tightly-linked genes on a chromosome that are likely to be inherited together. Haplotyping is used in linkage disequilibrium studies and it gives information on flow of genes. Earliness is governed by many genes and by different combination of alleles and they are additive. It is difficult to identify variation in heading date due to complexity of genes governing that character. Hence we use Marker Assisted Selection (MAS) method via haplotyping for identification of individual loci controlling that particular trait in different genotypes.

Keeping in view the above aspects, the present investigation was undertaken with the following objectives:

1. To evaluate genotypes for earliness and yield under irrigated conditions
2. To determine haplotype for earliness using linked SSR markers
3. To determine genotype x environment interaction and stability for earliness, grain yield and yield contributing characters.

REVIEW OF LITERATUTE

Chapter II

REVIEW OF LITERATURE

The present investigation is aimed at screening for early lines, studies on stability of rice during *Kharif* and *Rabi* seasons and genotyping and haplotyping for earliness.

A brief review of available literature in consonance with the objectives of the present investigation in respect of this crop are reviewed and presented under the following heads.

2.1 Genetic Variability

2.2 Heritability and Genetic Advance

2.3 Stability analysis

2.4 Character association

2.5 Path Coefficient Analysis

2.6 Genotyping and haplotyping for earliness using SSRs

2.1. GENETIC VARIABILITY

The nature and extent of variability forms the basis for all crop improvement programmes. According to Allard (1960), yield is polygenically controlled quantitative character and is highly influenced by environment.

Partitioning of observed variability into heritable and non-heritable components is very much essential to get a true indication of the genetic coefficient of variability as a useful measure of the magnitude of genetic variance present in the population.

A brief review of studies on genotypic and phenotypic coefficients of variation in rice is presented here under in tabular form in Table 2.1.

Table 2.1. Review of studies on genotypic and phenotypic coefficients of variation

S.No.	Character	Range	Reference
1.	Days to 50 % flowering	High	Bisne *et al.* (2008) Seyoum *et al*. (2012)
		Moderate	Singh *et al.* (2012) Bekele *et al.* (2013) Soni *et al.* (2013) Sravan *et al.* (2014)
		Low	Dhurai *et al.* (2014) Rahman *et al.* (2014) Islam *et al.* (2015a) Sindhumole *et al*. (2015) Mishu *et al*. (2016)
2.	Days to maturity	High	Devic *et al.* (2012)
		Low	Patel *et al.* (2014) Islam *et al.* (2015a) Mishu *et al.* (2016)
3.	Plant height(cm)	High	Seyoum *et al*. (2012) Gangashetty *et al*. (2013) Rahman *et al.* (2014) Sindhumole *et al.* (2015)
		Moderate	Soni *et al.* (2013) Vanisree *et al*.(2013) Dhurai *et al.* (2014) Sravan *et al.* (2014) Parmeshwar *et al.* (2015)
		Low	Prasad *et al*. (2013) Islam *et al.* (2015a) Roy *et al.* (2015)

S.No.	Character	Range	Reference
			Mishu *et al.* (2016)
4.	No. of total tillers per plant	High	Ravi *et al.* (2014) Sindhumole *et al.* (2015)
		Low	Patel *et al.* (2014)
5.	No. of productive tillers per plant	High	Soni *et al.* (2013) Dhurai *et al.* (2014) Parmeshwar *et al.* (2015)
		Moderate	Mohanty *et al.* (2012) Sravan *et al.* (2012) Dhanwani *et al.* (2013) Roy *et al.* (2015)
		Low	Garg *et al.* (2010). Yadav *et al.* (2010) Patel *et al.* (2014)
6.	Panicle length (cm)	High	Nayudu *et al.* (2007) Rahman *et al.* (2014)
		Moderate	Singh *et al.*(2013) Soni *et al.* (2013) Dhurai *et al.* (2014) Satish *et al.* (2014)
		Low	Sravan *et al.* (2014) Suresh *et al.* (2014) Roy *et al.* (2015) Sindhumole *et al.* (2015) Mishu *et al.* (2016)
7.	Panicle weight (g)	High	Soni *et al.* (2013)
8.	No. of total grains per panicle	High	Patel *et al.* (2014)

S.No.	Character	Range	Reference
9.	No. of filled grains per panicle	High	Dhurai *et al.* (2014) Lingaiah *et al*. (2014) Patel *et al. (*2014) Suresh *et al*. (2014) Parmeshwar *et al.* (2015)
		Moderate	Pandey *et al*. (2012) Sravan *et al*. (2012) Kishore *et al*. (2015) Islam *et al.* (2015a)
		Low	Nath and Talukdar (1997)
10.	No. of unfilled grains per panicle	High	Parmeshwar *et al.* (2015)
		Moderate	Rahman *et al.* (2014)
11.	Thousand grain weight (g)	High	Chakraborty and Chaturvedi (2014) Rahman *et al*. (2014) Satish *et al*. (2014) Roy *et al*. (2015)
		Moderate	Soni *et al.* (2013) Dhurai *et al.* (2014) Patel *et al*. (2014) Suresh *et al*. (2014)
		Low	Rahman *et al.* (2014) Sravan *et al.* (2014) Islam *et al*. (2015a)
12.	Single plant grain yield (g)	High	Dhurai *et al.* (2014) Rahman *et al*. (2014) Sravan *et al.* (2014) Suresh *et al*.(2014) Parmeshwar *et al*. (2015)

S.No.	Character	Range	Reference
	Single plant grain yield (g)	Moderate	Adilakshmi *et al*. (2012) Pandey *et al*. (2012) Soni *et al.* (2013) Roy *et al.* (2015)
		Low	Babu *et al*. (2012) Rahman *et al*. (2014)
13.	Spikelet fertility	High	Parmeshwar *et al.* (2015)
		Moderate	Dinesh *et al.* (2011)
14.	Sterility percentage	High	Mamun *et al.* (2012) Roy *et al.* (2015)
		Moderate	Mishu *et al.* (2016)
15.	Biomass per plant (g)	High	Patel *et al*. (2014)
16.	Biological yield per plant (g)	High	Soni *et al*. (2013) Satish *et al*. (2014) Parmeshwar *et al.* (2015)
		Low	Dinesh *et al.* (2011)
17.	Harvest index	High	Devic *et al.* (2012) Patel *et al*. (2014) Satish *et al*. (2014) Parmeshwar *et al*. (2015)
18.	Per day productivity (g)	High	Bhadru *et al*. (2012b)

2.2. HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN

Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. Basic information on heritability is a prerequisite for planning any breeding programme. High heritability indicates that it should be easy to conduct effective selection for the trait.

Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population**.** Johnson *et al.* (1955) reported that though the heritable estimates give useful indication of relative values of selection based on phenotypic expression, the genetic gain should also be considered to arrive at a more reliable conclusion.

A brief review of studies on broad sense heritability and genetic advance as per cent of mean in rice is presented here under in tabular form in Table 2.2.

Table 2.2. Brief review of studies on broad sense heritability and genetic advance as per cent of mean.

S.No	**Characters**	**Range**		**References**
		Heritability	**GAM**	
1.	Days to 50 % flowering	High	High	Dinesh *et al.* (2011) Soni *et al*. (2013) Kishore *et al.* (2015)
		High	Moderate	Idris and Mohamed (2013) Dhurai *et al.* (2014) Patel *et al.* (2014) Islam *et al.* (2015a) Sindhumole *et al.* (2015)
		High	Low	Yadav *et al*. (2010) Dinesh *et al.* (2011) Dhanwani *et al*. (2013) Mishu *et al*. (2016)
		Moderate	Moderate	Singh *et al.* (2013)
2.	Days to maturity	High	Moderate	Patel *et al*. (2014) Islam *et al.* (2015a)
		High	Low	Mishu *et al*. (2016)

3.	Plant height(cm)	High	High	Dhurai *et al.* (2014) Rahman *et al.* (2014) Rajput *et al.* (2014) Sravan *et al.* (2014) Roy *et al.* (2015) Sindhumole *et al.* (2015) Mishu *et al.* (2016)
		High	Moderate	Dinesh *et al.* (2011) Patel *et al.* (2014)
.		Moderate	Low	Islam *et al.* (2015a)
		Low	Low	Vijayalakshmi *et al.* (2008)
4.	No. of total tillers per plant	High	High	Ravi *et al.* (2014)
		High	Moderate	Patel *et al.* (2014)
		High	Low	Sindhumole *et al.* (2015)
		Low	Low	Patel *et al.* (2014)
5.	No. of productive tillers per plant	High	High	Dhurai *et al.* (2014) Khare *et al.* (2014) Rahman *et al.* (2014) Parmeshwar *et al.* (2015)
		High	Moderate	Patel *et al.* (2014)
		High	Low	Dinesh *et al.* (2011) Soni *et al.* (2013) Roy *et al.* (2015)
		Moderate	Moderate	Suresh (2001) Singh *et al.* (2011)
		Low	Low	Murthy *et al.* (1999) Singh *et al.* (2013)
6.	Panicle length (cm)	High	High	Nayudu *et al.* (2007) Lal and Devendra (2011) Dhurai *et al.* (2014)
		High	Moderate	Yadav *et al.* (2010) Parikh *et al.* (2011) Singh *et al.* (2011)

				Parmeshwar *et al*. (2015)
		Moderate	Moderate	Suresh (2001) Patel *et al*. (2014)
.		High	Low	Dinesh *et al*. (2011) Soni *et al*. (2013) Sindhumole *et al*. (2015) Roy *et al*. (2015) Mishu *et al*. (2016)
		Low	Low	Kole *et al*. (2008)
7.	Panicle weight (g)	High	Low	Soni *et al*. (2013)
8.	No. of total grains per panicle	High	High	Soni *et al*. (2013) Roy *et al*. (2015)
9.	No. of filled grains per panicle	High	High	Dinesh *et al*. (2011) Dhurai *et al*. (2014) Lingaiah *et al*. (2014) Rahman *et al*. (2014) Rajput *et al*. (2014)
	No. of filled grains per panicle	High	High	Sravan *et al*. (2014) Parmeshwar *et al*. (2015)
		High	Moderate	Kishore *et al*. (2015) Islam *et al*. (2015a)
		Moderate	Moderate	Singh *et al*. (2011)
10.	No. of unfilled grains	High	High	Rahman *et al*. (2014) Parmeshwar *et al*. (2015)
		Moderate	Moderate	Mamun *et al*. (2012)
11.	1000 grain weight (g)	High	High	Dhurai *et al*. (2014) Rahman *et al*. (2014)

	1000 grain weight (g)			Rao *et al*. (2014) Satish *et al*. (2014) Suresh *et al*. (2014)
		High	Moderate	Seyoum *et al*. (2012) Roy *et al*. (2015)
		High	Low	Soni *et al*. (2013) Islam *et al*. (2015a) Mishu *et al*. (2016)
12.	Single plant grain yield (g)	High	High	Dhurai *et al*. (2014) Lingaiah *et al*. (2014) Rahman *et al*. (2014) Rao *et al*. (2014) Satish *et al*. (2014) Suresh *et al*. (2014) Parmeshwar *et al*. (2015)
		High	Moderate	Singh *et al*. (2011) Singh *et al*. (2012)
		High	Low	Roy *et al*. (2015)
		Moderate	Moderate	Lalitha and Sreedar (1999)
13.	Spikelet fertility	High	High	Dinesh *et al*. (2011) Parmeshwar *et al*. (2015)
		Moderate	Moderate	Soni *et al*. (2013)

		Moderate	Low	Mishu *et al*. (2016)
14.	Sterility percentage	High	High	Roy *et al.* (2015)
15.	Biomass per plant	High	High	Patel *et al.* (2014)
16.	Biological yield per plant	High	High	Dinesh *et al*. (2011) Soni *et al.* (2013) Parmeshwar *et al*. (2015)
17.	Harvest index	High	High	Dinesh *et al*. (2011) Parmeshwar *et al*. (2015)
		High	Low	Soni *et al.* (2013)
18.	Productivity per day	High	High	Bhadru *et al*. (2012b)

2.3. STABILITY ANALYSIS

2.3.1 Genotype x Environment Interaction and Stability Analysis:

The performance of rice cultivars is likely to vary with changing environments. The level of performance of any character is a result of the genotype (G) of the cultivar, the environment in which it is grown (E), and the interaction between G and E (GEI). Genotype x environment interaction (GEI) exists when the responses of two genotypes to different levels of environmental stress are not consistent (Allard and Bradshaw, 1964). Understanding the causes of GxE interaction is important at all stages of plant breeding and can be used to establish breeding objectives. Identify ideal test conditions and formulate recommendations for areas of optimal cultivar adaptation and help breeders to overcome constraints encountered when developing or evaluating genotypes in different environments. These constraints are the basis for defining breeding strategies that would contribute to higher and more stable grain yield for variable environments, thereby reducing farmers risk and uncertainty while increasing productivity. GxE interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments, to help plant breeders in selecting varieties.

There are many univariate and multivariate biometrical approaches to assess stability. The Additive Main Effects and Multiplicative Interaction (AMMI) model has found more use recently since it incorporates both the classical additive main effects model for GxE interaction and the multiplicative components into an integrated least square analysis and thus becomes more effective in selection of stable genotypes (McLaren and Chaudhary *et al.*, 1994). It not only gives estimate of total GxE interaction effect of each genotype but also partitions it into interaction effects due to individual environments (Zobel *et al*., 1988).

AMMI model combines the analysis of variance for both genotype and environment main effects with principal component analysis of genotype and environment interaction. This model has been found to be useful for understanding complex interactions, gaining accuracy, improving selection, and increasing experimental accuracy. The results can be graphed in useful biplot that shows both main and interaction effects for both genotypes and environments (Gauch and Zobel, 1996). The AMMI model has been extensively applied in statistical analysis of multienvironment cultivar trials (Kempton 1984, Crossa *et al.,* 1990, Gauch and Zobel 1997). AMMI stability analysis is a good technique for measuring the adaptability of different crop varieties to varying environments. Therefore, the present study was undertaken to estimate the GxE interactions through stability parameters and performance of 18 characters of 59 rice genotypes across three environments and to identify suitable genotypes for future breeding programme.

Das *et al.* (2010) undertaken study to assess yield performance, stability and adaptability of thirty-six rice genotypes of three different maturity groups evaluated over 12 environments. Results indicated that two mid-early group genotypes, three mid-late group genotypes, and six late group genotypes yielded higher consistently over the 3 years in the different agro climatic zones.

Hasan *et al.* (2011) studied phenotypic stability of 12 rice genotypes for plant height, days to maturity and yield. The result showed highly significant genotypic and GxE interaction. Genotype Mayna showed low interaction effect with score nearest to zero with above average yield. Two genotypes exhibited high positive interaction effect, gave mean grain yield around 5 ton/ha and was better suited to favorable environments. Similarly AMMI characterized the environments and identified Satkhira as a favorable environment for the better expression of the trait studied.

Nassir and Ariyo (2011) studies indicated that genotype ‘TOX 3107’ is having a combination of stable and average yield. ‘TOX 3226-53-2-2-2’ and ‘ITA 230’ were high yielding but adjudged unstable by AMMI. These two varieties along with ‘WITA 1’ and ‘TOX 3180-32-2-1-3-5’ were identified with good inland swamp environment, which is essentially moisture based.

Rasyad *et al*. (2012) reported significant G and GxE interaction for five rice cultivars evaluated in three environments implying that G and GxE interaction accounted for great contribution to these traits than environment. Most cultivated rice cultivars having high yield potential are erratic in term of performance when exposed to varied growing conditions. This could be attributed to genotype x environment interaction caused by differences in genotypic adaptation.

Kulsum *et al.* (2013) carried out Genotype-environment interaction and stability performance investigation on grain yield with 13 hybrid rice promising combinations in five environments. The AMMI biplot for yield clearly indicated that seven hybrids were high yielding, stable and had general adaptability at all locations and among them BRRI hybrid dhan2 was more adapted to a wide range of environments than the rest of the genotypes.

Sangodele *et al*. (2013) conducted AMMI analysis and results showed that genotypes, environments and GEI components were significant. Out of twenty two genotypes evaluated for GEI effect in this study, six genotypes were found suitable for all environments; six genotypes for favorable environments while ten genotypes were identified as suitable for unfavorable environments.

Genotype x environment interaction and stability performance were investigated on grain yield with 12 rice genotypes in five environments by Akter *et al.* (2014) and reported hybrid BRRI 10A/BRRI 10R(G3) was best overall environments. Hence, the genotype G3 would be considered more adapted to a wide range of environments than the rest of genotypes. Environments, such as Gazipur (E1) and Jessore (E5) could be regarded as a more stable site for high yielding hybrid rice improvement than other location for grain yield due to IPCA score near zero which had no interaction effect.

Bose *et al.* (2014a) studied GxE interaction of nine rice genotypes possessing cold tolerance at seedling stage tested over four environments was analyzed to identify stable high yielding genotypes suitable for boro environments. The study revealed that genotypes GEN6 and GEN4 were found to be stable based on all stability statistics. Grain yield (GY) is positively and significantly correlated with rank-sum (RS) and YSI.

Genotype x Environment interaction of 17 early duration rice genotypes tested over four seasons was analyzed to identify stable high yielding genotypes by Bose *et al.* (2014b). Among them, three genotypes in genotype group GG-3 exhibited high yields across environments, low IPCA-1 scores, low stability index (*Di*) values, unit regression coefficient and minimum deviation from regression. Hence these genotypes were recognized as possessing stable high yielding attributes.

Field experiments were conducted with twelve rice genotypes by Bose *et al.* (2014c) and reported that the genotypic effect was a predominant source of variation followed by GE interaction and environment. The genotype effect was ~5 times higher than that of the GE interaction, suggesting the existence of different environment groups. AMMI stability value discriminated genotype 5 and 12 as the stable genotypes.

Study carried out by Dewi *et al.* (2014) concluded that six genotypes were stable for two or more stability parameters and combined with high yield potential. Based on AMMI biplot analysis, four genotypes were more stable and had minimal interaction with environment.

Lakew *et al.* (2014) conducted experiment using AMMI analysis and reported that variations due to environments accounted for 52.48% of the treatment sum of square (SS) while genotypes and genotype x environment interaction explained 12.06 % and 35.45% of SS, respectively. In GGE biplot, G15 and G7 respectively were the best genotypes in E1, E2, and E6. The Genotype G15 was relatively stable in grain yield across environments and it also showed relatively better resistance to major rice diseases.

Ogunbayo *et al.* (2014) studies indicated that ouedeme environment in benin republic was the most stable and ideal for rice cultivation. Five genotypes were established as the most promising and stable genotypes across the test environments. About five genotypes performed best for the grain thickness and 1000 grain weight while FARO51 performed best for grain width and NERICA-L55 performed best for grain length.

Islam *et al.* (2015b) reported genotypic contribution was much higher than the environmental effect on grain yield in the wet season, while the environmental contribution was much higher than genotypic effect during the dry season. The variety BRRI dhan54 was identified as the most suitable genotype with wider adaptability in the region during the wet season, followed by BRRI dhan40 and BRRI dhan53, while BRRI dhan47 was the most stable variety followed by BRRI dhan61 and BINA dhan8 for the dry season across all sites.

Katsura *et al.* (2015) results reported genotype IR42 showed the highest average yield among environments, but its yield stability was low. On the other hand, several genotypes including Amankwatia, a local aromatic cultivar adapted to irrigated and lowland environments, and IRBL9-W [RL], a blast-tolerant variety containing the *Sub1* gene for submergence tolerance, showed high and stable yield.

2.4. CHARACTER ASSOCIATION

Study of character association helps the breeder in fixing selection criteria for grain yield in parental lines, such that selections will be effective in isolating the plants with desired combination of characters. Various morphological and physiological plant characters contribute to yield and heading date. Yield contributing components are interrelated with each other and show a complex chain of relationship.

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

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

2.4.1. Association of yield component characters with single plant grain yield in rice

Character	**Nature of association**	**Reference**
Days to 50 % flowering	Positive significant	Reddy *et al.* (2013) Khare *et al*. (2014) Rashid *et al.* (2014) Sarker *et al.* (2014) Sindhumole *et al.* (2015)
	Positive non – significant	Rao *et al.* (2014) Patel *et al.* (2014) Ratna *et al*. (2015) Golam *et al.* (2015) Mishu *et al.* (2016)
	Negative significant	Babu *et al*. (2012) Yadav *et al.* (2012) Gangashetty *et al*. (2013) Hasan *et al*. (2013) Kumar and Verma (2015)
Days to 50 % flowering	Negative non – significant	Seyoum *et al.* (2012) Nagaraju *et al.* (2013) Nikhil *et al*. (2014) Kumar and Verma (2015)
Days to maturity	Positive significant	Ravi *et al.* (2014) Golam *et al.* (2015)
	Positive non-significant	Patel *et al.* (2014) Mishu *et al*. (2016)
	Negative significant	Hasan *et al*. (2013)
	Negative non – significant	Panwar (2006)

Character	Nature of association	Reference
Plant height (cm)	Positive significant	Patel *et al.* (2014) Ranwake and Amarasighe (2014) Ramanjaneyulu *et al.* (2014) Sindhumole *et al.* (2015)
	Positive non - significant	Madhavilatha *et al.* (2005) Hasan *et al.* (2013) Golam *et al.* (2015)
Plant height (cm)	Negative significant	Rao and Shrivastava (1999) Rashid *et al.* (2014) Sarker *et al.* (2014) Naseer *et al.* (2015) Ratna *et al.* (2015) Mishu *et al.* (2016)
	Negative non – significant	Seyoum *et al.* (2012) Rahman *et al.* (2014)
No. of total tillers per plant	Positive significant	Patel *et al*. (2014) Ranwake and Amarasighe (2014) Ramanjaneyulu *et al.* (2014)
No. of total tillers per plant	Positive significant	Ravi *et al.* (2014) Golam *et al*. (2015) Sindhumole *et al*. (2015) Ratna *et al*. (2015)
	Negative significant	Naseer *et al.* (2015)
No. of productive tillers per plant	Positive significant	Naseem *et al*. (2014) Rao *et al.* (2014) Rashid *et al.* (2014) Sarker *et al.* (2014) Ranwake and Amarasighe (2014) Ramanjaneyulu *et al*. (2014) Golam *et al.* (2015)

Character	Nature of association	Reference
No. of productive tillers per plant	Positive non – significant	Seyoum *et al*. (2012) Nikhil *et al*. (2014) Rahman *et al.* (2014)
	Negative significant	Roy *et al.* (2015)
	Negative non – significant	Nandan *et al.* (2010)
Panicle length (cm)	Positive significant	Soni *et al.* (2013) Ranwake and Amarasighe (2014) Rahman *et al.* (2014) Rao *et al.* (2014) Sindhumole *et al.* (2015) Mishu *et al*. (2016)
	Positive non – significant	Hasan *et al*. (2013) Seyoum *et al.* (2012) Moosavi *et al.* (2015) Golam *et al*. (2015)
Panicle length (cm)	Negative non – significant	Ravi *et al.* (2014) Roy *et al.* (2015)
Panicle weight (g)	Positive significant	Swain and Reddy (2006) Nandeshwar (2010) Bhadru *et al.* (2011) Awaneet and Senapati (2013) Soni *et al.* (2013) Ranwake and Amarasighe (2014)
	Positive non significant	Azarpour (2013)
	Negative significant	Moosavi *et al.* (2015)

Character	**Nature of association**	**Reference**
No. of total grains per panicle	Positive significant	Krishna *et al.* (2008) Yadav *et al.* (2010) Patel *et al.* (2014) Ranwake and Amarasighe (2014) Ramanjaneyulu *et al.* (2014) Naseer *et al.* (2015)
No. of filled grains per panicle	Positive significant	Nagesh *et al.* (2013) Reddy *et al.* (2013) Naseem *et al.* (2014) Patel *et al.* (2014) Ranwake and Amarasighe (2014) Rao *et al.* (2014) Sarker *et al.* (2014) Ratna *et al.* (2015)
	Positive non – significant	Rahman *et al.* (2014) Rashid *et al.* (2014) Golam *et al.* (2015)
No. of unfilled grains per panicle	Negative significant	Golam *et al.* (2015)
	Negative non-significant	Rahman *et al.* (2014) Ratna *et al.* (2015)
Thousand grain weight (g)	Positive significant	Naseem *et al.* (2014) Patel *et al.* (2014) Rahman *et al.* (2014) Rao *et al.* (2014) Rashid *et al.* (2014) Naseer *et al.* (2015) Roy *et al.* (2015) Mishu *et al.* (2016)
	Positive non – significant	Rahman *et al.* (2014) Golam *et al.* (2015)

Character	**Nature of association**	**Reference**
	Negative significant	Suman (2003)
	Negative non – significant	Ravi *et al.* (2014) Seyoum *et al*. (2012) Nikhil *et al*. (2014) Ratna *et al.* (2015)
Spikelet fertility	Positive significant	Hasan *et al.* (2013) Soni *et al.* (2013) Naseer *et al.* (2015)
	Positive non - significant	Nandeshwar (2010)
Sterility percentage	Negative significant	Panwar (2006) Roy *et al.* (2015) Mishu *et al.* (2016)
Biomass per plant (g)	Positive significant	Patel *et al*. (2014) Ramanjaneyulu *et al*. (2014)
Biological yield per plant (g)	Positive significant	Soni *et al.* (2013)
	Positive non - significant	Panwar (2006) Azarpour *et al*. (2013) Kumar and Verma (2015)
Harvest index	Positive significant	Panwar (2006) Soni *et al.* (2013) Patel *et al*. (2014) Ramanjaneyulu *et al.* (2014) Kumar and Verma (2015)
Per day productivity	Positive significant	Bhadru *et al*. (2012c)

2.4.2. Association among the yield component traits in rice, association of days to 50 per cent flowering with

Character	**Nature of association**	**Reference**
Days to maturity	Positive significant	Panwar (2006) Devic *et al*. (2012) Hasan *et al.* (2013) Patel *et al*. (2014) Ravi *et al.* (2014)
	Positive non - significant	Golam *et al.* (2015)
Plant height (cm)	Positive significant	Babu *et al.* (2012) Soni *et al*. (2013) Patel *et al*. (2014)
	Positive non - significant	Mishra *et al.* (2014) Sarker *et al.* (2014) Golam *et al*. (2015) Sindhumole *et al.* (2015)
	Negative significant	Chandra *et al.* (2009) Ravi *et al.* (2014)
	Negative non – significant	Nandan *et al.* (2010) Rao *et al.* (2014) Mishu *et al.* (2016)
No. of total tillers per plant	Positive significant	Patel *et al*. (2014)
	Positive non - significant	Ravi *et al.* (2014) Golam *et al.* (2015) Sindhumole *et al*. (2015)
No. of productive tillers per plant	Positive significant	Soni *et al*. (2013) Mishra *et al*. (2014) Rao *et al.* (2014) Golam *et al*. (2015)
	Positive non - significant	Sarker *et al.* (2014) Patel *et al.* (2014)

Character	**Nature of association**	**Reference**
	Negative significant	Padmaja *et al*. (2011) Babu *et al*. (2012) Hasan *et al.* (2013) Khare *et al.* (2014)
No. of productive tillers per plant	Negative non – significant	Madhavilatha (2002) Ratna *et al*. (2015)
Panicle length (cm)	Positive significant	Babu *et al.*(2012) Soni *et al*. (2013)
	Positive non - significant	Patel *et al.* (2014)
	Negative non - significant	Ravi *et al*. (2014) Ratna *et al*. (2015) Mishu *et al.* (2016)
Panicle weight (g)	Positive significant	Bhadru *et al.* (2011) Soni *et al.* (2013)
	Positive non - significant	Awaneet and Senapati (2013)
No. of total grains per panicle	Positive non - significant	Mishra *et al*. (2014)
	Negative significant	Yadav *et al.* (2012) Patel *et al*. (2014)
No. of filled grains per panicle	Positive significant.	Mamun *et al*. (2012) Seyoum *et al*. (2012) Nagesh *et al*. (2013) Reddy *et al*. (2013) Rao *et al.* (2014) Ratna *et al*. (2015)
No. of filled grains per panicle	Positive non – significant	Nandan *et al*. (2010) Sarker *et al.* (2014)
	Negative non - significant	Panwar (2006) Golam *et al.* (2015)
No. of unfilled grains per	Positive non - significant	Ratna *et al.* (2015)

Character	**Nature of association**	**Reference**
panicle		Golam *et al*. (2015)
	Negative significant	Mamun *et al.* (2012)
	Negative non - significant	Panwar (2006)
Thousand grain weight (g)	Positive significant	Kumar *et al*. (2011) Yadav *et al*. (2011) Sarker *et al.* (2014) Patel *et al*. (2014)
	Positive non - significant	Mishra *et al.* (2014) Rao *et al.* (2014) Ravi *et al*. (2014) Mishu *et al.* (2016)
	Negative significant	Sakthivel (2001) Bhadru *et al.* (2012a)
	Negative non- significant	Hasan *et al*. (2013) Ratna *et al.* (2015) Golam *et al*. (2015)
Spikelet fertility	Positive significant	Eradasappa *et al*. (2007) Soni *et al.* (2013)
	Positive non - significant	Panwar (2006) Mishra *et al*. (2014)
	Negative significant	Hasan *et al*. (2013)
	Negative non -significant	Bhadru *et al*. (2011)
Sterility percentage	Negative non- significant	Mishu *et al.* (2016)
Biomass per plant (g)	Positive significant	Patel *et al*. (2014)
Biological yield per plant (g)	Positive significant	Soni *et al.* (2013)
	Positive non- significant	Mishra *et al*. (2014)
Harvest index	Negative significant	Panwar (2006) Mishra *et al*. (2014)

Character	Nature of association	Reference
	Negative non-significant	Soni *et al*. (2013) Patel *et al.* (2014)
Per day productivity	Negative significant	Bhadru *et al.* (2012c)

2.4.3. Association among the yield component traits in rice, association of days to maturity with

Character	Nature of association	Reference
Plant height (cm)	Positive significant	Panwar (2006) Devic *et al.* (2012) Patel *et al*. (2014)
	Negative significant	Ganapati *et al*. (2014)
	Negative non significant	Hasan *et al*. (2013) Dilruba *et al.* (2014) Ravi *et al.* (2014) Kumar and Verma (2015) Mishu *et al*. (2016)
No. of total tillers per plant	Positive significant	Patel *et al.* (2014)
	Positive non - significant	Ravi *et al.* (2014) Golam *et al*. (2015)
No. of productive tillers per plant	Positive significant	Panwar (2006)
	Positive non –significant	Patel *et al.* (2014) Golam *et al*. (2015)
	Negative significant	Hasan *et al.* (2013) Kumar and Verma (2015)
Panicle length (cm)	Positive significant	Dilruba *et al*. (2014)
	Positive non – significant	Patel *et al.* (2014) Mishu *et al.* (2016)
	Negative non – significant	Panwar (2006) Hasan *et al*. (2013) Ganapati *et al.* (2014)

Panicle weight (g)	Positive non – significant	Awaneet and Senapati (2013)
No. of total grains per panicle	Negative non – significant	Ganapati *et al*. (2014) Patel *et al*. (2014)
No. of filled grains per panicle	Positive non – significant	Dilruba *et al*. (2014) Golam *et al.* (2015)
	Negative non – significant	Panwar (2006) Ganapati *et al.* (2014) Kumar and Verma (2015)
No. of unfilled grains per panicle	Positive non – significant	Golam *et al.* (2015)
	Negative non – significant	Panwar (2006) Ganapati *et al.* (2014)
Thousand grain weight (g)	Positive significant	Patel *et al.* (2014) Kumar and Verma (2015)
	Positive non – significant	Dilruba *et al*. (2014) Golam *et al*. (2015) Mishu *et al.* (2016)
	Negative non- significant	Hasan *et al*. (2013) Ganapati *et al*. (2014) Ravi *et al.* (2014)
Spikelet fertility	Negative significant	Hasan *et al*. (2013)
	Negative non- significant	Panwar (2006) Kumar and Verma (2015) Mishu *et al*. (2016)
Sterility percentage	Negative significant	Dilruba *et al*. (2014)
Biomass per plant (g)	Positive significant	Patel *et al.* (2014)
Biological yield per plant (g)	Negative non- significant	Kumar and Verma (2015)
Harvest index	Positive significant	Ganapati *et al*. (2014)
	Negative significant	Panwar (2006)
	Negative non –significant	Dilruba *et al.* (2014) Patel *et al*. (2014)

2.4.4. Association among the yield component traits in rice, association of plant height with

Character	**Nature of association**	**Reference**
No. of total tillers per plant	Positive significant	Patel *et al.* (2014) Ramanjaneyulu *et al.* (2014) Naseer *et al.* (2015) Sindhumole *et al.* (2015)
	Negative significant	Golam *et al.* (2015)
No. of productive tillers per plant	Positive significant	Chandra *et al.* (2009) Rahman *et al.* (2014) Patel *et al.* (2014)
	Positive non – significant	Hasan *et al. (*2013) Rao *et al.* (2014)
No. of productive tillers per plant	Negative significant	Bhadru *et al.* (2012a) Sarker *et al.* (2014) Ratna *et al.* (2015) Golam *et al.* (2015)
	Negative non – significant	Soni *et al.* (2013) Mishra *et al.* (2014)
Panicle length (cm)	Positive significant	Sarker *et al.* (2014) Ganapati *et al*. (2014) Patel *et al*. (2014) Golam *et al*. (2015) Moosavi *et al.* (2015) Ratna *et al*. (2015)
	Positive non – significant	Mishu *et al.* (2016)
	Negative significant	Padmaja *et al.* (2011)

Panicle length (cm)	Negative non – significant	Dilruba *et al.* (2014) Rahman *et al.* (2014) Ranwake and Amarasighe (2014)
Panicle weight (g)	Positive significant	Bhadru *et al.* (2011) Awaneet and Senapati (2013) Soni *et al*. (2013) Ranwake and Amarasighe (2014) Moosavi *et al.* (2015)
No. of total grains per panicle	Positive significant	Mishra *et al.* (2014) Patel *et al*. (2014)
	Positive non – significant	Ganapati *et al.* (2014) Ranwake and Amarasighe (2014)
No. of total grains per panicle	Negative significant	Nandeshwar (2010) Naseer *et al.* (2015)
No. of filled grains per panicle	Positive non – significant	Ganapati *et al.* (2014) Ranwake and Amarasighe (2014)
No. of filled grains per panicle .	Negative non – significant	Nandan *et al*. (2010) Dilruba *et al*. (2014) Ratna *et al*. (2015)
No. of unfilled grains per panicle	Positive non – significant	Ganapati *et al.* (2014) Rahman *et al*.(2014) Ratna *et al*. (2015) Golam *et al*. (2015)
	Negative non – significant	Panwar (2006)
Thousand grain weight (g)	Positive significant	Hasan *et al.* (2013) Soni *et al.* (2013) Mishra *et al.* (2014) Ramanjaneyulu *et al.* (2014)

		Kumar and Verma (2015)
Thousand grain weight (g)	Positive non-significant	Dilruba *et al*. (2014) Patel *et al.* (2014) Golam *et al*. (2015) Mishu *et al.* (2016)
Thousand grain weight (g)	Negative significant	Rahman *et al*. (2014) Rao *et al*. (2014) Sarker *et al.* (2014) Ratna *et al.* (2015)
	Negative non – significant	Khare *et al.* (2014) Naseer *et al.* (2015)
Spikelet fertility	Positive significant	Panwar (2006) Bhadru *et al*. (2011) Soni *et al.* (2013) Mishra *et al.* (2014)
	Positive non – significant	Hasan *et al.* (2013)
	Negative non – significant	Nandeshwar (2010)
	Positive non-significant	Dilruba *et al*. (2014) Roy *et al.* (2015)
	Negative non – significant	Mishu *et al.* (2016)
Biomass per plant (g)	Positive significant	Patel *et al*. (2014) Ramanjaneyulu *et al*. (2014)
Biological yield per plant (g)	Positive significant	Soni *et al.* (2013)
	Positive non – significant	Mishra *et al*. (2014)
	Negative significant	Panwar (2006)
Harvest index	Positive non – significant	Mishra *et al*. (2014)
	Negative significant	Panwar (2006) Ganapati *et al*. (2014)

	Negative non – significant	Soni *et al*. (2013) Patel *et al.* (2014) Ramanjaneyulu *et al*. (2014)
Per day productivity	Positive non – significant	Bhadru *et al*. (2012c)

2.4.5 Association among the yield component traits in rice association of no. of total tillers per plant with

Character	**Nature of association**	**Reference**
No. of productive tillers per plant	Positive significant	Patel *et al.* (2014) Ramanjaneyulu *et al.* (2014) Golam *et al*. (2015)
Panicle length (cm)	Positive non - significant	Ramanjaneyulu *et al*. (2014) Ranwake and Amarasighe (2014)
	Negative significant	Golam *et al.* (2015)
Panicle weight (g)	Positive non - significant	Ranwake and Amarasighe (2014)
No. of total grains per panicle	Positive significant	Patel *et al*. (2014) Ramanjaneyulu *et al.* (2014) Ranwake and Amarasighe (2014)
	Negative significant	Naseer *et al*. (2015)
No. of filled grains per panicle	Positive significant	Ranwake and Amarasighe (2014)
	Negative non significant	Golam *et al.* (2015)
No. of unfilled grains per panicle	Positive non - significant	Golam *et al.* (2015)
Thousand grain weight (g)	Positive significant	Ramanjaneyulu *et al.* (2014)
	Positive non - significant	Patel *et al.* (2014)
Thousand grain weight (g)	Negative significant	Golam *et al*. (2015)
	Negative non- significant	Naseer *et al*. (2015)
Spikelet fertility	Positive significant	Naseer *et al.* (2015)
Sterility percentage	Positive non - significant	Divya *et al.* (2015)

Biomass per plant (g)	Positive significant	Patel *et al.* (2014) Ramanjaneyulu *et al.* (2014)
	Negative non -significant	Patel *et al.* (2014)

2.4.6. Association among the yield component traits in rice association of no. of productive tillers per plant with

Character	**Nature of association**	**Reference**
Panicle length (cm)	Positive significant	Padmaja *et al.* (2011) Yadav *et al.* (2011) Nagaraju *et al.* (2013) Soni *et al.* (2013)
	Positive non - significant	Rao *et al.* (2014) Ranwake and Amarasighe (2014)
	Negative significant	Babu *et al.* (2012) Rahman *et al.* (2014) Ratna *et al*. (2015)
	Negative non – significant	Sandhyakishore (2007) Golam *et al.* (2015)
Panicle weight (g)	Positive significant	Soni *et al*. (2013)
	Positive non - significant	Ranwake and Amarasighe (2014)
No. of total grains per panicle	Positive significant	Patel *et al*. (2014) Ranwake and Amarasighe (2014) Ramanjaneyulu *et al.* (2014)
	Negative non - significant	Mishra *et al.* (2014)
No. of filled grains per panicle	Positive significant	Nagaraju *et al.* (2013) Ranwake and Amarasighe (2014)
	Positive non – significant	Rahman *et al.* (2014) Sarker *et al.* (2014)
	Negative significant	Satyavathi *et al.* (2001) Rao *et al.* (2014)

	Negative non - significant	Nayak *et al*. (2001) Golam *et al.* (2015)
No. of unfilled grains per panicle	Positive non significant	Rahman *et al*. (2014)
	Negative significant	Ratna *et al*. (2015)
	Negative non - significant	Panwar (2006) Golam *et al.* (2015)
Thousand grain weight (g)	Positive significant	Hasan *et al.* (2013) Soni *et al.* (2013)
	Positive non significant	Ratna *et al*. (2015)
	Negative significant	Padmaja *et al*. (2011) Mishra *et al.* (2014) Rahman *et al.* (2014)
	Negative non - significant	Ramanjaneyulu *et al*. (2014) Rao *et al.* (2014) Golam *et al*. (2015)
Spikelet fertility	Positive significant	Hasan *et al*. (2013) Soni *et al.* (2013) Mishra *et al.* (2014)
	Positive non – significant	Panwar (2006)
	Negative significant	Bhadru *et al.* (2011)
	Negative non - significant	Roy *et al*. (2015)
Sterility percentage	Positive non significant	Divya *et al.* (2015)
Biomass per plant (g)	Positive significant	Patel *et al*. (2014)
Biological yield per plant (g)	Positive significant	Panwar (2006) Soni *et al.* (2013)
	Positive non - significant	Mishra *et al.* (2014)
Harvest index	Positive significant	Ramanjaneyulu *et al*. (2014)
	Positive non-significant	Soni *et al*. (2013) Mishra *et al.* (2014) Patel *et al.* (2014)
Per day productivity	Positive significant	Bhadru *et al*. (2012c)

2.4.7. Association among the yield component traits in rice, association of panicle length with

Character	Nature of association	Reference
Panicle weight (g)	Positive significant	Bhadru *et al.* (2011) Awaneet and Senapati (2013) Soni *et al.* (2013)
	Positive non -significant	Nandeshwar (2010) Ranwake and Amarasighe (2014) Moosavi *et al*. (2015)
No. of total tillers per plant	Positive significant	Patel *et al.* (2014)
No. of productive tillers per plant	Positive significant	Patel *et al.* (2014) Rahman *et al*. (2014)
	Negative significant	Babu *et al.* (2012) Rahman *et al.* (2014)
No. of total grains per panicle	Positive significant	Ganapati *et al*. (2014) Patel *et al.* (2014) Ramanjaneyulu *et al*. (2014)
No. of filled grains per panicle	Positive significant	Padmaja *et al*. (2011) Ganapati *et al*. (2014) Golam *et al*. (2015)
	Positive non – significant	Rahman *et al*. (2014)
	Positive non – significant	Satyavathi *et al.* (2001) Rahman *et al.* (2014)
	Negative significant	Rao *et al.* (2014)
	Negative non – significant	Nandan *et al*. (2010) Dilruba *et al*. (2014) Ratna *et al*. (2015)
No. of unfilled grains per	Positive significant	Ganapati *et al.* (2014)

panicle	Positive non – significant	Panwar (2006) Rahman *et al*. (2014) Golam *et al.* (2015)
Thousand grain weight (g)	Positive significant	Babu *et al*. (2012) Hasan *et al*. (2013) Patel *et al.* (2014) Golam *et al.* (2015)
	Positive non – significant	Nandan *et al*. (2010) Dilruba *et al.* (2014) Rahman *et al.* (2014)
	Negative significant	Rao *et al.* (2014) Ratna *et al.* (2015) Mishu *et al.* (2016)
	Negative non significant	Ramanjaneyulu *et al.* (2014)
Spikelet fertility	Positive significant	Bhadru *et al*. (2011) Hasan *et al.* (2013) Soni *et al. (*2013)
	Positive non -significant	Panwar (2006)
	Negative non - significant	Nandeshwar (2010)
Sterility percentage	Positive non -significant	Mishu *et al.* (2016)
	Negative non - significant	Dilruba *et al*. (2014) Roy *et al*. (2015)
Biomass per plant (g)	Positive significant	Patel *et al.* (2014)
Biological yield per plant (g)	Positive significant	Soni *et al.* (2013)
	Negative non significant	Panwar (2006)
Harvest index	Positive significant	Ramanjaneyulu *et al.* (2014)
	Positive non significant	Soni *et al*. (2013)
	Negative non – significant	Dilruba *et al*. (2014) Ganapati *et al*. (2014)

2.4.8. Association among the yield component traits in rice, association of panicle weight with

Character	Nature of association	Reference
No. of total grains per panicle	Positive significant	Nandeshwar *et al*. (2010) Ranwake and Amarasighe (2014)
No. of filled grains per panicle	Positive significant	Bhadru *et al.* (2011) Ranwake and Amarasighe (2014)
Thousand grain weight (g)	Positive significant	Awaneet and Senapati (2013) Soni *et al.* (2013)
	Positive non – significant	Nandeshwar *et al*. (2010)
	Negative non – significant	Moosavi *et al*. (2015
Spikelet fertility	Positive significant	Nandeshwar *et al*. (2010) Bhadru *et al.* (2011) Awaneet and Senapati (2013) Soni *et al.* (2013)
Biological yield per plant (g)	Positive significant	Soni *et al.* (2013)
Harvest index	Positive non - significant	Soni *et al*. (2013)
	Negative non - significant	Moosavi *et al*. (2015)
Per day productivity	Negative non - significant	Bhadru *et al*. (2012c)

2.4.9. Association among the yield component traits in rice, association of number of total grains per panicle with

Character	Nature of association	Reference
No. of filled grains per panicle	Positive significant	Ganapati *et al*. (2014)
No. of unfilled grains per panicle	Positive significant	Ganapati *et al*. (2014)
Thousand grain weight (g)	Positive significant	Mishra *et al.* (2014) Naseer *et al.* (2015)

	Negative non - significant	Ganapati *et al.* (2014) Patel *et al.* (2014)
Spikelet fertility	Positive significant	Mishra *et al.* (2014) Naseer *et al*. (2015)
Sterility percentage	Negative non - significant	Roy *et al.* (2015)
Biomass per plant (g)	Positive significant	Patel *et al.* (2014)
Biological yield per plant (g)	Positive non - significant	Mishra *et al*. (2014)
Harvest index	Positive non- significant	Mishra *et al*. (2014) Patel *et al.* (2014)
	Negative non - significant	Ganapati *et al.* (2014)

2.4.10. Association among the yield component traits with number of filled grains per panicle

Character	**Nature of Association**	**References**
No. of unfilled grains per panicle	Positive significant	Ganapati *et al.* (2014) Golam *et al.* (2015)
	Positive non – significant	Panwar (2006) Rahman *et al.* (2014)
	Negative significant	Mamun *et al.* (2012)
	Negative non - significant	Ratna *et al.* (2015)
Thousand grain weight (g)	Positive significant	Panwar (2006) Rao *et al.* (2014)
	Positive non – significant	Chandra *et al.* (2009) Golam *et al*. (2015)
	Negative significant	Nayak *et al.* (2001) Dilruba *et al.* (2014) Rahman *et al.* (2014) Ratna *et al*. (2015)
	Negative non - significant	Nandan *et al*. (2010)
Spikelet fertility	Positive significant	Panwar (2006)
Sterility percentage	Negative significant	Mamun *et al*. (2012)
	Negative non - significant	Dilruba *et al.* (2014)

Biological yield per plant (g)	Negative non - significant	Panwar *et al.* (2006)
Harvest index	Positive significant	Panwar *et al.* (2006)
	Positive non - significant	Dilruba *et al.* (2014)

2.4.11. Association among the yield component traits with number of unfilled grains per panicle

Character	**Nature of Association**	**References**
Thousand grain weight (g)	Positive non - significant	Ratna *et al.* (2015)
	Negative non - significant	Ganapati *et al.* (2014) Rahman *et al.* (2014) Golam *et al.* (2015)
Sterility percentage	Positive significant	Mamun *et al.* (2012)
	Negative non - significant	Dilruba *et al.* (2014)
Harvest index	Positive non - significant	Dilruba *et al.* (2014)
	Negative non - significant	Ganapati *et al.* (2014)

2.4.12. Association among the yield component traits in rice, association of thousand grain weight with

Character	**Nature of association**	**Reference**
Spikelet fertility	Positive significant	Panwar (2006) Hasan *et al.* (2013) Mishra *et al.* (2014) Naseer *et al.* (2015)
	Negative non - significant	Nandeshwar *et al.* (2010)
Sterility percentage	Negatively significant	Panwar *et al.* (2006)
	Negatively non - significant	Roy *et al.* (2015) Mishu *et al.* (2016)
Biomass per plant (g)	Positive significant	Ramanjaneyulu *et al.* (2014)
	Positive non - significant	Patel *et al.* (2014)
Biological yield per plant (g)	Positive significant	Panwar (2006)
	Positive non - significant	Mishra *et al.* (2014)

Harvest index	Positive significant	Ramanjaneyulu *et al*. (2014)
	Positive non - significant	Patel *et al.* (2014)
	Negative non - significant	Mishra *et al*. (2014)
Per day productivity	Positive significant	Bhadru *et al*. (2012c)

2.4.13. Association among the yield component traits in rice, association of spikelet fertility with

Character	**Nature of association**	**Reference**
Sterility percentage	Negative significant	Divya *et al.* (2015)
Biological yield per plant (g)	Positive significant	Soni *et al.* (2013)
	Positive non - significant	Mishra *et al*. (2014)
	Negative non - significant	Panwar (2006)
Harvest index	Positive significant	Panwar (2006)
	Positive non - significant	Soni *et al.* (2013) Mishra *et al.* (2014)

2.4.14. Association among the yield component traits in rice, association of sterility percentage with

Character	**Nature of association**	**Reference**
Harvest index	Negative significant	Dilruba *et al*. (2014) Roy *et al*. (2015)

2.4.15. Association among the yield component traits in rice, association of biomass per plant with

Character	**Nature of association**	**Reference**
Harvest index	Positive significant	Ramanjaneyulu *et al*. (2014)
	Negative significant	Patel *et al*. (2014)

2.4.16. Association among the yield component traits in rice, association of biological yield per plant with

Character	**Nature of association**	**Reference**
Harvest index	Negative significant	Panwar (2006) Mishra *et al.* (2014)
	Negative non - significant	Soni *et al*. (2013)

2.5. PATH COEFFICIENT ANALYSIS

Selection for improvement of yield should not be based on yield alone but other components contributing to grain yield should also be considered. Interrelationship and relative contribution of each component towards yield is clearly described through path analysis. The path coefficient analysis which was initially developed by Wright (1921) and described by Dewey and Lu (1959) allows partitioning of correlation coefficient into direct and indirect effects of various traits towards dependent variable and thus helps in assessing the cause-effect relationship as well as effective selection. It is used in plant breeding programs to determine the nature of the relationships between yield and yield components that are useful as selection criteria to improve the crop yield. If the cause and effect relationship is well defined, it is possible to present the whole system of variables in the form of a diagram, known as path-diagram. In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield (Dewey and Lu, 1959).

The findings of earlier workers on the relative contribution of different characters to single plant grain yield in rice are furnished here under in a tabular form given below.

2.5.1. Direct effects

Character	**Positive direct effect on single plant grain yield**	**Negative direct effect on single plant grain yield**
Days to 50 % flowering	Mohanty *et al.* (2012) Seyoum *et al.* (2012) Nikhil *et al*. (2014)	Babu *et al*. (2012) Hasan *et al.* (2013) Soni *et al.* (2013)

	Ravi *et al.* (2014) Golam *et al*. (2015) Ratna *et al* (2015)	Mishra *et al.* (2014) Patel *et al*. (2014) Kumar and Verma (2015)
Days to maturity	Devic *et al.* (2012) Dilruba *et al.* (2014) Patel *et al.* (2014) Kumar and Verma (2015)	Panwar (2006) Ravi *et al.* (2014) Hasan *et al.* (2013)
Plant height (cm)	Hasan *et al*. (2013) Nagaraju *et al.* (2013) Dilruba *et al.* (2014) Rahman *et al*. (2014) Golam *et al.* (2015) Naseer *et al*. (2015)	Mishra *et al*. (2014) Nikhil *et al*. (2014) Patel *et al*. (2014) Ravi *et al*. (2014) Kumar and Verma (2015) Ratna *et al*. (2015)
No. of total tillers per plant	Patel *et al*. (2014) Golam *et al.* (2015)	Ravi *et al*. (2014) Naseer *et al.* (2015)
No. of productive tillers per plant	Naseem *et al.* (2014) Sarkar *et al.* (2014) Rahman *et al*. (2014) Rao *et al*. (2014) Golam *et al*. (2015) Ratna *et al*. (2015)	Hasan *et al*. (2013) Mishra *et al*. (2014) Nikhil *et al*. (2014) Patel *et al*. (2014) Kumar and Verma (2015)
Panicle length (cm)	Sarker *et al*. (2014) Lingaiah *et al*. (2014) Nikhil *et al*. (2014) Rahman *et al*. (2014) Moosavi *et al.* (2015) Ratna *et al.* (2015)	Hasan *et al*. (2013) Dilruba *et al*. (2014) Patel *et al*. (2014) Ravi *et al.* (2014) Golam *et al*. (2015) Kumar and Verma (2015)
Panicle weight (g)	Awaneet and Senapati (2013)	Soni *et al*. (2013)
No. of total grains per panicle	Yadav *et al.* (2010) Ganapati *et al.* (2014) Mishra *et al.* (2014) Kumar and Verma (2015) Naseer *et al*. (2015)	

No. of filled grains per panicle No. of filled grains per panicle	Dilruba *et al.* (2014) Ganapati *et al.* (2014) Naseem *et al.* (2014) Rahman *et al.* (2014) Rao *et al.* (2014) Sarker *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)	Akhtar *et al.* (2011) Rajamadhan *et al.* (2011) Babu *et al.* (2012)
No. of unfilled grains per panicle	Ganapati *et al.* (2014)	Panwar (2006) Rahman *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)
Thousand grain weight (g)	Hasan *et al.* (2013) Soni *et al.* (2013) Dilruba *et al.* (2014) Rahman *et al.* (2014) Rao *et al.* (2014) Ratna *et al.* (2015) Naseer *et al.* (2015) Golam *et al.* (2015)	Basavaraja *et al.* (2011) Babu *et al.* (2012) seyoum *et al.* (2012) Patel *et al.* (2014) Ravi *et al.* (2014)
Spikelet fertility	Panwar (2006) Hasan *et al.* (2013)	Gyanendra *et al.* (2011) Soni *et al.* (2013) Mishra *et al.* (2014) Kumar and Verma (2015) Naseer *et al.* (2015)
Sterility percentage		Dilruba *et al.* (2014) Krantikumar *et al.* (2016)
Biomass per plant (g)	Patel *et al.* (2014)	Krantikumar *et al.* (2016)
Biological yield per plant (g)	Panwar (2006) Soni *et al.* (2013) Mishra *et al.* (2014) Kumar and Verma (2015) Krantikumar *et al.* (2016)	

Harvest index Harvest index	Panwar (2006) Soni *et al*. (2013) Ganapati *et al.* (2014) Mishra *et al*. (2014) Patel *et al*. (2014) Kumar and Verma (2015) Moosavi *et al*. (2015) Krantikumar *et al.* (2016)	
Per day productivity	Bhadru *et al*. (2012)	

2.5.2. Indirect effects of days to 50 % flowering on single plant grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to maturity	Patel *et al*. (2014) Ravi *et al*. (2014) Golam *et al.* (2015)	Hasan *et al.* (2013) Kumar and Verma (2015)
Plant height (cm)	Yadav *et al*. (2012) Bhadru *et al.* (2012a) Golam *et al.* (2015) Kumar and Verma (2015)	Hasan *et al*. (2013) Mishra *et al*. (2014) Patel *et al.* (2014) Ravi *et al*. (2014) Ratna *et al.* (2015)
No. of total tillers per plant	Patel *et al*. (2014) Ravi *et al*. (2014) Golam *et al*. (2015)	
No. of productive tillers per plant	Bhadru *et al*. (2012a) Hasan *et al.* (2013) Golam *et al*. (2015) Kumar and Verma (2015)	Yadav *et al.* (2012) Mishra *et al*. (2014) Patel *et al.* (2014) Ratna *et al.* (2015)
Panicle length (cm)	Rajamadhan *et al*. (2011) Bhadru *et al*. (2012c) Golam *et al.* (2015) Kumar and Verma (2015)	Hasan *et al*. (2013) Patel *et al.* (2014) Ravi *et al*. (2014) Ratna *et al*. (2015)
Panicle weight (g)	Bhadru *et al.* (2011)	

No. of total grains per panicle	Mishra *et al.* (2014) Kumar and Verma (2015)	Patel *et al.* (2014)
No. of filled grains per panicle	Yadav *et al*. (2012) Bhadru *et al*. (2012a) Mamun *et al.* (2012) Ratna *et al*. (2015)	Padmaja *et al.* (2011) Rajamadhan *et al*. (2011) Babu *et al*. (2012) Yadav and Kumar (2012) Golam *et al*. (2015)
No. of unfilled grains per panicle		Mamun *et al*. (2012) Ratna *et al*. (2015) Golam *et al*. (2015)
Thousand grain weight (g)	Basavaraja *et al*. (2011) Yadav *et al*. (2012) Ravi *et al*. (2014)	Hasan *et al*. (2013) Mishra *et al*. (2014) Patel *et al*. (2014) Golam *et al.* (2015) Kumar and Verma (2015) Ratna *et al.* (2015)
Spikelet fertility	Panwar (2006) Bhadru *et al*. (2011) Kumar and Verma (2015)	Hasan *et al.* (2013) Mishra *et al.* (2014)
Sterility percentage	Mamun *et al.* (2012)	
Biomass per plant (g)	Patel *et al.* (2014)	
Biological yield per plant (g)	Panwar (2006) Mishra *et al*. (2014) Kumar and Verma (2015)	
Harvest index	Kumar and Verma (2015)	Panwar (2006) Mishra *et al*. (2014) Patel *et al.* (2014)
Per day productivity		Bhadru *et al*. (2012c)

2.5.3. Indirect effects of days to maturity on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Panwar (2006) Devic *et al*. (2012) Hasan *et al*. (2013) Golam *et al.* (2015)	Patel *et al.* (2014) Ravi *et al.* (2014)
Plant height (cm)	Devic *et al.* (2012) Ravi *et al.* (2014)	Hasan *et al*. (2013) Dilruba *et al*. (2014) Patel *et al*. (2014) Golam *et al*. (2015)
No. of total tillers per plant	Patel *et al.* (2014) Golam *et al*. (2015)	Ravi *et al*. (2014)
No. of productive tillers per plant	Panwar (2006) Hasan *et al*. (2013) Golam *et al*. (2015)	Patel *et al.* (2014)
Panicle length (cm)	Hasan *et al.* (2013) Golam *et al*. (2015)	Devic *et al*. (2012) Dilruba *et al.* (2014) Patel *et al.* (2014) Kumar and Verma (2015)
Panicle weight (g)	Awaneet and Senapati (2013)	
No. of total grains per panicle		Patel *et al*. (2014) Kumar and Verma (2015)
No. of filled grains per panicle	Panwar (2006) Golam *et al.* (2015)	Dilruba *et al.* (2014)
No. of unfilled grains per panicle		Panwar (2006) Golam *et al.* (2015)
Thousand grain weight (g)	Panwar (2006) Devic *et al*. (2012) Dilruba *et al*. (2014)	Hasan *et al*. (2013) Patel *et al*. (2014) Ravi *et al*. (2014)
Spikelet fertility Spikelet fertility		Panwar (2006) Hasan *et al.* (2013) Kumar and Verma (2015)

Sterility percentage	Dilruba *et al.* (2014)	
Biomass per plant (g)	Patel *et al.* (2014)	
Biological yield per plant (g)		Devic *et al.* (2012) Kumar and Verma (2015)
Harvest index	Kumar and Verma (2015)	Panwar (2006) Patel *et al.* (2014)

2.5.4. Indirect effects of plant height on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Panwar (2006) Ravi *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)	Padmaja *et al.* (2011) Bhadru *et al.* (2012a) Hasan *et al.* (2013) Patel *et al.* (2014)
Days to maturity	Hasan *et al.* (2013) Patel *et al.* (2014) Ravi *et al.* (2014)	Panwar (2006) Dilruba *et al.* (2014) Golam *et al.* (2015)
No. of total tillers per plant	Patel *et al.* (2014) Ravi *et al.* (2014)	Golam *et al.* (2015) Naseer *et al.* (2015)
No. of productive tillers per plant	Basavaraja *et al.* (2011) Pandey *et al.* (2012) Bhadru *et al.* (2012a) Mohanty *et al.* (2012) Reddy *et al.* (2013) Rahman *et al.* (2014)	Yadav *et al.* (2012) Hasan *et al.* (2013) Mishra *et al.* (2014) Patel *et al.* (2014) Ratna *et al.* (2015) Golam *et al.* (2015)
Panicle length (cm)	Babu *et al.* (2012) Pandey *et al.* (2012) Dilruba *et al.* (2014) Rahman *et al.* (2014) Ratna *et al.* (2015)	Bhadru *et al.* (2012c) Hasan *et al.* (2013) Patel *et al.* (2014) Ravi *et al.* (2014) Golam *et al.* (2015)
Panicle weight (g)	Bhadru *et al.* (2011)	
No. of total grains per	Yadav *et al.* (2010)	Yadav *et al.* (2012)

panicle	Kumar and Verma (2015)	Pandey *et al*. (2012) Mishra *et al*. (2014) Patel *et al*. (2014) Naseer *et al*. (2015)
No. of filled grains per panicle	Babu *et al*. (2012) Yadav *et al*. (2012) Rahman *et al*. (2014) Golam *et al*. (2015)	Suryanarayana (2000) Bhadru *et al*. (2012a) Dilruba *et al*. (2014) Ratna *et al*. (2015)
No. of unfilled grains per panicle	Panwar (2006)	Rahman *et al*. (2014) Golam *et al*. (2015) Ratna *et al*. (2015)
Thousand grain weight (g)	Bhadru *et al*. (2012a) Hasan *et al*. (2013) Dilruba *et al*. (2014) Rahman *et al*. (2014) Golam *et al*. (2015)	Pandey *et al*. (2012) Patel *et al*. (2014) Ravi *et al*. (2014) Naseer *et al*. (2015) Ratna *et al*. (2015)
Spikelet fertility	Hasan *et al*. (2013) Kumar and Verma (2015)	Panwar (2006) Bhadru *et al*. (2011) Mishra *et al*. (2014) Naseer *et al*. (2015)
Sterility percentage		Dilruba *et al*. (2014)
Biomass per plant (g)	Patel *et al*. (2014)	
Biological yield per plant (g)	Mishra *et al*. (2014)	Kumar and Verma (2015)
Harvest index	Mishra *et al*. (2014) Kumar and Verma (2015)	Panwar (2006) Dilruba *et al*. (2014) Patel *et al*. (2014)

2.5.5. Indirect effects of no of total tillers per plant on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Golam *et al*. (2015)	Patel *et al.* (2014) Ravi *et al.* (2014)
Days to maturity	Patel *et al*. (2014) Ravi *et al*. (2014) Golam *et al.* (2015)	
Plant height (cm)	Ravi *et al.* (2014) Naseer *et al.* (2015)	Patel *et al*. (2014) Golam *et al.* (2015)
No. of productive tillers per plant	Golam *et al.* (2015)	Patel *et al*. (2014)
Panicle length (cm)	Ravi *et al.* (2014) Golam *et al*. (2015)	Patel *et al*. (2014)
No. of total grains per panicle		Naseer *et al.* (2015)
No. of filled grains per panicle		Golam *et al.* (2015)
No. of unfilled grains per panicle		Golam *et al*. (2015)
Thousand grain weight (g)	Ravi *et al*. (2014)	Patel *et al.* (2014) Golam *et al.* (2015) Naseer *et al.* (2015)
Spikelet fertility		Naseer *et al.* (2015)
Biomass per plant (g)	Patel *et al.* (2014)	
Harvest index		Patel *et al*. (2014)
Per day productivity	Bhadru *et al.* (2012c)	

2.5.6. Indirect effects of number of productive tillers per plant on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Chandra *et al.* (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Basavaraja *et al*. (2011) Babu *et al*. (2012) Hasan *et al.* (2013)

Character	**Positive indirect effect**	**Negative indirect effect**
	Golam *et al.* (2015)	Patel *et al*. (2014) Ratna *et al*. (2015)
Days to maturity	Hasan *et al.* (2013) Patel *et al*. (2014) Golam *et al.* (2015)	Panwar (2006)
Plant height (cm)	Basavaraja *et al.* (2011) Rajamadhan *et al*. (2011) Hasan *et al.* (2013) Rahman *et al*. (2014) Ratna *et al*. (2015)	Chandra *et al.* (2009) Babu *et al*. (2012) Patel *et al.* (2014) Golam *et al*. (2015)
No. of total tillers per plant	Patel *et al*. (2014) Golam *et al*. (2015)	
Panicle length (cm)	Rajamadhan *et al*. (2011) Gangashetty *et al*. (2013) Rahman *et al*. (2014) Golam *et al*. (2015)	Yadav *et al*. (2010) Babu *et al*. (2012) Patel *et al.* (2014) Ratna *et al.* (2015)
No. of total grains per panicle	Patel *et al.* (2014)	Yadav *et al.* (2010) Mishra *et al*. (2014)
No. of filled grains per panicle	Rajamadhan *et al*. (2011) Seyoum *et al*. (2012) Rahman *et al.* (2014) Ratna *et al.* (2015)	Panwar (2006) Babu *et al*. (2012) Golam *et al*. (2015)
No. of unfilled grains per panicle	Ratna *et al*. (2015) Golam *et al.* (2015)	Panwar (2006) Rahman *et al.* (2014)
Thousand grain weight (g)	Hasan *et al.* (2013) Rahman *et al*. (2014) Patel *et al.* (2014) Ratna *et al*. (2015)	Padmaja *et al*. (2011) Babu *et al*. (2012) Mishra *et al.* (2014) Golam *et al*. (2015)
Spikelet fertility	Panwar (2006) Hasan *et al*. (2013) Kumar and Verma (2015)	Mishra *et al*. (2014)

Character	Positive indirect effect	Negative indirect effect
Biomass per plant (cm)	Patel *et al.* (2014)	
Biological yield per plant (cm)	Panwar (2006)	Mishra *et al.* (2014) Kumar and Verma (2015)
Harvest index	Mishra *et al*. (2014) Patel *et al*. (2014)	Panwar (2006) Kumar and Verma (2015)
Per day productivity	Bhadru *et al.* (2012c)	

2.5.7. Indirect effects of panicle length on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Rajamadhan *et al*. (2011) Babu *et al*. (2012) Bhadru *et al*. (2012a) Ravi *et al.* (2014)	Hasan *et al*. (2013) Patel *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)
Days to maturity	Hasan *et al.* (2013) Dilruba *et al.* (2014) Patel *et al.* (2014) Ravi *et al*. (2014) Kumar and Verma (2015)	Golam *et al.* (2015)
Plant height (cm)	Rajamadhan *et al.* (2011) Bhadru *et al.* (2012a) Hasan *et al.* (2013) Dilruba *et al.* (2014) Rahman *et al*. (2014)	Yadav *et al*. (2010) Patel *et al.* (2014) Ravi *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)
No. of total tillers per plant	Patel *et al.* (2014) Ravi *et al.* (2014)	Golam *et al.* (2015)
No. of productive tillers per plant	Rajamadhan *et al*. (2011) Mohanty *et al*. (2012) Hasan *et al*. (2013) Reddy *et al*. (2013) Rahman *et al*. (2014)	Babu *et al*. (2012) Bhadru *et al.* (2012a) Patel *et al.* (2014) Golam *et al*. (2015) Ratna *et al.* (2015)

Character	Positive indirect effect	Negative indirect effect
Panicle weight (g)	Bhadru *et al.* (2011)	
No. of total grains per panicle	Yadav *et al.* (2010) Patel *et al.* (2014) Kumar and Verma (2015)	Kole *et al.* (2008) Pandey *et al.* (2012)
No. of Filled grains per panicle	Yadav *et al.* (2010) Rahman *et al.* (2014)	Reddy *et al.* (2013) Dilruba *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)
No. of unfilled grains per panicle	Panwar (2006) Rahman *et al.* (2014)	Golam *et al.* (2015) Ratna *et al.* (2015)
Thousand grain weight (g)	Padmaja *et al.* (2011) Babu *et al.* (2012) Hasan *et al.* (2013) Dilruba *et al.* (2014) Patel *et al.* (2014)	Bhadru *et al.* (2012a) Rahman *et al.* (2014) Ravi *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)
Spikelet fertility	Hasan *et al.* (2013) Kumar and Verma (2015)	
Sterility percentage	Dilruba *et al.* (2014)	
Biomass per plant (g)	Patel *et al.* (2014)	
Biological yield per plant (g)	Kumar and Verma (2015)	Panwar (2006)
Harvest index	Dilruba *et al.* (2014) Patel *et al.* (2014) Kumar and Verma (2015)	

2.5.8. Indirect effects of panicle weight on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Bhadru *et al.* (2011) Awaneet and Senapati	

	(2013)	
Days to maturity		Awaneet and Senapati (2013)
Plant height (cm)	Bhadru *et al*. (2011)	Awaneet and Senapati (2013)
Panicle length (cm)	Awaneet and Senapati (2013)	Bhadru *et al*. (2011)
No. of filled grains per panicle	Bhadru *et al*. (2011)	
Thousand grain weight (g)		Bhadru *et al*. (2011) Awaneet and Senapati (2013)
Spikelet fertility	Awaneet and Senapati (2013)	Bhadru *et al*. (2011)

2.5.9. Indirect effects of number of total grains per panicle on single plant grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to50 % flowering	Padmaja *et al*. (2011) Patel *et al.* (2014)	Rajamadhan *et al*. (2011) Bhadru *et al*.(2012a)
Days to maturity	Ganapati *et al*. (2014)	Patel *et al*. (2014) Kumar and Verma (2015)
Plant height (cm)	Akhtar *et al*.(2011) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011) Bhadru *et al*. (2012a) Ganapati *et al*. (2014)	Kole *et al*. (2008) Chandra *et al.* (2009) Patel *et al.* (2014) Naseer *et al.* (2015)
No. of total tillers per plant	Patel *et al.* (2014) Naseer *et al.* (2015)	
No. of productive tillers per plant	Akhtar *et al*.(2011) Rajamadhan *et al.* (2011) Bhadru *et al*. (2012a)	Chandra *et al.* (2009) Padmaja *et al*. (2011) Patel *et al.* (2014) Kumar and Verma (2015)

Character	Positive indirect effect	Negative indirect effect
Panicle length (cm)	Chandra *et al.* (2009) Padmaja *et al*. (2011) Rajamadhan *et al*. (2011)	Bhadru *et al.* (2012a) Ganapati *et al*. (2014) Patel *et al.* (2014) Kumar and Verma (2015)
No. of filled grains per panicle	Ganapati *et al.* (2014)	
No. of unfilled grains per panicle	Ganapati *et al*. (2014)	
Thousand grain weight (g)	Rajamadhan *et al*. (2011) Bhadru *et al*. (2012a) Patel *et al.* (2014) Naseer *et al.* (2015)	Kole *et al.* (2008) Mishra *et al.* (2014)
Spikelet fertility		Mishra *et al.* (2014) Naseer *et al.* (2015)
Biomass per plant (g)	Patel *et al*. (2014)	
Biological yield per plant (g)	Mishra *et al.* (2014)	
Harvest index	Mishra *et al.* (2014) Patel *et al.* (2014)	Ganapati *et al.* (2014) Kumar and Verma (2015)

2.5.10. Indirect effects of number of filled grains per panicle on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering Days to 50 % flowering	Padmaja *et al*. (2011) Kiani and Nematzadeh (2012) Mamun *et al.* (2012) Seyoum *et al*. (2012)	Nayak *et al.* (2001) Panwar (2006) Bhadru *et al*. (2012a) Golam *et al.* (2015)

	Eidi kohanaki *et al*. (2013) Ratna *et al*. (2015)	
Days to maturity	Panwar (2006) Ganapati *et al*. (2014) Golam *et al.* (2015)	Dilruba *et al.* (2014)
Plant height (cm)	Akhtar *et al.* (2011) Padmaja *et al*. (2011) Bhadru *et al.* (2012a) Ganapati *et al*. (2014) Golam *et al.* (2015) Ratna *et al.* (2015)	Kole *et al*. (2008) Chandra *et al.* (2009) Dilruba *et al.* (2014) Rahman *et al.* (2014)
No. of total tillers per plant		Golam *et al.* (2015)
No. of productive tillers per plant	Akhtar *et al.* (2011) Rahman *et al*. (2014) Ratna *et al.* (2015)	Madhavilatha (2002) Chandra *et al.* (2009) Padmaja *et al.* (2011) Golam *et al.* (2015)
Panicle length (cm)	Padmaja *et al*. (2011) Dilruba *et al.* (2014) Rahman *et al.* (2014)	Bhadru *et al*. (2012a) Ganapati *et al.* (2014) Golam *et al.* (2015) Ratna *et al.* (2015)
Panicle weight	Bhadru *et al.* (2011)	
No. of unfilled grains per panicle	Panwar (2006) Ganapati *et al*. (2014) Rahman *et al.* (2014) Ratna *et al*. (2015)	Mamun *et al.* (2012) Golam *et al.* (2015)
Thousand grain weight (g)	Akhtar *et al.*(2011) Padmaja *et al*. (2011) Rahman *et al*. (2014)	Dilruba *et al.* (2014) Ganapati *et al.* (2014) Rantna *et al.* (2015) Golam *et al.* (2015)
Spikelet fertility	Panwar (2006)	
Sterility percentage	Mamun *et al*. (2012)	Dilruba *et al*. (2014)
Biological yield per plant		Panwar (2006)

(g)		
Harvest index	Panwar (2006) Dilruba *et al*. (2014)	Ganapati *et al.* (2014)
Productivity per day		Bhadru *et al.* (2012c)

2.5.11. Indirect effects of number of unfilled grains per panicle on single plant grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering	Golam *et al.* (2015) Ratna *et al*. (2015)	Panwar (2006) Mamun *et al*. (2012)
Days to maturity	Panwar (2006) Ganapati *et al.* (2014) Golam *et al.* (2015)	
Plant height (cm)	Panwar (2006) Ganapati *et al.* (2014) Golam *et al.* (2015)	Rahman *et al.* (2014) Ratna *et al*. (2015)
No. of total tillers per plant	Golam *et al.* (2015)	
No. of productive tillers per plant	Rahman *et al*. (2014)	Panwar (2006) Golam *et al.* (2015) Ratna *et al*. (2015)
Panicle length (cm)	Panwar (2006) Rahman *et al.* (2014) Ratna *et al.* (2015)	Ganapati *et al*. (2014) Golam *et al.* (2015)
No. of total grains per panicle		Ganapati *et al.* (2014)
No. of filled grains per panicle	Golam *et al*. (2015)	Mamun *et al.* (2012) Ganapati *et al*. (2014) Rahman *et al*. (2014) Ratna *et al*. (2015)
Thousand grain weight (g)	Ratna *et al*. (2015)	Panwar (2006) Ganapati *et al*. (2014) Rahman *et al*. (2014)

		Golam *et al.* (2015)
Spikelet fertility		Panwar (2006)
Sterility percentage	Mamun *et al.* (2012)	
Biological yield per plant (g0		Panwar (2006)
Harvest index	Panwar (2006)	Ganapati *et al.* (2014)

2.5.12. Indirect effects of thousand grain weight on single plant grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 % flowering	Chandra *et al.* (2009) Yadav *et al*. (2012) Kumar and Verma *et al.* (2015)	Babu *et al*. (2012) Bhadru *et al*. (2012a) Hasan *et al.* (2013) Patel *et al.* (2014) Ratna *et al*. (2015) Golam *et al.* (2015)
Days to maturity	Hasan *et al.* (2013) Dilruba *et al*. (2014) Patel *et al.* (2014) Golam *et al*. (2015)	Panwar (2006)
Plant height (cm)	Hasan *et al.* (2013) Dilruba *et al.* (2014) Rahman *et al*. (2014) Ratna *et al*. (2015) Golam *et al*. (2015)	Yadav *et al.* (2010) Padmaja *et al*. (2011) Bhadru *et al*. (2012a) Patel *et al.* (2014) Naseer *et al.* (2015)
No. of total tillers per plant	Patel *et al.* (2014) Naseer *et al.* (2015)	Golam *et al*. (2015)
No. of productive tillers per plant	Bhadru *et al*. (2012a) Rahman *et al*. (2014) Patel *et al.* (2014) Ratna *et al.* (2015)	Padmaja *et al*. (2011) Babu *et al*. (2012) Hasan *et al.* (2013) Golam *et al*. (2015)
Panicle length (cm)	Padmaja *et al*. (2011)	Hasan *et al.* (2013)

	Rajamadhan *et al*. (2011) Rahman *et al*. (2014) Kumar and Verma (2015)	Dilruba *et al.* (2014) Patel *et al.* (2014) Golam *et al.* (2015) Ratna *et al*. (2015)
Panicle weight (g)	Bhadru *et al*. (2011)	
No. of total grains per panicle	Naseer *et al.* (2015)	Yadav *et. al*. (2010) Bhadru *et.al*. (2012a) Patel *et al*. (2014) Kumar and Verma (2015)
No. of filled grains per panicle	Chandra *et al.* (2009) Padmaja *et al*. (2011) Yadav *et al*. (2012)	Rajamadhan *et al*. (2011) Dilruba *et al.* (2014) Rahman *et al*. (2014) Ratna *et al*. (2015) Golam *et al*. (2015)
No. of unfilled grains per panicle	Rahman *et al*. (2014) Golam *et al.* (2015)	Panwar (2006) Ratna *et al*. (2015)
Spikelet fertility	Bhadru *et al.* (2011) Hasan *et al.* (2013) Kumar and Verma (2015)	Panwar (2006) Naseer *et al.* (2015)
Sterility percentage	Dilruba *et al*. (2014)	
Biomass per plant (g)	Patel *et al.* (2014)	
Biological yield per plant (g)	Panwar (2006) Mishra *et al.* (2014)	
Harvest index	Patel *et al.* (2014)	Panwar (2006) Dilruba *et al.* (2014) Mishra *et al.* (2014)

2.5.13. Indirect effects of spikelet fertility on single plant grain yield through

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering	Panwar (2006) Kumar and Verma (2015)	Bhadru *et al*. (2011) Hasan *et al*. (2013)
Days to maturity	Panwar (2006) Hasan *et al*. (2013) Kumar and Verma (2015)	
Plant height (cm)	Panwar (2006) Hasan *et al*. (2013) Naseer *et al.* (2015)	Bhadru *et al*. (2011)
No. of total tillers per plant		Naseer *et al.* (2015)
No. of productive tillers per plant	Panwar (2006) Kumar and Verma (2015)	Bhadru *et al*. (2011) Hasan *et al*. (2013)
Panicle length (cm)	Kumar and Verma (2015)	Bhadru *et al*. (2011) Hasan *et al*. (2013)
Panicle weight (g)	Bhadru *et al*. (2011)	
No of total grains per panicle	Naseer *et al*. (2015)	
No. of filled grains per panicle		Panwar (2006)
No. of unfilled grains per panicle		Panwar (2006)
Thousand grain weight (g)	Bhadru *et al*. (2011) Hasan *et al*. (2013) Naseer *et al*. (2015)	Panwar (2006) Mishra *et al*. (2014)
Biological yield per plant (g)	Panwar (2006) Mishra *et al.* (2014)	Kumar and Verma (2015)
Harvest index	Mishra *et al*. (2014)	Panwar (2006) Kumar and Verma (2015)

2.5.14. Indirect effects of sterility percentage on single plant grain yield through:

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering	Mamun *et al.* (2012)	
Days to maturity		Dilruba *et al.* (2014)
Plant height (cm)	Dilruba *et al*. (2014)	
Panicle length (cm)	Dilruba *et al*. (2014)	
No. of filled grains per panicle	Mamun *et al.* (2012) Dilruba *et al.* (2014)	
No. of unfilled grains per panicle		Mamun *et al*. (2012)
Thousand grain weight (g)		Dilruba *et al*. (2014)
Biomass per plant (g)	Krantikumar *et al*. (2016)	
Biological yield per plant (g)		Krantikumar *et al.* (2016)
Harvest index		Dilruba *et al.* (2014) Krantikumar *et al.* (2016)

2.5.15. Indirect effects of Biomass per plant on single plant grain yield through:

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering		Patel *et al*. (2014)
Days to maturity	Patel *et al*. (2014)	
Plant height (cm)		Patel *et al*. (2014)
No. of total tillers per plant	Patel *et al*. (2014)	
No. of productive tillers per plant		Patel *et al*. (2014)
Panicle length (cm)		Patel *et al*. (2014)
No. of total grains per panicle	Patel *et al.* (2014)	
Thousand grain weight (g)		Patel *et al*. (2014)

Sterility percentage	Krantikumar *et al.* (2016)	
Biological yield per plant (g)	Krantikumar *et al.* (2016)	
Harvest index		Patel *et al.* (2014) Krantikumar *et al.* (2016)

2.5.16. Indirect effects of biological yield per plant on single plant grain yield through:

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering	Panwar (2006)	Kumar and Verma (2015)
Days to maturity		Panwar (2006) Kumar and Verma (2015)
Plant height (cm)	Kumar and Verma (2015)	Panwar (2006)
No. of productive tillers per plant	Panwar (2006)	
Panicle length (cm)	Kumar and Verma (2015)	Panwar (2006)
No. of total grains per panicle	Kumar and Verma (2015)	
No. of filled grains per panicle	Panwar (2006)	
No. of unfilled grains per panicle		Panwar (2006)
Thousand grain weight (g)	Panwar (2006) Kumar and Verma (2015)	
Spikelet fertility	Panwar (2006)	

	Kumar and Verma (2015)	
Sterility percentage	Krantikumar *et al.* (2016)	
Biomass per plant (g)		Krantikumar *et al.* (2016)
Harvest index	Kumar and Verma (2015)	Panwar (2006) Mishra *et al.* (2014)

2.5.17. Indirect effects of harvest index on single plant grain yield through:

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering	Patel *et al.* (2014)	Panwar (2006) Kumar and Verma (2015)
Days to maturity	Panwar (2006) Kumar and Verma (2015)	Dilruba *et al.* (2014) Ganapati *et al.* (2014) Patel *et al.* (2014)
Plant height (cm)	Patel *et al.* (2014)	Dilruba *et al.* (2014) Ganapati *et al.* (2014) Kumar and Verma (2015)
No of total tillers per plant		Patel *et al.* (2014)
No. of productive tillers per plant	Kumar and Verma (2015)	Patel *et al.* (2014)
Panicle length (cm)	Panwar (2006) Ganapati *et al.* (2014)	Dilruba *et al.* (2014) Patel *et al.* (2014)
No. of total grains per panicle	Ganapati *et al.* (2014) Patel *et al.* (2014)	Kumar and Verma (2015)
No. of filled grains per panicle		Dilruba *et al.* (2014) Ganapati *et al.* (2014)
No. of unfilled grains per panicle	Panwar (2006)	Ganapati *et al.* (2014)
Thousand grain weight (g)	Dilruba *et al.* (2014)	Patel *et al.* (2014) Kumar and Verma (2015)
Spikelet fertility	Kumar and Verma (2015)	Panwar (2006)
Sterility percentage	Dilruba *et al.* (2014)	
Biomass per plant (g)		Patel *et al.* (2014)

Biological yield per plant (g)	Panwar (2006)	

2.5.18. Indirect effects of per day productivity on single plant grain yield through:

Character	**Positive indirect effect**	**Negative indirect effect**
Days to 50 % flowering		Bhadru *et al*. (2012c)
Panicle length (cm)		Bhadru *et al*. (2012c)
No. of filled grains per panicle		Bhadru *et al*. (2012c)
Spikelet fertility		Bhadru *et al*. (2012c)

2.6. GENOTYPING AND HAPLOTYPING FOR EARLINESS USING SSRs

Heading date (HD) or flowering time is one of the key factors determining regional and seasonal adaptation and has been a major target of selection in rice breeding programs (Endo-Higashi and Izawa, 2011). In rice HD is a complex trait which is governed by multiple genes and regulated by environmental factors, such as day length, temperature, and soil conditions. Reducing the duration for days to heading in high yielding varieties, is a strategy in development of superior early varieties. Depending on conventional breeding for early flowering is slow in reaching progress due to poor understanding of genetic control of early flowering date. Molecular marker technology is the powerful tool for determining genetic variation in rice varieties.

Molecular markers helps in identification of marker(s) associated with heading date trait and indirect selection using marker assisted selection (Khatab *et al.*, 2016). The DNA-based molecular markers are universal, repeatable, stable and highly consistent (Song *et al.*, 2003). Among the several classes of available DNA markers, microsatellite or simple sequence repeat (SSR) markers are considered the most suitable due to their multi allelic nature, high reproducibility, co dominant inheritance, abundance and extensive genome coverage.

Khatab *et al.* (2016) carried out studies on genetic diversity associated with heading date in some rice (*Oryza sativa* L.) genotypes using microsatellite markers.

The overall results showed that some markers could be discriminated earlier heading than the late heading and these markers could be associated with heading date.

Table 2.6. List of markers showed variation in present study along with QTL or trait linked.

Marker	**Chromosome number**	**QTL linked**	**Trait linked**	**Reference**
RM84	1	qGPL1 qPPN-1-1 qGNP-1-1 qPH1-1	Grains per plant Productive panicle no Grain no per plant Plant height	Tian *et al.* (2006) Jing *et al.* (2010) Jing *et al.* (2010) Subudhi *et al.* (2015)
RM246	1	- Qph1.1 qGP-1 qPH-1	1000 grain weight Plant height No of filled grains/panicle Plant height	Cheema *et al.* (2008) Lin *et al.* (2011) Rabiei *et al.* (2015) Rabiei *et al.* (2015)
RM302	1	qDFF1.1 QPH-1.2	Days to 50% flowering Plant height	Balram *et al.* (2012) Shen *et al.* (2014b)
RM53	2	qPh2a -	Plant height Heading date	Tong *et al.* (2006) Xu *et al.* (2015)
RM263	2	Yldp2.2 Yld2.1 qDTF2.2 qDTY2.2 qDTY2.	Yield per plant Plot yield Days to flowering Grain yield Grain yield	Reddy *et al.* (2005) Reddy *et al.* (2005) Sandhu *et al.* (2014) Sandhu *et al.* (2014) Sandhu *et al.* (2014)
RM318	2	qtgw2 -	1000 grain weight Pollen fertility	Bai *et al.* (2011) Baliuag *et al.* (2015)
RM6	2	Tn2.2 QHD2	Tiller no Heading date	Liu *et al.* (2012) Shen and Xing (2014a)
RM48	2	qPh2b	Plant height	Tong *et al.* (2006)

RM22	3	qTINB-3 ST-3 Qhd3 Tn3.3 DH3	Tiller no per plant Sterility percentage Heading date Tiller no Heading date	Gutierrez *et al.* (2010) Gutierrez *et al.* (2010) Lin *et al.* (2011) Liu *et al.* (2012) Eizenga *et al.* (2013)
RM218	3	qPLT3-1 qgl3 qgs3.3 -	Panicle length Grain length Grain shape Heading date	Hittalmani *et al.* (2003) Seo *et al.* (2014) Seo *et al.* (2014) Xu *et al.* (2015)
RM168	3	qPHt3.3 qPL3.5 qYLD3.1 qSPP3.3 qTGW3.5 Tn3.2 -	Plant height Panicle length Yield per plant Spikelet's per plant 1000 grain weight Tiller no Pollen fertility	Balram *et al.* (2012) Balram *et al.* (2012) Balram *et al.* (2012) Balram *et al.* (2012) Balram *et al.* (2012) Liu *et al.* (2012) Baliuag *et al.* (2015)
RM307	4	dth4.1 qFLW4-1	Days to heading Flag leaf width	Thomson *et al.* (2003) Balram *et al.* (2012)
RM261	4	qPn4b - YLD-4 TGRWT-4	Panicle no per plant Grain yield Yield 1000 grain weight	Tong *et al.* (2006) Agrama *et al.* (2007) Gutierrez *et al.* (2010) Gutierrez *et al.* (2010)
RM273	4	qPP4-1 qSSD4-1	Panicles per plant Spikelet setting density	Balram *et al.* (2012) Balram *et al.* (2012)
RM241	4	Qpl4a gw4 qFGP4-1	Panicle length Grain width Filled grains per panicle	Ahamadi *et al.* (2008) Kwon *et al.* (2008) Balram *et al.* (2012)
RM153	5	pl5 pss5.1 -	Panicle length Percent seed set Spikelet fertility	Kwon *et al.* (2008) Thomson *et al.* (2003) Baliuag *et al.* (2015)
RM164	5	qpl5.1 qGW5 qGL5	Panicle length Grain width Grain length	Reddy *et al.* (2005) Bian *et al.* (2010) Subudhi *et al.* (2015)

		qTGW	1000 grain weight	Subudhi *et al.* (2015)
RM163	5	QS5	Panicle grain sterility	Ahamadi *et al.* (2008)
RM1369	6	qDH6	Heading date	Kobayashi *et al.* (2013)
RM1370	6	- - Hd6 -	Panicle no / meter square Spikelet's no / panicle Heading date Seed shattering	Takai *et al.* (2014) Takai *et al.* (2014) Hori *et al.* (2015) Subudhi *et al.* (2015)
RM30	6	qyd6 - Qph6.1	Yield per plant Grain yield Plant height	Tong *et al.* (2006) Rangel *et al.* (2008) Lin *et al.* (2011)
RM340	6	Qph6.2 - TGW6	Plant height 1000 grain weight 1000 grain weight	Lin *et al.* (2011) Venu *et al.* (2014) Xu *et al.* (2015)
RM248	7	qPh7a - qHD7.2 QHD7.3 QPH7.3	Plant height Grain yield Heading date Heading date Plant height	Tong *et al.* (2006) Rangel *et al.* (2008) Lee *et al.* (2013) Shen *et al.* (2014b) Shen *et al.* (2014b)
RM11	7	qFG7 qYP7 Qhd7 qHD7	Filled grains per panicle Yield per plant Heading date Heading date	Tian *et al.* (2006) Tian *et al.* (2006) Lin *et al.* (2011) Pinson *et al.* (2012)
RM234	7	qPh7b hd7 - qPH7.9	Plant height Heading date Heading date Plant height	Tong *et al.* (2006) Rabiei (2007) Yoo *et al.* (2007) Rabiei *et al.* (2015)
RM25	8	Se8 hd8 qDFF-8.1 qPHT-8.1 LH8	Heading date Heading date Days to 50 % flowering Plant height Heading date	Gu and Foley (2007) Rabiei (2007) Balram *et al.* (2012) Balram *et al.* (2012) Chen *et al.* (2014)
RM210	8	Yld8.1 -	Plot yield Grain yield	Reddy *et al.* (2005) Rangel *et al.* (2008)

		qGL8 Tn8	Grain length Tiller no	Bian *et al.* (2010) Liu *et al.* (2012)
RM264	8	qph8 qspp8 qtgw QHD8	Plant height Spikelet's per panicle 1000 grain weight Heading date	Bai *et al.* (2011) Bai *et al.* (2011) Bai *et al.* (2011) Shen *et al.* (2014b)
RM257	9	qHDD9 qph9.1	Heading date Plant height	Hittalmani *et al.* (2003) Reddy *et al.* (2005)
RM205	9	pl9.1 gw9.2 Yldp9.1	Panicle length Grain weight Yield per plant	Reddy *et al.* (2005) Reddy *et al.(*2005) Reddy *et al.* (2005)
RM311	10	pl10.1 gw10.1 -	Panicle length Grain weight Panicle no per plant	Thomson *et al.* (2003) Thomson *et al.* (2003) Zhang *et al.* (2014)
RM224	11	qTGW11.2 - -	1000 grain weight Heading date Heading date Seed shattering	Bian *et al.* (2010) Venu *et al.* (2014) Zhang *et al.* (2014) Subudhi *et al.* (2015)
RM202	11	qSSP-11-1 -	Seed set percentage Heading date	Jing *et al.* (2010) Yasui *et al.* (2010)
RM209	11	dth11.1 qhd11 qGN-11-2 qGWt11-2 -	Heading date Heading date Grain no per panicle 1000 grain weight Heading date	Septiningsih *et al.* (2003) Bai *et al.* (2011) Jing *et al.* (2010) Jing *et al.* (2010) Yasui *et al.* (2010)
RM206	11	QPl11.1b QS11 qSSD-11-1 qPSTE11-1 qPh11.2 - -	Panicle length Panicle grain sterility Spikelet setting density Percent sterility Plant height 1000 grain weight Seed shattering	Ahamadi *et al.* (2008) Ahamadi *et al.* (2008) Balram *et al.* (2012) Balram *et al.* (2012) Anuradha *et al.* (2013) Zhang *et al.* (2014) Subudhi *et al.* (2015)
RM19	12	qYd12 -	Yield per plant Grain width	Tong *et al.* (2006) Zhang *et al.* (2014)

		qSF12.2	Spikelet fertility	Vemireddy *et al.* (2015)
RM247	12	qYd12 -	Yield Heading date	Tong *et al.* (2006) Yasui *et al.* (2010)
RM270	12	qPn12 qPh12a qPH12	Grain no per plant Plant height Plant height	Tong *et al.* (2006) Tong *et al.* (2006) Eizenga *et al.* (2013)
RM101	12	qGL -	Grain length Panicle length	Yan *et al.* (2003) Susanto *et al.* (2008)

MATERIAL AND METHODS

Chapter III

MATERIAL AND METHODS

The present investigation on "Genetic analysis and haplotyping for earliness and yield traits in rice (*Oryza sativa* L.) using SSR markers" was undertaken to screen for early lines and study the stability of rice genotypes under three environments and also to identify stable early high yielding genotypes suitable for both *Kharif* and *Rabi* seasons of Telangana region. The material utilized and the methodologies adopted in the investigation to achieve the desired objectives are described under following major heads.

3.1 Screening for early lines and studies on stability

3.2 Statistical analysis

3.3 Genotyping and haplotyping for earliness

3.1. SCREENING FOR EARLY LINES AND STUDIES ON STABILITY

3.1.1. EXPERIMENTAL MATERIAL

The experimental material comprised of 83 lines and one check variety Prasanna (Early variety) obtained from the Crop Improvement Section, Indian Institute of Rice Research, Rajendranagar, Hyderabad. In the present study all 84 lines were used for genotyping but only 59 lines were used for phenotyping. The Details of genotypes are furnished in the Table 3.1.1.

Table 3.1.1. Details of 84 genotypes of rice

S.No	Name of the genotype	Source
1	*130 K	Indian Institute of Rice Research, Hyderabad
2	*14 – 3	Indian Institute of Rice Research, Hyderabad
3	*14 S	Indian Institute of Rice Research, Hyderabad
4	148 – 2	Indian Institute of Rice Research, Hyderabad
5	148 S	Indian Institute of Rice Research, Hyderabad
6	*148 S	Indian Institute of Rice Research, Hyderabad
7	166 – 2	Indian Institute of Rice Research, Hyderabad
8	166 - 2 – 10	Indian Institute of Rice Research, Hyderabad
9	*166 - 2 - 11	Indian Institute of Rice Research, Hyderabad
10	166 - 2 – 2	Indian Institute of Rice Research, Hyderabad

11	*166 - 2 – 3	Indian Institute of Rice Research, Hyderabad
12	166 - 2 – 4	Indian Institute of Rice Research, Hyderabad
13	166 - 2 – 5	Indian Institute of Rice Research, Hyderabad
14	*166 - 2 – 9	Indian Institute of Rice Research, Hyderabad
15	*166 – 23	Indian Institute of Rice Research, Hyderabad
16	*166 - 23 – 1	Indian Institute of Rice Research, Hyderabad
17	*166 – 30	Indian Institute of Rice Research, Hyderabad
18	*166 – 9	Indian Institute of Rice Research, Hyderabad
19	*166 S	Indian Institute of Rice Research, Hyderabad
20	*166-1	Indian Institute of Rice Research, Hyderabad
21	*220 S	Indian Institute of Rice Research, Hyderabad
22	*246 K	Indian Institute of Rice Research, Hyderabad
23	248 S 1	Indian Institute of Rice Research, Hyderabad
24	248 S	Indian Institute of Rice Research, Hyderabad
25	250 K	Indian Institute of Rice Research, Hyderabad
26	*258 S	Indian Institute of Rice Research, Hyderabad
27	*263 K	Indian Institute of Rice Research, Hyderabad
28	*27 K	Indian Institute of Rice Research, Hyderabad
29	3 – 1 K	Indian Institute of Rice Research, Hyderabad
30	*35 B	Indian Institute of Rice Research, Hyderabad
31	*51 B	Indian Institute of Rice Research, Hyderabad
32	65 S	Indian Institute of Rice Research, Hyderabad
33	7 K	Indian Institute of Rice Research, Hyderabad
34	70 S	Indian Institute of Rice Research, Hyderabad
35	*75 S	Indian Institute of Rice Research, Hyderabad
36	*93 B	Indian Institute of Rice Research, Hyderabad
37	*95 B	Indian Institute of Rice Research, Hyderabad
38	*Aditya	Indian Institute of Rice Research, Hyderabad
39	*ADT 43	Tamil Nadu Agricutural University, Coimbatore
40	*Anjali	Central Rice Research Institute, Cuttack
41	*Govindu	Govind Ballabh Pant University of Agriculture and Technology, Pantnagar
42	*IR 64	International Rice Research Institute, Philippines
43	*Jaldidhan	Indian Agricultural Research Institute, New delhi
44	*Jaya	Indian Institute of Rice Research, Hyderabad
45	*MTU1010	Andhra Pradesh Rice Research Institute, Maruteru
46	*Nagina 22	International Rice Research Institute, Philippines
47	Neela	Central Rice Research Institute, Cuttack
48	NL B	Indian Institute of Rice Research, Hyderabad
49	Pooja	Central Rice Research Institute, Cuttack
50	*Rasi	Indian Institute of Rice Research, Hyderabad
51	*Sabhagidhan	International Rice Research Institute, Philippines
52	*SM 1637	Indian Institute of Rice Research, Hyderabad
53	*SM 1876	Indian Institute of Rice Research, Hyderabad
54	*SM 219	Indian Institute of Rice Research, Hyderabad
55	*SM 349	Indian Institute of Rice Research, Hyderabad
56	SM 359	Indian Institute of Rice Research, Hyderabad

57	*SM 363	Indian Institute of Rice Research, Hyderabad
58	*SM 4014	Indian Institute of Rice Research, Hyderabad
59	*SM 4029	Indian Institute of Rice Research, Hyderabad
60	*SM 4071	Indian Institute of Rice Research, Hyderabad
61	*SM 4076	Indian Institute of Rice Research, Hyderabad
62	*SM 4078	Indian Institute of Rice Research, Hyderabad
63	*SM 4193	Indian Institute of Rice Research, Hyderabad
64	*SM 4226	Indian Institute of Rice Research, Hyderabad
65	SM 4230	Indian Institute of Rice Research, Hyderabad
66	*SM 4231	Indian Institute of Rice Research, Hyderabad
67	*SM 4371	Indian Institute of Rice Research, Hyderabad
68	*SM 4385	Indian Institute of Rice Research, Hyderabad
69	*SM 4406	Indian Institute of Rice Research, Hyderabad
70	*SM 4415	Indian Institute of Rice Research, Hyderabad
71	*SM 686	Indian Institute of Rice Research, Hyderabad
72	*SM 733	Indian Institute of Rice Research, Hyderabad
73	*SM 776	Indian Institute of Rice Research, Hyderabad
74	SM4244	Indian Institute of Rice Research, Hyderabad
75	*Sona	Indian Institute of Rice Research, Hyderabad
76	Swarna	Andhra Pradesh Rice Research Institute, Maruteru
77	*Tellahamsa	Agricultural Research Institute, Hyderabad
78	*Tulasi	Indian Institute of Rice Research, Hyderabad
79	Vandana	Central Rice Research Institute, Cuttack
80	*Varalu	Regional Agricultural Research Station, Warangal
81	WGL 14	Regional Agricultural Research Station, Warangal
82	WGL 505	Regional Agricultural Research Station, Warangal
83	WGL 915	Regional Agricultural Research Station, Warangal
	Check	
84	*Prasanna	Indian Institute of Rice Research, Hyderabad

Note: Star marked genotypes were used only for phenotyping.

3.1.2. EXPERIMENTAL TECHNIQUE

The present investigation was carried out under three environments during *Rabi* 2014-15, *Kharif* 2015 and *Rabi* 2015-16 at Indian Institute of Rice Research Farm, Hyderabad, India.

3.1.3. EXPERIMENTAL DESIGN

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was sown separately in raised nursery beds under three environments following uniform package of practices.

Thirty days old seedlings were transplanted following a spacing of 15 x 20 cm for each entry. All the recommended package of practices was adopted besides providing necessary prophylactic plant protection measures to raise a healthy crop under three environments.

3.1.4. RECORDING OF OBSERVATIONS

Observations were recorded for yield and yield attributing characters on five randomly selected plants for each entry in each replication, while the data on days to 50% flowering and days to maturity were noted on plot basis. The mean data obtained at each environment was considered for final statistical analysis. The method of recording data for each trait is described below character wise.

3.1.4.1. Days to 50% flowering (DFF)

The total number of days from the date of sowing to complete exertion of the panicle tip above the sheath of the flag leaf in 50 per cent of the total plants in the net plot.

3.1.4.2. Days to maturity (DM)

The number of days from sowing to grain ripening (85% of grains on panicle are mature).

3.1.4.3. Plant height (PH)

The plant height was recorded by measuring the total height from the base of the plant to the tip of the main panicle at the time of harvest and excluding awn if present and is expressed in centimeters (cm).

3.1.4.4. Number of tillers per plant (TN)

It was recorded as total no of panicles per plant at the time of maturity

3.1.4.5. Number of productive tillers per plant (PTN)

The number of ear bearing tillers, which produced healthy panicles were counted on each plant at the time of maturity.

3.1.4.6. Panicle length (PL)

The length of panicles from each plant was measured in centimeters from neck node to the tip of top most grain in a panicle and is expressed in centimeters (cm)

3.1.4.7. Panicle weight (PW)

It was recorded as single panicle weight of main tiller and is expressed in grams

3.1.4.8. Number of filled grains per panicle (FG)

The number of well filled grains were counted in each selected panicle per plant and expressed as filled grains per panicle.

3.1.4.9. Number of unfilled grains per panicle (UFG)

The number of unfilled grains were counted in each selected panicle per plant and expressed as unfilled grains per panicle.

3.1.4.10. Number of total grains per panicle (TG)

It was recorded as sum total of threshed filled grains and unfilled grains in each selected panicle per plant and expressed as total number of grains per panicle.

3.1.4.11. Spikelet fertility (SF)

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

3.1.4.12. Sterility percentage (SP)

Per cent sterility was calculated as the ratio of un-filled grains per panicle to the total number of grains in a panicle and expressed in percentage.

3.1.4.13. Thousand grain weight (TGW)

One thousand well filled grains were counted from a random sample of each entry in each replication and weighed with the help of electronic top pan balance in grams.

3.1.4.14. Single plant grain yield (SPY)

Panicles from a single plant were harvested at maturity, threshed, cleaned and sun dried to 12 per cent moisture content and the weight was recorded in grams.

3.1.4.15. Biomass per plant (BM)

It was recorded as dried straw yield per each plant and expressed in grams.

3.1.4.16. Biological yield per plant (BY)

It was recorded as sum of grain yield per plant and biomass per plant and expressed in grams.

3.1.4.17. Harvest index (HI)

Harvest index per plant was calculated as the ratio of grain yield per plant to the biological yield per plant and expressed in percentage.

3.1.4.18. Per day Productivity (PP)

Per day productivity was calculated as the ratio of grain yield per plant to the days to maturity of plant and expressed in grams.

3.2. STATISTICAL ANALYSIS

The data recorded on different traits were subjected to the following statistical analysis.

1. Analysis of variance
2. Genotypic and phenotypic coefficients of variation
3. Heritability and genetic advance
4. Stability Analysis
5. Estimation of correlation coefficients
6. Direct and indirect effects of characters using Path coefficient analysis.

3.2.1. Analysis of Variance

3.2.1.1. Analysis in Randomized Complete Block Design (RCBD)

The adopted design was Randomized Complete Block Design (RCBD) replicated thrice. The analysis of variance was carried out as per the method outlined by Panse and Sukhatme (1985).

$Y_{ij} = m + g_i + r_j + e_{ij}$

Where,

Y_{ij} = Phenotypic observation of i^{th} genotype in j^{th} replication

m = General mean

g_i = True effect of i^{th} genotype

r_j = True effect of j^{th} replication

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

Analysis of variance (ANOVA) was carried out for each character as indicated below:

Source of variation	d.f.	SS	MSS	F-ratio
Replications	r-1	RSS	M'r	M'r/M'e
Treatments	t-1	TSS	M't	M't/M'e
Error	(r-1) (t-1)	ESS	M'e	
Total	rt-1			

Where,

r = Number of replications

t = Number of treatments (genotypes)

M'r = Mean sum of squares of replications

M't = Mean sum of squares of treatments

M'e = Mean sum of squares of error

d.f = Degrees of freedom

MSS = Mean sum of squares

The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using ‘F’ test (Fisher and Yates, 1967).

SE(m) = $(Me/r)^{1/2}$

Where,

Me = Error mean of squares

r = Number of replications

C.D = S.E (d) x‘t’

Where,

S.E (d) = $(2Me/r)^{1/2}$

‘t’ = t Table value at error degrees of freedom

C.V = (S.D/ $\overline{X}$) x 100

Where,

S.D = Standard deviation of the population ,

X = Population mean

Mean

The mean value of each character was determined by taking sum of all the observations and dividing them by corresponding number of observations.

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

Where,

$\overline{X}$ = mean,

$\sum_{i=1}^{N} X_i$ = Sum of all observations

N = Number of observations

Range

The lowest and highest means values for each character were taken as the range.

Standard Error of Difference between Two Means [SE.d.(m)]

SE.d.(m) was calculated with the help of error mean square from ANOVA table.

$$S.E.d.(M) = \sqrt{\frac{2M.S.E.}{r}}$$

Where,

r = Number of replications, MSE = Mean sum of square due to error

3.2.1.2. Variance

The genotypic and phenotypic variances were calculated as per the formulae (Burton and Devane, 1953).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{(\text{TMSS} - \text{EMSS})}{\text{Number of replications}}$$

Where,

TMSS = Treatment mean sum of squares,

EMSS = Error mean sum of squares

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

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

3.2.2. Genotypic and Phenotypic Coefficients of Variance

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

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

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

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

< 10%	:	Low
10-20%	:	Moderate
> 20%	:	High

3.2.3. Heritability and Genetic Advance

Heritability

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

$$h^2_{(bs)} = \frac{\sigma^2 g}{\sigma^2 p}$$

Where,

h^2	=	heritability in broad sense
$\sigma^2 g$	=	genotypic variance
$\sigma^2 p$	=	phenotypic variance ($\sigma^2 g + \sigma^2 e$)
$\sigma^2 e$	=	environmental variance

As suggested by Johnson *et al.* (1955) (h^2) estimates were categorized as:

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

Genetic Advance (Expected)

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

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

Where,

GA = expected genetic advance

K = Selection differential, the value of which is 2.06 at 5 per cent selection intensity

σp = phenotypic standard deviation

h^2 (b) = heritability in broad sense

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

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

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

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

3.2.4. Stability Analysis

3.2.4.1. Methods to Measure Stable Performance of Genotypes:

Analysis of variance of genotypic mean was computed for each agronomic variable in each season. The data were as pooled over seasons to carry out AMMI stability analysis of variance to identify stable genotypes across all the three seasons.

The AMMI model (Gauch and Zobel, 1988) was used in analyzing the stability and interaction for yield traits. The results of the AMMI model analysis are interpreted on the basis of AMMI1 biplot where the graph is plotted with the main effect and first multiplicative axis term (PC1) for both genotypes and environments and are useful in supporting breeding program decisions such as specific adaptation and selection of environments (Gauch and Zobel, 1997; Ebdon and Gauch, 2002). Greater the Principal Component Axis (PC1) scores, either negative or positive, indicated the specific adaptation of a genotype to certain environments. The more PC1 scores approximate to zero, more stable the genotype among environments under study. The AMMI model is a combination of analysis of variance (ANOVA) and principal component analysis (PC). The analytical model can be written as

$$Y_{ij.} = \mu + \delta_i + \beta_j + \sum_{k=1}^{K} \lambda_k \delta_{ik} \beta_{jk} + \varepsilon_{ij.}$$

GGE biplots display both G (genotype) and GE (genotype–environment), variation (Kang, 1993) for genotype evaluation. The GGE biplot is based on the sites regression (SREG) linear–bilinear model (Cornelius *et al.*, 1996; Crossa and Cornelius, 1997; Crossa *et al.*, 2002). The sites regression model as a multiplicative model in the bilinear terms shows the main effects of cultivars plus the cultivar x environment interaction (GGE) and the Site regression model is:

$$Y_{ij.} = \mu + \beta_j + \sum_{k=1}^{K} \lambda_k \delta_{ik} \beta_{jk} + \varepsilon_{ij.}$$

Where $Y_{ij.}$ is the mean yield of i^{th} genotype in j^{th} environment, μ is the overall mean, δ_i is the genotypic effect, β_j is the environment effect, λ_k is the singular value for PC axis k: δ_{ik} is the genotype eigenvector value for PC axis n, β_{jk} is the environment eigenvector value for PC axis k and $\varepsilon_{ij.}$is the residual error assumed to be normally and independently distributed (0, σ^2/r), σ^2 is the pooled error variance and r is the number of replicates. The GGE biplot graphically represents G and GEI effect present in the multi-location trial data using environment centered data. GGE biplots were used to evaluate 1) mega environment analysis (which-won-where pattern), where by specific genotypes can be recommended to specific mega environments. 2) Genotype evaluation, stable genotype(s) across all locations and 3) location evaluation, explains discriminative power among genotypes in target locations.

ANOVA to estimate AMMI stability parameters

Source	d. f	S. S	M. S. S
Genotype	(g-1)		
Environment	(e-1)		
Interaction IPCA 1 IPCA 2 Residual	(g-1) (e-1)		
Error	(r-1)(ge-1)		
Total	(ger -1)		

3.2.5. Estimation of Correlation Coefficients

Correlation coefficients were calculated by using the formulae suggested by Karl Pearson (1920). Correlation coefficients were estimated based on pooled data of three seasons.

$$r_{xy} = \frac{\operatorname{cov}(xy)}{S_x \bullet S_y}$$

where,

r_{xy} = correlation between x and y

Cov (xy) = covariance for characters x and y

S = Standard deviation

r = correlation coefficient

xy = two independent variables

3.2.6. Path Coefficient Analysis

The direct and indirect effects both at genotypic and phenotypic level were estimated by taking seed yield as dependent variable, using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959). The following equations were formed and solved simultaneously for estimating the various direct and indirect effects. Direct and indirect effects were estimated based on pooled data of three seasons for 59 lines.

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

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

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

Where,

1, 2 .... n	=	Independent variable
y	=	Dependent variable (yield per plant)
$r_{1y}, r_{2y} \ldots\ldots\ldots r_{ny}$	=	Coefficient of correlation between causal factors '1' to 'n' on dependent character 1
$p_{1y}, P_{2y} \ldots\ldots P_{ny}$	=	Direct effect of characters 1 to n on character Y

The above equations can be written in matrix form as:

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

Then

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

Direct effects were as follows:

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

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

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

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

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

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

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

3.3. GENOTYPING AND HAPLOTYPING FOR EARLINESS

3.3.1. EXPERIMENTAL MATERIAL

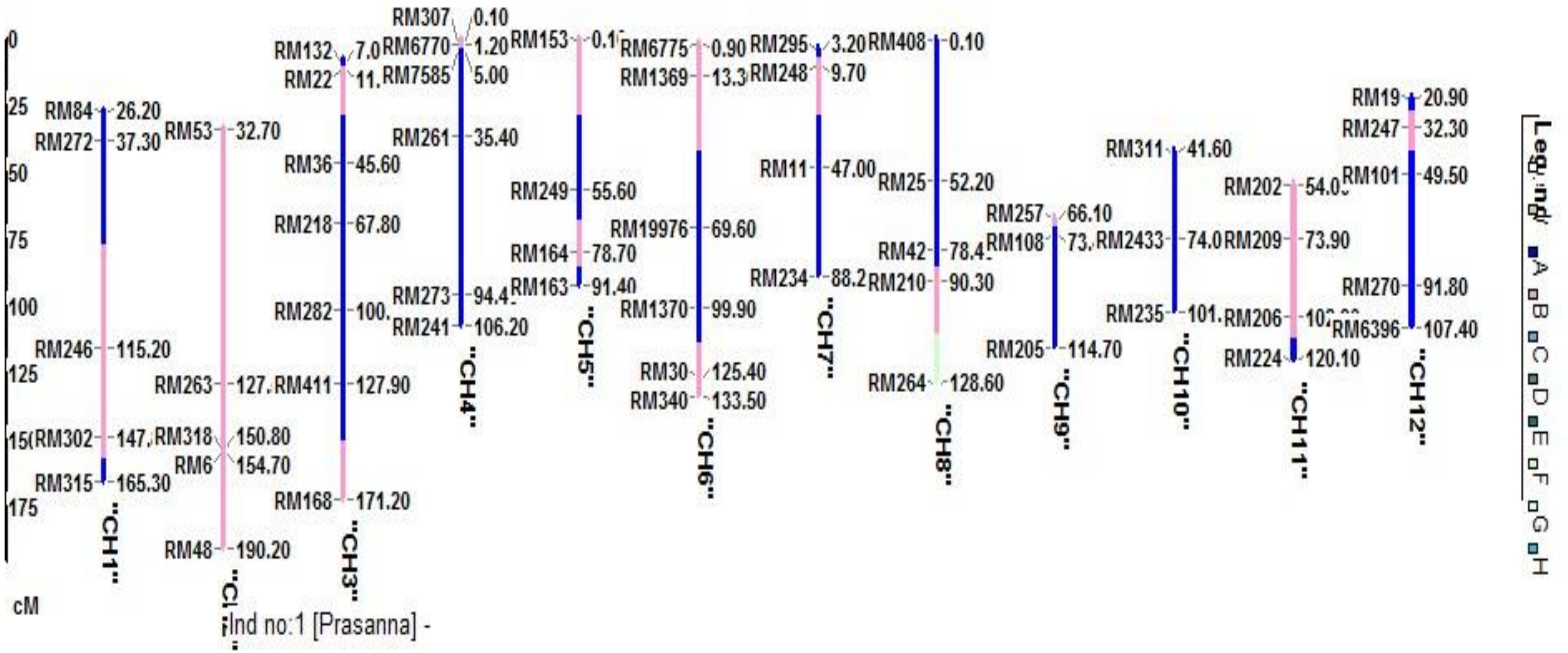
3.3.1.1. Leaf material

In addition to fifty nine genotypes used in phenotyping with a set of twenty five lines were used for genotyping and haplotyping in the present study for obtaining clear cut molecular divergence. Details of lines used for genotyping are furnished in Table 3.1.1. The leaf material of all the eighty five genotypes was collected from the Research farm, Indian Institute of Rice Research, Hyderabad. The distribution of markers along with their chromosome position on their respective chromosome is depicted in Fig 3.3.

3.3.1.2. Equipments required

1. Autoclaved and sterilized mortar and pestle
2. Micropipettes (1 ml, 20 µl and 200 µl range)
3. 1.5 ml micro - centrifuged tubes (autoclaved and dried)
4. 1 ml, 20 µl and 200 µl tips (autoclaved and dried)
5. Micro – centrifuge
6. Fume hood

Figure 3.3. Distribution of markers along with their chromosome position on their respective chromosome



3.3.2. METHODS

3.3.2.1. Preparation of buffers and stock solutions:

a) 1 M Tris HCl (pH = 8):

Tris base of about 60.578 g was dissolved in 400 ml of distilled water. Then the pH was adjusted to 8.0 with approximately 30 ml of 0.1N HCl and the solution was cooled to room temperature. After cooling the final volume was made up to 500 ml with distilled water and the solution was sterilized by autoclaving at 121°C temperature, 15 Psi pressure for 20 minutes. Then it was stored in transparent reagent bottle.

b) 0.5M EDTA (pH = 8):

Take 46.539 g of Disodium Ethylene Diamine Tetra Acetate (EDTA) and dissolve it in 100 ml of distilled water. Adjust the pH to 8.0 by adding approximately 6.25 g of NaOH pellets and stir vigorously on magnetic stirrer. The total volume was adjusted to 250 ml with distilled water and sterilized by autoclaving and it was stored at room temperature in transparent reagent bottle.

c) 5 M NaCl:

Dissolve 73.05 g of NaCl in 200 ml of distilled water. Adjust the total volume to 250 ml with distilled water and sterilized by autoclaving and it was stored at room temperature in transparent reagent bottle.

d) DNA Extraction Buffer

2 % (w/v) CTAB	10 g
100 mM Tris HCl (pH 8.0)	50 ml of 0.5 M Tris HCl (pH 8.0)
20 mM EDTA (pH 8.0)	20 ml of 0.5 M EDTA (pH 8.0)
1.4 M NaCl	140 ml of 5 M NaCl
1 % (w/v) PVP	5g

All the above ingredients except CTAB were added in respective quantities and final volume was made up to 500 ml with double distilled water, the solution was autoclaved. The solution was allowed to attain room temperature and 10 g of CTAB was dissolved by intense stirring, stored at room temperature.

e) Chloroform: Isoamyl alcohol (24:1):

Equal parts of equilibrated Chloroform and Isoamyl alcohol (24:1) were mixed and stored at 4^{o}C.

3.3.2.2. DNA isolation by CTAB method

Total genomic DNA was isolated from leaf tissue of 30 days old rice seedlings, following the protocol of Doyle and Doyle (1987).

1) The healthy leaf of about 2-3 cm was cut into small pieces and taken into autoclaved motor and about 1000 µl of CTAB (Cetyl Tri methyl Ammonium Bromide) buffer was added to the motor. The leaf tissues were macerated using autoclaved pestle for about 15-20 seconds till it was completely homogenized.
2) Using a micropipette of 1ml capacity (it's tip was cut at the bottom using a sterile scissor), the entire content was transferred into a 1.5 ml eppendorf tubes. And were kept in a water bath at 65°C with occasional mixing of tubes. These were removed from the water bath and allowed to cool at room temperature. Equal volume of Chloroform: Isoamyl alcohol mixture (24:1) was added into the tubes and mixed thoroughly by gentle inversion for 15 min (minutes) by keeping in rotator at 12,000 rpm (revolutions per minute) (eppendorf centrifuge) until clear separation of three layers was attained.
3) After the centrifugation, the clear aqueous phase (supernatant) was carefully aliquot into new tubes.
4) To the clear supernatant, cold Isopropanol of about 0.5 to 0.6 volumes (2/3rd of pipette volume) was added. The contents were mixed gently by inversion and kept at -20°C for overnight. Subsequently, the tubes were centrifuged at 12000 rpm for 12 min at 24°C temperature to pellet out DNA. The supernatant was discarded gently without disturbing the DNA pellet.
5) The obtained DNA pellet was washed with 70% Ethanol and centrifuged at 13,000 rpm for 4-5 min. This step was repeated twice. The supernatant was removed, the tubes were allowed to air dry completely and the pellet was dissolved in 100 µl T10E1buffer. DNA was stored at 4°C for further use.

3.3.2.3. Quantification of DNA isolated by Nanodrop method

The ratio of absorbance at 260 nm and 280 nm was used to assess the purity of DNA. A ratio of ~1.8 is generally accepted as "pure" for DNA and a ratio of ~2.0 is generally accepted as "pure" for RNA. If the ratio is appreciably lower in either case, it may indicate the presence of protein, phenol or other contaminants that absorb strongly at or near 280 nm.

The genomic DNA concentration was measured by using the formula:

Genomic DNA concentration in µg µl^{-1} = OD 260 x 50 µg µl^{-1} x dilution factor

The quantity of DNA in different samples varied from 263- 4028 ng/µl. After quantification, all the samples were diluted to 50 ng/µl and were used for PCR reactions.

3.3.2.4. Rice microsatellite markers used for analysis

In the present study, 57 rice microsatellite markers which have been mapped on 12 chromosomes of rice, were used. The list and details of SSR markers used in the present study were given in Table 3.3.2.4 a and 3.3.2.4 b

3.3.2.5. Polymerase Chain Reaction (PCR) amplification

The genomic DNA of 84 lines were subjected to PCR amplification using a thermal cycler with the components and cycles mentioned below in Tables 3.3.2.5 a and 3.3.2.5 b PCR reaction was performed in a 10 µl volume of mix containing the following. Annealing temperature for most of the primers was 55°C but for primer RM118 and 132 it was 67°C and for RM6770 and RM7585 it was 50°C.

Table 3.3.2.5 a Components of PCR reaction

Component	**Concentration**	**Reaction volume**
Taq buffer (10X) with MgCl2	1.0 X	1.0 µl
dNTP mix	2.5 Mm	1.0 µl
Taq DNA polymerase	3.0U/µl	0.1 µl
Forward primer	0.2 Mm	0.4 µl
Reverse primer	0.2 µM	0.4 µl
Genomic DNA	50.0 ng/µl	2.0 µl
Sterile distilled water		5.1 µl

Table 3.3.2.5 b PCR temperature regime

S.No.	Step	Temperature	Time	No. of cycles
1	Initial denaturation	94°C	5 minutes	1
2	Final denaturation	94°C	30 seconds	35
3	Annealing	55-67°C	30 seconds	
4	Initial Extension	72°C	1 minute	
5	Final extension	72°C	7 minutes	
6	Store	4°C	∞	1

The PCR products were stored at 4°C for short period and at -20°C for long duration. The amplified products were loaded on Ethidium bromide stained Agarose gels (3%), subjected to electrophoresis, visualized in a gel documentation system and the polymorphism was recorded.

3.3.2.6. Agarose Gel Electrophoresis for resolution of SSR markers PCR product

3.3.2.6.1. Materials used:

1. Gel casting unit
2. Gel trays
3. Power supply unit
4. Microwave oven
5. Reagent bottle
6. Electronic balance
7. Gel documentation system including UV trans-illuminator

3.3.2.6.2. Chemicals used:

1. Agarose
2. 10X TBE buffer, 1000ml: Add 108g of Tris base in 500ml double distilled water, then add 55g Boric acid, mix well by stirring and add 40 ml of 0.5m EDTA and make up the volume to 1000 ml using double distilled water. Filter sterilized solution using 0.45µm filter paper. Store at room temperature.
3. Ethidium Bromide: 10 mg^{-1} solution was prepared by dissolving 1 g of ethidium bromide in 100 ml of distilled water.
4. Bromophenol blue dye (0.25 percent bromophenol blue in 40 percent sucrose). This dye is to be used in the ratio of 1:6 (dye: DNA solution).

3.3.2.6.3. Method used:

Agarose gel (3%) electrophoresis was used to separate the amplified DNA products. The PCR amplified products were resolved on 3% agarose gel. The Agarose gel was prepared by adding 3 g of Agarose to 100 ml 1.0 X TBE (Tris Boric acid EDTA) buffer and boiled carefully till the Agarose was completely melted. Just before complete cooling 3 µ1 Ethidium bromide (10 mg/ml) was added and the gel was poured in the tray containing the comb carefully avoiding formation of air bubbles. The solidified gel was transferred to horizontal electrophoresis apparatus and 1.0 X TBE buffer was added to immerse the gel.

3.3.2.6.4. Loading the PCR products:

PCR product was mixed with 3 µl of 6X loading dye and loaded in the wells of the gel carefully. A 50 bp ladder was loaded as a reference marker. The gel was run at constant voltage of 70 V for about 4-6 hours, until the ladder got properly resolved. Gel was photographed using the ALPHA IMAGER gel documentation system (Alpha innotech, USA).

3.3.3. DATA ANALYSIS

3.3.3.1. Scoring

As we know haplotyping is genotyping based on allelic variation, and scoring will be done based on the number of alleles present in the population where each amplicon (band) was considered as an allele in SSR analysis. In present study a total of five allelic variations were observed. They were scored according to the relative position of the amplified DNA fragment. Allele amplified at lowest base pair is assigned as A and further were assigned as B, C, D, E (amplified at highest base pair in population).

3.3.3.2. Marker polymorphism

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

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

Where, ‘i’ is the total number of alleles detected for SSR marker and ‘Pi’ is the frequency of the i^{th} allele in the set of 84 genotypes investigated and j=i+1. This formula gives us an indicator of how many alleles a certain has, and how much these alleles divide evenly. The PIC value was calculated using the online software - ‘Polymorphism Information Content Calculator’ available at www.agri.huji.ac.

3.3.3.3. Cluster analysis:

The score data entered in excel sheet was subjected to cluster analysis. Genetic relatedness among the genotypes was calculated using unweighted pair group method with arithmetic averages algorithm (UPGMA) cluster analysis by using the program NTSYSpc 2.02i (Rohlf, 1989).

3.3.3.4. Haplotyping:

Genotypic analysis was conducted on the genotypes using previously reported markers linked to heading date. Amplified fragments were scored for the presence or absence of alleles for each primer genotype combination. Marker based haplotyping was carried out to understand genotypic constitution of the genotypes under study using HAPLOTYPE ANALYSIS v1.04 (Eliades and Eliades, 2009).

RESULTS AND DISCUSSION

Chapter IV

RESULTS AND DISCUSSION

The present investigation was conducted to evaluate 59 genotypes in three seasons *viz*., *Rabi* 2014-15, *Kharif* 2015 and *Rabi* 2015-16 of Telangana, to study mainly the stability of the early genotypes for yield and yield traits *viz*., days to 50 % flowering, days to maturity, plant height, number of total tillers per plant, number of productive tillers per plant, panicle length, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, number of total grains per panicle, spikelet fertility, sterility percentage, thousand grain weight, single plant grain yield, biomass per plant, biological yield per plant, harvest index and per day productivity and also to study genotyping and haplotyping of 84 genotypes for earliness. The results obtained from the experiment are presented below under the following headings.

The results obtained from the present experimental study on evaluation of fifty nine rice genotypes are furnished under the following heads.

4.1 Mean performance

4.2 Genetic variability, heritability and genetic advance

4.3 Stability analysis by AMMI biplot model and GGE biplot model

4.4 Character association

4.5 Path coefficient analysis

4.6 Genotyping and haplotyping for earliness using SSR markers

4.1. MEAN PERFORMANCE

The analysis of variance showed highly significant difference among the various genotypes for the characters under study in the present investigation among all the seasons. This indicate that the genotypes were possessing inherent genetic variances among themselves with respect to the characters studied. The results of analysis of variance are presented in Table 4.1 a. The mean values for 18 characters for fifty nine rice genotypes are given in Table 4.1 b.

Table 4.1 a Analysis of variance for single plant grain yield and its component traits in three different seasons

Source of Variation	df	Season	Days to 50 % flowering	Days to maturity	Plant height	No. of total tillers per plant	No. of productive tillers per plant	Panicle length	Panicle weight	No. of filled grains per panicle	No. of unfilled grains per panicle
Replications	2	*Rabi* 15	0.073	0.006	0.073	0.023	0.107	0.148	1.356	1802.650	32.836
		Kharif 15	0.141	0.277	0.959	3.006	3.819	2.479	0.875	1465.379	46.311
		Rabi 16	0.006	0.023	0.262	11.407	9.475	2.389	0.080	89.972	9.768
Genotypes	58	*Rabi* 15	425.764**	378.395**	1055.585**	124.188**	127.228**	27.905**	3.544**	6503.481**	262.474**
		Kharif 15	478.356**	446.191**	1107.511**	71.992**	68.961**	18.526**	2.487**	6112.503**	327.446**
		Rabi 16	901.883**	701.132**	300.956**	80.277**	54.438**	27.912**	1.320**	3594.070**	524.706**
Error	116	*Rabi* 15	2.522	2.632	17.670	14.804	14.849	2.322	0.604	589.552	86.888
		Kharif 15	1.750	1.656	31.652	11.891	11.469	4.015	0.488	1546.827	102.305
		Rabi 16	1.040	1.063	16.615	13.401	11.233	4.524	0.144	309.506	72.326

Continuation of table 4.1 a…

Source of Variation	df	Season	No. of total grains per panicle	Spikelet fertility	Sterility percentage	Thousand grain weight	Single plant grain yield	Biomass per plant	Biological yield per plant	Harvest index	Per day productivity
Replications	2	*Rabi* 15	1351.362	27.910	27.910	0.061	0.047	42.394	0.012	0.073	0.0002
		Kharif 15	1184.107	14.713	14.713	3.647	98.786	44.578	78.337	0.157	0.006
		Rabi 16	79.768	5.639	5.639	0.845	0.728	28.648	36.178	48.139	0.00007
Genotypes	58	*Rabi* 15	7893.964**	170.358**	170.358**	32.039**	406.671**	219.704**	1056.161**	325.736**	0.022**
		Kharif 15	7276.532**	113.602**	113.602**	34.585**	387.619**	409.325**	1321.165**	338.020**	0.022**
		Rabi 16	5438.737**	195.445**	195.455**	24.423**	93.073**	142.523**	341.181**	172.995**	0.006**
Error	116	*Rabi* 15	528.114	46.584	46.584	5.142	54.715	28.758	112.664	59.392	0.003
		Kharif 15	1587.659	43.577	43.577	4.425	60.11	62.558	148.841	73.511	0.003
		Rabi 16	448.062	34.235	34.235	0.678	17.380	19.233	56.297	22.121	0.001

* Significant at 0.05 level of probability   ** Significant at 0.01 level of probability

Table 4.1 b Mean performance table of 59 genotypes for eighteen characters under study for three seasons

S.NO	Genotype	Days to 50 % flowering				Days to maturity				Plant height			
		Rabi 15	*Kharif 15*	*Rabi 16*	Pooled	*Rabi 15*	*Kharif 15*	*Rabi 16*	Pooled	*Rabi 15*	*Kharif 15*	*Rabi 16*	Pooled
1	130K	116.00	121.00	96.00	111.00	147.00	151.00	129.00	142.33	99.00	104.67	86.67	96.78
2	14(S)	114.00	100.00	95.00	103.00	139.33	127.00	128.00	131.44	87.00	100.33	86.67	91.33
3	14-3	124.00	125.00	111.00	120.00	141.00	130.00	141.00	137.33	83.33	68.33	78.67	76.78
4	148S	98.00	105.00	86.00	96.33	121.00	121.00	116.00	119.33	157.67	161.33	118.33	145.78
5	166(S)	131.00	121.00	135.00	129.00	150.33	150.00	145.33	148.56	100.00	111.00	93.33	101.44
6	166-1	133.00	127.00	113.00	124.33	160.00	151.00	143.00	151.33	99.33	109.00	81.33	96.56
7	166-2-11	123.00	121.00	135.00	126.33	154.33	154.00	165.00	157.78	123.33	140.67	103.33	122.44
8	166-23	130.00	107.00	114.00	117.00	163.00	143.00	144.00	150.00	82.67	87.33	82.00	84.00
9	166-2-3	102.00	94.00	83.00	93.00	133.00	120.00	119.00	124.00	98.30	99.33	84.33	93.99
10	166-23-1	131.00	120.00	127.00	126.00	160.00	148.00	157.00	155.00	95.00	92.33	89.67	92.33
11	166-2-9	120.00	120.00	113.00	117.67	146.00	141.00	145.00	144.00	133.67	118.33	97.67	116.56
12	166-30	125.00	119.00	104.00	116.00	154.00	143.00	138.00	145.00	97.00	96.67	80.67	91.44
13	166-9	108.00	119.00	105.00	110.67	136.00	144.00	136.00	138.67	118.33	139.67	100.00	119.33
14	220S	115.00	101.00	98.00	104.67	139.00	132.00	134.00	135.00	89.67	74.00	85.00	82.89
15	246K	105.00	92.00	87.00	94.67	130.00	115.00	115.00	120.00	85.00	90.67	82.00	85.89
16	250(K)	131.00	121.00	129.00	127.00	145.00	148.00	131.00	141.33	104.67	119.00	100.00	107.89
17	258 S	113.00	116.00	99.00	109.33	143.00	141.00	135.00	139.67	91.67	97.33	80.67	89.89
18	263K	108.00	101.00	96.00	101.67	137.00	126.00	130.00	131.00	81.67	88.67	85.33	85.22
19	27(K)	119.00	118.00	95.00	110.67	148.33	138.33	134.00	140.22	96.33	98.67	80.33	91.78
20	35(B)	118.00	97.00	71.00	95.33	139.67	122.00	101.00	120.89	89.00	128.3	89.67	102.33
21	51(B)	124.00	108.00	126.00	119.33	146.00	128.00	151.00	141.67	69.33	89.67	82.67	80.56
22	75(S)	127.00	118.00	108.00	117.67	157.00	148.00	139.00	148.00	77.00	90.67	71.67	79.78

Continuation of table 4.1.b…

23	93(B)	122.00	97.00	115.00	111.33	152.00	125.00	147.00	141.33	82.00	89.67	82.33	84.67
24	95(B)	137.00	126.00	133.00	132.00	159.00	145.00	158.00	154.00	84.67	83.67	79.67	82.67
25	Adithya	94.00	90.00	88.00	90.67	119.00	123.00	117.00	119.67	100.67	102.33	89.67	97.56
26	ADT 43	106.00	98.00	100.00	101.33	136.00	123.00	136.00	131.67	81.67	84.00	79.00	81.56
27	Anjali	95.00	93.00	78.00	88.67	120.00	117.00	112.00	116.33	127.67	131.00	97.00	118.56
28	Govindu	107.00	95.00	88.00	96.67	139.00	126.00	122.00	129.00	82.67	84.33	85.00	84.00
29	IR-64	139.60	115.00	98.00	117.53	139.67	140.00	128.00	135.89	82.33	93.67	79.00	85.00
30	Jaldidhan	96.00	86.00	87.00	89.67	120.67	107.00	119.00	115.56	81.67	82.33	76.67	80.22
31	Jaya	131.00	117.00	117.00	121.67	158.33	139.00	150.00	149.11	96.67	111.67	84.33	97.56
32	MTU1010	114.66	105.00	95.00	104.89	139.67	135.00	125.00	133.22	93.00	103.67	85.33	94.00
33	Prasanna	95.00	81.00	74.00	83.33	120.00	102.00	103.00	108.33	80.33	81.00	100.47	87.27
34	Rasi	103.00	93.00	77.00	91.00	132.00	118.00	110.33	120.11	122.00	127.00	95.00	114.67
35	SBH	103.00	93.00	76.00	90.67	133.00	120.00	109.00	120.67	121.00	124.33	91.33	112.22
36	SM1637	94.00	86.00	80.00	86.67	119.67	116.00	110.00	115.22	126.00	127.33	95.33	116.22
37	SM1876	97.00	100.00	75.00	90.67	134.00	132.00	118.00	128.00	121.00	121.67	89.67	110.78
38	SM219	98.00	93.00	92.00	94.33	130.00	123.00	126.00	126.33	144.33	100.33	97.67	114.11
39	SM349	102.00	90.00	95.00	95.67	131.00	113.00	130.00	124.67	96.50	146.67	127.33	123.50
40	SM363	97.00	116.00	108.00	107.00	125.00	142.00	138.00	135.00	126.00	138.33	102.67	122.33
41	SM4014	107.67	95.00	76.00	92.89	135.67	121.00	107.00	121.22	124.67	119.67	95.67	113.33
42	SM4029	107.67	95.00	81.00	94.56	139.67	126.00	112.00	125.89	113.67	98.67	93.33	101.89
43	SM4071	106.00	91.00	88.00	95.00	137.67	120.00	118.00	125.22	98.00	126.67	96.00	106.89
44	SM4076	108.00	107.67	80.00	98.56	135.67	136.00	107.00	126.22	107.00	127.00	82.67	105.56
45	SM4078	108.00	91.00	73.00	90.67	138.00	125.00	106.00	123.00	91.33	106.00	88.00	95.11
46	SM4226	105.00	90.00	77.00	90.67	132.67	115.00	108.00	118.56	100.00	129.00	90.00	106.33

Continuation of table 4.1 b….

47	SM4231	97.00	103.00	82.00	94.00	122.67	121.00	116.00	119.89	108.00	134.67	97.33	113.33
48	SM4371	107.00	90.00	86.00	94.33	137.00	120.00	116.00	124.33	98.00	96.67	85.00	93.22
49	SM4385	119.00	91.00	69.00	93.00	149.00	121.00	100.00	123.33	130.33	112.33	90.67	111.11
50	SM4406	97.00	87.00	78.00	87.33	133.00	126.00	112.00	123.67	118.33	99.67	80.67	99.56
51	SM4415	97.00	94.00	84.00	91.67	127.00	121.00	117.00	121.67	104.00	108.67	95.67	102.78
52	SM686	98.00	95.00	92.00	95.00	127.00	121.00	125.00	124.33	126.67	100.00	95.00	107.22
53	SM733	99.00	95.67	90.00	94.89	132.33	127.00	126.00	128.44	133.33	103.33	93.00	109.89
54	SM776	97.00	89.00	72.00	86.00	135.00	126.00	111.00	124.00	93.00	110.00	89.67	97.56
55	Sona	109.00	104.00	87.67	100.22	139.00	135.00	123.00	132.33	108.33	100.00	82.67	97.00
56	Tellahamsa	107.00	97.00	89.00	97.67	134.67	122.00	120.00	125.56	116.33	106.67	99.67	107.56
57	Tulasi	107.00	91.00	92.00	96.67	136.33	125.00	126.00	129.11	98.67	99.33	88.33	95.44
58	Vandana	102.00	93.00	81.00	92.00	129.00	114.00	115.00	119.33	119.00	122.67	111.67	117.78
59	Varalu	106.00	94.00	89.00	96.33	132.33	115.00	121.00	122.78	106.33	109.67	90.00	102.00
	Mean	110.69	102.34	94.38	102.47	138.16	128.89	125.77	130.94	103.46	107.62	90.21	100.43
	CV%	1.44	1.29	1.08	7.29	1.17	0.99	0.81	5.51	4.06	5.22	4.51	10.5
	S.E ±	0.91	0.76	0.58	4.3	0.93	0.74	0.59	4.16	2.42	3.24	2.35	6.09
	C.D at 5%	2.56	2.13	1.64	12.09	2.62	2.08	1.66	11.66	6.79	9.09	6.59	17.06

Continuation of table 4.1 b…

S.NO	Genotype	Number of total tillers per plant				Number of productive tiller per plant				Panicle Length			
		Rabi 15	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**
1	130K	16.67	12.00	18.00	15.56	16.33	11.67	15.00	14.33	22.17	23.43	22.43	22.68
2	14(S)	21.00	19.67	30.00	23.56	20.00	14.67	25.33	20.00	22.73	25.10	22.33	23.39

Continuation of table 4.1 b….													
3	14-3	17.33	10.00	14.67	14.00	17.33	9.00	14.67	13.67	19.73	22.20	21.00	20.98
4	148S	13.00	13.67	13.33	13.33	12.33	13.67	11.67	12.56	24.20	28.70	25.50	26.13
5	166(S)	14.33	9.00	14.67	12.67	14.33	7.33	14.67	12.11	21.93	21.60	22.20	21.91
6	166-1	21.33	15.00	12.33	16.22	20.67	12.67	12.33	15.22	22.90	20.13	20.17	21.07
7	166-2-11	16.67	13.00	9.67	13.11	16.67	12.33	9.67	12.89	27.07	23.60	23.07	24.58
8	166-23	13.33	13.00	12.33	12.89	13.00	12.00	12.33	12.44	19.53	22.63	21.40	21.19
9	166-2-3	14.33	15.00	17.67	15.67	13.33	15.00	15.67	14.67	21.93	24.53	24.03	23.50
10	166-23-1	16.00	11.33	10.67	12.67	13.00	10.33	10.67	11.33	22.80	24.57	22.87	23.41
11	166-2-9	10.00	16.67	11.33	12.67	10.00	15.67	11.33	12.33	27.43	26.43	24.07	25.98
12	166-30	20.00	8.67	10.00	12.89	19.67	8.00	10.00	12.56	21.33	22.83	23.10	22.42
13	166-9	17.00	9.67	9.67	12.11	16.67	8.67	9.67	11.67	22.30	25.97	24.50	24.26
14	220S	15.00	25.67	29.33	23.33	15.00	20.33	24.00	19.78	23.77	23.73	21.93	23.14
15	246K	12.00	13.67	20.67	15.44	10.33	12.33	18.67	13.78	23.30	26.93	23.47	24.57
16	250(K)	24.00	13.00	12.67	16.56	23.67	12.67	12.67	16.33	24.87	24.07	25.40	24.78
17	258 S	17.67	13.67	17.33	16.22	17.67	13.67	15.33	15.56	20.57	22.47	20.57	21.20
18	263K	20.00	18.33	26.00	21.44	20.00	18.33	21.33	19.89	21.93	26.33	22.00	23.42
19	27(K)	21.67	21.67	20.00	21.11	21.00	16.67	17.00	18.22	24.30	26.17	21.53	24.00
20	35(B)	18.67	13.67	21.33	17.89	18.67	13.67	18.67	17.00	21.67	21.80	18.43	20.63
21	51(B)	28.00	36.00	14.67	26.22	28.00	36.00	14.67	26.22	17.97	20.13	17.73	18.61
22	75(S)	11.67	16.00	14.33	14.00	11.00	13.67	14.33	13.00	18.83	22.50	19.67	20.33
23	93(B)	31.67	14.33	20.67	22.22	31.33	11.67	20.67	21.22	17.70	21.60	13.20	17.50
24	95(B)	15.33	30.00	14.00	19.78	14.67	29.33	14.00	19.33	20.00	21.07	19.67	20.24
25	Adithya	16.00	17.33	27.00	20.11	15.33	17.33	25.00	19.22	20.10	23.97	22.67	22.24
26	ADT 43	14.33	20.33	19.33	18.00	14.00	19.67	15.33	16.33	22.57	24.30	22.83	23.23

Continuation of table 4.1 b….

27	Anjali	9.33	10.00	16.67	12.00	9.33	10.00	15.67	11.67	21.33	26.07	21.33	22.91
28	Govindu	16.33	17.67	15.67	16.56	16.00	17.00	14.33	15.78	21.97	26.10	20.10	22.72
29	IR-64	25.67	16.33	16.33	19.44	16.00	12.00	13.67	13.89	23.03	24.43	22.27	23.24
30	Jaldidhan	9.00	9.33	21.67	13.33	8.67	9.33	20.67	12.89	19.17	20.77	19.60	19.84
31	Jaya	15.67	13.67	16.33	15.22	15.67	12.33	16.33	14.78	24.40	24.97	22.13	23.83
32	MTU1010	25.33	16.67	15.33	19.11	25.33	14.33	12.67	17.44	23.33	25.50	21.80	23.54
33	Prasanna	17.00	18.00	23.67	19.56	16.33	17.33	23.33	19.00	21.83	22.40	21.77	22.00
34	Rasi	10.67	11.00	15.00	12.22	10.00	11.00	14.67	11.89	24.67	29.50	21.17	25.11
35	SBH	10.67	13.67	22.33	15.56	10.33	13.67	19.33	14.44	24.00	29.23	20.97	24.73
36	SM1637	14.67	15.33	16.00	15.33	14.00	15.33	15.33	14.89	17.27	21.23	19.03	19.18
37	SM1876	17.33	17.33	18.67	17.78	16.33	17.33	16.67	16.78	16.63	23.13	16.87	18.88
38	SM219	12.00	14.33	18.00	14.78	11.00	14.00	17.33	14.11	20.60	23.53	19.43	21.19
39	SM349	12.00	12.67	24.33	16.33	10.67	12.67	18.67	14.00	17.40	24.63	23.77	21.93
40	SM363	19.67	11.67	11.33	14.22	19.00	10.67	11.33	13.67	13.67	24.93	22.40	20.33
41	SM4014	14.33	13.00	24.00	17.11	14.00	13.00	21.33	16.11	14.20	20.93	18.63	17.92
42	SM4029	23.00	12.33	27.00	20.78	21.33	11.67	24.67	19.22	17.07	17.77	10.00	14.94
43	SM4071	15.33	20.33	26.67	20.78	14.33	20.33	23.67	19.44	19.03	21.63	15.77	18.81
44	SM4076	11.00	15.00	15.67	13.89	7.33	15.00	12.00	11.44	18.57	20.83	15.73	18.38
45	SM4078	15.67	14.00	22.33	17.33	15.00	9.67	20.00	14.89	19.53	20.70	18.27	19.50
46	SM4226	16.33	11.67	21.00	16.33	16.00	11.67	18.00	15.22	21.23	21.30	15.50	19.34
47	SM4231	19.33	9.67	13.67	14.22	19.00	9.67	11.00	13.22	17.60	24.27	17.83	19.90
48	SM4371	13.00	15.00	20.67	16.22	12.33	15.00	16.67	14.67	19.83	23.70	20.03	21.19
49	SM4385	15.67	12.67	24.33	17.56	15.67	12.67	21.33	16.56	24.93	19.87	15.70	20.17
50	SM4406	13.00	16.33	21.67	17.00	12.00	15.67	20.67	16.11	16.57	24.63	18.80	20.00

Continuation of table 4.1b….													
51	SM4415	13.00	11.00	20.67	14.89	9.33	9.00	19.33	12.56	17.17	18.40	16.93	17.50
52	SM686	11.00	16.33	27.33	18.22	10.67	16.33	23.33	16.78	18.13	22.60	19.87	20.20
53	SM733	9.33	17.67	18.67	15.22	8.67	17.33	17.33	14.44	16.40	25.07	20.77	20.74
54	SM776	34.67	20.33	19.67	24.89	34.33	20.33	17.33	24.00	23.00	19.80	16.53	19.78
55	Sona	11.33	9.00	17.67	12.67	11.00	9.00	13.00	11.00	25.23	25.50	23.00	24.58
56	Tellahamsa	24.00	14.33	13.00	23.78	23.67	14.00	12.00	23.22	25.40	25.33	24.83	25.19
57	Tulasi	16.67	17.00	21.00	18.22	16.00	17.00	20.00	17.67	21.87	24.70	18.47	21.68
58	Vandana	12.33	11.33	20.67	14.78	12.00	11.33	20.00	14.44	22.73	22.57	19.13	21.48
59	Varalu	11.00	11.67	15.33	12.67	10.00	10.67	14.67	11.78	23.07	21.80	18.27	21.04
	Mean	16.82	15.03	18.37	16.74	16.02	14.11	16.63	15.59	21.09	23.47	20.38	21.65
	CV%	22.87	22.94	19.92	31.23	24.04	23.99	20.15	32.08	7.22	8.53	10.43	9.21
	S.E ±	2.22	1.99	2.11	3.01	2.22	1.95	1.93	2.88	0.87	1.15	1.22	1.15
	C.D at 5%	6.22	5.57	5.92		6.23	5.47	5.42		2.46	3.24	3.43	3.22

Continuation of table 4.1b….

S.NO	Genotype	Panicle weight				Number of filled grains per panicle				Number of unfilled grains per panicle			
		Rabi 15	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**
1	130K	2.72	4.11	2.57	3.13	128.67	177.00	132.33	146.00	5.33	26.00	54.00	28.44
2	14(S)	2.11	3.13	2.18	2.47	91.00	160.00	91.67	114.22	20.67	12.33	15.67	16.22
3	14-3	0.36	1.56	2.13	1.35	38.67	118.00	114.00	90.22	25.00	17.67	11.00	17.89
4	148S	2.31	3.64	2.16	2.71	127.00	160.33	110.33	132.56	3.33	3.33	12.33	6.33
5	166(S)	1.83	2.51	2.50	2.28	123.00	167.67	123.00	137.89	7.33	27.33	30.67	21.78
6	166-1	3.13	1.73	2.44	2.43	184.33	127.67	129.33	147.11	12.67	39.00	17.00	22.89
7	166-2-11	4.05	3.83	3.07	3.65	225.33	230.33	142.33	199.33	32.33	22.33	20.33	25.00

Continuation of table 4.1 b….

8	166-23	1.41	3.31	2.65	2.46	80.33	228.67	205.33	171.44	19.67	41.67	36.33	32.56
9	166-2-3	3.65	2.95	2.69	3.09	118.00	128.67	113.67	120.11	14.67	29.33	26.67	23.56
10	166-23-1	2.93	4.27	2.64	3.28	162.33	241.00	128.00	177.11	30.00	13.00	43.67	28.89
11	166-2-9	4.72	3.57	3.77	4.02	206.00	186.00	186.67	192.89	34.00	16.67	31.67	27.44
12	166-30	5.54	5.79	3.86	5.06	290.67	305.00	209.00	268.22	42.00	29.67	62.67	44.78
13	166-9	4.02	4.88	2.55	3.82	171.00	185.00	89.67	148.56	7.33	20.33	47.33	25.00
14	220S	2.72	2.69	2.22	2.54	120.67	126.67	99.67	115.67	4.67	1.33	23.00	9.67
15	246K	2.05	2.91	2.64	2.54	102.00	132.33	135.33	123.22	5.67	19.67	26.00	17.11
16	250(K)	3.53	3.75	3.25	3.51	142.00	234.67	146.00	174.22	8.67	30.33	46.33	28.44
17	258 S	2.62	3.74	2.12	2.83	140.00	168.67	113.67	140.78	9.00	10.00	32.00	17.00
18	263K	2.05	3.25	1.92	2.41	93.00	132.00	88.67	104.56	11.33	7.33	14.33	11.00
19	27(K)	2.30	4.35	1.86	2.84	80.33	159.00	74.67	104.67	22.33	17.33	28.67	22.78
20	35(B)	3.06	1.56	1.47	2.03	148.00	121.67	63.33	111.00	20.67	19.33	10.00	16.67
21	51(B)	1.06	2.09	1.01	1.39	100.67	172.00	96.33	123.00	6.00	15.67	4.67	8.78
22	75(S)	1.42	2.61	1.57	1.87	96.33	163.33	91.67	117.11	2.67	4.33	18.67	8.56
23	93(B)	1.51	2.54	1.82	1.96	80.33	128.00	98.67	102.33	9.33	4.33	10.00	7.89
24	95(B)	2.47	2.22	2.20	2.30	178.67	212.00	156.67	182.44	7.33	4.00	4.67	5.33
25	Adithya	1.57	2.87	2.13	2.19	83.67	117.00	96.67	99.11	11.00	16.67	29.33	19.00
26	ADT 43	1.20	2.40	2.01	1.87	83.67	177.6667	131.33	130.89	18.00	5.67	44.67	22.78
27	Anjali	1.88	3.29	1.81	2.33	111.00	150.6667	80.00	113.89	4.00	9.67	13.67	9.11
28	Govindu	1.83	3.18	2.17	2.39	100.00	129.3333	83.67	104.33	22.67	9.00	28.00	19.89
29	IR-64	2.16	2.63	2.05	2.28	98.33	161.67	79.33	113.11	6.67	19.67	14.33	13.56
30	Jaldidhan	0.96	1.97	1.25	1.39	48.67	84.67	56.33	63.22	23.67	21.00	30.00	24.89
31	Jaya	3.06	3.31	2.75	3.04	129.00	169.00	101.67	133.22	4.00	25.33	12.33	13.89

Continuation of table 4.1 b….													
32	MTU1010	2.97	3.69	2.37	3.01	133.67	165.00	107.33	135.33	2.67	26.67	25.67	18.33
33	Prasanna	1.25	2.22	1.85	1.77	66.33	93.00	82.00	80.44	22.33	22.33	29.33	24.67
34	Rasi	2.30	4.54	2.01	2.95	145.33	182.00	92.67	140.00	3.33	6.67	7.67	5.89
35	SBH	2.03	3.92	2.19	2.71	113.67	157.67	118.33	129.89	2.67	6.67	13.67	7.67
36	SM1637	1.00	2.08	1.40	1.49	68.00	108.00	67.33	81.11	4.33	6.33	15.67	8.78
37	SM1876	0.94	2.30	1.12	1.45	83.00	145.00	61.00	96.33	1.00	8.00	15.00	8.00
38	SM219	1.75	3.08	2.01	2.28	119.33	147.00	102.67	123.00	9.33	5.00	13.67	9.33
39	SM349	0.98	2.91	2.10	1.99	62.33	151.00	139.33	117.56	6.67	11.67	27.67	15.33
40	SM363	0.92	3.55	3.12	2.53	57.67	141.67	110.33	103.22	2.33	42.00	21.67	22.00
41	SM4014	0.66	1.94	1.45	1.35	44.67	78.33	78.00	67.00	6.00	19.00	11.33	12.11
42	SM4029	3.10	1.53	1.04	1.89	76.00	79.33	76.67	77.33	4.67	3.33	8.67	5.56
43	SM4071	1.47	2.28	1.16	1.64	91.00	127.33	82.33	100.22	3.00	1.67	12.67	5.78
44	SM4076	1.02	1.79	1.38	1.40	69.33	99.67	69.33	79.44	7.00	5.33	9.00	7.11
45	SM4078	1.89	2.02	1.56	1.82	111.33	100.67	73.00	95.00	7.67	6.33	10.33	8.11
46	SM4226	1.37	1.87	1.07	1.44	97.67	108.00	67.33	91.00	24.00	6.33	3.00	11.11
47	SM4231	0.79	2.83	1.29	1.63	101.00	155.33	71.33	109.22	4.67	2.33	15.00	7.33
48	SM4371	1.35	3.12	1.60	2.02	98.00	182.00	69.33	116.44	15.00	17.00	16.00	16.00
49	SM4385	3.30	1.42	1.11	1.94	140.67	60.33	64.33	88.44	20.33	16.33	8.33	15.00
50	SM4406	0.70	3.94	1.53	2.06	60.33	152.67	63.67	92.22	2.00	15.67	41.00	19.56
51	SM4415	0.92	1.55	1.26	1.24	65.00	66.00	78.67	69.89	4.67	9.33	3.67	5.89
52	SM686	0.89	2.81	2.20	1.97	68.33	126.33	105.33	100.00	6.67	7.00	16.00	9.89
53	SM733	0.90	3.11	1.65	1.89	70.67	122.67	65.67	86.33	3.33	32.67	39.00	25.00
54	SM776	2.38	2.16	1.09	1.88	114.33	101.33	60.67	92.11	15.67	4.00	11.33	10.33
55	Sona	3.14	3.17	2.33	2.88	145.33	146.67	111.33	134.44	6.00	6.67	25.00	12.56

Continuation of table 4.1 b….													
56	Tellahamsa	2.63	3.04	2.28	2.65	136.67	126.33	111.67	124.89	10.33	9.00	20.00	13.11
57	Tulasi	2.17	2.55	1.15	1.95	101.33	110.67	52.67	88.22	13.00	4.67	13.33	10.33
58	Vandana	0.92	3.13	1.59	1.88	91.33	127.67	75.33	98.11	1.67	4.00	21.00	8.89
59	Varalu	2.52	2.65	1.49	2.22	180.67	133.00	75.67	129.78	17.33	17.00	24.67	19.67
	Mean	2.08	2.91	2.00	2.33	111.79	146.62	100.04	119.48	11.52	14.62	21.68	15.94
	CV%	37.42	23.98	18.96	26.82	21.71	26,.82	17.58	22.34	80.91	69.2	39.22	56.79
	S.E ±	0.44	0.4	0.21	0.36	14.01	22.7	10.15	15.41	5.38	5.83	4.91	5.22
	C.D at 5%	1.25	1.12	0.61	1.01	39.26	63.6	28.45	43.18	15.07	16.35	13.75	14.63

Continuation of table 4.1 b…

S.NO	Genotype	Number of total grains per panicle				Spikelet fertility				Sterility percentage			
		Rabi 15	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**
1	130K	134.00	203.00	186.33	174.44	96.12	84.53	70.46	83.70	3.88	15.47	29.54	16.30
2	14(S)	111.67	172.33	107.33	130.44	81.81	92.88	85.11	86.60	18.19	7.12	14.89	13.40
3	14-3	63.67	135.67	125.00	108.11	61.17	86.72	91.15	79.68	38.83	13.28	8.85	20.32
4	148S	130.33	163.67	122.67	138.89	97.53	97.96	89.85	95.12	2.47	2.04	10.15	4.88
5	166(S)	130.33	195.00	153.67	159.67	93.42	84.45	79.78	85.88	6.58	15.55	20.22	14.12
6	166-1	197.00	166.67	146.33	170.00	90.74	75.53	88.42	84.90	9.26	24.47	11.58	15.10
7	166-2-11	257.67	252.67	162.67	224.33	87.43	91.16	87.23	88.61	12.57	8.84	12.77	11.39
8	166-23	100.00	270.33	241.67	204.00	80.29	84.27	84.76	83.10	19.71	15.73	15.24	16.90
9	166-2-3	132.67	158.00	140.33	143.67	89.00	81.44	81.40	83.94	11.00	18.56	18.60	16.06
10	166-23-1	192.33	254.00	171.67	206.00	84.81	94.93	74.83	84.86	15.19	5.07	25.17	15.14
11	166-2-9	240.00	202.67	218.33	220.33	85.82	92.58	85.49	87.96	14.18	7.42	14.51	12.04

Continuation of table 4.1 b….													
12	166-30	332.67	334.67	271.67	313.00	87.15	91.99	76.99	85.38	12.85	8.01	23.01	14.62
13	166-9	178.33	205.33	137.00	173.56	96.18	89.85	65.23	83.76	3.82	10.15	34.77	16.24
14	220S	125.33	128.00	122.67	125.33	96.19	98.83	82.65	92.56	3.81	1.17	17.35	7.44
15	246K	107.67	152.00	161.33	140.33	94.51	87.51	84.73	88.92	5.49	12.49	15.27	11.08
16	250(K)	150.67	265.00	192.33	202.67	93.16	85.25	76.04	84.82	6.84	14.75	23.96	15.18
17	258 S	149.00	178.67	145.67	157.78	93.77	93.20	78.58	88.52	6.23	6.80	21.42	11.48
18	263K	104.33	139.33	103.00	115.56	89.18	94.76	86.14	90.03	10.82	5.24	13.86	9.97
19	27(K)	102.67	176.33	103.33	127.44	78.35	89.93	72.79	80.36	21.65	10.07	27.21	19.64
20	35(B)	168.67	141.00	73.33	127.67	87.66	84.90	86.26	86.27	12.34	15.10	13.74	13.73
21	51(B)	106.67	187.67	101.00	131.78	94.03	91.50	95.13	93.55	5.97	8.50	4.87	6.45
22	75(S)	99.00	167.67	110.33	125.67	97.22	97.54	83.07	92.61	2.78	2.46	16.93	7.39
23	93(B)	89.67	132.33	108.67	110.22	89.95	96.71	91.02	92.56	10.05	3.29	8.98	7.44
24	95(B)	186.00	216.00	161.33	187.78	96.31	98.05	97.22	97.19	3.69	1.95	2.78	2.81
25	Adithya	94.67	133.67	126.00	118.11	87.78	88.39	76.61	84.26	12.22	11.61	23.39	15.74
26	ADT 43	101.67	183.33	176.00	153.67	84.60	96.51	74.61	85.24	15.40	3.49	25.39	14.76
27	Anjali	115.00	160.33	93.67	123.00	97.21	93.57	85.81	92.20	2.79	6.43	14.19	7.80
28	Govindu	122.67	138.33	111.67	124.22	81.24	93.70	74.74	83.23	18.76	6.30	25.26	16.77
29	IR-64	105.00	181.33	93.67	126.67	94.30	88.52	84.94	89.25	5.70	11.48	15.06	10.75
30	Jaldidhan	72.33	105.67	86.33	88.11	66.60	81.44	64.90	70.98	33.40	18.56	35.10	29.02
31	Jaya	133.00	194.33	114.00	147.11	96.90	84.22	89.21	90.11	3.10	15.78	10.79	9.89
32	MTU1010	136.33	191.67	133.00	153.67	98.01	86.78	82.97	89.25	1.99	13.22	17.03	10.75
33	Prasanna	88.67	115.33	111.33	105.11	73.47	80.39	74.86	76.24	26.53	19.61	25.14	23.76
34	Rasi	148.67	188.67	100.33	145.89	97.79	96.41	92.34	95.51	2.21	3.59	7.66	4.49
35	SBH	116.33	164.33	132.00	137.56	97.70	96.05	90.15	94.63	2.30	3.95	9.85	5.37

Continuation of table 4.1 b….													
36	SM1637	72.33	114.33	83.00	89.89	94.31	94.60	81.57	90.16	5.69	5.40	18.43	9.84
37	SM1876	84.00	153.00	76.00	104.33	98.72	94.91	80.68	91.44	1.28	5.09	19.32	8.56
38	SM219	128.67	152.00	116.33	132.33	91.88	96.70	87.91	92.16	8.12	3.30	12.09	7.84
39	SM349	69.00	162.67	167.00	132.89	90.97	92.82	83.69	89.16	9.03	7.18	16.31	10.84
40	SM363	60.00	183.67	132.00	125.22	95.61	78.32	83.55	85.83	4.39	21.68	16.45	14.17
41	SM4014	50.67	97.33	89.33	79.11	88.53	81.24	88.01	85.93	11.47	18.76	11.99	14.07
42	SM4029	80.67	82.67	85.33	82.89	93.93	95.88	89.91	93.24	6.07	4.12	10.09	6.76
43	SM4071	94.00	129.00	95.00	106.00	96.74	98.66	86.88	94.09	3.26	1.34	13.12	5.91
44	SM4076	76.33	105.00	78.33	86.56	90.86	95.02	88.48	91.46	9.14	4.98	11.52	8.54
45	SM4078	119.00	107.00	83.33	103.11	93.51	94.48	88.18	92.05	6.49	5.52	11.82	7.95
46	SM4226	121.67	114.33	70.33	102.11	81.54	94.38	95.81	90.58	18.46	5.62	4.19	9.42
47	SM4231	105.67	157.67	86.33	116.56	95.90	98.54	83.34	92.60	4.10	1.46	16.66	7.40
48	SM4371	113.00	199.00	85.33	132.44	86.47	92.32	81.22	86.67	13.53	7.68	18.78	13.33
49	SM4385	161.00	76.67	72.67	103.44	87.26	77.56	88.70	84.50	12.74	22.44	11.30	15.50
50	SM4406	62.33	168.33	104.67	111.78	96.44	90.56	61.04	82.68	3.56	9.44	38.96	17.32
51	SM4415	69.67	75.33	82.33	75.78	93.29	87.57	95.56	92.14	6.71	12.43	4.44	7.86
52	SM686	75.00	133.33	121.33	109.89	91.11	94.72	86.96	90.93	8.89	5.28	13.04	9.07
53	SM733	74.00	155.33	104.67	111.33	95.52	78.25	60.68	78.15	4.48	21.75	39.32	21.85
54	SM776	130.00	105.33	72.00	102.44	86.79	96.35	85.31	89.48	13.21	3.65	14.69	10.52
55	Sona	151.33	153.33	136.33	147.00	95.68	95.26	81.58	90.84	4.32	4.74	18.42	9.16
56	Tellahamsa	147.00	135.33	131.67	138.00	93.02	93.34	84.97	90.44	6.98	6.66	15.03	9.56
57	Tulasi	114.33	115.33	66.00	98.56	88.74	95.91	79.61	88.09	11.26	4.09	20.39	11.91
58	Vandana	93.00	131.67	96.33	107.00	98.15	96.52	77.03	90.57	1.85	3.48	22.97	9.43
59	Varalu	198.00	150.00	100.33	149.44	91.41	89.59	75.30	85.43	8.59	10.41	24.70	14.57

Continuation of table 4.1 b….													
	Mean	123.31	161.23	121.72	135.42	90.40	90.78	82.74	87.97	9.60	9.22	17.26	12.03
	CV%	18.63	24.71	17.38	21.29	7.54	7.27	7.07	7.41	71.11	71.58	33.89	54.26
	S.E ±	13.26	23	12.22	16.65	3.94	3.81	3.37	3.76	3.96	3.81	3.37	3.76
	C.D at 5%	37.16	64.43	34.23	46.64	11.03	10.67	9.46	10.55	11.03	10.67	9.45	10.55

Continuation of table 4.1 b…

S.NO	Genotype	Thousand grain weight				Single plant grain yield				Biomass per plant			
		Rabi 15	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**	***Rabi 15***	***Kharif 15***	***Rabi 16***	**Pooled**
1	130K	23.33	19.97	22.47	21.92	37.80	21.11	19.29	26.06	29.33	24.67	21.50	25.17
2	14(S)	21.33	20.47	21.89	21.23	21.93	19.64	28.18	23.25	28.17	26.00	21.20	25.12
3	14-3	15.67	11.80	15.93	14.47	16.67	14.56	21.51	17.58	20.97	12.07	28.50	20.51
4	148S	25.33	22.83	23.47	23.88	14.23	35.28	13.32	20.95	31.70	45.33	29.93	35.66
5	166(S)	16.00	16.67	17.15	16.61	20.67	17.18	14.83	17.56	28.27	31.00	41.70	33.66
6	166-1	15.83	15.00	16.19	15.67	24.67	28.12	16.07	22.95	36.47	45.00	20.07	33.84
7	166-2-11	17.67	16.47	17.80	17.31	26.00	15.50	25.10	22.20	39.50	25.67	32.80	32.66
8	166-23	11.00	9.73	12.50	11.08	3.80	15.65	14.43	11.29	14.03	18.00	17.00	16.34
9	166-2-3	21.33	22.07	22.57	21.99	26.53	25.28	21.80	24.54	24.17	36.00	26.20	28.79
10	166-23-1	16.67	16.40	18.17	17.08	7.23	20.14	10.50	12.63	26.43	23.33	24.30	24.69
11	166-2-9	19.33	17.73	20.64	19.23	15.97	36.57	16.83	23.12	28.33	59.00	27.50	38.28
12	166-30	13.00	16.10	15.47	14.86	9.47	28.11	17.96	18.51	23.73	17.80	29.10	23.54
13	166-9	23.00	23.57	24.12	23.56	34.53	11.88	17.26	21.23	38.43	23.00	26.37	29.27
14	220S	21.00	19.00	22.45	20.82	17.63	31.02	32.23	26.96	24.90	23.33	29.83	26.02
15	246K	21.33	20.25	20.12	20.57	12.10	12.81	13.77	12.89	19.10	10.00	13.57	14.22
16	250(K)	18.67	19.91	19.89	19.49	25.40	24.65	27.47	25.84	28.10	41.67	27.53	32.43

Continuation of table 4.1 b….													
17	258 S	20.00	17.03	19.62	18.88	30.20	42.10	19.37	30.56	26.83	23.33	16.63	22.27
18	263K	21.33	21.03	22.14	21.50	21.83	30.25	20.29	24.13	24.50	20.67	23.00	22.72
19	27(K)	24.33	22.50	24.22	23.69	20.73	59.35	21.18	33.76	27.30	52.00	19.87	33.06
20	35(B)	19.00	16.03	18.40	17.81	31.03	27.33	11.84	23.40	25.17	19.33	13.23	19.24
21	51(B)	14.00	11.60	14.10	13.23	17.60	51.00	17.17	28.59	18.60	49.67	17.20	28.49
22	75(S)	17.67	13.30	17.72	16.23	10.97	27.61	13.31	17.29	10.90	20.67	17.07	16.21
23	93(B)	21.00	17.97	20.78	19.92	26.63	26.88	15.93	23.15	30.37	14.67	36.33	27.12
24	95(B)	13.00	10.13	13.77	12.30	10.20	62.80	10.70	27.90	18.00	43.63	21.47	27.70
25	Adithya	22.00	21.57	22.81	22.13	15.83	19.20	28.42	21.15	26.07	17.33	22.27	21.89
26	ADT 43	16.00	17.80	17.23	17.01	7.90	23.46	19.54	16.96	22.70	13.00	16.20	17.30
27	Anjali	21.67	21.28	20.77	21.24	15.10	26.96	17.33	19.80	22.50	16.00	14.83	17.78
28	Govindu	21.67	18.77	20.85	20.43	19.83	29.52	20.77	23.37	22.93	22.00	16.17	20.37
29	IR-64	22.67	22.53	22.67	22.62	9.13	24.96	20.14	18.08	19.80	23.33	17.10	20.08
30	Jaldidhan	20.67	22.35	20.76	21.26	12.37	10.32	15.02	12.57	21.77	4.00	11.77	12.51
31	Jaya	21.33	19.43	23.15	21.31	20.03	18.31	19.63	19.32	22.83	30.67	22.77	25.42
32	MTU1010	23.33	19.57	20.78	21.23	44.60	32.69	16.37	31.22	34.43	29.33	19.10	27.62
33	Prasanna	21.00	24.00	19.90	21.63	14.70	23.88	16.87	18.49	22.47	11.33	16.73	16.84
34	Rasi	20.00	22.23	20.20	20.81	17.00	28.20	18.47	21.22	37.77	13.33	13.10	21.40
35	SBH	24.33	21.37	20.59	22.10	21.57	29.58	16.70	22.62	23.07	16.67	11.50	17.08
36	SM1637	19.00	20.20	19.09	19.43	24.30	21.08	13.31	19.57	33.17	12.00	12.57	19.24
37	SM1876	17.00	15.53	17.02	16.52	12.37	27.28	10.80	16.81	22.07	19.33	12.43	17.94
38	SM219	24.33	17.10	19.19	20.21	32.67	33.42	18.27	28.12	29.47	17.33	21.60	22.80
39	SM349	13.33	14.67	15.56	14.52	5.47	40.57	19.30	21.78	27.07	47.33	26.70	33.70
40	SM363	14.10	22.87	25.14	20.70	7.03	34.91	17.22	19.72	25.90	22.00	24.73	24.21

Continuation of table 4.1 b….

41	SM4014	17.67	17.33	17.00	17.33	16.07	20.27	12.66	16.33	20.10	15.33	16.83	17.42
42	SM4029	20.33	15.80	15.40	17.18	9.50	7.14	16.62	11.09	28.67	10.67	17.17	18.83
43	SM4071	17.67	16.57	16.85	17.03	18.70	23.95	14.59	19.08	32.10	16.67	17.40	22.06
44	SM4076	19.67	13.97	17.12	16.92	33.53	12.13	6.42	17.36	29.00	16.00	8.93	17.98
45	SM4078	20.00	15.40	18.66	18.02	30.90	6.05	15.71	17.55	35.27	12.67	12.60	20.18
46	SM4226	20.67	17.73	17.12	18.51	29.37	21.54	8.61	19.84	28.27	17.33	12.37	19.32
47	SM4231	18.00	15.33	16.83	16.72	15.40	31.13	6.98	17.84	29.77	28.67	10.03	22.82
48	SM4371	20.00	20.93	20.05	20.33	44.70	38.12	22.42	35.08	39.90	34.67	22.10	32.22
49	SM4385	24.33	17.50	17.20	19.68	23.60	15.29	16.38	18.42	39.60	18.67	13.03	23.77
50	SM4406	16.67	20.73	21.70	19.70	18.43	32.94	23.46	24.94	28.03	26.67	20.47	25.06
51	SM4415	17.00	15.60	19.51	17.37	7.93	3.09	15.82	8.95	28.77	10.67	14.93	18.12
52	SM686	18.33	19.93	20.69	19.65	27.73	31.12	33.13	30.66	24.43	20.67	30.10	25.07
53	SM733	20.67	21.24	21.61	21.17	27.20	32.75	18.26	26.07	31.87	24.00	17.47	24.44
54	SM776	21.00	14.58	16.53	17.37	49.17	38.50	12.01	33.22	41.83	22.67	12.13	25.54
55	Sona	23.33	19.18	23.30	21.94	24.53	22.67	21.90	23.03	22.87	23.00	13.17	19.68
56	Tellahamsa	23.00	20.41	22.00	21.80	63.10	28.01	25.89	39.00	71.17	29.33	23.27	41.26
57	Tulasi	19.00	19.92	21.27	20.06	28.77	30.21	24.74	27.91	26.60	21.33	22.10	23.34
58	Vandana	23.00	22.27	21.43	22.23	4.00	22.46	19.48	15.31	23.83	15.33	19.63	19.60
59	Varalu	19.33	16.17	18.78	18.10	12.83	19.65	14.85	15.78	23.50	14.00	15.00	17.50
	Mean	19.54	18.30	19.50	19.11	21.17	26.21	17.94	21.77	27.85	23.71	20.00	23.85
	CV%	11.6	11.49	4.22	8.88	34.93	29.58	23.23	43.49	19.25	33.35	21.92	35.04
	S.E ±	1.3	1.21	0.47	0.98	4.27	4.47	2.4	5.46	3.09	4.56	2.53	4.82
	C.D at 5%	3.66	3.4	1.33	2.74	11.96	12.53	6.74		8.67	12.79	7.09	13.51

Continuation of table 4.1b…

S.NO	GENO	Biological yield per plant				Harvest Index				Per day productivity			
		Rabi 15	*Kharif 15*	*Rabi 16*	Pooled	*Rabi 15*	*Kharif 15*	*Rabi 16*	Pooled	*Rabi 15*	*Kharif 15*	*Rabi 16*	Pooled
1	130K	67.13	45.77	40.79	51.23	56.43	45.20	47.37	49.66	0.26	0.14	0.15	0.18
2	14(S)	50.10	45.64	49.38	48.37	42.58	42.58	56.90	47.35	0.16	0.15	0.22	0.18
3	14-3	37.63	26.62	50.01	38.09	43.28	53.83	42.55	46.55	0.12	0.11	0.15	0.13
4	148S	45.93	80.62	43.26	56.60	31.92	43.63	32.84	36.13	0.12	0.29	0.11	0.17
5	166(S)	48.93	48.18	56.53	51.21	42.22	35.89	46.13	41.41	0.14	0.11	0.10	0.12
6	166-1	61.13	73.12	36.13	56.80	39.64	36.73	44.09	40.15	0.15	0.19	0.11	0.15
7	166-2-11	65.50	41.16	57.90	54.85	39.88	37.43	43.41	40.24	0.17	0.10	0.15	0.14
8	166-23	17.83	33.65	31.43	27.64	23.42	46.24	45.34	38.33	0.02	0.11	0.10	0.08
9	166-2-3	50.70	61.28	48.00	53.33	52.12	40.31	45.45	45.96	0.20	0.21	0.18	0.20
10	166-23-1	33.67	43.48	34.80	37.31	20.12	45.70	29.60	31.80	0.05	0.14	0.07	0.08
11	166-2-9	44.30	95.57	44.33	61.40	35.72	39.63	37.95	37.77	0.11	0.26	0.12	0.16
12	166-30	33.20	45.91	47.06	42.06	30.39	54.94	37.90	41.08	0.06	0.20	0.13	0.13
13	166-9	72.97	34.88	43.63	50.49	46.51	33.69	39.86	40.02	0.25	0.08	0.13	0.15
14	220S	42.53	54.35	62.07	52.98	41.34	53.37	51.90	48.87	0.13	0.24	0.24	0.20
15	246K	31.20	22.81	27.34	27.12	35.80	55.43	50.34	47.19	0.09	0.11	0.12	0.11
16	250(K)	53.50	66.32	55.00	58.27	44.60	35.01	48.81	42.81	0.17	0.17	0.21	0.18
17	258S	57.03	65.43	36.00	52.82	55.91	56.00	55.93	55.94	0.21	0.30	0.14	0.22
18	263K	46.33	50.92	43.29	46.85	46.96	52.93	47.10	51.00	0.16	0.24	0.16	0.19
19	27(K)	48.03	111.35	41.05	66.81	42.72	54.23	51.62	49.52	0.14	0.43	0.16	0.24
20	35(B)	56.20	46.66	25.07	42.65	55.20	54.89	52.27	54.12	0.22	0.22	0.12	0.19
21	51(B)	36.20	100.67	34.37	57.08	49.07	50.71	50.02	49.93	0.12	0.40	0.11	0.21

Continuation of table 4.1 b….

22	75(S)	21.87	48.28	30.37	33.51	50.33	57.52	44.03	50.63	0.07	0.19	0.10	0.12
23	93(B)	57.00	41.54	52.26	50.27	46.69	55.10	41.28	47.69	0.18	0.22	0.11	0.17
24	95(B)	28.20	106.43	32.17	55.60	36.70	49.00	43.25	42.98	0.06	0.43	0.07	0.19
25	Adithya	41.90	36.53	50.69	43.04	38.03	52.95	55.66	48.88	0.13	0.16	0.24	0.18
26	ADT 43	30.60	36.46	35.74	34.26	34.85	52.44	54.63	47.31	0.06	0.19	0.14	0.13
27	Anjali	37.60	42.96	32.16	37.57	49.75	52.42	53.55	51.91	0.13	0.23	0.15	0.17
28	Govindu	42.77	51.52	36.94	43.74	47.99	55.29	55.12	52.80	0.14	0.23	0.17	0.18
29	IR-64	28.93	48.29	37.24	38.16	31.00	51.88	53.99	45.62	0.07	0.18	0.16	0.13
30	Jaldidhan	34.13	14.32	26.78	25.08	52.34	53.01	52.15	52.50	0.10	0.10	0.13	0.11
31	Jaya	42.87	48.97	42.40	44.75	46.69	36.87	46.27	43.28	0.13	0.13	0.13	0.13
32	MTU1010	79.03	62.03	35.47	58.84	56.52	53.00	45.82	51.78	0.32	0.24	0.13	0.23
33	Prasanna	37.17	35.22	33.61	35.33	48.25	50.60	49.85	49.56	0.12	0.23	0.16	0.17
34	Rasi	54.77	41.54	31.57	42.62	44.99	57.72	54.46	52.39	0.13	0.24	0.17	0.18
35	SBH	44.63	46.25	28.20	39.70	53.94	54.27	53.94	54.05	0.16	0.25	0.15	0.19
36	SM1637	57.47	33.08	25.88	38.81	53.65	54.71	51.57	53.31	0.20	0.18	0.12	0.17
37	SM1876	34.43	46.61	23.23	34.76	39.97	54.73	46.58	47.09	0.09	0.21	0.09	0.13
38	SM219	62.13	50.75	39.87	50.92	48.78	56.76	54.61	53.38	0.25	0.27	0.14	0.22
39	SM349	32.53	87.91	46.00	55.48	17.03	46.12	42.42	35.19	0.04	0.36	0.15	0.18
40	SM363	32.93	56.91	41.95	43.93	29.04	51.18	41.37	40.53	0.06	0.25	0.12	0.14
41	SM4014	36.17	35.60	29.50	33.76	44.16	56.48	42.92	47.85	0.12	0.17	0.12	0.13
42	SM4029	38.17	17.81	33.79	29.92	24.79	37.64	49.10	37.18	0.07	0.06	0.15	0.09
43	SM4071	50.80	40.62	31.99	41.13	40.60	54.92	45.33	46.95	0.14	0.20	0.12	0.15
44	SM4076	62.53	28.13	15.35	35.34	52.38	44.68	41.81	46.29	0.25	0.09	0.06	0.13
45	SM4078	66.17	18.72	28.31	37.73	46.53	33.20	55.35	45.03	0.22	0.05	0.15	0.14

Continuation of table 4.1 b….

46	SM4226	57.63	38.87	20.98	39.16	50.80	55.66	41.25	49.24	0.22	0.19	0.08	0.16
47	SM4231	45.17	59.79	17.01	40.66	33.93	51.75	39.22	41.63	0.13	0.26	0.06	0.15
48	SM4371	84.60	72.79	44.52	67.30	52.37	52.78	51.09	52.08	0.33	0.32	0.19	0.28
49	SM4385	63.20	33.96	29.41	42.19	37.53	45.43	55.96	46.31	0.16	0.13	0.16	0.15
50	SM4406	46.47	59.61	43.92	50.00	38.96	55.44	53.41	49.27	0.14	0.26	0.21	0.20
51	SM4415	36.70	13.75	30.75	27.07	21.43	22.79	51.24	31.82	0.06	0.03	0.14	0.07
52	SM686	52.17	51.78	63.23	55.73	54.01	55.03	53.15	54.06	0.22	0.26	0.27	0.25
53	SM733	59.07	56.75	35.73	50.51	46.08	57.54	51.22	51.62	0.21	0.26	0.14	0.20
54	SM776	91.00	61.16	24.14	58.77	52.61	52.91	53.45	53.09	0.37	0.31	0.11	0.26
55	Sona	47.40	45.67	35.07	42.71	51.75	49.44	52.59	51.39	0.18	0.17	0.18	0.17
56	Tellahamsa	134.27	57.35	49.16	80.26	46.57	49.17	52.71	49.48	0.47	0.23	0.22	0.30
57	Tulasi	55.37	51.55	46.84	51.25	53.71	55.46	52.96	54.04	0.21	0.24	0.20	0.22
58	Vandana	27.83	37.79	39.11	34.91	18.48	55.91	49.49	41.29	0.03	0.20	0.17	0.13
59	Varalu	36.33	33.65	29.85	33.28	35.08	57.51	49.81	47.46	0.10	0.17	0.12	0.13
	Mean	49.02	49.92	37.94	45.63	40.60	52.38	47.51	46.83	0.15	0.20	0.14	0.16
	CV%	21.65	24.43	19.77	35.7	18.98	16.36	9.91	19	35.20	28.80	23.29	42.06
	S.E ±	6.12	7.04	4.33	9.40	4.44	4.95	2.72	5.10	0.03	0.03	0.01	0.04
	C.D at 5%	17.16	19.72	12.13		12.45	13.86	7.62	14.39	0.08	0.09	0.05	

4.1.1. Days to 50 per cent flowering

Days to 50 per cent flowering ranged from 94 to 137 days with a general mean of 110.22 days during *Rabi* 2014-15. Among all the genotype, Adithya flowered earlier to the check Prasanna (95.00 days). 95B flowered late among all the genotypes.

Days to 50 per cent flowering ranged from 81 to 127 days with a general mean of 102.34 days during *Kharif* 2015. Among all the genotype, check Prasanna flowered earlier than others and the genotype 166-1 flowered late among all the genotypes.

Days to 50 per cent flowering ranged from 69 to 135 days with a general mean of 94.38 days during *Rabi* 2015-16 (Fig 4.1.1). Among all the genotype, SM4385 flowered five days earlier and 35 B flowered three days earlier to the check Prasanna (74 days). 166 S and 166-2-11 flowered late among all the genotypes Pooled analysis over three seasons revealed that among all the genotypes tested, days to 50 per cent flowering ranged from 83.33 to 132 days with a general mean of 102.47 days. Among all the genotype, check Prasanna flowered earlier. 95B flowered late among all the genotypes.

4.1.2. Days to maturity

Days to maturity ranged from 119 to 163 days with a general mean of 138.16 days during *Rabi* 2014-15. Among all the genotype, Adithya matured along with check Prasanna (120 days). While 166-23 genotype flowered late among all the genotypes.

Days to maturity ranged from 102 to 154 days with a general mean of 128.88 days during *Kharif* 2015. Among all the genotype, check Prasanna matured earlier than other genotypes, while 166-2-11 genotype flowered late among all the genotypes.

Days to maturity ranged from 100 to 165 days with a general mean of 125.77 days during *Rabi* 2015-16 (Fig. 4.1.2). Among all the genotype, SM4385 matured three days earlier to check Prasanna (103 days). While 166-2-11 genotype flowered late among all the genotypes.

Figure 4.1.1. Box plot for DFF

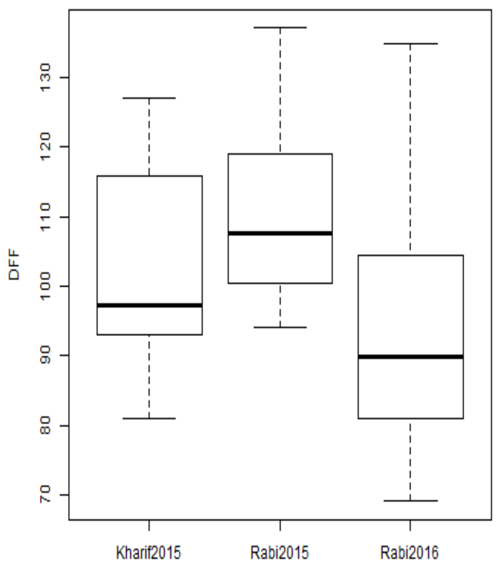


Figure 4.1.2. Box plot for DM

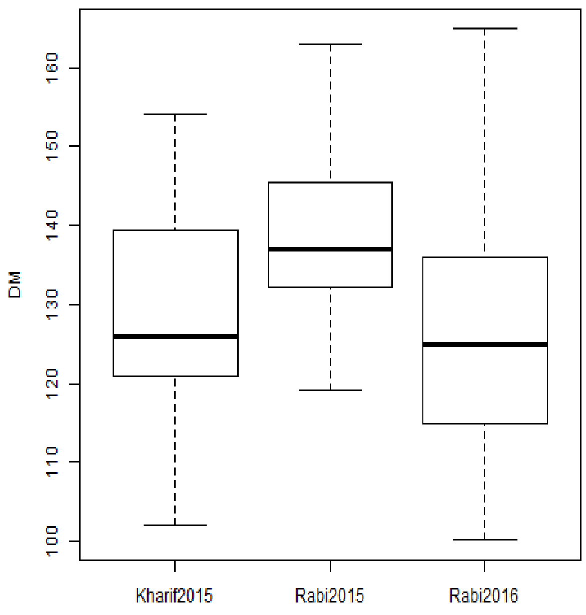
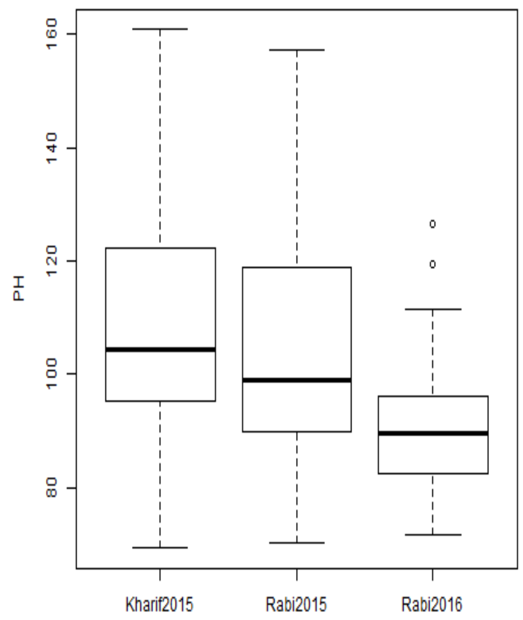


Figure 4.1.3. Box plot for PH



Pooled analysis over three seasons revealed that among all the genotypes tested, days to maturity ranged from 108.33 to 157.33 days with a general mean of 130.94 days. Among all the genotype, check Prasanna matured earlier. Among all the genotypes 166-2-11 genotype flowered late.

4.1.3. Plant height

Plant height ranged from 69.33 to 157.66 cm with a general mean of 103.46 cm during *Rabi* 2014-15. The shortest genotype was 51 B while the tallest genotype was 148 S which was 2.27 times taller than 51 B. Among all other genotypes 51 B and 75 S (77 cm) genotypes were lower in height compared to check Prasanna (80.33 cm).

Plant height ranged from 68.33 to 161.33 cm with a general mean of 107.62 cm during *Kharif* 2015. The shortest genotype was 14-3 while the tallest genotype was 148 S which was 1.99 times taller than check Prasanna. Among all other genotypes 14-3 and 220 S (74 cm) genotypes were lower in height compared to check Prasanna (81 cm).

Plant height ranged from 71.66 to 127.33 cm with a general mean of 90.21 cm during *Rabi* 2015-16 (Fig. 4.1.3). The shortest genotype was 75 S while the tallest genotype was SM349 which was 1.26 times taller than 75 S. Check Prasanna recorded plant height of about (100.46 cm).

Pooled analysis over three seasons revealed that among all the genotypes tested, plant height ranged from 76.77 to 145.77 cm with a general mean of 100.43 cm during. The shortest genotype was 14-3 while the tallest genotype was 148 S. Among all other genotypes Jaldidhan (80.22 cm), 51 B (80.55 cm), 95 B (82.33 cm), 220 S (82, 88 cm), 166-23 (84 cm), Govindu (84 cm), 93 B (84.66 cm), IR64 (85 cm), 263 K(85.22 cm) and 246 K (85.88 cm) genotypes were lower in height compared to check Prasanna (87.26 cm).

4.1.4. Number of total tillers per plant

The mean number of total tillers per plant ranged from 9 to 34.63 with a general mean of 16.81 during *Rabi* 2014-15. Lowest number of tillers per plant was seen in Jaldidhan and highest in SM776, where as check Prasanna beared total 16.33 tillers per plant.

The mean number of total tillers per plant ranged from 8.66 to 36 with a general mean of 15.06 during *Kharif* 2015 (Fig. 4.1.4). Lowest number of tillers per plant was seen in 166-30 and highest in 51 B, where as check Prasanna had total 18 tillers per plant.

The mean number of total tillers per plant ranged from 9.66 to 30 with a general mean of 18.37 during *Rabi* 2015-16. Lowest number of tillers per plant was seen in 166-9 and highest in 14 S, where as check Prasanna beared total 23.66 tillers per plant.

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean number of total tillers per plant ranged from 12 to 26.22 with a general mean of 16.74. Lowest number of tillers per plant was seen in Anjali and highest in 51 B, where as check Prasanna beared total 19.55 tillers per plant.

4.1.5. Number of productive tillers per plant

The mean number of productive tillers per plant ranged from 7.33 to 34.33 tillers with a general mean of 16.02 tillers per plant during *Rabi* 2014-15 (Fig. 4.1.5). Lowest productive tillers were seen in SM4076 genotype and highest productive tillers were recorded in genotype SM776. Whereas check Prasanna recorded 21.83 productive tillers per plant.

The mean number of productive tillers per plant ranged from 7.33 to 36 tillers with a general mean of 14.11 tillers per plant during *Kharif* 2015. Lowest productive tillers were seen in 166 S genotype and highest productive tillers were recorded in genotype 51 B. Whereas check Prasanna recorded 17.33 productive tillers per plant.

The mean number of productive tillers per plant ranged from 9.66 to 25.33 tillers with a general mean of 16.62 tillers per plant during *Rabi* 2015-16. Lowest productive tillers were seen in 166-9 and 166-2-11 genotype and highest productive tillers were recorded in genotype 14 S. Whereas check Prasanna recorded 23.33 productive tillers per plant.

Figure 4.1.4. Box plot for TN

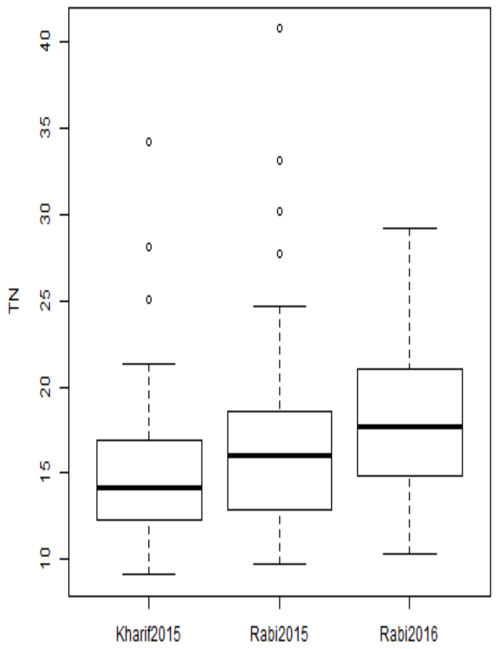


Figure 4.1.5. Box plot for PTN

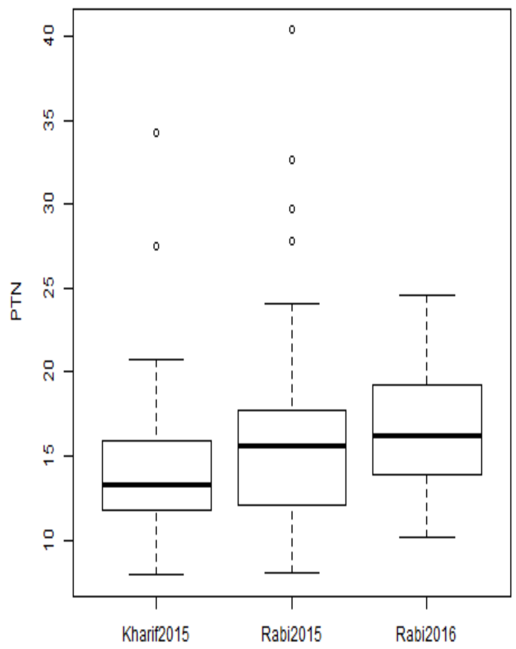
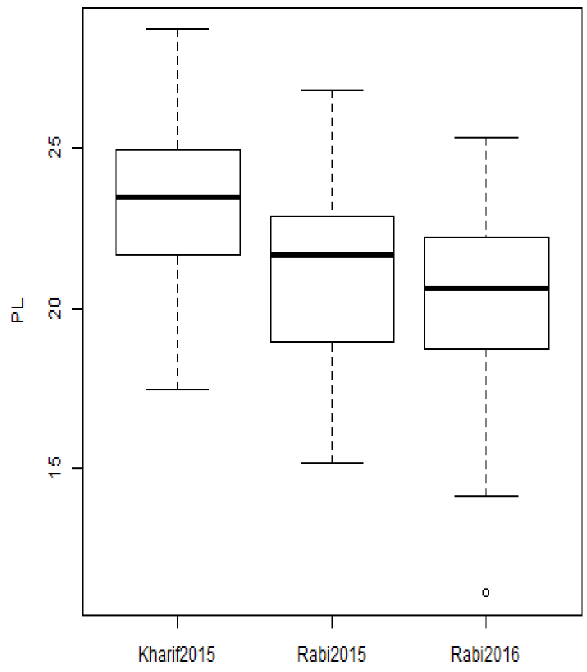


Figure 4.1.6. Box plot for PL



Pooled analysis over three seasons revealed that among all the genotypes tested, the mean number of productive tillers per plant ranged from 11 to 26.22 tillers with a general mean of 15.58 tillers per plant. Lowest productive tillers were seen in Sona and highest productive tillers were recorded in genotype 51 B. Whereas check Prasanna recorded 19 productive tillers per plant.

4.1.6. Panicle length

The panicle length ranged from 13.66 to 27.44 cm with a general mean of 21.09 cm during *Rabi* 2014-15. The genotype SM363 has recorded shorter panicle and the genotype 166-2-9 exhibited highest value, which was almost 5.61 cm longer than check Prasanna (21.8 cm).

The panicle length ranged from 17.76 to 29.5 cm with a general mean of 23.46 cm during *Kharif* 2015. The genotype SM4029 has recorded shorter panicle and the genotype Rasi exhibited highest value, which was almost 1.31 cm longer than check Prasanna (22.4 cm).

The panicle length ranged from 10 to 25.5 cm with a general mean of 20.38 cm during *Rabi* 2015-16 (Fig. 4.1.6). The genotype SM4029 has recorded shorter panicle and the genotype 148 S exhibited highest value, which was almost 3.74 cm longer than check Prasanna (21.76 cm).

Pooled analysis over three seasons revealed that among all the genotypes tested, the panicle length ranged from 14.94 to 26.13 cm with a general mean of 21.64 cm. The genotype SM4029 has recorded shorter panicle and the genotype 148 S exhibited highest value, where as check Prasanna recorded 22 cm panicle length.

4.1.7. Panicle weight

The mean value for panicle weight ranged from 0.36 to 5.53 g during *Rabi* 2014-15 with a general mean of 2.07 g. The genotype 14-3 recorded lowest panicle weight and the genotype 166-30 exhibited highest panicle weight, which has recorded 4.45 g more compared to check Prasanna (1.24 g).

The mean value for panicle weight ranged from 1.41 to 5.79 g during *Kharif* 2015 with a general mean of 2.91 g (Fig. 4.1.7). The genotype SM4385 recorded lowest panicle weight and the genotype 166-30 exhibited highest panicle weight, which has recorded 3.58 g more compared to check Prasanna (2.21 g).

The mean value for panicle weight ranged from 1.01 to 3.86 g during *Rabi* 2015-16 with a general mean of 1.99 g. The genotype 51 B has recorded lowest panicle weight and the genotype 166-30 exhibited highest panicle weight, which has recorded 1.98 g more compared to check Prasanna (1.85 g).

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean value for panicle weight ranged from 1.24 to 5.06 g with a general mean of 2.32 g. The genotype SM4415 recorded lowest panicle weight and the genotype 166-30 exhibited highest panicle weight, check Prasanna recorded 1.77g panicle weight.

4.1.8. Number of filled grains per panicle

The mean values for number of filled grains per panicle ranged from 38.66 to 290.66 with general mean of about 111.79 during *Rabi* 2014-15 (Fig. 4.1.8). The genotype 14-3 recorded lowest number of filled grains per panicle and genotype 166-30 exhibited highest number of filled grains per panicle, which was 4.38 times the number of filled grains per panicle of check Prasanna (66.33).

The mean values for number of filled grains per panicle ranged from 60.33 to 305 with general mean of about 146.61 during *Kharif* 2015. The genotype SM4385 recorded lowest number of filled grains per panicle and genotype 166-30 exhibited highest number of filled grains per panicle, which was 3.27 times double the number of filled grains per panicle of check Prasanna (93).

The mean values for number of filled grains per panicle ranged from 52.66 to 209 with general mean of about 100.04 during *Rabi* 2015-16. The genotype Tulasi recorded lowest number of filled grains per panicle and genotype 166-30 exhibited highest number of filled grains per panicle, which was 2.54 times double the number of filled grains per panicle of check Prasanna (82).

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for number of filled grains per panicle ranged from 63.22 to 268.22 with general mean of about 119.48. The genotype Jaldidhan recorded lowest number of filled grains per panicle and genotype 166-30 exhibited highest number of filled grains per panicle, check Prasanna recorded has 80.44 numbers of filled grains per panicle.

Figure 4.1.7. Box plot for PW

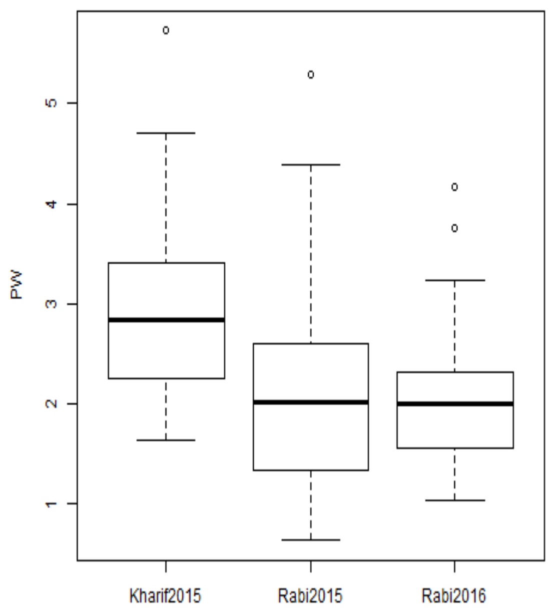


Figure 4.1.8. Box plot for FG

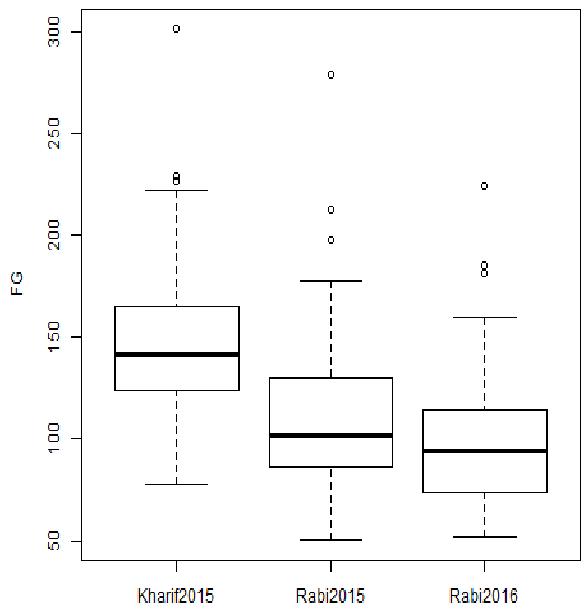
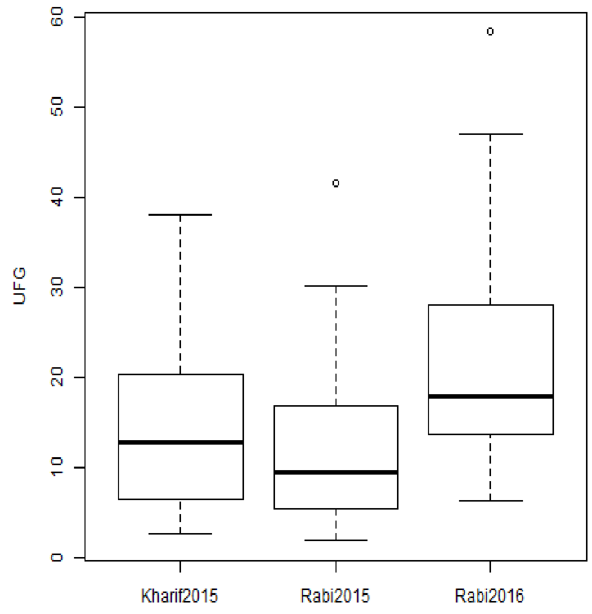


Figure 4.1.9. Box plot for UFG



4.1.9. Number of unfilled grains per panicle

The mean values for number of unfilled grains per panicle ranged from 1.00 to 42 with general mean 11.52 during *Rabi* 2014-15 (Fig. 4.1.9). The genotype SM1876 recorded lowest number of unfilled grains per panicle and genotype 166-30 exhibited highest number of unfilled grains per panicle, where as the number of unfilled grains per panicle of check Prasanna was 22.33.

The mean values for number of unfilled grains per panicle ranged from 1.33 to 42 with general mean 14.61 during *Kharif* 2015. The genotype 220 S recorded lowest number of unfilled grains per panicle and genotype SM363 exhibited highest number of unfilled grains per panicle, where as the number of unfilled grains per panicle of check Prasanna was 22.33.

The mean values for number of unfilled grains per panicle ranged from 3.00 to 62.66 with general mean 21.68 during *Rabi* 2015-16. The genotype SM4226 recorded lowest number of unfilled grains per panicle and genotype 166-30 exhibited highest number of unfilled grains per panicle, where as the number of unfilled grains per panicle of check Prasanna was 29.33.

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for number of unfilled grains per panicle ranged from 5.33 to 44.77 with general mean 15.93. The genotype 95 B recorded lowest number of unfilled grains per panicle and genotype 166-30 exhibited highest number of unfilled grains per panicle, where as the number of unfilled grains per panicle of check Prasanna was 24.66.

4.1.10. Number of total grains per panicle

The mean values for number of total grains per panicle ranged from 50.66 to 332.66 with general mean of 123.31 during *Rabi* 2014-15. The genotype SM4014 recorded lowest number of total grains per panicle and genotype 166-30 exhibited highest number of total grains per panicle, which was 1.39 times more than the number of total grains per panicle of check Prasanna (88.66).

The mean values for number of total grains per panicle ranged from 75.33 to 334.66 with general mean of 161.23 during *Kharif* 2015 (Fig. 4.1.10). The genotype

SM4415 recorded lowest number of total grains per panicle and genotype 166-30 exhibited highest number of total grains per panicle, which was 2.07 times more than the number of total grains per panicle of check Prasanna (115.33).

The mean values for number of total grains per panicle ranged from 66 to 271.66 with general mean of 121.72 during *Rabi* 2015-16. The genotype Tulasi recorded lowest number of total grains per panicle and genotype 166-30 exhibited highest number of total grains per panicle, which was only 1.09 times more than the number of total grains per panicle of check Prasanna (111.33).

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for number of total grains per panicle ranged from 75.77 to 313 with general mean of 135.42. The genotype SM4415 recorded lowest number of total grains per panicle and genotype 166-30 exhibited highest number of total grains per panicle, check Prasanna recorded 105.11 total grains per panicle.

4.1.11. Spikelet fertility

The mean values for spikelet fertility ranged from 61.16 to 98.71 with a general mean of about 90.43 during *Rabi* 2014-15 (Fig. 4.1.11). The genotype 14-3 showed lowest spikelet fertility and genotype SM1876 exhibited highest number of spikelet fertility, which was only 1.23 times more than the spikelet fertility of check Prasanna (73.46).

The mean values for spikelet fertility ranged from 75.53 to 98.83 with a general mean of about 90.77 during *Kharif* 2015. The genotype 166-1 shown lowest spikelet fertility and genotype 220 S exhibited highest number of spikelet fertility, which was only 1.12 times more than the spikelet fertility of check Prasanna (80.88).

The mean values for spikelet fertility ranged from 60.67 to 97.22 with a general mean of about 82.73 during *Rabi* 2015-16 (Fig. 4.1.11). The genotype SM733 has shown lowest spikelet fertility and genotype 95 B exhibited highest number of spikelet fertility, which was only 1.29 times more than the spikelet fertility of check Prasanna (74.85).

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for spikelet fertility ranged from 70.97 to 97.19 with a general mean of about 87.97. The genotype Jaldidhan shown lowest spikelet fertility

Figure 4.1.10. Box plot for TGP

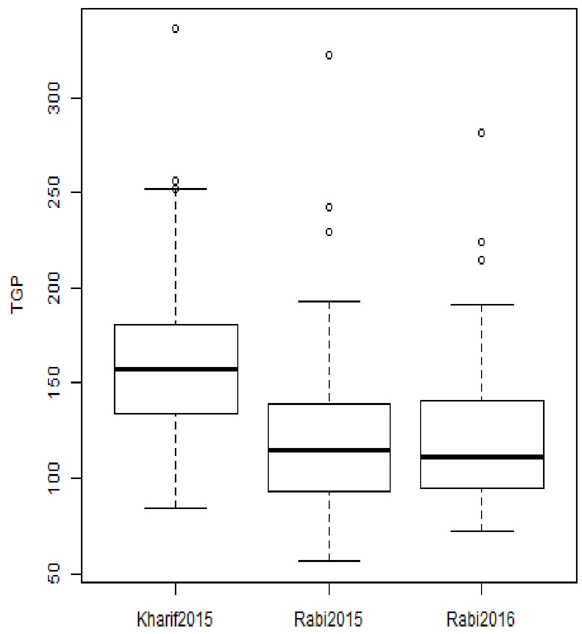


Figure 4.1.11. Box plot for SF

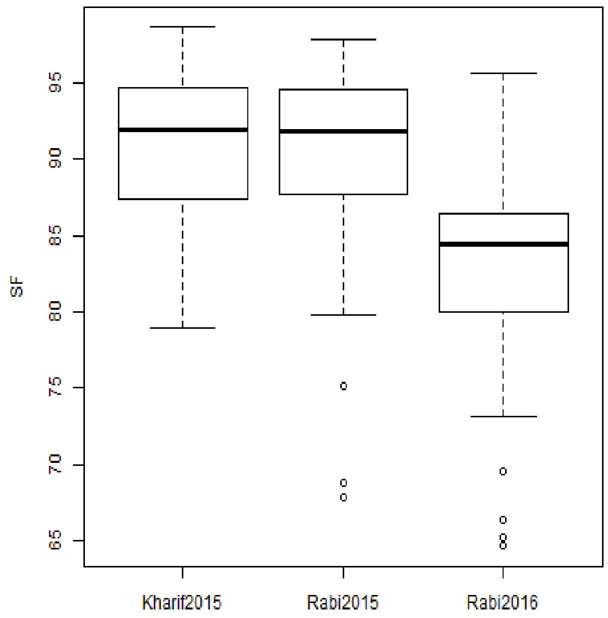
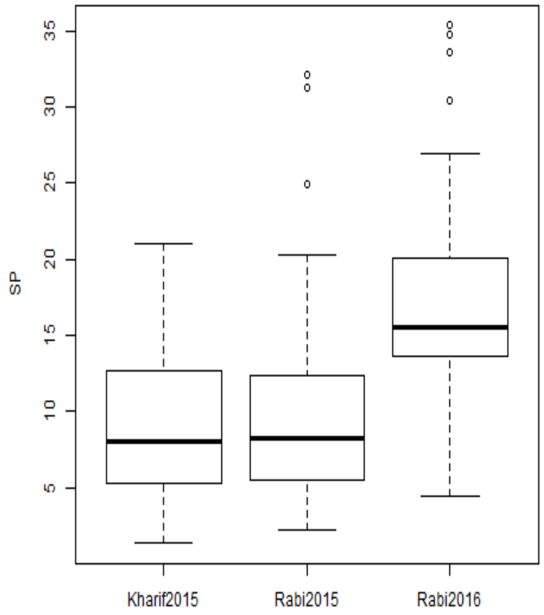


Figure 4.1.12. Box plot for SP



and genotype 95 B exhibited highest number of spikelet fertility, check Prasanna recorded spikelet fertility of about 76.23.

4.1.12. Sterility percentage

Sterility percentage mean values ranged from 1.28 to 38.83 with general mean of 9.59 during *Rabi* 2014-15 (Fig. 4.1.12). The genotype 166-30 shown lowest sterility percentage and genotype 148S exhibited highest number of sterility percentage, where as check Prasanna recorded sterility percentage of about 26.53.

Sterility percentage mean values ranged from 1.16 to 24.46 with general mean of 9.22 during *Kharif* 2015. The genotype 220 S shown lowest sterility percentage and genotype 166-1 exhibited highest number of sterility percentage, where as check Prasanna recorded sterility percentage of about 19.61.

Sterility percentage mean values ranged from 2.77 to 39.32 with general mean of 17.26 during *Rabi* 2015-16. The genotype 95 B shown lowest sterility percentage and genotype SM733 exhibited highest number of sterility percentage, where as check Prasanna recorded sterility percentage of about 25.14.

Pooled analysis over three seasons revealed that among all the genotypes tested, sterility percentage mean values ranged from 2.80 to 29.02 with general mean of 12.02. The genotype 95 B shown lowest sterility percentage and genotype Jaldidhan exhibited highest number of sterility percentage, where as check Prasanna recorded sterility percentage of about 23.76.

4.1.13. Thousand grain weight (g)

The general mean value of thousand grain weight was 19.54 g and the mean values ranged from 11.00 to 25.33 g during *Rabi* 2014-15 (Fig. 4.1.13). Among the genotypes investigated genotype 166-23 shown lowest thousand grain weight. 148S shown highest thousand grain weight which was 4.33 g more than the check Prasanna (21.00 g).

The general mean value of thousand grain weight was 18.29 g and the mean values ranged from 9.73 to 24 g during *Kharif* 2015. Among the genotypes investigated genotype 166-23 shown lowest thousand grain weight and the check Prasanna shown highest thousand grain weight.

The general mean value of thousand grain weight was 19.49 g and the mean values ranged from 12.5 to 25.14 g during *Rabi* 2015-16. Among the genotypes investigated genotype 166-23 shown lowest thousand grain weight. SM363 had shown highest thousand grain weight which was 5.42 g more than the check Prasanna (19.90 g).

Pooled analysis over three seasons revealed that among all the genotypes tested, the general mean value of thousand grain weight was 19.11 g and the mean values ranged from 11.07 to 23.87g. Among the genotypes investigated genotype 166-23 shown lowest thousand grain weight. 148 S had shown highest thousand grain weight. Check Prasanna recorded 21.63 g thousand grain weight.

4.1.14. Single plant grain yield

The general mean value for single plant grain yield was 21.17g and the mean value ranged from 3.80 to 63.10 g during *Rabi* 2014-15 (Fig. 4.1.14). The genotype 166-23 recorded lowest single plant grain yield while the genotype Tellahamsa exhibited highest single plant grain yield. Whereas check Prasanna has recorded 14.7 g for single plant grain yield.

The general mean value for single plant grain yield was 26.20 g and the mean value ranged from 3.08 to 62.80 g during *Kharif* 2015. The genotype SM4415 recorded lowest single plant grain yield while the genotype 95 B exhibited highest single plant grain yield. Whereas check Prasanna has recorded 23.88 g for single plant grain yield.

The general mean value for single plant grain yield was 17.93 g and the mean value ranged from 6.42 to 33.13 g during *Rabi* 2015-16. The genotype SM4076 recorded lowest single plant grain yield while the genotype SM686 exhibited highest single plant grain yield. Whereas check Prasanna has recorded 16.87g for single plant grain yield.

Pooled analysis over three seasons revealed that among all the genotypes tested, the general mean value for single plant grain yield was 21.77 g and the mean value ranged from 8.94 to 39 g. The genotype SM4415 recorded lowest single plant grain yield while the genotype Tellahamsa exhibited highest single plant grain yield. Whereas check Prasanna has recorded 18.48 g for single plant grain yield.

Figure 4.1.13. Box plot for TGW

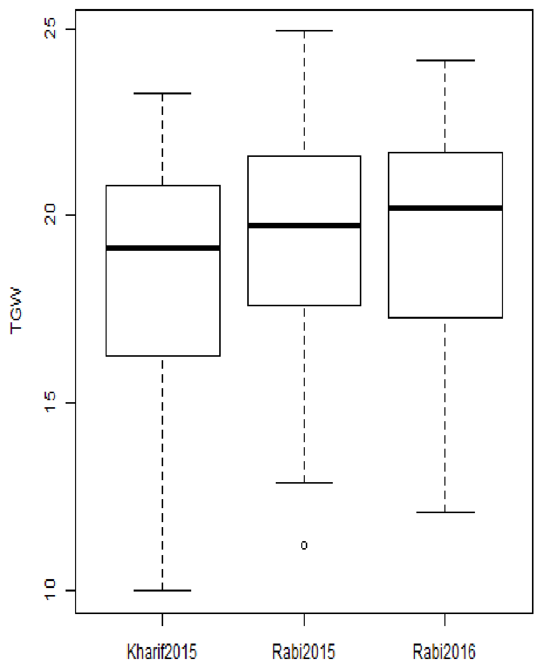


Figure 4.1.14. Box plot for SPY

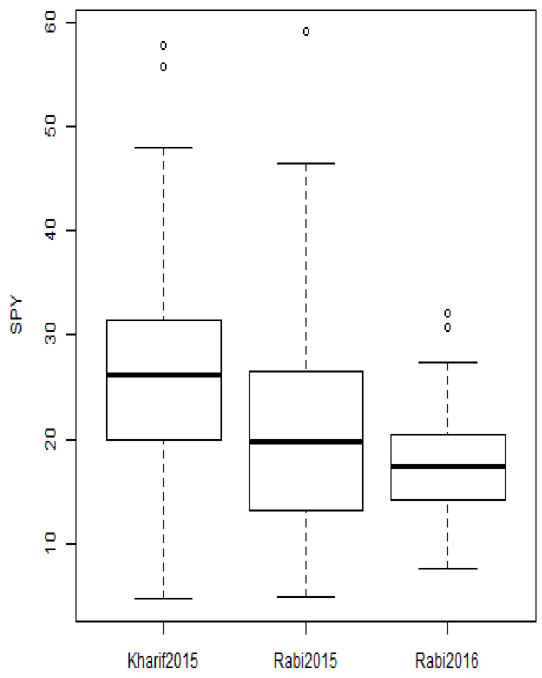
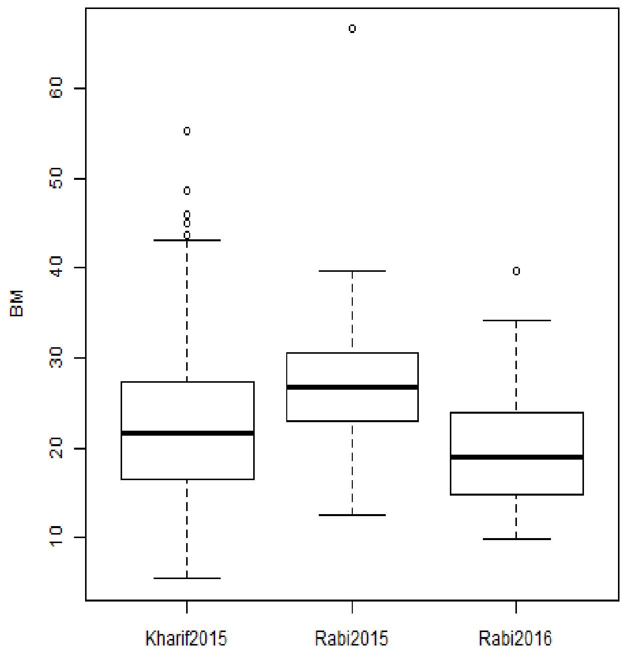


Figure 4.1.15. Box plot for BM



4.1.15. Biomass per plant

The mean values for biomass ranged from 10.90 to 71.16 g with a general mean of about 27.84 g during *Rabi* 2014-15 (Fig. 4.1.15). The genotype 75S shown lowest biomass per plant and genotype Tellahamsa exhibited highest biomass per plant, which was 2.55 times more than biomass per plant of check Prasanna (22.46 g).

The mean values for biomass ranged from 4 to 59 g with a general mean of about 23.71 g during *Kharif* 2015. The genotype Jaldidhan shown lowest biomass per plant and genotype 166-2-9 exhibited highest biomass per plant, which was 5.2 times more than biomass per plant of check Prasanna (11.33 g).

The mean values for biomass ranged from 8.93 to 41.7g with a general mean of about 20.00 g during *Rabi* 2015-16. The genotype SM4076 shown lowest biomass per plant and genotype 166 S exhibited highest biomass per plant, which was 2.54 times more than biomass per plant of check Prasanna (16.73 g).

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for biomass ranged from 12.51 to 41.25 g with a general mean of about 23.85 g. The genotype Jaldidhan shown lowest biomass per plant and genotype Tellahamsa exhibited highest biomass per plant, check Prasanna recorded 16.84 g biomass per plant.

4.1.16. Biological yield per plant

The mean values for biological yield per plant ranged from 17.83 to 134.26 g with a general mean of about 49.018 g during *Rabi* 2014-15 (Fig. 4.1.16). The genotype 166-23 shown lowest biological yield per plant and genotype Tellahamsa exhibited highest biological yield per plant, which was 97.1 g more than biological yield per plant of check Prasanna (37.16 g).

The mean values for biological yield per plant ranged from 13.75 to 111.35 g with a general mean of about 49.92 g during *Kharif* 2015. The genotype SM4415 shown lowest biological yield per plant and genotype 27 K exhibited highest biological yield per plant, which was 76.14 g more than biological yield per plant of check Prasanna (35.21 g).

The mean values for biological yield per plant ranged from 15.35 to 62.23 g with a general mean of about 37.94 g during *Rabi* 2015-16. The genotype SM4076 shown lowest biological yield per plant and genotype SM686 exhibited highest biological yield per plant, which was 28.63 g more than biological yield per plant of check Prasanna (33.6 g).

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for biological yield per plant ranged from 25.07 to 80.25 g with a general mean of about 45.62 g. The genotype Jalididhan shown lowest biological yield per plant and genotype Tellahamsa exhibited highest biological yield per plant, check Prasanna recorded 35.33 g of biological yield per plant.

4.1.17. Harvest index

The mean values for harvest index ranged from 15.48 to 56.51 with a general mean of about 40.60 during *Rabi* 2014-15. The genotype Vandana shown lowest harvest index and genotype MTU 1010 exhibited highest harvest index, which was 1.47 times more than the harvest index of check Prasanna (48.24).

The general mean value for harvest index was 52.38 during *Kharif* 2015. The genotype SM4415 (22.76) shown lowest harvest index and SM219 exhibited highest harvest index of about 56.76. Check Prasanna recorded harvest index of about 50.60

The general mean value for harvest index was 47.51 during *Rabi* 2015-16. The genotype 14 S exhibited highest harvest index of about 56.90, whereas check Prasanna recorded harvest index of about 49.85.

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for harvest index ranged from 31.80 to 55.94 with a general mean of about 46.83. The genotype 166-23-1 shown lowest harvest index and genotype 258 S exhibited highest harvest index, check Prasanna recorded harvest index of about 49.56

4.1.18. Per day productivity

The mean values for per day productivity ranged from 0.02 to 0.47 g with a general mean of about 0.15 g during *Rabi* 2014-15 (Fig. 4.1.18). The genotype 166-23 shown lowest per day productivity and genotype Tellahamsa exhibited highest

Figure 4.1.16.Box plot for BY

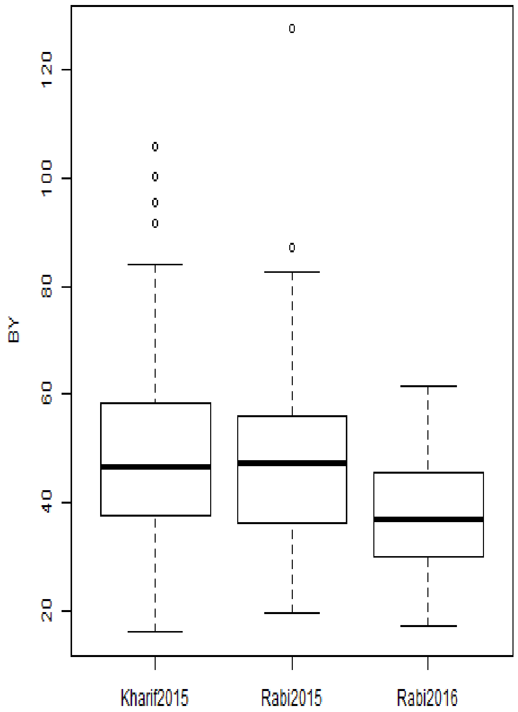
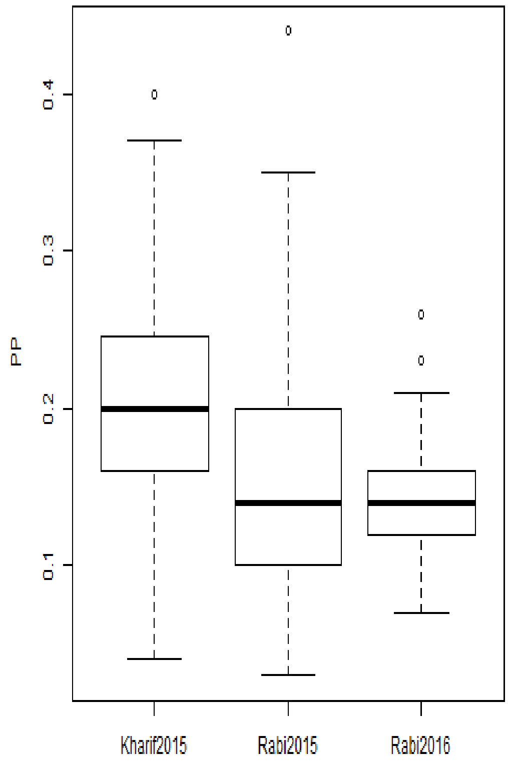


Figure 4.1.18. Box plot for PP



per day productivity, whereas check Prasanna recorded per day productivity of about 0.12 g.

The mean values for per day productivity ranged from 0.03 to 0.43 g with a general mean of about 0.20 g during *Kharif* 2015. The genotype SM4415 shown lowest per day productivity and genotype 95 B exhibited highest per day productivity, whereas check Prasanna recorded per day productivity of about 0.23 g.

The mean values for per day productivity ranged from 0.06 to 0.27 g with a general mean of about 0.14 g during *Rabi* 2015-16. The genotype 166-23-1 shown lowest per day productivity and genotype SM686 exhibited highest per day productivity, whereas check Prasanna recorded per day productivity of about 0.16 g.

Pooled analysis over three seasons revealed that among all the genotypes tested, the mean values for per day productivity ranged from 0.07 to 0.30 g with a general mean of about 0.16 g. The genotype 166-23 shown lowest per day productivity and genotype Tellahamsa exhibited highest per day productivity, whereas check Prasanna recorded per day productivity of about 0.17 g.

4.2. GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The genotypic and phenotypic coefficients of variation (Fig. 4.2 a), heritability and genetic advance as per cent of mean (Fig. 4.2 b) were estimated for fifty nine genotypes and results are furnished in Table 4.2.

4.2.1. Days to 50 per cent flowering

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation were moderate i.e., 10.77 and 10.87, respectively. The heritability observed for this trait was high (98.2%) with high genetic advance as per cent of mean (22.00) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the seed yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation were moderate i.e., 12.31 and 12.38, respectively. The heritability observed for this trait was high (98.9%) with high genetic advance as per cent of mean (25.23).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation were moderate i.e., 18.36 and 18.39, respectively. The heritability observed for this trait was high (99.7%) with high genetic advance as per cent of mean (37.75).

The results were in conformity with Singh *et al.* (2012), Bekele *et al.* (2013), Soni *et al.* (2013) and Sravan *et al.* (2014) for moderate gcv and pcv.

Dinesh *et al.* (2011), Soni *et al*. (2013) and Kishore *et al.* (2015) for high heritability coupled with high genetic advance as per cent of mean.

4.2.2. Days to maturity

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation were low i.e., 8.10 and 8.18, respectively. The heritability observed for this trait was high (97.9%) with moderate genetic advance as per cent of mean (16.51) indicating that this trait is governed by both additive and non additive gene effect. This trait can be improved through recurrent selection method or simple selection would be effective for this trait improvement.

Table 4.2. Estimates of range, variability, heritability, genetic advance for single plant grain yield and its components in 59 rice genotypes for three seasons

Genetic variability parameters		Days to fifty percent flowering			Days to maturity			Plant height		
		Rabi **15**	***Kharif*** **15**	***Rabi*** **16**	***Rabi*** **15**	***Kharif*** **15**	***Rabi*** **16**	***Rabi*** **15**	***Kharif*** **15**	***Rabi*** **16**
General Mean		110.26	102.34	94.38	138.16	128.88	125.77	103.46	107.62	90.21
Range	**Min**	94.00	81.00	69.00	119.00	102.00	100.00	69.33	68.33	71.66
	Max	137.00	127.00	135.00	163.00	154.00	165.00	157.66	161.33	127.33
PCV		10.87	12.38	18.39	8.18	9.47	12.17	18.43	18.35	11.70
GCV		10.77	12.31	18.36	8.10	9.44	12.14	17.97	17.59	10.79
h2(Broad Sense)		98.20	98.90	99.70	97.90	98.90	99.50	95.10	91.90	85.10
GA at 5%		24.25	25.82	35.63	22.81	24.93	31.39	37.37	37.39	18.49
GA as % of Mean at 5%		22.00	25.23	37.75	16.51	19.34	24.96	36.12	34.74	20.50

Continuation of table 4.2…

Genetic variability parameters		No. of total tillers per plant			No. of productive tillers per plant			Panicle Length		
		Rabi **15**	***Kharif*** **15**	***Rabi*** **16**	***Rabi*** **15**	***Kharif*** **15**	***Rabi*** **16**	***Rabi*** **15**	***Kharif*** **15**	***Rabi*** **16**
General Mean		16.81	15.02	18.37	16.02	14.11	16.62	21.09	23.46	20.38
Range	**Min**	9.00	8.66	9.66	7.33	7.33	9.66	13.66	17.76	10.00
	Max	44.00	36.00	30.00	43.66	36.00	25.33	27.43	29.50	25.50
PCV		42.57	37.59	32.51	45.13	39.21	30.45	15.61	12.67	17.22
GCV		35.90	29.78	25.69	38.19	31.01	22.82	13.84	9.37	13.70
h2(Broad Sense)		71.10	62.80	62.50	71.60	62.60	56.20	78.60	54.60	63.30
GA at 5%		10.49	7.30	7.68	10.67	7.13	5.86	5.33	3.34	4.57
GA as % of Mean at 5%		62.37	48.60	41.83	66.59	50.54	35.22	25.28	14.27	22.45

Continuation of table 4.2…

Genetic variability parameters		Panicle Weight			No. of filled grains per panicle			No. of unfilled grains per panicle		
		***Rabi* 15**	***Kharif* 15**	***Rabi* 16**	***Rabi* 15**	***Kharif* 15**	***Rabi* 16**	***Rabi* 15**	***Kharif* 15**	***Rabi* 16**
General Mean		2.07	2.91	1.99	111.79	146.61	100.03	11.52	14.61	21.68
Range	**Min**	0.36	1.41	1.01	38.66	60.33	52.66	1.00	1.33	3.00
	Max	5.53	5.79	3.86	290.66	305.00	209.00	42.00	42.00	62.66
PCV		60.60	36.88	36.64	45.26	37.78	37.46	104.68	91.11	68.88
GCV		47.67	28.02	31.35	39.71	26.60	33.07	66.41	59.27	56.63
h2(Broad Sense)		61.90	57.70	73.20	77.00	49.60	78.00	40.20	42.30	67.60
GA at 5%		1.60	1.27	1.10	80.24	56.59	60.18	9.99	11.60	20.79
GA as % of Mean at 5%		77.24	43.86	55.25	71.78	38.60	60.16	86.79	79.42	95.90

Continuation of table 4.2…

Genetic variability parameters		No. of total grains per panicle			Spikelet fertility			Sterility percentage		
		***Rabi* 15**	***Kharif* 15**	***Rabi* 16**	***Rabi* 15**	***Kharif* 15**	***Rabi* 16**	***Rabi* 15**	***Kharif* 15**	***Rabi* 16**
General Mean		123.31	161.23	121.73	90.40	90.77	82.73	9.59	9.22	17.26
Range	**Min**	50.66	75.33	66.00	61.16	75.53	60.67	1.28	1.16	2.77
	Max	332.66	334.66	271.66	98.71	98.83	97.22	38.83	24.46	39.32
PCV		44.29	36.60	37.75	10.36	9.01	11.33	97.65	88.71	54.32
GCV		40.18	27.00	33.50	7.10	5.32	8.86	66.92	52.39	42.46
h2(Broad Sense)		82.30	54.40	78.80	47.00	34.90	61.10	47.00	34.90	61.10
GA at 5%		92.60	66.18	74.57	9.06	5.87	11.80	9.06	5.87	11.80
GA as % of Mean at 5%		75.09	41.04	61.26	10.03	6.47	14.26	94.48	63.74	68.36

Continuation of table 4.2…

Genetic variability parameters		Thousand grain weight			Single plant yield			Biomass per plant		
		Rabi 15	*Kharif* 15	*Rabi* 16	*Rabi* 15	*Kharif* 15	*Rabi* 16	*Rabi* 15	*Kharif* 15	*Rabi* 16
General Mean		19.54	18.29	19.49	21.17	26.20	17.93	27.84	23.71	20.00
Range	**Min**	11.00	9.73	12.50	3.80	3.08	6.42	10.90	4.00	8.93
	Max	25.33	24.00	25.14	63.10	62.80	33.13	71.16	59.00	41.70
PCV		19.22	20.79	15.03	61.94	49.64	36.38	34.52	56.28	38.83
GCV		15.32	17.33	14.43	51.15	39.87	28.00	28.65	45.33	32.04
h2(Broad Sense)		63.60	69.40	92.10	68.20	64.50	59.20	68.90	64.90	68.10
GA at 5%		4.91	5.44	5.56	18.42	17.28	7.96	13.64	17.84	10.90
GA as % of Mean at 5%		25.16	29.74	28.52	87.02	65.95	44.38	48.98	75.22	54.48

Continuation of table 4.2…

Genetic variability parameters		Biological yield per plant			Harvest Index			Per day productivity		
		Rabi 15	*Kharif* 15	*Rabi* 16	*Rabi* 15	*Kharif* 15	*Rabi* 16	*Rabi* 15	*Kharif* 15	*Rabi* 16
General Mean		49.01	49.92	37.94	40.60	52.38	47.51	0.15	0.20	0.14
Range	**Min**	17.83	13.75	15.35	15.48	22.78	29.60	0.02	0.03	0.06
	Max	134.26	111.35	63.23	56.51	56.76	55.94	0.47	0.43	0.27
PCV		42.16	46.53	32.41	29.98	24.27	17.91	62.39	48.39	36.34
GCV		36.17	39.59	25.68	23.20	17.92	14.92	51.51	38.88	27.89
h2(Broad Sense)		73.60	72.40	62.80	59.90	54.50	69.40	68.20	64.60	58.90
GA at 5%		31.34	34.65	15.90	15.02	14.28	12.16	0.13	0.13	0.06
GA as % of Mean at 5%		63.94	69.41	41.92	37.00	27.26	25.59	87.61	64.37	44.11

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation were low i.e., 9.44 and 9.49, respectively. The heritability observed for this trait was high (98.9%) with moderate genetic advance as per cent of mean (19.34).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation were moderate i.e., 12.14 and 12.17, respectively. The heritability observed for this trait was high (99.5%) with high genetic advance as per cent of mean (24.96).

The results were in conformity with Kumar *et al.* (2013), Alam *et al*. (2014), Dhurai *et al*. (2014), Patel *et al.* (2014), Shahriar *et al.* (2014), Islam *et al.* (2015) and Mishu *et al.* (2016) for low gcv and pcv. The selection for this trait would offer very little scope for genetic improvement of the genotypes under study.

Idris and Mohamed (2013), Alam *et al*. (2014), Patel *et al*. (2014), Khare *et al*. (2014) and Islam *et al.* (2015a) for high heritability coupled with moderate genetic advance as per cent of mean. Rajkumar *et al*. (2015) and Shinde *et al.* (2015) for high heritability.

4.2.3. Plant height

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate i.e., 17.97 and 18.43, respectively. The observed heritability estimates for this character was high (95.1%) with high genetic advance as per cent of mean (36.12) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the seed yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation were moderate i.e., 17.59 and 18.35, respectively. The heritability observed for this trait was high (91.9%) with high genetic advance as per cent of mean (34.747) .

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate i.e., 10.79 and 11.7, respectively. The observed heritability estimates for this character was high (85.49%) with high genetic advance as per cent of mean (20.5)

The results were in conformity with Krishna *et al*. (2008), Padmaja *et al.* (2008), Singh *et al*. (2011), Sravan *et al*. (2012), Soni *et al.* (2013), Vanisree *et al*.

(2013), Dhurai *et al*. (2014), Sravan *et al*. (2014) and Parmeshwar *et al.* (2015) for moderate gcv and pcv .

Chandra *et al*. (2009), Mohanty *et al*. (2012), Singh *et al*. (2012), Sravan *et al*. (2012), Gangashetty *et al*. (2013), Chakraborty and Chaturvedi (2014), Dhurai *et al.* (2014), Lingaiah *et al*. (2014), Rahman *et al.* (2014), Rajput *et al*. (2014), Sravan *et al*. (2014), Roy *et al.* (2015), Sindhumole *et al*. (2015) and Mishu *et al.* (2016) for high heritability coupled with high genetic advance as per cent of mean.

4.2.4. Number of total tillers per plant

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation estimates observed for this trait were high i.e., 35.90 and 42.57, respectively. The observed heritability estimates for this character was high (71.1%) with high genetic advance as per cent of mean (36.12) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation estimates observed for this trait were high i.e., 29.78 and 37.59, respectively. The observed heritability estimates for this character was high (62.8%) with high genetic advance as per cent of mean (48.60).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation estimates observed for this trait were high i.e., 25.69 and 32.51, respectively. The observed heritability estimates for this character was high (62.5%) with high genetic advance as per cent of mean (41.83).

The results were in conformity with Alam *et al*. (2014), Ravi *et al.* (2014) and Sindhumole *et al*. (2015) for high gcv and pcv. Satish *et al.* (2014) for high pcv.

Osman *et al*. (2012), Alam *et al*. (2014) and Ravi *et al.* (2014) for high heritability coupled with high genetic advance as per cent of mean.

4.2.5. Number of productive tillers per plant

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 38.19 and 45.13, respectively. The observed heritability estimate was high (71.6%) with high genetic advance as per cent of mean (66.59) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the seed yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 31.01 and 39.21, respectively. The observed heritability estimate was high (62.6%) with high genetic advance as per cent of mean (50.54).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 22.82 and 30.45, respectively. The observed heritability estimate was moderate (56.2%) with high genetic advance as per cent of mean (35.24).

The similar findings were reported by Soni *et al.* (2013), Dhurai *et al.* (2014) and Parmeshwar *et al.* (2015) high gcv, pcv respectively. Jayasudha and Deepak (2010) and Shinde *et al*. (2015) for high pcv.

Jaiswal *et al*. (2007), Selvaraj *et al.* (2011), Gangashetty *et al*. (2013), Chakraborty and Chaturvedi (2014), Dhurai *et al*. (2014), Khare *et al.* (2014), Rahman *et al.* (2014) and Parmeshwar *et al.* (2015) for high heritability coupled with high genetic advance as per cent of mean.

4.2.6. Panicle length

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 13.84 and 15.61, respectively. The heritability observed for this trait was high (78.6%) with high genetic advance as per cent of mean (25.28) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the seed yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were low and moderate i.e., 9.37 and 12.67, respectively. The heritability observed for this trait was moderate (54.6%) with moderate genetic advance as per cent of mean (14.27).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 13.7 and 17.22, respectively. The heritability observed for this trait was high (63.3%) with high genetic advance as per cent of mean (22.45).

The similar findings were reported by Singh *et al*. (2013), Soni *et al.* (2013), Dhurai *et al.* (2014) and Sathish *et al*. (2014) for moderate gcv and pcv . Saikumar *et al.* (2014) for low gcv and moderate pcv. Shinde *et al*. (2015) for low gcv .

The similar results were observed by Nayudu *et al.* (2007), Lal and Devendra (2011) and Dhurai *et al.* (2014) for high heritability and genetic advance as per cent of mean. Suresh (2001) and Patel *et al.* (2014) for moderate heritability and genetic advance as per cent of mean. Yadav *et al*. (2010), Parikh *et al*. (2011), Singh *et al.* (2011), Lingaiah *et al.* (2014) and Parmeshwar *et al*. (2015) for high heritability.

4.2.7. Panicle weight

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 47.67 and 60.67, respectively. The observed heritability estimate was high (61.9%) with high genetic advance as per cent of mean (77.24) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the seed yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 23.98 and 36.88, respectively. The observed heritability estimate was moderate (57.7%) with high genetic advance as per cent of mean (43.86).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 31.35 and 36.64, respectively. The observed heritability estimate was high (73.2%) with high genetic advance as per cent of mean (55.25).

The similar findings were reported by Singh *et al.* (2000) and Soni *et al*. (2013) for high gcv and pcv. The similar results were observed by Awaneeth and Senapati (2013) for high heritability and genetic advance as percent of mean.

4.2.8. Number of filled grains per panicle

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 39.71 and 45.26, respectively. The heritability estimate for this trait was high (77%) with high genetic advance as per cent of mean (71.78) indicating presence of high genetic variability and preponderance of additive gene action. Hence this trait could be effectively improved by simple selection.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 26.08 and 37.78, respectively. The heritability estimate for this trait was moderate (49.6%) with high genetic advance as per cent of mean (38.6).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 33.07 and 37.46, respectively. The heritability estimate for this trait was high (78%) with high genetic advance as per cent of mean (60.16).

The results were in conformity with Padmaja *et al*. (2008), Chandra *et al*. (2009), Yadav *et al.* (2010), Singh *et al*. (2011), Yadav *et al*. (2011), Singh *et al*. (2012), Basavaraja *et al*. (2013), Singh *et al*. (2013), Dhurai *et al*. (2014), Lingaiah *et al*. (2014), Patel *et al*. (2014), Suresh *et al*. (2014) and Parmeshwar *et al.* (2015) for high gcv and pcv.

Krishna *et al*. (2008), Padmaja *et al*. (2008), Chandra *et al*. (2009), Yadav *et al*. (2010), Pandey *et al*. (2012), Singh *et al*. (2012), Sravan *et al*. (2012), Kumar *et al*. (2013), Singh *et al.* (2013), Chakraborty and Chaturvedi (2014), Dhurai *et al*. (2014), Lingaiah *et al*. (2014), Patel *et al*. (2014), Rahman *et al*. (2014), Rajput *et al*. (2014) and Parmeshwar *et al*. (2015) for high heritability and genetic advance as per cent of mean.

4.2.9. Number of unfilled grains per panicle

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 66.41 and 104.68, respectively. The heritability estimate for this trait was moderate (40.2%) with high genetic advance as per cent of mean (86.79).

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 59.27 and 91.11, respectively. The heritability estimate for this trait was moderate (42.3%) with high genetic advance as per cent of mean (79.42).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 56.63 and 68.88, respectively. The heritability estimate for this trait was high (67.6%) with high genetic advance as per cent of mean (95.9).

The results were in conformity with Parmeshwar *et al.* (2015) for high gcv and pcv. Rahman *et al*. (2014) and Parmeshwar *et al*. (2015) high heritability with high genetic advance.

4.2.10. Number of total grains per panicle

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 39.71 and 45.26, respectively. The heritability estimate for this trait was high (77%) with high genetic advance as per cent of mean (71.78) indicating presence of high genetic variability and preponderance of additive gene action. Hence this trait could be effectively improved by simple selection.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 27 and 36.6, respectively. The heritability estimate for this trait was moderate (54.4%) with high genetic advance as per cent of mean (41.04).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 28.19 and 35.33, respectively. The heritability estimate for this trait was high (63.7%) with high genetic advance as per cent of mean (46.34).

The results were in conformity with Khare *et al.* (2014) and Patel *et al.* (2014) for high gcv and pcv.

The similar findings were reported by Soni *et al.* (2013) and Roy *et al*. (2015) for high heritability and genetic advance as percent of mean.

4.2.11. Spikelet fertility

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were low gcv and moderate pcv i.e., 7.10 and 10.36, respectively. The heritability estimate for this trait was moderate (40.2%) with low genetic advance as per cent of mean (10.0).

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were low i.e., 5.32 and 9.01, respectively. The heritability estimate for this trait was moderate (34.9%) with low genetic advance as per cent of mean (6.47).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were low gcv and moderate pcv i.e., 8.86 and 11.33, respectively. The heritability estimate for this trait was high (61.1%) with moderate genetic advance as per cent of mean (14.26).

The results were in conformity with Nandeshwar *et al.* (2010) for low gcv and moderate pcv.

The similar findings were reported by Mishu *et al*. (2016) for moderate heritability and low genetic advance as percent of mean. Soni *et al.* (2013) for moderate genetic advance as per cent of mean. Jayasudha *et al*. (2010), Dinesh *et al.* (2011) and Parmeshwar *et al.* (2015) for high heritability. Seyoum *et al.* (2012) for low genetic advance as per cent of mean.

4.2.12. Sterility percentage

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 66.92 and 97.65, respectively. The heritability estimate for this trait was moderate (47%) with high genetic advance as per cent of mean (94.48).

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 52.39 and 88.71, respectively. The heritability estimate for this trait was moderate (34.9%) with high genetic advance as per cent of mean (63.74).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 42.46 and 54.32, respectively. The heritability estimate for this trait was high (61.1%) with high genetic advance as per cent of mean (68.36).

The results were in conformity with Mamun *et al.* (2012) and Roy *et al.* (2015) for high gcv and pcv.

The similar findings were reported by Chakraborty and Chakraborty (2010), Mamun *et al.* (2012) and Mishu *et al*. (2016) for moderate heritability and high genetic advance. Roy *et al.* (2015) for high heritability and genetic advance as per cent of mean.

4.2.13. Thousand grain weight

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 15.32 and 19.22, respectively. The observed heritability estimate was high (63.6%) with high genetic advance as per cent of mean (25.16) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the grain yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were moderate gcv and high pcv i.e., 17.33 and 20.79, respectively. The observed heritability estimate was high (69.4%) with high genetic advance as per cent of mean (29.74).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 14.43 and 15.03, respectively. The observed heritability estimate was high (92.1%) with high genetic advance as per cent of mean (28.52).

The results were in conformity with Soni *et al.* (2013) Dhurai *et al*. (2014), Patel *et al*. (2014) and Suresh *et al.* (2014) for moderate gcv and pcv. Seyoum *et al.* (2012) and Ravi *et al.* (2014) for high pcv. Kishore *et al*. (2015) for moderate gcv.

Chakraborty and Chaturvedi (2014), Dhurai *et al*. (2014), Lingaiah *et al*. (2014), Patel *et al.* (2014), Rahman *et al*. (2014), Rao *et al*. (2014), and Suresh *et al*. (2014) for high heritability coupled with high genetic advance per cent of mean.

4.2.14. Single plant grain yield

During *Rabi* 2014-15 the complex character single plant grain yield showed high gcv (51.15) and pcv (61.94) respectively. High heritability estimate (68.2%) coupled with high genetic advance as per cent of mean (87.02) indicating that simple direct selection in the present material may be effective for getting high yield.

During *Kharif* 2015 the complex character single plant grain yield showed high gcv (39.87) and pcv (49.64) respectively. High heritability estimate (64.5%) coupled with high genetic advance as per cent of mean (65.95).

During *Rabi* 2015-16 the complex character single plant grain yield showed high gcv (28) and pcv (36.38) respectively. Moderate heritability estimate (59.2%) coupled with high genetic advance as per cent of mean (25.9)

The results are in conformity with Yadav *et al*. (2010), Singh *et al*. (2011), Mohanty *et al*. (2012), Singh *et al*. (2012), Sravan *et al*. (2012), Dhanwani *et al*.

(2013), Gangashetty *et al*. (2013), Singh *et al*. (2013), Vanisree *et al*. (2013), Chakraborty and Chaturvedi (2014), Dhurai *et al*. (2014), Patel *et al*. (2014), Rajput *et al*. (2014), Rahman *et al*. (2014), Sravan *et al.* (2014), Suresh *et al*. (2014) and Parmeshwar *et al*. (2015) for high gcv and pcv.

Garg *et al*. (2010), Parikh *et al*. (2011), Mohanty *et al*. (2012), Pandey *et al*. (2012), Dhanwani *et al*. (2013), Gangashetty *et al*. (2013), Singh *et al*. (2013), Chakraborty and Chaturvedi (2014), Dhurai *et al.* (2014), Lingaiah *et al.* (2014), Patel *et al*. (2014), Rahman *et al*. (2014), Rao *et al*. (2014), Suresh *et al*. (2014) and Parmeshwar *et al*. (2015) for high heritability coupled with high genetic advance per cent of mean. Lalitha and Sreedhar (1999) for moderate heritability.

4.2.15. Biomass per plant

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 28.65 and 34.52, respectively. The heritability estimate for this trait was high (68.9%) with high genetic advance as per cent of mean (48.98) indicating presence of high genetic variability and preponderance of additive gene action. Hence this trait could be effectively improved by simple selection.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 45.33 and 56.28, respectively. The heritability estimate for this trait was high (64.9%) with high genetic advance as per cent of mean (75.22).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 32.04 and 38.83, respectively. The heritability estimate for this trait was high (68.1%) with high genetic advance as per cent of mean (54.48).

In pooled analysis the genotypic and phenotypic coefficients of variation for this trait were moderate and high i.e., 16.69 and 38.81, respectively. The heritability estimate for this trait was low (18.5%) with moderate genetic advance as per cent of mean (14.78).

The results are in conformity with Patel *et al*. (2014) for high gcv, pcv, heritability and genetic advance per cent of mean.

4.2.16. Biological yield per plant

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 36.17 and 42.16, respectively. The heritability estimate for this trait was high (73.6%) with high genetic advance as per cent of mean (63.94) indicating presence of high genetic variability and preponderance of additive gene action. Hence this trait could be effectively improved by simple selection.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 39.59 and 46.53, respectively. The heritability estimate for this trait was high (72.4%) with high genetic advance as per cent of mean (69.41).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 25.68 and 32.41, respectively. The heritability estimate for this trait was high (62.8%) with high genetic advance as per cent of mean (41.92).

The results are in conformity with Soni *et al*. (2013), Sathish *et al*. (2014) and Parmeshwar *et al.* (2015) for high gcv and pcv.

The similar findings were reported by Dinesh *et al*. (2011), Soni *et al.* (2013) and Parmeshwar *et al*. (2015) for high heritability coupled with high genetic advance per cent of mean.

4.2.17. Harvest index

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 23.2 and 29.98, respectively. The heritability estimate for this trait was moderate (59.9%) with high genetic advance as per cent of mean (37).

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were moderate gcv and high pcv i.e., 17.92 and 24.27, respectively. The heritability estimate for this trait was moderate (54.5%) with high genetic advance as per cent of mean (27.26).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were moderate i.e., 14.91 and 17.91, respectively. The heritability estimate for this trait was high (69.4%) with high genetic advance as per cent of mean (25.59).

The similar findings were reported by Devic *et al*. (2012), Patel *et al*. (2014), Satish *et al*. (2014) and Parmeshwar *et al*. (2015) for high gcv and pcv. Dhurai *et al*. (2014) for moderate gcv and pcv. Dinesh *et al.* (2011), Dhurai *et al*. (2014) and Parmeshwar *et al.* (2015) for high heritability and high genetic advance as per cent of mean.

4.2.18. Per day productivity

During *Rabi* 2014-15 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 51.51 and 62.39, respectively. The observed heritability estimate was high (68.2%) with high genetic advance as per cent of mean (87.61) indicating preponderance of additive gene action in controlling of the traits. Hence direct selection of the characters would be effective in improving the seed yield.

During *Kharif* 2015 the genotypic and phenotypic coefficients of variation for this trait were high gcv and high pcv i.e., 38.88 and 48.39, respectively. The observed heritability estimate was high (64.6%) with high genetic advance as per cent of mean (64.37).

During *Rabi* 2015-16 the genotypic and phenotypic coefficients of variation for this trait were high i.e., 27.89 and 36.34, respectively. The observed heritability estimate was moderate (58.9%) with high genetic advance as per cent of mean (44.11).

The results were in conformity Bhadru *et al.* (2012b) for high gcv and pcv. The similar findings were reported by Bhadru *et al.* (2012b) for high heritability coupled with high genetic for advance percent of mean.

A critical analysis and knowledge on of the genetic variability parameters, namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement for selection of superior genotypes over the existing cultivars. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Genotypic coefficient of variation (GCV) along with heritability estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that

Figure 4.2 a. Graphical representation of phenotypic and genotypic coefficients of various characters in 59 rice genotypes

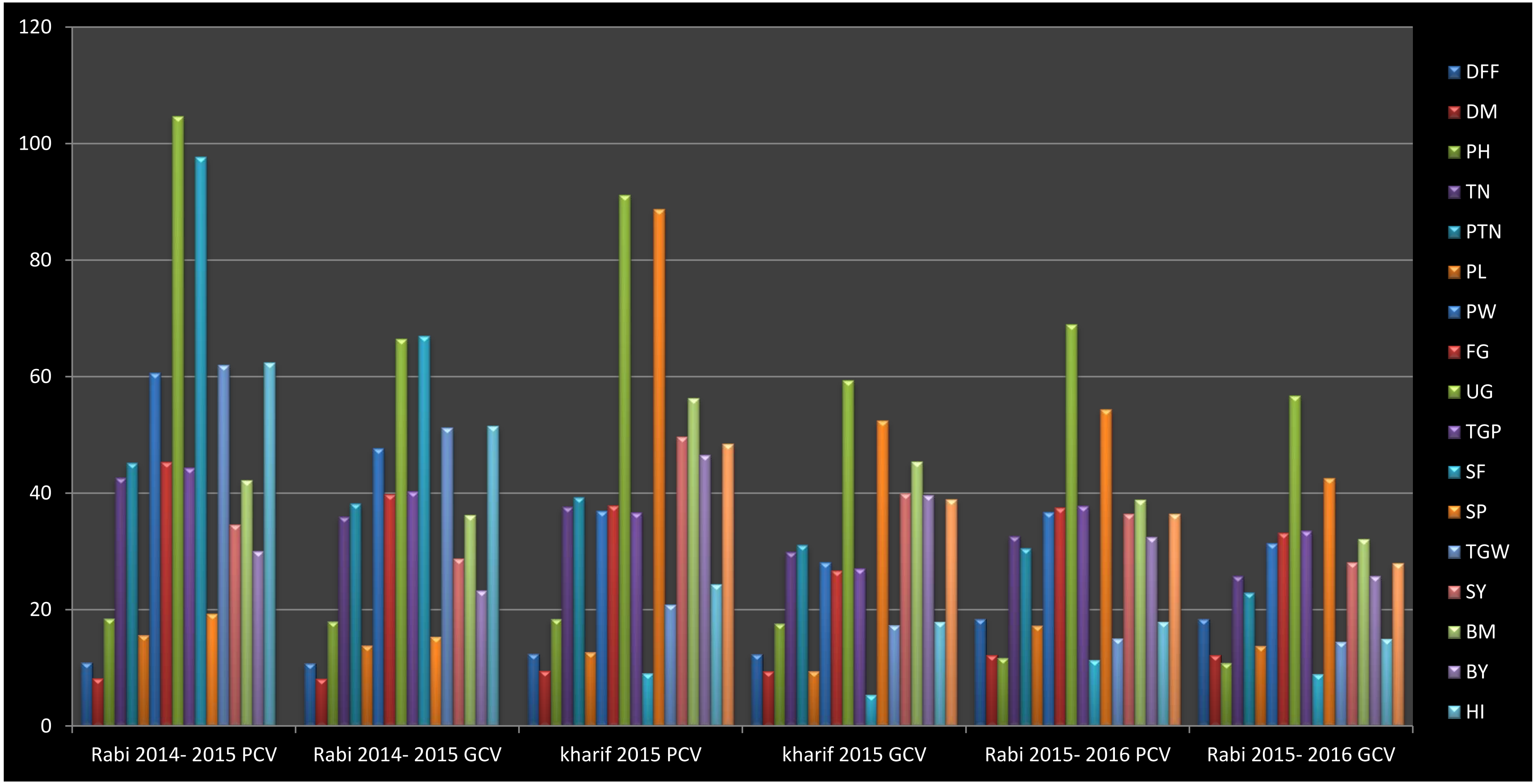
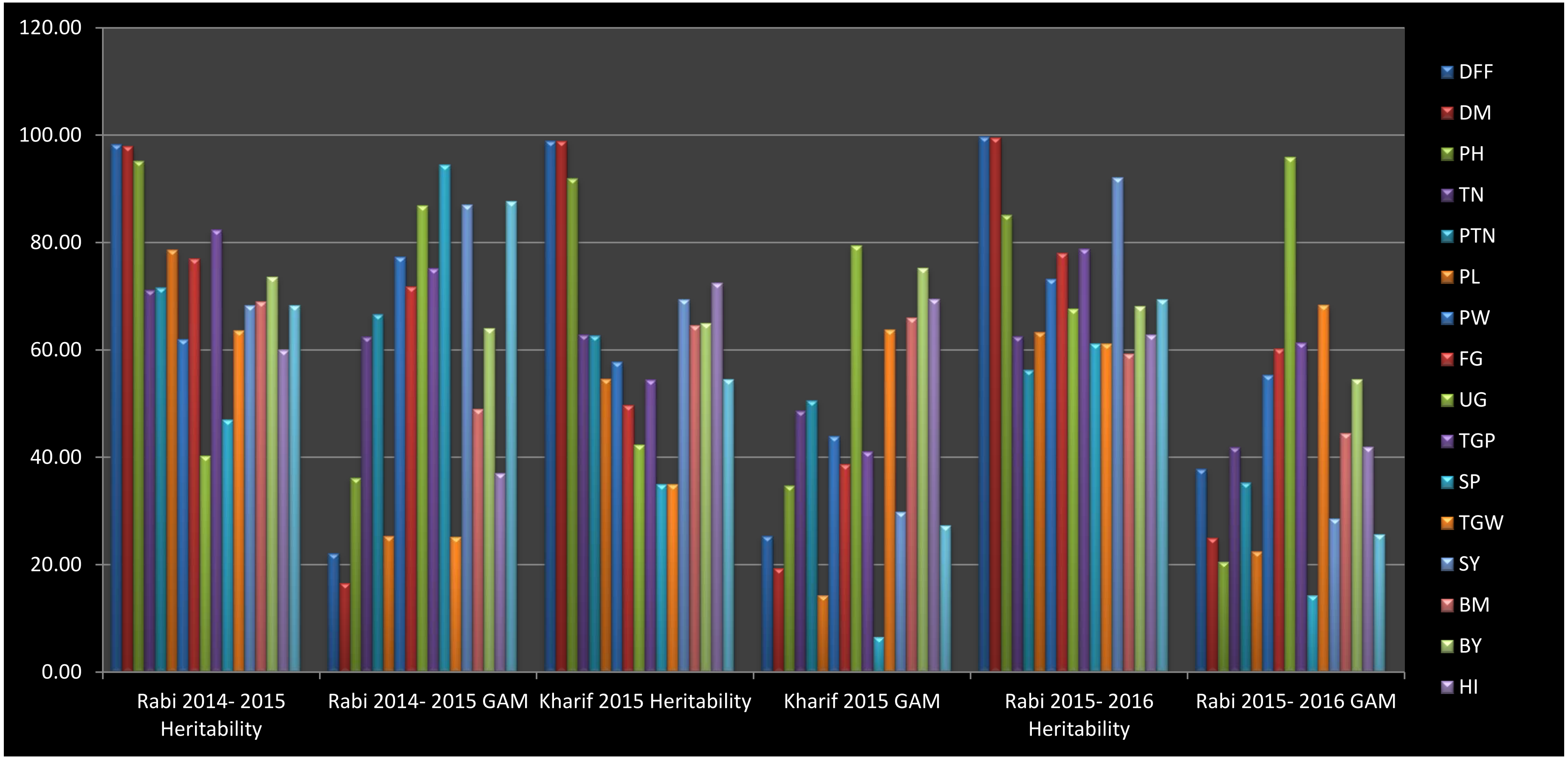


Figure 4.2 b. Graphical representation of heritability and genetic advance @ 5 % of mean for various characters in 59 rice genotypes



genetic gain should be considered in conjunction with heritability estimates (Johnson *et al*., 1955).

The information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study. High GCV, PCV indicate the existence of wide genetic base among the genotypes taken for study and possibility of genetic improvement through direct selection for these traits. And low GCV, PCV indicate little scope for improvement of those traits**.** Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all traits indicating less influence of environment on the manifestation of these traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection. Heritability in conjunction with genetic value would give a more reliable index of selection value. Characters which exhibited high degree of broad-sense heritability revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values. High heritability coupled with moderate genetic advance indicates that those traits are governed by both additive and non additive gene action and can be improved through recurrent selection method or simple direct selection. Heritability coupled with low genetic advance indicates that those traits are governed by additive gene action and heterosis and hybridization programme could be used to improve those traits.

The genetic advance as per cent of mean is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. The traits which recorded high heritability and high genetic advance indicate the control of additive gene action and selection may be effective for these characters.

4.3. STABILITY ANALYSIS BY AMMI BIPLOT MODEL AND GGE BIPLOT MODEL

4.3.1. AMMI and GGE biplot Analysis:

Analysis of variance was first conducted for each environment. Single plant grain yield , days to 50 % flowering, days to maturity, plant height, number of total tillers per plant, number of productive tillers per plant, panicle length, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, number of total grains per panicle, spikelet fertility, sterility percentage, thousand grain weight, biomass per plant, biological yield per plant, harvest index and per day productivity data for all three seasons were then subjected to combined analyses via additive main effect and multiplicative interaction (AMMI) analysis of variance and genotype effect and genotype x environment interaction effect (GGE).

AMMI uses ANOVA to analyze the main effects (additive part) and Principal Component Analysis (PCA) to analyze the non-additive residuals by the ANOVA (Gauch, 1993). The SS (%) was calculated comparing sum of square (SS) from AMMI ANOVA. When a genotype and environment have the same sign on their respective first PCA axis, their interaction is positive, if different, their interaction is negative (Tariku *et al.,* 2013). The AMMI biplot was used to visualize the interrelationships of genotypes and environments in a graph where the aspects are plotted on the same axis. This provides a pictorial view of the transformed GEI for any interpretation. In a biplot where PCA1 is on the vertical axis and mean yield on the horizontal axis, genotypes that appear almost on a perpendicular line had similar means and those almost on a horizontal line had similar interaction patterns. Genotypes or environments with large PCA1 scores, either positive or negative had large interactions, whereas genotypes with PCA1 score of zero or nearly zero had smaller interactions (Crossa *et al.*, 1990) and is considered as stable. The vertical line at the center of the biplot is the general grand mean. The best adapted genotype can plot far from the environment.

The GGE concept was used to visually analyze the yield from multi-environment trial (MET) data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also sources of variation in GEI analysis of MET data (Yan *et al.*, 2000; 2001). The GGE biplot is a graphical representation that displays the main genotype effect (G) and the genotype x environment interaction of multi-environment tests. GGE biplot symmetric view was used in this study to explain the ‘which-won-where’ patterns for genotypes and environments. Different polygons composed of one or several environment (s) and one or more genotype (s) can be used to determine which genotype(s) is performing best in which environment(s). It is constructed by plotting the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from singular value decomposition of the environment-centered data.

A specific option in GGE biplot analysis allows comparison among a set of genotypes with a reference genotype. This method defines the position of an ‘‘ideal’’ genotype, which will have the highest average value of all genotypes and be absolutely stable; that is, it expresses no genotype by environment interaction. A set of concentric circles are generated using the ideal genotype as the concentric center. The ideal genotype is used as a reference to rank the other genotypes. A performance line passing through the origin of the biplot is used to determine mean performance of a genotype. The arrow on the performance line represents increasing mean performance. A stability line perpendicular to the performance line is also passing through the origin of the biplot; the two arrows in opposite directions represent decrease in stability. A genotype farther from the biplot origin on either side on the stability line represents relatively lower stability. A genotype closer to the performance line is considered more stable than the one placed farther.

4.3.2. Analysis of Variance by AMMI model and GGE Model:

Combined Analysis of variance for the data showed that mean sum of square due to genotypes, environment and genotype x environment interaction was significant, indicating the presence of variability among the genotypes and environments. The significant mean sum of squares of genotype indicated that the genotypes were diverse with large differences among the mean yields. The significant genotype x environment interaction effect showed that the genotypes responded differently to the variation in environmental (seasonal fluctuations) conditions.

Table 4.3.2 a. Analysis of variance for AMMI stability model.

Source of variation	d.f	Days to 50 % flowering			Days to maturity			Plant height		
		Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)
Genotypes	58	86281.66	1487.61**	67.63	70373.19	1213.33**	67.78	104146.10	1795.62**	57.91
Environments	2	22210.40	11105.20**	17.41	14706.24	7353.12**	14.17	29261.51	14630.76**	16.27
G x E Interaction	116	18466.49	159.19**	14.47	18118.43	156.193**	17.45	38768.87	334.21**	21.56
IPCA1	59	12220.72	207.13**	66.18	12139.69	205.757**	67.00	22518.55	381.67**	58.10
IPCA2	57	6245.77	109.57**	33.82	5978.737	104.89**	33.00	16250.32	285.09**	41.90
Pooled error	348	616.23	1.77		620.72	1.7837		7648.66	21.98	
Total	530	127575.21			103819.19			179827.73		

Continuation of table 4.3.2 a….

Source of variation	d.f	No. of total tillers per plant			Number of productive tillers per plant			Panicle length		
		Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)
Genotypes	58	6519.69	112.41**	30.04	5833.34	100.57**	29.87	2926.35	50.45**	44.97
Environments	2	991.67	495.84**	4.57	609.64	304.82**	3.12	925.23	462.62**	14.22
G x E Interaction	116	9514.77	82.02**	43.83	8703.03	75.03**	44.57	1385.56	11.94**	21.29
IPCA1	59	6611.50	112.06**	69.50	5961.88	101.05**	68.50	928.67	15.74**	67.00
IPCA2	57	2903.27	50.93**	30.50	2741.15	48.09**	31.50	456.90	8.02**	33.00
Pooled error	348	4651.13	13.37		4355.86	12.52		1259.84	3.62	
Total	530	21706.14			19528.68			6507.02		

Source of variation	d.f	Panicle weight			Number of filled grains per panicle			Number of unfilled grains per panicle		
		Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)
Genotypes	58	290.585	5.01**	43.69	6292050.14	11931.90**	48.12	36131.40	622.96**	34.49
Environments	2	90.95	45.47**	13.67	207692.72	103846.36**	14.44	9607.733	4803.87**	9.17
G x E Interaction	116	135.75	1.17**	20.41	248133.06	2139.078**	17.25	28516.93	245.84**	27.22
IPCA1	59	98.98	1.68**	72.90	162070.35	2746.96**	65.30	16333.32	276.84**	57.30
IPCA2	57	36.77	0.65**	27.10	86062.71	1509.87**	34.70	12183.61	213.75**	42.70
Pooled error	348	143.25	0.41		283722.67	815.30		30336.17	87.17	
Total	530	665.16			1438314.58			104770.07		

Continuation of table 4.3.2 a…

Source of variation	d.f	Number of total grains per panicle			Spikelet fertility			Sterility percentage		
		Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)	Sum of squares	MSS	SS (%)
Genotypes	58	36131.40	15618.10**	54.08	12980.76	223.81**	26.16	12981.23	223.81**	26.16
Environments	2	9607.73	88542.33**	10.57	7292.84	3646.42**	14.70	7292.79	3646.40**	14.70
G x E Interaction	116	28516.93	2495.57**	17.28	14824.17	127.79**	29.87	14824.59	127.80**	29.87
IPCA1	59	16333.32	3560.21**	72.60	9474.70	160.59**	63.90	9475.03	160.59**	63.90
IPCA2	57	79433.24	1393.57**	27.40	5349.47	93.85	36.10	5349.57	93.85**	36.10
Pooled error	348	297404.86	854.612		14430.15	41.47		14430.09	41.47	
Total	530	1675055.51			49624.46			49625.25		

Continuation of table 4.3.2 a…

	Thousand grain weight			Single plant grain yield			Biomass per plant		
Source of variation	**Sum of squares**	**MSS**	**SS (%)**	**Sum of squares**	**MSS**	**SS (%)**	**Sum of squares**	**MSS**	**SS (%)**
Genotypes	4276.36	73.73**	64.26	20263.84	349.377**	27.70	20434.75	352.32**	32.31
Environments	176.79	88.40**	2.66	6144.43	3072.21**	8.40	5447.40	2723.70**	8.61
G x E Interaction	1004.34	8.66**	15.09	31203.20	268.99**	42.66	24315.27	209.61**	38.44
IPCA1	754.43	12.79**	75.10	20988.93	355.74**	67.30	16295.01	276.19**	67.00
IPCA2	249.91	4.38**	24.90	10214.28	179.20**	32.70	8020.26	140.71**	33.00
Pooled error	1188.40	3.41		15335.88	44.07		12823.78	36.85	
Total	6654.99			73146.48			63252.44		

Continuation of table 4.3.2 a…

	Biological yield per plant			Harvest index			Per day productivity		
Source of variation	**Sum of squares**	**MSS**	**SS (%)**	**Sum of squares**	**MSS**	**SS (%)**	**Sum of squares**	**MSS**	**SS (%)**
Genotypes	65294.09	1125.76**	31.02	20963.62	361.44**	26.53	1.19	0.021**	28.47
Environments	15751.43	7875.71**	7.48	12407.49	6203.75**	15.70	0.37	0.184**	8.80
G x E Interaction	92379.31	796.37**	43.88	27566.35	237.64**	34.88	1.73	0.015**	41.37
IPCA1	63183.01	1070.90**	68.40	17458.05	295.90**	63.30	1.15	0.019	66.60
IPCA2	29196.30	512.22**	31.60	10108.29	177.34**	36.70	0.58	0.010	33.40
Pooled error	36864.97	105.93		17993.91	51.71		0.88	0.003	
Total	210518.85			79028.00			4.17		

Table 4.3.2 b. Analysis of variance for GGE model

Source of variation	df	Days to 50 % flowering			Days to maturity			Plant height			No. of total tillers per plant		
		SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS
PC1	59	85.7	89783.4	1521.75**	81.4	72062.1	1221.39**	79.5	113667	1926.56**	48.3	746.726 1	31.30**
PC2	57	8.4	8759.28	153.67**	11.9	10530.7	184.75**	15.6	22329.5	391.74**	33.6	395.201	94.65**
PC3	55	5.9	6205.48	112.82**	6.7	5898.82	107.25**	4.8	6918.29	125.78**	18	892.537	52.59**

Continuation of table 4.3.2 b…..

Source of variation	df	No. of productive tillers per plant			Panicle length			Panicle weight			No. of filled grains per panicle		
		SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS
PC1	59	53.4	7765.17	131.61**	68.8	2965.11	50.25**	71.4	304.399	5.15**	75.4	708874	12014.80**
PC2	57	28.9	4196.72	73.62**	21.5	928.653	16.29**	21.7	92.5689	1.62**	16.9	158828	2786.46**
PC3	55	17.7	2574.49	46.80**	9.7	418.152	7.60**	6.9	29.366	0.53**	7.7	72481.6	1317.85**

Continuation of table 4.3.2 b….

Source of variation	df	No. of unfilled grains per panicle			No. of total grains per panicle			Spikelet fertility			Sterility percentage		
		SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS
PC1	59	61.6	39817.9	674.87**	76.3	911946	15456.70**	48	13343.5	226.16**	48	13343.8	226.16**
PC2	57	19.9	12859.5	225.60**	17.5	209534	3676.04**	33.6	9346.53	163.97**	33.6	9346.99	163.98**
PC3	55	18.5	11971	217.65**	6.2	73855.2	1342.82**	18.4	5114.95	92.99**	18.4	5114.98	92.99**

Continuation of table 4.3.2 b….

Source of variation	df	Thousnd grain weight			Single plant grain yield			Biomass per plant			Biological yield per plant		
		SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS
PC1	59	81.5	4301.92	72.91**	49.2	25346.2	429.59**	57.5	25747.3	436.39**	50.9	80237	1359.95**
PC2	57	14.2	751.156	13.17**	40.7	20922.8	367.06**	27.7	12388.9	217.34**	37.6	59318.7	1040.68**
PC3	55	4.3	227.622	4.13**	10.1	5198.03	94.50**	14.8	6613.85	120.25**	11.5	18117.8	329.41**

Continuation of table 4.3.2 b….

Source of variation	df	Harvest index			Per day productivity		
		SS%	Sum of Squares	MSS	SS%	Sum of Squares	MSS
PC1	59	45.9	22289.2	377.78**	49.4	1.4391	0.02
PC2	57	35.9	17417	305.56**	39.4	1.1478	0.02
PC3	55	18.2	8823.72	160.43**	11.2	0.327	0.005

The SS (%) showed that days to 50% flowering, days to maturity, plant height, panicle length, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, number of total grains per panicle and thousand grain weight were contributed mainly by genotype, followed by environment, and their interaction. But the characters *viz.*, single plant grain yield, number of tillers per plant, number of productive tillers per plant, spikelet fertility, sterility percentage, biomass per plant, biological yield per plant, harvest index and per day productivity were affected by mainly by interaction.

The principal component explains the contribution of genotype, environment and their interaction of the total sum of squares of the genotype x environment interaction. The first two principal components (PCA1 and PCA2) of AMMI analysis explains contribution of genotype and their environment, where as the three principal components (PCA1, PCA2 and PCA3) of GGE analysis explains the contribution of the genotype, environment and their interaction of the total sum of square of the genotype x environment interaction.

For all characters both PC1 and PC2 together showed 100% SS% in AMMI analysis. The PC1 value was higher than PC2 for all the traits explains higher contribution of genotype in the total sum of squares of the genotype x environment interaction. But compared to single plant grain yield IPCA1 (67.3) and IPCA2 (32.7) there was an increase in PC1 score and decrease in PC2 score for number of tillers per plant, number of productive tillers per plant, panicle weight, number of total grains per panicle and biological yield per plant showing increase in GxE interaction (Table 4.3.2 a.).

For all characters PC1, PC2 and PC3 together showed 100% explained SS% in GGE analysis. The PC1 value was higher than PC2 and PC3 for all the traits explains higher contribution of genotype in the total sum of squares of the genotype x environment interaction (Table 4.3.2 b).

4.3.3. Stability Analysis by AMMI Biplot Model and GGE Biplot Model:

The details of genotype code and season's code are given in Table 4.3.3. The genotypes were classified based on days to fifty per cent flowering duration as per DUS guidelines. The genotypes showing days to fifty per cent duration between 71 to 90 days are classified as early genotypes, genotypes showing duration of about 91 to 110 days to fifty per cent flowering are classified as medium duration lines and the genotypes showing duration of about 111 to 130 days to fifty per cent flowering are classified as late genotypes.

Table 4.3.3. Details of code used for genotypes and seasons in AMMI and GGE analysis along with classification of genotypes based on the duration.

S.No	Genotype	Code used in AMMI and GGE analysis	Genotype characteristic based on duration
1	130(K)	G1	Mid early line
2	14-3	G2	Late line
3	14(S)	G3	Mid early line
4	148(S)	G4	Early line
5	166-1	G5	Late line
6	166-2-11	G6	Late line
7	166-2-3	G7	Mid early line
8	166-2-9	G8	Late line
9	166-23	G9	Late line
10	166-23-1	G10	Late line
11	166-30	G11	Late line
12	166-9	G12	Mid early line
13	166(S)	G13	Late line
14	220(S)	G14	Mid early line
15	246(K)	G15	Mid early line
16	250(K)	G16	Late line
17	258(S)	G17	Mid early line
18	263(k)	G18	Mid early line
19	27(K)	G19	Mid early line
20	35(B)	G20	Mid early line
21	51B	G21	Late line
22	75(S)	G22	Late line
23	93B	G23	Late line
24	95B	G24	Late line
25	Aditya	G25	Early line
26	ADT43	G26	Early line
27	Anjali	G27	Early line
28	Govind	G28	Early line
29	IR64	G29	Mid early line
30	Jaldidhan	G30	Early line
31	Jaya	G31	Late line
32	MTU1010	G32	Mid early line
33	Prasanna	G33	Early line
34	Rasi	G34	Early line
35	SBH	G35	Early line
36	SM1637	G36	Mid early line

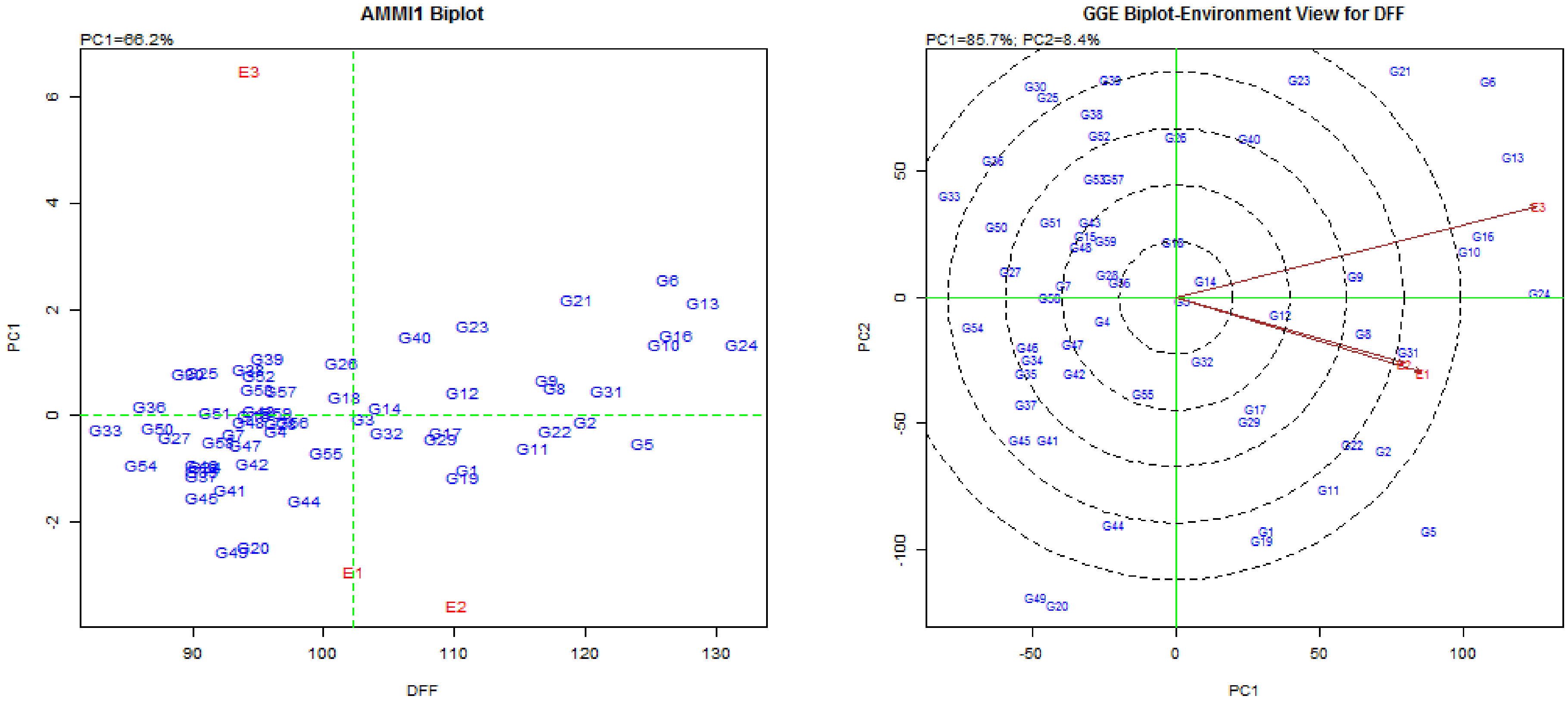
Continuation of table 4.3.3……			
37	SM1876	G37	Early line
38	SM219	G38	Mid early line
39	SM349	G39	Mid early line
40	SM363	G40	Mid early line
41	SM4014	G41	Early line
42	SM4029	G42	Early line
43	SM4071	G43	Early line
44	SM4076	G44	Early line
45	SM4078	G45	Early line
46	SM4226	G46	Mid early line
47	SM4231	G47	Early line
48	SM4371	G48	Early line
49	SM4385	G49	Early line
50	SM4406	G50	Early line
51	SM4415	G51	Early line
52	SM686	G52	Mid early line
53	SM733	G53	Early line
54	SM776	G54	Early line
55	Sona	G55	Mid early line
56	Tellahamsa	G56	Mid early line
57	Tulasi	G57	Early line
58	Vandana	G58	Early line
59	Varalu	G59	Early line
	Season	**Code used in AMMI and GGE analysis**	
1	Kharif 2015	E1	
2	Rabi 2014- 15	E2	
3	Rabi 2015- 16	E3	

4.3.3.1. Days to 50 % flowering:

As per AMMI biplot model and GGE biplot model the genotype G24 (95 B, late line) was identified as the best genotype across all the three seasons (Fig. 4.3.3.1). G33 (Prasanna, check), G54 (SM776) and G36 (SM1637) were identified as best in negative direction for days to fifty per cent flowering as early to medium varieties are preferred than late genotypes.

Among the seasons E2 was found to be the most suitable season for expression of this trait for longer duration lines, whereas E3 was found to be favorable season for early lines. As per GGE biplot analysis the genotype G31 (Jaya,

Figure 4.3.3.1. AMMI1 biplot and GGE biplot for days to 50 % flowering of 59 genotypes tested in three seasons



late line) was best suited for E1 (*Kharif* 2015) and E2 (*Rabi* 2014-15). The G16 (250 K, Late line) and G10 (166-23-1, Late line) are best suited for E3 (*Rabi* 2015-16).

4.3.3.2. Days to maturity:

As per AMMI biplot analysis and GGE biplot analysis G6 (166-2-11, late line) was identified as the best genotype across all the three seasons (Fig. 4.3.3.2). G33 (Prasanna, check), G36 (SM1637) and G30 (Jaldidhan) were identified as best in negative direction for days to maturity as early to medium varieties are preferred than late genotypes.

Among the seasons E2 was found to be the most suitable season for expression of this trait for long duration lines, whereas for early lines season E3 is more suitable. As per GGE biplot analysis the genotypes G9 (166-23, late line) and G13 (166 S, late line) are best suited for E1 (*Kharif* 2015). The genotypes G9 (166-23, Late line) and G11 (166-30, late line) are best suited for E2 (*Rabi* 2014-15). Genotypes G6 (166-2-11, late line) and G24 (95 B, late line) are best suited for E3 (*Rabi* 2015-16).

4.3.3.3. Plant height:

As per AMMI biplot model and GGE biplot model G4 (148 S, early line) was identified as the best genotype across all the three seasons (Fig. 4.3.3.3).

The seasons E1 and E2 were found to be the favorable seasons for expression of this trait. As per GGE biplot model best suited genotype for E2 it was genotype G4 and for E3 it was genotype G40 (SM363, mid early line).

4.3.3.4. Number of total tillers per plant:

As per AMMI biplot model and as per GGE biplot model the genotype G21 (51 B, late line) was identified as the best genotype across all the three seasons having highest tillering capacity (Fig. 4.3.3.4). As per GGE biplot model the genotype G23 was identified as best genotype across all the three seasons.

Among the seasons E3 was found to be the most suitable season for potential expression of this trait. As per GGE biplot model best suited genotype in E1 was G3 (14 S, mid early line), for E2 the best suited genotype was G23 (93 B, late line) and for E3 best suited genotype was G14 (220 S, mid early line).

Figure 4.3.3.2. AMMI1 biplot and GGE biplot for days to maturity of 59 genotypes tested in three seasons

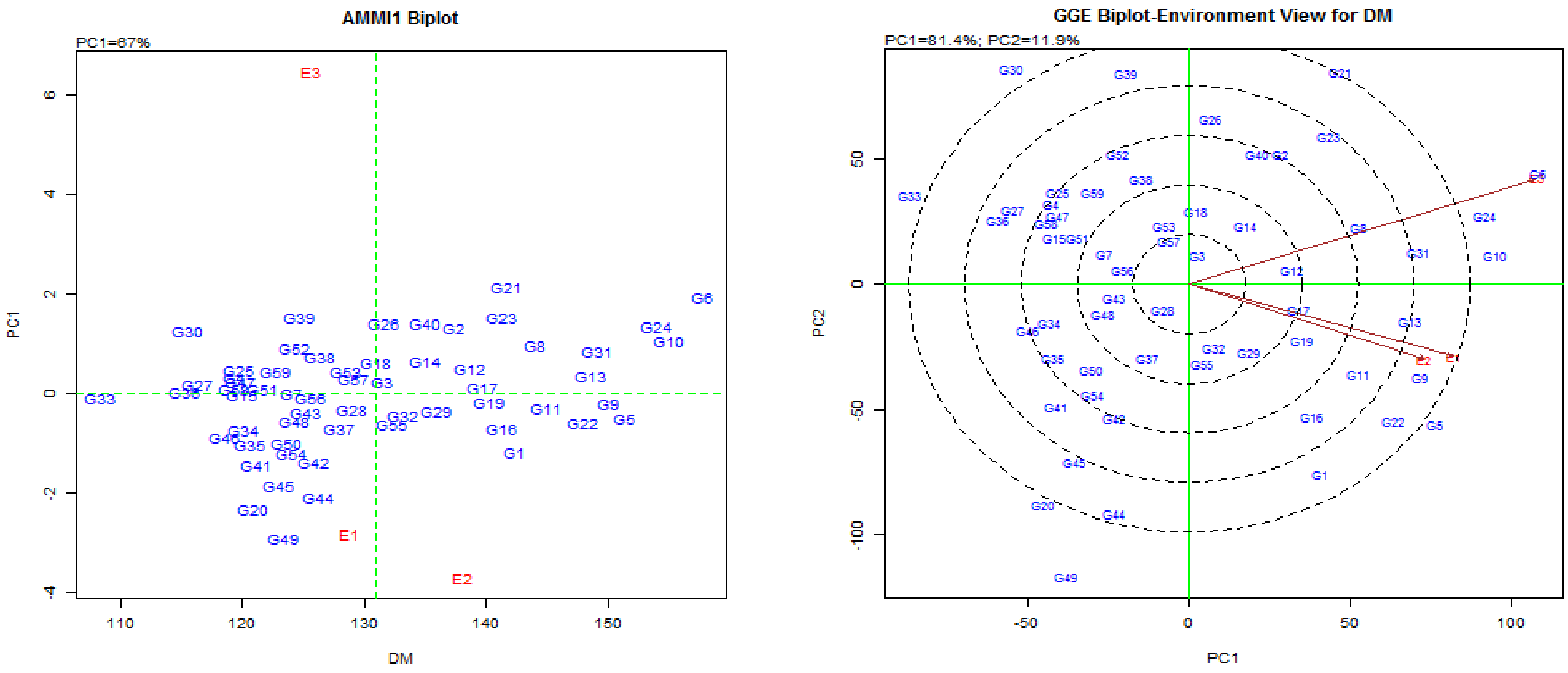


Figure 4.3.3.3. AMMI1 biplot and GGE biplot for plant height of 59 genotypes tested in three seasons

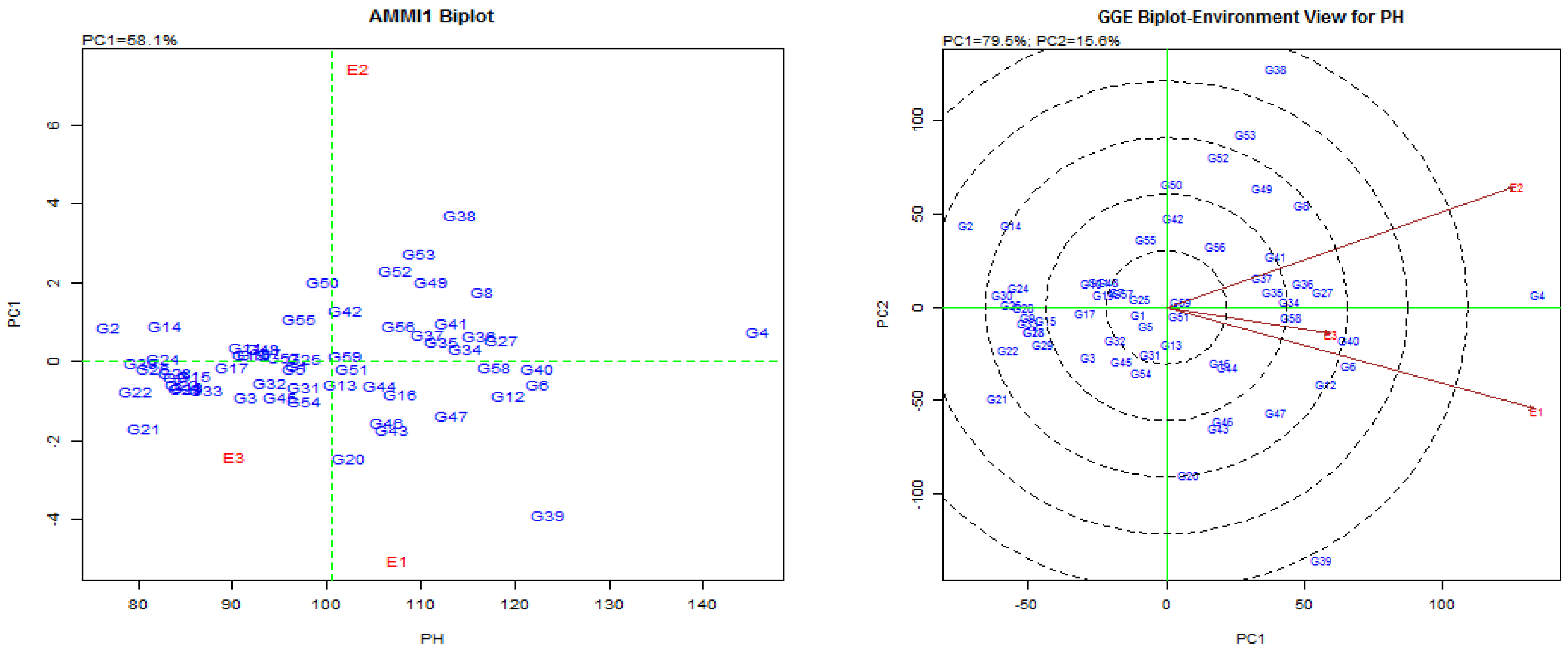
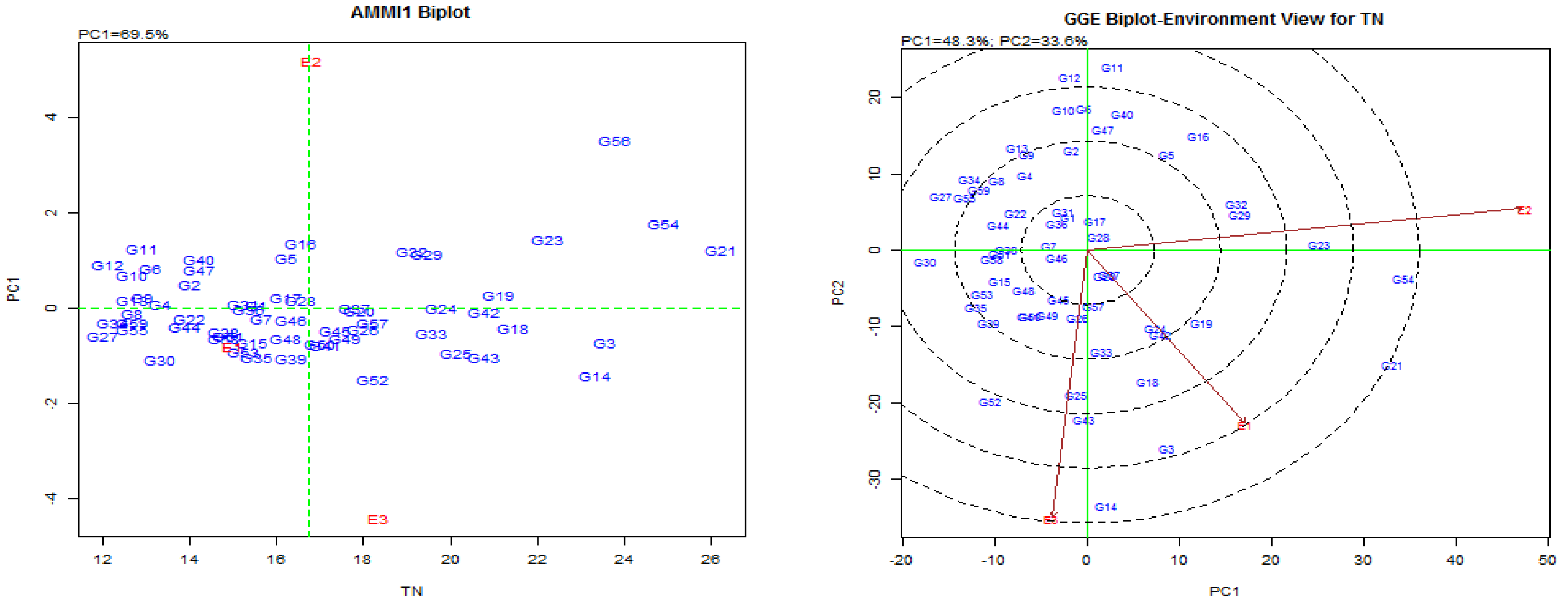


Figure 4.3.3.4. AMMI1 biplot and GGE biplot for number of total tiller per plant of 59 genotypes tested in three seasons



4.3.3.5. Number of productive tillers per plant:

As per AMMI biplot model the genotype G21 (51 B, late line) was identified as the best genotype across all the three seasons having highest tillering capacity (Fig. 4.3.3.5). As per GGE biplot analysis the genotype G23 was identified as the best genotype across all the three seasons.

Among the seasons E2 and E3 were found to be the most suitable seasons for potential expression of this trait. As per GGE biplot model best suited genotypes in E1 was G21 (51 B, late line) and G24 (95 B, late line), for E2 the best suited genotype was G23 (93 B, late line) and for E3 best suited genotype was G43 (SM4071, early line).

4.3.3.6. Panicle length:

As per AMMI biplot model G4 (148 S, early line) was identified as the best genotype across all the three seasons (Fig. 4.3.3.6). As per GGE biplot analysis G8 (166-2-9, late line) was identified as the best genotype across all the three seasons.

Among the seasons E1 was found to be the most suitable season for potential expression of this trait. As per GGE biplot model best suited genotype in E1 and E3 was G4 (148 S, early line), for E2 the best suited genotypes were G6 (166-2-11, late line), and G8 (166-2-9, late line).

4.3.3.7. Panicle weight:

As per AMMI biplot model and GGE model was the genotype G11 (166-30, late line) was identified as the best stable genotype across all the three seasons (Fig. 4.3.3.7).

Among the seasons E1 was found to be the most suitable season for expression of this trait. As per GGE biplot model the best suited genotype in E2 was G8 (166-2-9, late line) and for E3 genotype G12 (166-9, mid early line).

4.3.3.8. Number of filled grains per panicle:

As per AMMI biplot model and GGE biplot model G11 (166-30, late line) was identified as the best genotype across all the three seasons (Fig. 4.3.3.8).

Among the seasons E1 was found to be the most suitable season for expression of this trait potential. As per GGE biplot model best suited genotypes in

Figure 4.3.3.5. AMMI1 biplot and GGE biplot for number of productive tiller per plant of 59 genotypes tested in three seasons

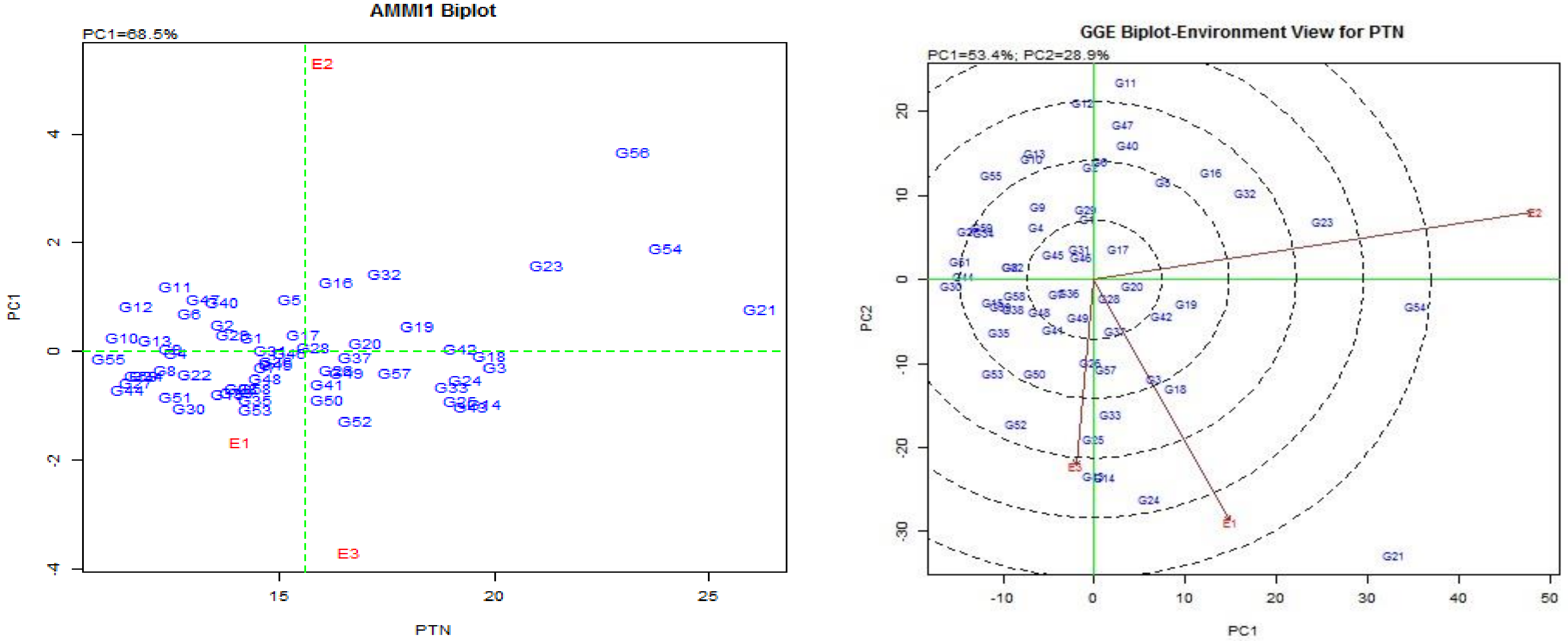


Figure 4.3.3.6. AMMI1 biplot and GGE biplot for panicle length of 59 genotypes tested in three seasons

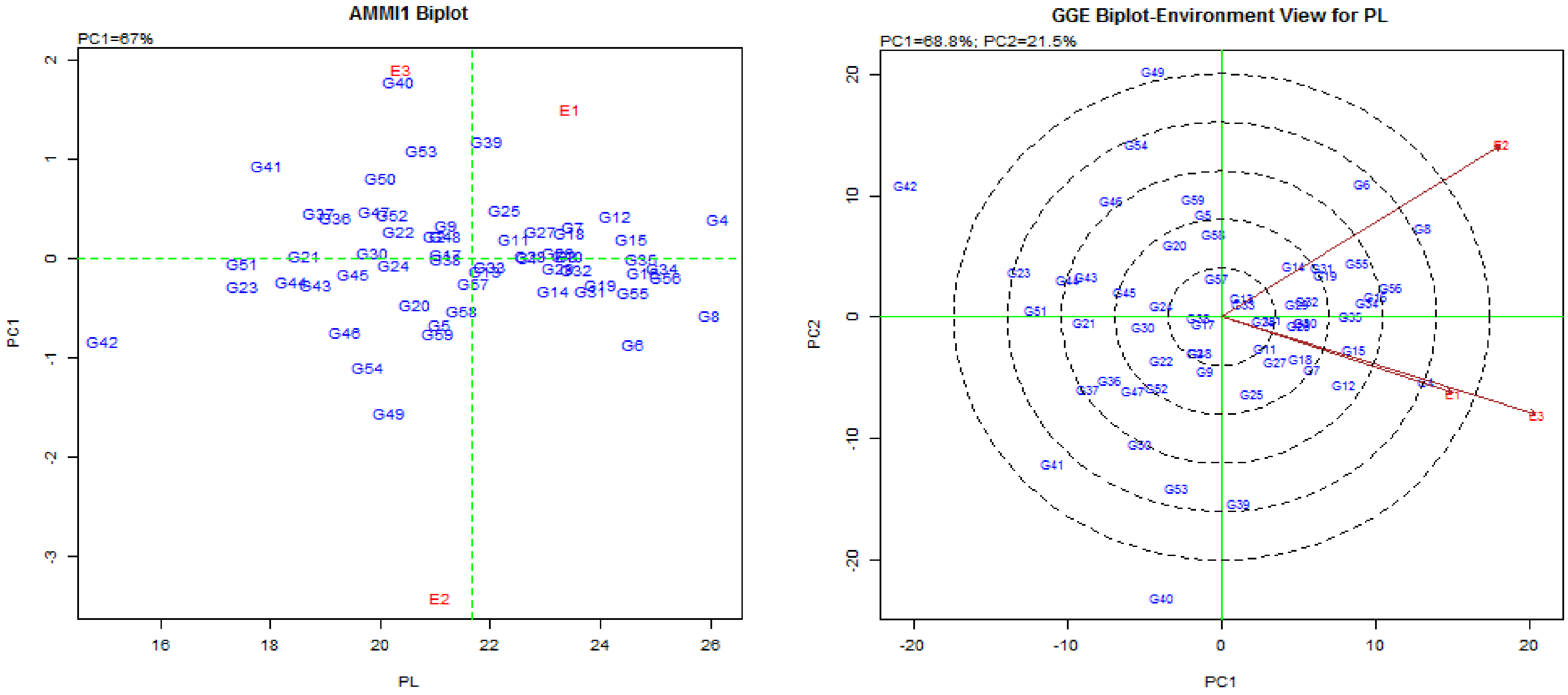


Figure 4.3.3.7. AMMI1 biplot and GGE biplot for panicle weight of 59 genotypes tested in three seasons

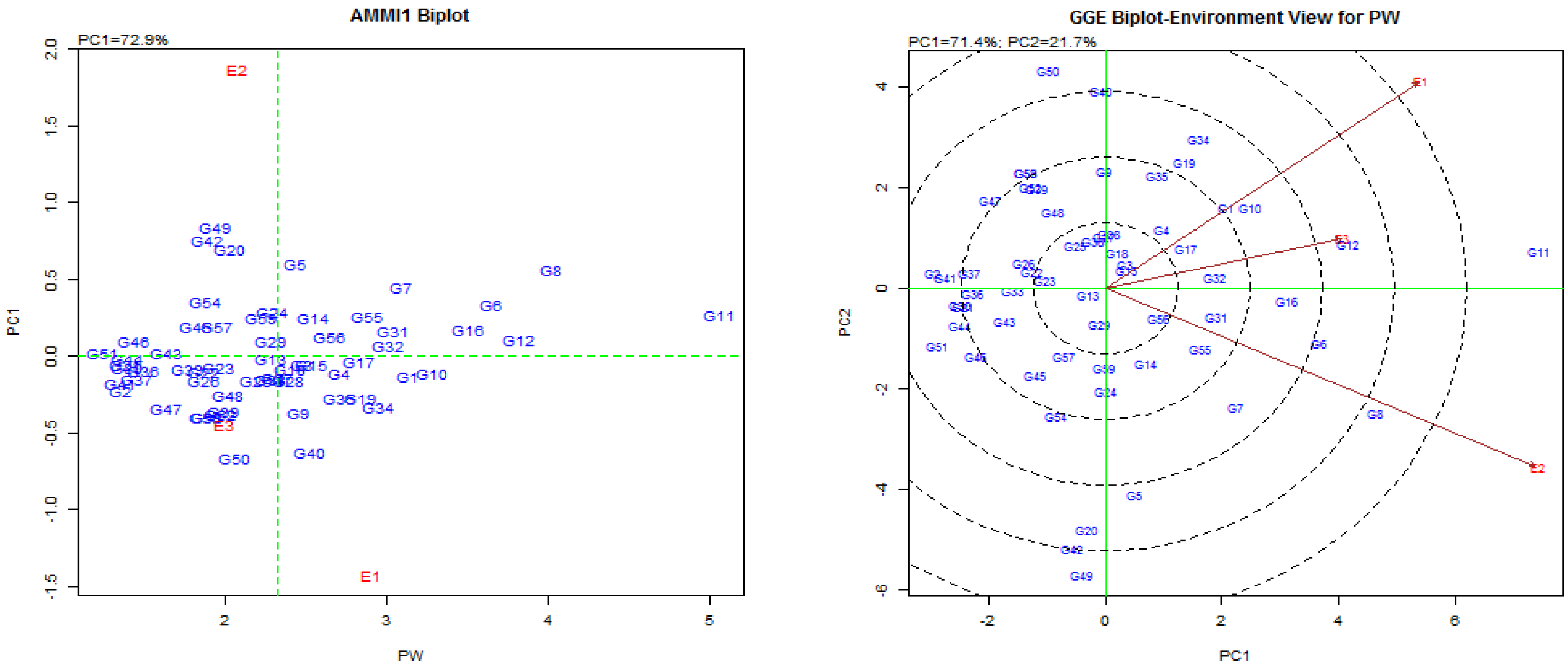
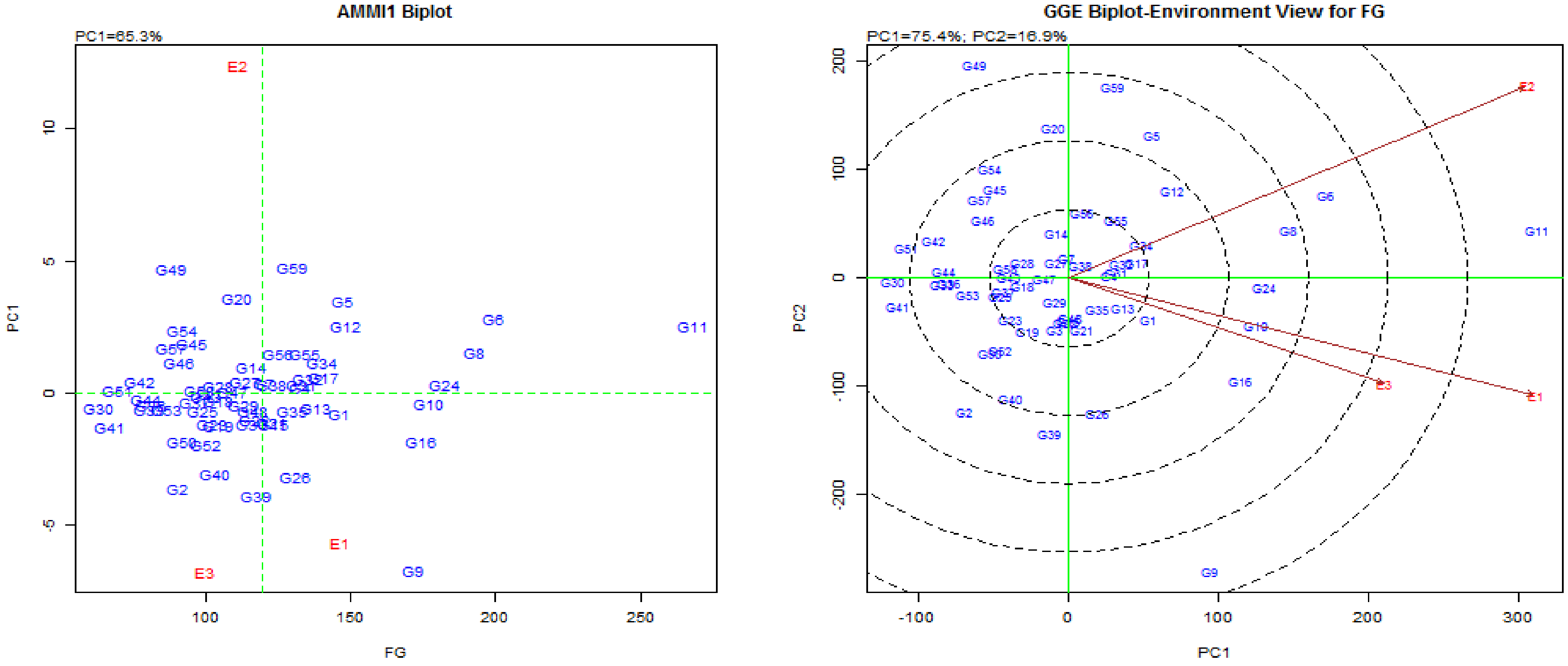


Figure 4.3.3.8. AMMI1 biplot and GGE biplot for number of filled grains per panicle of 59 genotypes tested in three seasons



E1 and E3 were G10 (166-23-1, late line) and G16 (250 K, late line), for E2 the best suited genotype was G11.

4.3.3.9. Number of unfilled grains per panicle:

As per AMMI biplot model genotype G8 was the best genotype and as per GGE model the genotype G11 (166-30, late line) was identified as stable suitable genotype across all the three seasons having highest number of unfilled grains per panicle (Fig. 4.3.3.9). G24, (95 B, late line), G42 (SM4029, early line), G43 (SM4071, early line) were identified as best in negative direction for number of unfilled grains per panicle as genotypes with low number of unfilled grains per panicle are preferred.

Among the seasons E3 was found to be the suitable season for higher expression of this trait, whereas seasons E2 and E1 had less potential in expression of this trait. As per GGE biplot model the best suited genotypes in E1and E3 was G9 (166-23, late line), for E2 the best suited genotype was G8 (166-2-9, late line).

4.3.3.10. Number of total grains per panicle:

As per AMMI biplot model and GGE model the genotype G11 (166-30, late line) was identified as the best, suitable genotype across all the three seasons having highest number of total grains per panicle. Followed by this genotype G6 (166-2-11, late line) and G8 are the best suitable genotypes across all the seasons (Fig. 4.3.3.10).

Among the seasons E1 was found to be the most suitable season for expression of this trait. As per GGE biplot model the best suited genotype in E1 and E3 was G16 (250 K, late line), for E2 the best suited genotype was G11.

4.3.3.11. Spikelet fertility:

As per AMMI biplot model genotype G43 (SM4071, early line) was identified as the best genotype and as per the GGE model genotype G34 (Rasi, early line) was identified as the best stable genotype across all the three seasons having high spikelet fertility (Fig. 4.3.3.11).

Among the seasons E1 and E2 were found to be the suitable seasons for expression of this trait. As per GGE biplot model the best suited genotypes in E2

Figure 4.3.3.9. AMMI1 biplot and GGE biplot for number of unfilled grains per panicle of 59 genotypes tested in three seasons

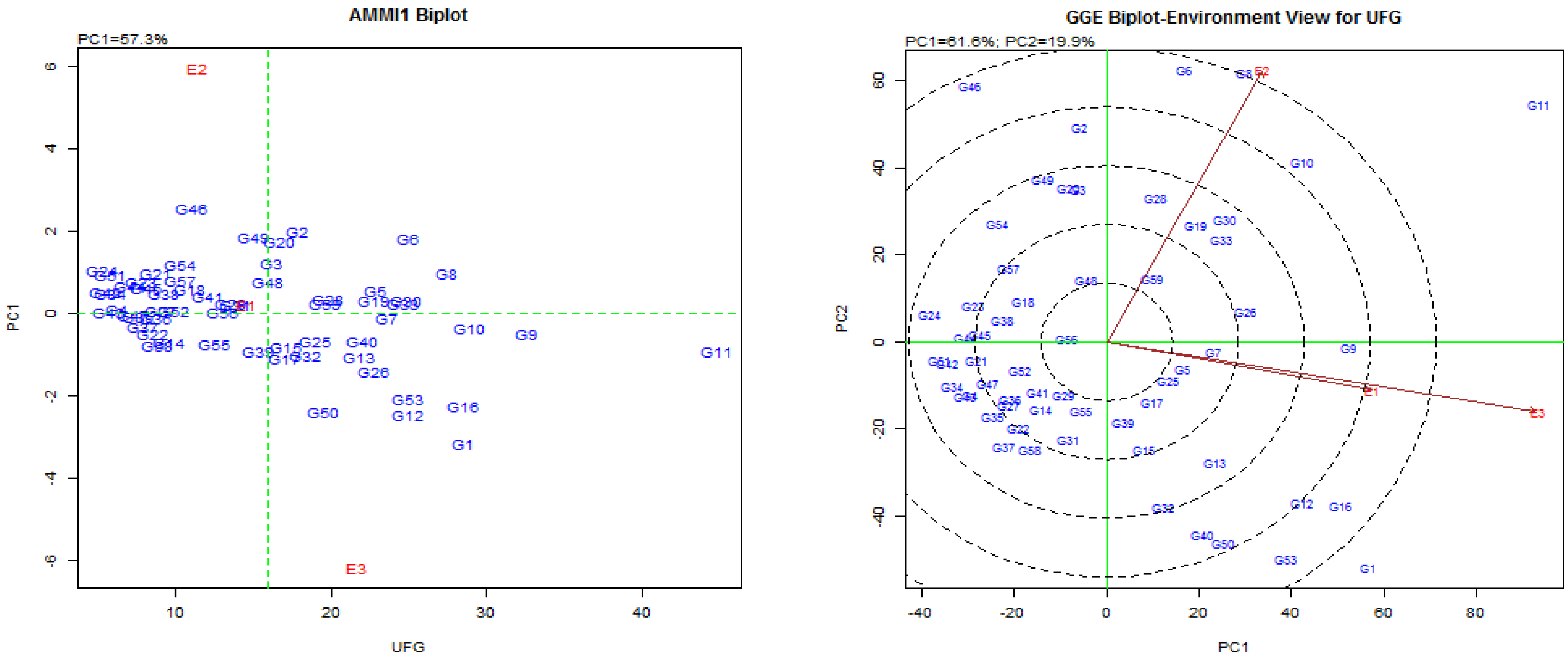


Figure 4.3.3.10. AMMI1 biplot and GGE biplot for number of total grains per panicle of 59 genotypes tested in three seasons

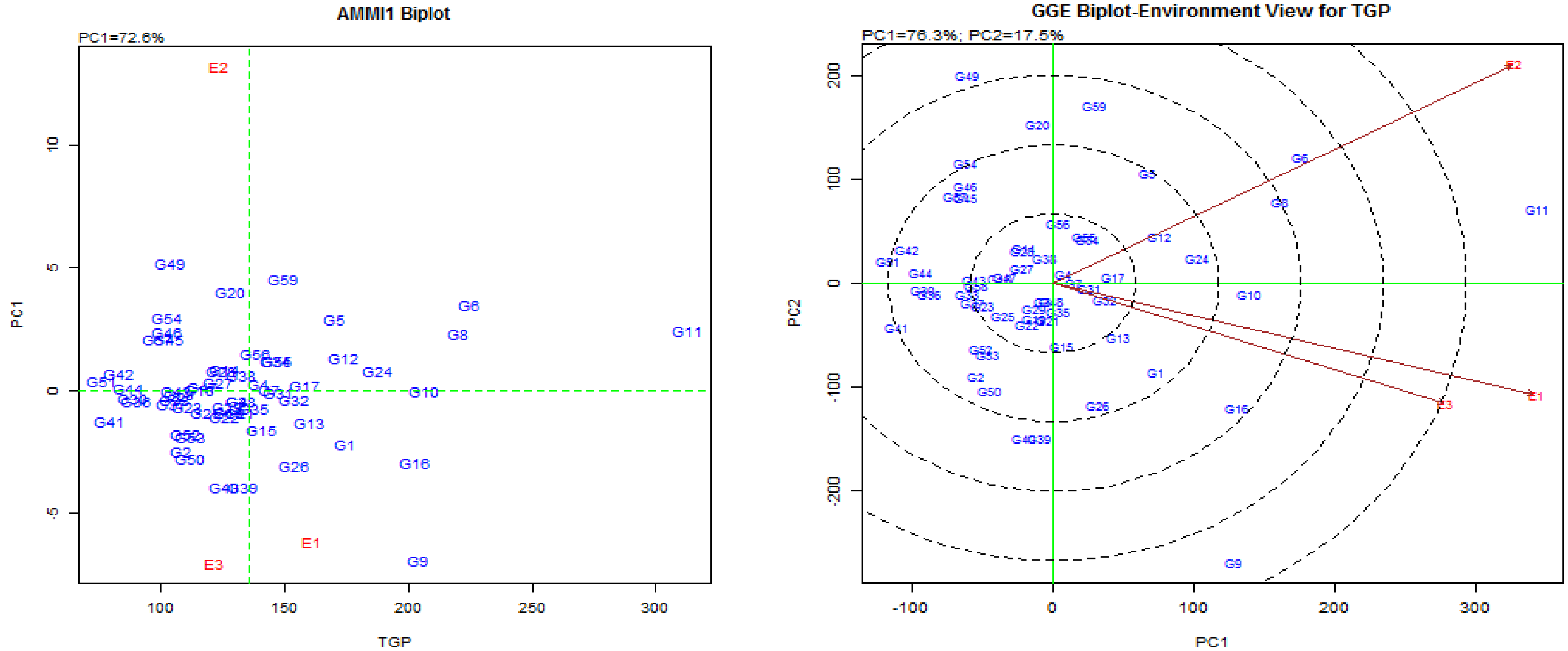
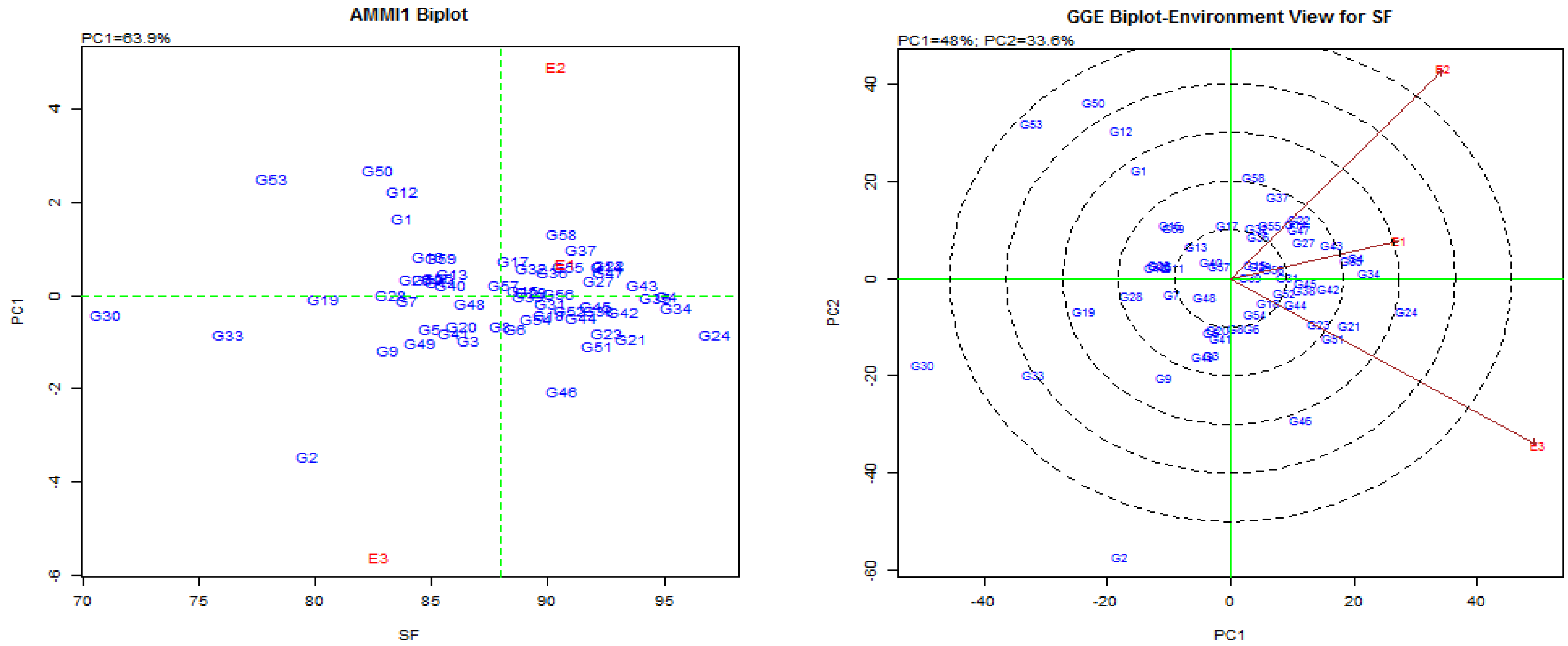


Figure 4.3.3.11. AMMI1 biplot and GGE biplot for spikelet fertility of 59 genotypes tested in three seasons



were G4 (148 S, early line), G35 (Sabhagidhan, early line) and G34, for E3 the best suited genotypes were G46 (SM4226, mid early line) and G24 (95 B, late line).

4.3.3.12. Sterility percentage:

As per AMMI biplot model genotype G53 (SM733, early line) has highest mean sterility percentage and is stable across all the seasons. As per the GGE model genotype G30 (Jaldidhan, early line) was identified as genotype with high mean and stable across all the three seasons. As per negative direction for sterility percentage the genotypes G24 (95 B, late line) and G34 (Rasi, early line) are stable and the best genotypes with low sterility percentage across all the seasons (Fig. 4.3.3.12). Among the seasons E3 was found to be the most suitable season for expression of this trait, whereas season E1 was found to be suitable for expression of this trait.

4.3.3.13. Thousand grain weight:

As per AMMI biplot model genotype G12 (166-9, mid early line) was identified as stable the best genotype across all the seasons. As per GGE model the genotype G4 (148 S, early line) was identified as the best, suitable genotype across all the three seasons having high mean value (Fig. 4.3.3.13).

Among the seasons E3 was found to be the most suitable season for expression of this trait. As per GGE biplot model the best suited genotype in E1 and E3 was G12, for E2 the best suited genotype was G4.

4.3.3.14. Single plant grain yield:

As per AMMI biplot model the genotype G19 (27 K, mid early line) was identified as the best stable genotype across all the three seasons having highest single plant yield (Fig. 4.3.3.14). As per GGE biplot model the genotypes G24 (95 B, late line) and G19 were identified as the best stable genotypes across all the seasons for single plant yield.

Among the seasons E1 was found to be the most suitable season for potential expression of yield trait. As per GGE biplot model genotype the best suited genotype in E1 was G19, for E2 was G56 (Tellahamsa, mid early line) and for E3 G5 (166-1, late line).

Figure 4.3.3.12. AMMI1 biplot and GGE biplot for sterility percentage of 59 genotypes tested in three seasons

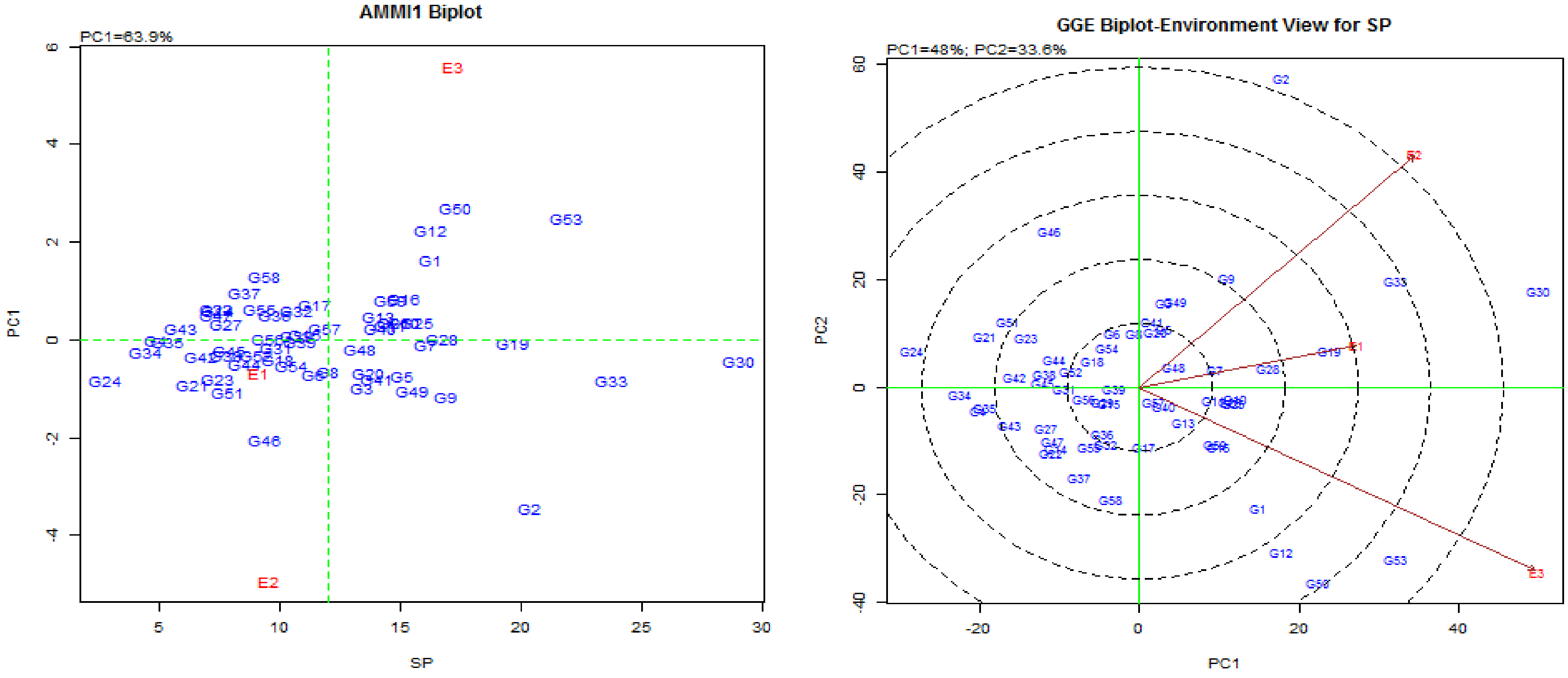


Figure 4.3.3.13. AMMI1 biplot and GGE biplot for thousand grain weight of 59 genotypes tested in three seasons

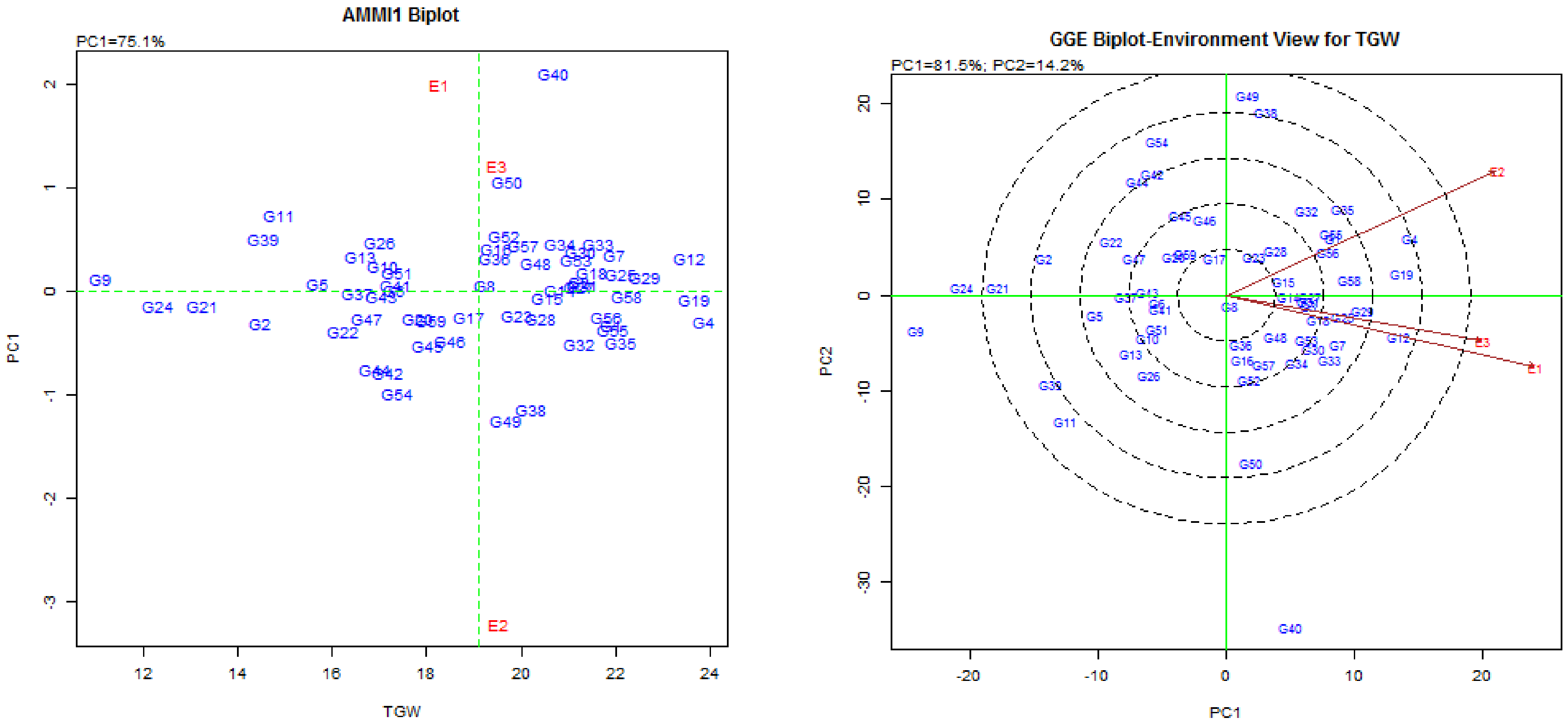
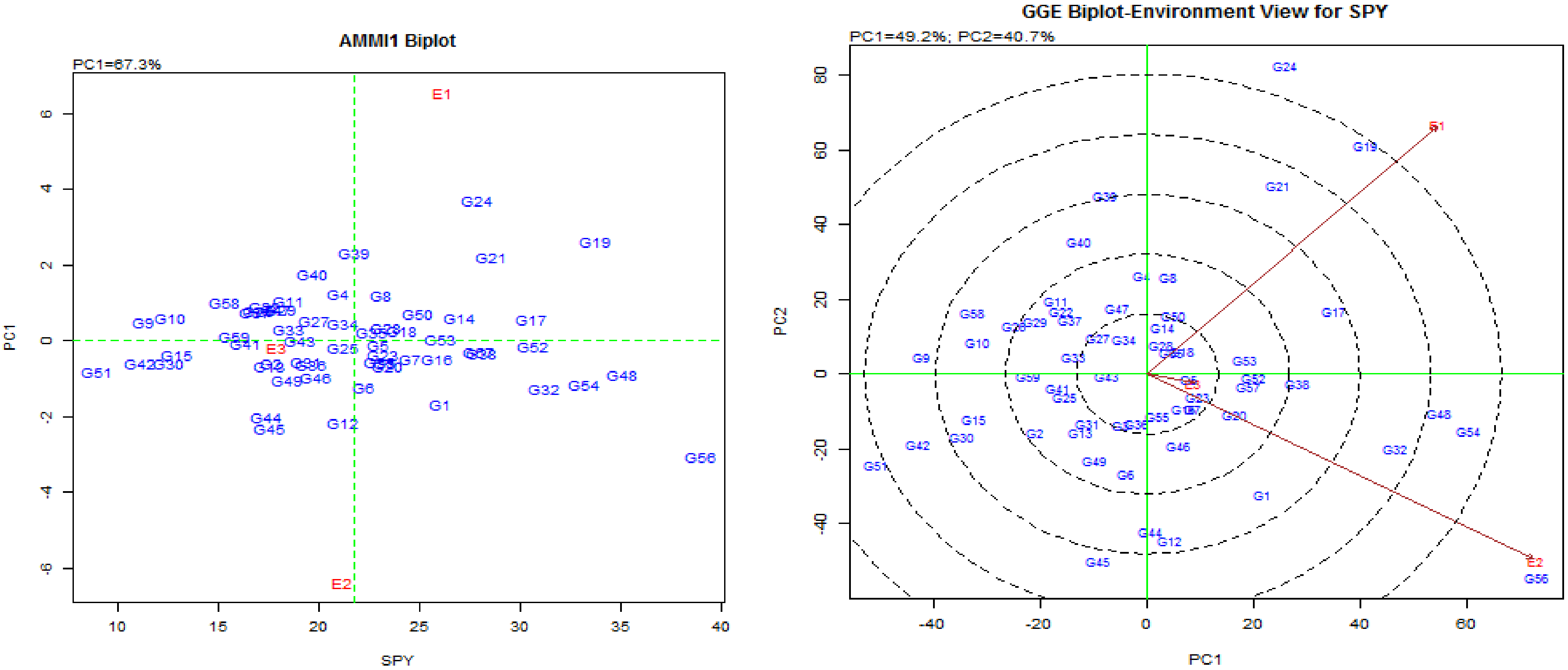


Figure 4.3.3.14. AMMI1 biplot and GGE biplot for single plant grain yield of 59 genotypes tested in three seasons



4.3.3.15. Biomass per plant:

As per AMMI biplot model the genotype G8 (166-2-9, late line) was identified as the best stable genotype across all the three seasons having high biomass per plant (Fig. 4.3.3.15). As per GGE biplot model the genotype G56 (Tellahamsa, mid early line) was identified as the best stable genotype across all the seasons for biomass per plant.

Among the seasons E2 was found to be the most suitable season for this trait. As per GGE biplot model genotype the best suited genotype in E1 was G8. For E2 the best suited genotypes were G6 (166-2-11, late line) and G12 (166-9, mid early line). For E3 the best suited genotype was G13.

4.3.3.16. Biological yield per plant:

As per AMMI biplot model and GGE model the genotype G19 (27 K, mid early line) was identified as the best, suitable genotype across all the three seasons having high biological per plant (Fig. 4.3.3.16).

Among the seasons E1 was found to be the most suitable season for expression of this trait. As per GGE biplot model genotype the best suited genotype in E1 was G19. For E2 the best suited genotype was G54 (SM776, early line). For E3 the best suited genotypes were G52 (SM686, mid early line), G57 (Tulasi, early line) and G53 (SM733, early line).

4.3.3.17. Harvest index:

As per AMMI biplot model and GGE biplot model the genotype G17 (258 S, mid early line) was identified as the best stable genotype across all the three seasons.

4.3.3.18. Per day productivity:

As per AMMI biplot model the genotype G19 (27 K, mid early line) was identified as the best stable genotype across all the three seasons (Fig. 4.3.3.18). As per GGE biplot model the genotypes G19 and G24 (95 B, late line) were identified as the best stable genotypes across all the seasons for this trait.

Among the seasons E1 was found to be the most suitable season for per day productivity. As per GGE biplot model genotype the best suited genotype in E1 was G19. For E2 the best suited genotype was G56 (Tellahamsa, mid early line). For E3

Figure 4.3.3.15. AMMI1 biplot and GGE biplot for biomass per plant of 59 genotypes tested in three seasons

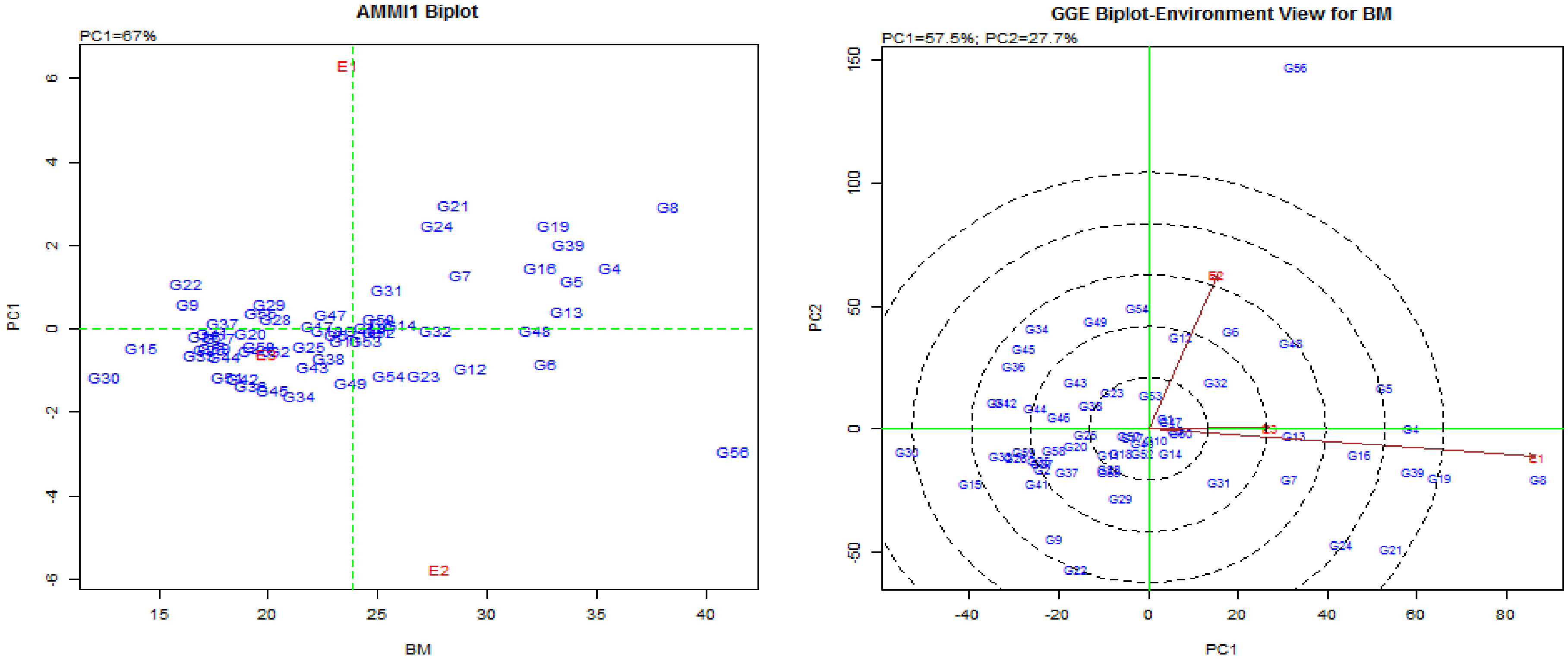


Figure 4.3.3.16. AMMI1 biplot and GGE biplot for biological yield per plant of 59 genotypes tested in three seasons

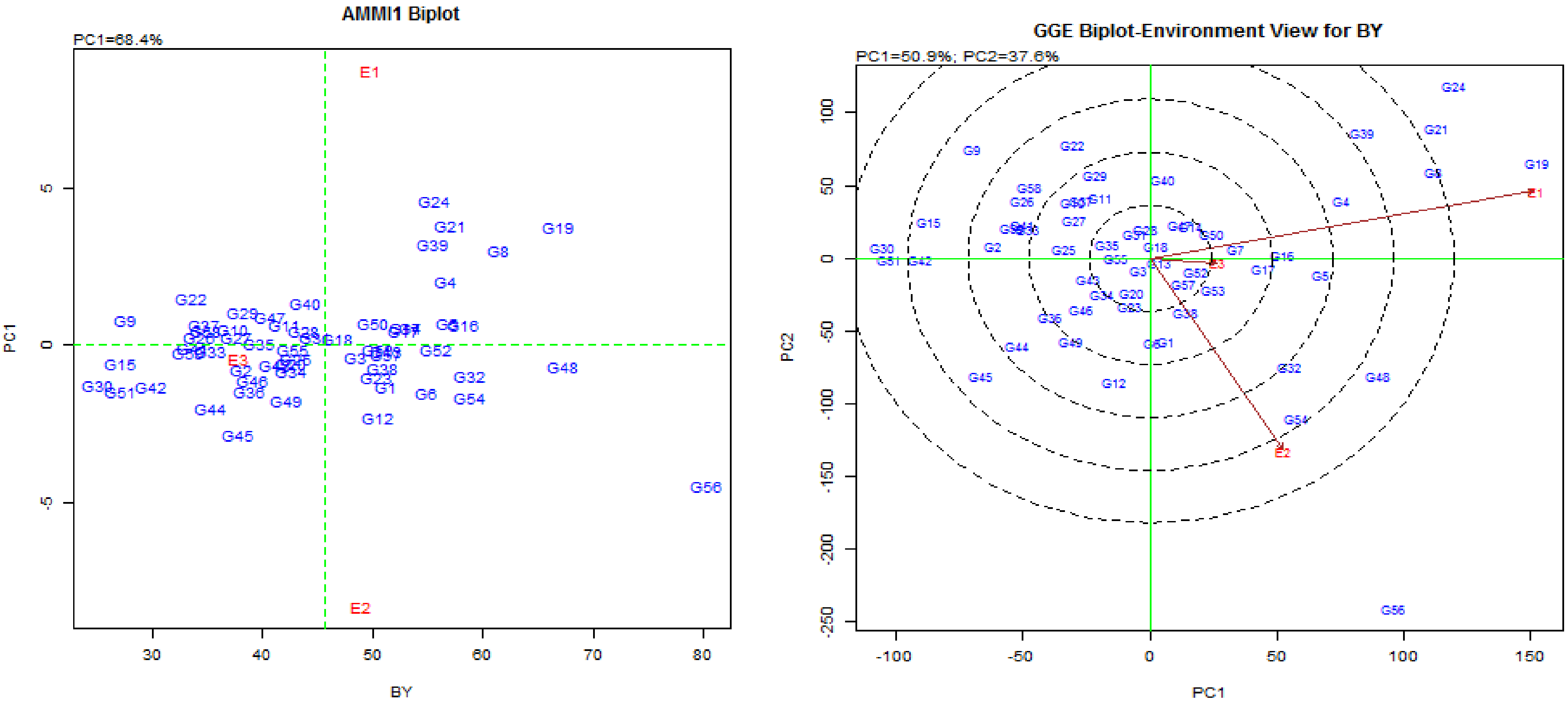
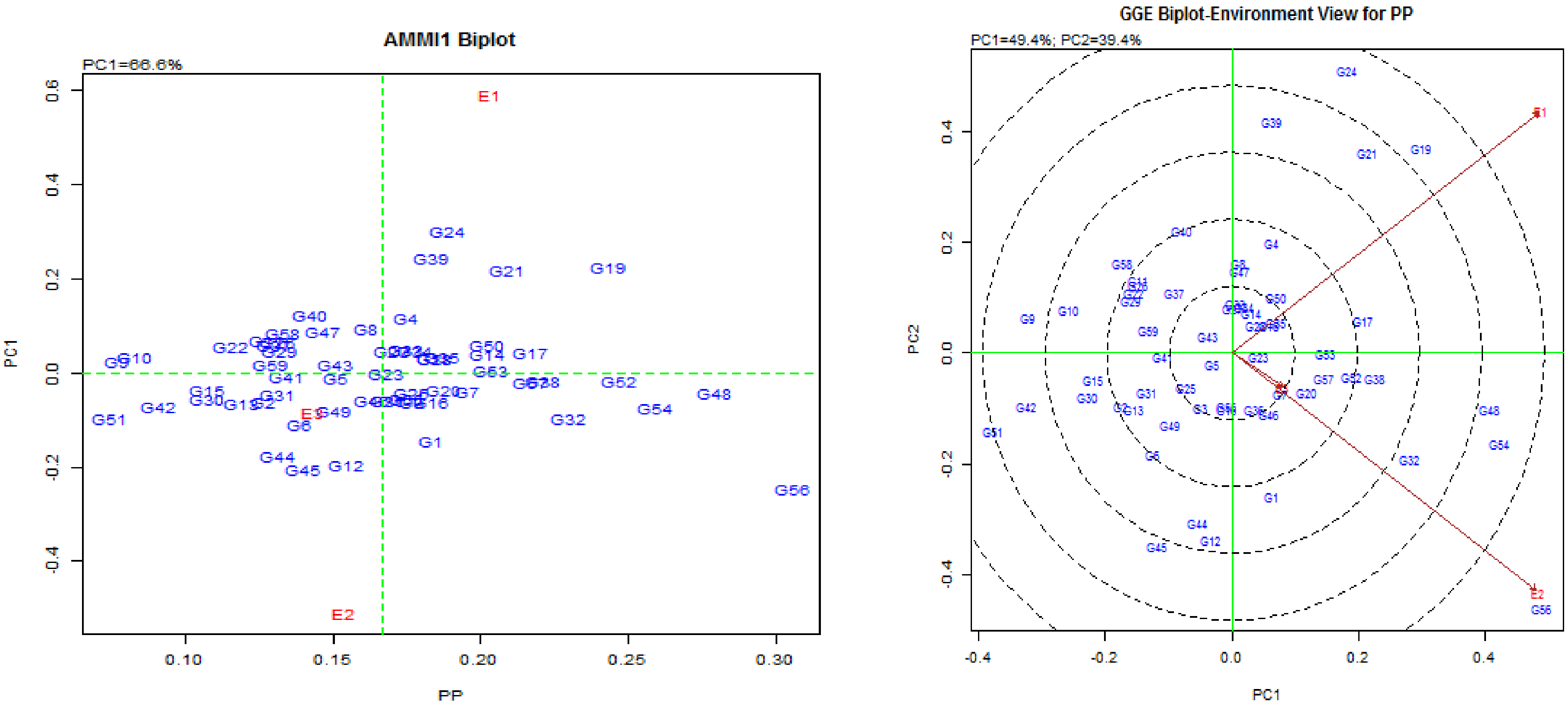


Figure 4.3.3.18. AMMI1 biplot and GGE biplot for per day productivity of 59 genotypes tested in three seasons



the best suited genotypes were G7 (166-2-3, mid early line), G20 (35 B, mid early line) and G57 (Tulasi, early line).

4.3.4. Adaptability of Genotypes across the Three Seasons:

Adaptability of genotypes across the environments was assessed based on GGE biplot – genotype view graph and GGE biplot polygon view graph (also called as Which- won- where graph). The ideal genotypes for traits were selected by GGE biplot – genotype graph and the best suited genotypes for particular season is identified by GGE biplot polygon view graph.

4.3.4.1. Days to 50 % flowering:

Genotype view of GGE biplot (Fig. 4.3.4.1) showed that G24 (95 B, late line) is ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G24, G13 (166 S, late line), G16 (250 K, late line), G6 (166-2-11, late line), G10 (166-23-1, late line), G5 (166-1, late line), G31 (Jaya, late line), G2 (14-3, mid early line), G22 (75 S, late line), G8 (166-2-9, late line), G9 (166-23, late line) and G11(166-30, late line) are the best stable late genotypes suitable across all the three seasons. But as the early to medium varieties are preferred than late genotypes so we have to choose the genotypes in negative direction for days to fifty per cent flowering and as per this the genotypes G53 (SM733, early line), G36 (SM1637, early line), G54 (SM776, early line), G50 (SM4406, early line), G27 (Anjali, early line) and G25 are the best suited stable early lines across all the seasons. The polygon view of GGE biplot (which won where graph) had shown that genotypes G6, G13, G24 and G5 are best suitable lines for all three seasons.

4.3.4.2. Days to maturity:

Genotype view of GGE biplot (Fig. 4.3.4.2) showed that G6 (166-2-11, late line) is ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G6, G10 (166-23-1, late line), G24 (95 B, late line), G5 (166-1, late line), G9 (166-23, late line), G13 (166 S, late line), G31 (Jaya, late line), G22 (75 S, late line), G11 (166-30, late line), G8 (166-2-9, late line), G16 (250 K, late line), G23 (93 B, late line) and G21 (51 B, late line) are the best stable late lines suitable across all the three seasons. But as the early to mid early lines are preferred the genotypes G33 (Prasanna, early line check), G36 (SM1637, mid early line), G30 (Jaldidhan, early line), G27 (Anjali, early line), G25 (Aditya, early line), G46

Figure 4.3.4.1. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for days to 50 % flowering in three seasons based on which-won-where pattern

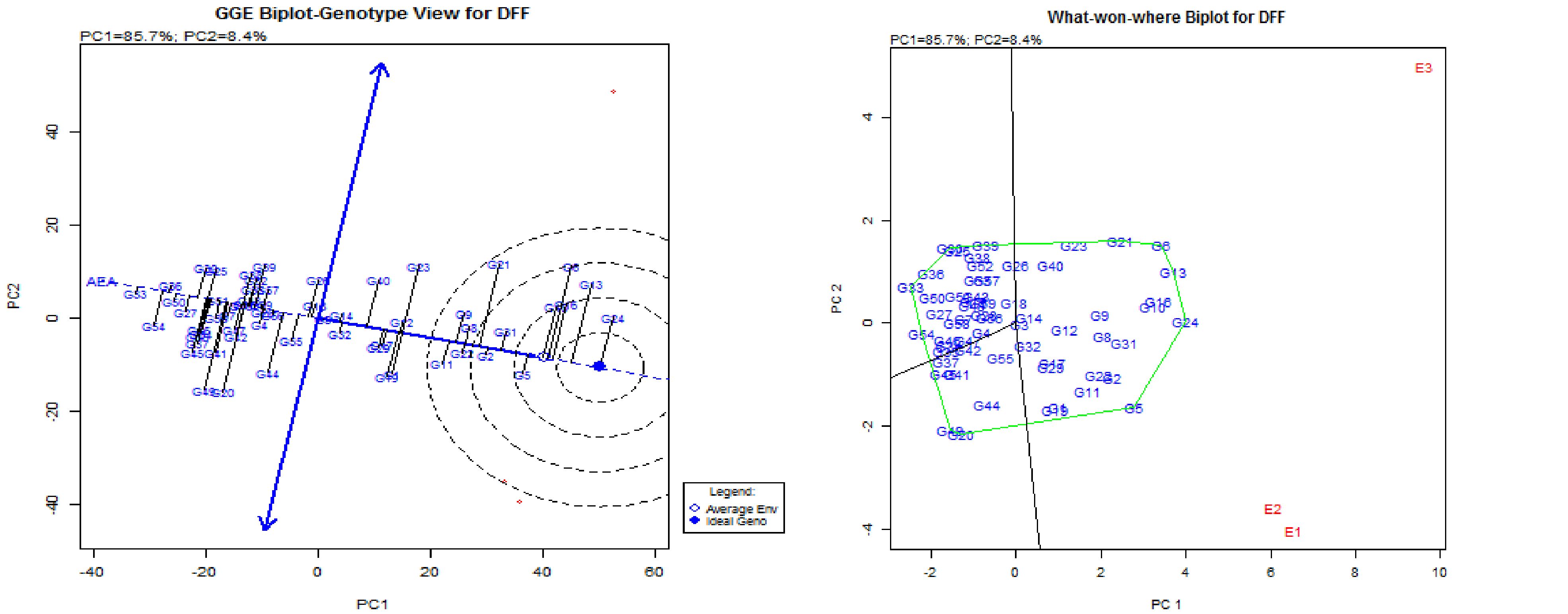
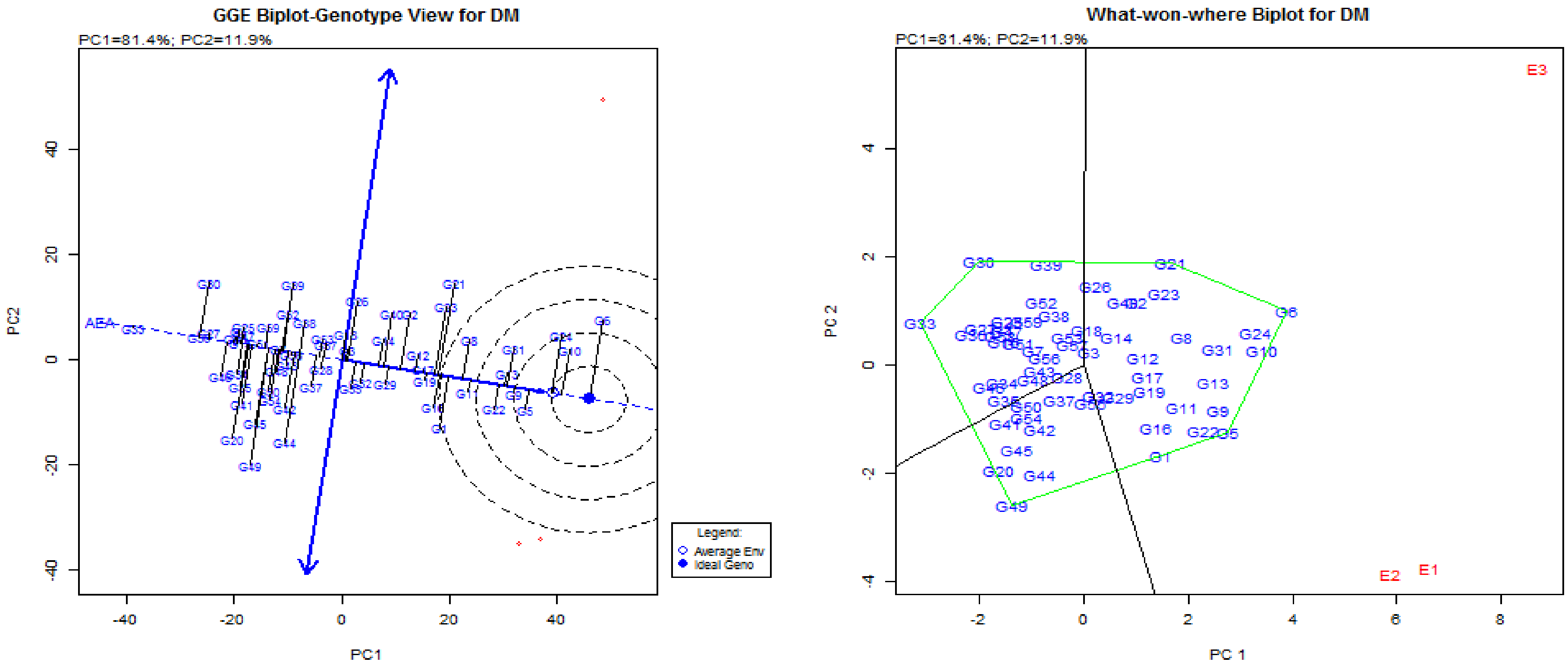


Figure 4.3.4.2. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for days to maturity in three seasons based on which-won-where pattern



(SM4226, mid early line), G47 (SM4231, early line), G35 (Sabhagidhan, early line) are the best stable early to mid early lines suitable cross all the three seasons. The polygon view of GGE biplot (which won where graph) had shown that genotypes G21, G6 and G5 are best suitable lines for all three seasons.

4.3.4.3. Plant height:

Genotype view of GGE biplot (Fig. 4.3.4.3) showed that G4 (148S, early line) is ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G4, G40 (SM363, mid early line), G6 (166-2-11, late line), G12 (166-9, mid early line), G59 (Varalu, early line) and G27 (Anjali, early line) are the best sable genotypes across all the three seasons. The polygon view of GGE biplot (which won where graph) had shown that genotypes G4 is the best suitable line for all three seasons.

4.3.4.4. Number of total tillers per plant:

Genotype view of GGE biplot showed that G21 (51B, late line) is ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G21, G54 (SM776, early line), G3 (14 S, mid early line), G14 (220 S, mid early line), G23 (93 B, late line), G18 (263 K, mid early line) and G19 (27 K, mid early line) are the best stable suitable lines across all the three seasons for this trait. The polygon view of GGE biplot (which won where graph) had shown that G11 (166-30, late line), G56 and G21 were best suited for both E1and E2. The genotype G14 and G52 (SM686, mid early line) were best suited for season E3.

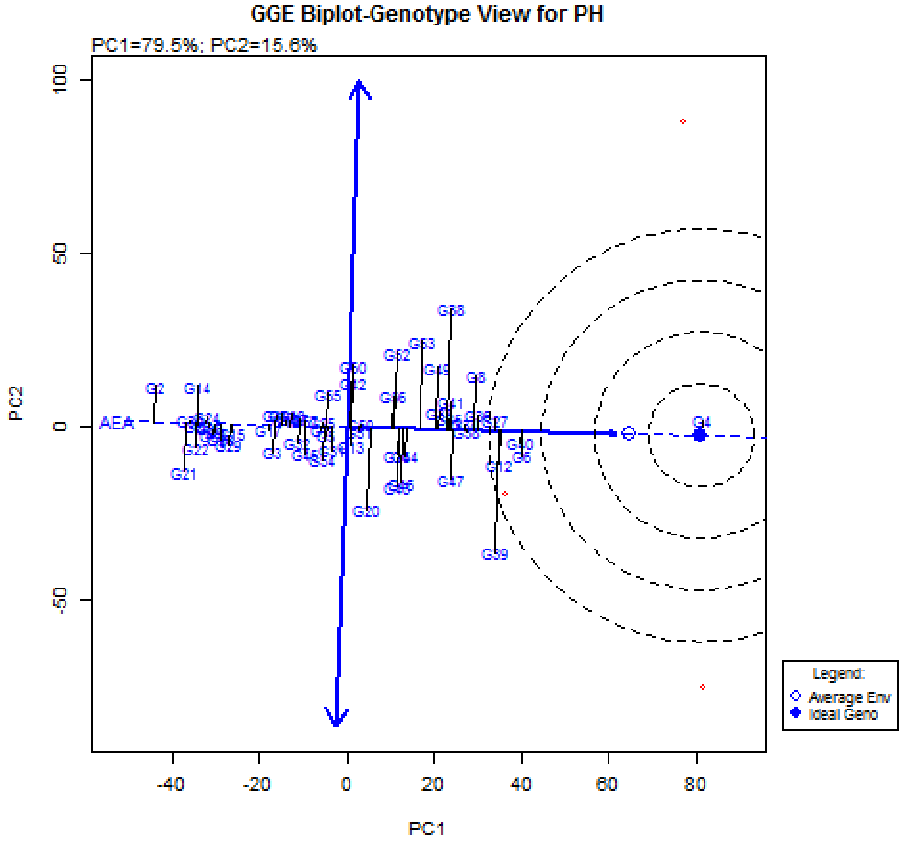
4.3.4.5. Number of productive tillers per plant:

Genotype view of GGE biplot showed that G21 is ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G21 and G54 are the best stable lines across all the seasons for productive tillers per plant. The polygon view of GGE biplot (which won where graph) had shown that G11 was the best suited genotype for E2. The genotype G52, G24 and G21 were best suited for seasons E1 and E3.

4.3.4.6. Panicle length:

Genotype view of GGE biplot (Fig. 4.3.4.6) showed that G4 (148 S, mid early line) and G8 (166-2-9, late line) were ideal genotypes for this trait in all the

Figure 4.3.4.3. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for plant height in three seasons based on which-won-where pattern



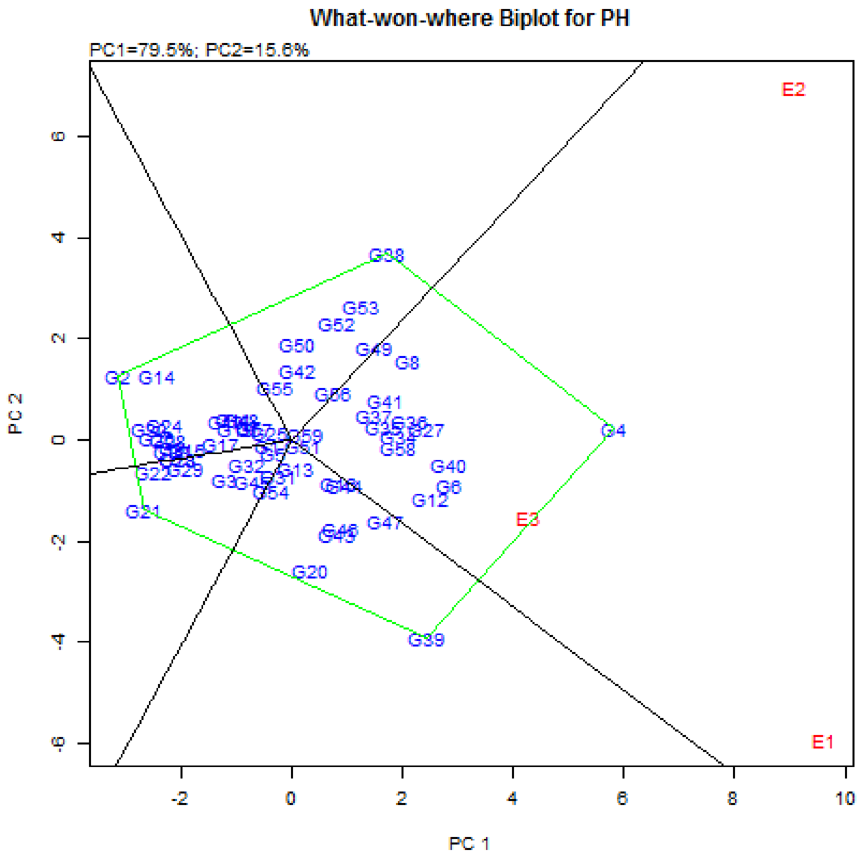
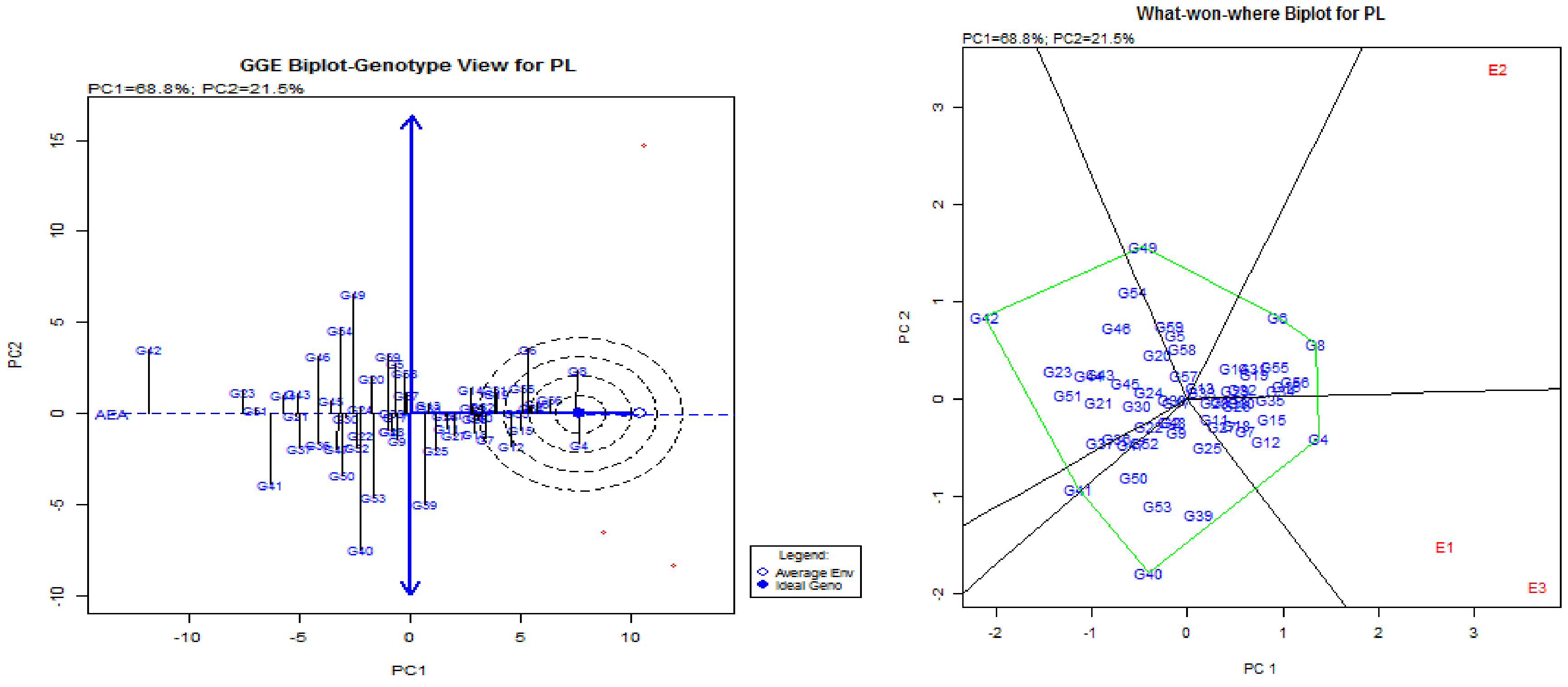


Figure 4.3.4.6. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for panicle length in three seasons based on which-won-where pattern



seasons compared to other genotypes. The genotypes G4, G8, G56 (Tellahamsa, mid early line), G34 (Rasi, early line), G55 (Sona, mid early line), G16 (250 K, late line), G6 (166-2-11, late line), G35 (Sabhagidhan, early line), G12 (166-9, mid early line), G15 (246 K, mid early line), G7 (166-2-3, mid early line), G32 (MTU1010, mid early line) and G19 (27 K, mid early line) are stable genotypes across all the three seasons. The polygon view of GGE biplot (which won where graph) had shown that G4 best suited for E1 and E3. The genotype G8 was best suited for season E2.

4.3.4.7. Panicle weight:

Genotype view of GGE biplot (Fig. 4.3.4.7) showed that G11 (166-30, late line) was identified as ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G11, G8 (166-2-9, late line), G12 (166-9, mid early line), G6 (166-2-11, late line) and G16 (250 K, late line) were best suited stable genotypes across all the seasons. The polygon view of GGE biplot (which won where graph) had shown that genotypes G11 and G8 are suited genotypes across all the three season.

4.3.4.8. Number of filled grains per panicle:

Genotype view of GGE biplot (Fig. 4.3.4.8) showed that G11 was identified as ideal genotype for this trait in all the seasons compared to other genotypes. The genotypes G11, G6, G8, G24 (95 B, late line) and G10 (166-23-1, late line) were identified as the best stable genotypes and are suitable for all the three seasons. The polygon view of GGE biplot (which won where graph) had shown that genotype G11 was the best suited genotype across all the three season.

4.3.4.9. Number of unfilled grains per panicle:

Genotype view of GGE biplot (Fig. 4.3.4.9) showed that G11 (166-30, late line) was identified as ideal genotype for this trait in all the seasons compared to other genotypes. As per this the stable genotypes having high mean value for unfilled grains are G9 (166-23, late line), G10 (166-23-1, late line), G1 (130 K, mid early line), G16 (250 K, late line) and G8 (166-2-9, late line). As genotypes having less mean for unfilled grains per panicle are preferred so we have to choose negative in direction. Based on this the genotypes G24 (95 B, late line), G42 (SM4029, early line), G51 (SM4415, early line), G4 (148 S, early line), G34 (Rasi, early line), G47 (SM4231, early line), G22 (75 S, late line), G42 (SM4029, early line), G37

Figure 4.3.4.8. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for number of filled grains per panicle in three seasons based on which-won-where pattern

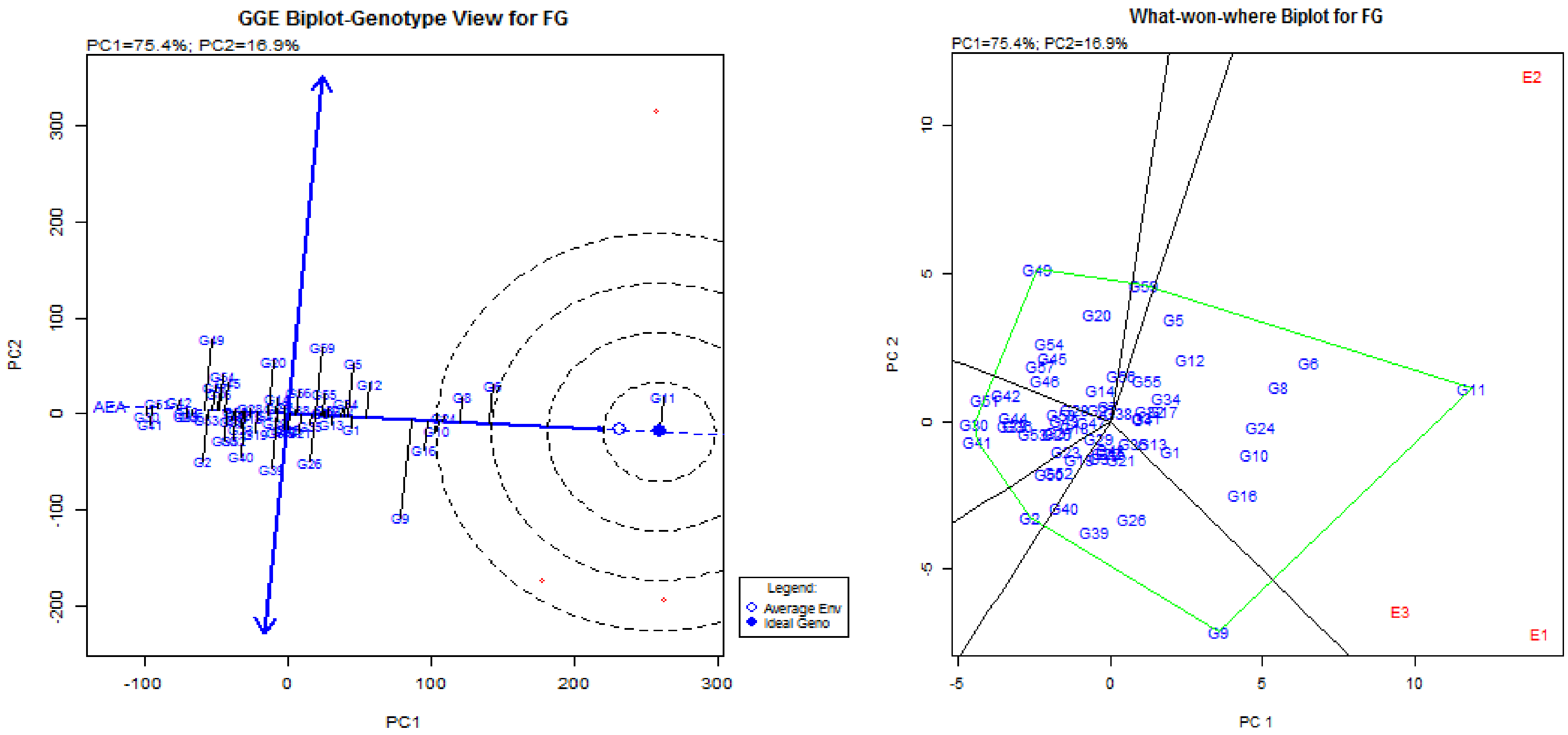
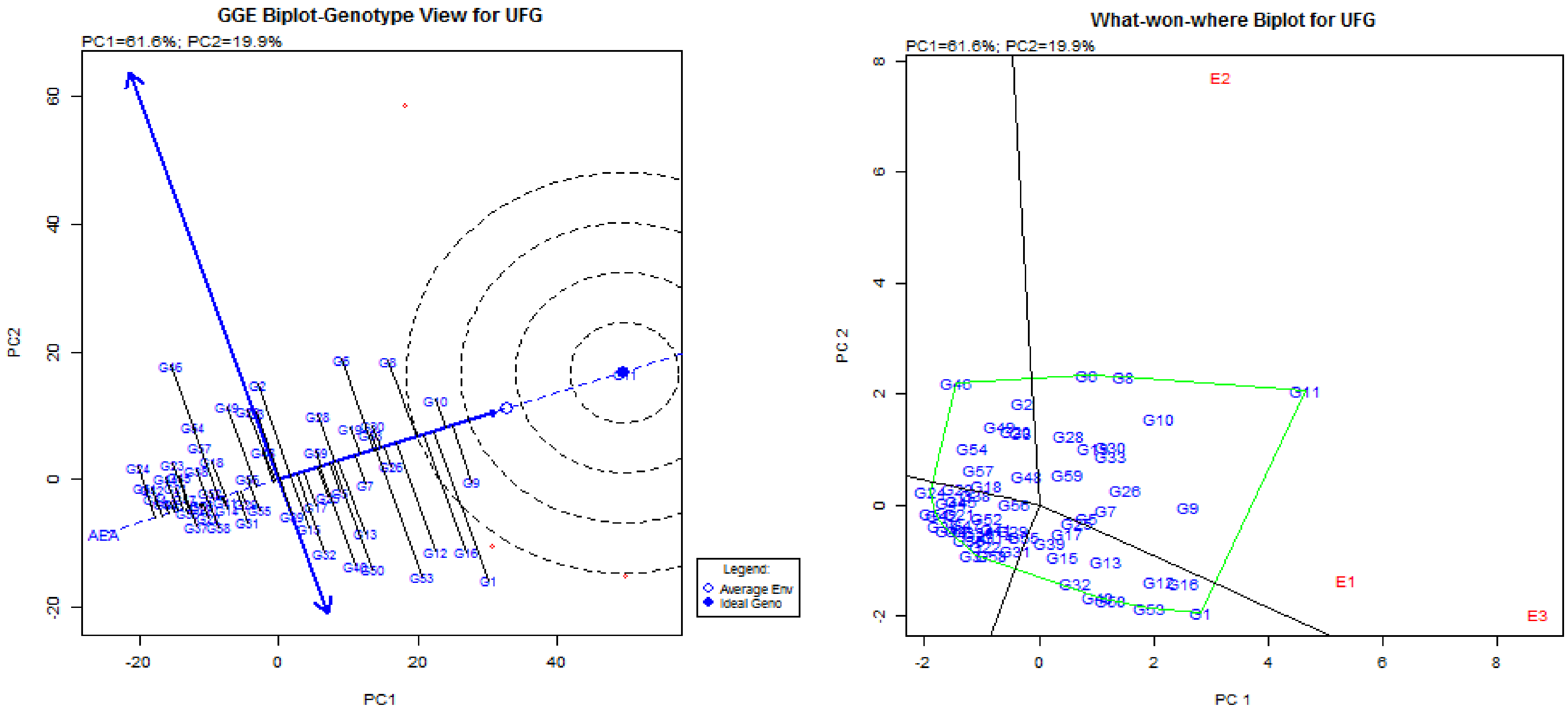


Figure 4.3.4.9. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for number of unfilled grains per panicle in three seasons based on which-won-where pattern



(SM1876, early line) and G58 (Vandana, early line) are the best stable genotypes suitable for all the seasons. The polygon view of GGE biplot (which won where graph) had shown that genotype G11 was the best suited genotype across all the three season.

4.3.4.10. Number of total grains per panicle:

Genotype view of GGE biplot (Fig. 4.3.4.10) showed that G11 was identified as ideal genotype for this trait in all the seasons compared to other genotypes having highest mean value. The genotypes G11 (166-30, late line), G6 (166-2-11, late line), G8 (166-2-9, late line), G10 (166-23-1, late line), G16 (250 K, late line) and G9 (166-23, late line) are identified as the best stable genotypes across all the three season. The polygon view of GGE biplot (which won where graph) had shown that genotype G11 was the best suited genotype across all the three season.

4.3.4.11. Spikelet fertility:

Genotype view of GGE biplot (Fig. 4.3.4.11) showed that G24 (95 B, late line) was identified as ideal genotype for this trait in all the seasons compared to other genotypes having highest mean value. The genotypes G24, G34 (Rasi, early line), G35 (Sabhagidhan, early line), G43 (SM4071, early line), G21 (51 B, late line), G42 (SM4029, early line), G51 (SM4415, early line), G23 (93 B, late line), G22 (75 S, late line), G47 (SM4231, early line) and G27 (Anjali, early line) are stable best suited genotypes across all the seasons. The polygon view of GGE biplot (which won where graph) had shown that genotype G24 was the best suited genotype for E1 and E3. Genotypes G50 (SM4406, early line) and G53 (SM733, early line) are suitable genotypes for E2.

4.3.4.12. Sterility percentage:

Genotype view of GGE biplot (Fig. 4.3.4.12) showed that G30 (Jaldidhan, early line) was identified as stable genotype for this trait in all the seasons compared to other genotypes having highest mean value. The genotypes G33 (Prasanna, check), G53 (SM733, early line), G2 (14-3, late line) and G19 (27 K, mid early line) are genotype across all the three season having high sterility percentage. As genotypes having low sterility percentage are preferred and are chosen based on negative direction for sterility percentage. Based on this genotypes G24 (95 B, late

Figure 4.3.4.10. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for number of total grains per panicle in three seasons based on which-won-where pattern

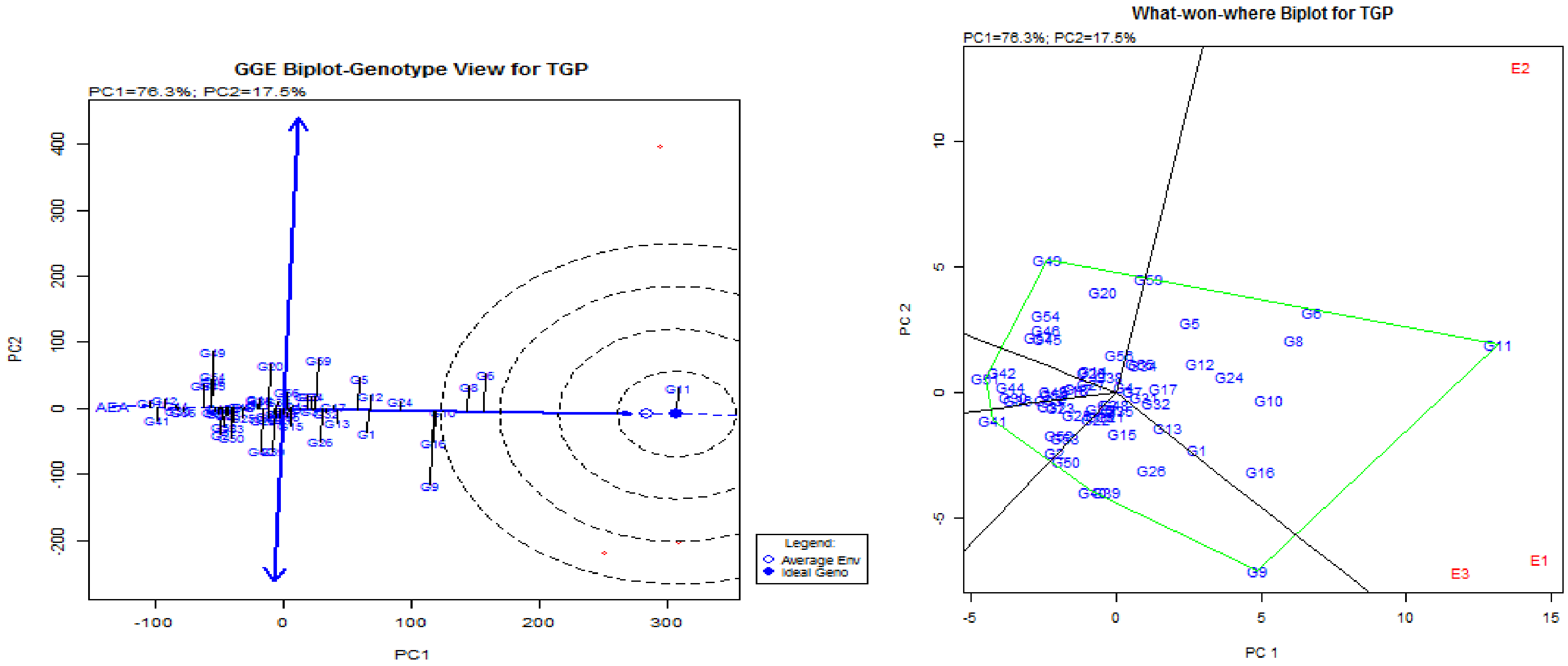


Figure 4.3.4.11. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for spikelet fertility in three seasons based on which-won-where pattern

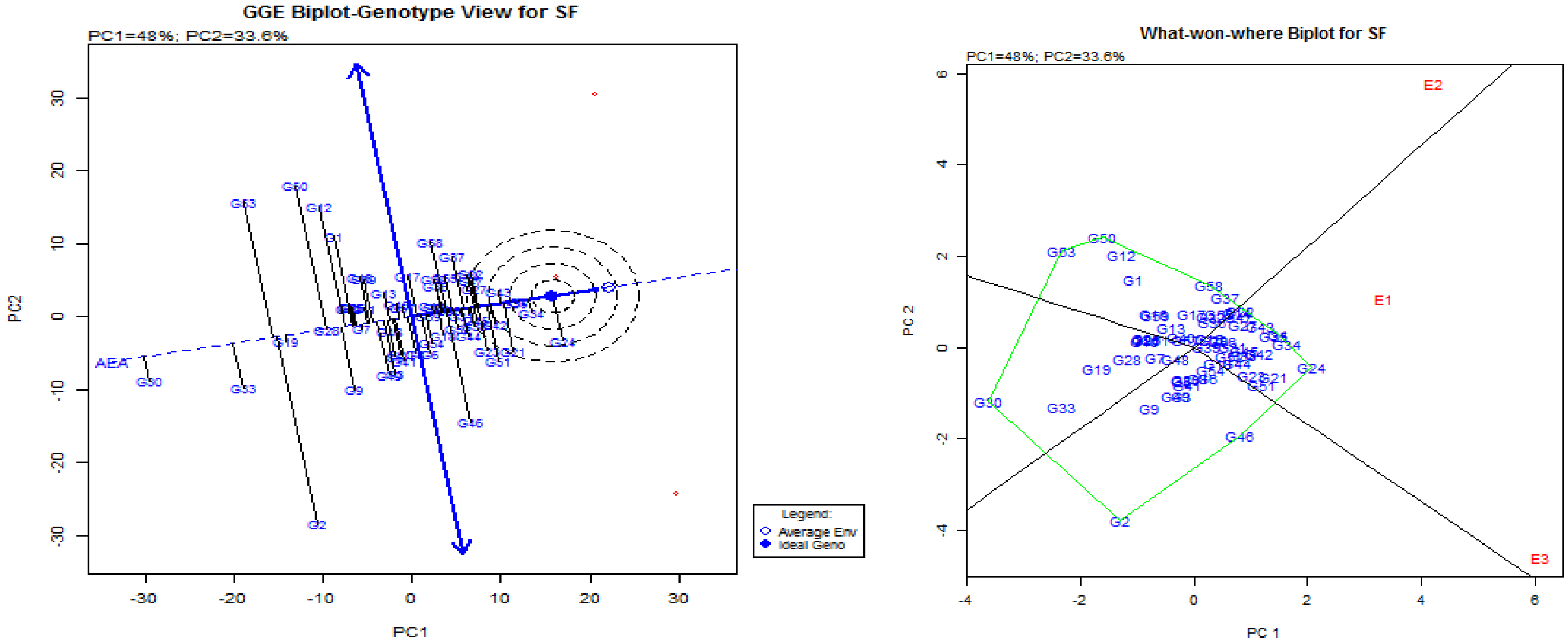
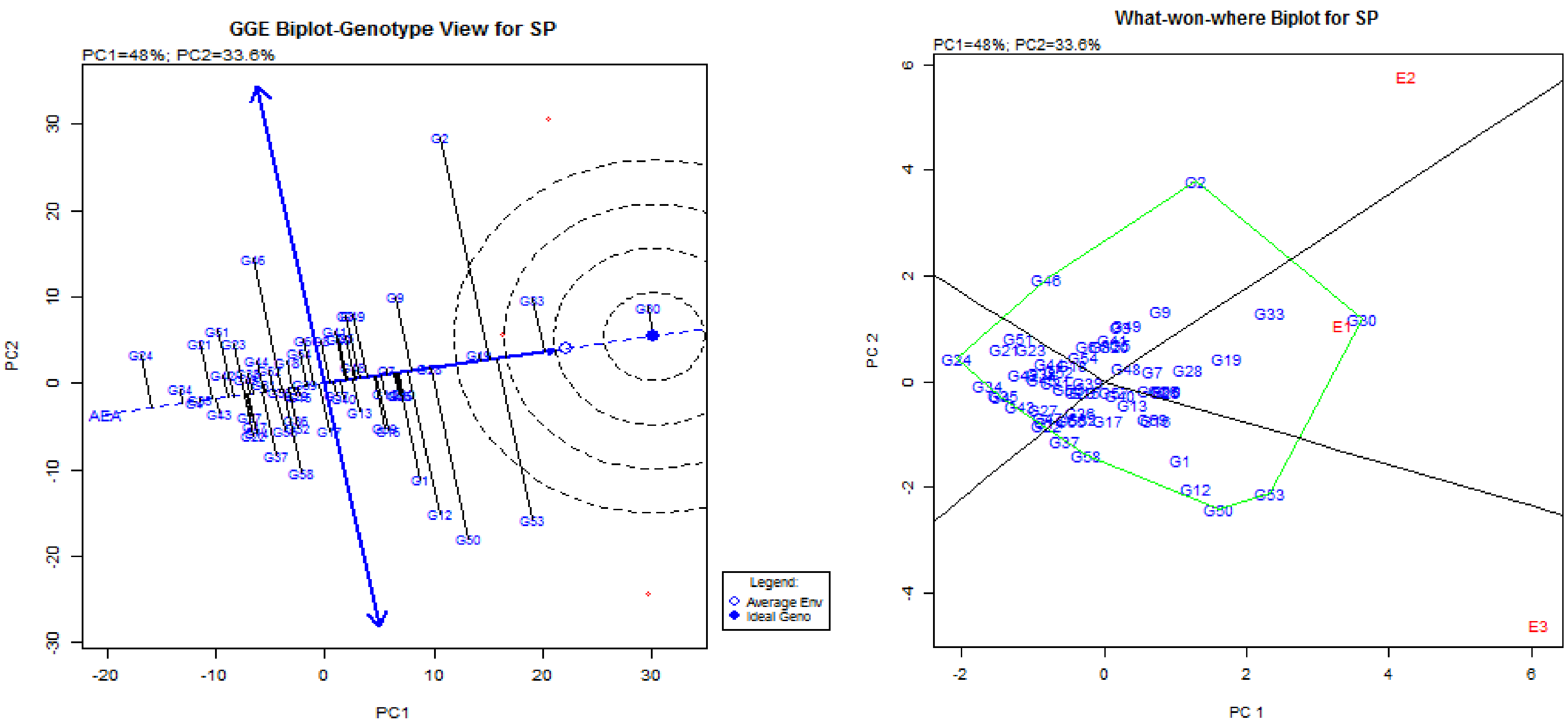


Figure 4.3.4.12. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for sterility percentage in three seasons based on which-won-where pattern



line), G34 (Rasi, early line), G4 (148 S, early line), G35 (Sabhagidhan, early line), G43 (SM4071, early line), G21 (51 B, late line), G42 (SM4029, early line), G51 (SM4415, early line), G23 (93 B, late line), G22 (75 S, late line), G47 (SM4231, early line), G27 (Anjali, early line), G14 (220 S, mid early line) and G44 (SM4076, early line) are the best stable genotypes for low sterility percentage and suitable across all the season. The polygon view of GGE biplot (which won where graph) had shown that genotype G30 was the best suited genotype for E1, G2 for E2. Genotypes G50 (SM4406, early line) and G53 are best suitable genotypes for E3.

4.3.4.13. Thousand grain weight:

Genotype view of GGE biplot (Fig. 4.3.4.13) showed that G4 (148 S, early line) was identified as ideal genotype for this trait in all the seasons compared to other genotypes having highest mean value. Followed by G4 genotype G19 (27 K, mid early line) and G12 (166-9, mid early line) were identified as the ideal genotypes across all the seasons. The genotypes G4, G19, G12, G29 (IR64, mid early line), G58 (Vandana, early line), G25 (Adithya, early line), G35 (Sabhagidhan, early line), G7 (166-2-3, mid early line), G55 (Sona, mid early line), G1(130 K, mid early line), G56 (Tellahamsa, mid early line) and G33 (Prasanna, check) are the best stable genotypes across all the seasons for thousand grain weight. The polygon view of GGE biplot (which won where graph) had shown that genotype G40 was the best suited genotype for E1, G4 for E2 and G12 for E3.

4.3.4.14. Single plant grain yield:

Genotype view of GGE biplot (Fig. 4.3.4.14) showed that G56 (Tellahamsa, mid early line) is ideal genotype in single plant grain yield in all the seasons compared to other genotypes.G54 is next to G56 is ideal genotype and it is most stable than G56, so it can be considered as best genotype across all the seasons than G56. The genotypes G56, G54 (SM776, early line), G48 (SM4371, early line), G19 (27 K, mid early line), G52 (SM686, mid early line), G17 (258 S, mid early line), G24 (95 B, late line), G21 and G38 (SM219 mid early line) are stable genotypes and best suited for all the three seasons. The polygon view of GGE biplot (which won where graph) had shown that G24 is best suitable to E1, followed by G19. These two genotypes are also high yielders in E1. G56 was observed to be best performing in both seasons E2 and E3.

Figure 4.3.4.13. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for thousand grain weight in three seasons based on which-won-where pattern

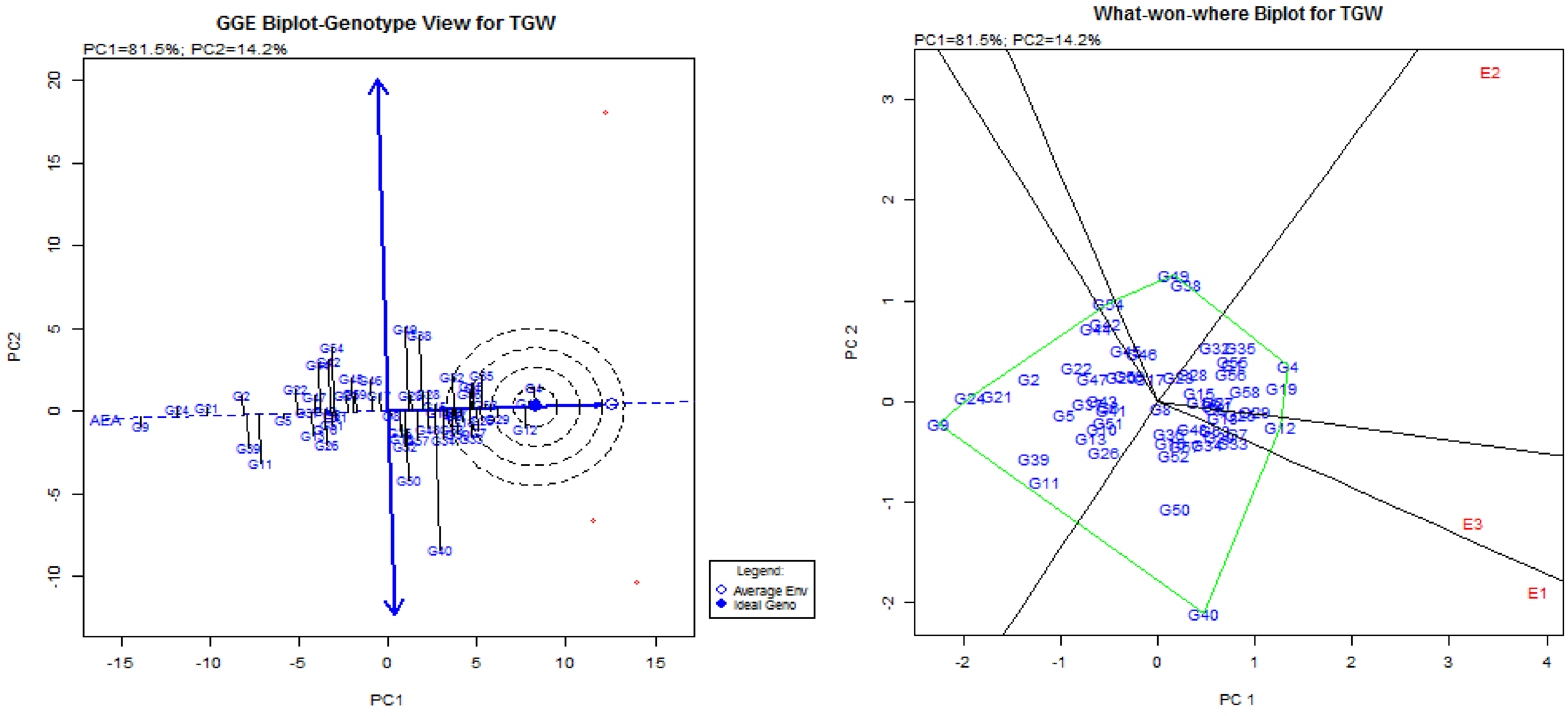
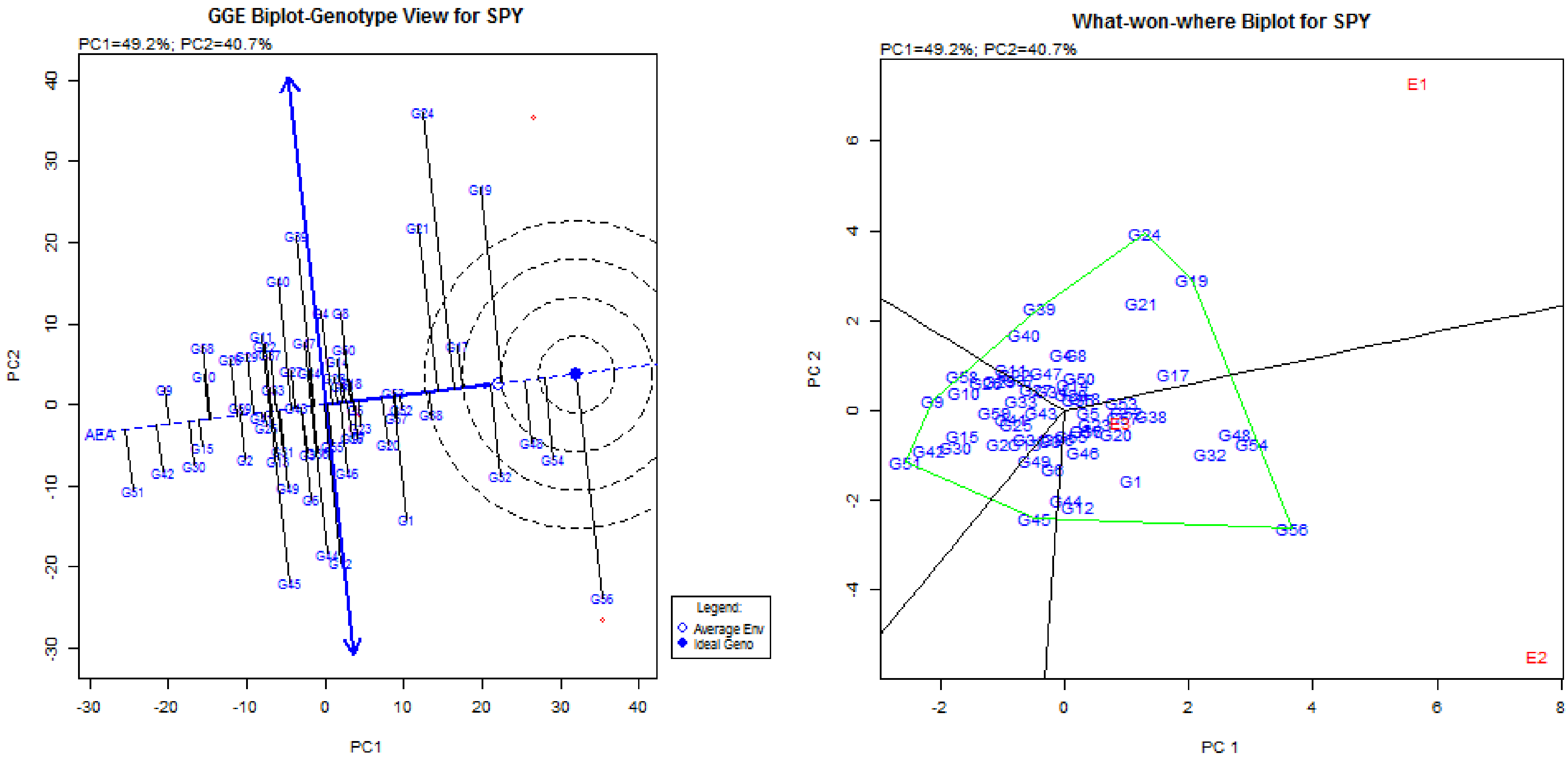


Figure 4.3.4.14. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for single plant grain yield in three seasons based on which-won-where pattern



4.3.4.15. Biomass per plant:

Genotype view of GGE biplot (Fig. 4.3.4.15) showed that G56 was identified as ideal genotype for this trait in all the seasons compared to other genotypes having highest mean value. Followed by G56, G8 (166-2-9, late line) was identified as the ideal genotypes across all the seasons. The genotypes G56, G8, G5 (166-1, late line), G4 (148 S, early line), G19 (27K, mid early line), G39 (SM349, mid early line), G48 (SM4371, early line) and G16 (250 K, late line) are the best stable genotypes across all the seasons for biomass per plant. The polygon view of GGE biplot (which won where graph) had shown that genotypes G8, G21 (51 B, late line) and G24 (95 B, late line) are best suited genotypes for E1 and E3. The genotype G56 was best suited for E2.

4.3.4.16. Biological yield per plant:

Genotype view of GGE biplot (Fig. 4.3.4.16) showed that G56 (Tellahamsa, mid early line) was identified as ideal genotype for this trait in all the seasons with highest mean value. The genotypes G56, G19 (27 K, mid early line), G48 (SM4371, early line), G54 (SM776, early line), G8 (166-2-9, late line), G32 (MTU1010, mid early line), G21 (35 B, late line), G24 (95 B, late line) and G6 (166-2-11, late line) are the best stable genotypes across all the seasons for biological yield per plant. The polygon view of GGE biplot (which won where graph) had shown that genotype G19 was the best suited genotype for E1 and E3. The genotypes G45 (SM4078, early line) and G56 are best suited genotypes for E2.

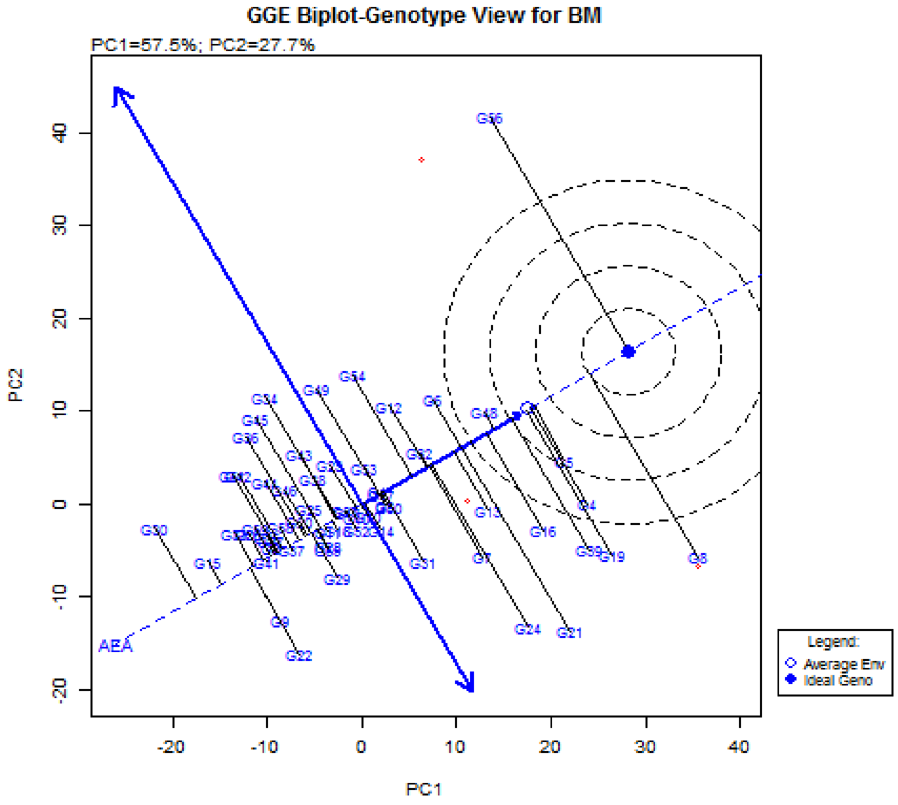
4.3.4.17. Harvest index:

Genotype view of GGE biplot showed that G17 (258 S, mid early line) was identified as ideal genotype for this trait in all the seasons with highest mean value. The polygon view of GGE biplot (which won where graph) had shown that genotype G1 (130 K, mid early line) was the best suited genotype for E2 and G17 for E3.

4.3.4.18. Per day productivity:

Genotype view of GGE biplot (Fig. 4.3.4.18) showed that G56 (Tellahamsa, mid early line) was identified as ideal genotype for this trait in all the seasons with highest mean value. Next to genotype G56 genotype G54 (SM776, early line) is considered as ideal genotype across all the seasons. The genotypes G56, G54, G48 (SM4371, early line), G32 (MTU1010, mid early line), G19 (27 K, mid early line),

Figure 4.3.4.15. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for biomass per plant in three seasons based on which-won-where pattern



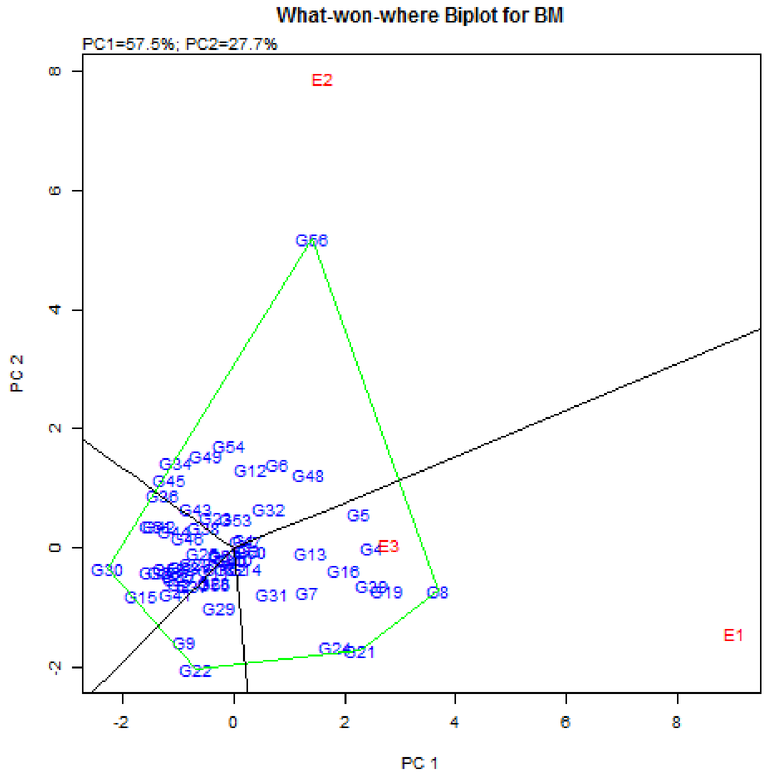


Figure 4.3.4.16. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for biological yield per plant in three seasons based on which-won-where pattern

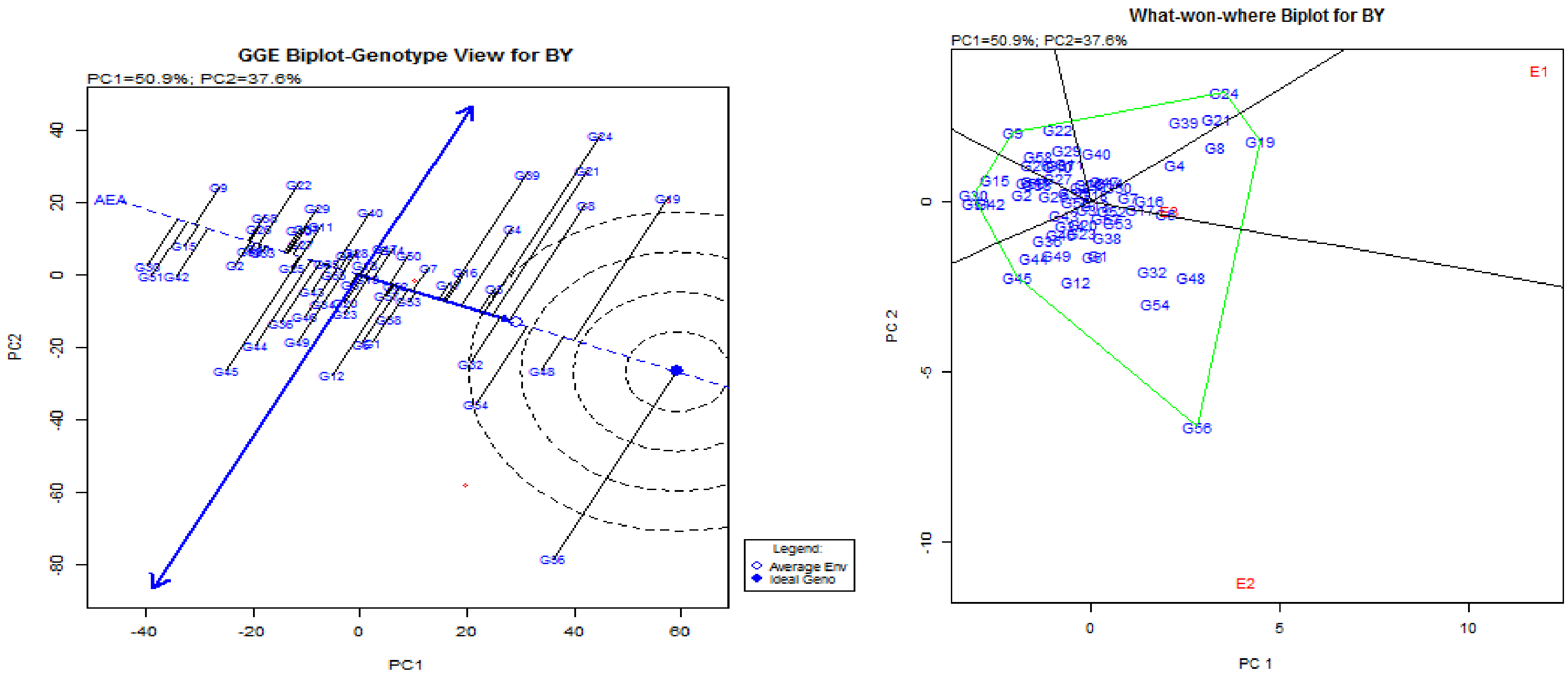
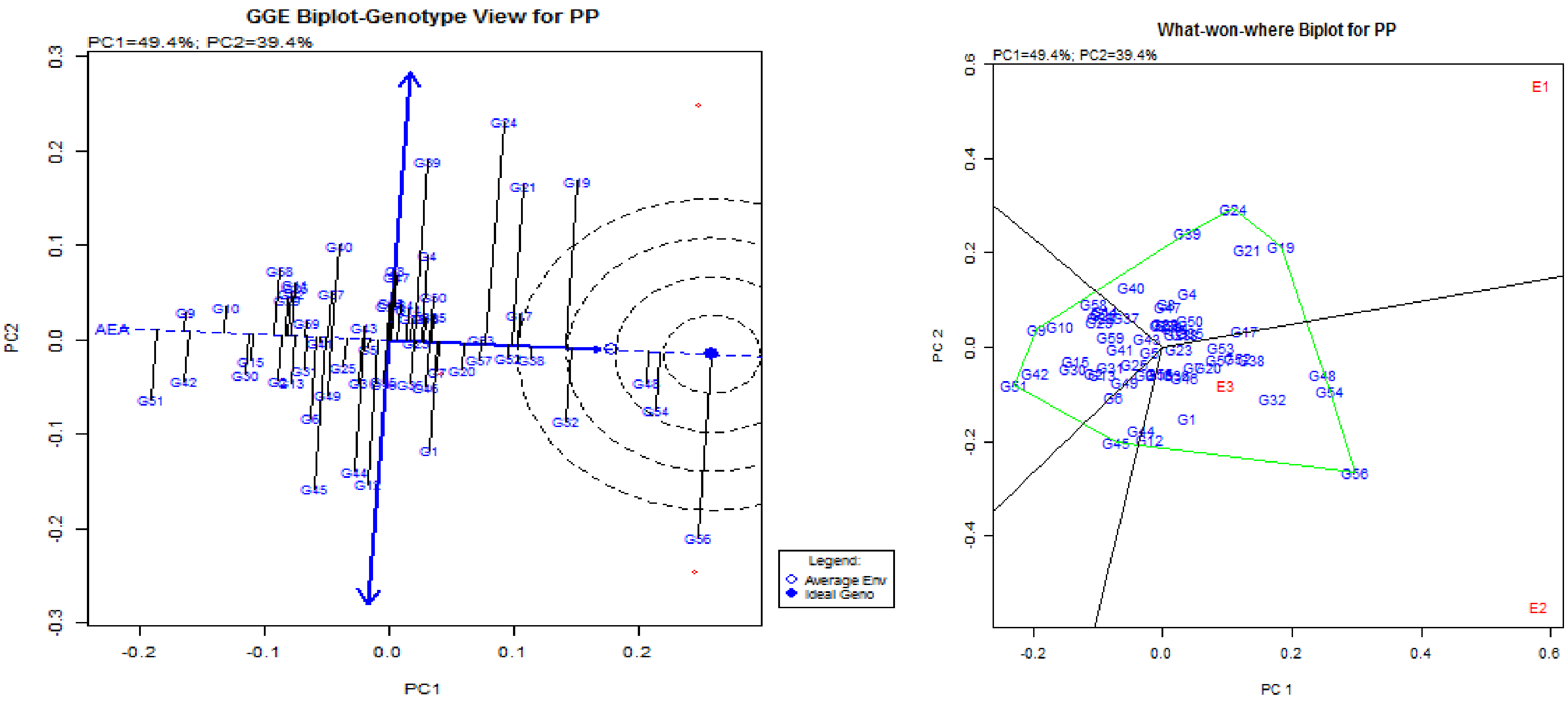


Figure 4.3.4.18. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with GGE biplot of 59 genotypes for per day productivity in three seasons based on which-won-where pattern



G38 (SM219, mid early line) and G17 (258 S, mid early line) are the best stable genotypes across all the seasons for per day productivity. The polygon view of GGE biplot (which won where graph) had shown that genotypes G24 (95 B, late line) and G19 was the best suited genotypes for E1. The genotypes G56 and G54 are best suited genotypes for E2 and E3.

4.4. CHARACTER ASSOCIATION

Crop yield is the end product of the interaction of a number of often interrelated attributes. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. Pooled genotypic correlations were worked out on single plant grain yield and yield contributing characters in fifty nine genotypes. Results of pooled genotypic correlation analysis were presented in Table 4.4.

4.4.1. Days to 50 % flowering

This trait showed positive significant association at genotypic level with days to maturity (0.9615**), panicle length (0.2247**), panicle weight (0.5067**), number of filled grains per panicle (0.7491**), number of unfilled grains per panicle (0.4846**), number of total grains per panicle (0.7293**), biomass per plant (0.6038**) and biological yield per plant (0.4028**). The similar findings were reported by Hasan *et al.* (2013), Patel *et al*. (2014) and Ravi *et al.* (2014) for days to maturity, Soni *et al*. (2013) for panicle length, panicle weight and biological yield per plant, Reddy *et al*. (2013), Rao *et al.* (2014) and Ratna *et al*. (2015) for number of filled grains per panicle and Patel *et al*. (2014) for biomass per plant. It showed positive non-significant association at genotypic level with spikelet fertility (0.0127) and single plant grain yield (0.0108). Similar results were reported by Panwar (2006) and Mishra *et al*. (2014) for spikelet fertility, Golam *et al.* (2015) and Mishu *et al.* (2016) for single plant grain yield.

Table 4.4. Pooled genotypic correlation coefficient analysis of single plant grain yield and yield contributing characters in rice

Character	Days to 50 % flowering	Days to maturity	Plant height(cm)	Number of total tillers / plant	Number of productive tillers / plant	Panicle length (cm)	Panicle weight (g)	Number of filled grains / panicle	Number of unfilled grains / panicle
Days to 50 % flowering	**1.0000**	0.9615**	-0.347**	-0.1074	-0.1049	0.2247**	0.5067**	0.7491**	0.4846**
Days to maturity		**1.0000**	-0.3743**	-0.0455	-0.0409	0.1693*	0.5589**	0.7656**	0.5028**
Plant height(cm)			**1.0000**	-0.6934**	-0.6179**	0.1510*	0.1304	-0.0311	-0.2776**
Number of total tillers / plant				**1.0000**	0.9475**	-0.5242**	-0.7531**	-0.8063**	-0.7847**
Number of productive tillers / plant					**1.0000**	-0.6111**	-0.7532**	-0.7240**	-0.6929**
Panicle length (cm)						**1.0000**	0.7205	0.5534**	0.3850**
Panicle weight (g)							**1.0000**	0.8746**	0.8808**
Number of filled grains / panicle								**1.0000**	0.7682**
Number of unfilled grains / panicle									**1.0000**
Number of total grains / panicle									
Spikelet fertility (%)									
Sterility percentage (%)									
Thousand grain weight (g)									
Biomass / plant (g)									
Biological yield /plant (g)									
Harvest index									
Per day productivity (g)									

*** Significant at 5 per cent level; ** Significant at 1 per cent level**

Continuation of table 4.4…

Character	Number of total grains / panicle	Spikelet fertility (%)	Sterility percentage (%)	Thousand grain weight (g)	Biomass / plant (g)	Biological yield / plant (g)	Harvest index	Per day productivity (g)	Single plant grain yield (g)
Days to 50 % flowering	0.7293**	0.0127	-0.0127	-0.4404**	0.6038**	0.4028**	-0.7479**	-0.4466**	0.0108
Days to maturity	0.7466**	0.0550	-0.0550	-0.4777**	0.5830**	0.4610**	-0.6355**	-0.3254**	0.1562**
Plant height (cm)	-0.0739	0.4400**	-0.4400**	0.2691**	0.3872**	0.1919*	-0.4810**	0.0465	-0.1273
Number of total tillers / plant	-0.8295**	0.5134**	-0.5134**	0.0705	-0.2288**	0.0924	0.5158**	0.4943**	0.4919**
Number of productive tillers / plant	-0.7429**	0.4517**	-0.4517**	-0.0701	-0.1887*	0.1281	0.5300**	0.5135**	0.5107**
Panicle length (cm)	0.5434**	-0.0683	0.0683	0.4892**	0.6295**	0.6064**	-0.1647*	0.2885**	0.3886**
Panicle weight (g)	0.9048**	-0.2266**	0.2266**	0.1939**	0.7300**	0.5824**	-0.6055**	-0.0759	0.2062**
Number of filled grains / panicle	0.9941**	0.0044	-0.0044	-0.3306**	0.5340**	0.3242**	-0.7425**	-0.3704**	-0.0552
Number of unfilled grains / panicle	0.8332**	-0.6574**	0.6574**	-0.1241	0.2284**	0.0563	-0.3819**	-0.3939**	-0.1904*
Number of total grains / panicle	**1.0000**	-0.1076	0.1076	-0.3066**	0.5000**	0.2896**	-0.7062**	-0.3868**	-0.0800
Spikelet fertility (%)		**1.0000**	-1.0000**	-0.1735*	0.2126**	0.2367**	-0.3381**	0.1644*	0.1960**
Sterility percentage (%)			**1.0000**	0.1735*	-0.2126**	-0.2367**	0.3381**	-0.1644*	-0.1960**
Thousand grain weight (g)				**1.0000**	0.096	0.2716**	0.4569**	0.5684**	0.4219**
Biomass / plant (g)					**1.0000**	0.9034**	-0.6309**	0.2320**	0.4962**
Biological yield / plant (g)						**1.0000**	-0.2728**	0.5906**	0.8206**
Harvest index							**1.0000**	0.5295**	0.2883**
Per day productivity (g)								**1.0000**	0.8864**

*** Significant at 5 per cent level; ** Significant at 1 per cent level**

This trait showed negative significant association at genotypic level with plant height (-0.3470**), thousand grain weight (-0.4404**) and per day productivity (-0.4466**). It expressed negative non – significant association at genotypic level with number of number of total tillers per plant (-0.1074), number of number of productive tillers per plant (-0.1049) and sterility percentage (-0.0127). Similar results were reported by Chandra *et al.* (2009) and Ravi *et al.* (2014) for plant height, Bhadru *et al* (2012a) for thousand grain weight and per day productivity, Madhavilatha (2002) and Ratana *et al*. (2015) for number of productive tillers per plant and Mishu *et al.* (2016) for sterility percentage.

4.4.2. **Days to maturity**

This trait showed positive significant association at genotypic level with panicle length (0.1693*), panicle weight (0.5589**), number of filled grains per panicle (0.7656**), number of unfilled grains per panicle (0.5028**), number of total grains per panicle (0.7466**), biomass per plant (0.5830**), biological yield per plant (0.4610**) and single plant grain yield (0.1562**). It showed positive non-significant association at genotypic level with spikelet fertility (0.0550). The similar findings were reported by Dilruba *et al*. (2014) for panicle length, Patel *et al*. (2014) for biomass per plant, Ravi *et al.* (2014) and Golam *et al.* (2015) for single plant grain yield

This trait showed negative significant association at genotypic level with plant height (-0.3743**), thousand grain weight (-0.4777**), harvest index (-0.6355**) and per day productivity (-0.3254**). It expressed negative non - significant association at genotypic level with number of number of total tillers per plant (-0.0455), number of productive tillers per plant (-0.0409) and sterility percentage (-0.0550). Similar results were reported by Ganapati *et al*. (2014) for plant height and Panwar *et al.* (2006) for harvest index.

4.4.3. **Plant height (cm)**

This trait showed positive significant association at genotypic level with panicle length (0.1510*), spikelet fertility (0.4400**), thousand grain weight (0.2691**), biomass per plant (0.3872**) and biological yield per plant (0.1919*). The similar findings were reported by Ganapati *et al*. (2014), Patel *et al*. (2014), Golam *et al*. (2015) and Moosavi *et al.* (2015) for panicle length, Soni *et al*. (2013)

and Mishra *et al*. (2014) for spikelet fertility and thousand grain weight, Patel *et al*. (2014) for biomass per plant and Soni *et al*. (2013) for biological yield per plant. It showed positive non-significant association at genotypic level with panicle weight (0.1304) and per day productivity (0.0465). These results are in accordance with Bhadru *et al*. (2012c) for per day productivity.

This trait showed negative significant association at genotypic level with number of total tillers per plant (-0.6934**), number of productive tillers per plant (-0.6179**), number of unfilled grains per panicle (-0.2776**), sterility percentage (-0.4400**) and harvest index (-0.4810**). It expressed negative non - significant association at genotypic level with number of filled grains per panicle (-0.0311), number of total grains per panicle (-0.0739) and single plant grain yield (-0.1273). Similar results were reported by Golam *et al.* (2015) for number of number of total tillers per plant and number of productive tillers per plant, Panwar (2006) and Ganapati *et al*. (2014) for harvest index, Dilruba *et al*. (2014) and Ratna *et al*. (2015) for filled grains per panicle, Seyoum *et al.* (2012) and Rahman *et al.* (2014) for single plant grain yield.

4.4.4. Number of total tillers per plant

This trait showed positive significant association at genotypic level with number of productive tillers per plant (0.9475**), spikelet fertility (0.5134**), harvest index (0.5158**), per day productivity (0.4943 **) and single plant grain yield (0.4919**). It showed positive non-significant association at genotypic level with thousand grain weight (0.0705) and biological yield per plant (0.0924). The similar findings were reported by Patel *et al.* (2014), Ramanjaneyulu *et al.* (2014) and Golam *et al*. (2015) for number of productive tillers per plant and single plant grain yield, Naseer *et al.* (2015) for spikelet fertility and Patel *et al.* (2014) for thousand grain weight.

This trait showed negative significant association at genotypic level with panicle length (-0.5242**), panicle weight (-0.7531**), number of filled grains per panicle (-0.8063 **), number of unfilled grains per panicle (-0.7847 **), number of total grains per panicle (-0.8295**), sterility percentage (-0.5134**) and biomass per plant (-0.2288**). Similar results were reported by Golam *et al.* (2015) for panicle length and Naseer *et al*. (2015) for number of total grains per panicle.

4.4.5. Number of productive tillers per plant

This trait showed positive significant association at genotypic level with spikelet fertility (0.4517**), harvest index (0.5300**), per day productivity (0.5135**) and single plant grain yield (0.5107**). It showed positive non-significant association at genotypic level with biological yield per plant (0.1281). The similar findings were reported by Hasan *et al*. (2013), Soni *et al*. (2013) and Mishra *et al*. (2014) for spikelet fertility, Ramanjaneyulu *et al*. (2014) for harvest index, Bhadru *et al*. (2012a) for per day productivity, Rashi *et al.* (2014), Sarker *et al.* (2014) and Golam *et al*. (2015) for single plant grain yield and Mishra *et al.* (2014) for biological yield per plant.

This trait showed negative significant association at genotypic level with panicle length (-0.6111**), panicle weight (-0.7532**), number of filled grains per panicle (-0.7240**), number of unfilled grains per panicle (-0.6929**), number of total grains per panicle (-0.7429**), sterility percentage (-0.4517**) and biomass per plant (-0.1887*). It expressed negative non-significant association at genotypic level with thousand grain weight (-0.0701). Similar results were reported by Babu *et al*. (2012), Rahman *et al*. (2014) and Ratna *et al*. (2015) for panicle length and Naseer *et al*. (2015) for total grains per panicle, Satyavathi *et al.* (2001) and Rao *et al*. (2014) for number of filled grains per panicle, Ratna *et al*. (2015) for number of unfilled grains per panicle and Golam *et al*. (2015) for thousand grain weight.

4.4.6. Panicle length (cm)

This trait showed positive significant association at genotypic level with number of filled grains per panicle (0.5534**), number of unfilled grains per panicle (0.3850**), number of total grains per panicle (0.5434**), thousand grain weight (0.4892**), biomass per plant (0.6295**), biological yield per plant (0.6064**) and single plant grain yield (0.3886**).It showed positive non-significant association at genotypic level with panicle weight (0.7205) and sterility percentage (0.0683). The similar findings were reported by Patel *et al.* (2014) and Ramanjaneyulu *et al.* (2014) for number of total grains per panicle, Ganapati *et al*. (2014) for number of filled and unfilled grains per panicle, Patel *et al.* (2014) for thousand grain weight and biomass per plant, Soni *et al*. (2013) for biological yield per plant, Rao *et al.* (2014),Sindhumole *et al.* (2015) and Mishu *et al*. (2016) for single plant grain yield, Nandeshwar (2010) and Moosavi *et al*. (2015) for panicle weight and Mishu *et al.* (2016) for sterility percentage.

This trait showed negative significant association at genotypic level with harvest index (-0.1647*). It also expressed negative non-significant association at genotypic level with spikelet fertility (-0.0683). Similar results were reported by Nandeshwar (2010) for spikelet fertility.

4.4.7. Panicle weight (g)

This trait showed positive significant association at genotypic level with filled grains per panicle (0.8746**), unfilled grains per panicle (0.8808**), total grains per panicle (0.9048**), sterility percentage (0.2266**), thousand grain weight (0.1939**), biomass per plant (0.7300**), biological yield per plant (0.5824**) and single plant grain yield (0.2062**). The similar findings were reported by Ranwake and Amarasighe (2014) for total grains per panicle and filled grains per panicle, Soni *et al.* (2013) for thousand grain weight and biological yield per plant and Nandeshwar (2010), Bhadru *et al.* (2011), Awaneet and Senapati (2013), Soni *et al.* (2013) and Ranwake and Amarasighe (2014) for single plant grain yield.

This trait showed negative significant association at genotypic level with spikelet fertility (-0.2266**) and harvest index (-0.6055**). It also expressed negative non-significant association at genotypic level with per day productivity (-0.0759). Similar results were reported by Bhadru *et al*. (2012c) for per day productivity.

4.4.8. Number of filled grains per panicle

This trait showed positive significant association at genotypic level with number of unfilled grains per panicle (0.7682**), number of total grains per panicle (0.9941**), biomass per plant (0.5340**) and biological yield per plant (0.3242**). It showed positive non-significant association at genotypic level with spikelet fertility (0.0044). The similar findings were reported by Ganapati *et al.* (2014) and Golam *et al.* (2015) for number of unfilled grains per panicle.

This trait showed negative significant association at genotypic level with thousand grain weight (-0.3306**), harvest index (-0.7425**) and per day productivity (-0.3704**). It also expressed negative non-significant association at genotypic level with sterility percentage (-0.0044) and single plant grain yield (-

0.0552). Similar results were reported by Dilruba *et al.* (2014), Rahman *et al.* (2014) and Ratna *et al*. (2015) for thousand grain weight, Dilruba *et al.* (2014) for sterility percentage.

4.4.9. Number of unfilled grains per panicle

This trait showed positive significant association at genotypic level with number of total grains per panicle (0.8332**), sterility percentage (0.6574**) and biomass per plant (0.2284**). It showed positive non-significant association at genotypic level with biological yield per plant (0.0563). The similar findings were reported by Mamun *et al.* (2012) for sterility percentage.

This trait showed negative significant association at genotypic level with spikelet fertility (-0.6574**), harvest index (-0.3819**), per day productivity (-0.3939**) and single plant grain yield (-0.1904*). It also expressed negative non-significant association at genotypic level with thousand grain weight (-0.0044). Similar results were reported by Golam *et al*. (2015) for single plant grain yield and Ganapati *et al*. (2014), Rahman *et al*. (2014) and Golam *et al.* (2015) for thousand grain weight.

4.4.10. Number of total grains per panicle

This trait showed positive significant association at genotypic level with biomass per plant (0.5000**) and biological yield per plant (0.2896**). It showed positive non-significant association at genotypic level with sterility percentage (0.1076). The similar findings were reported by Patel *et al.* (2014) for biomass per plant. This trait showed negative significant association at genotypic level with thousand grain weight (-0.3066**), harvest index (-0.7063**) and per day productivity (-0.3868**). It also expressed negative non-significant association at genotypic level with spikelet fertility (-0.1076) and single plant grain yield (-0.0800).

4.4.11. Spikelet fertility (%)

This trait showed positive significant association at genotypic level with biomass per plant (0.2126**), biological yield per plant (0.2367**), per day productivity (0.1644*) and single plant grain yield (0.1960**). The results are in accordance with Soni *et al.* (2013) for biological yield per plant and Hasan *et al.* (2013), Soni *et al.* (2013) and Naseer *et al.* (2015) for single plant grain yield. This trait showed negative significant association at genotypic level with sterility percentage (-1.0000**), thousand grain weight (-0.1735**) and harvest index (-0.3381**). The results are in similarity with Divya *et al.* (2015) for sterility percentage.

4.4.12. Sterility percentage (%)

This trait showed positive significant association at genotypic level with thousand grain weight (0.1735*) and harvest index (0.3381**). This trait showed negative significant association at genotypic level with biomass per plant (-0.2126**), biological yield per plant (-0.2367**), per day productivity (-0.1644**) and single plant grain yield (-0.1960**). The results are in similarity with Panwar *et al.* (2006), Roy *et al.* (2015) and Mishu *et al.* (2016) for single plant grain yield.

4.4.13. Thousand grain weight (g)

This trait showed positive significant association at genotypic level with harvest index (0.4569**), biological yield per plant (0.2716**), per day productivity (0.5684**) and single plant grain yield (0.4219**). It showed positive non-significant association at genotypic level with biomass per plant (0.0960). The results are in similarity with Patel *et al.* (2014) Rahman *et al.* (2014), Naseer *et al*. (2015), Roy *et al*. (2015) and Mishu *et al.* (2016) for single plant grain yield.

4.4.14. Biomass per plant (g)

This trait showed positive significant association at genotypic level with biological yield per plant (0.9034**), per day productivity (0.2320**) and single plant grain yield (0.4962**). It showed negative significant association at genotypic level with harvest index (-0.6309**). The results are in similarity with Patel *et al*. (2014) for harvest index and Patel *et al*. (2014) and Ramanjaneyulu *et al*. (2014) for single plant grain yield.

4.4.15. Biological yield per plant (g)

This trait showed positive significant association at genotypic level with per day productivity (0.5906**) and single plant grain yield (0.8206**). It showed negative significant association at genotypic level with harvest index (-0.2728 **). The results are in similarity with Panwar (2006) and Mishra *et al.* (2014) for harvest index and Soni *et al.* (2013) for single plant grain yield.

4.4.16. Harvest index

This trait showed positive significant association at genotypic level with per day productivity (0.5295**) and single plant grain yield (0.2883**). The results are in similarity with Panwar (2006), Soni *et al.* (2013), Patel *et al*. (2014) and Ramanjaneyulu *et al.* (2014) for single plant grain yield.

4.4.17. Per day productivity (g)

This trait showed positive significant association at genotypic level with single plant grain yield (0.8864**). The results are in similarity with Bhadru *et al*. (2012c) for single plant grain yield.

4.4.18. Single plant grain yield (g)

Genotypic correlations revealed that single plant grain yield had significant positive association with days to maturity (0.1562**), number of total tillers per plant (0.4919**), number of productive tillers per plant (0.5107**), panicle length (0.3886**), panicle weight (0.2062**), spikelet fertility (0.1960**), thousand grain weight (0.4219**), biomass per plant (0.4962**), biological yield per plant (0.8206**), harvest index (0.2883**) and per day productivity (0.8864**). It showed positive non - significant association with days to 50% flowering (0.0108) at genotypic level.

The trait showed negative significant association with number of unfilled grains per panicle (-0.1904*) and sterility percentage (-0.1960**). It showed negative non-significant association with plant height (-0.1273), number of filled grains per panicle (-0.0552) and number of total grains per panicle (-0.0800) at genotypic level. Pleiotropy or linkage may also be the genetic reasons for this type of negative association. According to NeWall and Eberhart (1961) when two characters show negative genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety. Hence, under such situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters.

Single plant grain yield showed positive significant association with days to maturity, number of total tillers per plant, number of productive tillers per plant, panicle length, panicle weight, spikelet fertility, thousand grain weight, biomass per plant, biological yield per plant, harvest index and per day productivity. Similar kind of association was revealed by Ravi *et al.* (2014) and Golam *et al.* (2015) for days to maturity, Ramanjaneyulu *et al.* (2014) and Golam *et al*. (2015) for number of total tillers per plant and number of productive tillers per plant, Soni *et al.* (2013) and Ranwake and Amarasighe (2014) for panicle length and panicle weight, Soni *et al.* (2013) for spikelet fertility and biological yield per plant, Rahman *et al.* (2014), Rao *et al.* (2014), Naseer *et al*. (2015) and Mishu *et al.* (2016) for thousand grain weight, Patel *et al*. (2014) and Ramanjaneyulu *et al*. (2014) for biomass per plant, Panwar (2006), Soni *et al.* (2013) and Patel *et al*. (2014) for harvest index and Bhadru *et al*. (2012c) for per day productivity. Hence, these characters could be considered as criteria for selection for higher yield as these were mutually and directly associated with grain yield.

4.5. PATH COEFFICIENT ANALYSIS

Correlation gives the relation between two variables whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921). Based on the data recorded on the genotypes across three seasons in the present investigation, the pooled genotypic correlations were estimated to determine direct and indirect effects of single plant grain yield and yield contributing characters. If the correlation coefficient between a casual factor and the effect is almost equal to its direct effect, it explains the true relationship and a direct selection through this trait may be useful. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects appear to be the cause of that positive correlation. In such situation the other factors are to be considered simultaneously for selection. However if the correlation coefficient is negative but direct effect is positive and high, a restriction has to be imposed to nullify the undesirable indirect effects in order to make use of direct effect.

Results of pooled genotypic path coefficient of single plant grain yield and yield contributing characters discussed here under which were presented in Table 4.5 and Fig. 4.5.

Table 4.5. Pooled genotypic path coefficient of single plant grain yield and yield contributing characters in rice

Character	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of total tillers / plant	Number of productive tillers / plant	Panicle length (cm)	Panicle weight (g)	Number of filled grains / panicle	Number of unfilled grains / panicle
Days to 50 % flowering	**0.0151**	-0.0043	-0.0001	0.0001	0.0006	-0.0022	0.0000	66.0697	8.3780
Days to maturity	0.0145	**-0.0045**	-0.0002	0.0000	0.0002	-0.0017	0.0000	67.5270	8.6922
Plant height (cm)	-0.0053	0.0017	**0.0004**	0.0005	0.0033	-0.0015	0.0000	-2.7412	-4.7990
Number of total tillers / plant	-0.0016	0.0002	-0.0003	**-0.0008**	-0.0051	0.0052	0.0000	-71.1146	-13.5665
Number of productive tillers / plant	-0.0016	0.0002	-0.0002	-0.0007	**-0.0054**	0.0061	0.0000	-63.8586	-11.9786
Panicle length (cm)	0.0034	-0.0008	0.0001	0.0004	0.0033	**-0.0100**	0.0000	48.8130	6.6563
Panicle weight (g)	0.0077	-0.0025	0.0001	0.0006	0.0041	-0.0072	**-0.0001**	77.1385	15.2268
Number of filled grains / panicle	0.0113	-0.0035	0.0000	0.0006	0.0039	-0.0055	-0.0001	**88.2010**	13.2810
Number of unfilled grains / panicle	0.0073	-0.0023	-0.0001	0.0006	0.0037	-0.0039	-0.0001	67.7569	**17.2883**
Number of total grains / panicle	0.0110	-0.0034	0.0000	0.0006	0.0040	-0.0054	-0.0001	87.6801	14.4038
Spikelet fertility (%)	0.0002	-0.0002	0.0002	-0.0004	-0.0024	0.0007	0.0000	0.39150	-11.366
Sterility percentage (%)	-0.0002	0.0002	-0.0002	0.0004	0.0024	-0.0007	0.0000	-0.3915	11.3656
Thousand grain weight (g)	-0.0067	0.0022	0.0001	-0.0001	0.0004	-0.0049	0.0000	-29.1580	-2.1457
Biomass / plant (g)	0.0091	-0.0026	0.0002	0.0002	0.0010	-0.0063	0.0000	47.0973	3.9480
Biological yield / plant	0.0061	-0.0021	0.0001	-0.0001	-0.0007	-0.0061	0.0000	28.5946	0.9725
Harvest index	-0.0113	0.0029	-0.0002	-0.0004	-0.0029	0.0016	0.0000	-65.4920	-6.6024
Per day productivity (g)	-0.0068	0.0015	0.0000	-0.0004	-0.0028	-0.0029	0.0000	-32.6716	-6.8100
Genotypic residual effect = 0.0088 BOLD values are direct effects									

Continuation of table 4.5…

Character	Number of total grains / panicle	Spikelet fertility (%)	Sterility percentage (%)	Thousand grain weight (g)	Biomass / plant	Biological yield / plant	Harvest index	Per day productivity (g)	Single plant grain yield (g)
Days to 50 % flowering	-74.4435	-0.8687	0.8685	-0.0026	-0.8081	0.8126	0.0031	-0.0073	0.0108
Days to maturity	-76.2151	-3.7616	3.7611	-0.0028	-0.7804	0.9301	0.0026	-0.0053	0.1562**
Plant height (cm)	7.5444	-30.0803	30.0763	0.0016	-0.5182	0.3873	0.0020	0.0008	-0.1273
Number of total tillers / plant	84.6811	-35.1031	35.0985	0.0004	0.3062	0.1865	-0.0021	0.0081	0.4919**
Number of productive tillers / plant	75.8370	-30.8824	30.8782	-0.0004	0.2525	0.2585	-0.0022	0.0084	0.5107**
Panicle length (cm)	-55.4667	4.6696	-4.6692	0.0029	-0.8425	1.2235	0.0007	0.0047	0.3886**
Panicle weight (g)	-92.3658	15.4949	-15.491	0.0012	-0.9771	1.1751	0.0025	-0.0012	0.2062**
Number of filled grains / panicle	-101.479	-0.3035	0.3034	-0.0020	-0.7147	0.6541	0.0031	-0.0061	-0.0552
Number of unfilled grains / panicle	-85.0494	44.948	-44.942	-0.0007	-0.3056	0.1135	0.0016	-0.0064	-0.1904*
Number of total grains / panicle	**-102.0815**	7.3576	-7.3566	-0.0018	-0.6692	0.5843	0.0029	-0.0063	-0.0800
Spikelet fertility (%)	10.9854	**-68.3704**	68.3613	-0.0010	-0.2845	0.4777	0.0014	0.0027	0.1960**
Sterility percentage (%)	-10.9854	68.3704	**-68.3613**	0.0010	0.2845	-0.4777	-0.0014	-0.0027	-0.1960**
Thousand grain weight (g)	31.3004	11.8652	-11.8639	**0.0060**	-0.1285	0.5480	-0.0019	0.0093	0.4219**
Biomass / plant (g)	-51.0403	-14.5329	14.5314	0.0006	**-1.3384**	1.8227	0.0026	0.0038	0.4962**
Biological yield / plant (g)	-29.5627	-16.1856	16.1836	0.0016	-1.2091	**2.0177**	0.0011	0.0097	0.8206**
Harvest index	72.0887	23.1129	-23.1098	0.0027	0.8444	-0.5505	**-0.0041**	0.0087	0.2883**
Per day productivity(g)	39.4822	-11.2370	11.2355	0.0034	-0.3105	1.1916	-0.0022	**0.0164**	0.8864**
Genotypic residual effect = 0.0088 BOLD values are direct effects									

4.5.1. Days to 50% flowering

The direct contribution of this character to single plant grain yield was positive (0.0151) at genotypic level. These results are in agreement with Mohanty *et al.* (2012), Nikhil *et al*. (2014), Ravi *et al.* (2014), Golam *et al*. (2015) and Ratna *et al.* (2015). This trait exhibited positive non-significant correlation (0.0108) with single plant grain yield due to indirect positive influence on single plant grain yield through number of total tillers per plant (0.0001), number of productive tillers per plant (0.0006), number of filled grains per panicle (66.0697), number of unfilled grains per panicle (8.3780), sterility percentage (0.8685), biological yield per plant (0.8126) and harvest index (0.0031) at genotypic level.

Whereas, days to maturity (-0.0043), plant height (-0.0001), panicle length (-0.0022), number of total grains per panicle (-74.4435), spikelet fertility (-0.8687), thousand grain weight (-0.0026), biomass per plant (-0.8081) and per day productivity
(-0.0073) showed negative indirect effect at genotypic level.

4.5.2. Days to maturity

The direct contribution of this character to single plant grain yield was negative (-0.0045) at genotypic level. These results are in agreement with Panwar (2006), Ravi *et al.* (2014) and Hasan *et al.* (2013). This trait exhibited positive significant correlation (0.1562**) with single plant grain yield due to indirect positive influence on single plant grain yield through days to 50% flowering (0.0145), number of productive tillers per plant (0.0002), number of filled grains per panicle (67.5270), number of unfilled grains per panicle (8.6922), sterility percentage (3.7611), biological yield per plant (0.9301) and harvest index (0.0026) at genotypic level.

This trait exhibited negative indirect effects with days to maturity (-0.0043), plant height (-0.0002), panicle length (-0.0017), number of total grains per panicle (-76.2151), spikelet fertility (-3.7616), thousand grain weight (-0.0028), biomass per plant (-0.7804) and per day productivity (-0.0053) showed negative indirect effects at genotypic level.

4.5.3. Plant height

The direct effect of this character on single plant grain yield was positive (0.0004) at genotypic level. These results are in agreement with Hasan *et al*. (2013), Nagaraju *et al.* (2013), Dilruba *et al.* (2014), Golam *et al.* (2015) and Naseer *et al*. (2015). This trait expressed negative non-significant correlation (-0.1273) with single plant grain yield due to indirect positive influence on single plant grain yield through days to maturity (0.0017), number of total tillers per plant (0.0005), number of productive tillers per plant (0.0033), number of total grains per panicle (7.5444), sterility percentage (30.0763), thousand grain weight (0.0016), biological yield per plant (0.3873), harvest index (0.0020) and per day productivity (0.0008) at genotypic level.

Whereas, days to 50% flowering (-0.0053), panicle length (-0.0018), number of filled grains per panicle (-2.7412), number of unfilled grains per panicle (-4.7990), spikelet fertility (-30.0803) and biomass per plant (-0.5182) showed negative indirect effect at genotypic level.

4.5.4. Number of total tillers per plant

The direct effect of this character on single plant grain yield was negative (-0.0008) at genotypic level. These results are in agreement with Ravi *et al*. (2014) and Naseer *et al.* (2015). This trait expressed positive significant correlation (0.4919**) with single plant grain yield due to indirect positive influence on single plant grain yield through days to maturity (0.0002), panicle length (0.0052), number of total grains per panicle (84.6811), sterility percentage (35.0985), thousand grain weight (0.0004), biomass per plant (0.3062), biological yield per plant (0.1865) and per day productivity (0.0081) at genotypic level.

This trait showed negative indirect effect through days to 50% flowering (-0.0016), plant height (-0.0003), number of productive tillers per plant (-0.0051), number of filled grains per panicle (-71.1146), number of unfilled grains per panicle (-13.5665), spikelet fertility (-35.1031) and harvest index (-0.0021) at genotypic level.

4.5.5. Number of productive tillers per plant

The direct effect of this character on single plant grain yield was negative (-0.0054) at genotypic level. These results are in agreement with Hasan *et al*. (2013), Mishra *et al*. (2014), Nikhil *et al*. (2014), Patel *et al*. (2014) and Kumar and Verma (2015). This trait expressed positive significant correlation (0.5107 **) with single plant grain yield due to indirect positive influence on single plant grain yield through days to maturity (0.0002), panicle length (0.0061), number of total grains per panicle (75.8370), sterility percentage (30.8782), biomass per plant (0.2525), biological yield per plant (0.2585) and per day productivity (0.0084) at genotypic level.

This trait showed negative indirect effect through days to 50% flowering (-0.0016), plant height (-0.0002), number of total tillers per plant (-0.0007), number of filled grains per panicle (-63.8586), number of unfilled grains per panicle (-11.9786), spikelet fertility (-30.8824), thousand grain weight (-0.0004) and harvest index (-0.0022) at genotypic level.

4.5.6. Panicle length

The direct effect of this character on single plant grain yield was negative (-0.0100) at genotypic level. These results are in agreement with Hasan *et al*. (2013), Dilruba *et al*. (2014), Patel *et al*. (2014), Ravi *et al.* (2014) and Golam *et al*. (2015). This trait expressed positive significant correlation (0.3886**) with single plant grain yield due to indirect positive influence on single plant grain yield through days to 50% flowering (0.0034), plant height (0.0001), number of total tillers per plant (0.0004), number of productive tillers per plant (0.0033), number of filled grains per panicle (48.8130), number of unfilled grains per panicle (6.6563), spikelet fertility (4.6696), thousand grain weight (0.0029), biological yield per plant (1.2235), harvest index (0.0007) and per day productivity (0.0047) at genotypic level.

Whereas, days to maturity (-0.0008), number of total grains per panicle (-55.4667), sterility percentage (-4.6692) and biomass per plant (-0.8425) showed negative indirect effect at genotypic level.

4.5.7. Panicle weight

The direct effect of this character on single plant grain yield was negative (-0.0001) at genotypic level. These results are in agreement with Soni *et al*. (2013). This trait expressed positive significant correlation (0.2062 **) with single plant grain yield due to indirect positive influence on single plant grain yield through days to 50% flowering (0.0077), plant height (0.0001), number of total tillers per plant (0.0006), number of productive tillers per plant (0.0041), number of filled grains per panicle (77.1385), number of unfilled grains per panicle (15.2268), spikelet fertility (15.4949), thousand grain weight (0.0012), biological yield per plant (1.1751) and harvest index (0.0025) at genotypic level.

Whereas, days to maturity (-0.0025), panicle length (-0.0072), number of total grains per panicle (-92.3658), sterility percentage (-15.4910), biomass per plant (-0.9771) and per day productivity (-0.0012) showed negative indirect effect at genotypic level.

4.5.8. Number of filled grains per panicle

The direct effect of this character on single plant grain yield was positive (88.2010) at genotypic level. These results are in agreement with Dilruba *et al.* (2014), Ganapati *et al*. (2014), Rao *et al*. (2014), Sarker *et al.* (2014) and Golam *et al.* (2015). This trait expressed negative non-significant correlation (-0.0552) with single plant grain yield due to indirect positive effects of this trait *via* days to 50% flowering (0.0113), number of total tillers per plant (0.0006), number of productive tillers per plant (0.0039), number of unfilled grains per panicle (13.2810), sterility percentage (0.3034), biological yield per plant (0.6541) and harvest index (0.0031) at genotypic level.

Whereas, days to maturity (-0.0035), panicle length (-0.0055), panicle weight (-0.0001), number of total grains per panicle (-101.479), spikelet fertility (-0.3035), thousand grain weight (-0.0020), biomass per plant (-0.7147) and per day productivity (-0.0061) showed negative indirect effect at genotypic level.

4.5.9. Number of unfilled grains per panicle:

The direct effect of this character on single plant grain yield was positive (17.2883) at genotypic level. These results are in agreement with Ganapati *et al.* (2014). This trait expressed negative significant correlation (-0.1904*) with single plant grain yield due to indirect positive effects of this trait *via* days to 50% flowering (0.0073), number of total tillers per plant (0.0006), number of productive tillers per plant (0.0037), number of filled grains per panicle (67.7569), spikelet fertility (44.948), biological yield per plant (0.1135) and harvest index (0.0016) at genotypic level.

Whereas, days to maturity (-0.0023), plant height (-0.0001), panicle length (-0.0039), panicle weight (-0.0001), number of total grains per panicle (-85.0494), sterility percentage (-44.942), thousand grain weight (-0.0007), biomass per plant (-0.3056) and per day productivity (-0.0064) showed negative indirect effect at genotypic level.

4.5.10. Number of total grains per panicle:

The direct effect of this character on single plant grain yield was negative (-102.0815) at genotypic level. These results are in agreement with Singh *et al.* (2000), Roy *et al* (2015). This trait expressed negative non-significant correlation (-0.0800) with single plant grain yield due to indirect positive effects of this trait *via* days to 50% flowering (0.0110), number of total tillers per plant (0.0006), number of productive tillers per plant (0.0040), number of filled grains per panicle (87.6801), number of unfilled grains per panicle (14.4038), spikelet fertility (7.3576), biological yield per plant (0.5843) and harvest index (0.0029) at genotypic level.

Whereas, days to maturity (-0.0034), panicle length (-0.0054), panicle weight (-0.0001), sterility percentage (-7.3566), thousand grain weight (-0.0018), biomass per plant (-0.6692) and per day productivity (-0.0063) showed negative indirect effect at genotypic level.

4.5.11. Spikelet fertility:

The direct effect of this character on single plant grain yield was negative (-68.3704) at genotypic level. These results are in agreement with Gyanendra *et al.* (2011), Soni *et al*. (2013), Mishra *et al*. (2014), Kumar and Verma (2015) and Naseer *et al*. (2015). This trait expressed positive significant correlation (0.1960**) with single plant grain yield due to indirect positive effects of this trait *via* days to 50% flowering (0.0002), plant height (0.0002), panicle length (0.0007), number of filled grains per panicle (0.3915), number of total grains per panicle (10.9854), sterility percentage (68.3613), biological yield per plant (0.4777), harvest index (0.0014) and per day productivity (0.0027) at genotypic level.

Whereas, days to maturity (-0.0002), number of total tillers per plant (-0.0004), number of productive tillers per plant (-0.0024), number of unfilled grains per panicle (-11.366), thousand grain weight (-0.0010) and biomass per plant (-0.2845) showed negative indirect effect at genotypic level.

4.5.12. Sterility percentage:

The direct effect of this character on single plant grain yield was negative (-68.3613) at genotypic level. These results are in agreement with Dilruba *et al.* (2014) and Krantikumar *et al.* (2016) This trait expressed negative significant correlation (-0.1960**) with single plant grain yield due to indirect positive effects of this trait *via* days to maturity (0.0002), number of total tillers per plant (0.0004), number of productive tillers per plant (0.0024), number of unfilled grains per panicle (11.366), spikelet fertility (68.3704), thousand grain weight (0.0010) and biomass per plant (0.2845) at genotypic level.

Whereas, days to 50% flowering (-0.0002), plant height (-0.0002), panicle length (-0.0007), number of filled grains per panicle (-0.3915), number of total grains per panicle (-10.9854), biological yield per plant (-0.4777), harvest index (-0.0014) and per day productivity (-0.0027) showed negative indirect effect at genotypic level.

4.5.13. Thousand grain weight (g)

The direct effect of this character on single plant grain yield was positive (0.0060) at genotypic level. These results are in agreement with Dilruba *et al.* (2014), Rahman *et al*. (2014), Rao *et al*. (2014), Ratna *et al*. (2015), Naseer *et al*. (2015) and Golam *et al.* (2015).

This trait expressed positive significant correlation (0.4219**) with single plant grain yield due to indirect positive effects of this trait *via* days to maturity (0.0022), plant height (0.0001), number of productive tillers per plant (0.0004), number of total grains per panicle (10.9854), spikelet fertility (11.8652), biological yield per plant (0.5480) and per day productivity (0.0093) at genotypic level.

Whereas, days to 50% flowering (-0.0067), number of total tillers per plant (-0.0001), panicle length (-0.0049), number of filled grains per panicle (-29.1580), number of unfilled grains per panicle (-2.1457), sterility percentage (-11.8639), biomass per plant (-0.1285) and harvest index (-0.0019) showed negative indirect effect at genotypic level.

4.5.14. Biomass per plant (g)

The direct effect of this character on single plant grain yield was negative

(-1.3384) at genotypic level. These results are in agreement with Krantikumar *et al.* (2016). This trait expressed positive significant correlation (0.4962**) with single plant grain yield due to indirect positive effects of this trait *via* days to 50% flowering (0.0091), plant height (0.0002), number of total tillers per plant (0.0002), number of productive tillers per plant (0.0010), number of filled grains per panicle (47.0973), number of unfilled grains per panicle (3.9480), sterility percentage (14.5314), thousand grain weight (0.0006), biological yield per plant (1.8227), harvest index (0.0026) and per day productivity (0.0038) at genotypic level.

Whereas, days to maturity (-0.0026), panicle length (-0.0063), number of total grains per panicle (-51.0403) and spikelet fertility (-14.5329) showed negative indirect effect at genotypic level.

4.5.15. Biological yield per plant

The direct effect of this character on single plant grain yield was positive (2.0177) at genotypic level. These results are in agreement with Soni *et al*. (2013), Mishra *et al*. (2014), Kumar and Verma (2015) and Krantikumar *et al*. (2016). This trait expressed positive significant correlation (0.9725**) with single plant grain yield due to indirect positive effects of this trait *via* days to 50% flowering (0.0061), plant height (0.0001), number of filled grains per panicle (28.5946), number of unfilled grains per panicle (0.9725), sterility percentage (16.1836), thousand grain weight (0.0016), harvest index (0.0011) and per day productivity (0.0097) at genotypic level.

Whereas, days to maturity (-0.0021), number of total tillers per plant (-0.0001), number of productive tillers per plant (-0.0007), panicle length (-0.0061), number of total grains per panicle (-29.5627), spikelet fertility (-16.1856), biomass per plant (-1.2091) showed negative indirect effect at genotypic level.

4.5.16. Harvest index:

The direct effect of this character on single plant grain yield was negative (-0.0041) at genotypic level. This trait expressed positive significant correlation (0.2883**) with single plant grain yield due to indirect positive effects of this trait *via* days to maturity (0.0029), panicle length (0.0016), number of total grains per panicle (72.0887), spikelet fertility (23.1129), thousand grain weight (0.0027), biomass per plant (0.8444) and per day productivity (0.0087) at genotypic level.

Whereas, days to 50% flowering (-0.0113), plant height (-0.0002), number of total tillers per plant (-0.0004), number of productive tillers per plant (-0.0029), number of filled grains per panicle (-65.4920), number of unfilled grains per panicle (-6.6024), sterility percentage (-23.1098) and biological yield per plant (-0.5505) showed negative indirect effect at genotypic level.

4.5.17. Per day productivity:

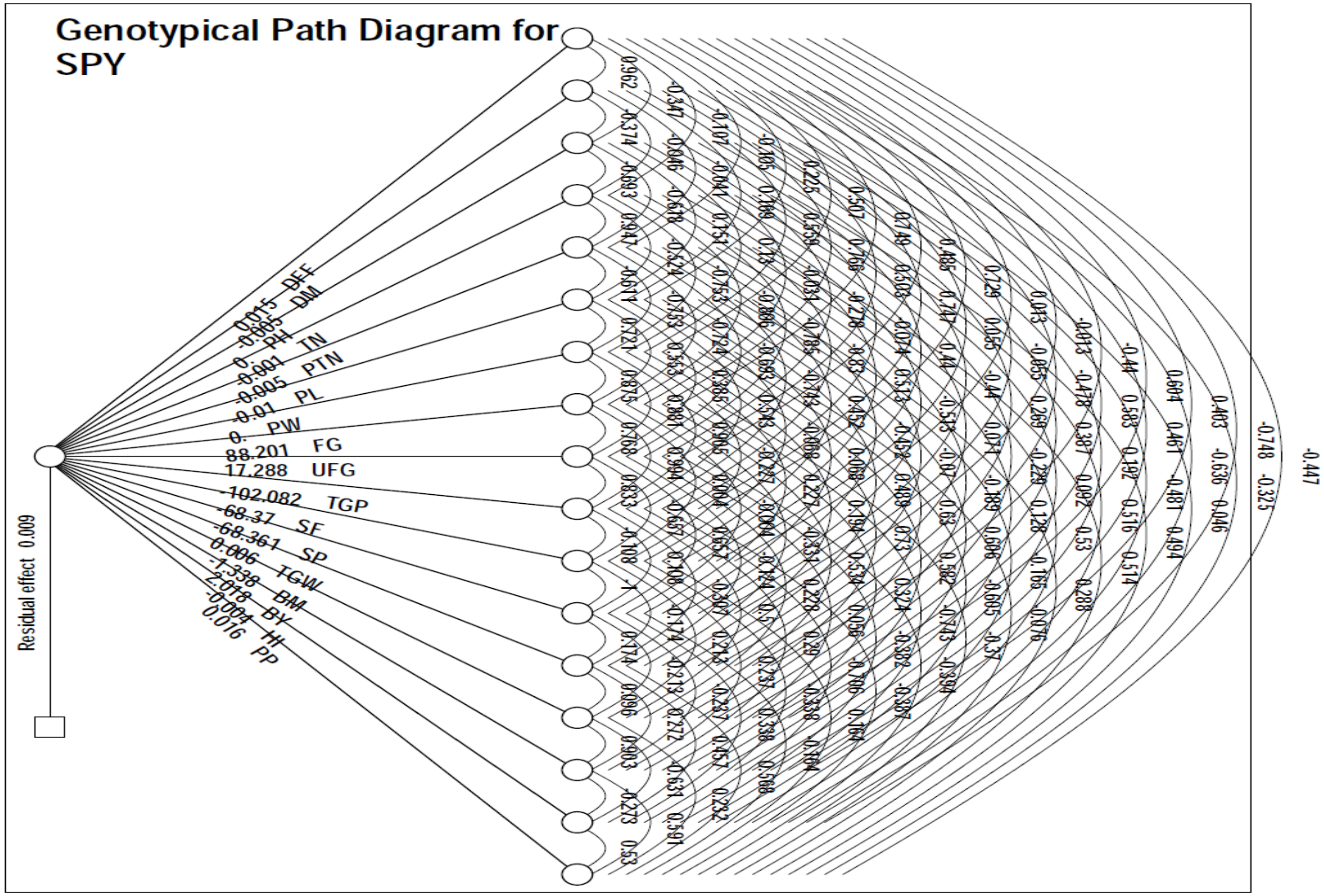
The direct effect of this character on single plant grain yield was positive (0.0164) at genotypic level. These results are in agreement with Bhadru *et al*. (2012). This trait expressed positive significant correlation (0.8864**) with single plant grain yield due to indirect positive effects of this trait *via* days to maturity (0.0015), number of total grains per panicle (39.4822), sterility percentage (11.2355), thousand grain weight (0.0034) and biological yield per plant (1.1916) at genotypic level.

Whereas, days to 50% flowering (-0.0068), number of total tillers per plant (-0.0004), number of productive tillers per plant (-0.0028), panicle length (-0.0029), number of filled grains per panicle (-32.6716), number of unfilled grains per panicle (-6.8100), spikelet fertility (-11.2370), biomass per plant (-0.3105) and harvest index (-0.0022) showed negative indirect effect at genotypic level.

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be some times fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria, indicating the selection for these characters is likely to bring about an overall improvement in single plant grain yield directly.

Path coefficient analysis revealed that number of filled grains per panicle exerted the highest positive direct effect on single plant grain yield followed by biological yield per plant, per day productivity, days to 50% flowering, thousand

Figure 4.5. Pooled genotypical path diagram of single plant grain yield



grain weight and plant height indicating that the selection for this characters was likely to bring about an overall improvement in single plant grain yield directly. Therefore, it is suggested that preference should be given to these characters in the selection programme to isolate superior lines with genetic potentiality for high yield in rice genotypes. Negative direct effect on grain yield was exhibited by days to maturity, number of total tillers per plant, number of productive tillers per plant, panicle length, panicle weight, spikelet fertility, sterility percentage, biomass per plant and harvest index.

4.6. GENOTYPING AND HAPLOTYPING FOR EARLINESS USING SSR MARKERS

Molecular characterization using SSR markers is playing an important role to identify gene for days to heading. They have become a popular type of co-dominant molecular marker in genetic analysis and plant breeding application (Choi *et al.*, 2011). Rice cultivars show a highly divergence of natural variability in heading date and photoperiod sensitivity, yet these differentiations of natural variation is not completely understood and there were rare information about it (Nonoue *et al.,* 2008). SSR markers used in this study shows amplified polymorphic bands using 84 rice genotypes.

SSR markers have facilitated the genetic analysis of heading date, and numerous quantitative trait loci (QTLs) have been identified using mapping populations (Nonoue *et al.*, 2008; Matsubara *et al.*, 2008 and Maas *et al.*, 2010). This study aimed to elucidate the diversity of heading date associated marker(s) using SSR markers in rice genotypes from different duration. Such markers would be of great importance in marker-assisted selection for early flowering time, which on the other hand would help to reduce the water requirement rice crop especially in drought prone areas.

4.6.1. Overall allelic diversity

Among the 57 SSR markers used in the present study 42 SSRs were polymorphic which produced varying number of alleles with different size ranges. A total of 99 alleles were detected among the 84 rice genotypes with an average of 2.35 alleles per locus. The number of microsatellite alleles of used markers ranged from 2 to 5 alleles of which RM1369 marker produced the highest numbers of alleles (5

Plate 1: Gel photograph of RM1369

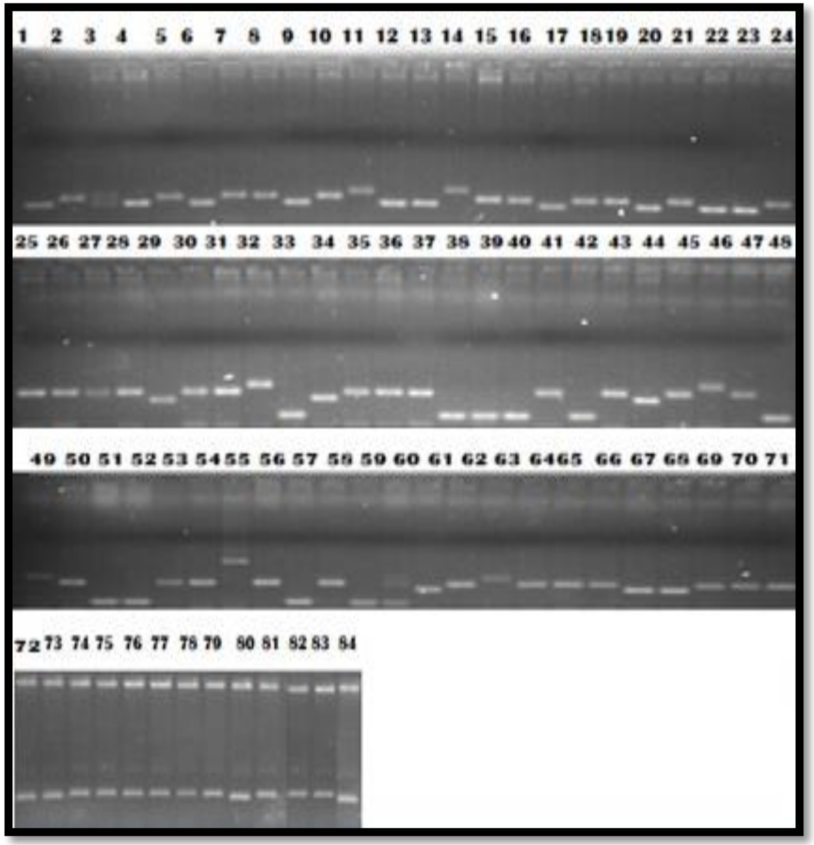
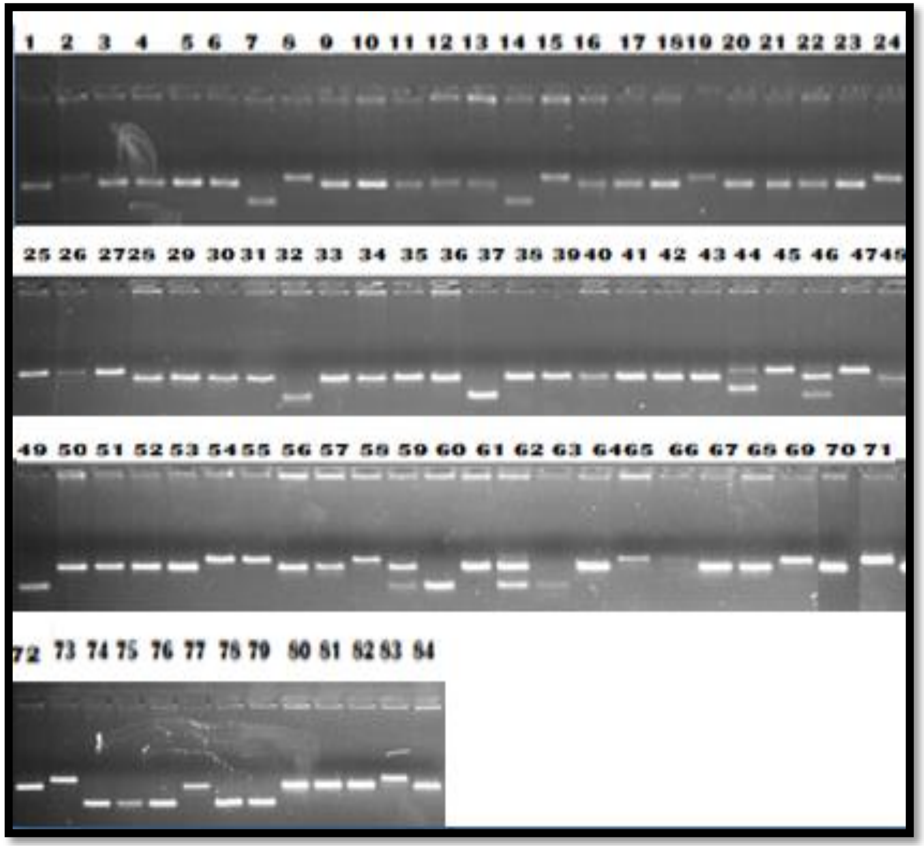


Plate 2: Gel photograph of RM340



Note: Lanes represent the genotypes used in present study

Plate 3: Gel photograph of RM11

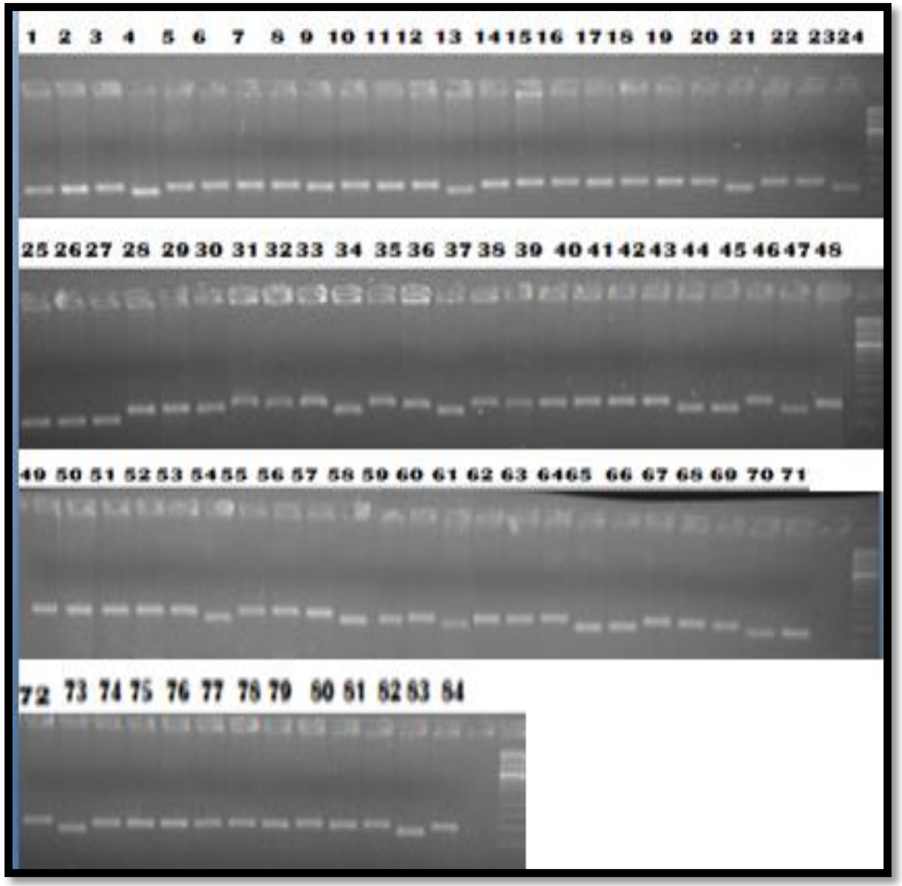
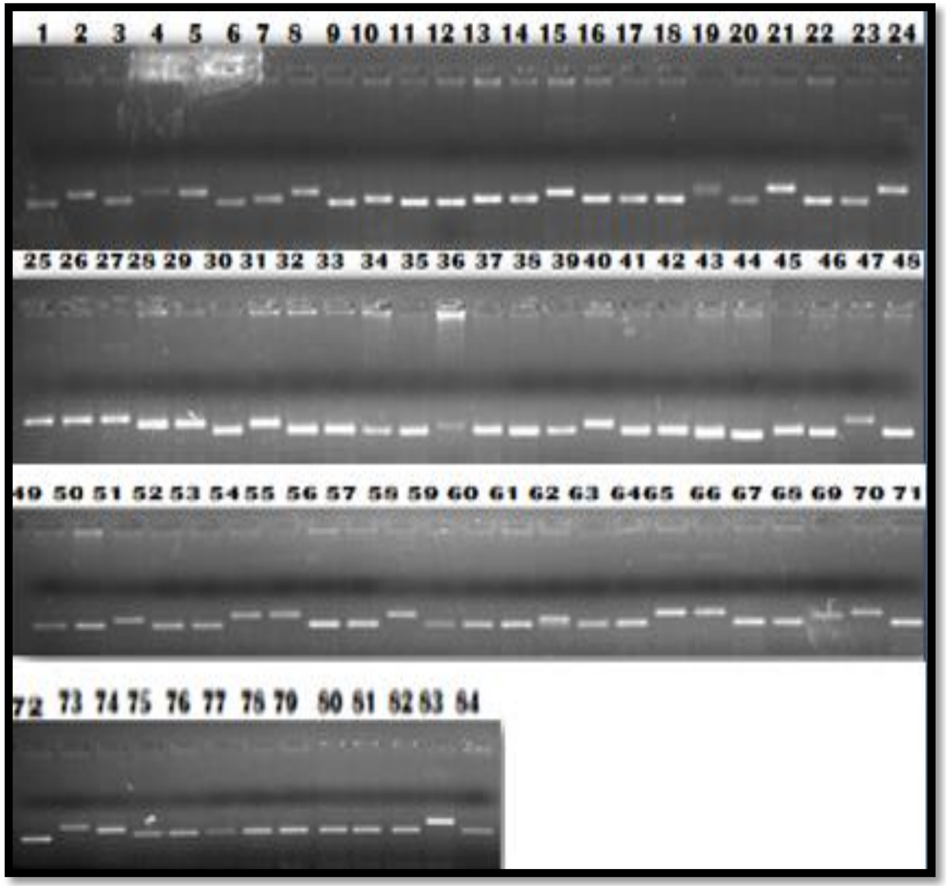


Plate 4: Gel photograph of RM209



Note: Lanes represent the genotypes used in present study

Plate5: Gel photograph of RM202

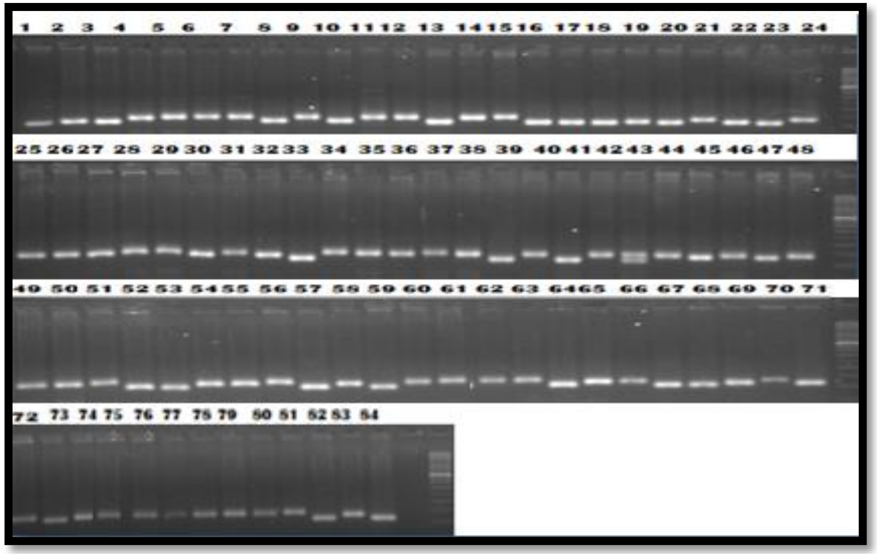
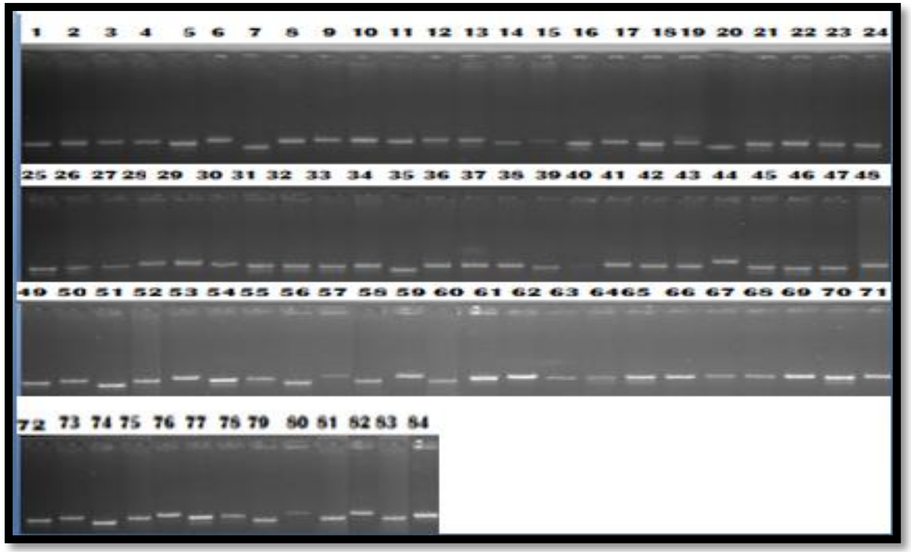


Plate 6: Gel photograph of RM206



Lanes represent the genotypes, where 1= Aditya, **2=** Anjali, **3=** Vandana, **4=** Prasanna, **5=** Neela, **6=** WGL 14, **7=** ADT43, **8=** Rasi, **9=** WGL505, **10=** Pooja, **11=** Govindu, **12=** WGL915, **13=** Varalu, **14=** Swarna, **15=** Jaldidhan, **16=** NL B, **17=** SM219, **18=** SM363, **19=** SM686, **20=** SM359, **21=** SM776, **22=** SM349, **23=** SM733, **24=** SM4071, **25=** SM1876**, 26=** SM4029, **27=** SM4076, **28=** 35 B, **29=** 51 B, **30=** 93 B, **31=** 95 B, **32=** 14-3, **33=** 130 K, **34=** 148 S, **35=** 148-2 S**, 36=** 220S, **37=** 246 K**, 38=** 248 S, **39=** 258 S, **40=** 166-2-4**, 41=** 166-30, **42=** 248 S, **43=** 166-2-3, **44=** SM4406, **45=** SM4415, **46=** 250 K, **47=** SM4244, **48=** 166-2-9 , **49=** 7K**, 50=** 166-2-5, **51=** IR64, **52=** 166-2-10, **53=** 166-23-1, **54=** SM4321, **55=** SM4230, **56=** 14 S, **57=** 166-2-2, **58=** SM4385, **59=** 166-9, **60=** 27 K , **61=** 75 S, **62=** 166-23, **63=** 148 S , **64=** Jaya, **65=** SM4078, **66=** SM4193, **67=** Tulasi, **68=** SM4371**, 69=** Sabhagidhan, **70=** SM4014, **71=** Tellahamsa, **72=** MTU1010, **73=** SM4226 , **74= 65 S, 75= 166-1, 76=** 70 S, **77=** 166-2-11, **78=** 3-1 K, **79=** 166 S, **80=** *263 K*, **81=** 166-2, **82=** Sona, **83=** SM1637, **84=** N22.

alleles) with motif (AG) 27 respectively (Plate 1). The SSR markers RM101, RM302, RM246, RM84 of chromosome 1, RM53, RM318, RM48, RM6 of chromosome 2, RM218, RM168, RM25, RM22, of chromosome 3, RM273, RM6770, RM261, RM7585 of chromosome 4, RM164 of chromosome 5, RM6775, RM30, RM1370 of chromosome 6,RM248, RM234 of chromosome 7, RM210 of chromosome 8, RM257 of chromosome 9, RM311 of chromosome 10, RM202 (Plate 5), RM224 of chromosome 11 and RM19, RM247, RM270 of chromosome 12 had shown 2 alleles per locus. RM263 of chromosome 2, RM241, RM307 of chromosome 4, RM153 of chromosome 5, RM340 of chromosome 6 (Plate 2), RM11 of chromosome 7 (Plate 3), RM264 of chromosome 8, RM205 of chromosome 9 and RM209 (Plate 4), RM206 (Plate 6) of chromosome 11 had shown 3 alleles per locus. RM163 of chromosome 5 had shown 4 alleles per locus. RM1369 of chromosome 6 had shown 5 alleles per locus of allele per locus. The overall size of amplified products ranged from 81bp in locus RM30 to 264 bp in locus RM164.

4.6.2. PIC value

A total of 57 SSRs distributed on all the chromosomes were selected and used in present study for 84 rice genotypes which includes early, mid early and late duration lines. Among the 57 markers used, 15 SSRs were monomorphic and 42 SSRs were clearly amplified and shown polymorphism. Polymorphic information content (PIC) value is a reflection of allele diversity and frequency among the varieties. Value polymorphic information content (PIC) provides an assessment of discriminating potential of any marker(s) based on the number of alleles at a locus and comparative rates of these alleles. PIC value of each marker can be evaluated on the basis of its alleles and it varied greatly for all the SSR loci tested. In the present study, the level of polymorphism among the 84 genotypes was evaluated by calculating PIC values for each of the 42 SSR loci. The PIC values ranged from 0.511 (RM270 and RM1370) to 0.939 (RM1369) with an average of 0.745 per locus (Table 4.6.2). The result revealed that markers RM1369 would be best in screening 84 rice genotypes due to its highest PIC value followed by RM163 (0.933), RM205 (0.863), RM340 (0.844), RM241 (0.8408), RM11 (0.8406), RM209 (0.837), RM206 (0.825), RM263 (0.824), RM264 (0.813) and RM307 (0.805) respectively. Whereas remaining markers PIC values were ranging from 0.511 to 0.793. High PIC value indicates that the SSR marker selected in the study RM1369 would be best in

Table. 4.6.2. Details on PIC value and no of alleles produced by markers used in present study

S.No	Marker	No of alleles	Polymorphic information content (PIC)
1	RM84	2	0.555981
2	RM101	2	0.586168
3	RM246	2	0.739725
4	RM302	2	0.740930
5	RM53	2	0.749858
6	RM263	3	0.824405
7	RM318	2	0.743977
8	RM6	2	0.732851
9	RM48	2	0.740930
10	RM22	2	0.646684
11	RM218	2	0.746457
12	RM168	2	0.744898
13	RM307	3	0.805886
14	RM261	2	0.735828
15	RM273	2	0.750000
16	RM241	3	0.840892
17	RM6770	2	0.743126
18	RM7585	2	0.684170
19	RM153	3	0.793556
20	RM164	2	0.743056
21	RM163	4	0.933957
22	RM6775	2	0.747732
23	RM1369	5	0.939853

24	RM1370	2	0.511763
25	RM30	2	0.741142
26	RM340	3	0.844199
27	RM248	2	0.743126
28	RM11	3	0.840608
29	RM234	2	0.722222
30	RM25	2	0.722222
31	RM210	2	0.698838
32	RM264	3	0.813256
33	RM257	2	0.717333
34	RM205	3	0.863757
35	RM311	2	0.747732
36	RM224	2	0.690122
37	RM202	2	0.731222
38	RM209	3	0.837349
39	RM206	3	0.825161
40	RM19	2	0.747732
41	RM247	2	0.739725
42	RM270	2	0.511763
	Average	2.357143	0.745719
	Total	99	31.32019

differentiating 84 rice genotypes due to its highest PIC value followed by RM163. The frequency of the most common allele at each locus ranged from 13.09% (RM307) on chromosome 4 to 98.80% (RM270 on chromosome 12 and RM1370 on chromosome 6).

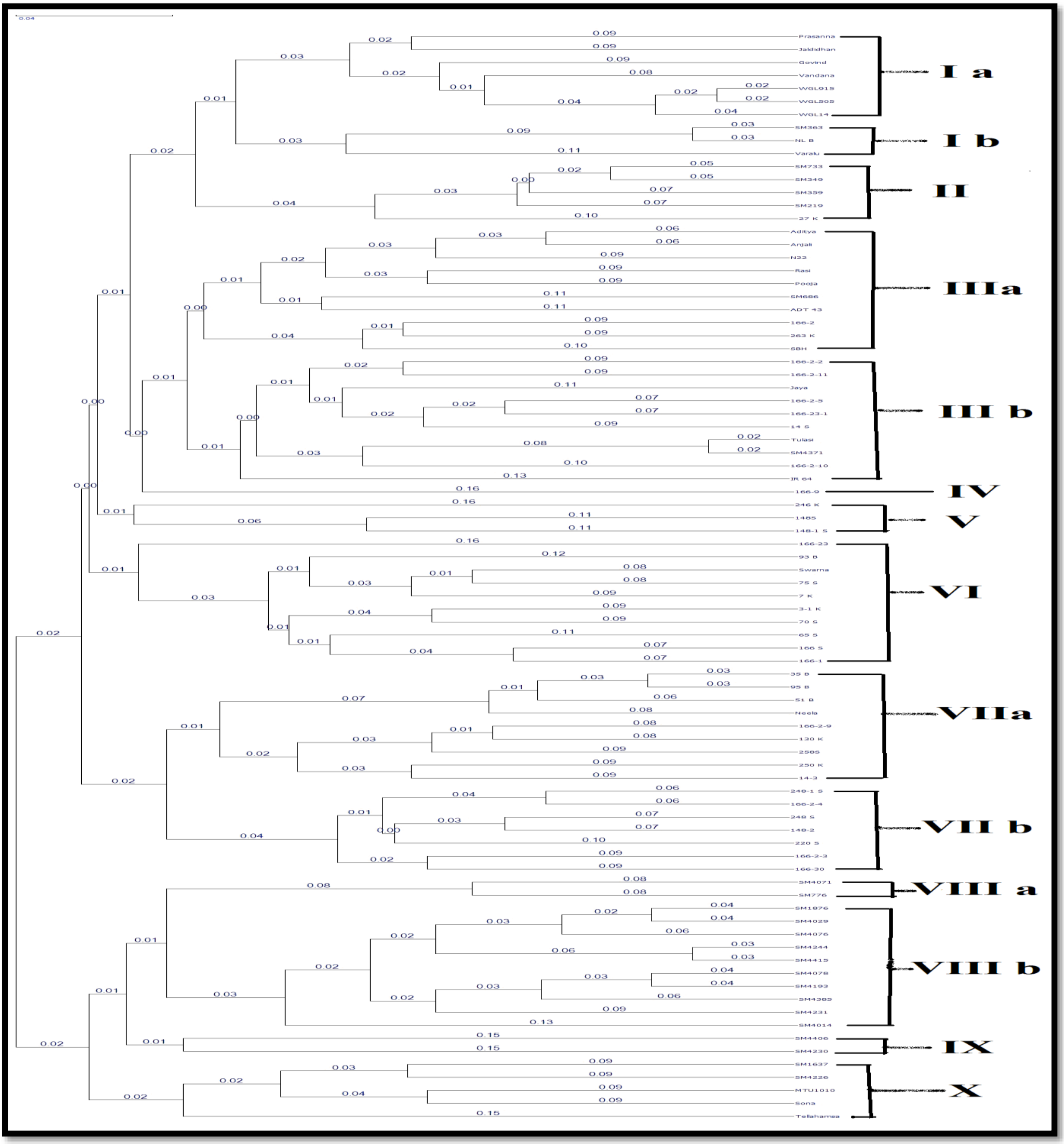
4.6.3. Conserved regions in the diverse germplasm

There were 15 SSR loci which were identified to be monomorphic or conserved in all the genotypes and were distributed on all chromosomes except 2, 4 and 11. All monomorphic SSR markers showed unique single allele in all the genotypes. These conserved monomorphic loci are reported to be associated with different agronomical traits. RM315 of chromosome 1 associated with trait heading date (Shen *et al.,* 2014). RM132, RM36 and RM282 of chromosome 3 are also associated with heading date (Lee *et al*., 2013 and Shen *et al.,* 2014) and grain yield per plant (Jing *et al.,* 2010). RM249 of chromosome 5, shown association for trait flowering time (Baliuag *et al.,* 2015). RM295 of chromosome 7 has shown association with heading date (Shen *et al.,* 2014). RM42 of chromosome 8 has shown association with shattering trait (Thomas *et al*., 2003). RM235 of chromosome 10 has shown association with trait plant height (Tong *et al.,* 2006). This shows the conserved regions in *indica* genotypes for very important domestication traits.

4.6.4. Cluster analysis

The dendrogram generated using UPGMA cluster analysis grouped 84 genotypes into ten major clusters and few clusters were divided into sub cluster (Fig. 4.6.4). The analysis revealed wide genetic variability among the genotypes. The genetic diversity relationships among rice genotypes are presented in a dendrogram based on informative microsatellite alleles. Details of clusters formed in genotyping and genotypes present in each cluster were presented in table form in Table 4.6.4.

Figure 4.6.4. Dendrogram generated by cluster analysis



Note: Details of genotypes classified under each cluster is presented in Table 4.6.4.

Table 4.6.4. Details of cluster analysis of 84 genotypes.

Cluster	No of genotypes	Genotypes	Characteristic of genotypes
I a	7	Prasanna (check), Jaldidhan, Govind, Vandana, WGL 915, WGL 505 and WGL 14.	This cluster has mixture of early to late duration lines and are medium tall to tall lines
I b	3	SM363, NL B and Varalu	They are mid early, tall lines
II	5	SM733, SM349, SM359, SM219 and 27K	These lines are mid early, medium tall lines.
III a	10	Adithya, Anjali, N22, Rasi, Pooja, SM686, ADT 43, 166-2, 263 K and SBH	These lines are mixture of early to late duration and consisting high yielding popular varieties
III b	10	166-2-2, 166-2-11, Jaya, 166-2-5, 166-23-1, 14S, Tulasi, SM4371, 166-2-10 and IR64.	These lines are mixture of mid early to late duration with very high grain yield.
IV	1	166-9	This line is mid early, medium tall line with good tillering capacity, medium panicle length and medium TGW.
V	3	246K, 148 S and 148-1 S	These are early lines with medium panicle length
VI	10	166-23, 93 B, Swarna, 75 S, 7 K, 3-1 K, 70 S, 65 S, 166 S, and 166-1	These lines are late duration, medium tall lines
VII a	9	35 B, 95 B, 51 B, Neela, 166-2-9, 130 K, 258 S, 250 K and 14-3	These lines are mixture of mid early to late duration and are medium tall lines
VII b	7	248-1 S, 166-2-4, 248 S, 148-2, 220 S, 166-2-3 and 166 -30	These lines are mixture of early to late duration. They are medium tall Swarna x *O. nivara* introgression

			lines.
VIII a	2	SM4071 and SM776	They are early tall N22 mutants.
VIII b	10	SM1876, SM4029, SM4076, SM4244, SM4415, SM4078, SM4193, SM4385, SM4231 and SM4014	These lines are early, medium tall N22 mutants
IX	2	SM4406 and SM4230	These N22 mutants are mid early with medium tillering capacity and medium thousand grain weight
X	5	SM1637, SM4226, MTU1010, Sona, Tellahamsa	These lines are mid early, high yielding genotypes.

In cluster analysis few clusters had all late, mid early and early lines, these results reveal that markers used in present study are effective to differentiate early and late lines and can be used for future breeding and marker assisted selection studies related to heading date. Results of this research indicated that the use of microsatellite markers associated with days to heading can differentiate genotypes for the traits related to growth duration. The findings provide a basement for the breeders to select diversified parents to exploit heterosis in hybrid progenies for growth duration.

4.6.5. Suitable markers for MAS in plant breeding

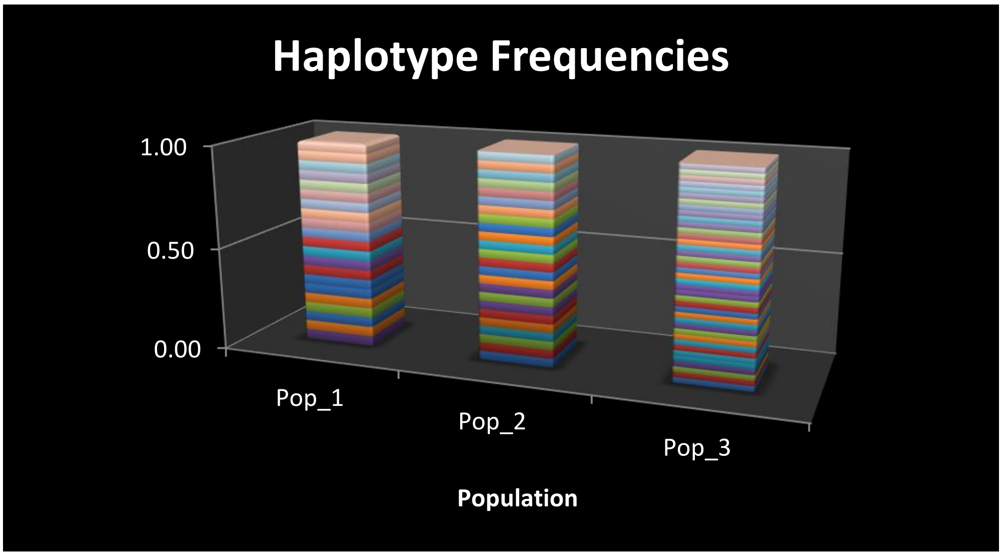
Analysis of genetic diversity revealed that the SSR marker, RM1369 was found to be superior and produced five different alleles and clearly differentiating the lines of different duration. It could be added to the potential marker for marker assisted breeding for heading date. Overall results showed that the RM164, RM261, RM311, RM11, RM340, RM6, RM318, RM53,RM263, RM7585 and RM163 markers could be able to discriminate the early heading and late heading efficiently for genotypes under study, and these markers could be associated with heading date. Such markers could be of great importance in marker-assisted selection of early flowering time in rice genotypes, which ultimately would help to produce short duration rice varieties with low input requirements.

4.6.6. Haplotyping

The genotypes were screened for reported markers linked to earliness and yield traits and the scoring data was subjected to haplotypes analysis. Inter-population haplotyping was conducted by classifying and comparing cultivars - *Oryza sativa* (population 1), N22 and derived mutants (population 2), Swarna and Introgresion lines from Swarna *nivara* cross (population 3) into three populations (Fig. 4.6.6 a and Fig. 4.6.6 b). Intra Population cluster analysis carried out among the genotypes under study showed the formation of 84 haplotypes showing each genotype has a unique allelic combination of for all the genes under study. Haplotypic richness was similar in all populations but the mean genetic distance between individuals were high in population consisting of *O. sativa* x *O. nivara* cross introgression lines than that of population consisting of cultivars or mutants (Table 4.6.6.1 a and Table 4.6.6.1 b). Total gene diversity was higher in population 3 but Proportion of the total genetic differentiation is more in population 1. Pairwise Population Matrix of Nei Genetic Distance showed that population 1 and population 2 show more similarity between them as they *O. sativa* genotypes compared to population 3 as it consist of *O. nivara* alleles in the population (Table 4.6.6.2)

The haplotype structure is presented in (Fig. 4.6.6 c). The results revealed that clear cut haplotype structure was not obtained in present study. As the markers used in present study were reported in haplotyping of *japonica* lines and the lines used in present study are *indica* derived lines, so those markers might not be expressed completely. So for further improvement of haplotype structure it is suggested to use further more number of SSR or SNP markers and also the markers which mapped in *indica* backgrounds.

Figure 4.6.6 a Haplotypes frequencies present in population 1 consist of cultivars and population 2 with N22 and derived mutants and population 3with Swarna and derived introgression lines



Note:

Number of loci = 57, Number of expected haplotype = 4.4E+12 and Number of observed haplotypes = 84

Figure 4.6.6 b Gene diversity within population from intra population haplotype identification

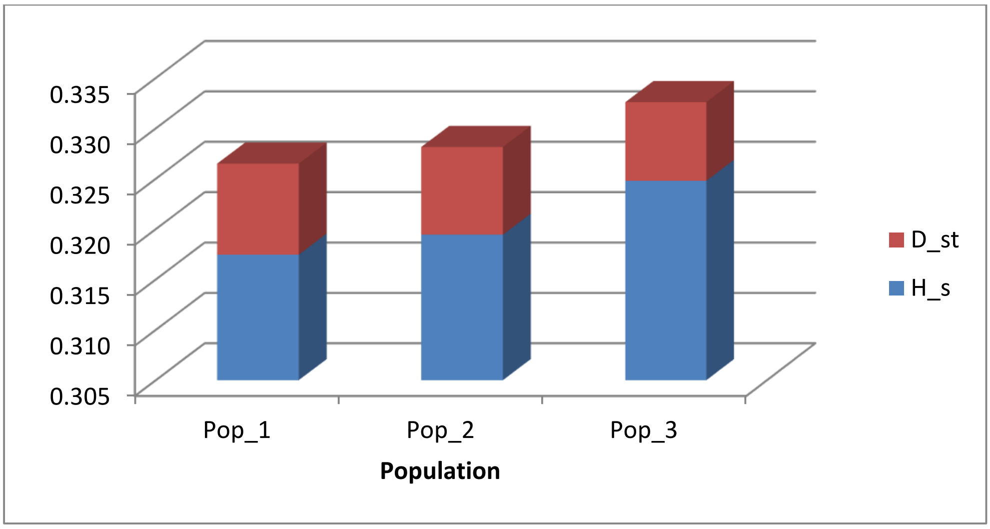


Table 4.6.6.1 a. Intra population cluster analysis for haplotype identification

Population	N	A	P	N_e	R_h	H_e	D^2_sh
Pop_1	21	21	21	21.000	20.000	1.000	4.548
Pop_2	24	24	24	24.000	20.000	1.000	4.690
Pop_3	39	39	39	39.000	20.000	1.000	4.795
Mean	28.000	28.000	28.000	28.000	20.000	1.000	4.678
Note:							
N: Sample size in each population							
A: Number of haplotypes detected in each population							
P: Number of private haplotypes							
N_e: Effective number of haplotypes							
R_h: Haplotypic richness							
H_e: Genetic diversity							
D^2_sh: Mean genetic distance between individuals							

Table 4.6.6.1 b. Intra Population haplotype identification for gene diversity within population

	N	c(j)	H_s(j)	D_st(j)	H_t(j)	F_st(j)
Pop_1	1	0.333	0.317	0.009	0.326	0.028
Pop_2	1	0.333	0.319	0.009	0.328	0.027
Pop_3	1	0.333	0.325	0.008	0.333	0.023

Note:

N : Sample size in each population

C : Relative contribution

H_s : Gene diversity within each population

D_st : Diversity due to differentiation

H_t : Total gene diversity

F_st : Proportion of the total genetic differentiation

Table 4.6.6.2. Pair wise population matrix of nei genetic distance

	Pop_1	**Pop_2**	**Pop_3**
Pop_1	0.000		
Pop_2	0.045	0.000	
Pop_3	0.037	0.034	0.000

SUMMARY AND CONCLUSION

Chapter V

SUMMARY AND CONCLUSIONS

Rice is one of the world's major staple food crops and a model cereal species. Rice feeds more than half the human population worldwide. Developing countries account for 95% of global rice production. The crop is the second most widely consumed food grain in the world next to wheat. Earliness is the emerging key agronomic character which provides greater adaptability to varieties to fit into different ecosystems, in different cropping seasons. Under existing scenario, in order to sustain the rice production growing of early high yielding varieties will enhance the rice productivity, resource and input use efficiency and profitability per unit area and per unit time.

The present investigation **"**Genetic analysis and haplotyping for earliness and yield traits in rice (*Oryza sativa* L.) using SSR markers" was undertaken to screen for early lines and study the stability of rice genotypes under three environments *Rabi* 2014-15, *Kharif* 2015 and *Rabi* 2015-16 and also to identify stable early high yielding genotypes suitable for both *Kharif* and *Rabi* seasons of Telangana region with fifty nine genotypes in three replications at Indian Institute of Rice Research Farm, Hyderabad.

Analysis of variance revealed significant differences for all the traits studied indicating the presence of sufficient amount of genetic variability among the genotypes studied. A perusal of genetic variability parameters revealed that high variability was observed for number of total tillers per plant, number of productive tillers per plant, panicle weight, number of filled grains per panicle, number of total grains per panicle, sterility percentage, single plant grain yield, biomass per plant, biological yield per plant and per day productivity across all the three seasons, indicating there is high potential for yield improvement by selection in these traits.

High heritability coupled with high genetic advance as per cent of mean was observed for days to fifty percent flowering, plant height, number of total tillers per plant, number of productive tillers per plant, number of filled grains per panicle, thousand grain weight, biomass per plant, biological yield per plant and per day productivity indicating the influence of additive gene action, as such simple selection would likely be effective for improvement of these traits.

Combined Analysis of variance for the data showed significant genotype, environment and genotype x environment interaction, indicating the presence of variability among the genotypes and environments. The significant genotype x environment interaction effect showed that the genotypes responded differently to the variation in environmental (seasonal fluctuations) conditions.

The PC1 value was higher than PC2 for all the traits explains higher contribution of genotype in the total sum of squares of the genotype x environment interaction. The SS% explained contribution of each trait and results revealed that days to 50% flowering, days to maturity, plant height, panicle length, panicle weight, number of filled grains per panicle, number of unfilled grains per panicle, number of total grains per panicle and thousand grain weight were contributed mainly by genotype, followed by environment, and their interaction. But the characters *viz.*, single plant grain yield, number of tillers per plant, number of productive tillers per plant, spikelet fertility, sterility percentage, biomass per plant, biological yield per plant, harvest index and per day productivity were affected significantly by G x E interaction.

As per AMMI biplot analysis the season *Kharif* 2015 was the best suited environment for potential expression of following traits *viz.*, panicle length, panicle weight, filled grains per panicle, low unfilled grains per panicle, total grains per panicle, spikelet fertility, low sterility percentage, biological yield per plant, harvest index and per day productivity. *Rabi* 2014-15 season was the best suited for expression of plant height, productive tiller number, low unfilled grains per panicle, spikelet fertility and biomass per plant. *Rabi* 2015-16 was the best suited seasons for potential expression of low days to fifty percent flowering and early to maturity, tiller number and productive tiller number, thousand grain weight and harvest index. Early wild introgression line, 148 S was identified as stable best suited line across all the three seasons for plant height and panicle length. Wild introgression line, 27 K of mid early duration was identified as stable best suited line across all the three seasons for single plant grain yield, biological yield per plant and per day productivity.

GGE biplot genotypic view graph provide information on the ideal genotype across all the three seasons. Based on that SM733 (early line) was identified as ideal genotype for days to fifty per cent flowering. Genotype Prasanna (check) was identified as the ideal genotype for days to maturity. Genotype 148 S was identified as the ideal genotype for the plant height, panicle length and thousand grain weight. Genotype 130 K (mid early line) was identified as the ideal genotype for total grains per panicle. Genotypes 27 K and 220 S (mid early lines) were identified as the ideal genotypes for thousand grain weight. Genotype tellahamsa mid early line was identified as the ideal genotype for single plant grain yield, biomass per plant, biological yield per plant and per day productivity. Genotype 258 S (mid early line) was identified as the ideal genotype for harvest index.

GGE biplot genotype graph illustrates stable genotypes across all the three seasons for each trait under study. Based on this genotypes SM1637 (mid early), Anjali (early line) and Adithya (early line) were identified as stable best suited lines for both days to fifty per cent flowering and days to maturity. Genotypes Tellahamsa (mid early line), SM776 (early line), SM4371 (early line), 27 K (mid early line), SM686 (mid early line), 258 S (mid early line) and SM219 (mid early line) were stable suited lines for single plant grain yield across all the three seasons. Genotype 166-2-3 (mid early line) identified as the best suited stable line for panicle length and thousand grain weight. Genotypes SM4071 and SM4029 were identified as best suited stable early line for spikelet fertility and low sterility percentage. Genotype Vandana (early line) was identified as the best suited for low unfilled grains per panicle and good thousand grain weight. Genotypes SM258 S and SM219 were identified as best suited stable mid early lines for harvest index and per day productivity. Genotype Prasanna (check) was identified as the best suited early line for thousand grain weight and harvest index. Genotypes SM4029 and SM4415 were identified as stable best suited early genotypes for low unfilled grains per panicle, low sterility percentage and good spikelet fertility. Genotype Sona (mid early line) was the best suited line for panicle length, thousand grain weight and harvest index. Genotype Rasi (early line) was identified as the best suited line for panicle length, and low sterility percentage and low unfilled grains per panicle. Genotype 166-9 (mid early line) was identified as the best suited stable line for panicle length, panicle weight and thousand grain weight. Genotype Sabhagidhan (early line) was identified as the best suited stable line for spikelet fertility, thousand grain weight, harvest index and low sterility percentage. Genotype 148 S (early line) was identified as stable line for plant height, thousand grain weight, biomass per plant, low unfilled grains per panicle and low sterility percentage. Genotype Anjali (early line) was identified as the best stable line for plant height, spikelet fertility, harvest index and low spikelet fertility. Genotype MTU1010 was identified as the best suited stable mid early line for panicle length, biological yield per plant, harvest index and per day productivity. Genotype Tellahamsa (mid early line) was identified as stable best suited line for panicle length, single plant yield, biomass per plant, biological yield per plant and per day productivity. Genotype SM4371 (early line) was identified as the best stable suitable genotype for single plant yield, biomass per plant, biological yield per plant, harvest index and per day productivity. Genotype 27 K (mid early line) was identified as the best suited stable line for panicle length, thousand grain weight, single plant yield, biomass per plant, biological yield per plant and per day productivity. Genotype SM776 was identified as the best stable suitable early line for tiller number per plant, productive tiller number per plant, single plant yield, harvest index and per day productivity.

The character association studies revealed that single plant grain yield had significant positive association with days to maturity, number of total tillers per plant, number of productive tillers per plant, panicle length, panicle weight, spikelet fertility, thousand grain weight, biomass per plant, biological yield per plant, harvest index and per day productivity indicating that this characters are very important for yield improvement and simultaneous selection of these characters will ultimately result in high yield.

Positive non- significant association of single plant grain yield was observed with days to 50 per cent flowering.

Path coefficient analysis revealed that number of filled grains per panicle exerted the highest positive direct effect on single plant grain yield followed by biological yield per plant, per day productivity, days to 50% flowering, thousand grain weight and plant height indicating that the selection for this characters was likely to bring about an overall improvement in single plant grain yield directly.

Critical analysis of results obtained from character association and path analysis indicated that days to 50% flowering exerted positive direct effect on single plant grain yield but it had positive non-significant association with yield which might be due to positive indirect effects manifested through other component traits. But thousand grain weight, biological yield per plant and per day productivity displayed significant positive correlation as well as positive direct effect on single plant grain yield. The positive direct effect of these traits on yield resulted in strong genetic correlation. Hence, due emphasis should be given to these traits in formulating selection criteria to bring yield improvement.

Among the 57 SSR markers used in the present study 42 SSR markers were polymorphic which produced varying number of alleles. A total of 99 alleles were detected among the 84 rice genotypes with an average of 2.35 alleles per locus. The number of microsatellite alleles of used markers ranged from 2 to 5 alleles of which RM1369 marker produced the highest numbers of alleles (5 alleles) followed by this RM163 showed four alleles per locus. The PIC values ranged from 0.511 (RM270 and RM1370) to 0.939 (RM1369) with an average of 0.745 per locus. High PIC value indicates that the SSR markers used in present study are informative and the best markers in differentiating of rice genotypes for heading date in diversity studies.

The dendrogram generated using UPGMA cluster analysis grouped 84 genotypes into ten major clusters and few clusters were divided into sub clusters. The clusters, I a (Prasanna (check), Jaldidhan, Govind, Vandana, WGL 915, WGL 505 and WGL 14), Cluster III (Adithya, Anjali, N22, Rasi, Pooja, SM686, ADT 43, 166-2, 263 K, SBH,166-2-2, 166-2-11, Jaya, 166-2-5, 166-23-1, 14S, Tulasi, SM4371, 166-2-10 and IR64) and cluster VII (35 B, 95 B, 51 B, Neela, 166-2-9, 130 K, 258 S, 250 K, 14-3,248-1 S, 166-2-4, 248 S, 148-2, 220 S, 166-2-3 and 166 -30) are having mixture of lines from early to late duration lines. Cluster I b (SM363, NL B and Varalu), II (SM733, SM349, SM359, SM219 and 27K) and X (SM1637, SM4226, MTU1010, Sona, Tellahamsa) are having mid early, tall lines. Cluster IV (166-9) and IX (SM4406 and SM4230) are having mid early medium, tall lines with medium thousand grain weight. Cluster V (246K, 148 S and 148-1 S) has early lines with medium panicle length. Cluster VI (166-23, 93 B, Swarna, 75 S, 7 K, 3-1 K, 70 S, 65 S, 166 S, and 166-1) has late duration, medium tall lines .Cluster VIII a (SM4071 and SM776) is having early, tall lines. Cluster VIII b (SM1876, SM4029,

SM4076, SM4244, SM4415, SM4078, SM4193, SM4385, SM4231 and SM4014) is having early, medium tall N22 mutants.

Overall results showed that the RM1369, RM163, RM261, RM311, RM11, RM340, RM6, RM318, RM53, RM263, RM7585 and RM164 markers could discriminate the early and late heading genotypes, and these markers showed significant association with heading date. Such markers could be of great importance in marker-assisted selection of early flowering rice genotypes, which ultimately would help to produce short duration rice varieties.

The genotypic data was subjected to haplotypes analysis. Intra Population cluster analysis showed the formation of 84 haplotypes showing their unique allelic combination for all the genes under study. The mean genetic distance between individuals and total gene diversity were high in population consisting of *O. sativa* x *O. nivara* cross introgression lines than that of other populations with popular cultivars or mutants.

Conclusion and future line of work:

The present research work reveals that the genotypes Prasanna, Anjali, Jaldidhan, SM776, SM1637 and SM4406 are the potential donors for earliness improvement and genotypes 166-30, 95 B, 130 K, Tellahamsa and 27 K for grain yield. Crosses between these genotypes may be prospective research area in the current scenario with high demand and low inputs for developing short duration high yielding lines. Secondly promising varieties Tellahamsa, Adithya, Rasi, MTU1010, Tulasi, Sona and mutants viz., SM219, SM686, SM776 and SM4371 and introgression lines 27 K, 130 K and 148 S which are stable for yield, earliness and other agronomic traits can be entered into multi location, multi environmental varietal testing. Other outstanding genotypes can be further advanced to obtain elite varieties with desirable economical characters. Breeding programmes may be designed by involving early and late varieties, mutants and introgression lines to study the genetics, gene action and interactions controlling heading date traits. The SSR markers viz., RM1369, RM164, RM261, RM311, RM11, RM340, RM6, RM318, RM53, RM263, RM7585 and RM163 were proved to enhance selection and breeding efforts to in introgression of desirable yield traits. Identification of clearly differentiating haplotypes were not successful among early and late genotypes comprising *indica* varieties, mutants and introgression lines and this will open new avenues for further research in mapping QTLs and association mapping for heading date involving *indica* genotypes.

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*Original not seen