

**EVALUATION OF RICE GENOTYPES SUITABLE FOR DIRECT
SEEDED CONDITION (*Oryza sativa* L.)**

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**EVALUATION OF RICE GENOTYPES SUITABLE FOR DIRECT
SEEDED CONDITION (*Oryza sativa* L.)**

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By

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CERTIFICATE

This is to certify that the thesis entitled "**EVALUATION OF RICE GENOTYPES SUITABLE FOR DIRECT SEEDED CONDITION (*Oryza sativa* L.)**" submitted by **Mr. GURURAJA M**, for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, to the University of Agricultural Sciences, Raichur is a record of research work done by him during the period of his study in this university under my guidance and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

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AFFECTIONATELY DEDICATED

TO

MY BELOVED PARENTS,

SRI. MANJANNA AND

SMT. RENUKAMMA

GRANDFATHER

NAGAPPA

AND BELOVED TEACHER,

DIWAN J. R.

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(GURURAJA M.)

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LIST OF ABBREVIATIONS USED

%	:	Percentage
/	:	Per
°C	:	Degree Celsius
ANOVA	:	Analysis of Variance
CD	:	Critical Difference
cm	:	Centimetre
CV	:	Coefficient of Variation
df	:	Degrees of freedom
EMS	:	Error mean sum of squares
ESS	:	Error sum squares
<i>et al.</i>	:	And others people
Fig.	:	Figure
GA	:	Genetic Advance
GAM	:	Genetic advance as percent of mean
GCV	:	Genotypic Coefficient of Variation
PCV	:	Phenotypic Coefficient of Variation
h^2	:	Heritability
ha	:	Hectare
Kg	:	Kilo grams
μ L	:	Micro liter
mL	:	Milli litre
sq m	:	Square metre

I. INTRODUCTION

Rice (*Oryza sativa* L.) is a unique grain used as human food and also as feed (Swaminathan, 1984). It belongs to the genus *Oryza* which has two cultivated and 22 wild species. The cultivated species are *Oryza sativa* and *Oryza glaberrima* and they belong to the family poaceae with a chromosome number of $2n=24$. It is the second most staple food crop of the world next to Wheat (Abodolereza and Raionzer, 2009), which provides 27 per cent of the dietary energy and 20 per cent of dietary protein intake in the developing world. In many developing countries, rice is the basis of food security and is intimately associated with traditional culture and customs in local regions. Rice is the predominant crop of Asia, where it covers half of the arable land. Global population estimated to increase from 6.2 billion in the year 2000 to about 8.2 billion by the year 2030 and the global rice demand will rise to about 533 mt of milled rice (Annon, 2002). The increasing population rate dictates the world's food requirements, especially for rice, so the extra rice required to feed the accelerating population ought to be met only by improving the productivity of rice, it is more so in India.

Globally, rice is cultivated an area about 161.40 million hectare and production of about 506.30 million tonnes with the productivity of 3.14 tonnes per hectare (Anon, 2015). In India, rice is being cultivated with an area of 44.8 million hectare and ranks second in production (104 million tonnes) next to china. The average yield of rice in India is 2400 kg/ha. India exports 9.3 million tonnes of rice to the countries around the world and earning a foreign exchange (Anon, 2015). The major rice growing states in India are Karnataka, Andhra Pradesh, Bihar, Uttar Pradesh, Madhya Pradesh, West Bengal and Punjab. In Karnataka, rice is being cultivated in an area of 1.34 million hectare with the annual production of 3.53 million tonnes and productivity of 3.09 t/ha (Anon, 2014).

Rice (*Oryza sativa* L.) is commonly grown by transplanting seedlings into puddled soil (wet tillage) in Asian countries. This production system is labor, water and energy intensive and is becoming less profitable as these resources are becoming increasingly scarce. It also deteriorates the physical properties of soil, adversely affects the performance of succeeding upland crops and contributes to methane emissions. These factors demand a major shift from puddled transplanting to direct seeding of rice (DSR) in irrigated rice ecosystems.

Direct seeding of rice refers to the process of establishing a rice crop from seeds sown in the field rather than by transplanting seedlings from the nursery.

There are three principal methods of direct seeding of rice (DSR):

- Dry seeding (sowing dry seeds into dry soil)
- Wet seeding (sowing pre-germinated seeds on wet puddled soils)
- Water seeding (seeds sown into standing water)

Dry seeding has been the principal method of rice establishment since the 1950s in developing countries. In recent years, there has been a shift from Transplanting rice (TPR) to DSR cultivation in several countries of Southeast Asia (Pandey and Velasco, 2002).

To date, no specific varieties have been developed for this purpose; however existing varieties used for TPR do not appear to be well-adapted for seedling growth in an initially oxygen-depleted microenvironment. As a result, farmers often resort to the costly practice of increasing the seeding rate for DSR by 2–3 times. New varieties suitable for DSR must be able to emerge and grow from a non-flooded soil (Flinn and Mandac, 1986).

In order to increase the area of cultivation and yield potential under water scarce area, it is essential to develop/ create a new plant type which are suitable for direct seeded rice condition system, it requires more efforts on the part of the plant breeder to understand the genetic background of the material being handled. Information on the nature and magnitude of variability among different genotypes under investigation help us to know the differential performance of genotypes under direct seeded condition and association among the various characters is a prerequisite for any breeding programme to develop high yielding and quality genotypes. Grain yield is a complex character not only influenced by its associated characters which are governed by number of genes, but also by environment. So to make selection effective, it is necessary to separate genetic variability from total variability which enables breeders to adopt suitable breeding programme.

Variability studies for different yield components among the different genotypes will be of much help for improvement of yield and its yield associated component

characters. Hence, it is essential to know the degree of mutual association (correlations) prevailing between yield and its component characters which forms a basis for selecting desirable genotypes (Wright, 1921).

Several genetic parameters viz., analysis of variance of each mean value, phenotypic and genotypic variances, phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2) and genetic gain as per cent of mean (GAM) on which the breeding methods are formulated for its further improvement. The extent of variability is measured by genotypic and phenotypic coefficient of variation which provides information about relative amount of variation present in different characters.

Molecular marker technologies can assist conventional breeding efforts and are valuable tools for the analysis of genetic relatedness and the identification and selection of desirable genotypes for breeding programme. DNA based molecular markers have proven to be powerful tool in the assessment of genetic variation and in the elucidation of genetic relationships within and among the species of rice (Ragunathanchari *et al.*, 2000).

Progress in plant breeding in terms of development of superior and high yielding varieties of agricultural crops was made possible by accumulation of beneficial alleles from vast plant genetic resources existing worldwide. Still, a significant portion of these beneficial/ superior alleles were not utilized as these were left behind during evolution and domestication. This untapped genetic variation existing in wild relatives and land races of crop plants could be exploited gainfully for development of agronomically superior cultivars. Introgressions of novel alleles from wild relatives of crop plants into cultivated varieties have clearly demonstrated that certain alleles and their combinations potentially make dramatic changes in trait expression when moved to a suitable genetic background by overcoming the genetic bottlenecks which restricted their introgression to cultivars these can be achieved through molecular techniques in breeding programmes (Mc Couch *et al.*, 2007).

The molecular marker systems used to identify and assess the genetic diversity and polymorphism for different traits which are suitable for direct seeded rice by using SSR markers. Simple sequence repeats (SSR) or microsatellites which are simple or tandemly repeated having di, tri, tetra- nucleotide sequence motifs flanked by unique sequences (Hamada *et al.*, 1982). These are useful markers for genetic diversity analysis

because they detect high level of allelic diversity, occur frequently throughout plant genomes, and are easily assayed by PCR and they have been extensively used to identify genetic variation among rice species (Ren *et al.*, 2003).

Considering the importance of the crop and the above indicated facts, it is need to generate more information on genetic diversity, variability, character association and molecular characterization for different rice genotypes. Keeping these things in view, the present investigation was undertaken with the following objectives.

1. Assessment of differential performance of rice genotypes for direct seeded condition
2. Association study among different traits relevant to direct seeded rice along with yield
3. Genetic diversity analysis of rice genotypes using suitable DNA markers

II. REVIEW OF LITERATURE

Direct-seeded rice (DSR) is a feasible alternative to conventional puddled transplanted rice with good potential to save water, reduce labour requirement, mitigate green-house gas (GHG) emission and adapt to climatic risks. The yields are comparable with transplanted rice if crop is properly managed. In recent years, efforts have been made in promoting the DSR technology by various organizations. Scientists are concentrating in developing suitable varieties and agronomic packages for promoting the DSR. However, the DSR suffers from some constraints particularly high weed infestation. The system has been proved cost-effective and farmers' friendly but require further improvement in technological approach to realize greater benefits.

Farooq *et al.* 2011 mentioned about looming water crisis, water-intensive nature of rice cultivation and escalating labour costs drive the search for alternative management methods to increase water productivity in rice cultivation. Direct seeded rice (DSR) has received much attention because of its low-input demand.

2.1 Genetic variability, heritability and genetic advance

Critical estimate of nature and magnitude of genetic variability is a prerequisite for any crop improvement programme. The variability observed in any population could be due to the genetic and environmental factors and also due to the interaction between these factors. The details of findings related to this study are reviewed below.

Venkataramana (1991) reported high phenotypic variability for grain yield, panicle weight, number of productive tillers and total number of tillers. Heritability was high for plant height, days to maturity and panicle exertion in both direct sown and irrigated conditions. The expected genetic advance was high for number of productive tillers.

Remabai *et al.* (1992) Evaluate the rice genotypes under aerobic condition, reported higher phenotypic coefficient of variation for the entire yield attributing parameters than genotypic coefficient of variation indicating the influence of extraneous factors on all the characters. Moderate to high estimate of heritability and genetic advance for plant height, flag leaf area, panicle exertion and grain yield per plant were observed.

Hajare *et al.* (1993) reported high GCV for the characters viz., number of filled grains per panicle, plant height and number of panicles per plant and high estimate of

genetic advance (GA) for straw yield per square meter, grain yield/ msq, number of filled grains per panicle and number of panicles per meter square under upland condition.

Borbora *et al.* (1998) studied significant variation among sixteen local rice varieties for eleven yield related traits and observed high to moderate GCV together with high heritability and GA as per cent of mean were recorded for test weight, grain yield per panicle and number of branches per panicles under transplanting condition.

Venkataramana and Hittalmani (1999) reported high phenotypic coefficient of variability for grain yield, panicle weight, number of productive tillers and total tillers. Heritability was high for plant height, days to maturity and panicle exertion in both direct sown rainfed and irrigated conditions. The expected genetic advance was high for productive tillers. Kaw *et al.* (1999) evaluated ninety-four rice genotypes in which thirty-eight were japonica x indica F₁'s, thirty six were indica x indica F₁'s and twenty parents. Results revealed that high genotypic variation for fertility per cent and fertile spikelet per panicle and low genotypic variance for flowering duration and panicle length.

Manna and Sasmal (2000) observed in high heritability coupled with moderate GCV and GA as per cent mean for grain yield, grain and endosperm weights in local rice genotypes under the upland condition. Shivapriya (2000) reported moderate GCV and PCV for days to first flowering, plant height, panicle length, days to maturity, grain breadth and L: B ratio in a study involving sixty eight local rice accessions under transplanting condition.

Bidhan *et al.* (2001) under direct seeded condition, reported high phenotypic and genotypic variances for grain yield, grain breadth and yield followed by number of filled grains per panicle. Heritability ranged from 50 per cent (grain yield) to 90 per cent (grain breadth). Genetic advance as per cent of mean was highest for number of filled grain per panicle followed by grain yield. Number of filled grain per panicle, 1000 grain weight, grain length and breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance

Nagabhushan (2003) studied eighty double haploid (DH) lines derived from IR 64 x Azucena cross and reported high GCV and PCV for grain yield per plant, moderate GCV and PCV for plant height and days to flowering and low GCV and PCV for days to maturity. Chand *et al.* (2004) under rainfed condition reported high phenotypic

coefficient of variation for grains per panicle and grains yield per plot. Heritability and genetic advance as percentage of mean were high in grains per panicle, 1000 grain weight, grains length, length to breadth ratio and grain yield. Grain yield showed significant positive correlation with grains per panicle and grain length.

Kuldeep *et al.* (2004) reported high heritability coupled with high genetic advance for yield components under transplanting condition. Seedling length, number of leaves per seedling, number of productive tillers per plant, panicle length, number of days to 50 per cent flowering, number of days to maturity and 100- seed weight showed positive and significant association with grain yield. Therefore, selection for these characters may be useful for developing rice varieties.

Mall *et al.* (2005) reported high heritability coupled with high genetic advance for plant height, number of tillers per plant, number of panicles per plant, number of spikelets per panicle and flag leaf length under the transplanting condition. Uttam *et al.* (2005) reported wide range of variability for grain yield per plant, effective tillers per plant, days to flowering, days to maturity, 1000 seed weight and protein content. High heritability coupled with moderate genetic advance was observed for days to flowering, days to maturity and plant height under transplanting condition.

Afzal *et al.* (2006) analysed phenotypic and genotypic variances, coefficient of variance (CV), genetic advance, heritability, correlation coefficient(r) and path coefficient for yield, yield components and grain quality characteristics in fourteen genotypes of Basmati rice under transplanting condition. High heritability estimates coupled with high genetic advance were observed for plant height and 1000 grain weight.

Manickavelu *et al.* (2006) under drought condition, recorded the high phenotypic and moderate genotypic coefficients of variation and high genetic advance for traits viz., days to 70 per cent relative water content, leaf rolling, leaf drying, harvest index, biomass yield and grain yield expressed high or moderate heritability, while traits viz., days to flowering, panicle length and plant height showed low heritability with low genetic advance.

Ali *et al.* (2007) studied regarding suitable rice varieties for direct seeding were conducted in RCBD. The experiment comprised 15 medium and fine grain rice varieties. The results revealed that short stature and low tillering, medium and fine grain varieties

viz ; KS-282, NIAB- IR9, IR-6, Basmati-2000, Super Basmati, 99512 and PK-5261-1-2-1 produced significantly higher yield than all the other varieties.

Kole *et al.* (2008) studied variability for twelve morphological characters on eighteen morphologically distinct rice mutants in M4 generation along with their two mother genotypes under transplanting conditions. Genotypic and phenotypic coefficients of variation were high for flag leaf angle and panicle number and moderate for grain number per panicle, straw weight, harvest index and grain yield per plant and low for days to flower, plant height, panicle length, spikelet number, spikelet fertility (per cent) and test weight. Abdus *et al.* (2009) reported significant differences among twenty five rice genotypes for all the morphological traits under direct seeded condition. Six genotypes used for the grain quality studies also showed significant differences among grain quality traits except volume expansion ratio and grain elongation ratio. Broad sense heritability (per cent) estimate was high for morphological traits ranging from 67.37 to 98.24.

Keshava Murthy *et al.* (2011) field experiment was conducted during wet season 2009 to study the response of rice genotypes under aerobic conditions. Variance studies revealed significant differences among the genotypes for the traits, days to flowering, plant height, harvest index, grain yield, panicle number, straw yield, panicle length, test weight and biomass. Higher values of heritability and genetic advance were observed for plant height and days to flowering.

Vange (2009) evaluate the performance and genetic diversity of some upland rice accessions. Preliminary results indicates highly significant ($P < 0.01$) differences on all traits studied except for grain length, grain width, grain length/width ratio and 1000 grain weight, indicating genetic diversity among these accessions. Grain yield ranged between 0.54 t/ha (TOX 1870-30-102) to 3.7 t/ha (TOX 1010-21-5-124). Genotypic coefficient of variability (GCV) was generally lower than phenotypic coefficient of variability (PCV). Days to 50% heading, days to maturity, flag leaf area, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle, grain weight/panicle and seed yield showed very low differences between their PCV and GCV values. Also these traits had high estimates for heritability and genetic advance.

Yadav *et al.* (2010) studied the extent of genetic variability under transplanting condition, among forty rice genotypes from diverse sources and reported that the mean

sum of squares due to genotypes were significant for all the characters. This suggests that the genotypes selected were genetically variable and considerable amount of variability exists among them.

Abarshahr *et al.* (2011) evaluated thirty rice different genotypes of native bred and upland cultivars of rice in both control and drought condition. Analysis of variance showed significant differences among genotypes in respect of all vegetative and morphological traits. Eight drought stress tolerance indices were calculated according to their grain yield under drought stress and normal conditions. Among rice cultivars 'IR24', 'Nemat', 'Sephidroud', 'Kadoos' and 'Bejar and 'Vandana', upland cultivar had the highest tolerance to drought stress and produced the highest grain yield.

Hasan *et al.* (2011) studied twenty four hybrid rice varieties of diverse origin for genetic variability under transplanting condition and reported that PCV values were greater than GCV. High values of heritability along with moderate genetic advance were observed for panicle/m², days to 50 per cent flowering and plant height.

Khriedinuo *et al.* (2011) reported the presence of high variability among the genotypes for all the traits under aerobic condition. GCV was high for flag leaf area, plant height, number of tillers per plant, number of ear bearing tillers, number of filled grains per panicle, panicle weight, root length and area, straw weight and grain yield. The broad sense heritability and genetic advance as percentage of mean indicated that panicle weight and grain yield per plant are the two most important yield components.

Hassan and Behzad (2011) studied based on Randomized Complete Block Design (RCBD) with three replications, experiment was conducted to compare differences between direct seeded rice and transplanting methods. Different cultivars were used "Hashemi", "Ali Kazemi", "Hassani", and "Hybrid Spring 1". According to analysis of variance, the effects of cultivars on all yield components (panicle/m², seed/panicle, and 1000 grain weight), plant height, panicle length, and total productive tiller were significant, except for grain weight. The largest and least number of seed/panicle was obtained under transplanting method of "Hybrid Spring 1" and direct seeded method "Ali Kazemi" respectively. The largest and least number of tillers and fertile productive tillers were obtained in direct seeded method of "Hybrid Spring 1" and transplanting method of "Hashemi", respectively.

Pathak *et al.* (2011) production of conventional puddled transplanted rice is facing severe constraints because of water and labour scarcity and climatic changes. Direct-seeded rice (DSR) is a feasible alternative to conventional puddled transplanted rice with good potential to save water, reduce labour requirement, mitigate green-house gas (GHG) emission and adapt to climatic risks. The yields are comparable with transplanted rice if crop is properly managed. In recent years, efforts have been made in promoting the DSR technology by various organizations. Scientists are concentrating in developing suitable varieties and agronomic packages for promoting the DSR.

Venkata Subbaiah *et al.* (2011) studied extent of variability and genetic parameters with 16 parents and 48 hybrids for nine yield and its components under direct seeded condition. High GCV and PCV were recorded for harvest index, and total number of productive tillers per plant in parents and for total number of productive tillers per plant, number of grains per panicle in hybrids. High heritability coupled with high genetic advance as per cent of mean were recorded for harvest index, total number of productive tillers per plant, number of grains per panicle, kernel length, kernel L/B ratio and grain yield per plant in case of parents, total number of productive tillers per plant, number of grains per panicle and harvest index in case of hybrids.

Ghosh and Sharma (2012) under transplanting condition reported narrow difference between PCV and GCV for days to 50 per cent flowering, sterile spikelet per panicle, fertile spikelet per panicle, panicle length, grain yield per plant, test weight and head rice recovery indicating less environmental influence. High heritability coupled with higher genetic advance as per cent of mean for grain yield per plant, sterile spikelet per panicle, fertile spikelet per panicle and 1000 seed weight was also reported

Khalid *et al.* (2012) reported high genotypic coefficient of variation and estimated genetic advance for number of tillers per plant and plant height; high heritability for plant height, number of tillers per plant and 1000 grain weight; high heritability with low genetic advance for days to 50 per cent flowering and days to maturity and concluded that traits such as panicle length, number of tillers per plant, number of filled grains per panicle and 1000 grain weight could be useful as index traits for improving the total grain yield.

Pratap *et al.* (2012) One hundred high yielding rice genotypes were evaluated under direct seeded condition to determine character variability and diversity for grain

yield, yield components and quality characters. High estimates of heritability, genetic advance, genotypic and phenotypic coefficients of variation were recorded for number of panicle per hill, flag leaf area and grain yield per hill.

Pandey *et al.* (2012) evaluated fifty two rice genotypes under stress condition to know the genetic relationship of various polygenetic traits on yield. Their results revealed that substantial amount of variability exists in entire gene pool for all traits studied, magnitude of PCV and GCV were high for biological yield, moderate for grain yield per plant, number of spikelet per panicle, however days to 50 per cent flowering, days to maturity, plant height, panicle length, per cent spikelet per panicle and harvest index had low estimates. They noticed high heritability coupled with high genetic advance in per cent mean for biological yield, grain yield per plant and spikelet per panicle.

Gulzar *et al.* (2013) reported high genotypic and phenotypic coefficients of variation for grain yield, secondary branches per panicle and panicle weight; moderate for grain number per panicle, grain length: breadth (L:B) ratio and panicle density. High heritability accompanied by high to moderate genetic advance for panicle density, days to 50% flowering, plant height and grain number.

Vanisree *et al.* (2013) studied variability under transplanting condition, reported high estimates of GCV for productive tiller per plant and filled grain per panicle where as low estimates of GCV were noticed for panicle length, days to 50 per cent flowering kernel breadth and kernel elongation ratio. Productive tiller per plant and filled grain per panicle exhibited high heritability and genetic advance.

Amit *et al.* (2014) studied 40 rice accessions, highest Phenotypic and Genotypic Coefficient of Variation were observed for grain yield per hill (g) and number of spikelet's per panicle whereas, lowest in days to maturity, test weight (g) and days to 50 per cent flowering. High heritability and genetic advance were observed for number of spikelet's per panicle.

Bhati *et al.* (2014) evaluated the 52 rice genotypes under transplanting conditions grown in a randomized block design (RBD) in three replications to estimate the genetic variability, heritability and genetic advance for grain yield and yield contributing traits in rice. Highly significant ($p < 0.01$) variation was obtained for almost all the characters studied. Grain weight per panicle and number of grains per panicle showed relatively high

GCV and PCV estimates. The range of heritability was from 60.10 % (Kernel breadth) to 99.30% (Number of grains per panicle). High estimates of heritability and genetic advance as percent of mean were obtained for plant height, number of tillers per plant, number of effective tillers per plant, panicle length, number of spikelet per panicle, number of grains per panicle, kernel length, grains weight per panicle, 1000-grains weight and grain yield per plant.

Lingaiah *et al.* (2014) reported about experiment which was carried out to study correlation and path analysis studies for yield and yield contributing characters in sixty four mid early group genotypes of rice. The correlation studies revealed that the genotypic correlation were higher than the corresponding phenotypic correlations. Yield exhibited positive association with effective tillers per plant, panicle length and test weight. And negative associate on with days to 50% flowering and plant height.

Masudrana *et al.* (2014) studied effect of planting methods on the yield and yield attributes of short duration aman rice varieties. The treatments comprised of three BRRI released high yielding varieties viz., BRRI dhan39, BRRI dhan49 and BRRI dhan57 and three planting methods viz., direct seeding of dry seed, direct seeding of sprouted seed and transplanting. It was conducted in a Randomized Complete Block Design with three replications. Planting methods had a significant effect on the growth duration of rice and yield related components like tiller number, grains per panicle, test weight . The rice crop established with direct seeding of the dry and sprouted seed matured 7 days earlier than transplanting because of absence of transplanting shock. The variety BRRI dhan39 gave the highest yield (4.9 t/ ha) when grown with direct seeding of sprouted seed compared to other varieties.

Muhammad Kamrul Islam *et al.* (2014) carried out study which was conducted in controlled field conditions by using Forty-three high yield rice varieties. The percentage of seedling establishment, first leaf, plant height, root length, leaf number and seeding depth parameters were observed, variety BR6 showing the highest seedling establishment percentage (85%) and longest first leaf (1.97) and seedling height (2.86), seeding depth 0.5, root length 1.65 at low land condition, the screening revealed that BR6 is the best variety for direct seeding in lowland conditions.

Patel *et al.* (2014) a studied to obtain information on genetic variability under rainfed upland conditions was carried out using 44 diverse genotypes. The analysis of

variance revealed the significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes for various traits. High estimate of genotypic and phenotypic coefficient of variation were observed for number of grains per panicle, grain yield per plant, straw yield per plant and harvest index indicated wider genetic variation for these traits. High value of heritability coupled with high expected genetic advance as per cent of mean were observed for the characters number of grains per panicle, grain yield per plant, straw yield per plant, harvest index, 1000 grain weight, grain L/B ratio and amylose content indicated that selection may be effective for this character.

Paikhomba *et al.* (2014) evaluated thirty F₁ rice hybrids along with complete set of thirteen parents and checks for variability, heritability and genetic advance in different yield and yield components under transplanting condition. The results revealed that the estimates of GCV was lower than the respective PCV, indicating the influence of environmental factors on the expression of the traits under studied. High heritability coupled with moderate genetic advance as per cent of mean were observed for per cent pollen fertility, grain yield per hill, harvest index and number of filled grains per panicle.

Krantikumar *et al.* (2015) carried out study on genetic variation for grain yield and its component traits in direct seeded rainfed upland rice was carried out using twenty rice varieties. High genotypic coefficient of variation (%) was exhibited for spikelet sterility (60.61), grain yield per plant (60.06 g) and grain weight per panicle (43.21).

In 2015, Mamta kumari carried out an experiment which was conducted to evaluate 24 rice genotypes under aerobic condition for yield and its thirteen attributing characters. Analysis of variance revealed significant difference among genotypes for all traits. High GCV and PCV were observed in number of spikelet's per panicle (23.35% and 23.62%) followed by grain yield per hill (21.10% and 21.39%). High heritability coupled with high genetic advance as per cent of mean were registered for number of spikelets per panicle (97.75% and 47.56%) followed by grain yield per hill (97.27% and 42.86%) and biological yield per hill (95.91% and 31.16%) suggesting preponderance of additive gene action in the expression of these traits.

Mahantashivayogayya *et al.* (2015) evaluated thirty six early maturing rice varieties/hybrids under Dry Direct Seeded condition, following randomized block design in three replications. Out of 36, only two varieties viz., MT4541 (7927 kg/ha) and UPR

2805-14-1-2 (7058 kg/ha) had expressed significantly superior grain yield over check Sahbhagidhan (6258 kg/ha) to an extent of 27 per cent and 13 per cent respectively. The variety 13K 4070 with medium slender grain type had yielded significantly higher grain yield (6970 kg/ha) with 11 per cent increase over Sahbhagidhan and 34 per cent over Local Check (ES-18).

Sandhyarani Das (2015) studied Genetic variability estimation for ten quantitative characters in 22 mid duration irrigated rice genotypes during *kharif* 2010. High estimates of heritability coupled with high genetic advance as percent of mean were recorded for most of the characters indicating the presence of additive gene effects in them. The genotypic and phenotypic coefficient of variation were maximum for flag leaf area, grain yield, number of effective tillers per plant, number of fertile grains per panicle, 100 seed weight and harvest index indicating selection for such characters would be more reliable.

Sandhya *et al.* (2015) carried out an investigation with 32 elite rice genotypes under transplanting condition to identify diverse genotypes. They were evaluated for thirteen yield and yield attributing characters *viz.* days to 50 percent flowering, plant height, number of tillers per plant, number of panicles per plant, panicle length, flag leaf length, flag leaf width, number of spikelets per panicle, days to maturity, biological yield, test weight, harvest index and grain yield per plant using Mahalanobis D² statistics. The characters like number of spikelets per panicle (21.17%), biological yield per plant (20.77%), test weight (15.93%), harvest index (13.10%) and days to 50 percent flowering (10.08%) contributed maximum towards genetic diversity.

Sunil Kumar *et al.* (2015) experimented with twenty eight rice genotypes with one check (NDR 359) were evaluated for yield and yield attributing traits at field experimentation under direct seeding condition, in randomized block design with three replications during *kharif* 2011. The minimum days to 50% flowering were taken by rice genotype COUDE (73.00) followed by GANZAOXIAN 4 (74.66), BINDESHWARI (75.33), maximum number of tillers per plant NDR 359 (20.73) and followed by RADHA 11 (17.00), ADT47 (16.26). High estimate of GCV and PCV were recorded for grain yield per hill (22.37, 22.97), number of tillers per hill (20.76, 21.41) and number of spikelets per panicle (20.74, 20.76). All the characters showed high heritability but plant height, biological yield showed high heritability with high genetic advance. So, these characters should be more preferred during selection.

2.2. Correlation among yield and yield contributing traits in rice.

Genetic correlation among yield and yield attributing traits determine the extent and direction of association of plant traits. While making selection for a character there may be simultaneous effect on the other characters also depending on the intensity of associations between two traits under consideration. If the correlation is strong between a set of desirable traits then if we make selection for one character, the other character will automatically be taken care. Correlation coefficient analysis can be used to determine the nature and degree of relationship between characters. Correlation between important characters is helpful in selection of suitable plant type. The details of findings related to this study are reviewed below.

Rao and Srivastav (1994) revealed that positive association of days to flowering with days to maturity, fertile spikelet's per panicle with fertility of spikelet's and grain yield and harvest index with grain yield in assessing association among yield and yield attributes in eighteen divergent rice genotypes under direct sown rain fed upland ecosystem.

Nath and Talukdar (1997) studied segregating populations of indigenous scented x high yielding non-scented crosses of rice. Results revealed that positive correlation of grain yield per plant with number of grains per panicle and 100- grain weight at genotypic level and negative significant correlation with plant height at phenotypic level. Meenakshi *et al.* (1999) under rainfed condition reported that productive tillers per plant, grains per panicle, dry matter production and harvest index were positively correlated with grain yield. Muhammad *et al.* (2002) under transplanting condition observed that total number of tillers, number of productive tillers, flag leaf area, straw yield, harvest index and fertility index except plant height revealed significant genotypic correlation to grain yield.

Vaishali (2003) recorded positive association of grain weight with plant height, days to flowering, panicle length and harvest index and negative association with panicle number, grains per panicle and biomass. Satoshi *et al.* (2007) evaluated the genotypic differences in grain yield of 14 rice (*Oryza sativa* L.) genotypes with different phenology under two growing conditions, transplanting (TP) and direct-seeding (DS). IR24 a semi-dwarf high yield, early maturing bred for irrigated low land. Genotypic differences in grain yield were significant in a combined analysis two growing conditions, and both high sink size (spikelet number per area) and high ripened grain percentage were associated

with high yield. High shoot dry matter production and large spikelet number per panicle were associated with high grain yield in DS genotypes in the lower field, whereas in TP genotypes with large numbers of panicles were required for high grain yield.

Abdus *et al.* (2009) reported positive and significant association of grain yield per plant with plant height, panicle length, flag leaf area and number of grains per panicle at genotypic level under aerobic condition. Keshava Murthy *et al.* (2011) Eight rice genotypes with increased yield advantage over checks have been identified as suitable entries for aerobic cultivation. Correlation revealed an ideal plant type of genotype under aerobic conditions should have high harvest index and biomass.

Vange (2009) genotypic correlation analysis of yield with other traits under upland condition revealed that yield had a significantly positive correlation with flag leaf area, number of tillers, number of panicles, panicle weight, panicle length, number of branches/panicle, number of seeds/panicle and seed weight/panicle, grain length and 1000 seed weight. Mina *et al.* (2011) reported that under the drought stress condition the number of spikelet per panicle, flag leaf length and flag leaf width had positive direct effects. Whereas, days to complete maturity days to 50 per cent flowering and plant height had negative direct effects on paddy yield under optimum irrigation condition.

Muhammad Ashfaq *et al.* (2012) noticed significant correlation with yield for panicle length, seeds per panicle whereas seed weight per panicle showed significant positive correlation with grain yield under the aerobic condition. Pratap *et al.* (2012) One hundred high yielding rice genotypes were evaluated under direct seeded condition to determine character association majority of the traits showed significant and positive associations between yield and yield components like biological yield per hill followed by harvest-index.

Ramya *et al.* (2012) reported significant and positive associations of grain yield per plant with total number of tillers per plant and number of productive tillers per plant under transplanting condition. Rangare *et al.* (2012) studied forty exotic and Indian accessions and found the positive significant positive genetic association of grain yield with biological yield per plant, number of fertile tillers per plant, number of spikelets per panicle, test weight, panicle length and days to maturity under aerobic condition.

Saravan *et al.* (2012) reported that grain yield per plant had significant positive correlation with biological yield per plant, harvest index, panicles per plant, plant height, spikelets per panicle, panicle length, test weight, spikelet fertility and flag leaf length.

Chakravorty *et al.* (2013) evaluated fifty one land races under recommended package of practice under direct seeded condition and reported positive significant genetic association of kernel weight with leaf length, leaf breadth, plant height, flag leaf angle, Culm diameter, panicle length, grain length, grain breadth, grain L/B ratio and days to maturity. Gulzar *et al.* (2013) recorded grain yield is positively and significantly correlated with number of tiller per plant, panicle density per meter square and number of grain per panicle at both genotypic and phenotypic levels under temperate region.

Prakash *et al.* (2013) studied on forty two non-basmati genotypes and observed significant and positive association for number of tillers per plant, number of productive tillers per plant, panicle weight, grain breadth and test weight with grain yield per plant at both genotypic and phenotypic level. The negative and significant correlation noticed for plant height and days to 50 per cent flowering at both genotypic and phenotypic level.

Shivaprasad *et al.* (2013) evaluated fifty two genotypes and the study depicted significant positive genetic association of cold tolerance with days to 50 per cent flowering, plant height, seedling maturity after transplanting, number of productive tillers and panicle exertion. Vanisree *et al.* (2013) reported significant correlation of productive tiller per plant, filled grain per panicle, panicle length and days to 50 per cent flowering with harvest index under transplanting condition.

Amit *et al.* (2014) studied 40 rice accessions and reported that seed yield has a strong positive significant association with tillers per hill, panicles per hill, panicle length (cm), biological yield (gm), harvest Index, spikelet's per panicle, and test weight (g).

Patel *et al.* (2014) associated study for yield and yield contributing traits under rainfed upland conditions was carried out using 44 diverse genotypes. The results of correlation studies indicated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for most of the traits. Grain yield per plant was found positively and significantly associated with plant height, panicle length, number of total tillers per plant, number of effective tillers per plant, number of grains per panicle, harvest index and 1000-grain weight at both

genotypic and phenotypic levels indicating that these traits were main yield attributing traits.

Ramanjaneyulu *et al.* (2014) under aerobic condition reported significant and positive correlation of grain yield with number of tillers/plant (1.11), number of productive tillers/plant (0.99), number of grains/spikelet (0.84) and spikelet length (0.59) among the rice genotypes.

Satish Kumar Rai *et al.* (2014) conducted an experiment with 40 rice genotypes under transplanting condition. Correlation and path-coefficient analysis, concluded that, biological yield per plant and harvest index exhibited maximum positive direct effect on grain yield seems to be primary yield contributing characters and could be relied upon for selection of genotypes to improve genetic yield potential of rice. Hence, utmost importance should be given to these characters during selection for single plant yield improvement.

Venkanna *et al.* (2014) studied association between yield traits in F₂ generation in 36 crosses of rice which revealed seed yield had highly significant positive correlations with total biomass both phenotypically and genotypically and 1000 weight at genotypic level. Mamta Kumari *et al.* (2015) conducted an experiment to evaluate 24 rice genotypes under aerobic condition for yield and its thirteen attributing characters. Grain yield per hill had positive significant association with biological yield per hill (0.88 and 0.88), harvest index (0.72 and 0.71), panicle length (0.57 and 0.53), plant height (0.40 and 0.39) and number of spikelet's per panicle (0.36 and 0.35) at both genotypic and phenotypic level respectively.

Krantikumar *et al.* (2015) carried out studies on inter relationship of grain yield and its component traits in direct seeded upland rice was carried out using twenty rice varieties. Grain yield per plant was positively and significantly correlated with grain weight per panicle (0.97), biological yield (0.92), harvest index (0.87), number of filled grains per panicle (0.84), 1000 grain weight (0.80), straw yield per plant (0.79), panicle length (0.77), number of spikelet's per panicle (0.84) and plant height at maturity (0.57). Study proved that selection for characters such as higher biological yield, higher harvest index and more number of filled spikelet's per panicle proved to be effective for further crop improvement programmes.

Lingaraja *et al.* (2015) carried out study on correlation among various yield and yield contributing characters revealed that grain yield per hill was significantly and positively correlated at $p = 0.001$ (1% level of significance) with harvest index (0.85), biological yield (0.48) and panicle length (0.39) at both phenotypic and genotypic level. The characters like harvest index, biological yield per hill, number of panicles per hill, flag leaf length and plant height exhibited positive direct effect on grain yield per hill at both phenotypic and genotypic paths and direct selection of these characters may be helpful for yield improvement in aerobic rice.

Sandhyarani Das (2015) carried out character association studies which were estimated for ten quantitative characters in 22 mid duration irrigated rice genotypes. In this study all the component traits exhibited positive association with grain yields except plant height and panicle length although the level of association varied.

2.3. Genetic diversity analysis of rice genotypes using suitable DNA markers.

In recent years, the development of molecular markers techniques has allowed new opportunity in plant breeding. DNA markers provide powerful and reliable tools for evaluating genetic variation both within and between populations and have greatly enhanced the genetic analysis of crop plants. A variety of molecular markers, including RFLPs, RAPDs, AFLPs, and SSRs have been developed in different crop plants.

Neeraja *et al.* (2005) characterized a set of tall rice landraces using 17 gene-derived SSRs and eight other genomic SSRs. Gene-derived SSRs (0.68) revealed a lower polymorphism information content than the other SSRs (0.87). Upon UPGMA analysis of gene-derived SSRs they observed that tall landraces and high-yielding varieties, which were nitrogen responsive, were grouped into a major cluster and other landraces which were nonresponsive to nitrogen into a minor cluster at 0.37 similarity.

Bibi *et al.* (2009) studied rice cultivars IR6 and IR8 were exposed to different doses of gamma radiation and stable mutants along with parents were studied for genetic diversity on the basis of molecular marker (RAPD). The genetic variation was determined through RAPD. A total of 74 scorable bands were observed, out of which 47 (63.6%) were polymorphic and 27 (36.5%) were monomorphic. The size of fragments ranged from 201bp – 3.2 kbp. The number of fragments produced by various primers ranged from 1-12 with an average of 4.93 fragments per primer. Maximum 12 bands were

amplified with primer A-03 and minimum one band was amplified with primer A-15, A-19 and B-10. Some specific RAPD bands were also identified reflecting the RAPDs application for the identification of rice cultivars/genotypes. Results revealed that variety Sarshar and IR8-178 contain a specific segment of 451bp amplified with primer A-19. The highest similarity was observed between IR8-15A and IR8-178 (96%) and the least similarity was recorded between IR-8 and IR6-15/B (69%). On the basis of RAPD studies, genotypes were grouped on the basis of their similarities and distinctness.

Random Amplified Polymorphic DNA (RAPD) assay was initiated for molecular genetic analysis among 13 F₃ rice lines and their parents. Four out of 15 decamer random primers were used to amplify genomic DNA and the primers yielded a total of 41 RAPD markers of which 37 were considered as polymorphic with a mean of 9.25 bands per primer. The percentage of polymorphic loci was 90.24. The highest percentage of polymorphic loci (14.63) and gene diversity (0.0714) was observed in 05-6 F₃ line and the lowest polymorphic loci (0.00) and gene diversity (0.00) was found in 05-12 and 05-15 F₃ lines. So, relatively high level of genetic variation was found in 05-6 F₃ line and it was genetically more diverse compared to others. The average co-efficient of gene differentiation (GST) and gene flow (Nm) values across all the loci were 0.8689 and 0.0755, respectively. The UPGMA dendrogram based on the Nei's genetic distance differentiated the rice genotypes into two main clusters: PNR-519, 05-19, 05-14, 05-12 and 05-17 grouped in cluster 1. On the other hand, Baradhan, 05-9, 05-13, 05-11, 05-5, 05-6, 05-1, 05-4, 05-15 and 05-25 were grouped in cluster 2. The highest genetic distance (0.586) was found between 05-4 and 05-17 F₃ lines and they remain in different cluster as reported by Rahman *et al.* (2009).

Prabakaran *et al.* (2010) investigated the genetic divergence of 12 rice land races using five SSR markers. A total of 11 alleles were detected in 12 land races and the number of alleles per locus ranged from 2 to 3 with an average of 2.2 per locus. Among the primers used RM 481 identified more number of alleles and average PIC was 0.43. The dendrogram based on SSR marker analysis grouped the 12 rice accession into six clusters, where cluster VI was the largest with three accessions. The similarity coefficient through Jaccard's revealed that Anna samba and Chetti virippu were ascertained to be the genetically diverse from the other land races. The study also highlighted use of more number of markers for efficient characterizing the land races used for the present study.

The quantitative trait loci (QTLs) of three traits for rice seed vigor during the germination stage, including germination rate, final germination percentage, and germination index, were investigated using one recombinant inbred line (RIL) population derived from a cross between *japonica* Daguandao and *indica* IR28, and using the multiple interval mapping (MIM) approach. The results show that *indica* rice presented stronger seed vigor during the germination stage than *japonica* rice. A total of ten QTLs, and at least five novel alleles, were detected to control rice seed vigor, and the amount of variation (R^2) explained by an individual QTL ranged from 7.5% to 68.5%, with three major QTLs with $R^2 > 20\%$. Most of the QTLs detected here are likely to coincide with QTLs for seed weight, seed size, or seed dormancy, suggesting that the rice seed vigor might be correlated with seed weight, seed size, and seed dormancy. At least five QTLs are novel alleles with no previous reports of seed vigor genes in rice, and those major or minor QTLs could be used to significantly improve the seed vigor by marker-assisted selection (MAS) in rice as revealed by Zhou-fei wang *et al.* (2010).

Molecular characterization of the genotypes gives precise information about the extent of genetic diversity which helps in the development of an appropriate breeding program. Total of 24 SSR markers were used across 12 elite aromatic rice genotypes for their characterization and discrimination. Among these 24 markers 9 microsatellite markers were showed polymorphism. The number of alleles per locus ranged from 2 alleles (RM510, RM244, and RM277) to 6 alleles (RM 163), with an average of 3.33 alleles across 9 loci obtained in the study. The polymorphic information content values ranged from 0.14 (RM510) to 0.71 (RM163) in all 9 loci with an average of 0.48. RM163 was found the best marker for the identification of 12 genotypes as revealed by PIC values. The frequency of most common allele at each locus ranged from 41% (RM163, RM590, and RM413) to 91% (RM510). The pair-wise genetic dissimilarity co-efficient indicated that the highest genetic distance was obtained between Basmati PNR 346 and Deepa, Basmati PNR 346 and Patnai-23; Dolargura and Sugandha, Bhogganijia and Sugandha and finally between Dolargura and Chinikani (88.89%). Opchaya, Basmati PNR 346 and Sugandha had close similarity among them but showed wide dissimilarity with other genotypes. Being grouped into distant clusters Dolargura and Opchaya could be utilized as potential parents for the improvement of fine grain aromatic rice varieties. Genotypes Deepa and Patnai-23 (having zero dissimilarity) might have possessed

somewhat similar genetic background and more markers are needed to discriminate them as studied by Abdul *et al.* (2012).

Rajani *et al.* (2012) performed RAPD analysis to assess the genetic diversity in ten selected cultivars of rice, *Oryza sativa* L. using 30 decamer random primers. Out of 30, 25 RAPD primers revealed polymorphism while the remaining 5 primers showed no reaction. The primers produced a total of 428 bands of which 363 were polymorphic (85.02%). The number of polymorphic fragments for each primer varied from 7 to 23 with an average of 14 polymorphic fragments. The primer OPB-17 produced the maximum number of polymorphic bands. The RAPD data was analyzed to determine the genetic similarity coefficients which ranged from 0.46 to 0.81 and genotypes were grouped into two major clusters using UPGMA.

Berilus *et al.* (2013) evaluated Twenty four genotypes of rice for polymorphisms after amplification with 30 SSR primer pairs. The results obtained depicted a wide range of variation among the varieties. The diversity parameters confirmed that Bordungsha F₁, S5 and Baodhan Bordungsha (deep water rice) were most diverse and were distinctly different from the rests of the genotype and the dissimilarity coefficient ranged from 0.06 to 0.94. This study provides a clear picture of the genetic diversity of rice. Among the set of SSR primers tested, RM44 (0.942), RM495 (0.932), RM125 (0.998) and OSR13 (0.970) were more informative in comparison to other primers.

Nitika Sandhu *et al.* (2014) reported the development of rice varieties for dry direct-seeded conditions can be accelerated by selecting suitable traits which includes seedling emergence, early vegetative vigour, nutrient uptake, nodal root number, and root hair length and density, for these traits characterized by using markers like RM168, RM252, RM26 to study the genetic control of these traits and their relationship with grain yield by identifying the QTLs under seedling and reproductive-stage drought stress. Two BC₂F₄ mapping populations derived from crosses of Aus 276, a drought tolerant aus variety, with MTU1010 and IR64, high-yielding indica mega-varieties, and studied to identify quantitative trait loci (QTLs) that showed large and consistent effects. qGY6.1, qGY10.1, qGY1.1, and qEVV9.1 were found to be effective in both populations under a wide range of conditions. QTLs for several seedling-stage traits co-located with QTLs for grain yield, including early vegetative vigour and root hair length. Six lines were selected from both populations based on grain yield and the presence of QTLs, and these lines

typically showed improved seedling-stage traits (nodal root number, dry shoot weight, and root hair length and density) these lines can be used for rainfed rice to direct-seeded planting conditions.

Ashu singh and Sengar (2015) evaluated the genetic divergence of 30 rice varieties (Basmati, Non-Basmati, Aerobic) using 10 ISSR, RAPD markers each. SSR primers RM-263 is highly informative since it recorded high PIC value (0.995). The resolving power varies between 0.132 (RM-256) to 4.662 (RM-222) with an average value of 2.7502. In RAPD analysis PIC values varies from 0.811 (OPD-08) to 0.9925 (OPF-13) with average of 0.9635 and resolving power varies from 1.32 (OPJ-08) to 2.066 (OPJ-13) with average of 1.8256. In ISSR analysis, PIC value ranged from 0.8791 (ISSR6) to 0.9916 (ISSR5) with an average value of 0.9482. The resolving power varies between 1.6 (ISSR3) and 8.366 (ISSR2) with an average value of 5.2708. The PIC values and Resolving power were calculated for individual primers. The analysis indicated that ISSR expressed maximum resolving power of 8.336 and RAPD gave maximum PIC values of 0.9925. RAPD primer OPF-13 gave the maximum accessions coverage (depending on the value of PIC) in the rice genome. Out of 52 amplified bands, 49 bands were polymorphic and 3 bands were monomorphic. The cluster analysis using the marker systems could distinguish the different genotypes.

Mahender *et al.* (2015) studied, early seedling vigour, which is the characteristic of seed quality and describes the rapid, uniform germination and the establishment of strong seedlings in any environmental condition. A rice cultivar with a better seedling vigour, plant height, stem length, root length, leaf area trait are more desirable in case of direct seeding. And for these traits can be characterized by using a markers like RM 528, RM 480, RM 223 and identifying the QTLs in rice cultivars. Marker-assisted selection approach has facilitated efficient and precise transfer of genes/QTLs into many crop species and suggests a speedy and efficient technique over conventional breeding and selection methods.

III. MATERIALS AND METHODS

The present investigation on “Evaluation of Rice Genotypes Suitable for Direct Seeded Condition” was conducted during *Kharif* 2015 at Agricultural Research Station, Gangavati, which is situated in the Northern Dry Zone of Karnataka between 15° -15'40" North latitude and 76° -31'40" East longitude and at an altitude of 419 m above mean sea level. The Agricultural Research Station represents irrigated transplanted rice belt of Tungabhadra command area. The details on genetic material used and statistical methods followed are presented under the following headings.

3.1 Description of the experimental material

The experimental material for the present investigation consisted of an about 40 early maturing (110-125 days to maturity), 40 mid-early maturing (125-135 days to mature) and 36 (> 140 days to mature) medium maturing rice genotypes were used, which are consists of different genotypes includes, land races, hybrids, which were supplied by IRRI- INDIA (Table 1, 2 and 3).

3.2 Method:

Experiment was laid out at Agricultural Research Station (ARS), Gangavati during *Kharif* 2015. All the genotypes were sown separately in each experimental unit having two replications by following Randomized Block Design (RBD). The field experiment was taken up by using dibbling method of direct seed sowing into two replicated blocks of 4m length and 1.6 m width with spacing of 20 x 15 cm.

3.3 Experimental Details:

The fertilizers were applied at the rate of 120 kg N, 40 kg P₂O₅, and 40 kg K₂O per hectare. One third dose of nitrogen and entire dose of P₂O₅ and 1/2 of the K₂O were applied as basal dose. The remaining nitrogen was applied in two equal split doses one at 30 days after sowing (DAS) and another at 60 DAS, remaining 1/2 of the K₂O applied along with last dose of N. The intercultural operations like weeding was done at regular intervals and necessary plant protection measures were adopted during the crop growth period (Table 4).

Table 1. List of Early maturing rice genotypes (110-125 days to maturity)

Table 1. List of Early maturing rice genotypes (110-125 days to maturity)

Sl. No	Entry no	Entry name	Sl. No	Entry no	Entry name
1	101	GNV 14-4	21	121	EC 811547
2	102	MT 4533	22	122	EC 811512
3	103	RYC 339	23	123	IR 14K 10450
4	104	IR 14K 9922	24	124	UPR 3912-21-2-1
5	105	IR 14K 11350	25	125	EC 811543
6	106	EC 811508	26	126	IR 14K 11353
7	107	OR 2521-5	27	127	RYT 3448
8	108	IR 14K 11463	28	128	IR 14K 10214
9	109	IR 13K 5179	29	129	Sahbhagidhan
10	110	IR 14K 11381	30	130	MT 4552
11	111	MT 4060	31	131	EC 811511
12	112	IR 13K 5173	32	132	MT 4534
13	113	IR 14K 10003	33	133	RYT 3443
14	114	MT 4074	34	134	AD 09219
15	115	IR 14K 11485	35	135	MT 4375
16	116	IET-19251	36	136	BPT 2671
17	117	UPR 3906-18-2-1	37	137	IR 14K 10405
18	118	EC 811508	38	138	OR 2567-2
19	119	MT 4252	39	139	IR 14K 11465
20	120	GNV-14-3	40	140	IR13K5177

Table 2. List of mid-early maturing rice genotypes (125 - 135 days to maturity)

Sl. No.	Entry no.	Entry name	Sl. No.	Entry no	Entry name
1	301	MT 4124	21	321	GGV-05-01
2	302	BPT 2570	22	322	NLR 3444
3	303	MT 4039	23	323	MT 4124
4	304	GNV 14-2	24	324	BPT 2613
5	305	IR 14K 9269	25	325	MT 4389
6	306	RYT 3447	26	326	OR 2512-6
7	307	OR 2153-3	27	327	MTU 1081
8	308	MT 4111	28	328	RYC 242
9	309	IR 14K 10485	29	329	IR 14K 9805
10	310	MTU 1010	30	330	IR 14K 10475
11	311	IR 14K 9802	31	331	IR 14K 10197
12	312	IR 13K 5165	32	332	IR 13K 4099
13	313	IR 14K 10147	33	333	BPT 2605
14	314	GNV 14-1	34	334	IR 14K 9762
15	315	UPRI 2013-4	35	335	MT 4393
16	316	UPR 3837-7-2-1-1	36	336	MT 4037
17	317	IR 14K 10158	37	337	RYT 3449
18	318	IR 14K 10174	38	338	IR 14K 10164
19	319	IR 14K 10503	39	339	IR 13K 5168
20	320	MT 4852	40	340	MT 4269

Table 3. List of medium duration maturing rice genotypes (≥ 140 days to maturity)

Sl. No.	Entry no.	Entry name	Sl. No.	Entry no	Entry name
1	501	IR 13K 5129	21	521	IR 14K 10485
2	502	IR 13K 5156	22	522	BPT 5204
3	503	IR 14K 10041	23	523	IR 13K 5121
4	504	RYT 3438	24	524	BPT 5204
5	505	IR 14K 10455	25	525	IR 14K 10045
6	506	IR 14K 10042	26	526	MT 4091
7	507	IR 14K 10236	27	527	IR 14K 10231
8	508	UPR 3926-6-1-1	28	528	IR 14K 10451
9	509	IR 14K 9977	29	529	MT 4316
10	510	UPR 3946-20-1-1	30	530	MTU 1121
11	511	MT 2808	31	531	OR 2542-4
12	512	MTU 3626	32	532	IR 14K 10056
13	513	IR 14K 10452	33	533	IR 14K 10037
14	514	IR 14K 10048	34	534	IR 14K 10530
15	515	OR 2517-5	35	535	IR 14K 10203
16	516	IR 13K 5144	36	536	IR 14K 10477
17	517	NDR 359			
18	518	RYT 3450			
19	519	IR 14K 10115			
20	520	IR 14K 11414			

Table 4. Experimental details of evaluation of rice genotypes.

Total number of rice genotypes	116
No. of rows/plot	8
Plot length	4 m
Width of plot	1.6 m
Replications	2
Spacing	20×15 cm
Net plot size	6.4 sq.mtr.
Date of sowing	First fortnight of August.
Checks	IET-19251, Sahbhagidhan (Early) MTU-1010, GGV-05-01 (Mid early) NDR 359, BPT 5204 (Medium)

3.4 Observations Recorded

The observations were recorded for five plants selected at random per genotype per replication and their means were used for statistical analysis. However, observations were taken for the following characters.

- Field Emergence.
- Plant Height (cm).
- Tiller Number/Plant.
- Reproductive Tiller Number/Plant.
- Days to 50% Flowering.
- Grain Filling Duration (days).
- Number of plants/Square Meter.
- Panicle Length (cm).
- Panicle Weight (g).
- Filled and Unfilled Grains/panicle.
- Test weight (1000 seeds).
- Grain Yield/ Plant.
- Grain Yield/Hectare.

The detailed method of recording of observations is listed below character wise.

3.4.1 Field Emergence

Number of emerging seedling was counted for each genotype per square meter area and the percentage emergence was calculated.

$$\text{Field Emergence (\%)} = \frac{\text{Number of emerging seedlings}}{\text{Number of seeds sown/sq mtr}} \times 100$$

3.4.2 Plant height (cm)

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

3.4.3 Tiller number/plant.

The total number of tillers per plant including both productive and unproductive tillers were counted and recorded in each genotype randomly selected five plants was counted and average it at maturity.

3.4.4 Reproductive tiller number/plant

The number of tillers bearing panicles per plant was recorded by excluding the tillers which do not bear panicles.

3.4.5 Days to 50% flowering

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

3.4.6 Grain filling duration (days)

Record number of days to be taken for grain filling from flowering time.

3.4.7 Number of plants / sq mtr

Take count of number of plants per square meter area of each genotype.

3.4.8 Panicle length(cm)

Length of panicle was measured from the neck of panicle to the tip of the top most spikelet.

3.4.9 Panicle weight

Take weight of five randomly selected panicles from each genotype at maturity and average value is taken into consideration for further calculation.

3.4.10 Filled grains/panicle

Number of filled grains for each panicle was counted for five randomly selected panicles from each genotype and the average was calculated.

3.4.11 Unfilled grains/panicle

Number of unfilled grains per each panicle was counted for five randomly selected panicles from each genotype and the average was calculated.

3.4. 12 Test weight (g)

One thousand well filled grains from each genotype were counted by using a seed counter machine and weighed at optimum seed moisture level.

3.4.13 Grain yield per plant (g)

Weight of grains from the five plants of each genotype was measured in grams and averaged to single plant.

3.4.14 Grain yield (kg/ha)

Grain yield of entire plot except the two border rows were recorded in kg separately and averaged.

3.5 Statistical analysis

3.5.1 Analysis of variance

The analysis of variance for each character was computed as per the standard statistical procedure given by Cochran and Cox (1950) for randomized block design.

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

Where,

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

μ = general mean

b_i = effect of i^{th} block

t_j = effect of j^{th} genotype

e_{ij} = random error associates with i^{th} block and j^{th} genotype.

Table 5. The analysis of variance for each character was carried out as indicated below

Source of variation	df	SS	MSS	F ratio
Replications	r-1	RSS	$Mr = \sigma^2e + \sigma^2r$	Mr/Me
Treatments (Genotypes)	t-1	TrSS	$Mt = \sigma^2e + \sigma^2g$	Mt/Me
Error	(r-1)(t-1)	ESS	$Me = \sigma^2e$	
Total	(rt-1)	TSS		

Where,

r = Number of replications

t = Number of genotypes

df = Degrees of Freedom

SS = Sum of Squares

MSS = Mean Sum of Squares

σ^2e = Error Variance

σ^2g = Variance due to genotypes

σ^2r = Variance due to replications

M r = Mean squares due to replications

M t = Mean squares due to treatments

M e = Mean squares due to error

The test of significance was carried out using 'F' table values given by Fisher and Yates (1963).

3.5.2 Estimation of Genetic Parameters

3.5.2.1 Coefficient of Variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

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

$$GCV = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

As suggested by Shivasubramanian and Menon (1973), GCV and PCV were categorized into

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

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

Heritability in broad sense was estimated as per Allard (1960).

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

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

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

3.5.2.3 Genetic advance as per cent of mean (GAM)

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

$$\text{Genetic Advance (GA)} = K \times \sigma_p \times h^2 (b)$$

Where,

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

$h^2 (b)$ = heritability in broad sense.

σ_p^2 = Phenotypic standard deviation.

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

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%

3.5.2.4 Correlations

Phenotypic and genotypic correlations were worked out by using the formulae suggested by Falconer (1964).

Phenotypic coefficient of correlation (r_p)

$$\text{GAM} = \frac{\text{Cov}(x_i, x_j)p}{\sqrt{V(x_i)p \cdot V(x_j)p}} \times 100$$

Where,

$r (X_i, X_j)p$ = Phenotypic correlation between i^{th} and j^{th} character.

$\text{COV} (X_i, X_j)p$ = Phenotypic covariance between i^{th} and j^{th} character.

$V (X_i)p$ = Phenotypic variance of i^{th} character.

$V (X_j)p$ = Phenotypic variance of j^{th} character.

Genotypic coefficient of correlation (r_g)

$$r(x_i, x_j)_g = \frac{Cov(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(X_i, X_j)_g$ = Genotypic correlation between i^{th} and j^{th} character.

$COV(X_i, X_j)_g$ = Genotypic covariance between i^{th} and j^{th} character.

$V(X_i)_g$ = Genotypic variance of i^{th} character.

$V(X_j)_g$ = Genotypic variance of j^{th} character.

3.5.2.5 Test of significance

Significance of correlation coefficients was tested by comparing phenotypic correlation coefficients with the table values (Fisher and Yates, 1963) at 5% and 1%.

3. 6 Screening of rice genotypes using suitable DNA markers

Fifty one rice genotypes were selected based on their performance and morphological characters under field condition (Table 6) which were subjected to screening and characterization using four different Simple Sequence Repeats (SSR) molecular markers.

3.6.1 DNA extraction

The DNA was extracted from the 51 genotypes by following DNA extraction quick (TPS buffer) method

1. Cut fresh leaf sample around 100mg and put it in 2ml micro centrifuge tube. Put two steel beads in each well
2. Add 400 µl TPS buffer to each tube (100 mM Tris-HCl 100ml (PH8), 10mM EDTA 20ml, 1M KCl 74.55g, make up to 1lit by using a nano pure water)
3. Grind the samples in the Genogrinder
4. Centrifuge the tubes at 3000 rpm for 15min (A)
5. Prepare new 96 well plates (PCR plate) with 80 µl 2 propanol in each well (B)
6. Add supernatant solution of A into B and mix well by using a pipette

7. Centrifuge the plates at 2000 rpm for 20 min

8. Pour supernatant and dry up the tubes

9. Rehydrated with 100 µl of 1x TE buffer

3.6.2. Polymerase chain reaction

1. SSR primers: The decamers were used for the study

2. Template DNA: Crude genomic DNA extracts of different genotypes

3. Emerald AMPTGTPCR master mix (Takara) made in Japan using for PCR cycle

4. Thermocycler - Eppendorf thermal cycler gradient was used for cyclic amplification of DNA

Table 6. List of direct seeded rice genotypes used for screening by using DNA markers

Sl. No.	Genotypes	Sl. No.	Genotypes
1	EC 811512	30	GGV-05-01
2	Sahbhagidhan	31	MT 4393
3	IR 14K 11485	32	IR 14K 9805
4	RYT 3448	33	IR 14K 10503
5	OR 2567-2	34	MTU 1010
6	EC 811511	35	UPR 3837-7-2-1-1
7	IR 13K 5173	36	IR 13K 4099
8	OR 2567-2	37	IR 14K 10455
9	RYC 339	38	UPR 3926-6-1-1
10	AD 09219	39	IR 14K 10048
11	MT 4534	40	IR 14K 10045
12	GNV 14-4	41	IR 13K 5156
13	IET-19251	42	MTU 1121
14	IR 14K 11381	43	IR 14K 10056
15	IR 14K 10214	44	MT 4316
16	IR 14K 11353	45	IR 14K 10115
17	EC 811547	46	IR 14K 11414
18	IR 13K 4099	47	OR 2542-4
19	GNV 14-2	48	IR 14K 10037
20	RYC 242	49	RYT 3450
21	IR 14K 10197	50	BPT 5204
22	MT 4124	51	NDR 359
23	MTU 1081		
24	MT 4269		
25	OR 2153-3		
26	IR 14K 10158		
27	IR 14K 9269		
28	UPRI 2013-4		
29	IR 14K 10174		

Table 7. List of Simple Sequence Repeat (SSR) Markers used for characterization

Sl. No.	Marker Name	Forward Primer (5' – 3')	Reverse Primer (5' - 3')
1	RM13	TCCAACATGGCAAGAGAGAG	GGTGGCATTTCGATTCCAG
2	RM306	CAAGGTCAAGAATGCAATGG	GCCACTTTAATCATTGCATC
3	RM5389	TCTTGCATGAGAGCCAACAC	GCTATTGCGCGAGATTATCC
4	RM161	TGCAGATGAGAAGCGGCGCCTC	TGTGTCATCAGACGGCGCTCCG

3.6.3 Amplification reaction mixture for SSR markers (ICRISAT LAB)

Amplification reaction mixture for SSR markers was prepared in 1.2 mL thin walled PCR tubes containing following components in a total volume of 12 µL.

Sl. No.	Components	Quantity (µl/reaction)
1.	Emerald master mix	6.0
2	Primer (5 pm/µl)	2.0
3	Template (15 ng/µl)	2.0
4	Sterile distilled water	2.0

Except template, the master mix was distributed to PCR tubes (10µl/tube) and later 2µl of template DNA from the respective genotypes was added making the final volume of 12µl.

3.6.4 The PCR amplification profile for SSR marker

	Step	Temperature (oC)	Duration (min.)	Number of cycles
1	Initial denaturation	94	5.00	1
2	Denaturation	94	0.45	35
3	Annealing	55	0.45	
4	Extension	72	0.30	
5	Final extension	72	7.00	1
6	Dump	4	-	-

3.6.5 Separation of amplified products by Agarose Gel

The amplified products from each tube along with 2µl of loading dye (Bromophenol blue) were separated on 4 per cent agarose gel containing syber safe at 90 volts using 1x TAE buffer of pH 8.0. Lambda DNA double digest was used as DNA molecular weight marker. The gel was photographed by using documentation system (Bio Rad).

3.6.6 Scoring the amplified fragments

The amplified fragments were scored as '1' for presence of single band, and '0' for the absence of a band generating the 0 and 1 matrix and per cent polymorphism was calculated by using the following formula.

$$\text{Per cent polymorphism} = \frac{\text{Number of polymorphic bands}}{\text{Total number of bands}} \times 100$$

IV. EXPERIMENTAL RESULTS

The present study was conducted to estimate nature and magnitude of genetic variation with respect to different morphological traits in different maturity groups viz early, mid-early and medium maturing direct seeded rice genotypes. The results obtained are presented under the following broad headings:

1. Assessment of differential performance of rice genotypes for direct seeded condition.
2. Association study among different traits relevant to direct seeded rice along with yield.
3. Genetic diversity analysis of rice genotypes using suitable DNA markers.

4.1 Analysis of variance

The analysis of variance for different characters is presented in Table 8, 9 and 10. The treatments *i.e.* mean sum of squares due to genotypes showed significant differences for all characters under study at 1% level of significance and some traits like days to 50% flowering, grain filling duration in early maturing rice genotypes whereas in mid early maturing rice genotypes for the traits like tiller number/plant, days to 50% flowering, grain filling duration and grain yield per plant and in case of medium maturing genotypes days to 50% flowering, grain yield per plant showed significance at 5% level, suggesting that genotypes were genetically diverse for majority of the characters in all the three viz early, mid early and medium maturing genotypes.

According to the mean performance (appendix 1, 2 and 3) a wide range of variation was found for most of characters. Through this study an attempt was made to assess the mean performance and extent of variability in direct seeded rice genotypes which depicts the mean performance of 40 early, 40 mid early, 36 medium duration rice genotypes, for 14 quantitative characters along with the coefficient of variation. This is elaborated individually here as under.

4.2 Assessment of differential performance of rice genotypes for direct seeded condition

4.2.1 In early maturing direct seeded rice genotypes

The results of the study are presented in table 11.

Table 8. Analysis of variance (ANOVA) for different yield and yield related characters in early maturing rice genotypes.

Source of variance	Mean Sum of Squares														
	df	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
Genotypes	39	54.23**	119.24**	8.26**	7.77**	14.90*	5.08*	17.02**	4.03**	0.49**	1152.35**	32.05**	11.03**	7.11**	2230205**
Error	39	9.92	15.34	0.57	0.43	7.50	2.20	1.73	1.17	0.02	28.78	0.10	2.89	1.67	144409
CV		3.69	4.29	6.27	5.78	3.24	4.96	4.39	5.08	5.25	4.59	3.98	7.20	6.98	6.78

** and * indicates Significance at 1 and 5% level respectively

X1: Field emergence

X2: Plant Height (cm)

X3: Tiller number/plant

X4: Reproductive tiller number /plant

X5: Days to 50% flowering

X6: Grain Filling Duration

X7: Plants/square meter

X8: Panicle Length (cm)

X9: Panicle Weight (g)

X10: Filled Grains/panicle

X11: Unfilled Grains /panicle

X12: Test Weight (g)

X13: Yield/plant (g)

X14: Yield/hectare (Kg)

Table 9. Analysis of variance (ANOVA) for different yield and yield related characters in mid- early maturing rice genotypes

Source of variance	Mean Sum of Squares														
	df	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
Genotypes	39	318.36**	237.34**	6.86*	6.16**	34.12*	4.36*	15.17**	5.39**	0.82**	1441.54**	116.47**	17.35**	4.97*	1596417**
Error	39	10.85	30.09	2.76	1.33	16.46	1.54	2.53	1.82	0.08	3.96	3.20	3.29	2.70	150852
CV		4.64	5.68	12.60	9.61	4.59	4.02	6.16	5.9	8.38	4.22	11.72	8.02	7.43	6.81

** and * indicates Significance at 1 and 5% level

X1: Field emergence

X2: Plant Height (cm)

X3: Tiller number/plant

X4: Reproductive tiller number /plant

X5: Days to 50% flowering

X6: Grain Filling Duration

X7: Plants/square meter

X8: Panicle Length (cm)

X9: Panicle Weight (g)

X10: Filled Grains/panicle

X11: Unfilled Grains /panicle

X12: Test Weight (g)

X13: Yield/plant (g)

X14: Yield/hectare (Kg)

Table 10. Analysis of variance (ANOVA) for different yield and yield related characters in medium maturing rice genotypes

Source of variance	Mean Sum of Squares														
	df	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14
Genotypes	35	606.94**	287.94**	8.39**	8.82**	42.71*	5.22**	33.76**	4.86*	1.02**	1659.05**	39.10**	16.01**	1.65*	890713.00**
Error	35	7.57	21.51	0.60	0.60	24.85	0.69	4.64	2.14	0.02	52.08	0.73	3.38	0.86	229781
CV		4.28	5.02	5.33	5.74	5.54	2.63	8.02	6.70	5.01	5.49	8.69	7.64	4.71	9.12

** and * indicates Significance at 1 and 5% level

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

Table 11. Estimates of mean, range and other genetic parameters for different yield and yield attributing characters in early maturing rice genotypes

Sl. No	Character	Mean	Range		Variances		Coefficient of variation (%)		h ² bs (%)	GA	GAM (%)
			Min.	Max.	Phenotypic	Genotypic	PCV	GCV			
1	Field emergence	85.34	72.45	93.95	32.07	22.15	6.63	5.51	69	8.05	9.44
2	Plant height (cm)	91.28	77.70	110.30	67.29	51.94	8.98	7.89	77	13.04	14.29
3	Number of tillers/plant	12.06	9.00	18.70	4.41	3.84	17.42	16.25	87	3.76	31.23
4	Number of reproductive tillers/plant	11.35	8.50	18.15	4.10	3.67	17.84	16.88	89	3.73	32.89
5	Days to 50% flowering	84.38	78.00	89.50	11.20	3.70	3.96	2.27	33	2.27	2.69
6	Grain filling duration(days)	29.88	27.00	33.50	3.64	1.44	6.38	4.01	39	1.55	5.20
7	Number of Plants /square meter	29.97	22.00	34.50	9.38	7.64	10.21	9.22	81	5.14	17.14
8	Panicle length(cm)	21.34	19.10	25.20	2.60	1.43	7.56	5.60	54	1.82	8.55
9	Panicle weight (g)	2.89	1.60	3.94	0.25	0.23	17.53	16.72	91	0.94	32.86
10	Number of filled grains	116.72	59.30	170.50	590.56	561.77	20.81	20.30	95	47.62	40.79
11	Number of unfilled grains	8.21	2.80	22.90	16.08	15.97	48.84	48.68	99	8.20	99.95
12	1000 grain weight (g)	23.64	16.60	30.96	6.96	4.06	11.16	8.53	58	3.17	13.42
13	Grain yield / plant (g)	18.54	15.62	22.20	4.39	2.71	11.30	8.88	61	2.66	14.39
14	Grain yield / hectare (kg)	5602	3430	7445	1187307.00	1042897.97	19.45	18.23	87	1.63	35.19

PCV: Phenotypic coefficient of variation,
GAM: Genetic advance as per cent of mean,

GCV: Genotypic coefficient of variation,
h² bs: Heritability (Broad sense)

GA: Genetic advance,

4.2.1.1 Field emergence

The mean value of field emergence was 85.34 with a range from 72.45 to 93.95. The genotype IR 14K 11485 was performed better among all the genotypes (93.95), while, IR 14K 11353 recorded low field emergence (72.45). The Phenotypic and genotypic variances were estimated to be 32.07 and 22.15 respectively, while the coefficients of variability at phenotypic and genotypic levels were low and were estimated to be 6.63 and 5.51 respectively. Heritability was recorded (69 percent) high and GA as per cent of mean recorded (9.44) was low.

4.2.1.2 Plant height (cm)

Plant height exhibited a wide range of values from 77.70 cm (AD 09219) to 110.30 cm (IR 14K 11485) with a mean value of 91.28 cm. Phenotypic variance of 67.29 and genotypic variance of 51.94 were recorded. Phenotypic and genotypic coefficients of variability were low and estimated to be 8.98 and 7.89 respectively. Heritability (77 percent) was high and genetic advance as per cent mean (14.29 %) was moderate.

4.2.1.3 Number of tillers per plant

The data revealed that the number of tillers per plant ranged from 9.00 to 18.70 with the mean value of 12.06, the more number of tillers were recorded in IR14K11485 (18.70). The minimum numbers of tillers were recorded in IR14K11353 (9.00). Phenotypic and genotypic variances were estimated to be 4.14 and 3.84 respectively. The moderate PCV and GCV were recorded to be 17.42 and 16.25 respectively. Heritability (87 percent) and genetic advance as per cent of mean (31.23) were high.

4.2.1.4 Number of reproductive tillers per plant

The mean value recorded for number of reproductive tillers per plant was 11.35 with a range from 8.50 to 18.15. Highest number of reproductive tillers/plant was recorded in IR 14K 11485 (18.15) while, AD 09219 recorded lowest value for number of productive tillers/plant (8.50). The Phenotypic and genotypic variances were estimated to be 4.10 and 3.67 respectively. The moderate PCV and GCV were recorded to be 17.84 and 16.88 percent respectively. Heritability (89 percent) and genetic advance (32.89) were high.

4.2.1.5 Days to 50 per cent flowering

The mean value for days to 50 per cent flowering was 84.38 with a range from 78.00 to 89.50 days. The genotype IET-19251 was recorded as earliest to flower (78 days) while, IR 14K 10405 took as many as (89.50) days to flower. The Phenotypic and genotypic variances were estimated to be 11.20 and 3.70 respectively. The low PCV and GCV were recorded to be 3.96 and 2.27 percent respectively. Heritability (33 percent) was moderate and GAM (2.69) was low for this trait.

4.2.1.6 Grain filling duration (days)

The mean value of days to grain filling duration was 29.88 with a range from 27.00 to 33.50 days. The genotype AD 09219 was recorded as less as (27 days) to require to grain filling while, IR 14K11485 took as many as (33.50 days) to grain filling. The Phenotypic and genotypic variances were estimated to be 3.64 and 1.44 respectively. The low PCV and GCV were recorded to be 6.38 and 4.01 percent respectively. Heritability (39 percent) was moderate and genetic advance as per cent mean (5.20) was low.

4.2.1.7 Number of plants per square meter

The mean value for number of plants per square meter was 29.97 with a range from 22.00 to 34.50. Highest number of plants per square meter was recorded in IR14K9922 (34.50) genotype while, AD09219 genotype recorded lowest value for number of plants per square meter (22). The Phenotypic and genotypic variances were estimated to be 9.38 and 7.64 respectively. The low PCV and GCV were recorded to be 10.21 and 9.22 percent respectively. Heritability (81 percent) was high and GAM (17.14 %) was moderate for this trait.

4.2.1.8 Panicle length (cm)

The experimental data on panicle length revealed that this character ranged from 19.10 cm to 25.20 cm with the mean of 21.34 cm. The longest panicle length was observed in genotype GNV 14-3 (25.20) and shortest panicle length was observed in genotype IR14K11353 (19.10). The phenotypic variance of 2.60 and genotypic variance of 1.43 were recorded. Phenotypic and genotypic coefficients of variability were low and estimated to be 7.56 and 5.60 respectively and moderate heritability value of (54 percent) and low genetic advance value of (8.55%) as per cent mean.

4.2.1.9 Panicle weight (g)

The character panicle weight was ranged from 1.60 g to 3.94 g with the mean of 2.89 g. The maximum panicle weight was recorded in IR 14K 11485 (3.94). The lowest panicle weight was recorded in AD 09219 (1.60). The phenotypic and genotypic variances observed were 0.25 and 0.23 respectively. Phenotypic coefficient of variation (17.53) and genotypic coefficients of variation (16.72) were moderate. Heritability (91 percent) and genetic advance as per cent mean (32.86) were high.

4.2.1.10 Number of filled grains per panicle

The number of filled grains per panicle was counted and varied from 59.30 to 170.50 with mean performance of 116.72. The genotype IR14K11485 (170.50) had highest number of filled grains per panicle, while the lowest number of filled grains recorded in AD09219 (59.30). Large variance was obtained for this character. The values of phenotypic and genotypic variances were very high and found to be 590.56 and 561.77 respectively. The PCV (20.81) and GCV (20.30) were high. Heritability (95 percent) and genetic advance as percent mean (40.79) were high.

4.2.1.11 Number of unfilled grains per panicle

The number of unfilled grains per panicle varied from 2.80 to 22.90 with mean performance of 8.21. The genotype AD 09219 (22.90) had highest number of unfilled grains per panicle, while the lowest number of unfilled grains recorded in IR14K11350 (2.80). The values of phenotypic and genotypic variances were estimated to be 16.08 and 15.97 respectively. The PCV (48.84) and GCV (48.68) were high. Heritability (99 percent) and genetic advance as percent mean (99.95) were high.

4.2.1.12 Test weight (g)

Range of variation with respect to test weight was recorded from 16.60 to 30.96 with a mean value of 23.64. The minimum test weight was recorded in IR14K11353 (16.60) and maximum test weight in IR14K11485 (30.96). The Phenotypic and genotypic variances were estimated to be 6.96 and 4.04 respectively. The moderate PCV and low GCV were recorded to be 11.16 and 8.53 percent respectively. Heritability (58 percent) and genetic advance as per cent mean (13.42) were moderate.

4.2.1.13 Grain yield per plant (g)

The grain yield per plant ranged from 15.62 g to 22.20 g with a mean value of 18.54g. The highest grain yield per plant was recorded in IR 14K 11350 (22.20 g) and lowest grain yield per plant was recorded in EC 811508 (15.62 g). The Phenotypic and genotypic variances were estimated to be 4.39 and 2.71 respectively. The moderate PCV and low GCV were recorded to be 11.30 and 8.88 percent respectively. Heritability (61 percent) was high and genetic advance as per cent mean (14.39) was moderate.

4.2.1.14 Grain yield per hectare (kg)

The grain yield varied from 3430 Kg/ha to 7445 Kg/ha with the mean performance of 5602 Kg/ha. The maximum grain yield was recorded in IR 14K 11485 (7445 Kg), while low grain yield was recorded by the genotype AD09219 (3430 Kg). The phenotypic and genotypic variances observed for this trait were 1187307.00 and 1042897.97 respectively, while the coefficients of variability at phenotypic and genotypic levels were moderate and were estimated to be 19.45 and 18.23 respectively. Heritability (87 percent) and genetic advance as per cent mean (35.19) were high.

Early maturing rice genotypes with superior performance presented in (Plate1), while the PCV, GCV, h^2 , and Genetic advance for these traits were presented graphically in (Fig. 1 and 2). The top ten genotypes with high grain yield/hectare and character wise better performing genotypes is given in Fig. 3 and 4.



Entry Name: IR 14K 11350

Grain Yield: 7333kg/ha, 56.74% superior over check Sahbhagidhan



Entry Name: IR 14K 9922

Grain Yield: 7258kg/ha.54.38% superior over check Sahbhagidhan

Plate 1. Early maturing rice genotypes with superior performance

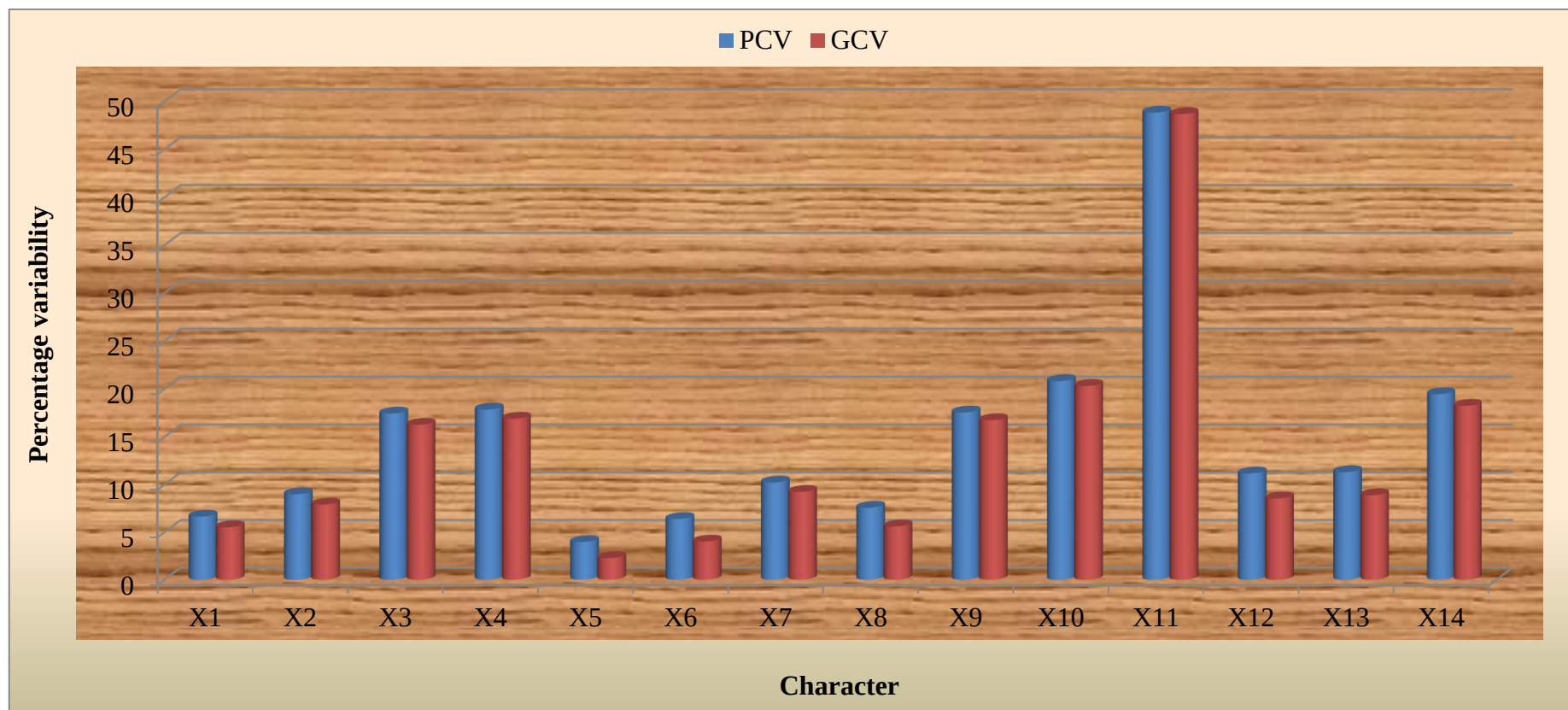


Fig 1. Phenotypic and genotypic coefficient of variability for plant and yield attributing characters in early maturing rice genotypes

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

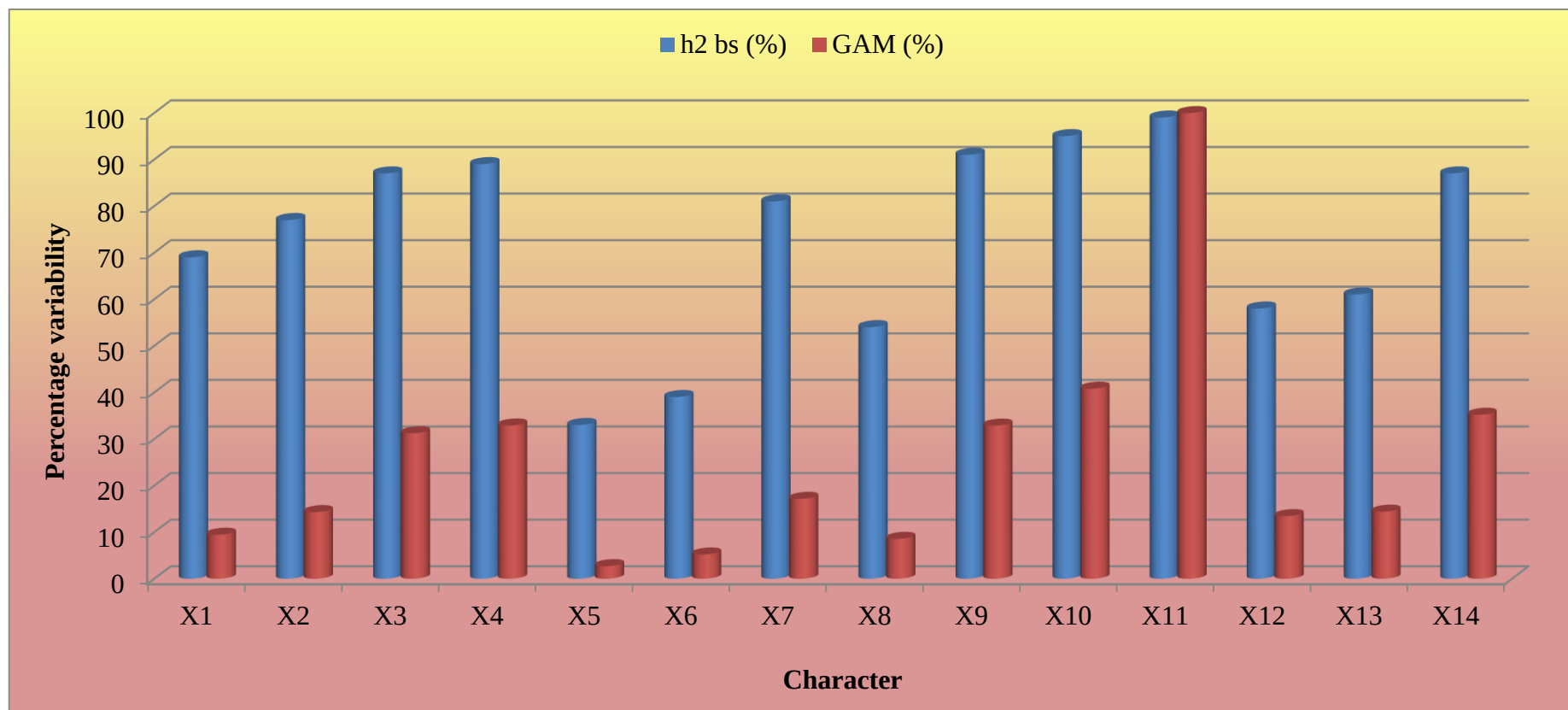


Fig 2. Heritability and genetic advance for plant and yield attributing characters in early maturing rice genotypes.

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

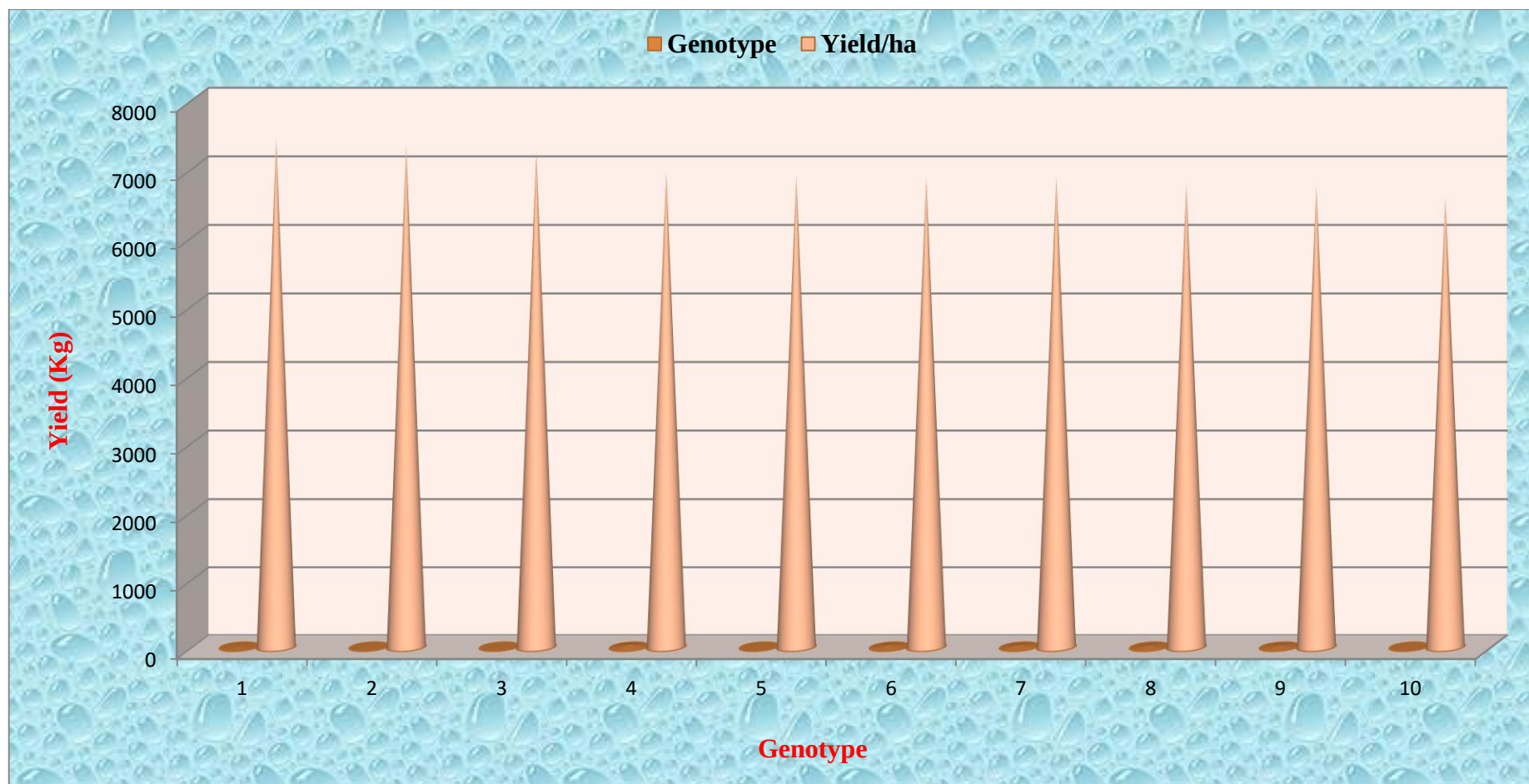
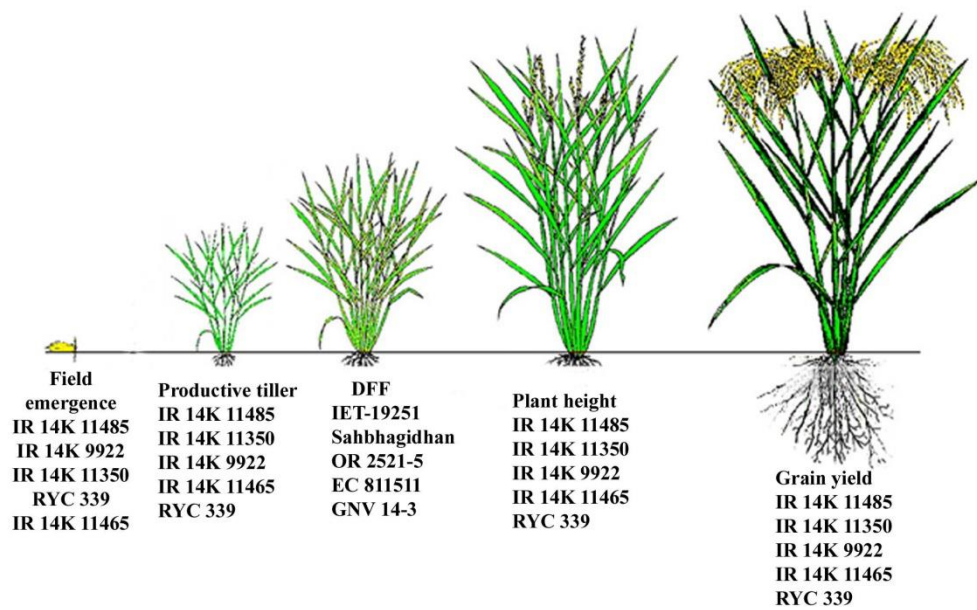


Fig 3. Top ten rice genotypes having high grain yield per hectare in early maturing direct seeded rice genotypes.

- | | | | | |
|-----------------|-----------------|----------------|-----------------|--------------|
| 1. IR 14K 11485 | 2. IR 14K 11350 | 3. IR 14K 9922 | 4. IR 14K 11465 | 5. RYC 339 |
| 6. MT 4534 | 7. RYT 3443 | 8. EC 811543 | 9. IR 14K 10214 | 10. GNV 14-4 |



Test weight
IR 14K 11485
IR 14K 11350
IR 14K 9922
IR 14K 11465
RYC 339



Filled grains / panicle	Panicle length
IR 14K 11485	GNV 14-3
IR 14K 11350	EC 811508
IR 14K 9922	BPT 2671
IR 14K 11465	OR 2521-5
RYC 339	IR 14K 10405

Fig 4: Trait wise superior performing early maturing direct seeded rice genotypes

4.2.2 In mid early maturing direct seeded rice genotypes.

The results of the study are presented in table 12.

4.2.2.1 Field emergence

The mean value of field emergence was 70.93 with a range from 42.21 to 92.68. The genotype IR 14K 10158 performed best among all the genotypes (92.68), while, RYT 3449 recorded low value for field emergence (42.21). The Phenotypic and genotypic variances were estimated to be 164.61 and 153.75 respectively, while the coefficients of variability at phenotypic and genotypic levels were low and estimated to be 18.08 and 17.47 respectively. Heritability (93 percent) and GA as per cent mean (34.79) were high.

4.2.2.2 Plant height (cm)

Plant height exhibited a wide range of values from 80.50 cm (RYT 3449) to 119.00 (IR 14K 10158) cm with a mean value of 96.53 cm. Phenotypic variance of 133.71 and genotypic variance of 103.62 were recorded. Phenotypic and genotypic coefficients of variability were moderate and estimated to be 11.97 and 10.54 respectively. High heritability value of (77 percent) per cent and moderate genetic advance value of (19.12) as per cent of mean.

4.2.2.3 Number of tillers per plant

The data revealed that the number of tillers per plant ranged from 8.95 to 18.20 with the mean value of 13.19. More number of tillers were recorded in IR 14K 10158 (18.20). The minimum numbers of tillers were recorded in RYT 3449 (8.95). Phenotypic and genotypic variances were estimated to be 4.81 and 2.04 respectively. The moderate PCV and GCV were recorded to be 16.63 and 10.84 respectively. Heritability (42 percent) was moderate and genetic advance as per cent of mean was (14.57) was moderate for this trait.

4.2.2.4 Number of reproductive tillers per plant

The mean value recorded for number of reproductive tillers per plant was 12.01 with a range from 8.35 to 17.40. Highest number of reproductive tillers/plant was recorded in IR 14K 10158 (17.40) while, RYT 3449(8.35) recorded lowest number of reproductive tillers/plant. The Phenotypic and genotypic variances were estimated to be

Table 12. Estimates of mean, range and other genetic parameters for different yield and yield characters in mid early duration maturing rice genotypes

Sl. No.	Character	Mean	Range		Variances		Coefficient of variation (%)		h ² bs (%)	GA	GAM (%)
			Min.	Max.	Phenotypic	Genotypic	PCV	GCV			
1	Field emergence	70.93	42.21	92.68	164.61	153.75	18.08	17.47	93	24.68	34.79
2	Plant height (cm)	96.53	80.50	119.00	133.71	103.62	11.97	10.54	77	18.46	19.12
3	Number of tillers/plant	13.19	8.95	18.20	4.81	2.04	16.63	10.84	42	1.92	14.57
4	Number of reproductive tillers/plant	12.01	8.35	17.40	3.74	2.41	16.12	12.93	64	2.56	21.38
5	Days to 50% flowering	88.28	81.00	100.00	25.29	8.83	5.64	3.36	34	3.61	4.09
6	Grain filling duration (days)	30.83	28.50	35.00	2.95	1.41	5.57	3.85	47	1.69	5.48
7	Number of Plants /square meter	25.80	19.50	31.00	8.85	6.32	11.53	9.74	71	4.37	16.96
8	Panicle length(cm)	22.64	18.95	24.75	3.61	1.78	8.39	5.89	49	1.93	8.54
9	Panicle weight (g)	3.42	2.23	4.93	0.45	0.36	19.63	17.75	81	1.13	33.07
10	Number of filled grains	139.96	88.80	190.50	738.24	703.28	19.41	18.94	95	53.32	38.09
11	Number of unfilled grains	15.28	5.10	33.20	59.84	56.63	50.62	49.25	94	15.08	98.70
12	1000 grain weight (g)	22.62	15.30	26.90	10.32	7.02	14.20	11.71	68	4.50	19.91
13	Grain yield / plant (g)	22.10	19.55	25.68	3.83	1.13	8.85	4.82	29	1.19	5.40
14	Grain yield / hectare (kg)	5703	4297	7352	873635	722782	16.38	14.90	82	1.98	27.93

PCV: Phenotypic coefficient of variation,
GAM: Genetic advance as per cent of mean,

GCV: Genotypic coefficient of variation,
h² bs: Heritability (Broad sense)

GA: Genetic advance,

3.74 and 2.41 respectively. The moderate PCV and GCV were recorded to be 16.12 and 12.93 respectively. Heritability (64 percent) and GAM (21.38) were high for this trait.

4.2.2.5 Days to 50 per cent flowering

The mean value for days to 50 per cent flowering was 88.28 with a range from 81.00 to 100 days. The genotype MT 4037 were recorded as earliest to flower (81 days) while, GNV 14-2 took as many as (100 days) to flower. The Phenotypic and genotypic variances were estimated to be 25.29 and 8.83 respectively. The low PCV and GCV were recorded to be 5.64 and 3.36 percent respectively. Heritability (34 percent) was moderate and low GAM (4.09) for this trait.

4.2.2.6 Grain filling duration (days)

The mean value of days to grain filling duration was 30.83 with a range from 28.50 to 35.00 days. The line NLR 3444 was earliest for grain filling (28.50 days) while, IR 13K 5144 took as many as (35 days) to grain filling. The Phenotypic and genotypic variances were estimated to be 2.95 and 1.41 respectively. The low PCV and GCV were recorded to be 5.57 and 3.85 percent respectively. Moderate heritability value of (47 percent) and coupled with low GAM (5.48) for this trait.

4.2.2.7 Number of plants per square meter

The mean value for number of plants per square meter was 25.80 with a range from 19.50 to 31.00. Highest number of plants per square meter was recorded in MT 4111 (31) while, BPT 2570 genotype recorded lowest number of plants per square meter (19.50). The Phenotypic and genotypic variances were estimated to be 8.85 and 6.32 respectively. The moderate PCV and low GCV were recorded to be 11.53 and 9.74 percent respectively. Heritability (71 percent) was high and coupled with moderate GAM (16.96) for this trait.

4.2.2.8 Panicle length (cm)

The experimental data on panicle length revealed that this character ranged from 18.95 cm to 24.75 cm with the mean of 22.64cm. The longest panicle length was observed in genotype MT 4111(24.75) and shortest panicle length was observed in genotype RYT3449 (18.95).The phenotypic variance of 3.61 and genotypic variance of

1.78 were recorded. Phenotypic and genotypic coefficients of variability were low and estimated to be 8.39 and 5.89 respectively. Moderate heritability value of (49 percent) and low genetic advance as per cent of mean (8.54) was recorded for this character.

4.2.2.9 Panicle weight (g)

The character panicle weight was ranged from 2.23g to 4.93g with the mean of 3.42g. The maximum panicle weight was reported in the genotype IR 14K 10158 (4.93g). The lowest panicle weight was recorded in the genotype RYT 3449(2.23g). The phenotypic and genotypic variances observed were 0.45 and 0.36 respectively. Phenotypic coefficient of variation (19.63) and genotypic coefficients of variation (17.75) were moderate. Heritability (81 percent) and genetic advance as per cent mean (33.07) were high.

4.2.2.10 Number of filled grains per panicle

The number of filled grains per panicle was counted and varied from 88.80 to 190.50 with mean performance of 139.96. The genotype IR14K10158 (190.50) had highest number of filled grains per panicle, while the lowest number of filled grains recorded in RYT 3449 (88.80). Large variation was observed for this character. The values of phenotypic and genotypic variances were very high and found to be 738.24 and 703.28 respectively. The PCV (19.41) and GCV (18.94) were moderate. Heritability (95 percent) and genetic advance as percent of mean (38.09) were high.

4.2.2.11 Number of unfilled grains per panicle

The number of unfilled grains per panicle was counted and varied from 5.10 to 33.20 with mean performance of 15.28. The genotype RYT 3449 (33.20) had highest number of unfilled grains per panicle, while the lowest number of unfilled grains recorded in IR14K10158 (5.10). The values of phenotypic and genotypic variances were estimated to be 59.84 and 56.63 respectively. The PCV (50.62) and GCV (49.25) were high. Heritability (94 percent) and genetic advance as percent of mean (98.70) were high.

4.2.2.12 Test weight (g)

The variation with respect to test weight was recorded with range from 15.30 to 26.90 with a mean value of 22.62. The minimum test weight was recorded in RYT 3449 (15.30g) and maximum test weight in BPT 2613 (26.90g). The Phenotypic and genotypic

variances were estimated to be 10.32 and 7.02 respectively. The moderate PCV and GCV were recorded to be 14.20 and 11.71 percent respectively. Heritability (68 percent) was high and GAM (19.91) was moderate for this trait.

4.2.2.13 Grain yield per plant (g)

The grain yield per plant ranged from 19.55g to 25.68g with a mean value of 22.10g. The highest grain yield per plant was recorded in IR 14K 9269(25.68g) and lowest grain yield per plant was recorded in IR 14K 9805(19.55g). The Phenotypic and genotypic variances were estimated to be 3.83 and 1.13 respectively. The low PCV and GCV were recorded to be 8.85 and 4.82 percent respectively. Heritability (29 percent) was low and coupled with low GAM (5.40) for this trait.

4.2. 2.14 Grain yield per hectare (kg)

The grain yield varied from 4297 kg/ha to 7352 kg/ha with the mean performance of 5703 kg/ha the maximum grain yield recorded in IR14K10158 (7352 kg). The low grain yield was recorded by the RYT3449 (4297 kg). The phenotypic and genotypic variances observed for this trait were 873635.00 and 722782.00 respectively, while the coefficients of variability at phenotypic and genotypic levels were moderate and estimated to be 16.38 and 14.90 respectively. Heritability (82 percent) and GA as per cent of mean observed (27.93) were high.

Mid early maturing rice genotypes with superior performance presented in (Plate2), while the PCV, GCV, h^2 , and Genetic advance for these traits were presented graphically in (Fig. 5 and 6). The top ten genotypes with high grain yield/hectare and character wise better performing genotypes is given in (Fig. 7 and 8).



Entry Name: IR 14K 10158

Grain Yield: 7352kg/ha. 21.73% over the check MTU-1010



Entry Name: GNV 14-2

Grain yield: 6922kg/ha. 14.62% over check MTU-1010

Plate 2. Mid early maturing rice genotypes with superior performance

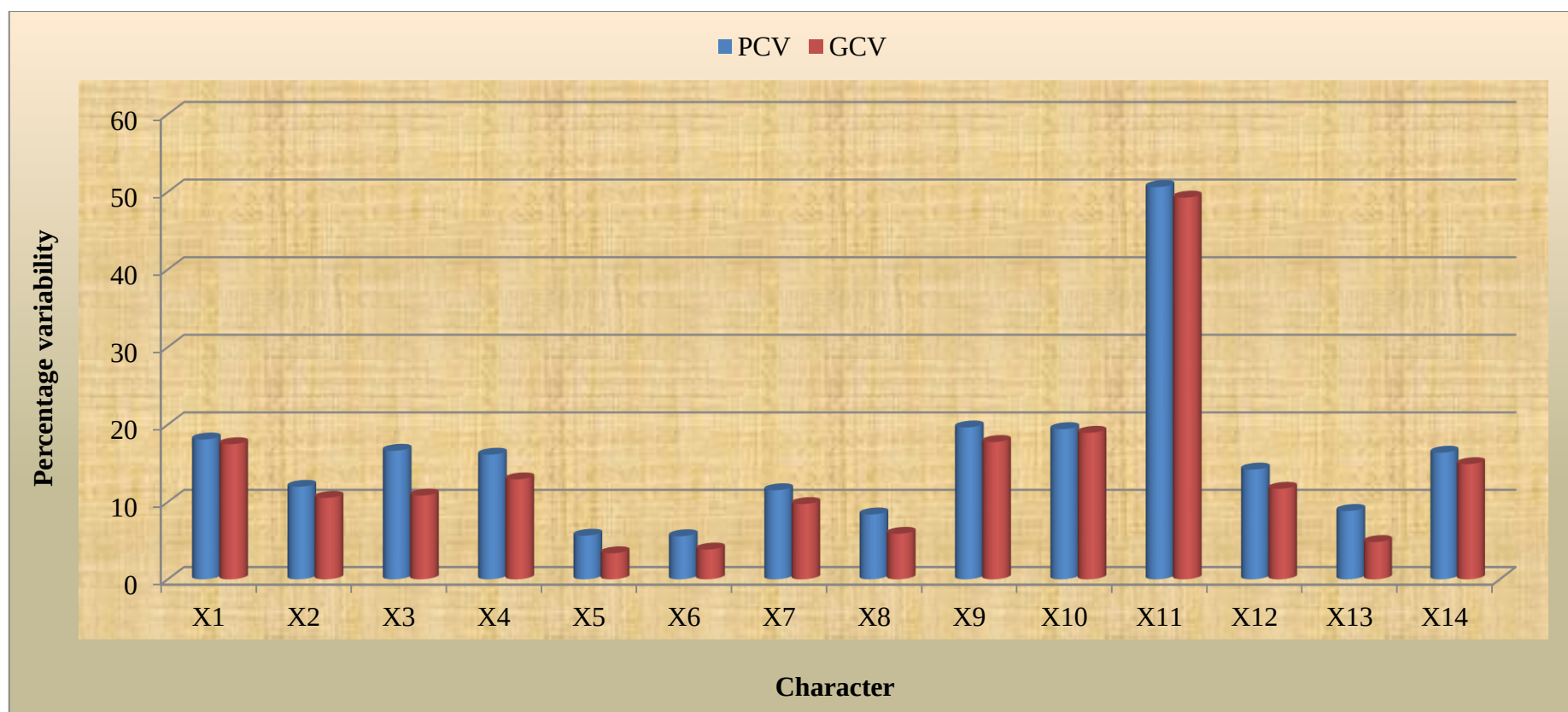


Fig 5. Phenotypic and genotypic coefficient of variability for plant and yield attributing characters in mid early maturing rice genotypes

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

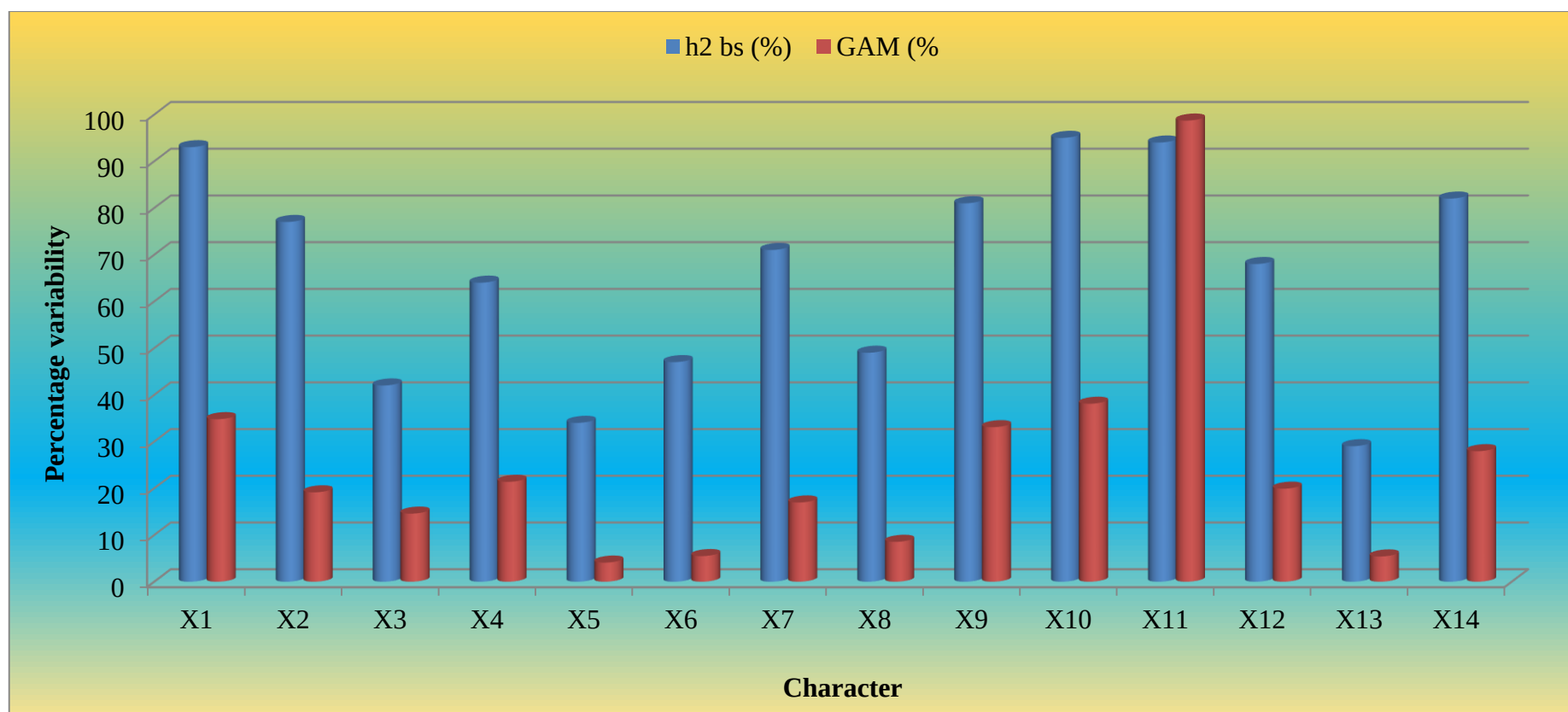


Fig 6. Heritability and genetic advance for plant and yield attributing characters in mid early maturing rice genotypes

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

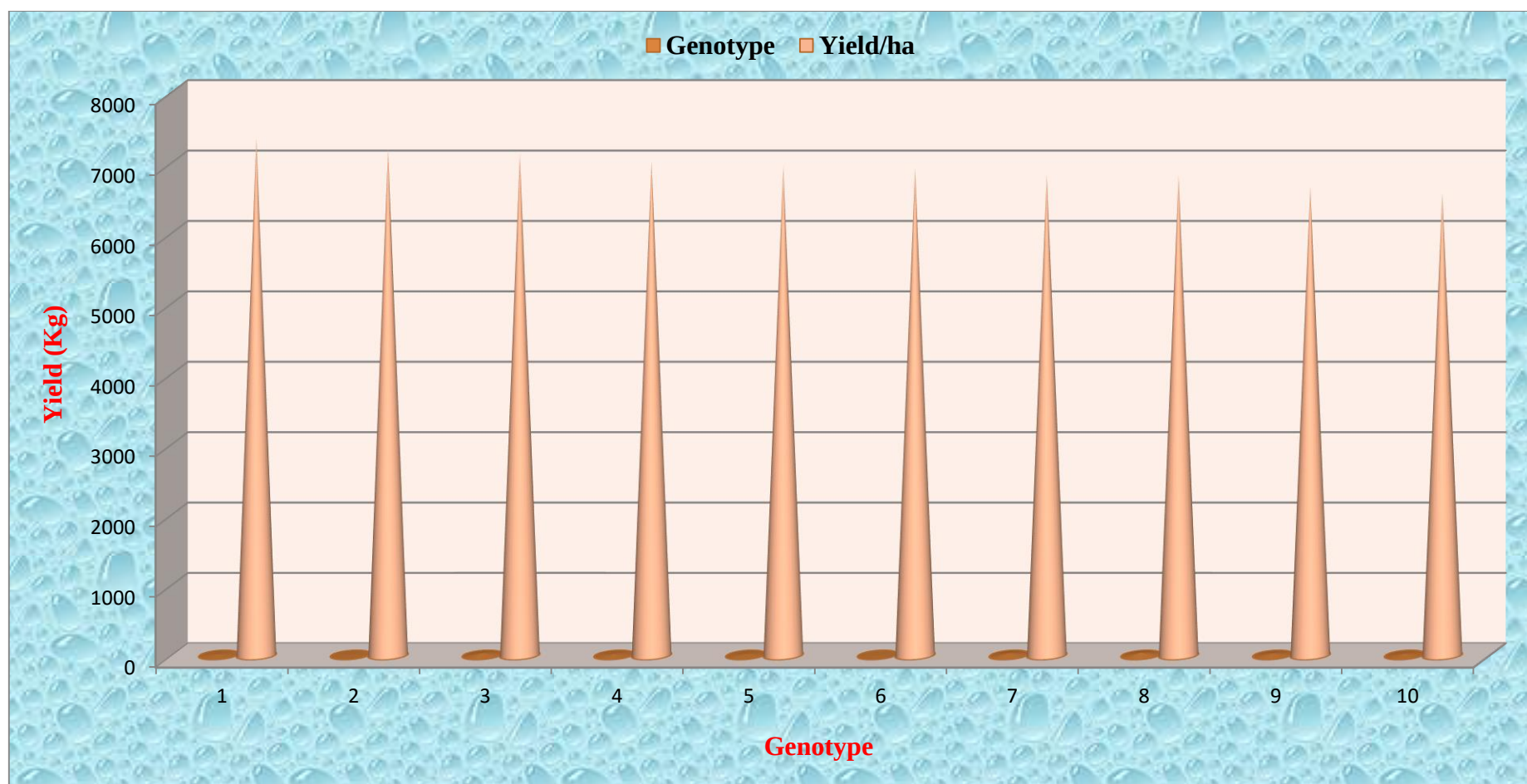
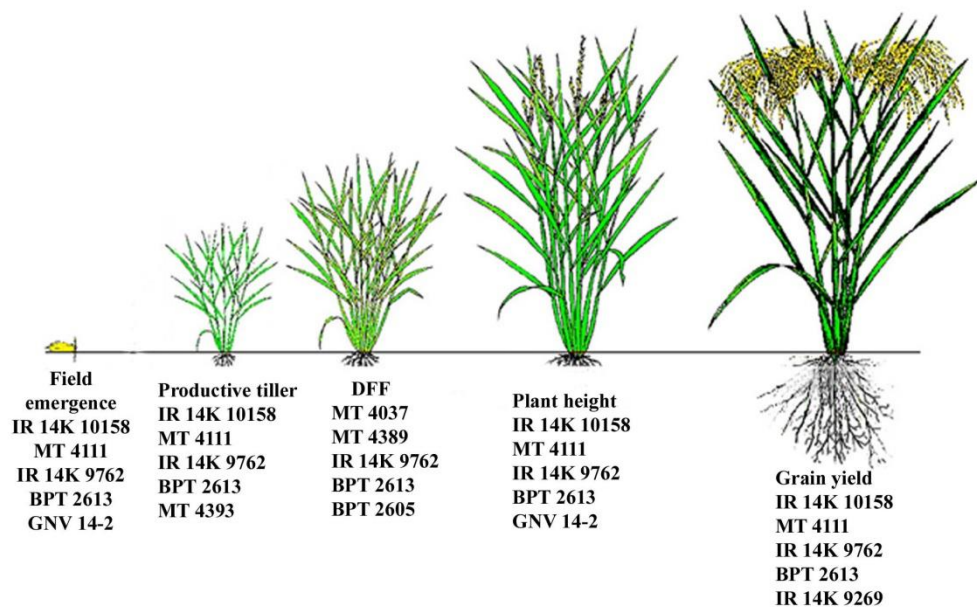


Fig 7. Top ten rice genotypes having high grain yield per hectare in mid early maturing direct seeded rice genotypes

- | | | | | |
|-----------------|------------|----------------|---------------|--------------|
| 1. IR 14K 10158 | 2. GNV14-2 | 3. IR 14K 9762 | 4. BPT 2613 | 5. GGV-05-01 |
| 6. MT 4111 | 7. MT4393 | 8. MT4269 | 9. IR14K10197 | 10. MT4389 |



Test weight
BPT 2613
MT 4111
IR 14K 9762
IR 14K 10158
GGV -05-01



Filled grains / panicle	Panicle length
IR 14K 10158	IR 14K 10158
MT 4111	IR 14K 9762
IR 14K 9762	MT 4111
BPT 2613	GNV 14-2
GGV-05-01	GGV-05-01

Fig 8: Trait wise superior performing mid early maturing direct seeded rice genotypes

4.2.3 In medium maturing direct seeded rice genotypes

The results of the study are presented in table 13

4.2.3.1 Field emergence

The mean value of field emergence was 64.31 with a range from 31.20 to 91.99. The genotype UPR 3926-6-1-1 was performed best among all the genotypes (91.99), while, IR13K 5144 was recorded as low field emergence (31.20). The Phenotypic and genotypic variances were estimated to be 307.26 and 299.68 respectively, while the coefficients of variability at phenotypic and genotypic levels were high and estimated to be 27.25 and 26.91 respectively. Heritability (97 percent) and GA as per cent of mean (54.76) were high.

4.2.3.2 Plant height (cm)

Plant height exhibited a wide range of values from 67.30 cm (IR 13K 5144) to 118.10 cm (IR 14K 10477) with a mean value of 92.36 cm. Phenotypic variance of 154.73 and genotypic variance of 133.21 were recorded. Phenotypic and genotypic coefficients of variability were moderate and estimated to be 13.46 and 12.49 respectively. High heritability value of (80 percent) and moderate genetic advance as per cent of mean was (23.88).

4.2.3.3 Number of tillers per plant

The data revealed that the number of tillers per plant ranged from 10.50 to 18.60 with the mean value of 14.57, the more number of tillers were recorded in IR 14K 10485 (18.60). The minimum numbers of tillers were recorded in UPR 3946-20-1-1 (10.50). Phenotypic and genotypic variances were estimated to be 4.49 and 3.89 respectively. The moderate PCV and GCV were recorded to be 14.54 and 13.53 respectively. Heritability (86 percent) and genetic advance as per cent of mean (25.94) were high for this trait.

4.2.3.4 Number of reproductive tillers per plant

The mean value recorded for number of reproductive tillers per plant was 13.62 with a range from 9.85 to 17.40. Highest number of reproductive tillers/plant was recorded in IR 14K 10485 (17.40) while, UPR 3946-20-1-1 (9.85) recorded lowest number of productive tillers/plant (9.85). The Phenotypic and genotypic variances were estimated to be 4.71 and 4.11 respectively. The moderate PCV and GCV were recorded to

Table 13. Estimates of mean, range and other genetic parameters for different yield and yield attributing characters in medium maturing rice genotypes

Sl. No.	Character	Mean	Range		Variances		Coefficient of variation (%)		h ² bs (%)	GA	GAM (%)
			Min.	Max.	Phenotypic	Genotypic	PCV	GCV			
1	Field emergence	64.31	31.2	91.99	307.26	299.68	27.25	26.91	97	35.21	54.76
2	Plant height (cm)	92.36	67.3	118.1	154.73	133.21	13.46	12.49	80	22.06	23.88
3	Number of tillers/plant	14.57	10.5	18.6	4.49	3.89	14.54	13.53	86	3.78	25.94
4	Number of reproductive tillers/plant	13.62	9.85	17.4	4.71	4.11	16.05	14.98	87	3.90	28.83
5	Days to 50% flowering	89.88	80.5	100	33.78	8.93	6.46	3.32	26	3.16	3.52
6	Grain filling duration(days)	31.65	29.5	37.5	2.95	2.26	5.43	4.75	76	2.71	8.56
7	Number of Plants /square meter	26.84	20	33	19.20	14.56	16.32	14.21	75	6.84	25.49
8	Panicle length(cm)	21.86	14.5	23.95	3.50	1.35	8.56	5.33	38	1.49	6.83
9	Panicle weight (g)	3.10	2.23	5.05	0.52	0.49	23.26	22.71	95	1.42	45.70
10	Number of filled grains	131.41	73.80	188.5	855.56	803.48	22.25	21.56	93	56.58	43.05
11	Number of unfilled grains	9.83	2.2	19.1	19.91	19.18	45.36	44.51	96	8.85	90.01
12	1000 grain weight (g)	24.05	17.45	30.8	9.69	6.31	12.94	10.44	65	4.17	17.36
13	Grain yield / plant (g)	19.69	18.29	21.86	1.26	0.39	5.69	3.19	31	0.72	3.69
14	Grain yield / hectare (kg)	5252	4063	6492	560247.15	330466.03	14.25	10.94	58	9.50	17.31

PCV: Phenotypic coefficient of variation,
GAM: Genetic advance as per cent of mean,

GCV: Genotypic coefficient of variation,
h² bs: Heritability (Broad sense)

GA: Genetic advance,

be 16.05 and 14.98 respectively. Heritability (87 percent) was high and with high GAM (28.83) for this trait.

4.2.3.5 Days to 50 per cent flowering

The mean value for days to 50 per cent flowering was 89.88 with a range from 80.50 to 100 days. The genotypes IR 14K 10477, IR 14K 10530 were recorded as earliest to flower (80.50 days) while, OR 2542-4 took as many as (100 days) to flower. The Phenotypic and genotypic variances were estimated to be 33.78 and 8.93 respectively. The low PCV and GCV were recorded to be 6.46 and 3.32 percent respectively. Heritability (26 percent) and GAM (3.52) were recorded as low.

4.2.3.6 Grain filling duration (days)

The mean value for days to grain filling duration was 31.65 with a range from 29.50 to 37.50 days. The genotypes IR 14K 10203, IR 14K 10045 were earliest grain filling (29.50 days) while; IR 13K 5144 took as many as (37.50 days) to grain filling duration. The Phenotypic and genotypic variances were estimated to be 2.95 and 2.26 respectively. The low PCV and GCV were recorded to be 5.43 and 4.75 percent respectively. Heritability (76 percent) was high and genetic advance as per cent mean (8.56) was low.

4.2.3.7 Number of plants per square meter

The mean value for number of plants per square meter was 26.84 with a range from 20 to 33. Highest number of plants per square meter was recorded in the genotypes UPR 3926-6-1-1, IR 14K 9977 (33) while, IR 14K 10048, IR 13K 5144 genotypes recorded lowest number of plants per square meter (20). The Phenotypic and genotypic variances were estimated to be 19.20 and 14.56 respectively. The moderate PCV and GCV were recorded to be 16.32 and 14.21 percent respectively. Heritability (75 percent) and GAM (25.49) were high.

4.2.3.8 Panicle length (cm)

The experimental data on panicle length revealed that this character ranged from 14.50 to 23.95 cm with the mean of 21.86 cm. The longest panicle length was observed in genotype UPR 3946-20-1-1(23.95) and shortest panicle length was observed in genotype OR2542-4 (14.50). The phenotypic variance of 3.50 and genotypic variance of 1.35 were

recorded. Phenotypic and genotypic coefficients of variability were low and estimated to be 8.56 and 5.33 respectively and moderate heritability value of (38 percent) and low genetic advance as per cent of mean was (6.83).

4.2.3.9 Panicle weight (g)

The character panicle weight was ranged from 2.23g to 5.05g with the mean of 3.10g. The maximum panicle weight was reported in the genotype UPR 3926-6-1-1(5.05g). The lowest panicle weight was recorded in the genotype IR 13K 5144(2.23). The phenotypic and genotypic variances observed were 0.52 and 0.49 respectively. Phenotypic coefficient of variation (23.26) and genotypic coefficients of variation (22.71) were high. Heritability (95 percent) was high and genetic advance as per cent of mean (45.70) was high.

4.2.3.10 Number of filled grains per panicle

The number of filled grains per panicle was varied from 73.80 to 188.50 with mean performance of 131.41. The genotype UPR 3926-6-1-1(188.50) had highest number of filled grains per panicle, while the lowest number of filled grains recorded in IR 14K 10477 (73.80). Large variance was obtained for this character. The values of phenotypic and genotypic variances were very high and found to be 855.56 and 803.48 respectively. The PCV (22.25) and GCV (21.56) were high. Heritability (93 percent) and genetic advance as percent of mean (43.05) were recorded high.

4.2.3.11 Number of unfilled grains per panicle

The number of unfilled grains per panicle was counted and varied from 2.20 to 19.10 with mean performance of 9.83. The genotype IR 13K 5144(19.10) had highest number of unfilled grains per panicle, while the lowest number of unfilled grains recorded in UPR 3926-6-1-1(2.20). The values of phenotypic and genotypic variances were estimated to be 19.91 and 19.18 respectively. The PCV (45.36) and GCV (44.51) were high. Heritability (96 percent) and genetic advance as percent of mean (90.01) were high.

4.2.3.12 Test weight (g)

Range of variation with respect to 1000 grain weight was recorded to be 17.45 to 30.80 with a mean value of 24.05. The minimum test weight was recorded in IR 13K 5144(17.45g) and maximum test weight in UPR 3926-6-1-1(30.80g). The Phenotypic and

genotypic variances were estimated to be 9.69 and 6.31 respectively. The moderate PCV and GCV were recorded to be 12.94 and 10.44 percent respectively. Heritability (65 percent) was high and coupled with moderate GAM (17.36) for this trait.

4.2.3.13 Grain yield per plant (g)

The grain yield per plant ranged from 18.29 to 21.86 with a mean value of 19.69 g. The highest grain yield per plant was recorded in IR 14K 10048 (21.29) and lowest grain yield per plant was recorded in IR 14K 10452 (18.29). The Phenotypic and genotypic variances were estimated to be 1.26 and 0.39 respectively. The low PCV and GCV were recorded to be 5.69 and 3.19 percent respectively. Heritability (31 percent) was high and genetic advance as per cent mean (3.69) was low.

4.2.3.14 Grain yield per hectare (kg)

The grain yield varied from 4063 kg/ha to 6492 kg/ha with the mean performance of 5252 kg/ha the maximum grain yield recorded in UPR 3926-6-1-1(6492 kg). The less grain yield was recorded by the IR 13K 5144 (4063 kg).The phenotypic and genotypic variances observed for this trait were 560247.15 and 330466.03 respectively, while the coefficients of variability at phenotypic and genotypic levels were moderate and were estimated to be 14.25 and 10.94 respectively. Moderate heritability (58 percent) was recorded with moderate GA as per cent of mean (17.31).

Medium maturing rice genotypes with superior performance presented in (Plate 3), while the PCV, GCV, h^2 and Genetic advance for these traits were presented graphically in (Fig. 9 and 10). The top ten genotypes with high grain yield/hectare and character wise better performing genotypes is given in (Fig. 11 and 12).



Entry Name: UPR 3926-6-1-1

Grain Yield: 6492kg/ha. 9.33% over check NDR 359



Entry Name: IR 14K 10236

Grain Yield: 6352kg/ha. 6.96% over check NDR 359

Plate 3. Medium maturing rice genotypes with superior performance

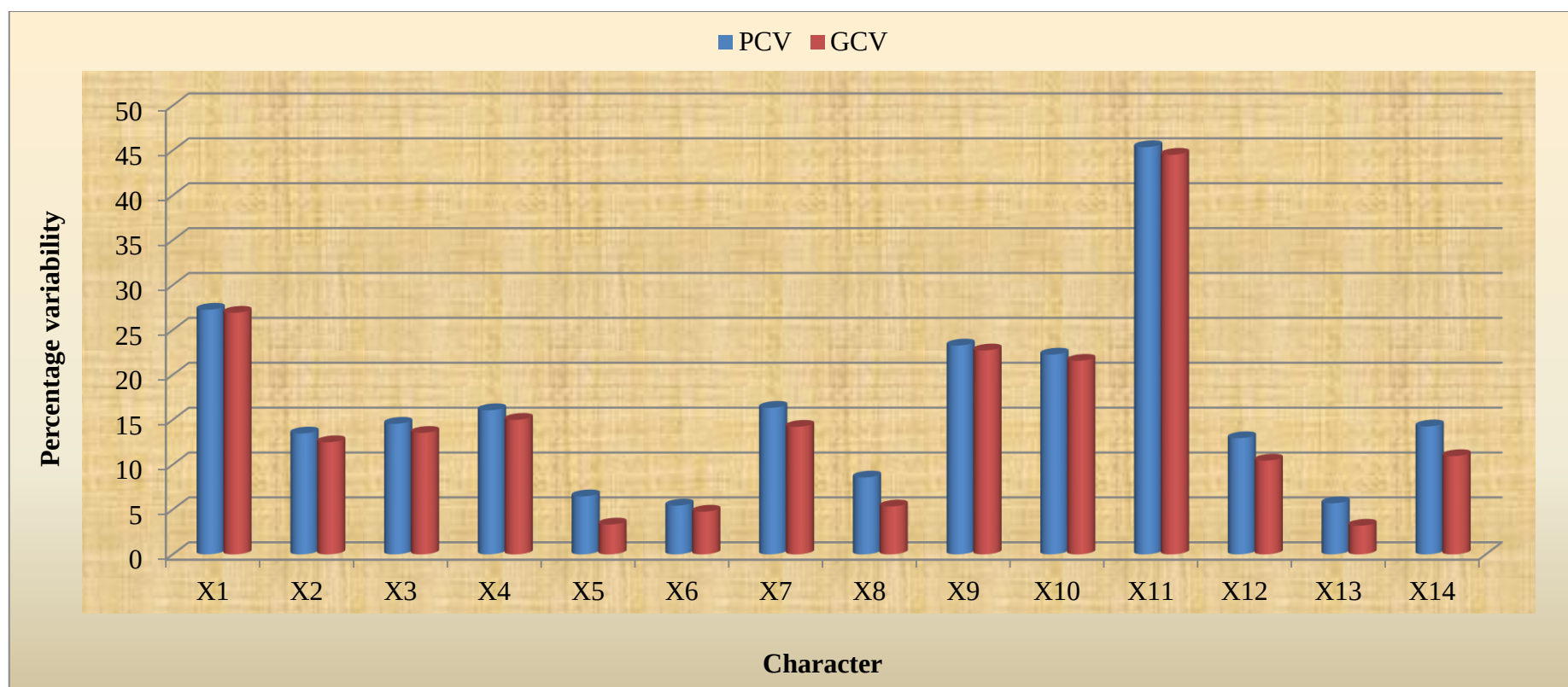


Fig 9. Phenotypic and genotypic coefficient of variability for plant and yield attributing characters in medium maturing rice genotypes

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

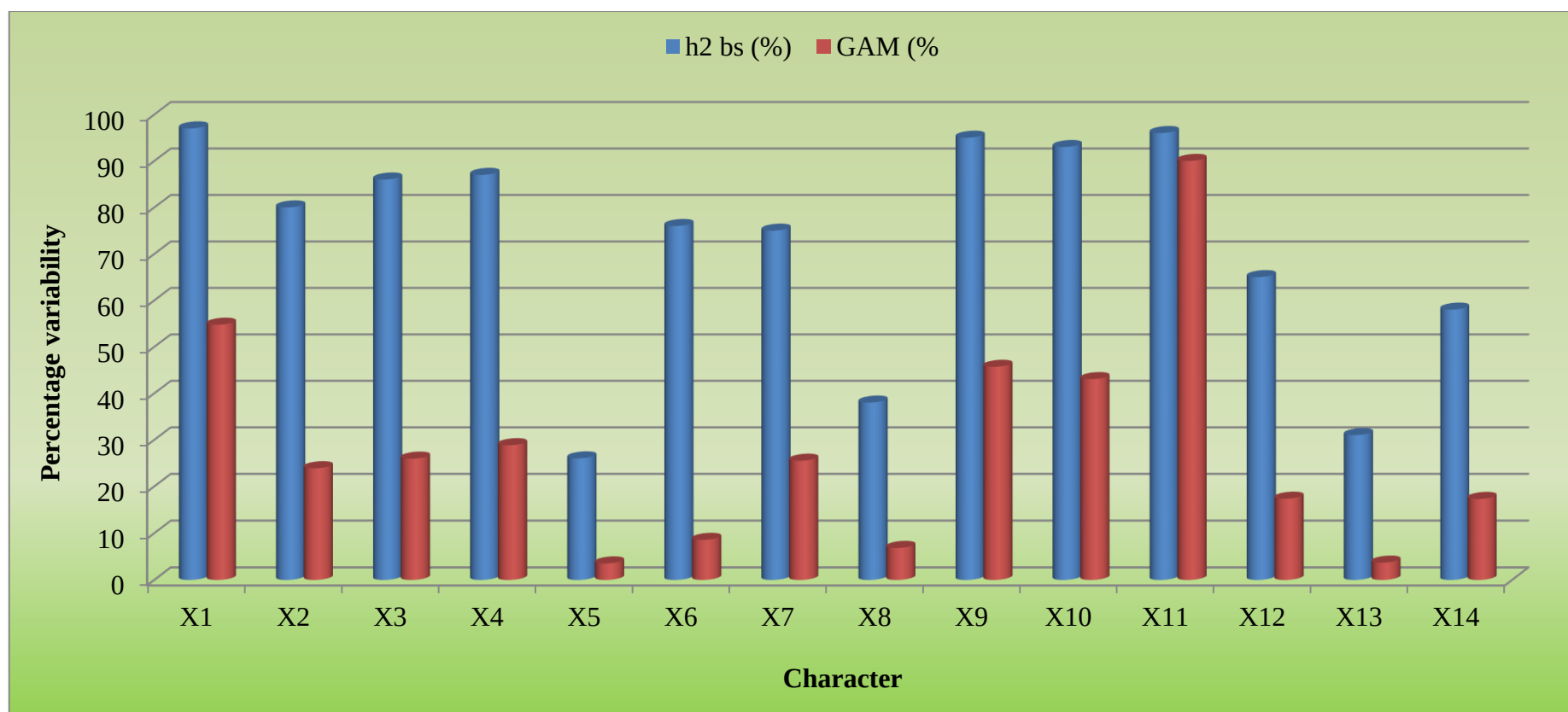


Fig 10. Heritability and genetic advance for plant and yield attributing characters in medium maturing rice genotypes.

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)	X14: Yield/hectare (Kg)		

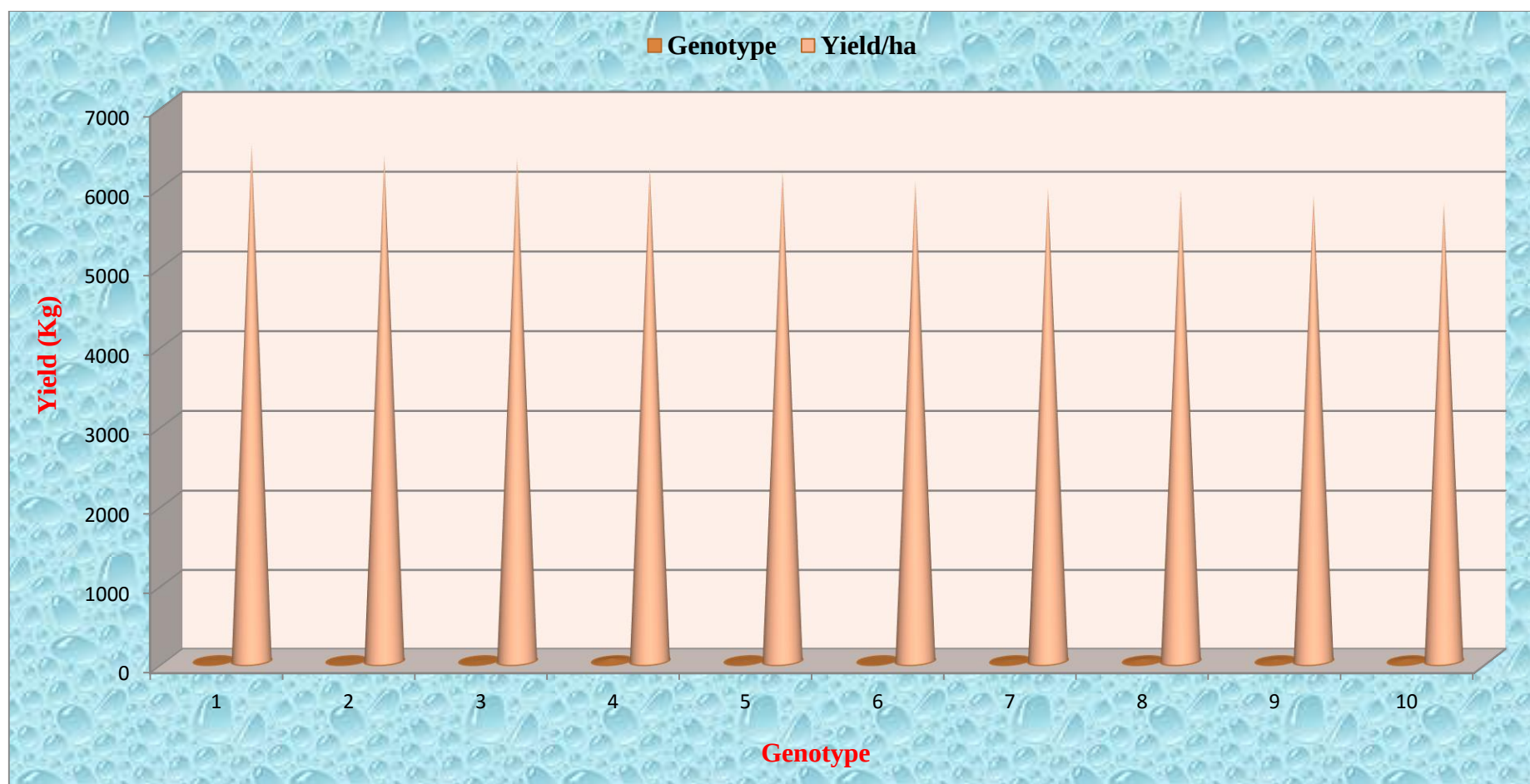
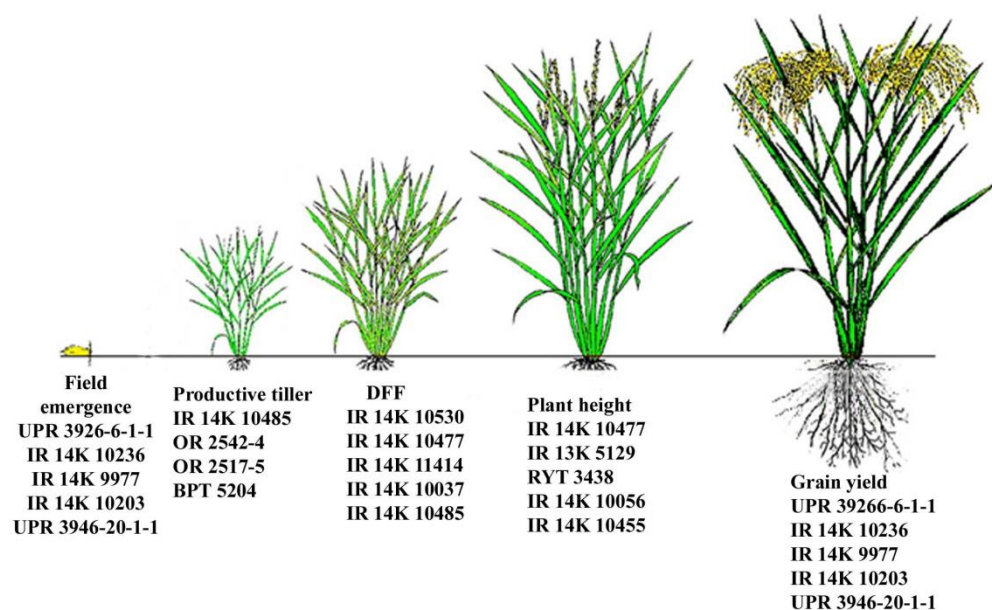


Fig 11. Top ten rice genotypes having high grain yield per hectare in medium maturing direct seeded rice genotypes

- | | | | | |
|-------------------|--------------------|-----------------|-----------------|--------------------|
| 1. UPR 3926-6-1-1 | 2. IR 14K 10236 | 3. IR 14K 9977 | 4. IR 14K 10203 | 5. UPR 3946-20-1-1 |
| 6. IR 13K 5156 | 7. NDR 359 (Check) | 8. IR 14K 10231 | 9. IR 14K 10115 | 10. MT 4316 |



Test weight
 UPR 3926-6-1-1
 IR 14K 10236
 IR 14K 9977
 IR 14K 10115
 IR 14K 5156



Filled grains / panicle
 UPR 3926-6-1-1
 IR 14K 9977
 IR 14K 10236
 IR 14K 10203
 IR 13K 5156

Panicle length
 MT 2808
 IR 14K10485
 IR 14K 10048
 MTU 3626
 IR 14K 10451

Fig 12: Trait wise superior performing medium maturing direct seeded rice genotypes

4.3 Association study among different traits relevant to direct seeded rice along with yield.

The results of Genotypic and Phenotypic association among the plant and yield attributing characters are given in all the three different maturing direct seeded rice genotypes. Genotypic correlations were higher than phenotypic correlation.

4.3.1 Phenotypic association studies in early maturing direct seeded rice genotypes.

The results of the study presented in table 14.

4.3.1.1 Correlation between grain yield and its components

Grain yield per plant exhibited significant positive correlations with field emergence percentage (0.69), plant height (0.76), number of tillers/plant (0.73), number of reproductive tillers/plant (0.71), grain filling duration (0.62), number of plants/square meter (0.69), panicle weight (0.77), filled grains/panicle (0.83) and test weight (0.58). Significant negative association with unfilled grains per panicle (-0.72).

4.3.1.2 Field emergence

Field emergence percentage showed significant positive correlations with plant height (0.81), number of tillers/plant (0.78), number of reproductive tillers/plant (0.78), grain filling duration (0.70), number of plants/square meter (0.86), panicle weight (0.81), filled grains/panicle (0.85) and test weight (0.75). Significant negative correlation with unfilled grains / panicle (-0.86).

4.3.1.3 Plant height (cm)

Plant height exhibited significant positive correlations with number of tillers/plant (0.87), number of reproductive tillers/plant (0.86), grain filling duration (0.76), number of plants/square meter (0.83), panicle weight (0.83), filled grains/panicle (0.93) and test weight (0.74). But significant negative correlation with unfilled grains/ panicle (-0.80).

4.3.1.4 Number of tillers per plant

Total number of tillers per plant had significant positive correlation with number of reproductive tillers/plant (0.98), grain filling duration (0.73), number of plants/square

Table 14. Estimates of phenotypic correlation coefficients for yield and yield attributing characters in early maturing rice genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1.00												
X2	0.81**	1.00											
X3	0.78**	0.87**	1.00										
X4	0.78**	0.86**	0.98**	1.00									
X5	0.09	-0.04	-0.06	-0.03	1.00								
X6	0.70**	0.76**	0.73**	0.74**	0.03	1.00							
X7	0.86**	0.83**	0.76**	0.75**	0.03	0.75**	1.00						
X8	-0.01	0.03	-0.08	-0.09	-0.11	0.10	-0.02	1.00					
X9	0.81**	0.83**	0.84**	0.84**	0.02	0.75**	0.80**	-0.04	1.00				
X10	0.85**	0.93**	0.89**	0.88**	-0.01	0.77**	0.89**	-0.01	0.90**	1.00			
X11	-0.86**	-0.80**	-0.74**	-0.74**	0.01	-0.72**	-0.89**	-0.09	-0.84**	-0.89**	1.00		
X12	0.75**	0.74**	0.73**	0.74**	-0.02	0.63**	0.67**	0.02	0.66**	0.73**	-0.73**	1.00	
X13	0.69**	0.76**	0.73**	0.71**	-0.04	0.62**	0.69**	0.05	0.77**	0.83**	-0.72**	0.58**	1.00

** and * indicates Significance at 1 and 5% level

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)			

meter (0.76), panicle weight (0.84), filled grains/panicle (0.89) and test weight (0.73). Significant negative correlation with unfilled grains/panicle (-0.74).

4.3.1.5 Number of reproductive tillers per plant

Total number of reproductive tillers per plant exhibited a significant positive correlation with grain filling duration (0.74), number of plants/square meter (0.75), panicle weight (0.84), filled grains/panicle (0.88) and test weight (0.74). Significant negative correlation with unfilled grains/panicle (-0.74).

4.3.1.6 Days to 50 per cent flowering

Days to fifty per cent flowering exhibited non significant positive correlations with grain filling duration (0.03), number of plants/square meter (0.03), panicle weight (0.02), unfilled grains/plant (0.01). Non-significant negative correlation with filled grains/plant (-0.01) and test weight (-0.02).

4.3.1.7 Grain filling duration

Days to grain filling duration had significant positive correlations with number of plants/square meter (0.75), panicle weight (0.75), filled grains/panicle (0.77) and test weight (0.63). Significant negative correlations with unfilled grains /panicle (-0.72).

4.3.1.8 Number of plants per square meter

Number of plants per square meter had significant positive correlations with panicle weight(0.80), filled grains/panicle (0.89) and test weight (0.67) and significant negative correlations with character unfilled grains /panicle (-0.89).

4.3.1.9 Panicle length

Panicle length exhibited non significant positive correlations with test weight (0.02). Non significant negative correlations with panicle weight (-0.04), filled grains/panicle (-0.01), and unfilled grains /panicle (-0.09).

4.3.1.10 Panicle weight

Panicle weight exhibited significant positive correlations with filled grains/panicle (0.90) and test weight (0.66). Significant negative correlations with unfilled grains/panicle (-0.84).

4.3.1.11 Filled grains per panicle

Filled grains per plant had significant positive correlations with test weight (0.73). Significant negative correlations with unfilled grains /panicle (-0.89).

4.3.1.12 Unfilled grains per panicle

Unfilled grains had significant negative correlations with test weight (-0.73).

4.3.2 Phenotypic association studies in mid early maturing direct seeded rice genotypes

The results of the study presented in table 15.

4.3.2.1 Correlation between grain yield and its components.

Grain yield per plant had significant positive correlations with field emergence percentage (0.51), plant height (0.64), number of tillers/plant (0.35), number of reproductive tillers/plant (0.46), number of plants/square meter (0.30), panicle length (0.43), panicle weight (0.55), filled grains/panicle (0.57) and test weight (0.43). Significant negative correlations with unfilled grains /panicle (-0.46).

4.3.2.2 Field emergence

Field emergence exhibit significant positive correlation with plant height (0.87), number of tillers/plant (0.77), number of reproductive tillers/plant (0.80), number of plants/square meter (0.86), panicle length (0.84), panicle weight (0.89), filled grains/panicle (0.93) and test weight (0.87). Significant negative correlation with unfilled grains /panicle (-0.94),

4.3.2.3 Plant height (cm)

Plant height had significant positive correlation with number of tillers/plant (0.81), number of reproductive tillers/plant (0.83), number of plants/square meter (0.75), panicle length (0.70), panicle weight (0.89), filled grains/panicle (0.91) and test weight (0.81). Significant negative correlation with the unfilled grains /panicle (-0.83).

4.3.2.4 Number of tillers per plant

Total number of tillers per plant had significant positive correlation with number of reproductive tillers/plant (0.90), number of plants/square meter (0.76), panicle length (0.61), panicle weight (0.83), filled grains/panicle (0.80) and test weight (0.74). But significant negative correlation with unfilled grains/panicle (-0.74).

Table 15. Estimates of phenotypic correlation coefficients for yield and yield attributing characters in mid early maturing rice genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1.00												
X2	0.87**	1.00											
X3	0.77**	0.81**	1.00										
X4	0.80**	0.83**	0.90**	1.00									
X5	-0.11	-0.17	-0.15	-0.17	1.00								
X6	-0.06	-0.01	-0.10	-0.05	0.12	1.00							
X7	0.86**	0.75**	0.76**	0.76**	-0.16	-0.02	1.00						
X8	0.84**	0.70**	0.61**	0.63**	-0.07	-0.05	0.76**	1.00					
X9	0.89**	0.89**	0.83**	0.85**	-0.19	-0.09	0.83**	0.76**	1.00				
X10	0.93**	0.91**	0.80**	0.83**	-0.15	-0.01	0.84**	0.82**	0.93**	1.00			
X11	-0.94**	-0.83**	-0.74**	-0.77**	0.17	0.01	-0.87**	-0.84**	-0.89**	-0.93**	1.00		
X12	0.87**	0.81**	0.74**	0.74**	-0.19	-0.03	0.81**	0.78**	0.85**	0.86**	-0.89**	1.00	
X13	0.51**	0.64**	0.35**	0.46**	-0.12	0.03	0.30**	0.43**	0.55**	0.57**	-0.46**	0.43**	1.00

** and * indicates Significance at 1 and 5% level

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)			

4.3.2.5 Number of reproductive tillers per plant

Total number of reproductive tillers per plant was found to be significant positive correlations with number of plants/square meter (0.76), panicle length (0.63), panicle weight (0.85), filled grains/panicle (0.83) and test weight (0.74). Significant negative correlations with unfilled grains /panicle (-0.77).

4.3.2.6 Days to 50 per cent flowering

Days to fifty per cent flowering had non significant positive correlations with grain filling duration (0.12), unfilled grains/panicle (0.17). Non significant negative correlation with number of plants/square meter (-0.16), panicle length (-0.07), panicle weight (-0.19), filled grains/panicle (-0.15) and test weight (-0.19).

4.3.2.7 Grain filling duration

Days to grain filling duration exhibited non significant positive correlations with unfilled grains/panicle (0.01). But non significant negative correlation with number of plants/square meter (-0.02), panicle length (-0.05), panicle weight (-0.09), filled grains/panicle (-0.01) and test weight (-0.03).

4.3.2.8 Number of plants per square meter

Number of plants per square meter was found to be significant positive correlations with panicle length (0.76), panicle weight (0.83), filled grains/panicle (0.84) and test weight (0.81) and significant negative association with unfilled grains /panicle (-0.87).

4.3.2.9 Panicle length

Panicle length had significant positive correlations with panicle weight (0.76), filled grains/panicle (0.82) and test weight (0.78). But significant negative correlations with unfilled grains /panicle (-0.84)

4.3.2.10 Panicle weight

Panicle weight had significant positive correlations with filled grains/panicle (0.93) and test weight (0.85). Significant negative correlations with unfilled grains /panicle (-0.89).

4.3.2.11 Filled grains per panicle

Filled grains exhibited significant positive correlations with test weight (0.86). Significant negative association with unfilled grains /panicle (-0.93)

4.3.2.12 Unfilled grains per panicle

Unfilled grains had significant negative correlations with test weight (-0.89).

4.3.3 Phenotypic association studies in medium maturing direct seeded rice genotypes.

The results of the study are presented in table 16

4.3.3.1 Correlation between grain yield and its components

Grain yield per plant had significant positive correlations with number of tillers/plant (0.33), number of reproductive tillers/plant (0.31), unfilled grains/panicle (0.47). Significant negative association with field emergence (-0.52), plant height (-0.60), number of plants/square meter (-0.58), filled grains/panicle (-0.43), test weight (-0.40).

4.3.3.2 Field emergence

Field emergence exhibited a significant positive correlations with plant height (0.75), number of plants/square meter (0.92), panicle weight (0.88), filled grains/panicle (0.95) and test weight (0.83). Significant negative correlations with number of tillers/plant (-0.54), number of reproductive tillers/plant (-0.51), grain filling duration (-0.35), unfilled grains /panicle (-0.96).

4.3.3.3 Plant height (cm)

Plant height was found to be significant positive correlations with number of plants/square meter (0.72), panicle weight (0.51), filled grains/panicle (0.65), test weight (0.58). Significant negative correlations with number of tillers/plant (-0.51), number of reproductive tillers/plant (-0.52), grain filling duration (-0.30), unfilled grains /panicle (-0.70).

4.3.3.4 Number of tillers per plant

Total number of tillers per plant had significant positive correlation with number of reproductive tillers/plant (0.97), unfilled grains/panicle (0.50). Significant negative correlations with number of plants/square meter (-0.51), panicle weight (-0.41), filled grains/panicle(-0.45),testweight(-0.43).

Table 16. Estimates of phenotypic correlation coefficients for yield and yield attributing characters in medium duration maturing rice genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1.00												
X2	0.75**	1.00											
X3	-0.54**	-0.51**	1.00										
X4	-0.51**	-0.52**	0.97**	1.00									
X5	0.11	-0.08	-0.05	0.01	1.00								
X6	-0.35*	-0.30*	-0.01	0.06	0.24	1.00							
X7	0.92**	0.72**	-0.51**	-0.52**	0.01	-0.34*	1.00						
X8	-0.15	-0.14	-0.05	-0.10	-0.14	-0.03	-0.06	1.00					
X9	0.88**	0.51**	-0.41**	-0.39**	0.12	-0.29*	0.78**	-0.12	1.00				
X10	0.95**	0.65**	-0.45**	-0.43**	0.11	-0.36*	0.87**	-0.16	0.92**	1.00			
X11	-0.96**	-0.70**	0.50**	0.48**	-0.08	0.36*	-0.89**	0.11	-0.91**	-0.94**	1.00		
X12	0.83**	0.58**	-0.43**	-0.40**	0.07	-0.34*	0.79**	-0.05	0.77**	0.80**	-0.81**	1.00	
X13	-0.52**	-0.60**	0.33**	0.31**	0.12	0.18	-0.58**	0.05	-0.27	-0.43**	0.47**	-0.40**	1.00

** and * indicates Significance at 1 and 5% level

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)			

4.3.3.5 Number of reproductive tillers per plant

Total number of reproductive tillers per plant had significant positive correlations with unfilled grains/panicle (0.48). Significant negative correlations with number of plants/square meter (-0.52), panicle weight (-0.39), filled grains/panicle (-0.43), test weight (-0.40).

4.3.3.6 Days to 50 per cent flowering

Days to fifty per cent flowering exhibited non significant positive correlations with grain filling duration (0.24), number of plants/square meter (0.01), panicle weight (0.12), filled grains/panicle (0.11) and test weight (0.07). It had also showed non significant negative correlation with panicle length (-0.14), unfilled grains /panicle (-0.08).

4.3.3.7 Grain filling duration

Days to grain filling duration had significant positive correlations with unfilled grains /panicle (0.36). Significant negative correlation with number of plants/square meter (-0.34), panicle weight (-0.29), filled grains/panicle (-0.36) and test weight (-0.34).

4.3.3.8 Number of plants per square meter

Number of plants per square meter had significant positive correlation with panicle weight (0.78), filled grains/panicle (0.87), test weight (0.79) and significant negative correlation with unfilled grains/panicle (-0.89).

4.3.3.9 Panicle length

Panicle length had non significant positive correlation with unfilled grains/panicle (0.11). it had also showed non significant negative correlation with the panicle weight (-0.12), filled grains/ panicle (-0.16) and test weight (-0.05).

4.3.3.10 Panicle weight

Panicle weight exhibited significant positive correlations with filled grains/panicle (0.92) and test weight (0.77) and significant negative correlations with unfilled grains / panicle (-0.91).

4.3.3.11 Filled grains per panicle

Filled grains had significant positive correlations with test weight (0.80) and significant negative correlations with unfilled grains / panicle (-0.94).

4.3.3.12 Unfilled grains per panicle

Unfilled grains showed significant negative correlation test weight (-0.81).

4.3.4 Genotypic correlation studies in early maturing direct seeded rice genotypes.

The results of the study presented in table 17

4.3.4.1 Correlation between grain yield and its components

Grain yield per plant had a significant positive correlation with field emergence (0.96), plant height (0.98), number of tillers per plant (0.97), number of reproductive tillers/plant (0.95), grain filling duration (0.98), number of plants/square meter (0.97), panicle weight (0.98), filled grains/panicle (0.99) and test weight(0.87) and it had also showed significant negative correlation with unfilled grains/panicle (-0.94).

4.3.4.2 Field emergence

Field emergence exhibit significant positive correlation with plant height (0.95), number of tillers/plant (0.90) number of reproductive tillers/plant (0.88), grain filling duration (0.99), number of plants/square meter (0.98), panicle weight (0.96), filled grains/panicle (0.97) and test weight (0.87) and it had also showed significant negative correlation with unfilled grains/ panicle (-0.94).

4.3.4.3 Plant height

Plant height exhibited a significant positive correlation with number of tillers/plant (0.98), number of reproductive tillers/plant (0.97), grain filling duration (0.99), number of plants/square meter (0.94), panicle weight (0.93), filled grains/ panicle (0.99) and test weight (0.86) and it had also showed significant negative correlation with unfilled grains/panicle (-0.87).

4.3.4.4 Number of tillers per plant

Total number of tillers per plant had significant positive correlated with number of reproductive tillers/plant (0.98), grain filling duration (0.96), number of plants/square

Table 17. Estimates of genotypic correlation coefficients for yield and yield attributing characters in early maturing rice genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1.00												
X2	0.95**	1.00											
X3	0.90**	0.98**	1.00										
X4	0.88**	0.97**	0.98**	1.00									
X5	-0.05	0.06	-0.04	-0.05	1.00								
X6	0.99**	0.99**	0.96**	0.96**	-0.10	1.00							
X7	0.98**	0.94**	0.86**	0.84**	0.04	0.95**	1.00						
X8	0.05	-0.04	-0.11	-0.11	-0.15	-0.09	0.03	1.00					
X9	0.96**	0.93**	0.92**	0.91**	0.07	0.98**	0.91**	-0.08	1.00				
X10	0.97**	0.99**	0.96**	0.95**	0.01	0.96**	0.98***	-0.03	0.95**	1.00			
X11	-0.94**	-0.87**	-0.81**	-0.78**	0.05	-0.90**	-0.96**	-0.12	-0.88**	-0.91**	1.00		
X12	0.87**	0.86**	0.85**	0.85**	-0.07	0.86**	0.83**	-0.10	0.78**	0.84**	-0.84**	1.00	
X13	0.96**	0.98**	0.97**	0.95**	0.10	0.98**	0.97**	-0.02	0.98**	0.99**	-0.94**	0.87**	1.00

** and * indicates Significance at 1 and 5% level

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)			

meter (0.86), panicle weight (0.92), filled grains/ panicle (0.96) and test weight (0.85) and it had also showed significant negative correlation with unfilled grains / panicle (-0.81).

4.3.4.5 Number of reproductive tillers per plant

Total number of reproductive tillers per plant found to be significant positive correlation with grain filling duration (0.96), number of plants/square meter (0.84), panicle weight (0.91), filled grains/panicle (0.95) and test weight (0.85) and negative significant correlation with unfilled grains / panicle (-0.78).

4. 3.4.6 Days to 50 per cent flowering

Days to fifty per cent flowering had non significant positive correlations with number of plants/square meter (0.04), panicle weight (0.07), filled grains/plant (0.01), unfilled grains / panicle (0.05) and non significant negative correlated with grain filling duration (-0.10), panicle length (-0.15) test weight (-0.07).

4.3.4.7 Grain filling duration

Days to grain filling duration exhibited significant positive correlations with number of plants/square meter (0.95), panicle weight (0.98), filled grains/panicle (0.96) and test weight (0.86). Negative significant correlations with unfilled grains/panicle (-0.90).

4.3.4.8 Number of plants per square meter

Number of plants per square meter exhibited significant positive correlations with panicle weight (0.91), filled grains/plant (0.98), test weight (0.83). Negative significant correlations with unfilled grains / panicle (-0.96).

4.3.4.9 Panicle length

Panicle length had non-significant negative correlations with panicle weight(-0.09), filled grains/panicle (-0.02), unfilled grains/panicle (-0.02) and test weight (-0.10).

4.3.4.10 Panicle weight

Panicle weight exhibited significant positive correlations with filled grains/panicle (0.95) and test weight (0.78). Negative significant correlations with unfilled grains / panicle (-0.88).

4.3.4.11 Filled grains per panicle

Filled grains per panicle exhibited significant positive correlations with test weight (0.84). Negative significant correlation with unfilled grains/panicle (-0.91).

4.3.4.12 Unfilled grains per panicle

Unfilled grains had significant negative correlations with test weight (-0.84).

4.3.5 Genotypic correlation studies in mid early maturing direct seeded rice genotypes.

The results of the study presented in table 18.

4.3.5.1 Correlation between grain yield and its components

Grain yield per plant exhibited significant positive correlations with field emergence percentage (0.78), plant height (0.94), number of tillers/plant (0.85), number of reproductive tillers/plant (0.81), number of plants/square meter (0.75), panicle length (0.73), panicle weight (0.89), filled grains/panicle (0.90) test weight (0.76). Negative significant association with unfilled grains / panicle (-0.72).

4.3.5.2 Field emergence

Field emergence percentage exhibited significant positive correlations with plant height (0.95), number of tillers/plant (0.95), number of reproductive tillers/plant (0.93), number of plants/square meter (0.99), panicle length (0.99), panicle weight (0.97), filled grains/panicle (0.97) and test weight (0.99). Negative significant correlations with unfilled grains/panicle (-0.98).

4.3.5.3 Plant height (cm)

Plant height exhibited significant positive correlations with number of tillers/plant (0.96), number of reproductive tillers/plant (0.94), number of plants/square meter (0.93), panicle length (0.92), panicle weight (0.98), filled grains/ panicle (0.99) and test weight (0.92). Negative significant correlations with unfilled grains/ panicle (-0.91).

4.3.5.4 Number of tillers per plant

Total number of tillers per plant was found to be significant positive correlation with number of reproductive tillers/plant (0.98), number of plants/square meter (0.93),

Table 18. Estimates of genotypic correlation coefficients for yield and yield attributing characters in mid early maturing rice genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1.00												
X2	0.95**	1.00											
X3	0.95**	0.96**	1.00										
X4	0.93**	0.94**	0.98**	1.00									
X5	-0.23	-0.13	-0.18	-0.12	1.00								
X6	-0.04	0.08	0.07	-0.07	-0.04	1.00							
X7	0.99**	0.93**	0.93**	0.91**	-0.43**	0.05	1.00						
X8	0.99**	0.92**	0.92**	0.89**	-0.47**	0.05	0.99**	1.00					
X9	0.97**	0.98**	0.98**	0.96**	-0.21	0.12	0.96**	0.94**	1.00				
X10	0.97**	0.99**	0.96**	0.93**	-0.26	0.03	0.96**	0.95**	0.99**	1.00			
X11	-0.98**	-0.91**	-0.91**	-0.88**	0.29	0.07	-0.99**	-0.99**	-0.94**	-0.95**	1.00		
X12	0.99**	0.92**	0.94**	0.90**	0.25	0.04	0.98**	0.99**	0.94**	0.95**	-0.98**	1.00	
X13	0.78**	0.94**	0.85**	0.81**	-0.25	0.06	0.75**	0.73**	0.89**	0.90**	-0.72**	0.76**	1.00

** and * indicates Significance at 1 and 5% level

X1: Field emergence	X2: Plant Height (cm)	X3: Tiller number/plant	X4: Reproductive tiller number /plant
X5: Days to 50% flowering	X6: Grain Filling Duration	X7: Plants/square meter	X8: Panicle Length (cm)
X9: Panicle Weight (g)	X10: Filled Grains/panicle	X11: Unfilled Grains /panicle	X12: Test Weight (g)
X13: Yield/plant (g)			

panicle length (0.92), panicle weight (0.98), filled grains/ panicle (0.96) and test weight (0.94). Significant negative correlation with unfilled grains/ panicle (-0.91).

4.3.5.5 Number of reproductive tillers per plant

Total number of reproductive tillers per plant exhibited positive significant correlation with number of plants/square meter (0.91), panicle length (0.89), panicle weight (0.96), filled grains/ panicle (0.93) and test weight (0.90). Negative significant association with unfilled grains / panicle (-0.88).

4.3.5.6 Days to 50 per cent flowering

Days to fifty per cent flowering showed non-significant positive correlations with unfilled grains/panicle (0.23) and test weight (0.25). Negative significant correlation with number of plants/square meter (-0.43), panicle length (-0.47).

4.3.5.7 Grain filling duration

Days to grain filling duration exhibited non-significant positive correlations with number of plants per square meter (0.05), panicle length (0.05), panicle weight (0.12), filled grains/plant (0.03), unfilled grains/panicle (0.07), test weight (0.04) .

4.3.5.8 Number of plants per square meter

Number of plants per square meter exhibited positive significant correlation with panicle length (0.99), panicle weight (0.96), filled grains/panicle (0.96) and test weight (0.98). Negative significant correlation with unfilled grains/panicle (-0.99) .

4.3.5.9 Panicle length

Panicle length exhibited significant positive correlations with panicle weight (0.94), filled grains/ panicle (0.95) and test weight (0.99). Negative significant correlation with unfilled grains /panicle (-0.99)

4.3.5.10 Panicle weight

Panicle weight exhibited significant positive associations with filled grains/plant (0.99) and test weight (0.94). Negative significant correlation with unfilled grains/ panicle (-0.94)

4.3.5.11 Filled grains per panicle

Filled grains per panicle was exhibited significant positive correlation with Test weight (0.95). Negative significant association with unfilled grains/panicle (-0.95).

4.3.5.12 Unfilled grains per panicle

Unfilled grains per panicle exhibited significant negative association with test weight (-0.98).

4.3.6 Genotypic correlation studies in medium maturing direct seeded rice genotypes.

The results of the study are presented in Table 19

4.3.6.1 Correlation between grain yield and its components

Grain yield per plant exhibited significant positive correlations with number of tillers/plant (0.59), number of reproductive tillers/plant (0.62), grain filling duration (0.39), unfilled grains/ panicle (0.91). Negative significant correlation with field emergence percentage (-0.97), plant height (-0.99), number of plants/square meter (-0.98), panicle weight (-0.60), filled grains/panicle (-0.80) and test weight (-0.72).

4.3.6.2 Field emergence

Field emergence percentage exhibited significant positive correlations with plant height (0.81), number of plants/square meter (0.98), panicle weight (0.92), filled grains/panicle (0.99), test weight (0.96). Negative significant association with number of tillers/plant (-0.59), number of reproductive tillers/plant (-0.57), grain filling duration (-0.43) and unfilled grains/panicle (-0.98).

4.3.6.3 Plant height (cm)

Plant height exhibited significant positive correlations with number of plants /square meter (0.88), panicle weight (0.58), filled grains/panicle (0.74), test weight (0.76). Negative significant correlations with number of tillers/plant (-0.60), number of reproductive tillers/plant (-0.59), grain filling duration (-0.41) and unfilled grains/panicle (-0.76)

Table 19. Estimates of genotypic correlation coefficients for yield and yield attributing characters in medium duration maturing rice genotypes.

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13
X1	1.00												
X2	0.81**	1.00											
X3	-0.59**	-0.60**	1.00										
X4	-0.57**	-0.59**	0.99**	1.00									
X5	0.10	-0.15	-0.05	-0.02	1.00								
X6	-0.43**	-0.41**	0.01	0.04	0.42**	1.00							
X7	0.98**	0.88**	-0.69**	-0.63**	0.12	-0.37**	1.00						
X8	-0.27	-0.35	-0.30	-0.33	-0.51**	-0.06	-0.24	1.00					
X9	0.92**	0.58**	-0.46**	-0.42**	0.23	-0.33**	0.95**	-0.17	1.00				
X10	0.99**	0.74**	-0.50**	-0.48**	0.14	-0.42**	0.95**	-0.21	0.97**	1.00			
X11	-0.98**	-0.76**	0.56**	0.53**	-0.18	0.45**	-0.96**	0.26	-0.94**	-0.98**	1.00		
X12	0.96**	0.76**	-0.59**	-0.56**	0.29	-0.41**	0.95**	-0.44**	0.91**	0.96**	-0.98**	1.00	
X13	-0.97**	-0.99**	0.59**	0.62**	0.26	0.39**	-0.98**	-0.02	-0.60**	-0.80**	0.91**	-0.72**	1.00

** and * indicates Significance at 1 and 5% level

X1: Field emergence

X2: Plant Height (cm)

X3: Tiller number/plant

X4: Reproductive tiller number /plant

X5: Days to 50% flowering

X6: Grain Filling Duration

X7: Plants/square meter

X8: Panicle Length (cm)

X9: Panicle Weight (g)

X10: Filled Grains/panicle

X11: Unfilled Grains /panicle

X12: Test Weight (g)

X13: Yield/plant (g)

4.3.6.4 Number of tillers per plant

Total number of tillers per plant exhibited significant positive correlations with number of reproductive tillers/plant(0.99), unfilled grains/panicle(0.56). Negative significant correlations with number of plants/square meter(-0.69), panicle weight (-0.46), filled grains/ panicle (-0.50) and test weight (-0.59).

4.3.6.5 Number of reproductive tillers per plant

Total number of reproductive tillers per plant exhibited significant positive correlations with unfilled grains/panicle (0.53) and significant negative correlations with number of plants/square meter (-0.63), panicle weight (-0.42), filled grains/panicle (-0.48) and test weight (-0.56).

4.3.6.6 Days to 50 per cent flowering

Days to fifty per cent flowering exhibited positive significant correlations with grain filling duration (0.42). Negative significant correlation with panicle length (-0.51) .

4.3.6.7 Grain filling duration

Days to grain filling duration exhibited positive significant correlations with unfilled grains/panicle (0.45). Negative significant correlation with number of plants/square meter (-0.37), panicle weight (-0.33), filled grains/panicle (-0.42) and test weight (-0.41).

4.3.6.8 Number of plants per square meter

Number of plants per square meter exhibited significant positive correlations with panicle weight (0.95), filled grains/panicle (0.95), test weight (0.95). Negative significant correlations with unfilled grains / panicle (-0.96).

4.3.6.9 Panicle length

Panicle length exhibited a significant negative correlations with test weight (-0.44) and negative non-significant correlations with the panicle weight (-0.17), filled grains/panicle (-0.21).

4.3.6.10 Panicle weight

Panicle weight had significant positive correlations with filled grains/panicle (0.97) and test weight (0.91). Negative significant correlation with unfilled grains/panicle (-0.94).

4.3.6.11 Filled grains per panicle

Filled grains exhibited significant positive correlations with test weight (0.96). Significant negative correlations with unfilled grains / panicle (-0.98).

4.3.6.12 Unfilled grains per panicle

Unfilled grains had significant negative correlation with test weight (-0.98).

4.4 Genetic diversity analysis of rice genotypes using suitable DNA markers

In the present study, four rice SSR primers (RM 13, RM 5389, RM 161, RM 306) were used for screen fifty one rice genotypes. Among 4 SSR primers, only 2 primers showed the polymorphism while 2 primers showed monomorphic bands. (List of genotypes used table 6).

4.4.1 Similarity index

The range of similarity was from 0.39 to 1. The most of the genotypes are showing highest similarity coefficient value 1. The similarity coefficient for remaining genotypes ranged from 0.40 to 0.80.

4.4.2 Clusters analysis

The genetic similarity matrix generated from the 4 primer combinations was used to perform cluster analysis using the UPGMA clustering method following the Sequential Agglomerative Hierarchical Nested (SAHN) cluster analysis module of NTSYS. Fifty one rice genotypes were grouped into eight clusters (Fig.13) at 0.80 Jaccard's similarity coefficient, which contain 2, 2, 1, 2, 1, 5, 32 and 6 rice genotypes, respectively. Group 1 was comprised of 2 genotypes viz., UPR3926-6-1-1, IR13K 4099 with similarity coefficients of 80 per cent. Group 2 was comprised of 2 genotypes viz., RYT3448, NDR 359 with similarity coefficients of 55 per cent. Group 3 was comprised of 1 genotype viz., UPRI 2013-4 with similarity coefficients of 54 per cent. Group 4 was comprised of 1 genotype viz., IR 14K 9805 with similarity coefficients of 75 per cent. Group 5 was

comprised of 2 genotypes viz., UPR3837-7-2-1-1, IR14K9805 with similarity coefficients of 75 per cent. Group 6 was comprised of 5 genotypes viz., RYC339, OR2153-3, IR14K9269, MT4316, RYT 3450 with similarity coefficients of 80 per cent. Group 7 was the largest comprising of thirty two genotypes with similarity coefficients of 80 per cent, which was further subdivided into two clusters, group A and group B with 2 and 30 genotypes, respectively with similarity coefficients of 80 per cent. Group 8 was comprised of 6 genotypes viz., EC811512, Sabhagidhan, AD 09219, BPT5204, MT4534, and GNV14-4 with similarity coefficients of 74 per cent.

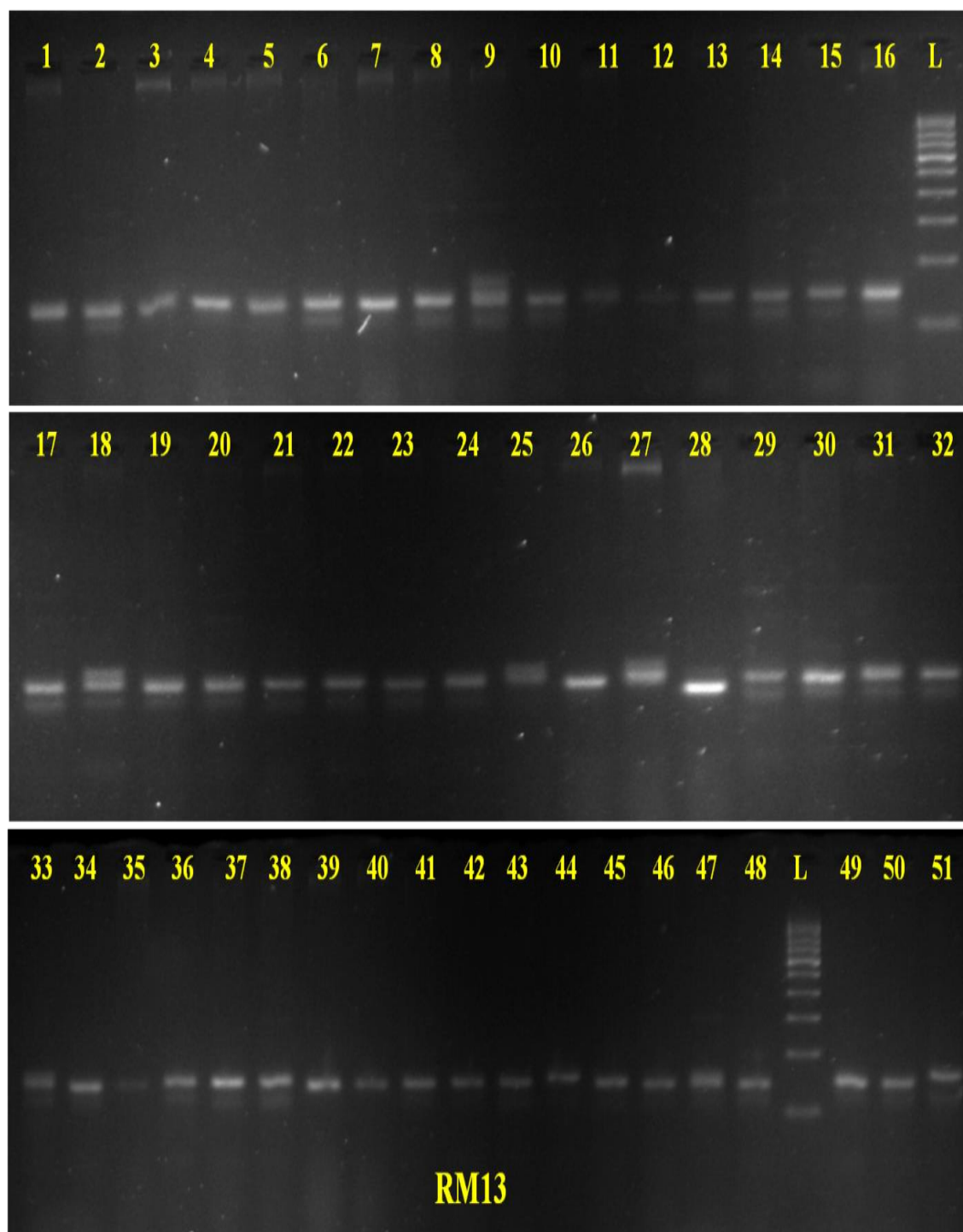


Plate 4. Molecular profiling of SSR marker RM13 in 51 genotypes.

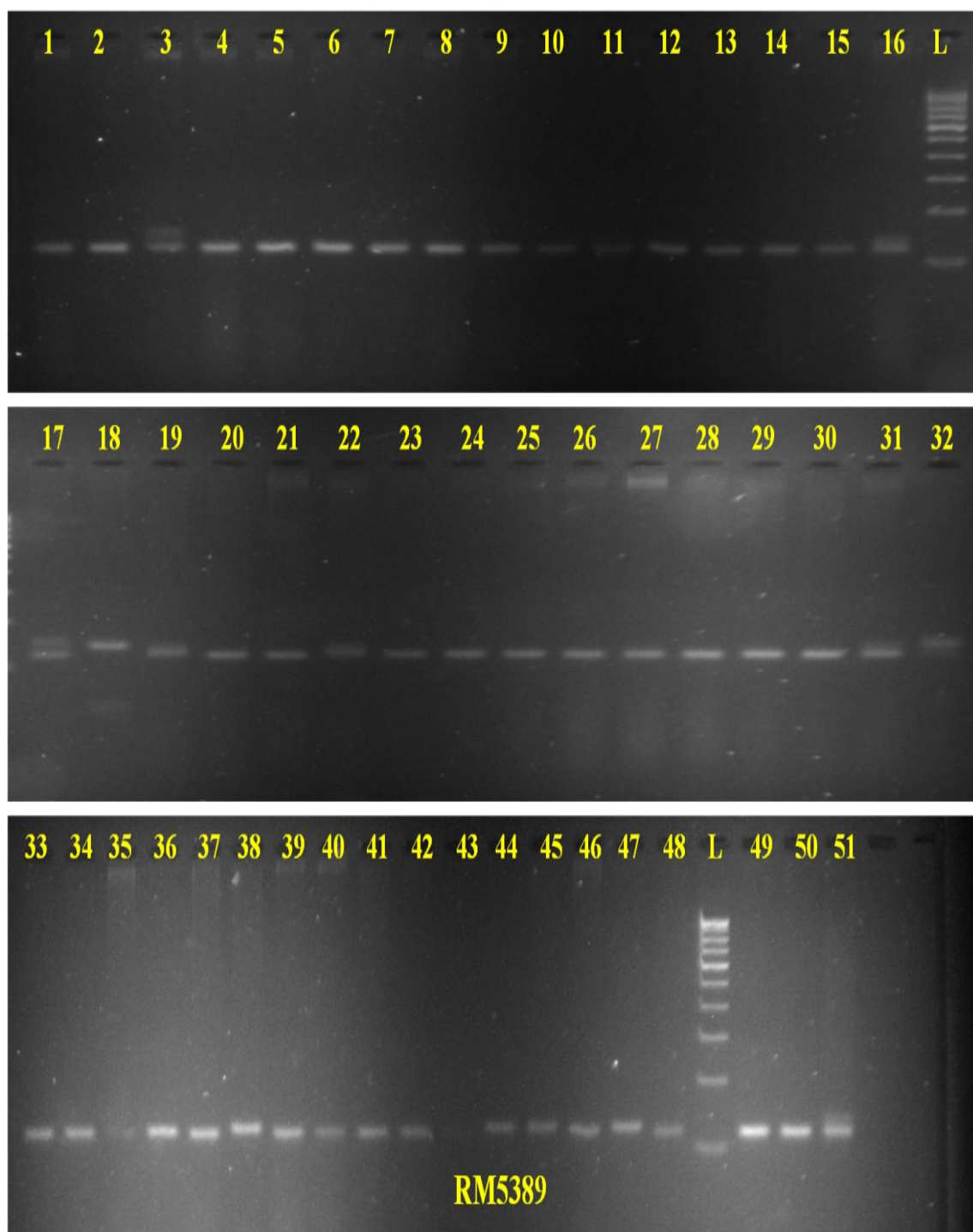


Plate 5. Molecular profiling of SSR markers RM5389 in 51 genotypes.

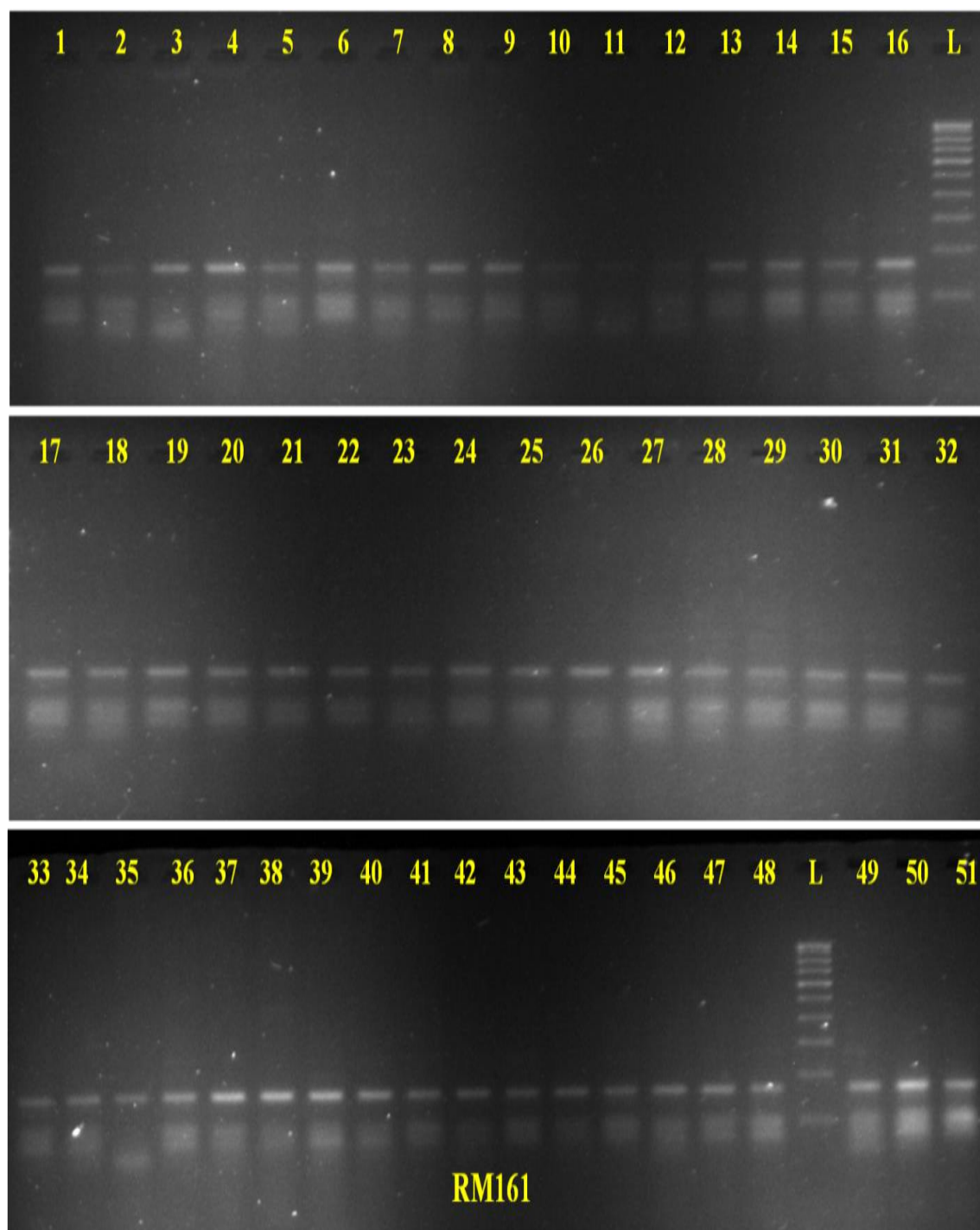
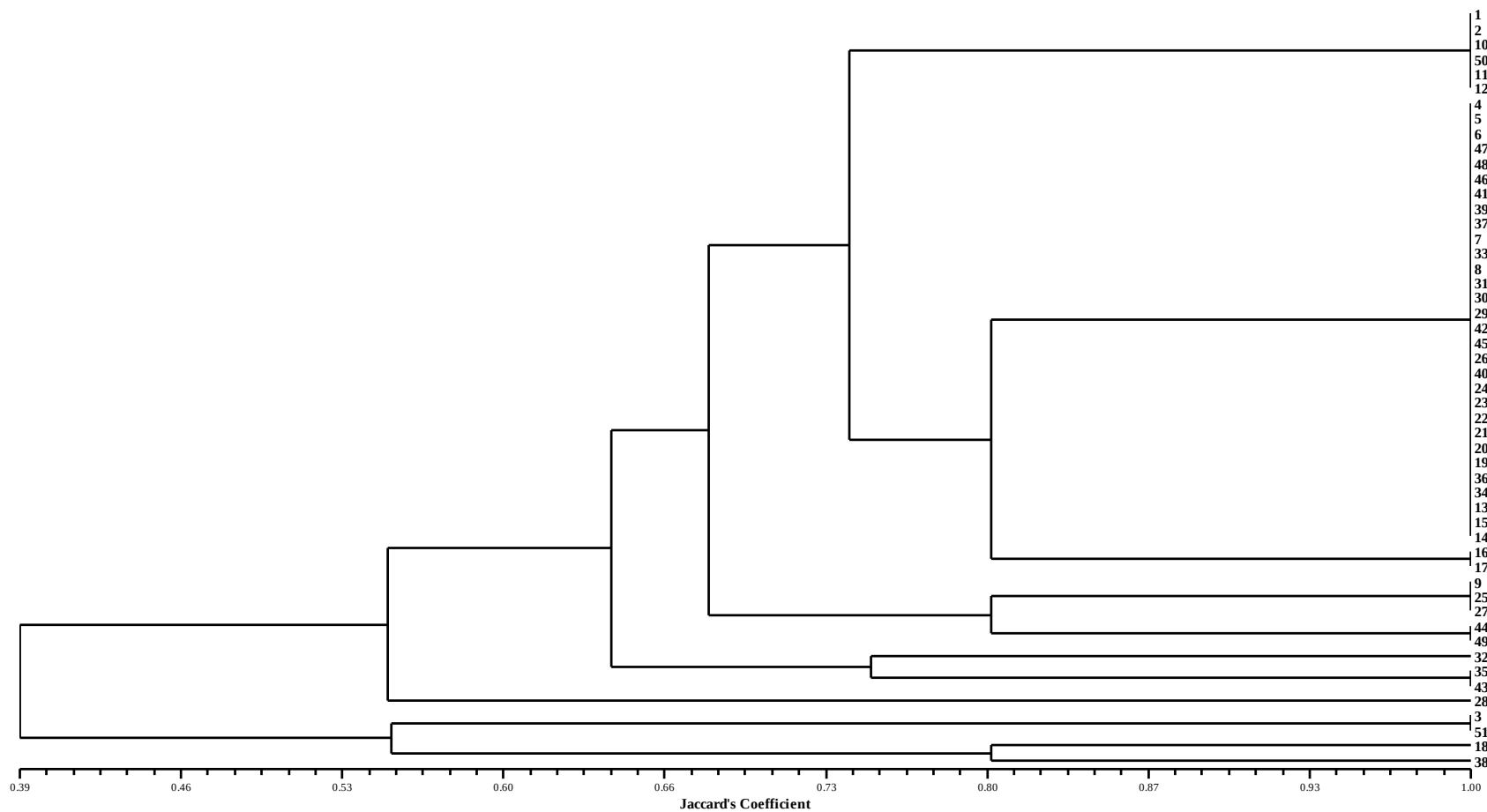


Plate 6. Molecular profiling of SSR markers RM161 in 51 genotypes



V. DISCUSSION

The collection, conservation and evaluation of genetically diverse rice germplasm is important for crop improvement programme. As on date, thousands of rice germplasm lines have been collected, documented and conserved from across the world (Siddiq 2003). The whole genome sequence of 3000 rice germplasm is stored in database by IRRI and accessible to researchers. However, only a few germplasm lines have been extensively utilized in breeding programmes possessing good traits, but still large amounts of rich diversity has been left untapped.

The success of any crop improvement programme depends on the presence of genetic variability for different characters and the extent to which the desirable trait is heritable. The utility of such material in the germplasm could be judged based on the knowledge of extent of variability, genetic diversity, character association among yield and yield attributing traits.

The present investigation was undertaken to assess the variability, character association among yield and yield attributing in rice for thirteen characters. All the information is discussed here under.

- 5.1 Assessment of differential performance of rice genotypes for direct seeded condition
- 5.2 Association study among different traits relevant to direct seeded rice along with yield.
- 5.3 Genetic diversity analysis of rice genotypes using suitable DNA markers.

5.1 Assessment of differential performance of rice genotypes for direct seeded condition

Variability was measured by estimation of mean, coefficient of variation (genotypic and phenotypic), heritability, genetic advance. Environment plays an important role in the expression of phenotype and genotype facts are inferred from phenotypic observations. Hence, variability can be observed through biometric parameters like genotypic and phenotypic coefficient of variation, heritability (broad

sense) and genetic advance. This would be of great help to breeders in evolving a selection programme for suitable gene or genotype.

The coefficient of variation expressed at phenotypic (PCV) and genotypic (GCV) levels have been compared for different characters. The PCV indicates the amount of phenotypic variability present in the character. The GCV indicates the amount of genetic variability present in the character. While, the heritability estimates aid in determining the relative amount of heritable portion of variation for that character. In fact, heritability estimates in broad sense would be reliable if accompanied by high genetic advance.

Less difference in the estimates of genotypic and phenotypic variance and higher genotypic values compared to environmental variances for all the characters suggested that the variability present among the genotypes were mainly due to genetic reason with minimum influence of environment and hence heritable.

The estimates of variance, coefficient of variation, heritability and genetic advance for all the 14 characters studied discussed here as under:

5.1.1 Field emergence

In early maturing genotypes the phenotypic and genotypic coefficients of variability were low, indicating that variation among the genotypes were low for this trait. This character had high heritability and low genetic advance as per cent mean, indicating additive and non additive gene action in the inheritance of this trait. These results are contradictory to the findings of Okelola *et al.* (2007).

In mid early maturing genotypes the phenotypic and genotypic coefficients of variability were moderate, indicating that variation among the genotypes were moderate variation for this trait. This character had high heritability coupled with high genetic advance as per cent mean indicating additive gene action in the inheritance of this trait these results are in agreement with findings of Dadlani *et al.* (1990).

In medium maturing rice genotypes the phenotypic and genotypic coefficients of variability were high, indicating that variation among the genotypes were high for this trait. This character had high heritability coupled with high genetic advance as per cent mean, indicating additive gene action in the inheritance of this trait, these results are in agreement with findings of Kharb *et al.* (1994) and Okelola *et al.* (2007).

Among three different maturing genotypes, medium duration genotypes have high heritability and genetic advance as per cent mean for field emergence, simple selection will be highly rewarding for improving this character in medium duration rice genotypes. The differences in early, mid early, medium genotypes may be due to change in genetic makeup of individual genotype and its interaction with environment.

5.1.2 Plant height

In early maturing genotypes, the phenotypic and genotypic coefficients of variability were low in early maturing genotypes, indicating that variation among the genotypes was low for this trait. This character had high heritability and moderate genetic advance as per cent mean, indicating operation of additive and non additive gene action in the inheritance of this trait. These results are in agreement with findings of Chaudhary and Motiramani (2003) and Monalisa Manna *et al.* (2006)

Mid-early maturing genotypes had moderate phenotypic and genotypic coefficients of variability indicating that variation among the genotypes was moderate for this trait. This character showed high heritability and moderate genetic advance as per cent mean, these results are in agreement with findings of Nagajyothi (2001), Patil *et al.* (2003), Krishna (2004).

Medium maturing genotypes had moderate phenotypic and genotypic coefficients of variability indicating that variation among the genotypes were moderate for this trait. Heritability and genetic advance as per cent mean were high, indicating that operation of additive gene action in the inheritance of this trait. These results are in agreement with findings of Mamta Singh *et al.* (2007), Laxuman *et al.* (2010) and Nagajyothi (2001).

Among three different maturing genotypes, medium duration genotypes had high heritability and genetic advance as per cent mean for plant height.

5.1.3 Number of tillers per plant

In early maturing genotypes, phenotypic coefficient of variability and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate for this trait. This character showed high heritability and high genetic advance as per cent mean indicate that more of additive gene action in the inheritance of this trait These results are in agreement with findings of Bhavana (2003) and Prasad *et al.* (2009).

In mid-early maturing genotypes phenotypic coefficient of variability and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate for this trait. These results are in agreement with findings of Nagajyothi (2001). Heritability and genetic advance as per cent mean were moderate indicating that presence of additive and non additive gene action in the inheritance of this trait, which agrees with the results obtained by Monalisa Manna *et al.* (2006).

In medium maturing genotypes phenotypic coefficient of variability and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate for this trait. This character showed high heritability and high GAM indicating that predominance of additive gene action in the inheritance of this trait which agrees with the results obtained by Swarup and Chaugle (1962), Swain and Reddy (2006).

Among three different maturing genotypes, early maturing genotypes have high heritability and genetic advance as per cent mean value for plant height. So more scope for selection in early maturing genotypes for this trait.

5.1.4 Number of reproductive tillers per plant

In early maturing genotypes phenotypic coefficient of variability and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate for this trait, which are in agreement with the results obtained by Karthikeyan *et al.* (2007), Kuchanur *et al.* (2009). This character showed high heritability and high genetic advance as per cent mean, indicating that predominance of additive gene action in the inheritance of this trait, which agrees with the results obtained by Singh *et al.* (2005) and Rita Binse *et al.* (2006)

In mid-early maturing genotypes phenotypic and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate for this trait. which are in agreement with the results obtained by Karthikeyan *et al.* (2007), Kuchanur *et al.* (2009). High heritability and high genetic advance as per cent mean, indicating that predominance additive gene action in the inheritance of this trait, which agrees with the results obtained by Mamta Singh *et al.* (2007), Vijaya Lakshmi *et al.* (2008).

In medium maturing genotypes phenotypic and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate for this trait, which are in agreement with the results obtained by Satish (2000), Singh *et al.* (2005). Heritability and GAM were high, indicating that more of additive gene action in the inheritance of this trait, which are in agreement with the results obtained by Monalisa Manna *et al.* (2006), Mamta Singh *et al.* (2007), Vijaya Lakshmi *et al.* (2008).

Among three different maturing genotypes, early maturing genotypes had high heritability and genetic advance as per cent mean value for this trait.

5.1.5 Days to 50 per cent flowering

In early and mid early maturing genotypes phenotypic and genotypic coefficient of variability were low, indicating that variation among the genotypes was low for this trait, which are in agreement with the results obtained by Krishna *et al.* (2008), Prasad *et al.* (2009). This character showed moderate heritability and low genetic advance as per cent mean, indicating the presence of additive and non additive gene action in the inheritance of this trait, which agrees with the results obtained by Patil *et al.* (2003), Rita Binse *et al.* (2006).

In medium maturing genotypes phenotypic and genotypic coefficient of variability were low, indicating that variation among the genotypes was low for this trait. which are in agreement with the results obtained by Laxuman *et al.* (2010), Saidaiah *et al.* (2010). This character showed low heritability and low GAM, indicating the presence of additive and non additive gene action in the inheritance of this trait, which are in agreement with the results obtained by Mamta Singh *et al.* (2007).

Among three different maturing genotypes, mid early maturing genotypes had high heritability and GAM for this trait.

5.1.6 Grain filling duration

The Phenotypic and genotypic coefficient of variability were low, indicating that variation among the genotypes was low. This character showed moderate heritability and low genetic advance as per cent mean in early and mid early maturing genotypes, indicating operation of non additive gene action in the inheritance of this trait, which are in agreement with the results obtained by Cho *et al.* (1987).

In medium maturing genotypes, phenotypic and genotypic coefficient of variability were low indicating that variation among the genotypes was low. This character showed high heritability and low genetic advance as per cent mean, indicating predominance of non additive gene action in the inheritance of this trait.

Among the three groups medium maturing rice genotypes showed high heritability with low genetic advance as per cent of mean.

5.1.7 Number of plants per square meter

In early and mid early maturing genotypes phenotypic coefficient of variability was moderate and genotypic coefficient of variability was low, indicating that variation among the genotypes was low to moderate. This character showed high heritability estimates and moderate genetic advance as per cent mean, indicating the presence of additive and non additive gene action in the inheritance of this trait, which are in agreement with the results obtained by Baloch *et al.* (2002), Mobasser *et al.* (2012) and Ogunbayo *et al.* (2014).

In medium maturing rice genotypes the phenotypic coefficient of variability and genotypic coefficient of variability were moderate, indicating that variation among the genotypes were moderate. Heritability and genetic advance as per cent mean were high indicating the more of additive gene action in the inheritance of this trait. which are in agreement with the results obtained by Romel Biswash *et al.* (2015) and Akinwale *et al.* (2011).

Among the three different maturing genotypes, medium maturing genotypes showed high Heritability and high genetic advance as per cent mean.

5.1.8 Panicle length

In early, mid early and medium maturing genotypes, phenotypic and genotypic coefficient of variability were low, indicating that variation among the genotypes are low, which are in agreement with the results obtained by Laxuman *et al.* (2010), Paikhomba *et al.* (2014) and Gampala *et al.* (2015). This character showed moderate heritability estimates and low genetic advance as per cent mean in all the three early, mid early and medium maturing rice genotypes, indicating the presence of additive and non additive gene action in the inheritance of this trait, which agrees with the results obtained by Bhavana (2003), Paikhomba *et al.* (2014), Gampala *et al.* (2015).

Among three different maturing genotypes, early maturing genotypes have high values of variability, heritability and genetic advance as per cent mean as compare to other two different group.

5.1.9 Panicle weight

In early, mid early and medium maturing genotypes, moderate estimates of both PCV and GCV were reported, indicating that variation among the genotypes are moderate these similar results are reported by Choubey and Singh (1994) and Sobita Devi *et al.* (2006). High heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the predominance of additive gene action in the inheritance of this trait which are in agreement with the results obtained by Choubey and Singh (1994) and Akinwale *et al.* (2011).

Among three different maturing genotypes, medium maturing genotypes have high variability value and these genotypes showed high heritability and genetic advance as per cent mean for this trait.

5.1.10 Filled grains per panicle

In early and medium maturing genotypes, phenotypic and genotypic coefficient of variability were high, indicating variation among the genotypes was high for this trait, which are in agreement with the results obtained by Krishna *et al.* (2008) and Prasad *et al.* (2009). This character showed high heritability and high genetic advance as per cent mean, indicating that predominance of additive gene action in the inheritance of this trait, which are in agreement with the results obtained by Singh *et al.* (2005) and Rita Binse *et al.* (2006)

In mid-early maturing genotypes, phenotypic and genotypic coefficient of variability were moderate, indicating that variation among the genotypes was medium for this trait which agrees with the results obtained by Singh *et al.* (2005). High heritability and high genetic advance as per cent mean, indicating predominance of additive gene action in the inheritance of this trait, which are in agreement with the results obtained by Sharma and Sharma (2007) and Prasad *et al.* (2009).

Among three groups early maturing genotypes showed high value for heritability and high GAM.

5.1.11 Unfilled grains per panicle

In early, mid-early and medium maturing genotypes, the estimates of both PCV and GCV were high indicating that variation among the genotypes was high. These results are in agreement with results noticed by Saidaiah *et al.* (2010). High heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the predominance of additive gene action in the inheritance of this trait. These findings are in agreement with the results reported by Khalid *et al.* (2012), Sharma and Sharma (2007) and Singh *et al.* (2005).

Among three different maturing genotypes, early maturing genotypes had high PCV and GCV value, heritability and genetic advance as per cent mean were also high.

5.1.12 Test weight

In early maturing genotypes, the moderate PCV and low GCV were reported, indicating that variation among the genotypes was low to moderate. These results were in agreement with the results obtained by Vijaya Lakshmi *et al.* (2008) and Kuchanur *et al.* (2009). Heritability and genetic advance as per cent of mean were moderate, indicating the operation of additive and non additive gene action in the inheritance of this trait. These results were in agreement with the results obtained by Kuchanur *et al.* (2009).

In mid early and medium maturing genotypes, moderate PCV and GCV were reported, indicating that variation among the genotypes is medium. These results were in agreement with the results obtained by Mamta Singh *et al.* (2007) and Sarkar *et al.* (2007). High heritability coupled with Moderate genetic advance as per cent of mean was observed for this trait, indicating that operation of additive and non additive gene action in different proportion in the inheritance of this trait. These results were in agreement with the results obtained by Satish (2000) and Khare *et al.* (2014).

5.1.13 Grain yield per plant

In early maturing genotypes, phenotypic coefficient of variability was moderate and genotypic coefficient of variability was low, indicating that variation among the genotypes are low to medium. These results were in agreement with the results obtained by Satish (2000) and Bhavana (2003). High heritability estimates and moderate genetic advance as per cent mean for grain yield per plant, indicating that operation of additive

and non additive gene action in the inheritance of this trait which are in agreement with the results obtained by Khare *et al.* (2014).

In mid-early maturing genotypes, the phenotypic coefficient and genotypic coefficient of variability were low, indicating that variation among the genotypes is low which agrees with the results obtained by Krishna (2004). Heritability and genetic advance as per cent mean were low, indicating the operation of additive and non additive gene action in the inheritance of this trait. These results were in agreement with the results obtained by Gampala *et al.* (2015)

In medium maturing genotypes, the phenotypic coefficient and genotypic coefficient of variability were low, indicating that variation among the genotypes was low. These results were agreement with the results obtained by Krishna (2004). Heritability was moderate and genetic advance as per cent mean was low, indicating the operation of additive and non additive gene action in the inheritance of this trait. These results were in agreement with the results obtained by Mamta Singh *et al.* (2007) and Satish Chandra *et al.* (2009).

Yield per plant is a major parameter to choose as a superior genotype. Among three different maturing genotypes, early maturing genotypes showed low to medium variability and high heritability with moderate genetic advance as per cent of mean for this trait as compared to mid early and medium maturing genotypes.

5.1.14 Grain yield per hectare

In early and mid early maturing rice genotypes were showed moderate for phenotypic coefficients and genotypic coefficients of variability for grain yield per hectare. High heritability coupled with high genetic advance was recorded for this trait. indicating that variation among the genotypes are medium and operation of additive gene action in the inheritance of this trait. These results were in agreement with the findings of Karthikeyan *et al.* (2007), Sharma and Sharma (2007), Prasad *et al.* (2009), Khare *et al.* (2014) and Patel *et al.* (2014).

In case of medium maturing rice genotypes phenotypic and genotypic coefficients of variability were moderate for grain yield per hectare. Moderate heritability coupled with moderate genetic advance was recorded for this trait, indicating that variation among the genotypes are medium and operation of additive and non additive gene action in the

inheritance of this trait. These results were in agreement with the results obtained by Mamta Singh *et al.* (2007) and Khare *et al.* (2014).

Among three different maturing genotypes, early maturing genotypes have high variability value and these genotypes were exhibited high heritability and genetic advance as per cent mean for grain yield per hectare as compared with other two different maturing genotypes.

5.2 Association study among different traits relevant to direct seeded rice along with yield.

Direct selection for yield and yield attributing traits is not effective as they are complex quantitative characters, highly influenced by environment. High genotype and environment interaction will restrict improvement if selection is based on yield *per se*. The effective improvement in yield may be brought about through selection on yield component characters. The aim of correlation studies is primarily to know the suitability of various characters for indirect selection because any particular trait may bring about undesirable changes in other associated characters (Singh, 1998).

Yield component characters show associations among themselves and also with yield. The unfavorable associations between the desired attributes under selection may limit genetic advance. Hence, knowledge of associations between the yield and yield components and also among the yield components is essential for planning a sound selection programme (Falconer, 1964).

The correlation estimates obtained for 13 characters of rice (*Oryza sativa* L.) are discussed here under.

5.2.1 Correlation between yield and yield components in direct seeded rice genotypes.

The degree of association among the plant and yield attributing characters at phenotypic and genotypic level as discussed here under. The study of association of yield components with yield assumes special importance and forms basis for selecting desired strains. Breeder has to establish and understand the existing relationships between yield and yield attributing characters as the genetic correlation between different characters within a plant often arise because of their genetic linkage or pleiotropy (Herald, 1939).

5.2.1.1 In early maturing direct seeded rice genotypes

5.2.1.1.1 Correlation between yield and yield components

Grain yield per plant exhibited a significant positive correlations with field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, grain filling duration, number of plants/square meter, panicle weight, filled grains/panicle and test weight. These results were in agreement with the results obtained by Amirthadevarathinam and Edwin (1990), Eradasappa *et al.* (2007), Shashidhar *et al.* (2005), Panwar (2006) and Kranti kumar *et al.* (2015). But significant negative association with unfilled grains/panicle at both phenotypic and genotypic level, these results are agreement with the results observed by Eradasappa *et al.* (2007) and Khalid *et al.* (2012).

5.2.1.1.2 Correlation among yield components

Association of yield components with yield assumes special importance and the study of which forms the basis for selecting the desired genotypes. Correlation coefficient measures the magnitude and direction of association among the characters. The genotypic correlations between different characters within a plant often arise because of either genetic linkages or pleiotropy (Herald, 1939). It is important to the breeders to establish and understand the existing relationship between the yield and yield contributing characters. It is intended to consider the issues concerning the significant inter relationships among yield character other than grain yield which might aid in conceiving an ideal plant type.

Field emergence exhibited significant positive correlations with plant height, number of tillers/plant, number of reproductive tillers/plant, grain filling duration, number of plants/square meter, panicle weight, filled grains/panicle and test weight. But significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These results are agreement with the results observed by Muhammad Akram *et al.* (2007), Adebisi *et al.* (2010).

Seedling vigor is mainly determined by the field emergence and rapid early growth of both the shoot and roots (Williams and Peterson 1973 and Sasahara *et al.* (1986). So that in early maturing genotypes, field emergence had a significant positive correlated with all most all the morphological traits so that it is essential criteria while selection in breeding programmes.

Plant height exhibited significant positive correlations with number of tillers/plant, number of reproductive tillers/plant, grain filling duration, number of plants/square meter, panicle weight, filled grains/panicle and test weight. But significant negative correlations with unfilled grains/panicle at both phenotypic and genotypic level, these results are agreement with the reported by Eradasappa *et al.* (2007), Shashidhar *et al.* (2005), Khare *et al.* (2014) and Khalid *et al.* (2012).

Total number of tillers per plant had significant positive correlation with number of reproductive tillers/plant, grain filling duration, number of plants/square meter, panicle weight, filled grains/panicle and test weight. But this trait was significant negative correlation with unfilled grains /panicle at both phenotypic ally and genotypic ally. The results are in confirmation to the findings of Swain and Reddy (2006), Krishna *et al.* (2008), Panwar and Mashiat Ali (2007) and Khalid *et al.* (2012).

Number of reproductive tillers per plant had significant positive correlation with grain filling duration, number of plants/square meter, panicle weight, filled grains/panicle and test weight but significant negatively correlations with unfilled grains/panicle at both phenotypic and genotypic level. These results are agreement with the results reported by Woonho Yang *et al.*(2008), Eradasappa *et al.* (2007), Patel *et al.* (2014), Janardhanam *et al.* (2001), Panwar (2006) and Khalid *et al.* (2012).

Grain filling duration had significant positive correlations with number of plants/square meter, panicle weight, filled grains/panicle and test weight, while significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These results are in agreement with the results observed by Jones *et al.* (1979) and Satish kumar rai *et al.* (2014).

Number of plants per square meter showed significant positive correlations with panicle weight, filled grains/panicle and test weight and significant negative correlations with unfilled grains/panicle at both phenotypic and genotypic level. These results are agreement with the results reported by Akinwale *et al.* (2011), Khalid *et al.* (2012) .

Panicle weight exhibit significant positive correlations with filled grains/panicle and test weight and significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. The present results are supported by Choubey and Singh (1994), Akinwale *et al.* (2011).

Filled grains per plant had significant positive correlations with test weight and significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These results are in agreement with the results obtained by Panwar and Mashiat Ali (2007), Patel *et al.* (2014).

A perusal of the results on character associations for grain yield, yield components revealed phenotypic and genotypic correlation to be of similar direction and significance. The genotypic correlation values were also in general higher than the phenotypic correlation values indicating the masking effects of environment on these traits. Similar results were reported by Rajput *et al.* (1996).

From the above study it can be concluded that for increasing grain yield, genotypes should possess increased field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, number of plants/square meter, panicle weight, filled grains/panicle. The results suggested that these characters are important yield contributing traits and selection of these traits would be most effective for further improvement in grain yield, the similar results were found by Amirthadevarathinam (1990), Eradasappa *et al.* (2007), Ogunbayo *et al.* (2014) and Patel *et al.* (2014).

5.2.1.2 In mid early maturing direct seeded rice genotypes

5.2.1.2.1 Correlation between yield and yield components

In mid-early maturing genotypes grain yield had significant positive correlations with field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, number of plants/square meter, panicle length, panicle weight, filled grains/panicle and test weight, while significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These results are agreement with the results obtained by Sasaki *et al.* (1999), Muhammad Akram *et al.* (2007), Bhavana (2003), Ogunbayo *et al.* (2014) and khalid *et al.* (2012).

5.2.1.2.2 Correlation among yield components

Field emergence exhibit significant positive correlations with plant height, number of tillers/plant, number of reproductive tillers/plant, number of plants/square meter, panicle length, panicle weight, filled grains/plant and test weight, while significant negative correlations observed with unfilled grains /plant at both phenotypic and

genotypic level. These results are agreement with the results reported by Muhammad Akram *et al.* (2007), Adebisi *et al.* (2010).

Field emergence was significant positive correlations with almost all the traits in direct seeded so that it is very essential criteria to incorporate this trait into direct seeded rice genotypes. Seedling vigor is genetically controlled and modified by the environment (Perry, 1972), it is essential trait under direct seeded condition so that it is possible to incorporate this trait in high yielding varieties (Seshu & Krishnasamy, 1987) and seedling vigor in rice is associated with several quantitative characters (Petersen *et al.*, 1978).

Plant height had significant positive correlations with number of tillers/plant, number of reproductive tillers/plant, number of plants/square meter, panicle length, panicle weight, filled grains/panicle and test weight and significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These results are in agreement with the results reported by Janardhanam *et al.* (2001), Satish Chandra *et al.* (2009), Neelima *et al.* (2007), Patel *et al.* (2014) and Khalid *et al.* (2012).

Total number of tillers per plant had significant positive correlations with number of reproductive tillers/plant, number of plants/square meter, panicle length, panicle weight, filled grains/panicle and test weight. But significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These results are in agreement with the results reported by Panwar and Mashiat Ali (2007), Shashidhar *et al.* (2005), Swain and Reddy (2006)

Total number of reproductive tillers per plant exhibited a significant positive correlations with number of plants/square meter, panicle length, panicle weight, filled grains/panicle and test weight, while significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. These similar results are also found by Janardhanam *et al.* (2001), Eradasappa *et al.* (2007), Panwar (2006) and Khalid *et al.* (2012).

Number of plants per square meter had a significant positive correlations with panicle length, panicle weight, filled grains/panicle and test weight at both phenotypic and genotypic level. These results are agreement with the results noticed by Akinwale *et al.* (2011), Ogunbayo *et al.* (2014) and Khalid *et al.* (2012).

Panicle length had significant positive correlation with panicle weight, filled grains/panicle and test weight and significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. The similar results were observed by Panwar (2006), Hasib (2005) and Khalid *et al* (2012). Panicle weight had significant positive correlations with filled grains/panicle and test weight but significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level. The results were in confirmation to the findings of Choubey and Singh (1994) and Akinwale *et al.* (2011).

Filled grains exhibited significant positive correlations with test weight as also found by Panwar *et al.* (2006) and Khalid *et al.* (2012).

Grain yield per plant in mid early maturing genotypes showed the positive and significant association with field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, number of plants/square meter, panicle length, panicle weight, filled grains/panicle, which indicated that grain yield can be increased if there is an increase in traits showing positive and significant association with grain yield, hence, these characters can be given priority while selecting for higher yield as these were mutually and directly associated with yield. Similar findings were found by Shashidhar *et al.* (2005), Eradasappa *et al.* (2007) and Hasib (2005)

5.2.1.3 In medium maturing direct seeded rice genotypes

5.2.1.3.1 Correlation between yield and yield components

Grain yield per plant had significant positive correlations with number of tillers/plant, number of reproductive tillers/plant, and unfilled grains/panicle at both phenotypic and genotypic level. The results are in confirmation to the findings of Swain and Reddy (2006) and Shashidhar *et al.* (2005). But significant negative association with field emergence, plant height, number of plants/square meter, filled grains/panicle, test weight at both phenotypic and genotypic level. The results are in confirmation to the findings of Borbora *et al.* (2005), Monalisa Manna *et al.* (2006) and Swain and Reddy (2006).

At genotypic level grain yield per plant exhibited significant positive correlation with grain filling duration and also it shows significant negative association with the panicle weight, where as in case phenotypic level it shows positive non-significant

association with grain filling duration and negative non-significant association with the panicle weight.

5.2.1.3.2 Correlation among yield components

Field emergence exhibits significant positive correlations with plant height, number of plants/square meter, panicle weight, filled grains/panicle and test weight. The results were in confirmation to the findings of Muhammad Akram *et al.* (2007) and Adebisi *et al.* (2010). Significantly negative correlation with number of tillers/plant, number of reproductive tillers/plant, Grain filling duration, unfilled grains/panicle at both phenotypic and genotypic level.

Plant height had significant positive correlations with number of plants/square meter, panicle weight, filled grains/panicle and test weight, while significant negative correlations with number of tillers/plant, number of reproductive tillers/plant, grain filling duration, unfilled grains/panicle at both phenotypic and genotypic level, the results were in confirmation to the findings of Janardhanam *et al.* (2001), Satish Chandra *et al.* (2009), Neelima *et al.* (2007), Patel *et al.* (2014) and Khalid *et al.* (2012).

Total number of tillers per plant had significant positive correlation with number of reproductive tillers/plant, unfilled grains /panicle. The results were in confirmation to the findings of Shashidhar *et al.* (2005). But significant negative correlations with number of plants/square meter, panicle weight, filled grains/panicle and test weight at both phenotypic and genotypic level. These results are in agreement with the findings of Rita Binse *et al.* (2006), Monalisa Manna *et al.* (2006) and Borbora *et al.* (2005).

Total number of reproductive tillers per plant had significant positive correlations with unfilled grains/panicle, while significant negative correlations with number of plants/square meter, panicle weight, filled grains/panicle, test weight at both phenotypic and genotypic level. The results were in confirmation to the findings of Rita Binse *et al.* (2006), Manna *et al.* (2006), Sharma and Sharma (2007) and Borbora *et al.* (2005).

Number of plants per square meter had significant positive correlation with panicle weight, filled grains/panicle and test weight. The results were in confirmation to the findings of Akinwale *et al.* (2011), Ogunbayo *et al.* (2014), Khalid *et al.* (2012) and significant negative correlation with unfilled grains/panicle at both phenotypic and genotypic level.

Filled grains had significant positive correlations with test weight and significant negative correlations with unfilled grains /panicle at both phenotypic and genotypic level, these results are in agreement with the findings of Panwar *et al.* (2006) and Khalid *et al.* (2012).

Unfilled grains had significant negative correlations with test weight as it observed that medium maturing genotypes were exposed to cold stress during flowering so more number of unfilled grains found for seed setting.

In association study reported that positive significant association between yield and number of tillers, number of reproductive tillers these traits are consider as a major parameters responsible for grain yield (Yadav, 1992, Girish *et al.* 2006).

Grain yield per plant in medium maturing genotypes showed the positive and significant association with number of tillers/plant, number of reproductive tillers/plant, grain filling duration indicated that grain yield can be increased if there is an increase in traits showing positive and significant association with grain yield, These results are similar with the findings of Shashidhar *et al.* (2005), Swain and Reddy (2006) and Satish Kumar Rai *et al.* (2014).

5.3 Genetic diversity analysis of rice genotypes using suitable DNA markers

Individual identification based on morphological characterization is the most common practice. The continued usage of morphological characterization to describe a genotype/cultivar indicates its popularity as descriptors. The constraints on usage of morphological data are (i) narrow range of morphological diversity, (ii) effect of environment on morphology and (iii) the inability of morphological data to estimate genetic distance accurately.

The morphological data cannot provide reliable information of calculation of genetic distance in terms of validation of pedigree. The recent advances in molecular biology has provided opportunity to describe cultivars/genotypes based on protein and DNA as an aid to plant breeding programme. Genetic diversity caused by sexual reproduction i.e. hybridization, selection and mutation results in genome changes from one base pair to entire chromosome. The molecular markers that are not influenced by environmental changes provide an opportunity to examine the genetic relationship

between accessions more precisely and also acts as valuable tool for identification of parental lines and varieties for protection of plant breeder's right.

The detection of Simple Sequence Repeats (SSR) polymorphism has become one of most frequently used technique in molecular finger printing. SSRs are the most reliable markers for cultivar identification, genetic diversity evaluation and property rights protection, due to their random distribution, high polymorphism, co-dominant mendelian inheritance coupled with high mutation rate, these SSR markers provide highest polymorphic information content. Therefore SSR markers have become one of the principle classes of DNA markers used for DNA finger printing, genetic mapping and molecular breeding in crop plants.

Population structure and diversity is commonly estimated by using SSR derived information, because of the proven usefulness of this type of markers for population genetics inferences and their higher information content when compared to biallelic markers.

Genetic diversity is the extent to which the heritable material differs within a group of plants, which is a result of evolution, including domestication and plant breeding. Assessing genetic diversity of cultivated crop plants is important to select proper genotype for hybridization programme.

To define the phylogenetic relationship between 51 DSR genotypes with 4 SSR markers were used in present study. Genetic similarity of rice genotypes was calculated using Jaccards similarity coefficient by analysing 4 SSR markers. These similarity coefficients were used to generate dendrogram by UPGMA analysis in order to determine the phylogenetic relationship based on grouping of different genotypes.

The genetic similarity computed considering pooled data of SSR markers showed very wide range from 0.33 to 1 indicating the presence of high variability among 51 rice genotypes. Similar results were reported by Erasmus (2008).

In this study we used both superior and low performing rice genotypes for screening using SSR markers. The DNA isolated from individual genotype was amplified and scored, which indicated both mono and polymorphism. The monomorphism indicated presence of similar genomic regions while polymorphism indicated diverse regions, which is depicted through different clusters. In the present study the markers

were selected based on previous reports which were found to be associated with traits relevant to performance of direct seeded rice, however no clear association was found hence more DNA markers need to be used for screening, which will further help in establishing marker-trait association and ultimately Marker Assisted Selection (MAS).

VI. SUMMARY AND CONCLUSIONS

An investigation was carried out involving forty early, forty mid early and thirty six medium maturing direct seeded rice genotypes. The objectives were to assess the relative performance, estimation of genetic variability, heritability, genetic advance, genetic divergence and association study among the rice genotypes for grain yield and yield contributing traits. The experiment was conducted at the Agricultural Research Station, Gangavati, University of Agricultural Sciences, Raichur, during *Kharif* 2015. The field layout was Randomized Block Design (RBD) with two replications.

Fourteen quantitative characters like field emergence, plant height, tiller number, reproductive tiller number, days to 50% flowering, grain filling duration, number of plants per square meter, panicle length, panicle weight, filled and unfilled grains, test weight, grain yield per plant and grain yield per hectare were studied. The salient results of the study and conclusions drawn from the experiment are summarized below.

The analysis of variance revealed highly significant mean sum of squares for all traits in direct seeded condition for all the three different maturing genotypes, indicating that there was ample scope for selection of promising lines from present genotypes which are suitable for direct seeded condition.

The experimental results concluded that IR 14K 11485, IR 14K 11350, IR 14K 9922, IR 14K 11465, RYC 339 recorded best performance for grain yield in early maturing genotypes, whereas in case of mid early maturing genotypes IR 14K 10158, MT 4111, IR 14K 9762, BPT 2613, GGV-05-01 recorded best performance for grain yield and in case of medium maturing genotypes UPR 3926-6-1-1, IR 14K 10236, IR 14K 9977, IR 14K 10203, UPR 3946-20-1-1 recorded best performance for grain yield.

Phenotypic coefficients of variability values for all yield attributing traits were higher than genotypic coefficients of variability. However, difference between PCV and GCV were less for these characters, indicating low environmental influence and predominance of genetic factor controlling variability in these traits.

In case of early maturing genotypes high PCV and GCV values were recorded for characters viz., number of filled grains per panicle, number of unfilled grains per panicle whereas number of tillers/plant, number of reproductive tillers /plant, panicle weight,

and grain yield/plot shows moderate PCV and GCV. The characters like field emergence, plant height, days to 50% flowering, panicle length, grain filling duration showed low PCV and GCV. Whereas character like test weight, number of plants/square meter, grain yield/plant are shows moderate PCV and low GCV.

In case of mid early maturing rice genotypes high PCV and GCV values were observed for character like number of unfilled grains per panicle. The character like field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, number of filled grains per panicle, panicle weight, test weight showed moderate PCV and GCV. While traits like days to 50% flowering, panicle length, grain filling duration, grain yield/plant showed low PCV and GCV. The character like number of plants/square meter showed moderate PCV and low GCV.

In case of medium maturing rice genotypes high PCV and GCV values were observed for characters viz., number of field emergence, number of filled grains per panicle, unfilled grains per panicle, panicle weight. The characters viz., plant height, number of tillers/plant, number of reproductive tillers /plant, test weight, number of plants/square meter exhibited moderate PCV and GCV, while characters like days to 50% flowering, panicle length, grain filling duration, grain yield/plant observed low PCV and GCV.

In early maturing rice genotypes the characters viz., field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, number of filled grains per panicle, unfilled grains per panicle, panicle weight, number of plants/square meter, grain yield/plant, grain yield/plot recorded high heritability and characters like panicle length, test weight, grain filling duration, days to 50% flowering showed moderate heritability, while the characters like number of tillers/plant, number of reproductive tillers/plant, number of filled grains per panicle, unfilled grains per panicle, panicle weight, grain yield/plot observed high genetic advance percent mean. Whereas characters like plant height, test weight, number of plants/square meter, grain yield/plant showed moderate genetic advance percent mean and also characters like field emergence, days to 50% flowering, panicle length, grain filling duration exhibited low genetic advance as percent mean.

In mid early maturing rice genotypes the characters viz., field emergence, plant height, number of reproductive tillers /plant, number of filled grains per panicle, unfilled

grains per panicle, panicle weight, test weight, number of plants/square meter, grain yield/plant, grain yield/plot showed high heritability and characters like number of tillers/plant, days to 50% flowering, panicle length, grain filling duration showed moderate heritability, whereas character like grain yield/plant observed low heritability. The characters like field emergence, number of reproductive tillers/plant, number of filled grains per panicle, unfilled grains per panicle, panicle weight, grain yield/plot recorded high genetic advance percent mean, whereas character like plant height, number of tillers/plant, test weight, number of plants/square meter showed moderate genetic advance percent mean and character like days to 50% flowering, panicle length, grain filling duration, grain yield/plant exhibited low genetic advance percent mean.

In medium maturing rice genotypes the characters viz., field emergence, plant height, number of tillers/plant, number of reproductive tillers /plant, number of filled grains per panicle, unfilled grains per panicle, panicle weight, test weight, number of plants/square meter, grain filling duration were recorded high heritability. Whereas the characters like panicle length, grain yield/plant, grain yield/plot shows moderate heritability and character like days to 50% flowering showed low heritability. The field emergence, plant height, number of tillers/plant, number of reproductive tillers / plant, number of filled grains per panicle, unfilled grains per panicle, panicle weight , number of plants/square meter showed high genetic advance percent mean. Whereas, test weight and grain yield/plot showed moderate genetic advance percent mean and also the character like days to 50% flowering, panicle length, grain filling duration and grain yield/plant exhibited low genetic advance percent mean.

In the correlation study among yield and yield attributing traits, the study revealed that in early maturing rice genotypes, grain yield exhibited significant positive correlation with field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, grain filling duration, number of plants/square meter, panicle weight, filled grains/plant, test weight and significant negative association with the unfilled grains per plant at both phenotypic and genotypic level.

In mid early maturing rice genotypes grain yield per plant exhibited significant positive correlations with field emergence, plant height, number of tillers/plant, number of reproductive tillers/plant, number of plants/square meter, panicle length, panicle

weight, filled grains/plant and test weight and significant negative association with the unfilled grains per plant at both phenotypic and genotypic level.

Grain yield per plant in medium duration maturing rice genotypes exhibited significant positive correlations with number of tillers/plant, number of reproductive tillers/plant and unfilled grains, Hence, the traits having significant association are useful in selection in breeding programme for improving grain yield in a direct seeded genotypes.

Molecular diversity assessment among fifty one rice genotypes using SSR markers revealed that the genetic similarity index computed considering data of SSR markers showed very wide range from 0.33 to 1 indicating high variability among DSR genotypes. The dendrogram separated 51 rice genotypes into eight main clusters at 0.80 Jaccard's similarity coefficient. Which contain 2, 2, 1, 2, 1, 5, 32 and 6 rice genotypes, respectively.

From the present study, it is evident that genotypes studied under direct seeded condition may provide good source of material for further breeding program. Therefore, information on the genetic parameters such as coefficient of variation, heritability, genetic advance, correlation coefficients can help the breeder to evolve suitable cultivars for DSR condition within a short time. On the basis of results as summarized above, it is concluded that the great deal of variability for the important characters observed even in highly selected lines under the present investigation. High heritability with high genetic advance with positive significant correlation characters act as a due importance for improving the grain yield under DSR condition. The superior performing rice genotypes can be further evaluated under different locations to know their stability performance across the locations and released for cultivation under DSR condition. But many of these genotypes are having large bold seed size hence these genotypes can be used in breeding programme to derive genotypes suitable to DSR condition along with acceptable grain quality features ..

Future line of work

- ✓ The Variability present for different yield and yield attributing traits in all the three different maturing direct seeded rice genotypes can be exploited by direct selection.

- ✓ Hybridization work can be planned between genotypes superior for different traits to tailor desired genotypes suitable for direct seeded condition.
- ✓ The genotypes identified on the mean performance basis as high yielding genotype can be further evaluated under crop densities preferably over locations and years to confirm their superiority and further release as variety suitable to DSR condition.
- ✓ The Molecular analysis of genotypes can be planned to identify markers linked to the traits important to DSR condition which would be useful in Marker Assisted Selection.

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APPENDIX -1

Mean performance of 40 early maturing direct seeded rice genotypes for plant and yield attributing characters

Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
1	GNV 14-4	88.90	94.25	12.65	10.70	84.00	30.50	31.50	20.95	3.31	131.80	5.40	24.50	20.86	6575.00	LB
2	MT 4533	84.15	87.00	10.70	10.55	86.00	28.50	29.50	21.20	2.75	106.40	8.60	23.75	17.66	5200.00	LB
3	RYC 339	92.35	103.00	14.10	13.10	84.50	31.50	33.50	21.00	3.58	150.20	3.50	25.30	20.62	6900.00	LB
4	IR 14K 9922	93.45	106.00	15.80	15.00	84.00	32.50	34.50	19.15	3.84	158.00	3.30	26.30	21.06	7257.82	LB
5	IR 14K 11350	93.20	107.70	17.50	16.45	82.00	32.50	33.00	20.85	3.93	162.80	2.80	27.05	22.20	7332.82	LB
6	EC 811508	81.50	83.00	11.10	10.20	85.50	28.50	28.00	20.45	2.28	96.20	10.70	22.66	15.63	4375.00	LB
7	OR 2521-5	79.70	82.00	10.40	9.55	79.00	28.00	26.00	23.40	2.22	91.60	12.30	21.39	16.16	4200.00	LB
8	IR 14K 11463	89.70	93.60	13.00	12.40	86.50	31.50	33.00	21.60	3.21	128.40	6.00	24.68	19.07	6275.00	LB
9	IR 13K 5179	89.85	93.70	13.30	12.20	84.50	30.00	32.50	22.80	3.22	135.30	5.70	24.78	20.22	6575.00	LB
10	IR 14K 11381	86.95	91.60	12.00	11.30	84.50	30.50	30.50	22.90	2.97	116.80	6.80	24.11	19.26	5875.00	LB
11	MT 4060	82.55	85.50	10.65	9.65	82.50	28.50	29.00	20.90	2.57	102.70	8.70	22.65	16.98	4925.00	LB
12	IR 13K 5173	89.20	93.00	12.70	11.90	84.00	30.50	31.50	21.75	3.17	123.50	6.40	24.54	19.87	6250.00	LB
13	IR 14K 10003	85.90	91.70	11.00	10.30	86.50	29.50	32.00	19.95	2.96	116.70	7.20	24.05	18.10	5775.00	LB
14	MT 4074	82.10	85.00	10.85	10.25	85.00	29.00	28.00	20.40	2.50	99.90	9.90	22.90	16.91	4725.00	LB
15	IR 14K 11485	93.95	110.30	18.70	18.15	82.00	33.50	34.50	19.15	3.94	170.50	2.90	30.96	21.60	7445.32	LB

Cont...

Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
16	IET-19251	82.75	88.00	11.05	10.65	78.00	29.50	29.50	20.85	2.81	109.50	7.70	23.74	17.81	5250.00	MS
17	UPR 3906-18-2-1	83.50	87.85	10.90	10.50	84.00	29.50	28.50	20.90	2.75	105.50	8.50	23.10	17.83	5075.00	LB
18	EC 811508	82.30	88.20	10.60	10.15	86.00	28.50	27.50	24.15	2.69	104.00	8.80	23.74	18.26	5025.00	LS
20	GNV 14-3	82.55	89.90	10.35	9.70	85.00	30.00	29.50	25.20	2.55	109.00	8.40	23.59	17.79	5250.00	LB
21	EC 811547	89.20	93.30	11.85	11.30	88.00	30.50	31.50	20.30	3.05	122.65	6.80	24.24	19.38	6100.00	LB
22	EC 811512	85.90	92.80	12.60	11.90	81.50	30.50	30.50	20.45	2.98	118.90	7.20	24.40	19.62	5975.00	LB
23	IR 14K 10450	82.10	81.10	10.35	9.60	83.50	28.00	25.00	21.85	2.70	86.00	16.10	16.61	16.44	4100.00	LB
24	UPR 3912-21-2-1	93.95	91.00	12.45	11.20	83.00	31.00	29.50	21.70	2.94	116.30	7.60	23.75	19.32	5700.00	LB
25	EC 811543	82.75	96.80	12.95	12.55	84.00	31.50	31.50	22.50	3.36	134.50	5.60	25.01	21.52	6773.44	LB
26	IR 14K 11353	83.50	79.20	9.00	8.55	87.50	27.00	25.00	19.10	2.09	79.40	18.30	16.60	16.23	4055.00	LB
27	RYT 3448	82.30	84.10	11.10	10.45	84.00	28.50	27.50	22.90	2.56	94.70	10.60	22.79	16.54	4550.00	LB
28	IR 14K 10214	80.95	95.60	12.50	11.80	83.50	31.50	31.50	20.20	3.08	134.40	5.70	25.11	21.43	6742.19	MS
29	Sahbhagidhan	82.40	86.60	11.05	10.10	84.50	28.50	28.50	21.05	2.36	100.50	8.60	23.06	16.70	4750.00	LB
30	MT 4552	89.15	82.20	9.80	9.25	83.50	27.50	25.50	19.25	2.23	85.30	12.40	20.95	16.26	4150.00	LB
31	EC 811511	87.40	91.40	12.00	11.20	78.50	30.50	30.50	22.40	3.05	114.80	7.50	23.71	17.94	5475.00	LB
32	MT 4534	77.70	96.80	12.80	12.40	87.50	31.50	33.50	20.85	3.30	141.90	4.90	24.96	20.52	6875.01	LB

Cont...

Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
33	RYT 3443	85.55	101.70	14.10	13.10	80.00	30.50	34.00	21.85	2.75	145.10	5.10	24.84	20.26	6875.00	LB
34	AD 09219	90.40	77.70	9.00	8.50	89.00	27.00	22.00	20.10	1.61	59.30	22.90	21.46	15.63	3429.69	LB
35	MT 4375	72.45	87.25	10.90	10.35	86.00	28.50	29.00	20.00	2.70	104.10	8.70	23.06	17.25	5000.00	LB
36	BPT 2671	82.10	93.20	12.70	12.10	85.50	30.50	31.50	23.50	2.64	123.40	7.00	23.73	19.30	6075.00	LB
37	IR 14K 10405	84.55	90.40	12.30	11.85	89.50	30.50	29.00	23.35	3.05	115.50	8.00	23.01	18.61	3.46	LB
38	OR 2567-2	85.30	90.00	10.90	10.40	87.50	29.50	30.00	21.20	2.84	110.50	8.30	23.33	17.51	3.36	MB
39	IR 14K 11465	92.00	104.40	14.80	14.00	87.00	32.50	34.00	22.40	3.49	154.60	4.10	25.90	20.45	4.45	LB
40	IR 13K 5177	85.55	90.65	11.90	11.10	85.00	29.50	31.00	20.85	3.00	117.70	8.10	22.82	17.07	3.38	MS
Grand Total		3413.8	3651.2	482.7	454.05	3375.5	1195.5	1199	853.85	115.6	4669.0	328.4	945.69	741.9	224064.4	
Mean		85.35	91.28	12.07	11.35	84.39	29.89	29.98	21.35	2.89	116.73	8.21	23.64	18.55	3.59	
CV (%)		3.69	4.29	6.27	5.78	3.25	4.97	4.40	5.08	5.26	4.60	3.98	7.20	6.99	6.77	
S.E.		2.23	2.77	0.54	0.46	1.94	1.05	0.93	0.77	0.31	10.85	0.66	3.44	2.62	0.49	
C.D. 5%		6.37	7.92	1.53	1.33	5.54	3.00	2.67	2.19	0.41	14.53	0.89	4.61	3.51	0.66	

X1: Field emergence

X5: Days to 50% flowering

X9: Panicle Weight (g)

X13: Yield/plant (g)

MS: Medium Slender

X2: Plant Height (cm)

X6: Grain Filling Duration

X10: Filled Grains/panicle

X14: Yield/hectare (Kg)

MB: Medium Bold

X3: Tiller number/plant

X7: Plants/square meter

X11: Unfilled Grains /panicle

LB: Long Bold

X4: Reproductive tiller number plant

X8: Panicle Length (cm)

X12: Test Weight (g)

LS: Long Slender

APPENDIX -2

Mean performance of 40 mid early maturing direct seeded rice genotypes for plant and yield attributing characters

Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
1	MT 4124	76.80	102.80	13.90	12.35	87.00	32.50	28.00	23.76	3.85	156.10	9.00	24.30	22.87	6390.63	LB
2	BPT 2570	50.48	83.35	11.00	9.95	94.50	35.00	19.50	19.16	2.53	102.70	30.00	17.75	23.21	4523.44	MS
3	MT 4039	73.50	95.35	14.90	10.45	85.50	31.50	26.50	23.16	3.46	145.90	11.90	22.80	21.42	5671.88	LB
4	GNV 14-2	85.07	113.00	15.00	13.70	100.00	30.50	27.00	24.56	4.03	175.20	7.80	25.65	25.68	6921.88	MB
5	IR 14K 9269	65.38	91.90	12.50	10.55	94.00	30.50	25.50	22.06	3.01	122.80	18.90	21.70	20.86	5296.88	LB
6	RYT 3447	73.65	92.20	13.05	11.90	93.00	28.50	25.50	22.96	3.43	140.50	12.00	22.25	21.87	5570.32	MB
7	OR 2153-3	70.53	90.75	12.70	11.85	84.00	31.50	26.00	22.36	3.14	127.80	15.70	22.85	20.68	5359.38	MB
8	MT 4111	90.90	117.05	16.90	15.60	86.50	31.00	31.00	24.75	4.71	188.50	5.40	26.80	23.23	7195.32	LB
9	IR 14K 10485	72.12	88.30	12.05	10.75	92.50	28.50	24.00	21.56	2.93	114.80	21.30	21.30	20.33	4875.01	LB
10	MTU 1010	77.25	100.60	13.95	12.65	90.50	29.50	26.50	23.36	3.69	152.80	10.80	24.30	22.80	6039.07	LB
11	IR 14K 9802	55.48	85.15	11.65	9.85	92.50	30.00	23.00	20.56	2.78	111.10	25.20	18.25	20.25	4656.26	LB
12	IR 13K 5165	60.48	87.40	12.30	11.40	91.00	29.50	24.50	21.36	2.89	113.90	21.80	21.40	19.95	4875.00	LS
13	IR 14K 10147	73.70	94.50	13.60	12.10	85.00	30.00	26.50	23.36	3.41	147.20	11.50	24.35	21.79	5773.44	LS
14	GNV 14-1	73.95	93.10	12.25	11.80	87.50	31.50	27.50	22.96	3.41	135.60	13.40	22.80	21.66	5523.44	LB
15	UPRI 2013-4	63.65	89.45	11.95	10.60	92.50	32.00	23.00	21.76	2.99	120.50	20.20	20.80	21.81	5000.00	LB
16	UPR 3837-7-2-1-1	65.18	90.10	12.30	11.40	86.50	30.50	23.50	21.96	2.97	122.30	19.90	21.75	22.45	5281.25	LB

Cont...

Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
17	IR 14K 10158	92.68	119.00	18.20	17.40	90.00	29.50	29.00	24.76	4.93	190.50	5.10	26.65	25.39	7351.57	LB
18	IR 14K 10174	44.05	81.25	10.20	9.30	90.00	30.00	20.00	19.16	2.40	99.90	31.90	16.45	22.41	4476.57	MS
19	IR 14K 10503	75.47	99.30	13.80	12.80	88.00	29.50	27.00	23.36	3.59	151.40	10.90	23.90	21.68	5843.75	LB
20	MT 4852	77.35	102.00	13.95	12.40	85.00	29.00	28.00	23.55	3.78	152.30	10.30	24.20	21.80	6101.57	LB
21	GGV-05-01	84.60	112.20	15.00	13.40	90.00	31.50	29.50	24.56	4.22	175.60	7.10	25.90	23.65	6953.13	MS
22	NLR 3444	72.02	93.15	12.80	12.00	87.50	28.50	26.00	22.76	3.21	129.90	15.60	22.80	20.92	5429.69	LB
23	MT 4124	79.18	103.90	13.50	12.45	85.00	31.50	27.50	23.96	3.96	157.20	9.90	25.40	23.75	6523.44	LB
24	BPT 2613	86.73	113.55	16.00	14.55	82.00	30.00	28.50	24.56	4.28	180.10	7.10	26.90	24.74	7023.44	LB
25	MT 4389	79.13	105.60	14.60	13.20	81.50	29.50	26.50	24.16	4.06	160.00	8.30	24.70	24.81	6570.32	LB
26	OR 2512-6	55.43	84.25	10.85	10.25	91.50	29.50	22.00	20.56	2.73	110.00	25.10	17.90	21.04	4625.01	LB
27	MTU 1081	73.93	97.40	13.30	12.10	89.00	30.50	27.00	23.36	3.54	148.10	10.90	23.60	21.40	5929.69	LB
28	RYC 242	72.02	92.85	12.85	12.30	91.50	31.50	26.00	22.96	3.31	133.50	14.80	22.25	20.92	5265.63	LB
29	IR 14K 9805	63.65	88.30	11.40	10.55	86.50	32.50	25.00	21.56	2.97	115.50	20.90	21.20	19.55	4875.01	LB
30	IR 14K 10475	68.65	92.00	12.75	12.30	87.50	31.50	26.00	22.36	3.12	125.80	16.00	22.30	20.59	5351.57	LB
31	IR 14K 10197	83.27	107.25	13.90	12.90	92.50	33.00	27.50	24.36	4.03	166.90	7.90	25.50	24.24	6664.07	MS
32	IR 13K 4099	56.52	85.40	12.00	11.05	88.50	30.00	23.50	20.96	2.81	118.30	22.90	19.30	20.10	4703.13	LB

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Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
33	BPT 2605	50.48	83.45	10.70	10.20	82.50	31.50	22.00	20.16	2.77	109.60	25.70	18.45	20.98	4593.76	LB
34	IR 14K 9762	88.78	115.65	16.35	14.90	81.50	31.50	29.50	24.76	4.39	182.60	6.90	26.70	24.21	7125.01	LB
35	MT 4393	83.78	110.30	14.80	13.80	85.00	32.50	29.50	24.36	4.04	171.90	7.80	25.15	23.22	6828.13	LB
36	MT 4037	73.55	94.20	12.90	11.60	81.00	29.50	26.00	23.16	3.41	143.60	11.90	23.40	21.79	5648.44	LB
37	RYT 3449	42.22	80.50	8.95	8.35	84.50	30.00	20.00	18.96	2.23	88.80	33.20	15.30	21.53	4296.88	LB
38	IR 14K 10164	57.02	86.10	11.90	11.05	90.50	32.50	24.00	21.36	2.78	114.60	22.00	20.30	20.27	4851.57	LB
39	IR 13K 5168	65.33	89.90	12.70	11.30	89.50	33.50	25.00	22.36	3.05	124.40	16.40	22.35	21.36	5320.32	LB
40	MT 4269	83.68	108.80	14.35	13.40	88.50	32.50	29.50	24.35	4.14	170.20	7.80	25.35	23.20	6820.32	LB
Grand Total		2837.6	3861.3	527.75	480.45	3531.5	1233.5	1032	905.88	136.98	5598.4	611.2	905	884.32	228125.0	
Mean		70.94	96.53	13.19	12.01	88.29	30.84	25.80	22.65	3.42	139.96	15.28	22.63	22.11	5703.13	
CV (%)		4.65	5.68	12.61	9.62	4.60	4.03	6.17	5.97	8.38	4.22	11.72	8.03	7.43	6.81	
S.E.		2.33	3.88	1.18	0.82	2.87	0.88	1.13	0.96	0.20	4.18	1.27	1.28	1.16	274.64	
C.D. 5%		6.67	11.10	3.36	2.34	8.21	2.51	3.22	2.74	0.58	11.96	3.62	3.67	3.32	785.61	

X1: Field emergence

X2: Plant Height (cm)

X3: Tiller number/plant

X4: Reproductive tiller number plant

X5: Days to 50% flowering

X6: Grain Filling Duration

X7: Plants/square meter

X8: Panicle Length (cm)

X9: Panicle Weight (g)

X10: Filled Grains/panicle

X11: Unfilled Grains /panicle

X12: Test Weight (g)

X13: Yield/plant (g)

X14: Yield/hectare (Kg)

LB: Long Bold

LS: Long Slender

MS: Medium Slender

MB: Medium Bold

APPENDIX -3

Mean performance of 36 medium maturing direct seeded rice genotypes for plant and yield attributing characters

Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	Grain Type
1	IR 13K 5129	76.45	113.60	12.50	11.70	92.00	32.50	28.50	20.10	3.22	143.30	7.30	24.45	19.51	5562.51	LB
2	IR 13K 5156	82.02	92.05	13.85	13.25	89.50	32.50	31.00	21.75	3.73	173.20	5.30	26.40	19.49	6039.07	LS
3	IR 14K 10041	57.68	90.25	15.30	14.25	92.00	33.00	26.00	21.75	2.61	117.90	11.20	23.20	18.91	4914.07	MB
4	RYT 3438	71.46	111.90	14.90	13.45	86.50	31.00	29.00	21.90	3.49	141.90	8.00	24.30	18.87	5468.76	LB
5	IR 14K 10455	69.45	106.50	11.55	10.40	85.00	29.50	29.00	20.90	2.86	135.70	8.40	24.10	18.67	5414.07	LB
6	IR 14K 10042	67.54	91.45	15.70	14.60	88.50	30.00	28.00	22.30	2.86	127.80	10.10	24.00	18.75	5234.38	MB
7	IR 14K 10236	91.30	97.40	14.20	13.55	93.50	32.50	31.50	20.65	4.89	185.30	2.50	29.75	20.18	6351.57	MB
8	UPR 3926-6-1-1	91.99	96.75	14.05	13.10	92.50	30.50	33.00	21.75	5.05	188.50	2.20	30.80	19.70	6492.19	LB
9	IR 14K 9977	91.01	97.25	13.00	11.55	90.00	30.00	33.00	20.90	4.47	185.50	2.40	28.30	19.16	6320.32	MB
10	UPR 3946-20-1-1	84.71	92.60	10.50	9.85	92.00	31.50	32.00	22.65	3.93	144.70	2.90	26.20	19.29	6164.07	LB
11	MT 2808	67.59	91.65	12.50	10.60	94.50	31.50	28.50	23.95	2.83	128.80	10.00	24.30	18.72	5335.94	LB
12	MTU 3626	42.20	80.45	16.55	15.60	91.00	32.50	22.00	23.35	2.61	105.00	13.50	20.50	20.42	4492.19	LB
13	IR 14K 10452	67.51	106.10	12.80	11.95	92.00	33.50	29.50	22.50	2.91	134.70	9.00	24.40	18.29	5375.01	LS
14	IR 14K 10048	37.51	74.80	12.20	11.00	92.50	33.50	20.00	23.70	2.32	88.10	16.50	24.30	21.87	4367.19	LB
15	OR 2517-5	51.66	84.75	17.55	16.70	94.50	31.00	23.00	21.80	2.61	110.20	13.20	22.20	20.94	4812.51	LB

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Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	
16	IR 13K 5144	31.20	67.30	14.55	13.75	93.50	37.50	20.00	22.40	2.23	73.80	19.10	17.45	20.40	4062.51	LB
17	NDR 359	82.20	104.00	13.65	12.40	88.50	30.50	31.00	22.90	3.62	156.70	6.80	26.40	19.19	5945.32	LB
18	RYT 3450	54.65	87.55	15.80	15.05	88.00	31.50	24.00	22.95	2.73	116.90	12.80	23.50	20.22	4835.94	LB
19	IR 14K 10115	80.02	101.70	11.85	11.25	93.50	30.00	30.00	21.55	3.45	156.20	6.80	26.55	19.55	5859.38	LS
20	IR 14K 11414	52.45	86.05	15.50	13.80	81.50	30.00	24.00	21.45	2.65	114.10	13.00	23.55	20.11	4734.38	LB
21	IR 14K 10485	41.15	80.15	18.60	17.40	82.00	31.00	21.50	23.80	2.52	104.20	13.90	20.50	20.66	4437.5	LB
22	BPT 5204	64.48	90.95	16.90	15.90	93.00	31.00	27.50	21.30	2.84	124.30	10.60	24.30	18.86	5164.07	MS
23	IR 13K 5121	36.76	72.95	15.45	14.25	83.50	32.50	20.50	22.10	2.26	86.30	18.10	18.45	21.37	4359.38	LB
24	BPT5204	59.56	89.45	17.05	16.45	92.50	33.50	26.50	20.95	2.81	121.80	11.00	23.90	19.29	5109.38	MS
25	IR 14K 10045	41.50	77.35	16.70	15.20	91.50	29.50	21.00	22.55	2.49	104.00	14.60	20.45	21.13	4421.88	MB
26	MT 4091	50.05	80.90	15.85	15.15	88.50	31.00	22.50	22.30	2.62	110.30	13.20	21.40	20.07	4492.19	LS
27	IR 14K 10231	82.55	102.80	13.30	12.20	93.50	31.50	30.50	22.10	3.72	160.60	5.90	26.40	19.47	5937.51	MB
28	IR 14K 10451	53.35	86.65	16.50	15.45	89.50	31.50	24.50	23.00	2.74	116.40	12.70	23.50	19.69	4812.51	LB
29	MT 4316	76.70	99.55	11.55	10.50	89.50	33.50	30.00	21.80	3.36	155.00	7.20	25.55	19.21	5765.63	LB
30	MTU 1121	40.73	76.25	15.70	14.55	94.50	33.50	20.50	22.70	2.37	99.00	14.60	19.55	21.49	4390.63	MB
31	OR 2542-4	56.52	88.75	17.70	16.95	100.00	32.50	23.50	14.50	2.75	118.40	12.00	23.40	20.70	4867.19	LB

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Sl. No.	Genotypes	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	
32	IR 14K 10056	71.65	109.05	12.95	11.85	91.50	31.00	29.00	22.45	3.00	136.40	8.40	24.50	18.70	5414.07	LB
33	IR 14K 10037	59.40	90.40	16.10	15.00	81.50	30.00	26.00	22.00	2.79	118.10	11.20	23.40	19.59	5085.94	MB
34	IR 14K 10530	64.52	91.35	15.90	15.10	80.50	32.50	27.50	20.45	2.84	126.60	9.90	24.30	18.96	5187.51	LB
35	IR 14K 10203	89.41	96.40	14.25	13.05	93.00	29.50	32.50	22.45	4.28	176.90	2.60	26.40	19.12	6210.94	LB
36	IR 14K 10477	76.45	118.10	11.75	10.20	80.50	31.00	30.00	21.50	3.40	144.40	7.30	25.40	18.74	5617.19	LB
Grand Total		2315.3	3325.1	524.75	487	3236	1139.5	966.5	787.15	111.86	4731	354.2	866.05	709.19	189054.8	
Mean		64.31	92.37	14.58	13.53	89.89	31.65	26.85	21.87	3.11	131.42	9.84	24.06	19.70	5251.52	
CV (%)		4.28	5.02	5.33	5.74	5.55	2.64	8.03	6.70	5.01	5.49	8.69	7.65	4.72	9.13	
S.E.		1.95	3.28	0.55	0.55	3.53	0.59	1.52	1.04	0.11	5.10	0.60	1.30	0.66	338.96	
C.D. 5%		5.59	9.42	1.58	1.58	9.56	1.69	4.37	2.98	0.32	14.65	1.74	3.73	1.89	973.14	

X1: Field emergence

X5: Days to 50% flowering

X9: Panicle Weight (g)

X13: Yield/plant (g)

MS: Medium Slender

X2: Plant Height (cm)

X6: Grain Filling Duration

X10: Filled Grains/panicle

X14: Yield/hectare (Kg)

MB: Medium Bold

X3: Tiller number/plant

X7: Plants/square meter

X11: Unfilled Grains /panicle

LB: Long Bold

X4: Reproductive tiller number plant

X8: Panicle Length (cm)

X12: Test Weight (g)

LS: Long Slender

Evaluation of rice genotypes suitable for direct seeded condition (*Oryza sativa* L.)

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Major Advisor

Rice (*Oryza sativa* L.) is one of the most important food crop grown worldwide. It is the staple food for half of the world's population. The present investigation was carried out to evaluate rice genotypes suitable for direct seeded condition. The experimental material consists of forty early, forty mid early and thirty six medium maturing direct seeded rice genotypes. Analysis of variance showed significant difference among the genotypes studied for all the characters like field emergence, plant height, tiller number, reproductive tiller number, days to 50% flowering, grain filling duration, number of plants per square meter, panicle length, panicle weight, filled and unfilled grains, test weight, grain yield per plant and grain yield per hectare in all the three viz., early, mid early and medium maturing rice genotypes. The genetic variability components like PCV, GCV, broad sense heritability and genetic advance as percent mean were studied in all the three group. Genotype IR 14K 11485 was performed better followed by IR 14K 11350 and IR 14K 9922 in early maturing group. In case of mid early maturing group the genotype IR 14K 10158 was superior followed by MT 4111 and IR 14K 9762, while in medium maturing group, the genotype UPR 3926-6-1-1 performed better followed by IR 14K 10236 and IR 14K 9977. The correlation study revealed that grain yield exhibited significant positive correlation with field emergence, plant height, number of reproductive tillers/plant, panicle weight, filled grains/plant and test weight in both early and mid early maturing group, whereas in medium maturing group grain yield exhibited significant positive correlation with number of tillers/plant and number of reproductive tillers/plant. Genetic diversity of 51 rice (consist of both high performing and low performing) genotypes using four SSR markers revealed high variability among genotypes. The dendrogram separated genotypes into eight main clusters at 0.80 Jaccard's similarity coefficient, which contains 2, 2, 1, 2, 1, 5, 32 and 6 rice genotypes, respectively.