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PARAMETERS IN RICE
(*Oryza sativa* L.) VARIETIES OF
DIFFERENT AGRO-CLIMATIC ZONES**

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ABSTRACT

The present investigation was carried out during *kharif*, 2004-05 to study the genetic divergence, genetic parameters for yield, grain quality characters, character association and path coefficient analysis in seventy rice genotypes belonging to the different agro-climatic zones of India. The experiment was laid out at Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad in a Randomized Block Design with three replications. Data were recorded on yield, yield attributing characters and grain quality characters.

Analysis of variance indicated that the existence of significant genotypic differences for all the eighteen characters. The genotypes *viz.*, Vikas, NLR-30491, VRS-3, PR-111, NDR-359 and PR-116 showed high mean performance for grain yield and grain quality characters.

Small differences between GCV and PCV were recorded for all the characters studied which indicated the less influence of environment on these characters. The characters *viz.*, days to 50 per cent flowering, plant height, water uptake and gel consistency exhibited high heritability coupled with high genetic advance indicating that simple selection could be effective for improving these characters.

The results of D^2 statistic revealed that existence of significant diversity in 70 rice genotypes which were grouped into nine clusters. The mode of distribution of genotypes from different agro-climatic zones into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters like water uptake, gel consistency and head rice recovery percentage contributed maximum towards genetic diversity.

Correlation studies revealed significant positive association of grain yield per plant with number of grains per panicle and 1000-grain weight, whereas, characters like number of productive tillers per plant and number of grains per panicle with days to 50 per cent flowering; panicle length, number of grains per panicle, 1000-grain weight with plant height; panicle length with 1000-grain weight have shown positive association among themselves. Hence, these characters could be used as criteria for selection of genotypes with high seed yield.

Path coefficient analysis revealed that 1000-grain weight, number of grains per panicle, productive tillers per plant, plant height and days to 50 per cent flowering have shown positive direct effects on grain yield.

CHAPTER I

INTRODUCTION

Rice is a grain belonging to the grass family. The origin of rice cultivation is traced back to 3000 BC India when people discovered the plant growing in the wild and began to experiment with it. “Rice means life” was the theme of International year of rice, 2004 denoting its overwhelming importance as an item of food and commerce. Today, rice is grown and harvested on every continent except Antarctica. Rice produced in over 100 countries of the world. Rice remains a staple food for the majority of the world’s population. More than two thirds of the world rely on the nutritional benefits of rice.

Rice plays a pivotal role in Indian economy being the staple food for two third of the population. In India, it is grown in an area of 42.5 million hectares with a production of 88.2 million tonnes and productivity of 2077 kg/ha, while in Andhra Pradesh it is grown in an area of 29.8 lakh hectares with a production of 89.5 lakh tonnes and productivity of 3009 kg/ha (CMIE, 2004).

With liberalization, India emerged as an important rice exporter. During, 2003-04, India exported 0.77 million tonnes of Basmati rice, 2.60 million tonnes of non-basmati rice and earned foreign exchange of Rs. 1990.92 crores and Rs. 2142.16 crores, respectively. Most of India’s rice export are long-grain non-basmati rice varieties like PR-106, White Ponni, Kavya, Kamini, Sona Masuri,

IR-64, Sambamasuri and high quality basmati varieties like Bas-370, Taroari Basmati and Pusabasmati-1.

Rice grows under most diverse ecological situations i.e., rainfed to waterlogged conditions. Consumer preference plays a dominant role in localization and adoption of varieties. So, the genetic diversity among rice varieties brought forth by natural processes, the human selection due to socio-economic compulsions. Socio-religious traditions also played a major role in adding diversity to morphological features. In grain quality characters, milling characteristics, grain shape, size and appearance and cooking quality characters like kernel elongation ratio are being given preference. Keeping these points in view, plant breeders should evolve high yielding rice varieties associated with good grain quality characteristics.

A thorough knowledge of nature and magnitude of genetic variability and association of characters in crop species is a pre-requisite for a successful breeding programme. Information on direct and indirect effects contributed by each character towards yield will be an added advantage in aiding the selection.

A population with more diverse genotypes is of considerable value as the success of any breeding programme relies on the genetic variability present in the base population for effective selection and recombination breeding. Hence, the present investigation was carried out by taking the genotypes from ten different agro-climatic zones with the following objectives:

1. To study the genetic diversity among the rice genotypes for yield and quality characters.
2. To study the variability, heritability, GA (%) among the different high yielding rice genotypes.
3. To study the extent of association between yield and its component characters.
4. To determine the direct and indirect effects of different yield components on yield.

CHAPTER II

REVIEW OF LITERATURE

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

- 2.1 Genetic parameters
- 2.2 Genetic divergence
- 2.3 Character association
- 2.4 Path coefficient analysis

2.1 GENETIC PARAMETERS

2.1.1 Variability

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

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

2.1.1.1 Days to 50 per cent flowering

Maurya *et al.* (1986), Chookar *et al.* (1994), Surendra Singh and Choudhary (1996), Kaw *et al.* (1999) and Awasthi and Pandey (2000) reported high genotypic and phenotypic coefficients of variation for days to 50 per cent flowering in rice. However, moderate amount of variability was observed for days to 50 per cent flowering by Manonmani *et al.* (1996), Vange and Ojo (1997) and Chikkalingaiah *et al.* (1999).

Nayak *et al.* (2002), Patil *et al.* (2003), Suman (2003) and Sinha *et al.* (2004) observed low genotypic and phenotypic coefficients of variation for days to 50 per cent flowering, while Balan *et al.* (1999) reported low genotypic coefficient of variation for this trait.

2.1.1.2 Plant height (cm)

Chikkalingaiah *et al.* (1999) and Patil *et al.* (2003) observed low genotypic coefficient of variation for plant height.

Ganesan and Subramanian (1990), Surendra Singh and Choudary (1996), Vange and Ojo (1997), Manonmani *et al.* (1996), Nagajyothi (2001), Tara Satyavathi (2001), Nayak *et al.* (2002) and Patil *et al.* (2003) observed moderate amount of variability for plant height in rice, while studies of Remabai *et al.* (1992) and Chookar *et al.* (1994) indicated a high phenotypic coefficient of variation for plant height in rice.

Tripathi *et al.* (1999), Awasti and Pandey (2000) and Sinha *et al.* (2004) observed high genotypic and phenotypic coefficients of variation for plant height in rice.

2.1.1.3 Number of productive tillers per plant

Chookar *et al.* (1994), Surendra Singh and Choudhary (1996), Manonmani *et al.* (1996), Chikkalingaiah (1999) and Sinha *et al.* (2004) reported high genotypic coefficient of variation and phenotypic coefficient of variation for number of productive tillers per plant in rice.

Chaudhary *et al.* (2003) studied high phenotypic coefficient of variation for number of productive tillers per plant, whereas Vange and Ojo (1997) and Nagajyothi (2001) reported moderate amount of variability for this trait.

Niranjana Murthy *et al.* (1999), Tarasatyavathi *et al.* (2001) and Surender Raju (2002) observed low genotypic and phenotypic coefficient of variation for number of productive tillers per plant.

2.1.1.4 Panicle length (cm)

Chookar *et al.* (1994) and Kaw *et al.* (1999) reported wide range of variation for panicle length in rice whereas Manonmani *et al.* (1996), Vange and Ojo (1997), Chikkalingaiah *et al.* (1999), Nagajyothi (2001), Tarasatyavathi *et al.* (2001) and Patil *et al.* (2003) reported low genotypic and phenotypic coefficient of variation for panicle length in rice.

Tripathi *et al.* (1999) reported high genotypic and phenotypic coefficient of variation for panicle length in rice, while Nayak *et al.* (2002) observed moderate amount of variability.

2.1.1.5 Number of grains per panicle

Rao and Shrivastav (1994), Reddy and De (1996), Borbora and Hazarika (1998), Debchoudhary and Das (1998), Nagajyothi (2001), Nayak *et al.* (2002) and Madhavalatha (2002) reported high genotypic and phenotypic coefficient of variation for this trait.

Sarma and Roy (1993) and Tara Satyavathi *et al.* (2001) observed moderate genotypic and phenotypic coefficient of variation for number of grains per panicle.

Suman (2003) reported high genotypic coefficient of variation for this trait.

Nath and Talukdar (1997) observed low genotypic and phenotypic coefficient of variation for number of grains per panicle.

2.1.1.6 1000-grain weight (g)

High estimates of phenotypic coefficient of variation and genotypic coefficient of variation for 1000-grain weight were reported by Paramasivam *et al.* (1995), Manonmani *et al.* (1996), Surendra Singh and Choudhary (1996), Mokate *et al.* (1998), Leenakumari (1998), Kaw *et al.* (1999) and Singh *et al.* (2004).

Chaudhary *et al.* (2003) and Patil *et al.* (2003) reported high phenotypic coefficient of variation for 1000-grain weight of rice.

Moderate to low genotypic variability for this trait was reported by Vange and Ojo (1997), Satya Priya Lalitha and Sreedhar (1999) and Nayak *et al.* (2002).

Vange *et al.*, (1999), Chikkalingaiah *et al.* (1999) and Tara Satyavathi *et al.* (2001) reported low genotypic and phenotypic variability for 1000-grain weight of rice.

2.1.1.7 Grain yield per plant (g)

Amirthadevarathinam (1983) and Ganesan and Subramanian (1990) observed a wide range of phenotypic and genotypic coefficient of variation for grain yield in rice.

Chookar *et al.* (1994), Rao and Shrivastav (1994), Satya Priya Lalitha and Sreedhar (1999), Balan *et al.* (1999), Nayak *et al.* (2002), Madhavalatha (2002), Patil *et al.* (2003), Suman (2003) and Sinha *et al.* (2004) observed high phenotypic and genotypic coefficients of variation for single plant yield in rice.

Chaudhary *et al.* (2003) observed high phenotypic coefficient of variation for single plant yield, while moderate variability for this trait was reported by Nagajyothi (2001) and Tara Satyavathi *et al.* (2001), while low genotypic coefficient of variation for single plant yield in rice was reported by Supriyo Chakraborty and Hazarika (1994).

2.1.1.8 Hulling percentage

Nayak *et al.* (2003) reported moderate genotypic and phenotypic coefficients of variation for hulling per cent in rice.

Pathak and Sharma (1996), Nagajyothi (2001) Surender Raju (2002) and Madhavalatha (2002) reported low genotypic and phenotypic coefficients of variation for hulling per cent in rice.

2.1.1.9 Milling percentage

Chikkalingaiah *et al.* (1999) reported high genotypic and phenotypic coefficients of variation for this trait in rice.

Nayak *et al.* (2003) observed moderate amount of variability for milling per cent in rice.

Nagajyothi (2001) and Chaudhary *et al.* (2003) reported low genotypic and phenotypic coefficients of variation for this trait.

2.1.1.10 Head rice recovery percentage

Nayak *et al.* (2003) reported moderate genotypic and phenotypic coefficients of variation for this trait in rice.

Chaudhary *et al.* (2003) and Patil *et al.*(2003) observed low genotypic and phenotypic coefficients of variation for this trait.

2.1.1.11 L/B ratio

Pathak and Sharma (1996), Vivekanandan and Giridharan (1998), Sarawgi *et al.* (2000) and Madhavalatha (2002) reported high genotypic and phenotypic coefficients of variation for L/B ratio in rice.

Moderate amount of variability for L/B ratio in rice was observed by Satya Priya Lalitha and Sreedhar (1999), Nagajyothi (2001), Sakthivel (2001), Nayak *et al.* (2002), Nayak *et al.* (2003), Chaudary *et al.* (2003) and Patil *et al.* (2003).

Ramesh Kumar (1989), Chikkalingaiah *et al.* (1999) and Tara Satyavathi *et al.* (2001) observed low genotypic and phenotypic coefficients of variation for this trait.

2.1.1.12 Kernel length after cooking (KLAC) (mm)

Tarasatyavathi *et al.* (2001) observed low genotypic and phenotypic coefficients of variation for this trait.

Nayak *et al.* (2003), Chaudhary *et al.* (2003) and Patil *et al.* (2003) reported moderate variability for this trait.

2.1.1.13 Elongation ratio

Pathak and Sharma (1996) and Chikkalingaiah *et al.* (1999) reported high genotypic and phenotypic coefficients of variation for elongation ratio in rice.

Vivekanandan and Giridharan (1998), Sarawgi *et al.* (2000), Tarasatyavathi *et al.* (2001), Madhavalatha (2002) and Patil *et al.* (2003) observed low genotypic and phenotypic coefficients of variation for this trait.

2.1.1.14 Water uptake

Nayak *et al.* (2003) reported moderate genotypic and phenotypic coefficients of variation for water uptake in rice.

2.1.1.15 Volume expansion ratio

A wide range of variability was observed by Deosarkar *et al.* (1989) and Sakthivel (2001) for volume expansion ratio in rice.

Moderate amount of variability was observed for this trait in rice by Satya Priya Lalitha and Sreedhar (1999) and Nayak *et al.*(2003) while Nagajyothi (2001) reported moderately high genotypic and phenotypic coefficients of variation for this trait.

Chauhan *et al.* (1991) and Tara Satyavathi *et al.* (2001) observed a low variation for this trait, whereas absence of variation was recorded by Chauhan *et al.* (1992).

2.1.1.16 Alkali spreading value (Gelatinization temperature)

Good amount of variation for alkali value was recorded by Chauhan *et al.* (1991), while high genotypic and phenotypic coefficients of variation for this trait was observed by Nagajyothi (2001) and Sakthivel (2001).

Moderate variation (from 3 to 6) for alkali value in rice were reported by Sarkar *et al.* (1994) and Chaudhary *et al.* (2003).

Larger variation (from 1 to 6) for this trait in rice was reported by Jagannadha Rao and Murthy (1997).

Larger variation (from 2 to 7) for alkali spread value in rice was observed by Nayak *et al.* (2003) and Patil *et al.* (2003).

2.1.1.17 Gel consistency

Tarasatyavathi *et al.* (2001) reported high genotypic and phenotypic coefficient of variation for this trait in rice.

2.1.1.18 Amylose content

Hussain *et al.* (1989) and Kikuchi (1988) observed, a wide range of variation, while Deosarkar *et al.* (1989), Chikkalingaiah *et al.* (1999) and Tarasatyavathi *et al.* (2001) reported high variation for this trait.

Chauhan and Nanda (1983) and Nayak *et al.* (2003) observed moderate to high variability for amylose content.

Kihupi (1987), Chauhan *et al.* (1991), Nagajyothi (2001) and Patil *et al.* (2003) reported low variation for this trait.

2.1.2 Heritability and genetic advance

Heritability in broad sense refers to the genetic variation present in the population in relation to the total observed variance.

Genetic advance refers to the improvement in the mean genotypic value of the selected plants over the base population.

High heritability coupled with high genetic advance suggests that character improvement could be made by selection based on phenotypic performance. This estimation of broad sense heritability and genetic advance for different characters by different workers are reviewed below.

2.1.2.1 Days to 50 per cent flowering

Marimuthu *et al.* (1990) and Rao and Shrivastav (1994) studied high heritability coupled with moderate genetic advance for days to 50 per cent flowering.

Chikkalingaiah *et al.* (1999) reported high heritability estimates for days to 50 per cent flowering.

Madhavalatha (2002) and Nayak *et al.* (2002) observed high heritability coupled with high genetic advance to 50 per cent flowering in rice.

Sinha *et al.* (2004), Patil *et al.* (2003), Suman (2003), Niranjana Murthy *et al.* (1999) and Balan *et al.* (1999) reported high heritability coupled with low genetic advance.

2.1.2.2 Plant height (cm)

Mokate *et al.* (1998), Chikkalingaiah (1999) and Kaw *et al.* (1999) reported high heritability estimates. High heritability coupled with high genetic advance for plant height in rice was reported by Nagajyothi (2001), Venkata Suresh (2001), Nayak *et al.* (2003), Patil *et al.* (2003), Suman (2003) and Sinha *et al.* (2004) observed high heritability along with moderate or low genetic advance.

Sahdev Singh *et al.* (1996) reported low to high heritability and low genetic advance in F_3 populations of the cross Jhona-349 x IR-8.

2.1.2.3 Number of productive tillers per plant

Borbora and Hazarika (1998), Chikkalingaiah *et al.* (1999), Nagajyothi (2001), Nayak *et al.* (2002), Suman (2003) and Patil *et al.* (2003) reported high

heritability coupled with high genetic advance as per cent of mean for number of productive tillers per plant in rice.

Satya Priya Lalitha and Sreedhar (1998) and Venkata Suresh (2001) studied moderate heritability coupled with moderate genetic advance.

Medium to high heritability and low genetic advance were reported by Sahdev Singh *et al.* (1996) for number of productive tillers per plant in rice.

Ramesh Kumar (1989) and Niranjana Murthy *et al.* (1999) studied low heritability with very low genetic advance.

2.1.2.4 Panicle length (cm)

Paramasivam *et al.* (1995), Chikkalingaiah *et al.* (1999) and Nayak *et al.* (2002) reported high heritability coupled with high genetic advance for panicle length.

Borbora and Hazarika (1998), Nagajyothi (2001) and Suman (2003) reported high heritability and low genetic advance for panicle length in rice.

Satya Priya Lalitha and Sreedhar (1996) and Venkata Suresh (2001) observed moderate heritability and moderate genetic advance for panicle length in rice.

2.1.2.5 Number of grains per panicle

Satyapriyalalitha and Sreedhar (1996) studied moderate heritability and moderate genetic advance for number of grains per panicle in rice.

Borbora and Hazarika (1998), Gupta *et al.* (1999), Venkata Suresh (2001), Nayak *et al.* (2002) and Patil *et al.* (2003) reported high heritability coupled with high genetic advance for this trait in rice.

2.1.2.6 1000-grain weight (g)

High heritability estimates for this character in rice was observed by Paramasivam *et al.* (1995) and Mokate *et al.* (1998) and Chaudhary *et al.* (2003).

Mishra *et al.* (1996), Chikkalingaiah *et al.* (1999), Nagajyothi (2001) and Suman (2003) revealed high heritability with low genetic advance for 1000-grain weight in rice.

Reddy and De (1996), Reddy *et al.* (1997) and Sinha *et al.* (2004) observed high heritability coupled with moderate values of genetic advance, whereas Ramesh Kumar (1989) recorded moderate to high heritability with low to moderate genetic advance.

Borbora and Hazarika (1998), Mokate *et al.* (1998) and Nayak *et al.* (2002) reported high heritability values coupled with high genetic advance for 1000-grain weight in rice.

2.1.2.7 Grain yield per plant (g)

Balan *et al.* (1999), Nirajana Murthy *et al.* (1999), Nagajyothi (2001), Madhavilatha (2002), Nayak *et al.* (2002), Patil *et al.* (2003) and Suman (2003) studied high heritability estimates coupled with high genetic advance as percentage of mean.

Satya Priya Lalitha and Sreedhar (1999) revealed moderate heritability and moderate genetic advance, while Ramesh Kumar (1989) and Suman (2003) studied high heritability with very low expected genetic advance.

Sinha *et al.* (2004) revealed high heritability with moderate genetic advance for this trait.

2.1.2.8 Hulling percentage

Singh *et al.* (1998) revealed high heritability with high genetic advance was observed for hulling percentage.

Chikkalingaiah *et al.* (1999) observed moderate heritability with medium genetic advance for this trait.

For hulling percentage, Surender Raju (2000) reported high heritability coupled with low genetic advance.

Nagajyothi (2001) observed low heritability with low genetic advance for hulling percentage in rice.

Nayak *et al.* (2003) revealed high heritability coupled with moderate genetic advance.

2.1.2.9 Milling percentage

Chikkalingaiah *et al.* (1999) reported high heritability coupled with high genetic advance for milling percentage in rice.

For milling percentage in rice, Nagajyothi (2001) reported moderate heritability with low genetic advance.

Nayak *et al.* (2003) revealed high heritability with moderate genetic advance for this trait.

2.1.2.10 Head rice recovery percentage

Nayak *et al.* (2003) studied high heritability with high genetic advance for head rice recovery percentage in rice.

Patil *et al.* (2003) observed high heritability and low genetic advance for this trait.

2.1.2.11 L/B ratio

High heritability and high genetic advance for L/B ratio in rice was revealed by Vivekanandan and Giridharan (1998), Sarwagi *et al.* (2000), Nagajyothi (2001), Nayak *et al.* (2002) and Nayak *et al.* (2003).

High heritability coupled with moderate genetic advance for L/B ratio was observed by Satya Priya Lalitha and Sreedhar (1999).

Sakthivel (2001), Venkata Suresh (2001), Madhavalatha (2002) observed high heritability coupled with low genetic advance.

2.1.2.12 Kernel length after cooking (mm)

High heritability with high genetic advance for kernel length after cooking was observed by Nayak *et al.* (2003).

Patil *et al.* (2003) reported high heritability with moderate genetic advance for this trait.

2.1.2.13 Elongation ratio

Chikkalingaiah *et al.* (1999) reported high heritability coupled with high genetic advance for elongation ratio in rice.

Patil *et al.* (2003) and Nayak *et al.* (2003) observed high heritability with moderate genetic advance for this trait.

2.1.2.14 Volume expansion ratio

Satya Priya Lalitha and Sreedhar (1998) revealed moderate heritability with moderate genetic advance.

Singh *et al.* (1998) and Nagajyothi (2001) recorded high heritability and high genetic advance for volume expansion ration.

Sakthivel (2001), Madhavalatha (2002), Surender Raju (2002) and Nayak *et al.* (2003) observed high heritability with low genetic advance.

2.1.2.15 Water uptake

Nayak *et al.* (2003) reported high heritability with high genetic advance for this trait.

2.1.2.16 Amylose content (%)

Chikkalingaiah *et al.* (1999) and Nayak *et al.* (2003) reported high heritability with high genetic advance.

Patil (2003) and Nagajyothi (2001) studied high heritability with moderate genetic advance.

2.1.2.17 Alkali spreading value (Gelatinization temperature)

High heritability for alkali digestion value in rice was observed by Sakthivel (2001).

Sarawgi *et al.* (2000), Nagajyothi (2001) and Nayak *et al.* (2003) recorded high heritability and high genetic advance for gelatinization temperature.

2.1.2.18 Gel consistency (mm)

High heritability estimates for gel consistency was observed by Guo and Xie (1983).

Deosarkar *et al.* (1989) and Nagajyothi (2001) recorded high heritability coupled with high genetic advance for this trait.

2.2 GENETIC DIVERGENCE

Genetic improvement in any crop mainly depends upon the amount of genetic variability present in the population. The importance of genetic diversity in crop plants was first realized by Darwin (1859) and the term “morphism” employing genetic morphs was given by Huxley (1955), which means the existence of distinct genetic forms in balance in a population.

2.2.1 Mahalanobis's D^2 analysis

Mahalanobis's D^2 analysis is a powerful tool in quantifying the degree of divergence between biological populations at genetic level and provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

Estimation of degree of divergence between populations and contribution of different characters to total divergence was done by Mahalanobis's D^2 statistic (Maurya and Singh, 1977) which is more reliable method in selection of parents for hybridization programme.

Murthy and Arunachalam (1966) emphasized the importance of genetic diversity in selection of parents for hybridization in different crops and reported that the greatest contributing characters to genetic diversity in grain crops were flowering time, plant height and tiller number per plant.

From genetic divergence studies, Kanwal *et al.* (1983) grouped various strains into nine groups and concluded that panicle weight, days to maturity, plant height and grain size had contributed maximum to genetic divergence in rice.

Ratho (1984) while studying on quality characters of scented rice varieties reported that kernel length followed by volume expansion, kernel breadth and protein content contributed to genetic divergence in descending order.

Kotaiah *et al.* (1987) grouped thirty six long duration genotypes into 10 clusters by D^2 analysis. Days to 50% heading and 1000-grain weight were the main contributors to total divergence.

Gomathinayagam *et al.* (1990) grouped 40 rice entries into four different clusters and revealed that there is a lack of parallelism between geographic distribution and genetic divergence. Similarly, Pradhan and Roy (1990) conducted D^2 analysis in 25 rice cultures and grouped them into 6 clusters. Test weight contributed maximum to genetic divergence.

Vivekanandan and Sukanya Subramanian (1993) carried out genetic divergence using D^2 analysis in 28 genotypes of rainfed rice and grouped them into five clusters. Plant height and grain yield contributed considerably (85 %) to the total divergence. The geographical diversity was not found to be related to genetic diversity.

Barauah *et al.* (1994) grouped 144 rice varieties into 55 clusters and observed that there is a lack of correspondence between ecological situation and genetic divergence. They reported that days to flowering, plant height, ear bearing tillers per hill, test weight and grain yield contributed maximum towards divergence.

Kaw (1995) from his investigation on genetic divergence in 94 cold tolerant rice varieties reported that the genotypes were grouped into 18 clusters using D^2 statistic and canonical analysis. The maximum contribution of plant height, days to 50 percent flowering, fertile spikelets per panicle and fertility percentage towards genetic divergence was observed.

Singh *et al.* (1996) measured the degree of genetic divergence in 40 scented and fine genotypes of rice and grouped them into six clusters. It was observed that grain yield and plant height had contributed greatly to the divergence.

Genetic divergence was assessed by using 40 rice genotypes at two different locations by Rao and Gomatinayagam (1997). Genetic divergence has not been found to be related to geographic diversity. They also noted the differential response of genotypes to the environments which has altered the clustering pattern too. It was also observed that stable genotypes having less interaction with environment were tend to

group into one cluster and such genotypes were found to be good breeding material for heterosis.

Sardana *et al.* (1997) conducted D^2 analysis in 82 local rice varieties and grouped them into 18 clusters based on 15 agro-morphological characters. Cluster I with 15 genotypes was the largest one. They observed that number of grains per panicle, number of effective tillers per plant and grain yield per plant were major characters contributing to the genetic diversity.

Ushakumari and Rangaswamy (1997) carried out genetic divergence among 74 rice genotypes and grouped them into six clusters by multivariate analysis using D^2 statistic. The characters grain yield per plant and plant height contributed maximum towards divergence. Relation between geographic diversity and genetic diversity was not observed.

Hanamaratti *et al.* (1998) evaluated fifty rice genotypes for 10 yield components in low and upland environments by D^2 statistic and grouped them into 18 and 17 clusters, respectively of their geographic origin.

Studies on fifty rice genotypes by Pandey *et al.* (1999) using Mahalanobis's D^2 statistic assigned the genotypes into six clusters and revealed no correlation between genetic diversity and geographical diversity. The characters, days to 50 per cent flowering, Plant height and 1000-seed weight contributed maximum to the genetic diversity.

Kandhola and Panwar (1999) grouped 52 indigenous and exotic genotypes of rice using D^2 statistic into 11 clusters based on 16 agro-morphological and quality characters. Cluster I with 26 genotypes was the largest, while clusters VII, VIII, IX

and XI were monogenotypic and revealed that no association between genetic and geographic diversity. The inter-cluster distance was maximum between genotypes of clusters V and XI. Hence, hybridization among these genotypes drawn from widely divergent clusters with high yield potential is likely to produce more heterotic effect.

In a genetic divergence study of 132 genotypes by Soni *et al.* (1999) for quality traits led to their grouping into 10 clusters. Grouping of genotypes in different clusters indicated the presence of significant amount of variability for quality traits. Based on mean performance and cluster distances, hybridization among the genotypes Kranchi, X-12, Motibakiya, Assam chudi, Baka B. Jondhara, Than, Poorva, IR-36, Gondajhul and Kranthi were suggested in order to recover desirable segregants for grain quality.

Hegde *et al.* (2000) assessed the genetic divergence in 40 genotypes of rainfed rice and grouped into seven clusters. Total spikelets per panicle, photosynthetic rate and 1000-grain weight were contributed maximum to total genetic divergence.

D^2 analysis of divergence grouped the 56 diverse rice cultivars into eight clusters. Geographical origin was not found to be a good parameter of genetic divergence. The 100 grain weight and L:B ratio of grain were important components of divergence. Based on mean performance for plant height, grain yield and inter-cluster distance, the genotypes from clusters II and IV may be used for initiating the hybridization programme (Rather *et al.*, 2001).

Sakthivel (2001) grouped 81 genotypes of rice using D^2 statistics into 21 clusters based on thirteen quantitative and qualitative characters. No relationship between geographic origin and genetic diversity was observed. The character alkali

spreading value contributed maximum towards genetic divergence besides days to 50 per cent flowering and volume expansion.

Chaudhary *et al.* (2002) grouped the 54 genotypes into five clusters by D^2 analysis. Genetic divergence was studied for nineteen morphological and quality traits. The analysis of variance indicated that the genotypes differed for almost all the morphological and quality traits.

Genetic divergence studies carried out with 54 rice genotypes which were grouped into nine clusters. The mode of distribution of genotypes from different eco-geographical regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The characters, plant height and days to 50 per cent flowering were contributed maximum towards genetic divergence (Madhavi Latha, 2002).

Surender Raju (2002) assessed the genetic divergence among 42 genotypes by Mahalanobis's D^2 statistic and grouped them into 12 clusters. The characters 100-grain weight, volume expansion ratio, kernal length and days to 50% flowering have contributed maximum to the genetic divergence.

Manonmani *et al.* (2003) studied nature and magnitude of genetic divergence among fourteen *indica* rice genotypes and grouped them into five clusters. The cluster I consisted of ten genotypes and the clusters II, III, IV and V had one genotype each. Number of filled grains per panicle, days to 50 per cent flowering and plant height showed maximum contribution to the genetic divergence.

Vanaja *et al.* (2003) carried out genetic divergence among 56 high yielding rice genotypes representing different eco-geographical regions and grouped them into

nine clusters. It was concluded that there was no association between geographical distribution and genetic diversity. At the same time the relationship between genetic divergence and geographical origin also exists to some extent.

Nayak *et al.* (2004) assessed nature and magnitude of genetic divergence among 200 rice genotypes of scented rice for the quantitative traits and grouped the genotypes into 10 clusters. It was observed that no relationship was found between clustering pattern and geographic distribution. Among the different characters i.e., grain length and days to 50 per cent flowering played an important role in the formation of clusters.

Patil *et al.* (2004) grouped 135 rice genotypes into 10 different clusters based on different morphological and quality traits. The analysis of variance revealed significant differences among the genotypes for each character studied. These differences for morphological and quality characters may be utilised in future breeding programme to evolve desirable recombinants.

Senapathi and Sarkar (2005) evaluated forty tall *indica* rice genotypes for grain yield and seven yield related traits. The genotypes were grouped into five clusters. Cluster IV showed maximum genetic distance from cluster V suggested wide diversity between these groups. Panicle number per hill, panicle lengths, yield per plot and 1000-grain weight contributed maximum towards genetic divergence.

2.3 CHARACTER ASSOCIATION

Study of character associations helps the breeder in fixing a selection criteria for grain yield in parental lines, such that selections will be effective in isolating the plants with desired combination of characters. Phenotypic correlation is the

correlation of phenotypic values and is subjected to changes in the environment. It measures the environment deviation together with non-additive gene action. Genotypic correlation is the correlation of breeding value (Additive + Additive x Additive epistatic) gene action. Hence, knowledge of association between different characters is highly essential for planning a sound breeding programme.

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

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

2.3.1 Association of yield component characters with grain yield per plant in rice

Character	Nature of association	Reference
Days to 50% flowering	Positive significant	Selvarani and Rangaswamy (1998) Balan <i>et al.</i> (1999) Sakthivel (2001) Madhavalatha (2002) Suman (2003) Mahto <i>et al.</i> (2003) Kuldeep <i>et al.</i> (2004)
	Positive non-significant	Kumar <i>et al.</i> (1998) Rao and Shrivastav (1999) Vange <i>et al.</i> (1999)
	Negative non-significant	Sarma and Roy (1993) Yolanda and Vijendra Das (1995) Meenakshi <i>et al.</i> (1999)
Plant height	Positive significant	Deb Chaudhury and Das (1998) Bala (2001) Nayak <i>et al.</i> (2001) Sakthivel (2001) Madhavalatha (2002)
	Positive non-significant	Suman (2003)

Character	Nature of association	Reference
	Negative significant	Yolanda and Vijendra Das (1995) Reddy <i>et al.</i> (1997) Rao and Shrivastav (1999) Tarasatyavathi <i>et al.</i> (2001) Mahto <i>et al.</i> (2003)
	Negative non-significant	Chauhan <i>et al.</i> (1993) Gupta <i>et al.</i> (1998) Meenakshi <i>et al.</i> (1999)
No. of productive tillers per plant	Positive significant	Janardhanam <i>et al.</i> (2001) Nayak <i>et al.</i> (2001) Sakthivel (2001) Tarasatyavathi <i>et al.</i> (2001) Madhavalatha (2002) Chaudhary and Motiramani (2003) Suman (2003) Kuldeep <i>et al.</i> (2004)
	Positive and non-significant	Chaubey and Singh (1994) Yolanda and Vijendra Das (1995) Reddy <i>et al.</i> (1997)
	Negative Non-significant	Awasthi and Borthakur (1986) Haque <i>et al.</i> (1991)
Panicle length	Positive significant	Bala (2001) Nayak <i>et al.</i> (2001) Sakthivel (2001) Madhavalatha (2002) Suman (2003) Kuldeep <i>et al.</i> (2004)
	Positive Non-significant	Rao and Shrivastav (1999) Vange <i>et al.</i> (1999) Tarasatyavathi <i>et al.</i> (2001)
	Negative Non-significant	Chauhan <i>et al.</i> (1993) Ramesh Babu (1999)
Number of grains per panicle	Positive significant	Reddy <i>et al.</i> (1997) Debchaudhary and Das (1998) Tarasatyavathi <i>et al.</i> (2001) Madhavalatha (2002)
	Positive Non-significant	Sarma and Roy (1993) Chaubey and Singh (1994) Paul and Sarmah (1997)

Character	Nature of association	Reference
1000-grain weight	Positive significant	Sakthivel (2001) Madhavalatha (2002) Tarasatyavathi <i>et al.</i> (2002) Sinha <i>et al.</i> (2004) Kuldeep <i>et al.</i> (2004)
	Positive Non-significant	Supriyo Chakraborty and Hazarika (1994) Gupta <i>et al.</i> (1998) Vange <i>et al.</i> (1999)
	Negative Non-significant	Suman (2003)
	Negative Non-significant	Wilfred manuel and Rangaswamy (1993) Geeta <i>et al.</i> (1994)

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

Character	Nature of association	Reference
Plant height	Positive significant	Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001) Sakthivel (2001) Madhavalatha (2002)
	Positive Non-significant	Chauhan <i>et al.</i> (1993) Ramesh Babu (1999)
	Negative Non-significant	Debchoudhary and Das (1998) Rao and Shrivastav (1999)
Number of production tillers per plant	Positive significant	Sawant <i>et al.</i> (1995) Sakthivel (2001)
	Positive Non-significant	Kavitha and Sree Rama Reddi (2001) Surendar Raju (2002)
	Negative Non-significant	Yolanda and Vijendra Das (1995) Meenakshi <i>et al.</i> (1999)

Character	Nature of association	Reference
Panicle length	Positive significant	Vange <i>et al.</i> (1999) Nayak <i>et al.</i> (2001) Sakthivel (2001) Madhavalatha (2002) Suman (2003)
	Positive Non-significant	Sarma and Roy (1993) Sawant <i>et al.</i> (1995) Kavitha and Sri Rama Reddi (2001)
	Negative Non-significant	Chauhan <i>et al.</i> (1993) Ramesh Babu (1999)
Number of grains per panicle	Positive significant	Debchoudhury and Das (1998) Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001) Madhavalatha (2002)
	Positive Non-significant	Chauhan <i>et al.</i> (1993) Yolanda and Vijendra Das (1995) Vange <i>et al.</i> (1999)
	Negative Non-significant	Sawant <i>et al.</i> (1995) Meenakshi <i>et al.</i> (1999)
1000-grain weight	Positive significant	Ravindranath <i>et al.</i> (1982)
	Positive and non-significant	Roy <i>et al.</i> (1995)
	Negative significant	Ramesh Babu (1999) Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001) Sakthivel (2001)
	Negative non-significant	Sawant <i>et al.</i> (1995) Vange <i>et al.</i> (1999)

2.3.3 Association among the yield component traits in rice association of plant height with

Character	Nature of association	Reference
Number of productive tillers per plant	Positive significant	Janardhanam <i>et al.</i> (2001) Kavitha and Sree Rama Reddi (2001) Sakthivel (2001) Surendra Raju (2002)

Character	Nature of association	Reference
	Positive	Roy <i>et al.</i> (1995)
	Non-significant	Yolanda and Vijendra Das (1995) Pradyumna Rao <i>et al.</i> (1996)
	Negative significant	Satya Priaya Lalitha and Sreedhar (1996) Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001)
Panicle length	Positive significant	Janardhanam <i>et al.</i> (2001) Sakthivel (2001) Tarasatyavathi <i>et al.</i> (2001) Madhavalatha (2002) Suman (2003) Sinha <i>et al.</i> (2004)
	Positive non-significant	Reddy <i>et al.</i> (1997) Debchaudhury and Das (1998) Rao and Shrivastav (1999)
	Negative significant	Ananda Kumar (1992)
Number of grains per panicle	Positive significant	Yolanda and Vijendra Das (1995) Satya Priya Lalitha and Sreedhar (1996) Nayak <i>et al.</i> (2001) Madhavalatha (2002)
	Positive non-significant	Geeta <i>et al.</i> (1994) Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Debchoudhury and Das (1998) Surender Raju (2002)
	Negative non-significant	Chauhan <i>et al.</i> (1993) Sawant <i>et al.</i> (1995) Reddy <i>et al.</i> (1997)
1000-grain weight	Positive and significant	Reddy <i>et al.</i> (1997) Suman (2003) Yogameenakshi <i>et al.</i> (2004)
	Positive and non-significant	Awasthi and Borthakur (1986) Ramesh Babu (1999)
	Negative significant	Sukanya Subramanian and Rathinam (1984)
	Negative non-significant	Roy <i>et al.</i> (1995) Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001)

2.3.4 Association among the yield component traits in rice association of number of productive tillers per plant with

Character	Nature of association	Reference
Panicle length	Positive significant	Roy <i>et al.</i> (1995) Janardhanam <i>et al.</i> (2001) Sakthivel (2001)
	Positive non-significant	Yolanda and Vijendra Das (1995) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Chaubey and Richharia (1993) Tarasatyavathi <i>et al.</i> (2001) Suman (2003)
	Negative non-significant	Satya Priya Lalitha and Sreedhar (1996) Reddy <i>et al.</i> (1997)
Plant height	Positive significant	Sakthivel (2001)
Number of grains per panicle	Positive significant	Sundaram <i>et al.</i> (1990) Meenakshi <i>et al.</i> (1999) Janardhanam <i>et al.</i> (2001)
	Positive non-significant	Geetha <i>et al.</i> (1994) Yolande and Vijendra Das (1995) Satya Priya Lalitha and Sreedhar (1996)
	Negative significant	Chaubey and Richharia (1993) Tarasatyavathi <i>et al.</i> (2001)
	Negative non-significant	Roy <i>et al.</i> (1995) Reddy <i>et al.</i> (1997) Kavitha and Sree Rama Reddy (2001) Nayak <i>et al.</i> (2001)
1000-grain weight	Positive and significant	Suryanarayana (2000) Sakthivel (2001)
	Positive and non-significant	Yolanda and Vijendra Das (1995) Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddy (2001) Tarasatyavathi <i>et al.</i> (2001)
	Negative significant	Gopinath <i>et al.</i> (1984) Nayak <i>et al.</i> (2001)
	Negative non-significant	Nanja Reddy <i>et al.</i> (1995) Roy <i>et al.</i> (1995) Reddy <i>et al.</i> (1997)

2.3.5 Association among the yield component traits in rice association of panicle length with

Character	Nature of association	Reference
Number of productive tillers per plant	Positive significant	Bala (2001)
Number of grains per panicle	Positive significant	Satya Priya Lalitha and Sreedhar (1996) Ganesan <i>et al.</i> (1997) Janardhanam <i>et al.</i> (2001) Kavitha and Sree Rama Reddy (2001) Yogameenakshi <i>et al.</i> (2004)
	Positive non-significant	Reddy <i>et al.</i> (1997) Deb Choudhury and Das (1998) Tarasatyavathi <i>et al.</i> (2001)
	Negative significant	Gopinath <i>et al.</i> (1984)
	Negative non-significant	Sawant <i>et al.</i> (1995)
Days to 50 per cent flowering	Positive significant	Bala (2001) Sakthivel (2001)
Plant height	Positive significant	Bala (2001) Sakthivel (2001)
1000-grain weight	Positive significant	Gopinath <i>et al.</i> (1984) Yogameenakshi <i>et al.</i> (2004)
	Positive and non-significant	Reddy <i>et al.</i> (1997) Kavitha and Sree Rama Reddi (2001)
	Negative significant	Sukanya Subramanian and Rathinam (1984)
	Negative and non-significant	Roy <i>et al.</i> (1995) Vange <i>et al.</i> (1999) Nayak <i>et al.</i> (2001)

2.3.6 Association among the yield component traits in rice association of number of grains per panicle with

Character	Nature of association	Reference
1000-grain weight	Positive significant	Ravindranath <i>et al.</i> (1982)
	Positive non-significant	Nanja Reddy <i>et al.</i> (1995) Meenakshi <i>et al.</i> (1999)
	Negative significant	Geetha <i>et al.</i> (1994) Nayak <i>et al.</i> (2001)
	Negative non-significant	Reddy <i>et al.</i> (1997) Vange <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001)

2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis, a statistical device developed by Wright (1921) helps in partitioning of the correlation coefficients into direct and indirect effects of independent variable on dependent variable. As grain yield is a complex character influenced by several factors, selection based on simple correlation without taking into consideration between the component characters is not effective. Hence, path analysis is of much importance in any plant breeding programme. Correlation in combination with path analysis would give a better insight into cause and effect relationship between different pairs of characters. Dewey and Lu (1959) and Frakes (1961) demonstrated the utility of path coefficient analysis in plant selection and since then its application has been extended to almost to every crop.

The findings of earlier workers on the relative contribution of different characters to grain yield in rice are furnished hereunder in a tabular form:

2.4.1 Direct effects

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Days to 50 per cent flowering	Saravanan <i>et al.</i> , (1996) Selvarani and Rangaswamy (1998) Balan <i>et al.</i> (1999) Bala (2001) Madhavalatha (2002) Suman (2003) Khedikar <i>et al.</i> (2004)	Debchoudhury and Das (1998) Gupta <i>et al.</i> (1998) Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001)
Plant height	Meenakshi <i>et al.</i> (1999) Bala (2001) Janardhanam <i>et al.</i> (2001) Kavitha and Sree Rama Reddi (2001) Nagajyothi (2001) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Gupta <i>et al.</i> (1998) Tarasatyavathi <i>et al.</i> (2001) Suman (2003)

Character	Positive direct effect on grain yield	Negative direct effect on grain yield
Number of productive tillers per plant	Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish <i>et al.</i> (2003) Khedikar <i>et al.</i> (2004)	Valarmathi and Leenakumary (1998) Kavitha and Sree Rama Reddi (2001)
Panicle length	Kavitha and Sree Rama Reddi (2001) Nagajyothi (2001) Suman (2003) Khedikar <i>et al.</i> (2004)	Ganesan <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Madhavalatha (2002)
Number of grains per panicle	Janardhanam <i>et al.</i> (2001) Nayak <i>et al.</i> (2001) Madhavalatha (2002) Satish <i>et al.</i> (2003) Yogameenakshi <i>et al.</i> (2004)	Amirthadevarathinam (1990) Gupta <i>et al.</i> (1998)
1000-grain weight	Sinha <i>et al.</i> (1999) Nayak <i>et al.</i> (2001) Tarasatyavathi <i>et al.</i> (2001) Madhavalatha (2002) Suman (2003) Khedikar <i>et al.</i> (2004) Yogameenakshi <i>et al.</i> (2004)	Reddy <i>et al.</i> (1997) Gupta <i>et al.</i> (1998) Selvarani and Rangaswamy (1998) Kavitha and Sree Rama Reddi (2001)

2.4.2 Indirect effects

2.4.2.1 Indirect effects of days to 50 per cent flowering on grain yield through

Character	Positive indirect effect	Negative indirect effect
Plant height	Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Saravanan <i>et al.</i> (1996) Debchoudhury and Das (1998)
Number of productive tillers per plant	Gupta <i>et al.</i> (1998) Madhavalatha (2002)	Meenakshi <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001)
Panicle length	Gupta <i>et al.</i> (1998) Kavitha and Sree Rama Reddi (2001)	Sinha <i>et al.</i> (1999) Nayak <i>et al.</i> (2001) Madhavalatha (2002)
Number of grains per panicle	Debchoudhury and Das (1998) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Gupta <i>et al.</i> (1998) Meenakshi <i>et al.</i> (1999)
1000-grain weight	Kavitha and Sree Rama Reddi (2001) Madhavalatha (2002)	Meenakshi <i>et al.</i> (1999) Nayak <i>et al.</i> (2001)

2.4.2.2 Indirect effects of plant height on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Gupta <i>et al.</i> (1998) Madhavilatha (2002)	Sinha <i>et al.</i> (1999) Kavitha and Sree Rama Reddi (2001)
Number of productive tillers per plant	Valarmathi and Leenakumary (1998) Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Madhavilatha (2002)	Ganesan <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Tarasatyavathi <i>et al.</i> (2001)
Panicle length	Nagajyothi (2001) Tarasatyavathi <i>et al.</i> (2001)	Nayak <i>et al.</i> (2001) Madhavilatha (2002)
Number of grains per panicle	Debchoudhury and Das (1998) Madhavilatha (2002)	Valarmathi and Leenakumary (1998) Suryanarayana (2000)
1000-grain weight	Sarvanan <i>et al.</i> (1996) Sinha <i>et al.</i> (1999) Nagajyothi (2001) Madhavilatha (2002)	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001)

2.4.2.3 Indirect effects of number of effective tillers per plant on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Nayak <i>et al.</i> (2001) Madhavilatha (2002)	Amirthadevarathinam (1990) Kavitha and Sree Rama Reddi (2001)
Plant height	Janardhanam <i>et al.</i> (2001) Nagajyothi (2001) Madhavilatha (2002)	Ravindra Babu (1996) Reddy <i>et al.</i> (1997)
Panicle length	Gupta <i>et al.</i> (1998) Nagajyothi (2001) Madhavilatha (2002)	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001)
Number of grains per panicle	Gupta <i>et al.</i> (1998) Janardhanam <i>et al.</i> (2001) Tarasatyavathi <i>et al.</i> (2001)	Valarmathi and Leenakumary (1998) Nayak <i>et al.</i> (2001) Madhavilatha (2002)
1000-grain weight	Reddy <i>et al.</i> (1997) Nagajyothi (2001) Tarasatyavathi <i>et al.</i> (2001)	Ganesan <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Madhavilatha (2002)

2.4.2.4 Indirect effects of panicle length on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Bala (2001) Kavitha and Sree Rama Reddi (2001) Madhavalatha (2002)	Debchoudhury and Das (1998)
Plant height	Valarmathi and Leenakumary (1998) Bala (2001) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Tarasatyavathi <i>et al.</i> (2001) Janardhanam <i>et al.</i> (2001)
Number of productive tillers per plant	Valarmathi and Leenakumary (1998) Bala (2001) Nayak <i>et al.</i> (2001)	Tarasatyavathi <i>et al.</i> (2001) Madhavalatha (2002)
Number of grains per panicle	DebChoudhury and Das (1998) Nayak <i>et al.</i> (2001)	Amirthadevarathinam (1990)
1000-grain weight	Ganesan <i>et al.</i> (1997) Nagajyothi (2001) Madhavalatha (2002)	Nayak <i>et al.</i> (2001)

2.4.2.5 Indirect effects of number of grains per panicle on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Gupta <i>et al.</i> (1998) Madhavalatha (2002)	Kavitha and Sree Rama Reddi (2001) Nayak <i>et al.</i> (2001)
Plant height	Valarmathi and Leenakumari (1998) Nayak <i>et al.</i> (2001) Madhavalatha (2002)	Reddy <i>et al.</i> (1997) Debchoudhury and Das (1998)
Number of effective tillers per plant	Amrithadevarathinam (1993) Valarmathi and Leenakumary (1998)	Satya Priya Lalitha and Sreedhar (1996) Ganesan <i>et al.</i> (1997) Nayak <i>et al.</i> (2001) Madhavalatha (2002)
Panicle length	Amirthadevarathinam (1990) Satya Priya Lalitha and Sreedhar (1996) Reddy <i>et al.</i> (1997)	Nayak <i>et al.</i> (2001) Madhavalatha (2002)
1000-grain weight	Ganesan <i>et al.</i> (1997) Reddy <i>et al.</i> (1997) Madhavalatha (2002)	Tarasatyavathi <i>et al.</i> (2001)

2.4.2.6 Indirect effects of 1000-grain weight on grain yield through

Character	Positive indirect effect	Negative indirect effect
Days to 50 per cent flowering	Nayak <i>et al.</i> (2001) Madhaviatha (2002)	Sinha <i>et al.</i> (1999)
Plant height	Reddy <i>et al.</i> (1997) Nagajyothi (2001) Madhaviatha (2002)	Ganesan <i>et al.</i> (1997)
Number of productive tillers per plant	Tarasatyavathi <i>et al.</i> (2001) Nagajyothi (2001)	Kavitha and Sree Rama Reddi (2001) Madhaviatha (2002)
Panicle length	Nagajyothi (2001) Nayak <i>et al.</i> (2001)	Gupta <i>et al.</i> (1998) Madhaviatha (2002)
Number of grains per panicle	Tarasatyavathi <i>et al.</i> (2001) Madhaviatha (2002)	Reddy <i>et al.</i> (1997) Nayak <i>et al.</i> (2001)
Hulling percentage	Nagajyothi (2001) Madhaviatha (2002)	Roy <i>et al.</i> (1995)
Kernel length	Reddy <i>et al.</i> (1997)	Ganesan <i>et al.</i> (1997) Madhaviatha (2002)
Kernel breadth	Ramesh Babu (1999) Madhaviatha (2002)	Sinha <i>et al.</i> (1999)
Kernel L/B ratio	Nagajyothi (2001) Tarasatyavathi <i>et al.</i> (2001)	Madhaviatha (2002)
Kernel elongation ratio		Tarasatyavathi <i>et al.</i> (2001) Madhaviatha (2002)

CHAPTER III

MATERIAL AND METHODS

The present experiment was conducted during *kharif*, 2004 at Directorate of Rice Research Farm, ICRISAT Campus, Patancheru, Hyderabad, Andhra Pradesh, India, situated at 17.5°N latitude, 78.27°E longitude and altitude of 545 m above mean sea level.

The experimental materials used and methods adopted in the present study are outlined below:

3.1 MATERIALS

The materials comprised of 70 rice genotypes which were obtained from Department of Plant Breeding and Genetics, Directorate of Rice Research, Rajendranagar, Hyderabad. The details of genotypes are furnished in Table 1.

3.2 METHODS

The experiment was laid out in a Randomized Block Design (RBD) with three replications. The experimental material was planted in three blocks. Each block consisted of 70 rice genotypes. These genotypes were randomized and replicated within each block. Thirty days old seedlings were transplanted 20 cm apart between rows and 15 cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment per replication.

All the recommended package of practices were adopted besides providing necessary prophylactic plant protection measures to raise a good crop.

3.3 COLLECTION OF DATA

Single plant observations were recorded on five selected plants at random from middle of the rows for each treatment per replication and their means were used for statistical analysis.

Following observations were recorded at appropriate growth stages.

3.3.1 Quantitative characters

Total of seven yield and yield attributing characters were recorded on five randomly selected plants in each plot. These characters were measured as per the standard techniques and are described below:

3.3.1.1 Days to 50 per cent flowering

The number of days from sowing to the days when primary panicles in 50 per cent plants were in heading was recorded.

3.3.1.2 Plant height (cm)

Plant height is measured in centimeters from ground level to the tip of the tallest panicle in each plant at the time of harvest.

3.3.1.3 Number of productive tillers per plant

Number of tillers bearing ears at maturity were counted.

3.3.1.4 Panicle length (cm)

It was measured in centimeters from the panicle base node to the tip of last spikelet prior to harvesting.

3.3.1.5 Number of grains per panicle

Number of grains were counted from five panicles of each selected plant and averaged was recorded.

3.3.1.6 1000-grain weight (g)

One thousand well filled grains were counted at random from each plant and weighed after thorough drying at 15 per cent moisture content and recorded in grams.

3.3.1.7 Grain yield per plant (g)

The weight of filled grains harvested from each plant was recorded in grams after bringing the grains to get required moisture content.

3.3.2 Quality characters

Data was recorded on physico-chemical quality characters from the bulk samples. The detailed methods of recording the observations are presented hereunder character wise:

The milling characteristics were computed following the methods given by Ghosh *et al.* (1971).

3.3.2.1 Hulling percentage

Sample of two hundred grams of well dried paddy (12-14% moisture) from each entry were dehulled in Satake Dehusker (Type-THU 35A) and the weight of brown rice was recorded. Hulling percentage was computed as:

$$\text{Hulling per cent} = \frac{\text{Weight of brown rice}}{\text{Weight of paddy}} \times 100$$

3.3.2.2 Milling percentage

The brown rice obtained after dehulling was passed through Satake Grain Testing Mill (Type-TM 05) for 1 minute 30 seconds to obtain uniformly 5-6 per cent polish. The weight of polished rice was recorded. Milling percentage was calculated as:

$$\text{Milling per cent} = \frac{\text{Weight of milled rice}}{\text{Weight of paddy}} \times 100$$

3.3.2.3 Head rice recovery (%)

The milled samples were sieved to separate whole kernels from the broken ones. Small proportion of whole kernels which passed along with broken grains were separated by hand. Full rice and three-fourth kernels were taken as whole milled rice for computation. Head rice recovery (HRR) was calculated in percentage as:

$$\text{Head rice recovery} = \frac{\text{Weight of whole milled rice}}{\text{Weight of paddy}} \times 100$$

3.3.2.4 L/B ratio

Ten polished kernels with their tips intact from each replication of the bulk samples of each entry were measured for their length and breadth using a Satake Grain Shape Tester. Average of length and breadth were taken in millimeters and L/B ratio was calculated. Based on length and L/B ratio following Ramaiah (1969) classification, the grain type was assigned.

Grain type	Length	L/B ratio
Long Slender (LS)	6 mm and above	3 and above
Short Slender (SS)	Less than 6 mm	3 and above
Medium Slender (MS)	Less than 6 mm	2.5 – 3.0
Long Bold (LB)	6 mm and above	Less than 3.0
Short Bold (SB)	Less than 6 mm	Less than 2.5

Source: Rice Research in India, ICAR Publication, 1985

3.3.2.5 Kernel length after cooking (mm)

A sample of five grams was taken in a labelled test tube and 15 ml tap water was added and soaked for ten minutes. The tubes were placed in a water bath maintained at boiling temperature (100°C) for 20 minutes. After cooking, the cooked rice from the test tubes was emptied into petri plates. Ten cooked grains (intact on both ends) were measured using a graph paper mounted in a glass frame. The average length of the cooked kernels was expressed in millimeters.

3.3.2.6 Elongation ratio

The elongation ratio was calculated by dividing the length of the cooked kernels by original average length of raw rice kernels.

$$\text{Elongation ratio (ER)} = \frac{\text{Kernel length after cooking}}{\text{Kernel length before cooking}} \times 100$$

3.3.2.7 Volume expansion ratio

Fifteen ml tap water was taken in a 50 ml graduated centrifuge tube to which 5 g rice sample was added. The increase in volume was noted after allowing the sample to soak for 10 minutes. The samples were boiled for 20 minutes and the cooked kernels were poured into a petri plate. The cooked rice was then transferred to a 100 ml measuring cylinder having 50 ml water and the increased volume was noted down. Volume expansion ratio was computed as per Juliano *et al.*, 1965.

$$\text{Volume expansion ratio (VER)} = \frac{\text{Increase in volume after cooking}}{\text{Increase in volume before cooking}}$$

Aroma is determined when the cooked rice sample was transferred into the petri dish.

3.3.2.8 Water uptake (ml)

Ten ml of tap water was added to 2 g of rice samples and allowed to soak for 30 minutes. Then the samples were boiled by placing the tubes in a constant temperature both maintained at 77°C to 80°C for 45 minutes. Another 2-3 test tubes with 10 ml water were also kept as control along with the test samples in the water

both. After boiling, the tubes were taken out, cooled and the supernatant water was poured into a graduated cylinder to note the water level. The actual amount of water absorbed during cooking was calculated by subtracting the supernatant water from the water used for cooking (after considering the evaporation loss, Beachell and Stansel, 1963).

$$\text{Water uptake (ml)} = \frac{100 \text{ g}}{2 \text{ g}} \times \text{Actual water absorbed during cooking}$$

3.3.2.9 Amylose content (%)

Amylose is the linear fraction of starch in the non-glutinous genotypes. Amylopectin, the branch fraction makes up the remainder of the starch. Amylose content has a major influence on the texture of cooked milled rice.

For standard curve, 40 mg of potato amylose was wetted with 1 ml ethyl alcohol and 9 ml of 1 N NaOH heated for 5-10 minutes in a boiling water bath, cooled and made up to 100 ml with distilled water. 1, 2, 3, 4 and 5 ml solution was taken followed by 0.2, 0.4, 0.6, 0.8 and 1.0 ml of 1N acetic acid and 2ml Iodine solution + KI and factor was derived as per Julanio, 1971. For amylose estimation of the rice sample, 100 mg rice flour passed through 100 mm sieve was taken in a test tube (2x19.5 cm), 1 ml rectified spirit and 9 ml of 1N NaOH was added to it and the mixture was shaken well. The tubes were heated over water bath for 15 minutes and the contents were transferred to 100 ml volumetric flask and volume made up to 100 ml with distilled water. From this, 5 ml of solution was taken in 100 ml volumetric flask (in three replications) and 1 ml acetic acid and 2 ml KI+I₂ reagent were added and final volume was made up to 100 ml. These flasks were covered with

black cloth for colour development and after 20 minutes, the transmission values at 620 nm were recorded. Then the amylose content of the sample was calculated by multiplying the mean of the transmission values of that sample with the factor calculated by using the standard curve and expressed as percentage.

3.3.2.10 Alkali spreading value (Gelatinization temperature)

Time required for cooking is determined by the gelatinization temperature. Gelatinization temperature, a physical property of starch, is the range of temperature within which the starch granules begin to swell irreversibly in hot water. The gelatinization temperature ranges from 55 to 79°C and is divided into three main groups: low (< 70°C), intermediate (70-74°C) and high (75-79°C). Gelatinization temperature is estimated by the extent of alkali spreading and clearing of milled rice soaked in 1.7% KOH for 23 hours at room temperature. Rices with low gelatinization temperature disintegrate completely, whereas, rice with intermediate gelatinization temperature show only partial disintegration. Rices with high gelatinization temperature remain largely unaffected in the alkali solution.

Six whole milled grains per replication were spread evenly in transparent plastic boxes containing 10 ml of 1.7 per cent potassium hydroxide solution (KOH). These boxes were kept undisturbed in an incubator 27-30°C for 23 hours. The genotypes IR 8 and CP 231 were used as checks for high and low alkali spreading values, respectively. The alkali spreading of kernels noted on a 7 point scale was expressed as average of six values. Scoring was done by following the method described by Little *et al.*, 1958.

Spreading scale

- 1 - Kernel not affected
- 2 - Kernel swollen
- 3 - Kernel swollen, collar incomplete and narrow
- 4 - Kernel swollen, collar complete and wide
- 5 - Kernel split or segmented, collar complete wide
- 6 - Kernel dispersed, merging with collar
- 7 - Kernel completely dispersed and intermingled

According to alkali spreading score, the gelatinization temperature of the entries was classified as follows:

<u>Alkali spreading value</u>	<u>Rating</u>	<u>GT</u>
1 – 2	Low	High
3	Low Intermediate	High Intermediate
4 – 5	Intermediate	Intermediate
6 – 7	High	Low

3.3.2.11 Gel consistency (mm)

100 mg of rice flour passed through 100 mm mesh was taken in triplicates in 13 x 100 mm test tubes. Ethanol (0.2 ml) containing 0.25% thymol blue and 0.2 N

KOH was added following the procedure given by Cagampang *et al.* (1973) and the solution was mixed on a vortex mixer. The test tubes were kept in water bath at 98-100°C for 8 minutes and then removed, cooled for 5 minutes and then mixed again on a vortex mixer. After mixing, these test tubes were kept in ice bath (1-6°C) for 20 minutes, removed and then laid horizontally for one hour over graph paper. Length of the blue coloured gel from the inside bottom of the test tube to the gel front was then measured as gel consistency of the sample.

Gel length	Type of gel consistency
26-40 mm	Hard
41-60 mm	Medium
61-100 mm	Soft

3.4 STATISTICAL PROCEDURE

The data with respect to the above characters were subjected to the following analysis with the help of standard statistical procedures:

1. Analysis of variance
2. Genotypic and phenotypic coefficients of variation
3. Heritability and genetic advance
4. Estimation of genetic divergence using Mahalanobis's generalized distances (D^2)
5. Estimation of correlation coefficients
6. Direct and indirect effects of characters using path coefficient analysis

3.4.1 Analysis of variance

Analysis of variance was computed based on randomized block design for each of the character separately as per standard statistical procedure (Panse and Sukhatme, 1978). The significance was tested by referring to the values of 'F' table (Fisher and Yates, 1967).

$$y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

y_{ij} = phenotypic observation of i^{th} genotype and j^{th} replication

μ = general mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

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

The structure of analysis of variance:

Source	Degrees of freedom	Mean sum of squares	F-ratio
Replications	(r-1)	M's	M's/M'e
Treatments	(t-1)	M't	M't/M'e
Error (e)	(r-1) (t-1)	M'e	
Total	(tr-1)	TMSS	

Where,

r and t = number of replications and treatments, respectively

M's, M't and M'e = mean sum of squares due to replications, treatments and error respectively

Variance

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

$$\text{Genotypic variance } (\sigma^2g) = \frac{(\text{Mean sum of squares due to treatments} - \text{Mean sum of squares due to error})}{\text{Number of replications}}$$

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

$$(\sigma^2e) = \text{Error variance}$$

3.4.2 Genotypic and phenotypic coefficients of variation

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

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

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

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

Less than 10% : Low

10-20% : Moderate

More than 20% : High

3.4.3 Heritability and genetic advance

3.4.3.1 Heritability

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

$$h^2 = \frac{\sigma^2g}{\sigma^2p}$$

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

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

- Low : 0-30%
- Medium : above 30-60%
- High : above 61%

3.4.3.2 Genetic advance

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

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

Where, GA = expected genetic advance
 K = selection differential, the value of which is 2.06 at 5 per cent selection intensity
 σ_p = phenotypic standard deviation
 $h^2(b)$ = heritability in broad sense

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

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

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

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

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

A measure for group distance based on multiple characters was given by Mahalanobis (1936) using D^2 statistics. With the help of this, genetic divergence between genotypes was estimated.

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

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

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for 't' character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for 't' character

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

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

3.4.4.1 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation values of the differences in mean values of various characters of the two genotypes i.e., d_i^2 . Therefore, transformation of correlated variables to uncorrelated one was done before working out the D^2 values. Transformation was done by using pivotal consideration method.

3.4.4.2 Computation of D^2 values

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

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

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for 't' character

Y_{jt} = Uncorrelated mean values of j^{th} genotype for 't' character

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

3.4.4.3 Testing of significance of D^2 values

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

3.4.4.4 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their combination towards divergence between two entries ($d_i = r_i^i - r_i^j$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where P is the total number of characters. Percentage contribution of each character towards genetic divergence was calculated using the formula:

$$\text{Percentage contribution of character X} = \frac{N \times 100}{M}$$

Where,

N = Number of genotype contribution where the character was ranked first

M = All possible combinations of number of genotypes considered

3.4.4.5 Grouping of genotypes into various clusters

Grouping of populations into different clusters was done using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two varieties belonging to the same cluster should at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of magnitude in a tabular form as described by Singh and Chaudhary (1979). To start

with two populations having the smallest distance from each other were considered to which a third population having the smallest D^2 value from the first two populations was added. Similarly, next nearest fourth population was considered and this procedure was continued. At certain stage where it was felt that after adding a particular population there was abrupt increase in the average D^2 value, that population was not considered for including in that cluster. The group of the first cluster was then omitted and the rest was treated in a similar way. This process was continued till the genotypes were included into one or other clusters.

3.4.4.6 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $3D_i^2/n$

Where,

$3D_i^2$ = Sum of distances between all possible combinations (n) of the populations included in a cluster

n = Number of clusters

3.4.4.7 Average inter-cluster distance

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

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

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

n_1 and n_2 are the number of genotypes of two clusters

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

3.4.4.8 Canonical analysis

Canonical analysis was used to compare the clustering pattern obtained by Mahalanobis's D^2 statistic. The canonical roots vectors were calculated to present the genotypes in the graphical form (Rao, 1952).

3.4.4.9 Calculation of sum of squares and sum of products

The correlated means were transformed into uncorrelated variables. From the transformed variables, sum of squares and sum of product for each character and character combinations were computed to obtain the matrix of variances and co-variance (matrix-A). Matrix $(A)^P$ was then divided from matrix A where P is the number of characters.

3.4.4.10 Calculation of first vector

Taking the sum column totals of matrix $(A)^P$, dividing by the highest quantity among them, the first approximate trial vector was estimated. The first approximate trial vector can be checked by interaction, multiply each column of matrix $(A)^P$ with

the first trial vector to get another column vector. Dividing each value of the second column vector by the highest value among them, the second approximation vector was obtained. This new vector was taken them as a trial vector and the procedure was repeated till the elements of the second approximation vectors were the same. Then the vectors were standardized by dividing them by correlated sum of squares of these vectors. The first root 'n' was calculated pth root of the highest column total of the last approximation.

3.4.4.11 Calculation of second vector

For getting the second vector ω^2 , the original (A)^p matrix was transformed and represented (B)^p. In (B)^p, each (i, j)th element was calculated as follows:

$$(I,j)^{th} \text{ element} = (A)^p - \lambda_1 X_1^{th} \text{ element} X_j^{th} \text{ element of the first vector}$$

The procedure followed in case of matrix A was repeated to obtain the second canonical root.

3.4.4.12 Estimation of Z values

From the values of Y₁, Y₂ Y_{ij} the mean values of characters considered Z₁, Z₂, Z₃ were calculated as:

$$Z_1 = (Y) (V_1); \quad Z_2 = (Y) (V_2)$$

Where,

(Y) = mean transformed value

V₁, V₂ = the first and second vectors, respectively

The mean values Z_1 , and Z_2 for each genotype were represented in a 2-dimensional diagram

3.4.4.13 Contribution of Vectors towards divergence

Total contribution of all the vectors was given by the sum of diagonal elements in matrix A.

$$\text{Per cent contribution of vector '1' (X}_1\text{)} = \frac{\lambda_1 \times 100}{\text{Total contribution of all vectors}}$$

$$\text{Per cent contribution of vector '2' (X}_2\text{)} = \frac{\lambda_2 \times 100}{\text{Total contribution of all vectors}}$$

$$\text{Per cent contribution of vector '3' (X}_3\text{)} = \frac{\lambda_3 \times 100}{\text{Total contribution of all vectors}}$$

Where, ' λ ' are canonical roots.

3.4.5 Estimation of correlation coefficients

Correlation coefficients were calculated at genotypic and phenotypic level using the formulae suggested by Falconer (1964).

$$\text{Genotypic coefficient of correlation (r}_g\text{)} = r(x_i . x_j)_g = \frac{\text{Cov.}(x_i . x_j)_g}{\sqrt{v(x_i)_g \cdot v(x_j)_g}}$$

Where,

$r(x_i . x_j)_g$ is genotypic correlation between i^{th} and j^{th} characters

$\text{Cov.}(x_i . x_j)_g$ is genotypic covariance between i^{th} and j^{th} characters

$v(x_i)_g$ is genotypic variance of i^{th} character

$v(x_j)_g$ is genotypic variance of j^{th} character

$$\text{Phenotypic coefficient of correlation (r}_p) = r(x_i, x_j)_p = \frac{\text{Cov.}(x_i, x_j)_p}{\sqrt{v(x_i)_p \cdot v(x_j)_p}}$$

Where,

$r(x_i, x_j)_p$ is phenotypic correlation between i^{th} and j^{th} characters

$\text{Cov.}(x_i, x_j)_p$ is phenotypic covariance between i^{th} and j^{th} characters

$v(x_i)_p$ is phenotypic variance of i^{th} character

$v(x_j)_p$ is phenotypic variance of j^{th} character

3.4.6 Path coefficient analysis

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

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

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

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

Where,

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

The above equations can be written in matrix form as:

$$\begin{matrix} & \mathbf{A} & & \mathbf{C} & & \mathbf{B} \\ \left(\begin{array}{c} r_{1y} \\ r_{2y} \\ \vdots \\ r_{ny} \end{array} \right) & = & \left(\begin{array}{cccc} 1 & r_{12} & r_{13} & \dots\dots r_{1n} \\ r_{21} & 1 & r_{23} & \dots\dots r_{2n} \\ \vdots & \vdots & \vdots & \\ \vdots & \vdots & \vdots & \\ r_{n1} & r_{n2} & r_{n3} & \dots\dots 1 \end{array} \right) & = & \left(\begin{array}{c} p_{1y} \\ p_{2y} \\ \vdots \\ p_{ny} \end{array} \right)
 \end{matrix}$$

Then

$$\mathbf{B} = [\mathbf{C}]^{-1} \mathbf{A} \text{ where } \mathbf{C}^{-1} = \left(\begin{array}{cccc} c_{11} & c_{12} & c_{13} & \dots\dots c_{1n} \\ c_{21} & c_{22} & c_{23} & \dots\dots c_{2n} \\ \vdots & \vdots & \vdots & \\ \vdots & \vdots & \vdots & \\ c_{n1} & c_{n2} & c_{n3} & \dots\dots c_{nn} \end{array} \right)$$

Direct effects were as follows:

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

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

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

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

$$p_{ry} = \sqrt{1 - (p_{1y} r_{1y} + p_{2y} r_{2y} + \dots\dots + p_{ny} r_{ny})}$$

Where, p_{ny} = Direct effect of x_n on Y
 r_{iy} = Correlation coefficient of x_n on y.

CHAPTER IV

RESULTS

The experimental findings obtained from the present study on evaluation of 70 rice genotypes for seven quantitative and eleven quality characters are presented hereunder the following heads:

- 4.1 Analysis of variance
- 4.2 Mean, genetic variability, heritability and genetic advance
- 4.3 Genetic divergence
- 4.4 Character association
- 4.5 Path coefficient analysis

4.1 ANALYSIS OF VARIANCE

Analysis of variance showed significant difference for all the traits *viz.*, days to 50 per cent flowering, plant height (cm), number of productive tillers per plant, panicle length, number of grains per panicle, 1000-grain weight (g), grain yield per plant (g), hulling percentage, milling percentage, head rice recovery percentage, L/B ratio, kernel length after cooking (mm), elongation ratio, volume expansion ratio, water uptake (ml), amylose content (%), alkali spreading value and gel consistency (mm). The results of analysis of variance are presented in Table 3.

4.2 MEAN, GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The genotypic coefficient of variability and phenotypic coefficient of variability, heritability, genetic advance and genetic advance as per cent of mean were estimated for 70 rice genotypes.

The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among the yield characters, grain yield per plant recorded highest PCV (39.31) followed by number of grains per panicle (29.55) and the lowest (12.84) recorded for panicle length. Highest GCV values were recorded for grain yield per plant (36.89) followed by number of grains per panicle (28.55), whereas, lowest value was recorded for number of productive tillers per plant (9.39). Among the grain quality characters highest PCV (28.96) for water uptake and lowest (3.40) for amylose content, whereas, highest GCV (28.84) for gel consistency and lowest for hulling percentage (3.23) was recorded.

Heritability is classified as low (below 30%), medium (30-60%) and high (above 60%). The characters studied in the present investigation expressed medium to high heritability estimates ranging from 38.91 to 99.38 per cent. Among the yield characters, highest heritability was recorded by plant height (97.14%) followed by days to 50 per cent flowering (96.70%), number of grains per panicle (93.35%), whereas, in grain quality characters gel consistency (99.38%) recorded highest heritability and amylose content recorded lowest heritability value (38.91%).

Genetic advance was highest for plant height (26.38) followed by days to 50 per cent flowering (25.75) among yield characters. In case of grain quality

characters water uptake recorded highest genetic advance (116.94) followed by gel consistency (37.27). The genetic advance as per cent of mean was highest (71.20) in grain yield per plant, while lowest (1.52) recorded by number of grains per panicle. Among grain quality characters gel consistency (59.15) recorded the highest genetic advance per cent mean, while the lowest (2.36) was recorded by hulling percentage.

4.2.1 Mean

The mean performance of 18 characters is presented in Table 4. Based on mean performance it was observed that PTB-39 found early (77.3 days), while Kalanamak was late (123.7 days). Productive tillers per plant observed more in Yamini (14) and low (8.1) in ASG 4002. Number of grains per panicle were low (48.7) in Basmati 386, whereas this trait was high (226.7) in ASG-4005. Chittimutyalu exhibited low value (8.6 g) for 1000-grain weight, while NDR-359 showed more (33.4 g) for this trait. High mean grain yield per plant (26.8 g) exhibited by Vikas, while this trait was low (5.8 g) in Ranbir Basmati.

Among the grain quality parameters, milling recovery was more in Karjat-3 (78.13 %) and low in ADT-41 (60.7 %). The maximum mean value for HRR percentage observed in Karjat-3 (76.63%) and low value in PTB-39 (29.47%). L/B ratio varied from 4.76 (Pusa Basmati) to 1.916 (ASG-4002) whereas, KLAC is ranging from 15.4 mm (Taroari Basmati) to 6.9 mm (Chittimutyalu). Gel consistency observed with a maximum value of 105.67 (Gurjari) to 25.67 (NLR-336.54). Other characters like amylose content, alkali spreading value ranged between medium to high values.

4.2.2 Genetic variability, heritability and genetic advance

4.2.2.1 Plant height (cm)

Plant height showed high genetic variability varying from 73.40 (Poornima) to 177.1 cm (Amritbhog) with a mean of 107.24 cm. The genotypic and phenotypic coefficient of variation estimates observed high i.e., 24.25 and 24.59, respectively. The observed heritability estimate for this character was high (97.14) per cent with high genetic advance (26.38) and genetic advance as per cent mean (24.59).

4.2.2.2 Days to 50 per cent flowering

This trait ranged from 77.30 (PTB-39) to 123.70 days (Kalanamak) with mean of 94.63 days, suggesting that it possessed considerable variability. The genotypic and phenotypic coefficient of variability were moderate i.e., 12.77 and 12.98, respectively. The observed heritability estimate for this trait was high (96.70) with genetic advance (25.75) and genetic advance as per cent mean (27.20) were high.

4.2.2.3 Number of productive tillers per plant

The range of variation observed for this character was from 8.10 (Amritbhog) to 14.00 (Yamini) with a mean value of 10.95. The genotypic coefficient of variability for this trait was low i.e., 9.39, whereas phenotypic coefficient of variability was moderate (14.64). The observed heritability estimate was moderate i.e., 41.17 with a low genetic advance of 1.36 and moderate genetic advance as per cent mean (12.40).

4.2.2.4 Panicle length

The mean panicle length was 24.96 cm with a minimum of 18.30 cm (GR-103) and maximum of 32.30 cm (Atmashital). The GCV (11.68) and PCV (12.84) were found to be moderate. The heritability observed for this trait was high (82.73). This character recorded low genetic advance (5.46) and moderate genetic advance as per cent of mean (21.88).

4.2.2.5 Number of grains per panicle

The wide range of variability from 48.70 (BAS-386) to 226.70 (Atmashital) observed for this character with a mean value of 125.70, suggested that this trait possess high variability which also reflected in high genotypic and phenotypic coefficients of variation i.e., 28.55 and 29.55, respectively. The heritability estimate for this trait was very high (93.35) with low genetic advance (1.92) and genetic advance as per cent of mean (1.52).

4.2.2.6 1000-grain weight (g)

1000-grain weight ranged from 8.60 (Chittimutyalu) to 33.40 g (NDR-359) with a mean value of 20.92 g. High GCV (26.36) and PCV (27.73) were recorded with high heritability estimate of 90.40. The genetic advance was moderate (10.80) and with a high genetic advance as per cent of mean (51.65).

4.2.2.7 Grain yield per plant (g)

The grain yield per plant ranged from 5.80 (Ranbir Basmati) to 27.10 g (NDR-359) with a mean value of 13.97 g. The genotypic and phenotypic coefficient of variation for this trait were high 36.89 and 39.31, respectively. The heritability

estimate for this trait was high (88.06) with a low genetic advance (9.96) and with a high genetic advance as per cent of mean (71.20).

4.2.2.8 Hulling percentage

The range of variation observed for this characters is 70.27 (GR-11) to 83.38 per cent (NLR-33654) with a mean value of 77.89 per cent. The GCV and PCV for this trait were low i.e., 3.23 and 3.41, respectively. The observed heritability estimate was high (89.78 %) with low genetic advance (1.84) and genetic advance as per cent of mean (2.36).

4.2.2.9 Milling percentage

The variability recorded for this trait ranges from 60.77 (ADT-41) to 78.13 per cent (Karjat-3) with a mean value of 69.69 per cent. The GCV and PCV for this character were low i.e., 4.61 and 4.74, respectively. The heritability estimate for this trait was very high (94.00) coupled with low genetic advance (6.40) and genetic advance as per cent of mean (9.18).

4.2.2.10 Head rice recovery percentage (HRR %)

Head rice recovery percentage varied from 29.47 (PTB-39) to 76.63 per cent (Karjat-3) with a mean value of 61.18 per cent. The GCV and PCV for this trait were moderate i.e., 14.35 and 14.50, respectively. The heritability estimate for this trait was very high (97.80) with a moderate genetic advance (17.87) and high genetic advance as per cent of mean (29.20).

4.2.2.11 L/B ratio

This trait ranged from 1.91 (Amrit bhog) to 4.76 (Pusa Basmati-1) with a mean value of 3.113. High GCV and PCV were recorded i.e., 21.57 and 21.97, respectively. The heritability estimate for this character was very high (96.37) coupled with low genetic advance (1.35) and high genetic advance as per cent of mean (43.40).

4.2.2.12 Kernel length after cooking (KLAC)

Kernel length after cooking from 6.9 (Chittimutyalu) to 15.40 mm (Taroari Basmati) with a mean value of 10.54 mm. Moderate GCV and PCV values were recorded for this character i.e., 17.91 and 18.17, respectively. Very low heritability estimate (97.18) coupled with low genetic advance (3.82) and with a high genetic advance as per cent mean (36.27) was observed for this trait.

4.2.2.13 Elongation ratio (ER)

The range of variation observed for this character was 1.29 (MTU-3626) to 2.68 (ASG-4006) with a mean value of 1.74. The GCV and PCV were moderate i.e., 15.43 and 15.85, respectively. This character recorded a high heritability of 94.70 coupled with low genetic advance (0.53) and with a high genetic advance as per cent of mean (30.82).

4.2.2.14 Volume expansion ratio (VER)

Volume expansion ratio was observed between 3.58 (BPT-11711) to 6.19 (Karjat-3) with a mean value of 4.62. The GCV and PCV for this character were moderate i.e., 10.23 and 10.81, respectively. The estimate of heritability was high

(93.50). Low values of genetic advance (0.95) and high genetic advance as per cent of mean (20.78) observed.

4.2.2.15 Water uptake

The mean water uptake was 200.04 ml with a minimum value of 103.33 ml (ADT-43) and with a maximum value of 329.67 ml (Vijetha). The GCV and PCV were found to be high i.e., 28.73 and 28.96, respectively. The heritability estimate for this trait was very high (98.40), coupled with high genetic advance (116.94) and with a high genetic advance as per cent of mean (58.40).

4.2.2.16 Amylose content

Amylose content ranged from 17.60 (Kasturi) to 26.16 (Basmati-386) with a mean value of 21.89. The GCV and PCV were recorded very low i.e., 2.12 and 3.40, respectively. The moderate estimate of heritability (38.91) coupled with very low genetic advance (0.59) and genetic advance as per cent of mean (2.72).

4.2.2.17 Alkali spreading value

Alkali spreading value ranged from 2.10 (PR-113) to 7.00 (Rasi, Vijetha and Mandya Vijaya) with a mean value of 5.95. The GCV and PCV for this character were moderate i.e., 16.53 and 16.68, respectively. The high estimate heritability (98.20) coupled with low genetic advance (2.00) and high genetic advance as per cent of mean (33.61) were observed for this trait.

4.2.2.18 Gel consistency

This character ranged with a mean value of 63.00 mm and with a minimum volume of 25.67 mm (NLR-33654) with a maximum value of 105.67 mm (Gurjari). The GCV and PCV for this character were moderate i.e., 28.84 and 28.93, respectively with a high heritability of 99.38. High genetic advance (37.27) and genetic advance as per cent of mean (59.15) were observed for this character.

4.3 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was taken up by adopting Mahalanobis's D^2 statistic using yield contributing characters and grain quality characters. Genetic divergence was estimated for 70 rice genotypes and the results obtained from the study are presented here.

4.3.1 Mahalanobis's generalized distance D^2

In order to assess the genetic diversity among 70 genotypes, D^2 statistic was used following the procedure given by Rao (1952). Since the yield and grain quality characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method. The statistical distance (Mahalanobis's D^2) between a pair of genotypes was obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated values of any two genotypes considered at a time.

4.3.2 Grouping of genotypes into various clusters

4.3.2.1 Canonical analysis

Canonical analysis was carried out in 70 genotypes, the values of six canonical roots and percentage of variation by them are presented in Table 6.

The first canonical root accounted for 29.161 per cent of total variability, second for 18.867 per cent, third for 14.396 per cent, fourth for 8.642 per cent, fifth for 7.918 per cent and sixth for 5.028 per cent. The six canonical roots were responsible for 84.00 per cent of total variability. The first three vectors contributed 62.14 per cent of total variability only.

The coefficients attached to different characters in six canonical roots are presented in Table 6 and mean values of canonical variates for 70 genotypes in three roots Z_1 (x), Z_2 (y) and Z_3 (z) were furnished in Table 8. The mean values of the canonical variates Z_1 on x-axis, Z_2 on y-axis were plotted in a 2-D graph (Fig. 1). The figure clearly depicted the six distant clusters.

The characters *viz.*, water uptake (0.51053), HRR percentage (0.46654) contributed highest towards divergence in vector Z_1 , water uptake (0.67633), gel consistency (0.48128) in vector Z_2 , gel consistency (0.58213), HRR percentage (0.46757) in vector Z_3 , days to 50 per cent flowering (0.62702) in vector Z_4 , plant height (0.48192) in vector Z_5 , water uptake (0.28620) in vector Z_6 contributed more towards genetic divergence. This was in conformity with the relative contribution of characters through D^2 statistic.

4.3.2.2 Cluster analysis

The quantum of genetic divergence was also observed by cluster analysis using Mahalanobis's Euclidean square distances which groups the entire material into more précised clusters and estimates the average distance between them. The Euclidean squared distance grouped the material into nine clusters. The cluster composition given in Table 9. The clustering pattern was depicted by Ward's minimum variance dendogram (Fig. 2). Among the clusters, cluster I was the largest comprising of 18 genotypes followed by cluster IV with 14 genotypes, cluster VI with nine genotypes, cluster IX with eight genotypes, cluster V with seven genotypes, cluster VIII with six genotypes, cluster III with four genotypes, cluster II with three genotypes, cluster VII with one genotype.

4.3.3 Intra and inter Euclidean cluster average distances

The average intra and inter cluster D^2 values are presented in Table 10 and Fig. 3. Most of the intra clusters were related and cluster D^2 values ranged from 0.00 (cluster VII) to 1365.297 (cluster VIII).

From the inter cluster D^2 values of the nine clusters, it can be observed that the highest divergence was between cluster VII and VIII (3902.050), while, lowest divergence was noticed between cluster I and cluster VI (1382.263). The clusters II and III, IV and IX, II and VIII were moderately divergent.

Mean values of clusters for yield and grain quality characters are presented in Table 11. From the data it can be concluded that considerable differences existed for all the characters studied. The data indicated that days to 50 per cent flowering

was highest in cluster II (120.00) and the lowest in cluster VII (78.33), plant height was highest in cluster IX (156.55 cm) and lowest in cluster VII (78.66 cm). Cluster II recorded highest number of productive tillers per plant (11.79) and the lowest number of productive tillers per plant was recorded in cluster VII (9.73). Highest panicle length recorded in cluster IX (29.16 cm) and lowest was in cluster VII (22.33 cm). Cluster II recorded the highest number of grains per panicle (158.56), while, cluster V recorded the lowest number of grains per panicle (109.24). 1000-grain weight observed highest in cluster V (24.76 g), lowest in cluster II (12.38 g). Cluster I recorded highest grain yield per plant (17.43 g) and lowest in cluster VII (9.30 g).

Hulling percentage was high in cluster VII (80.20) and low in cluster VI (76.65). Highest milling percentage observed in cluster VII (72.13) and lowest in cluster III (63.68). HRR per cent was highest in cluster I (66.69) and lowest in cluster V (41.68). Cluster III recorded the highest L/B ratio (3.75) and the lowest in cluster VII (2.63). KLAC was low in cluster II (9.72) and high in cluster V (11.85).

Cluster IX was high for elongation ratio (2.01) and low in cluster III (1.45). Volume expansion ratio was high in cluster I (4.78) and low in cluster VII (4.21). Cluster VI recorded lowest water uptake (132.30) and highest was recorded in cluster VII (301.33). Amylose content was high (23.70) in cluster VII and low in cluster III (18.77). ASV was high (6.88) in cluster III and low in cluster VII (2.10). Cluster VIII recorded the highest (92.28) gel consistency and lowest (48.34) in cluster I.

4.3.4 Relative contribution of characters towards genetic divergence

The number of times that each of character appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 12 and Fig. 4. The results showed that the contribution of water uptake was highest towards genetic divergence (26.00%) by taking 628 times ranking first, followed by gel consistency (24.80%) by 599 times, HRR percentage (17.10%) by 413 times, days to 50 per cent flowering (10.23%) by 247 times, plant height (7.12%) by 172 times, ASV (7.00%) by 169 times, milling percentage (1.90%) by 46 times, KLAC (1.70%) by 41 times, VER (1.41%) by 34 times, elongation ratio (1.16%) by 28 times, amylose content (0.41%) by 10 times, number of grains per panicle (0.25%) by six times, 1000-grain weight (0.17%) by four times and grain yield per plant (0.08%) by two times.

4.4 CHARACTER ASSOCIATION

Phenotypic and genotypic correlations between yield and yield components *viz.*, days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle and 1000-grain weight were estimated for rice genotypes. The genotypic and phenotypic correlations between yield and yield component characters were computed separately. The results are presented in Table 13.

The results revealed that the estimates of genotypic coefficients were higher than phenotypic correlation coefficients for most of the characters under study. The results obtained from the phenotypic and genotypic correlations coefficients are presented character-wise hereunder:

4.4.1 Days to 50 per cent flowering

Days to 50 per cent flowering registered positive and significant correlation with number of grains per panicle (0.3125**/0.3217**).

4.4.2 Plant height (cm)

This trait exhibited positive and significant correlation with panicle length (0.6289**/0.6860**), number of grains per panicle (0.2423*/0.2503*), while a negative and significant association with 1000-grain weight (0.4552**/-0.4917**).

4.4.3 Number of productive tillers per plant

Number of productive tillers per plant registered positive and non-significant correlation with grain yield per plant, while, it is negative and non-significant correlation with panicle length.

4.4.4 Panicle length

Panicle length had a negative and significant correlation (-0.3170**/-0.3755**) with 1000-grain weight.

4.4.5 Number of grains per panicle

This trait exhibited positive and significant correlation with grain yield per plant (0.3697**/0.3995**).

4.4.6 1000-grain weight

This trait registered positive and significant correlation with grain yield per plant (0.3911**/0.4512**).

4.5 PATH COEFFICIENT ANALYSIS

Path coefficient analysis was done for grain yield per plant and its component characters in rice genotypes. The estimates of path coefficient analysis are furnished for yield and yield component characters in Tables 14.

4.5.1 Days to 50 per cent flowering

Days to 50 per cent flowering exhibited a positive direct effect of 0.1158 on grain yield per plant. It recorded positive indirect effect on grain yield per plant via plant height (0.0088), number of productive tillers per plant (0.0083) and number of grains per panicle (0.1267).

4.5.2 Plant height

Plant height had shown a positive direct of 0.1537 on grain yield per plant. It recorded positive indirect effects via number of grains per panicle (0.0982) and days to 50 per cent flowering (0.0066) towards grain yield.

4.5.3 Number of productive tillers per plant

It recorded a positive direct effect of 0.1036 on grain yield per plant, while, it had shown indirect effects via panicle length (0.0268), number of grains per panicle (0.0203) and days to 50 per cent flowering (0.0092).

4.5.4 Panicle length

Panicle length exhibited a negative direct effect of -0.1759 on grain yield per plant, while, it was recorded positive indirect effect via days to 50 per cent flowering (0.0016), plant height (0.0967) and number of grains per panicle (0.0691).

4.5.5 Number of grains per panicle

Number of grains per panicle showed positive direct (0.4055) effect on grain yield per plant, while, this trait exhibited positive indirect effects via days to 50 per cent flowering (0.0362), plant height (0.0372) and number of productive tillers per plant (0.0052).

4.5.6 1000-grain weight

This trait showed the highest positive direct effect of 0.4958 on grain yield per plant, while, it was recorded positive indirect effect via panicle length (0.0558).

Table 1: Details of experimental material (70 rice genotypes)

S.No.	Genotype	Source / Origin
1.	NLR-30491	Andhra Pradesh
2.	NLR-145	Andhra Pradesh
3.	NLR-33654	Andhra Pradesh
4.	IR-30864	Karnataka
5.	Vikas	Haryana
6.	IET-8116	Karnataka
7.	KRH-2	Karnataka
8.	NDR-359	Uttar Pradesh
9.	Rasi	DRR, Hyderabad
10.	Tellahamsa	Andhra Pradesh
11.	SGT-1	Andhra Pradesh
12.	IET-16775	DRR, Hyderabad
13.	PR-111	Punjab
14.	Yamini	DRR, Hyderabad
15.	Kranthi	Madhya Pradesh
16.	Mahamaya	Madhya Pradesh
17.	PR-116	Punjab
18.	Vijetha	Andhra Pradesh
19.	Mandya Vijaya	Karnataka
20.	BAS-370	Punjab
21.	BAS-386	Punjab
22.	IR-64	Tamil Nadu
23.	PTB-39	Kerala
24.	Kasturi	Himachal Pradesh
25.	Ranbir Basmati	Jammu & Kashmir
26.	Karjat-3	Maharashtra
27.	VRS-3	Gujarat
28.	Poornima	Madhya Pradesh
29.	White Ponni	Tamil Nadu
30.	Pusa Basmati-1	IARI, New Delhi
31.	Vasumati	DRR, Hyderabad
32.	Taraori Basmati	Haryana
33.	ADT-41	Tamil Nadu
34.	ADT-43	Tamil Nadu

(Contd...)

Table 1: (Contd...)

(1)	(2)	(3)
35.	BPT-5204	Andhra Pradesh
36.	Jaya	DRR, Hyderabad
37.	Cotondora Sannalu	Andhra Pradesh
38.	Type-3	Uttar Pradesh
39.	PR-113	Punjab
40.	Suraksha	DRR, Hyderabad
41.	Mugadsugandha	Karnataka
42.	ADT-36	Tamil Nadu
43.	BPT-11711	Andhra Pradesh
44.	PR-114	Punjab
45.	Pant Dhan-16	Uttar Pradesh
46.	Pant Dhan-14	Uttar Pradesh
47.	Triguna	DRR, Hyderabad
48.	Amrit bhog	Chattisgarh
49.	Himashital	Chattisgarh
50.	Tilakchandani	Uttar Pradesh
51.	Badshaw bhog	West Bengal
52.	RAU 3030	Chattisgarh
53.	RAU 3043	Chattisgarh
54.	Kalanamak	Uttar Pradesh
55.	Krishnakamod	Gujarat
56.	Chittimutyalu	Andhra Pradesh
57.	GR-103	Gujarat
58.	MTU 1001	Andhra Pradesh
59.	MTU-3626	Andhra Pradesh
60.	GR-11	Gujarat
61.	Gurjari	Gujarat
62.	Dhandi	Gujarat
63.	GR-104	Gujarat
64.	GR-7	Gujarat
65.	Shashi	West Bengal
66.	Giri	West Bengal
67.	Satabdi	West Bengal
68.	Khitish	West Bengal
69.	Sabita	West Bengal
70.	PNR-519	Himachal Pradesh

Table 6: Canonical root values, per cent variation observed and cumulative total variation for different genotypes

Canonical root	Value of canonical root	Per cent variation observed	Cumulative total per cent variation
Z ₁	19546.06	29.16179	29.16179
Z ₂	12646.08	18.86735	48.02915
Z ₃	9649.69	14.39689	62.42604
Z ₄	5792.93	8.64278	71.06882
Z ₅	5307.50	7.91855	78.98737
Z ₆	3370.17	5.02815	84.01552

Table 9: Clustering pattern among different rice genotypes under study (cluster-analysis)

Cluster No.	No. of genotypes	Name of the genotype
I	18	NLR-30491, Pant Dhan-14, Vasumati, Type-3, NLR-145, SGT-1, Gurjari, Khitish, MTU-3626, IR-30864, IET-8116, Sabita, NDR-359, PR-111, GR-103, MTU-1001, NLR-33654, VRS-3
II	3	White ponni, Kalanamak, RAU 3043
III	4	Vikas, Giri, Ranbir basmati, BPT-5204
IV	14	Rasi, Tellahamsa, Shashi, IET-16775, PR-114, PR-116, Dhandi, KRH-2, Mandya Vijaya, Vijetha, Triguna, Satabdi, PR-113, Taraori-Basmati
V	7	Yamini, Bas-386, Mahamaya, Kasturi, PNR-519, Pusa Basmati-1, IR-64
VI	9	PTB-39, Tilakchandam, Poornima, Suraksha, GR-11, Cotton Dora Sannalu, Karjat-3, Mugadsugandha, Pent Dhan-16
VII	1	ADT-36
VIII	6	Kranthi, GR-7, BPT-711, ADT-43, Jaya, ADT-41
IX	8	Bas-370, Badshawbhog, RAU 3030, Krishna Kamood, Chittimuthyalu, Amritbhog, Atmashital, GR-104

Table- 12: Relative contribution of yield and quality characters to genetic diversity in rice

S.No.	Character	Times ranked first	Contribution (%)
1.	Days to 50 per cent flowering	247	10.23
2.	Plant height (cm)	172	7.12
3.	Number of productive tillers/plant	0	0.00
4.	Panicle length (cm)	0	0.00
5.	Number of grains/panicle	6	0.25
6.	1000-grain weight (g)	4	0.17
7.	Grain yield/plant (g)	2	0.08
8.	Hulling percentage	8	0.33
9.	Milling percentage	46	1.90
10.	Head rice recovery (%)	413	17.10
11.	L/B ratio	8	0.33
12.	Kernel length after cooking (mm)	41	1.70
13.	Elongation ratio	28	1.16
14.	Volume expansion ratio	34	1.41
15.	Water uptake (ml)	628	26.00
16.	Amylose content (%)	10	0.41
17.	Alkali spreading value (ASV)	169	7.00
18.	Gel consistency (mm)	599	24.80

Table 3: ANOVA for yield and quality characters in different rice genotypes

S.No.	Character	Mean sum of squares		
		Replications (d.f.=2)	Treatments (d.f.=68)	Error (d.f.=136)
1.	Days to 50 per cent flowering	14.34	443.41**	4.99
2.	Plant height (cm)	59.22	2049.48**	19.90
3.	Number of productive tillers/plant	2.89	4.69**	1.51
4.	Panicle length (cm)	4.57	27.28**	1.78
5.	Number of grains/panicle	260.39	3957.42**	91.82
6.	1000-grain weight (g)	0.70	94.45**	3.23
7.	Grain yield/plant (g)	4.08	83.37**	3.60
8.	Hulling percentage (%)	2.13	19.84**	0.72
9.	Milling percentage (%)	1.53	32.24**	0.59
10.	Head rice recovery (%)	4.17	233.04**	1.67
11.	L/B ratio	0.01	1.37**	0.02
12.	Kernel length after cooking	0.05	10.80**	0.10
13.	Elongation ratio	0.01	0.22**	0.00
14.	Volume expansion ratio	0.05	0.72**	0.02
15.	Water uptake (ml)	158.26	9963.98**	53.00
16.	Amylose content (%)	0.99	12.05**	0.34
17.	Alkali spreading value	0.01	2.92**	0.02
18.	Gel consistency (mm)	4.41	992.87**	2.05

** Significant at 1 per cent level

Table 7: Canonical root vectors for different characters contributing to genetic diversity (D^2) in rice

Character	Vector 1	Vector 2	Vector 3	Vector 4	Vector 5	Vector 6
Days to 50 per cent flowering	0.2208	0.0760	0.3842	0.6270	0.4171	0.0857
Plant height (cm)	0.0183	-0.1028	0.3213	-0.4534	0.4819	0.0703
Number of productive tillers/plant	-0.0079	-0.0002	-0.0868	0.0690	-0.0936	-0.0386
Panicle length (cm)	-0.0149	0.0126	-0.0016	0.0372	0.0350	0.0278
Number of grains/panicle	0.0046	-0.0047	0.0592	-0.0548	-0.0080	0.1496
1000-grain weight (g)	0.0074	0.0733	-0.1306	0.2250	-0.2241	-0.0117
Grain yield/plant (g)	0.0709	0.0308	0.0769	0.1871	-0.0376	0.0706
Hulling percentage (%)	0.0439	-0.0413	-0.0515	-0.0865	-0.1479	0.0699
Milling percentage (%)	0.1304	-0.0764	-0.1046	-0.0814	-0.3721	-0.0138
Head rice recovery (%)	0.4665	-0.4067	0.4675	-0.0951	-0.4332	0.0392
L/B ratio	0.0041	0.0378	-0.1133	0.2757	0.0320	-0.2453
Kernel length after cooking (mm)	-0.1601	-0.0399	-0.2667	0.0108	0.0223	-0.32117
Elongation ratio	-0.0301	-0.2404	0.0377	-0.1794	0.1091	-0.1160
Volume expansion ratio	0.1549	-0.0185	0.0253	0.3131	-0.2141	-0.0285
Water uptake (ml)	0.5101	0.6763	-0.1782	-0.2379	-0.0108	0.2862
Amylose content (%)	-0.0786	-0.0529	-0.0487	-0.0236	-0.0632	-0.1034
Alkali spreading value	0.3391	0.2261	0.1461	-0.1313	0.06328	-0.8233
Gel consistency (mm)	-0.5256	0.4813	0.5821	-0.0492	-0.3412	-0.0567

Table 8: Mean values of canonical variates in different genotypes of rice

S.No.	Genotype	X Vector	Y Vector	Z Vector
(1)	(2)	(3)	(4)	(5)
1.	NLR-30491	114.976	-0.061	73.800
2.	NLR-145	126.330	7.650	81.603
3.	NLR-33654	137.016	-0.378	77.087
4.	IR-30864	110.741	15.649	84.972
5.	Vikas	112.802	40.094	85.407
6.	IET-8116	117.072	20.456	89.796
7.	KRH-2	126.570	25.889	80.144
8.	NDR-359	114.088	15.178	80.290
9.	Rasi	119.806	33.141	73.724
10.	Tellahamsa	118.663	27.178	76.197
11.	SGT-1	113.204	7.744	81.449
12.	IET-16775	119.979	30.359	70.700
13.	PR-111	103.687	19.851	75.119
14.	Yamini	85.394	8.576	53.696
15.	Kranthi	99.605	35.981	91.680
16.	Mahamaya	85.554	45.039	63.514
17.	PR-116	133.648	20.527	75.433
18.	Vijetha	139.198	35.687	82.223
19.	Mandya Vijaya	131.822	22.093	92.651
20.	BAS-370	88.688	6.531	79.263
21.	BAS-386	74.073	14.505	56.030
22.	IR-64	93.210	5.601	73.137
23.	PTB-39	72.496	42.300	73.871
24.	Kasturi	103.723	42.814	77.157
25.	Ranbir Basmati	87.389	6.675	72.658
26.	Karjat-3	138.880	-3.736	78.717
27.	VRS-3	106.817	11.913	79.187
28.	Poornima	125.775	16.194	84.636
29.	White Ponni	111.430	2.175	66.900
30.	P. Basmati	135.624	23.282	49.747
31.	Vasumati	93.545	5.885	83.635
32.	Taroari Basmati	77.331	22.622	78.813
33.	ADT-41	104.089	39.541	83.800
34.	ADT-43	101.275	4.556	82.362

(Contd...)

Table 8: (Contd...)

(1)	(2)	(3)	(4)	(5)
35.	BPT-5204	112.672	-5.569	70.012
36.	Jaya	130.903	30.991	60.501
37.	Cottondora Sannalu	96.980	12.590	90.367
38.	Type-3	86.813	1.610	79.567
39.	PR-113	107.240	23.879	52.002
40.	Suraksha	100.279	22.146	115.208
41.	Mugadsugandha	126.628	41.454	78.919
42.	ADT-36	89.588	-0.740	58.208
43.	BPT-11711	105.114	-5.145	70.590
44.	PR-114	129.574	22.104	58.542
45.	Pant Dhan-16	87.271	22.878	96.726
46.	Pant Dhan-14	106.705	16.397	87.406
47.	Triguna	94.665	7.952	79.340
48.	Amrit bhog	93.733	-2.130	85.096
49.	Himashital	106.084	0.441	91.132
50.	Tilakchandani	102.907	14.463	86.424
51.	Badshaw bhog	123.539	4.062	99.871
52.	RAU 3030	105.060	1.386	86.780
53.	RAU 3043	107.504	14.968	89.726
54.	Kalanamak	110.246	6.132	84.019
55.	Krishnakamod	106.140	8.175	90.886
56.	Chittimutyalu	116.603	15.886	84.347
57.	GR-103	96.986	7.783	85.419
58.	MTU 1001	125.726	16.439	78.189
59.	MTU-3626	136.006	18.139	73.679
60.	GR-11	92.670	21.234	86.730
61.	Gurjari	90.163	37.870	90.369
62.	Dhandi	111.840	33.966	82.700
63.	GR-104	116.171	43.630	92.483
64.	GR-7	117.145	23.270	68.476
65.	Shashi	123.050	17.217	81.812
66.	Giri	113.540	15.181	92.512
67.	Satabdi	89.393	27.472	75.171
68.	Khitish	97.016	30.858	58.456
69.	Sabita	79.512	29.423	91.121
70.	PNR-519	87.679	26.234	73.148

Table 2: Rice genotypes of different agro-climatic zones

S.No.	Name of the zone	Comprising states	Genotypes collected
1.	Western Himalayan Zone	Sub zones of Jammu & Kashmir, Himachal Pradesh, Uttar Pradesh hills	Ranbir Basmati Kasturi PNR-519
2.	Lower Gangetic plains	West Bengal	Badshawbhog, Shashi, Giri, Satabdi, Khitish, Sabita
3.	Upper gangetic plains	32 districts of Uttar Pradesh	Pant Dhan-16 Pant Dhan-14 NDR-359, Type-3 Kalnamak Tilkchandan
4.	Trans Gangetic plains	Punjab, Haryana, Union Territories of Delhi, Chandigarh and Sriganganagar district of Rajasthan	Vikas, PR-111, PR-116, Bas-370, Bas-386, Pusa Basmati-1, Taroari Basmati, PR-113, PR-114
5.	Central Plateau and hills	42 districts of Madhya Pradesh, Uttar Pradesh and Rajasthan	Kranti, Poornima, Mahamaya
6.	Western Plateau and hills	Major parts of Maharashtra, parts of Madhya Pradesh and one district of Rajasthan	Karjat-3, Amritbhog, Atmashital, RAU 3030, RAU 3043
7.	Southern plateau and hills	35 districts of Andhra Pradesh, Karnataka, Tamil Nadu	NLR-30491, NLR-145, NLR-33654, Rasi, Tellahamsa, SGT-1, IET-16775, Yamini, BPT-5204, Vijetha, Jaya, Cotton Dora Sannalu, Suraksha, BPT-11711, Triguna, Chittimutyalu, MTU-1001, MTU-3626, Vasumati
8.	East coast plains and hills	Orissa coastal, North coastal, South coastal Andhra, North coastal Tamil Nadu, South Coastal Tamil Nadu and Tanjavur	IR-64, White ponni, ADT-41, ADT-43, ADT-36
9.	West coast plains and Ghats	Parts of Tamil Nadu, Kerala, Karnataka, Maharashtra and Goa	IR-30864, IET-8116, KRH-2, Mandya Vijaya, PTB-39, Mugad Sugandha
10.	Gujarat plains and hills	19 districts of Gujarat	VRS-3, Krishnakamood, GR-103, GR-11, Gurjari, Dhandi, GR-104, GR-7

Table 5: Estimates of variability, heritability, genetic advance and genetic advance as per cent mean in rice genotypes

S.No.	Character	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (h ²) (%)	GA (5%)	GA as per cent mean
1.	Days to 50 per cent flowering	151.12	146.14	12.98	12.77	96.7	25.75	27.20
2.	Plant height (cm)	696.42	676.52	24.59	24.25	97.14	26.38	24.59
3.	Number of productive tillers/plant	2.57	1.05	14.64	9.39	41.17	1.35	12.40
4.	Panicle length (cm)	10.27	8.50	12.84	11.68	82.73	5.46	21.88
5.	Number of grains/panicle	1380.35	1288.53	29.55	28.55	93.35	1.92	1.52
6.	1000-grain weight (g)	33.64	30.40	27.73	26.36	90.40	10.80	51.64
7.	Grain yield/plant (g)	30.19	26.58	39.31	36.89	88.06	9.96	71.20
8.	Hulling percentage (%)	7.09	6.37	3.41	3.23	89.78	1.84	2.36
9.	Milling percentage (%)	10.94	10.33	4.74	4.61	94.00	6.40	9.18
10.	Head rice recovery (%)	78.79	77.12	14.50	14.35	97.80	17.87	29.20
11.	L/B ratio	0.46	0.45	21.97	21.57	96.37	1.35	43.4
12.	Kernel length after cooking (mm)	3.66	3.56	18.17	17.91	97.18	3.82	36.27
13.	Elongation ratio	0.07	0.07	15.85	15.43	94.70	0.53	30.82
14.	Volume expansion ratio	0.24	0.23	10.81	10.23	93.50	0.95	20.78
15.	Water uptake (ml)	3356.65	3303.66	28.96	28.73	98.40	116.94	58.40
16.	Amylose content (%)	0.55	0.21	3.40	2.12	38.91	0.59	2.72
17.	Alkali spreading value	0.98	0.96	16.68	16.53	98.20	2.00	33.61
18.	Gel consistency (mm)	332.32	330.27	28.93	28.84	99.38	37.27	59.15

Table 13: Estimates of phenotypic and genotypic correlation coefficients between yield and yield component characters

Character	Days to 50 per cent flowering	Plant height (cm)	Productive tillers/plant	Panicle length	Grains per panicle	1000-grain weight	Grain yield/plant
Days to 50 per cent flowering	1.0000 (1.0000)	0.0571 (0.0588)	0.0797 (0.1188)	0.0138 (0.0173)	0.3125** (0.3217)**	-0.1099 (-0.1149)	0.2026 (0.2226)
Plant height (cm)		1.0000 (1.0000)	-0.0774 (-0.1483)	0.6289** (0.6860)**	0.2423* (0.2503)*	-0.4552** (-0.4917)**	-0.0858 (-0.0926)
No. of productive tillers/plant			1.0000 (1.0000)	-0.1525 (-0.2271)	0.0501 (0.0207)	-0.0846 (-0.1517)	0.1062 (0.1691)
Panicle Length				1.0000 (1.0000)	0.1704 (0.1889)	-0.3170** (-0.3755)**	-0.1815 (-0.2200)
No. of grains/panicle					1.0000 (1.0000)	-0.1702 (-0.1875)	0.3697** (0.3995)**
1000-grain weight						1.0000 (1.0000)	0.3911** (0.4512)**
Grain yield/plant							1.0000 (1.0000)

** Significant at 1 per cent level

* Significant at 5 per cent level

Figures in parenthesis are genotypic correlation coefficients

Table 14: Estimates of direct and indirect effects between yield and yield components

Character	Days to 50 per cent flowering	Plant height	Number of productive tillers/plant	Panicle length	Number of grains per panicle	1000-grain weight	Grain yield
Days to 50 per cent flowering	0.1158 (0.1113)	0.0088 (0.0165)	0.0083 (0.0286)	-0.0024 (-0.0035)	0.1267 (0.1441)	-0.0545 (-0.0743)	0.2026 (0.2226)
Plant height (cm)	0.0066 (0.0065)	0.1537 (0.2807)	-0.0080 (-0.0357)	-0.1106 (-0.1382)	0.0982 (0.1121)	-0.2257 (-0.3180)	-0.0858 (-0.0926)
No. of productive tillers/plant	0.0092 (0.0132)	-0.0119 (-0.0416)	0.1036 (0.2406)	0.0268 (0.0458)	0.0203 (0.0093)	-0.0419 (-0.0981)	0.1062 (0.1691)
Panicle length	0.0016 (0.0019)	0.0967 (0.1926)	-0.0158 (-0.0546)	-0.1759 (-0.2015)	0.0691 (0.0846)	-0.1572 (-0.2429)	-0.1815 (-0.2200)
No. of grains/panicle	0.0362 (0.0358)	0.0372 (0.0703)	0.0052 (0.0050)	-0.0300 (-0.0381)	0.4055 (0.4478)	-0.0844 (-0.1213)	0.3697 (0.3995)
1000-grain weight	-0.0127 (-0.0128)	-0.0700 (-0.1380)	-0.0088 (-0.0365)	0.0558 (0.0757)	-0.0690 (-0.0840)	0.4958 (0.6468)	0.3911 (0.4512)

Residual effect (Phenotypic) = 0.3971

Residual effect (Genotypic) = 0.5545

Figures in parentheses are genotypic effects

Table 11: Cluster means for yield and quality characters in different rice genotypes (cluster analysis)

	Days to 50% flow.	Plant height (cm)	No. of prod. tillers/plant	Panicle length (cm)	No. of grains/panicle	1000-grain weight (g)	Grain yield/plant (g)	Hulling (%)	Milling (%)	HRR (%)	L/B ratio	KLAC (mm)	Elong. Ratio	VER	Water uptake (ml)	Amylose content (%)	ASV	Gel consistency (mm)
Cluster I	98.37	105.61	11.04	24.19	136.80	23.15	17.43	78.71	70.92	66.69	2.94	9.83	1.73	4.78	175.41	21.89	6.09	48.34
Cluster II	120.00	140.14	11.79	27.67	158.56	12.38	10.81	79.18	69.08	61.98	2.72	9.72	2.00	4.62	205.22	20.34	5.49	51.22
Cluster III	94.75	101.19	10.12	25.42	137.42	19.38	12.25	72.83	63.68	58.04	3.75	10.18	1.45	4.71	274.75	18.77	6.88	81.21
Cluster IV	97.31	97.98	10.98	24.00	113.79	22.01	13.69	79.00	71.79	63.46	3.30	10.54	1.63	4.64	275.86	21.55	6.76	56.52
Cluster V	86.05	101.83	11.23	25.19	109.24	24.76	13.24	77.61	67.93	41.68	3.46	11.86	1.74	4.51	184.95	23.13	6.16	76.45
Cluster VI	88.33	86.78	11.22	23.48	111.30	21.19	13.95	76.65	68.86	63.02	3.14	10.58	1.76	4.54	132.30	21.28	4.68	63.87
Cluster VII	78.33	78.66	9.73	22.33	117.33	19.49	9.30	80.20	72.13	57.37	2.63	10.40	1.65	4.21	301.33	23.70	2.10	69.40
Cluster VIII	101.83	97.38	10.72	24.78	129.94	22.60	12.96	78.64	69.98	58.64	3.32	11.64	1.70	4.45	168.72	22.96	5.58	92.28
Cluster IX	83.25	156.55	10.64	29.17	131.88	13.19	10.81	77.00	68.50	63.45	2.57	10.62	2.01	4.50	183.50	22.52	5.95	67.19

Table 4: Mean performance of genotypes for various characters

S.No	Name of variety	Days to 50% flowering	Plant height (cm)	Productive tillers/plant	Panicle length (cm)	No. of grains/panicle	1000 Gr. Wt (g)	Grain yield/plant(g)	Hulling percentage	Milling percentage	Head rice recovery percentage	L/B ratio	Kernel length after cooking (mm)	Elongation ratio	Volume expansion ratio	Water uptake (ml)	Amylose content	Alkali spreading value	Gel consistency (mm)
(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)	(17)	(18)	(19)	(20)
1	NLR-30491	83.33	90.72	12.50	22.00	179.00	20.32	24.64	79.16	72.67	70.60	2.64	9.47	1.72	4.07	147.67	20.03	6.13	41.67
2	NLR-145	112.33	100.00	12.40	23.67	169.67	20.55	19.09	80.80	73.67	69.27	3.14	9.33	1.54	4.30	184.33	20.24	5.60	43.17
3	NLR-33654	111.67	108.33	11.97	26.33	166.67	19.07	13.54	83.38	77.57	71.33	2.80	9.27	1.56	4.93	172.33	20.63	6.22	25.67
4	IR-30864	95.00	101.22	11.10	27.33	98.00	24.66	12.06	80.37	73.63	67.23	3.39	8.77	1.39	4.43	162.67	22.06	6.12	67.17
5	VIKAS	96.67	90.37	8.67	25.67	149.33	25.09	13.91	70.87	63.43	59.30	3.42	9.47	1.44	5.10	262.33	18.01	6.94	75.67
6	IET-8116	95.33	134.28	10.53	24.33	159.67	22.94	23.76	78.00	69.00	68.17	2.47	9.60	1.71	4.34	235.33	22.18	6.60	64.33
7	KRH-2	98.33	113.09	13.17	28.00	142.67	21.03	25.60	80.80	72.30	67.20	3.07	10.20	1.61	5.33	274.33	18.66	5.80	63.17
8	NDR-359	99.33	119.00	8.63	26.33	190.67	33.35	27.09	78.33	71.80	63.47	3.24	10.60	1.41	4.89	191.67	21.30	5.67	56.33
9	RASI	80.33	76.22	11.97	19.00	147.33	26.51	15.09	78.67	72.10	65.30	2.45	9.17	1.65	5.01	272.67	24.25	7.00	72.17
10	TELLAHAMSA	81.33	89.89	10.40	20.67	86.67	24.47	8.80	79.87	71.70	68.43	3.18	10.30	1.65	5.18	257.67	24.78	6.70	70.00
11	SGT-1	108.67	106.44	11.87	22.67	95.67	27.96	18.70	79.50	70.43	64.47	3.81	11.20	1.52	4.33	148.33	22.57	6.37	48.00
12	IET-16775	106.33	112.22	10.53	26.00	93.67	21.65	8.37	76.47	68.87	55.10	4.40	12.53	1.68	4.42	280.00	23.72	6.70	56.50
13	PR-111	98.00	95.83	11.50	25.00	145.67	24.05	22.02	78.90	70.27	56.50	3.67	11.67	1.75	5.58	189.67	24.01	5.60	66.83
14	YAMINI	80.33	91.77	13.97	22.67	88.33	23.28	11.23	75.87	66.03	46.33	4.62	15.37	2.04	4.68	150.33	19.88	5.63	50.67
15	KRANTHI	98.33	105.77	10.43	24.33	126.33	28.93	18.35	79.80	70.50	59.43	2.22	9.40	1.71	3.87	234.33	23.77	6.07	96.50
16	MAHAMAYA	80.67	99.00	10.53	21.67	128.33	32.19	20.10	80.13	67.57	38.13	2.55	11.30	1.71	5.35	255.00	25.04	6.27	94.00
17	PR-116	93.33	99.32	10.87	22.67	129.33	26.92	21.69	80.03	75.17	71.30	3.36	9.57	1.42	4.54	249.67	23.13	7.00	50.67
18	VIJETHA	106.67	106.67	11.73	22.67	113.33	23.69	16.51	78.87	69.00	67.97	2.83	10.40	1.62	5.35	329.67	14.01	7.00	56.67
19	MANDYA VIJAYA	111.33	131.05	11.87	25.00	173.67	17.08	16.88	80.07	72.30	70.70	3.00	8.43	1.52	4.06	249.67	22.37	7.00	57.17
20	BAS-370	80.33	142.16	11.33	28.33	109.33	22.25	9.93	76.30	60.83	61.00	3.89	14.47	2.18	4.59	181.00	21.13	5.30	61.33
21	BAS-386	78.33	123.63	12.33	26.33	48.67	23.13	7.93	73.57	64.37	37.77	4.14	14.47	1.96	4.14	150.33	26.16	6.00	61.67
22	PTB-39	77.33	80.83	10.43	20.33	91.00	27.78	11.96	78.73	70.80	63.90	2.61	10.50	1.52	4.23	117.00	21.91	5.30	63.17
23	KASTURI	95.67	110.38	9.50	30.67	123.67	23.83	12.44	78.70	66.03	29.47	2.69	9.27	1.50	4.38	166.67	24.50	7.00	96.33
24	RANBIR BASMATI	77.67	113.89	10.87	25.33	74.00	20.71	5.81	73.37	64.37	56.33	3.87	11.27	1.61	5.42	295.67	17.60	6.60	86.50
25	KARJAT-3	94.33	90.72	12.97	23.67	126.33	19.53	18.27	75.67	67.27	54.40	3.81	13.30	2.03	5.43	128.67	23.49	4.50	63.17
26	VRS-3	100.33	124.99	11.30	22.67	142.33	23.49	23.80	82.07	78.13	76.63	2.67	9.37	1.67	6.19	177.67	21.49	6.00	26.67
27	POORNIMA	81.67	73.44	11.07	20.67	75.00	21.30	19.69	74.27	71.20	70.43	2.24	9.40	1.83	4.35	178.33	22.51	5.23	66.33
28	WHITE PONNI	115.33	135.43	11.97	26.00	146.33	14.46	13.86	79.67	68.00	64.40	3.67	8.77	1.37	4.77	229.33	15.03	5.30	47.00
29	VASUMATI	81.67	106.00	11.53	27.67	126.67	14.53	7.96	77.37	67.90	64.47	2.75	10.60	2.10	4.56	196.33	21.17	5.13	39.67
30	TAROARI BASMATI	97.33	93.70	12.33	26.00	73.67	23.06	7.01	76.07	70.20	57.10	4.76	14.40	1.89	4.16	320.33	22.31	7.00	27.67
31	ADT-41	97.67	76.72	10.50	24.00	75.00	25.89	7.15	80.80	71.20	67.43	4.45	14.33	1.85	5.14	119.33	21.59	4.68	71.67
32	ADT-43	97.33	66.33	11.00	23.00	110.00	16.28	7.16	76.00	67.00	50.40	4.26	15.40	2.09	4.74	145.67	21.27	5.60	87.17
33	BPT-5204	104.67	87.38	10.83	24.00	203.33	13.03	14.90	70.73	60.77	53.17	4.33	11.23	1.47	4.31	249.67	19.39	6.97	76.17
34	COTTNDORA SANNALU	93.67	77.11	10.77	25.00	96.00	24.63	11.50	75.20	67.80	66.57	3.15	7.57	1.42	4.52	103.33	19.04	4.73	57.50
35	TYPE-3	83.67	135.72	9.22	27.33	145.67	20.76	8.14	75.33	67.97	64.37	3.02	9.57	1.78	4.72	151.67	21.81	5.57	27.67
36	PR-113	97.67	92.44	8.77	25.33	139.33	28.02	17.02	78.40	71.00	55.37	2.54	8.63	1.42	5.10	297.67	22.12	6.00	46.67
37	SURAKSHA	98.33	99.55	12.20	27.67	162.67	21.50	20.11	76.40	68.23	64.97	3.40	10.60	1.59	4.90	138.67	19.96	5.00	73.17

(Contd...)

Table-4: (Contd....)

(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)	(17)	(18)	(19)	(20)
38	MUGADSUGANDHA	94.67	99.88	11.40	29.00	103.67	20.08	18.99	77.10	67.60	64.33	3.44	12.50	1.90	3.96	146.67	22.63	2.12	71.67
39	ADT-36	78.33	78.66	9.73	22.33	117.33	19.49	9.30	80.20	72.13	57.37	2.63	10.40	1.65	4.21	301.33	23.70	2.10	69.40
40	BPT-711	122.00	131.11	10.07	25.00	207.33	16.35	15.45	77.00	69.07	66.73	2.56	7.43	1.34	4.68	149.67	24.07	5.13	91.67
41	PR-114	119.33	90.83	9.77	26.33	94.67	18.29	8.27	77.97	69.43	56.60	4.22	11.73	1.65	4.63	308.67	22.00	6.96	67.50
42	PANT DHAN-16	78.33	80.09	9.77	22.67	117.33	24.94	8.50	77.13	66.80	55.80	3.18	12.37	2.17	4.27	143.33	21.40	3.90	48.00
43	PANT DHAN-14	84.33	95.00	9.77	27.00	109.00	25.65	13.42	78.30	71.10	65.47	2.73	11.50	2.33	3.58	132.67	21.13	5.97	38.97
44	TRIGUNA	79.67	77.46	10.87	22.67	80.67	17.81	9.97	77.13	71.13	65.10	3.70	9.43	1.35	3.80	266.33	22.03	7.00	42.33
45	ASG-4002	86.33	177.11	8.07	30.33	104.67	10.05	12.35	78.90	73.10	57.37	2.22	10.77	1.94	4.39	193.00	23.23	6.00	96.00
46	ASG-4005	79.67	156.50	9.97	32.33	226.67	9.44	9.72	80.47	72.17	67.20	2.79	10.53	1.67	4.21	224.33	20.60	5.97	71.50
47	ASG-4006	79.00	84.97	10.27	22.33	77.67	18.09	6.60	77.20	71.30	66.63	3.80	9.67	1.58	4.72	123.00	19.97	4.97	71.00
48	ASG-4016	80.33	170.74	11.53	30.67	191.00	9.63	8.01	74.80	70.10	64.10	1.92	14.47	2.08	4.84	155.33	24.06	5.63	55.67
49	ASG-4011	81.00	164.50	10.20	31.67	108.33	12.02	9.30	79.43	72.10	71.07	2.20	9.10	2.27	4.66	168.67	22.53	5.70	60.17
50	ASG-4013	121.00	114.67	12.20	25.67	206.67	10.86	10.10	77.47	69.33	52.33	2.18	12.20	2.68	4.79	192.00	23.11	5.77	60.00
51	KALANAMAK	123.67	170.33	11.20	31.33	122.67	11.82	8.46	80.40	69.90	69.20	2.31	8.20	1.96	4.29	194.33	22.87	5.40	46.67
52	KRISHNAKAMOD	90.00	157.47	10.40	26.00	75.33	11.36	8.66	80.47	69.17	65.60	2.39	9.57	2.36	4.91	173.00	22.73	5.57	55.33
53	CHITTIMUTYALU	88.33	163.40	11.87	26.67	108.33	8.65	10.09	75.40	66.10	61.83	2.13	7.53	1.84	4.48	200.00	22.93	6.90	60.67
54	GR-103	106.33	91.77	11.43	18.33	117.33	17.58	11.23	76.60	67.37	63.70	2.80	10.67	2.16	5.17	148.00	25.88	6.67	47.67
55	MTU-1001	109.33	104.14	11.07	24.00	118.33	23.13	15.77	78.17	68.30	65.87	2.73	9.57	1.83	4.88	145.33	23.97	5.20	61.00
56	MTU-3626	98.67	88.23	10.77	24.67	116.00	27.20	16.86	78.40	67.87	65.80	2.07	6.90	1.72	4.54	178.33	19.59	6.53	54.67
57	GR-11	97.67	94.47	12.07	20.00	152.00	12.82	9.89	78.13	68.70	60.20	2.63	9.30	1.83	4.52	111.67	20.63	6.33	60.83
58	GURJARI	98.33	89.10	13.87	21.00	142.67	23.87	19.55	77.73	70.90	68.17	2.84	10.17	1.70	5.07	215.33	22.20	7.00	48.00
59	DHANDI	98.33	106.07	11.40	25.33	125.67	23.13	11.49	79.23	75.13	70.63	2.82	11.30	1.70	4.46	274.33	21.63	6.53	44.00
60	GR-104	80.00	120.50	11.77	27.33	131.33	22.10	18.35	70.27	64.43	59.47	3.05	8.53	1.72	3.88	172.67	22.97	6.53	76.83
61	GR-7	99.67	111.87	13.10	25.00	123.00	21.70	15.45	81.07	72.77	54.03	2.81	11.20	1.69	3.75	221.67	22.87	6.00	105.67
62	SHASHI	95.33	101.48	9.99	24.00	105.33	21.45	10.30	82.53	73.30	60.33	2.54	10.33	1.81	4.29	256.67	21.03	7.00	81.00
63	GIRI	100.00	113.11	10.11	26.57	123.00	18.67	14.38	76.33	66.17	63.37	3.37	8.73	1.29	4.00	291.33	20.07	7.00	86.50
64	SATABDI	97.00	81.33	10.11	22.17	87.00	15.08	14.59	79.87	73.43	57.27	3.35	11.07	1.82	4.65	224.33	19.68	7.00	55.83
65	KHITISH	102.67	74.05	11.00	22.67	107.00	19.25	15.27	77.43	69.13	67.73	3.04	9.40	1.64	5.32	192.00	22.63	7.00	51.17
66	SABITA	101.67	136.11	8.22	22.00	132.33	28.27	20.79	76.97	68.93	67.20	3.04	9.30	1.61	5.07	188.00	21.13	6.17	61.50
67	PNR-519	97.33	80.26	10.77	22.00	117.00	21.03	17.72	78.03	69.90	48.00	3.57	11.10	1.73	4.40	165.00	20.17	6.20	80.67
68	IR-64	85.67	100.11	11.97	25.33	143.00	28.35	14.43	79.93	71.23	42.80	3.17	10.37	1.58	4.28	224.67	21.20	6.00	69.67
69	JAYA	96.00	92.50	9.20	27.33	138.00	26.45	14.20	77.17	69.33	53.83	3.61	12.07	1.54	4.54	141.67	24.20	6.00	101.00
70	P.BASMATI	84.33	107.66	9.53	27.33	115.67	21.52	8.82	77.07	70.40	49.23	3.51	11.13	1.66	4.34	182.67	24.98	6.00	82.17
	General Mean	94.64	107.24	10.96	24.96	125.70	20.91	13.97	77.90	69.70	61.18	3.11	10.54	1.74	4.61	200.01	21.81	5.95	63.01
	SEm±	1.82	3.63	1.00	1.06	7.82	1.46	1.54	0.69	0.62	1.05	0.10	0.26	0.08	0.10	5.94	0.48	0.10	1.36
	CD (P=0.05)	3.57	7.11	1.96	2.07	15.30	2.86	3.01	1.35	1.21	2.05	0.20	0.51	0.16	0.20	11.64	0.93	0.20	2.66
	CV (%)	2.35	4.15	11.20	5.30	7.60	8.60	13.60	1.09	1.10	2.11	4.20	3.00	3.60	2.70	3.63	2.60	2.10	2.20

Plant height	Productive tillers/plant	Panicle length	No. of		Grain		Gr.yield (kg/ha)
			grains/pa nicle	1000 Wt	yield/plan t(g)		
91.00	13.60	22	176	20.18	25.77	4974.00	
90.16	11.30	21	171	20.38	27.49	4526.00	
91.00	12.60	23	190	20.39	20.66	5159.00	
103.00	13.30	25	161	20.55	17.64	5977.00	
104.00	10.60	23	180	21.19	19.59	6613.00	
93.00	13.30	23	168	19.90	20.05	6231.00	
112.00	13.00	26	172	19.64	14.32	5833.00	
110.66	12.30	24	166	20.39	12.34	6367.00	
102.33	10.60	29	162	17.18	13.98	5451.00	
104.33	12.00	26	104	23.16	13.00	3623.00	
97.33	10.30	28	94	26.33	12.14	3497.00	
102.00	11.00	28	96	24.50	11.03	3344.00	
96.00	10.00	26	145	25.30	12.36	3115.00	
89.50	8.00	26	148	24.94	14.18	2985.00	
85.60	8.00	25	155	25.04	15.20	2151.00	
138.00	12.00	24	158	23.35	20.49	4423.00	
135.53	9.00	24	160	22.55	25.40	4772.00	
129.30	10.60	25	161	22.92	25.38	5338.00	
113.33	14.60	27	148	21.03	26.80	5738.00	
113.33	12.60	28	138	19.72	25.58	5155.00	
112.60	12.30	29	142	22.32	24.41	5633.00	
121.33	9.60	27	202	33.84	27.31	5818.00	
122.66	8.30	27	180	34.08	24.30	5254.00	
113.00	8.00	25	190	32.15	29.66	5531.00	
79.00	12.60	20	152	25.10	12.45	3082.00	
75.00	11.30	18	141	28.40	15.97	3241.00	
74.66	12.00	19	149	26.04	16.84	3256.00	
91.33	10.60	20	80	24.95	8.13	2751.00	
89.33	11.30	22	96	24.44	8.24	3110.00	
89.00	9.30	20	84	24.00	10.04	3492.00	
110.66	9.60	22	88	27.60	17.65	5577.00	
108.66	14.00	23	107	27.64	19.83	6136.00	
100.00	12.00	23	92	28.64	18.63	5326.00	
112.66	13.00	25	110	20.34	9.72	3736.00	
115.00	10.00	26	88	22.42	8.31	3562.00	
109.00	8.60	27	83	22.20	7.08	2944.00	
94.66	11.30	23	148	23.65	23.34	4690.00	
96.83	12.60	25	139	24.30	21.03	5069.00	
96.00	10.60	27	150	24.20	21.69	4562.00	
90.66	13.60	23	85	25.36	10.62	1982.00	
90.00	15.00	22	89	22.24	12.81	2023.00	
94.66	13.30	23	91	22.26	10.27	2090.00	
105.00	10.30	25	130	28.32	20.55	4910.00	
104.66	11.00	24	130	28.48	16.25	4690.00	
107.66	10.00	24	119	30.00	18.24	4026.00	
105.00	11.00	23	135	32.32	17.55	3664.00	
97.00	9.30	22	130	32.48	21.63	3497.00	
95.00	11.30	20	120	31.78	21.13	2997.00	
100.00	12.30	23	125	27.08	25.19	6333.00	
97.66	10.00	23	124	27.96	18.45	6826.00	
100.30	10.30	22	139	25.72	21.43	6569.00	
110.00	12.00	23	107	21.80	16.47	6133.00	
107.00	10.60	23	118	24.13	18.07	6367.00	
103.00	12.60	22	115	25.12	14.99	5085.00	
131.66	12.00	25	170	16.50	15.38	6500.00	
129.50	13.30	24	176	17.91	18.31	6536.00	
132.00	10.30	26	175	16.82	16.94	6862.00	

Plant hight	Productive tillers/plant	Panicle length	No. of grains/pa nicle	1000 Gr. Wt	Gr. yield/plan t(g)	Gr.yield (kg/ha)
141.66	12.00	28	102	22.81	8.75	2246.00
146.83	9.00	29	112	22.34	11.33	1959.00
138.00	13.00	28	114	21.59	9.72	2344.00
125.66	10.00	26	50	22.30	8.24	2362.00
128.00	14.00	27	48	24.12	8.69	2185.00
117.23	13.00	26	48	22.96	6.88	2015.00
83.50	10.00	21	95	24.25	11.50	1654.00
82.66	10.00	21	90	29.94	13.48	2010.00
76.33	11.30	19	88	29.16	10.91	2336.00
116.83	10.60	32	124	23.18	10.38	4008.00
110.66	9.30	28	121	25.14	12.00	4121.00
103.66	8.60	32	126	23.18	14.95	4523.00
116.66	11.00	27	80	20.25	6.37	1579.00
110.00	9.30	26	70	21.01	5.70	1682.00
115.00	12.30	23	72	20.87	5.37	1213.00
88.50	12.60	25	120	21.62	15.14	5877.00
91.66	13.30	23	127	16.30	19.78	6413.00
92.00	13.00	23	132	20.69	19.88	6572.00
127.00	11.60	23	145	21.02	28.11	3964.00
120.66	10.00	21	142	22.80	21.71	3841.00
127.30	12.30	24	140	26.65	21.58	4679.00
75.00	11.60	22	70	23.68	17.82	5454.00
75.33	10.00	20	69	20.51	18.13	6372.00
70.00	11.60	20	86	19.71	23.13	5910.00
135.66	12.60	26	145	16.40	14.17	6287.00
136.33	11.30	25	150	15.72	11.15	6405.00
134.30	12.00	27	144	11.26	16.26	5123.00
107.33	11.00	30	122	14.96	8.27	4636.00
102.66	12.30	26	124	13.63	9.07	4846.00
108.00	11.30	27	134	15.01	6.53	5133.00
90.80	12.00	28	72	23.63	8.08	2741.00
89.00	11.00	25	69	21.31	6.30	2062.00
101.30	14.00	25	80	24.24	6.66	1995.00
78.33	10.60	25	75	26.64	6.81	2282.00
77.50	11.60	24	70	26.44	6.06	2482.00
74.33	9.30	23	80	24.60	8.59	2077.00
66.33	11.00	25	117	14.67	5.72	1918.00
68.33	10.00	22	105	17.96	7.32	2377.00
64.33	12.00	22	108	16.20	8.44	2528.00
88.83	11.60	25	195	13.34	13.17	5210.00
83.66	10.30	23	205	14.44	15.40	5859.00
89.66	10.60	24	210	11.32	16.13	6085.00
80.00	10.00	23	90	27.29	11.98	1890.00
68.00	10.00	25	93	20.76	10.38	1861.00
83.33	12.30	27	105	25.84	12.15	2103.00
139.66	9.00	28	158	20.54	10.14	4069.00
133.83	10.00	27	145	22.20	7.03	4841.00
133.66	8.66	27	134	19.55	7.25	4733.00
91.66	9.30	26	139	30.87	16.31	5303.00
91.00	9.00	24	144	24.32	15.66	4741.00
94.66	8.00	26	135	28.88	19.10	4615.00
100.66	12.00	29	150	21.48	17.30	5505.00
96.00	10.30	28	170	21.30	22.60	5403.00
102.00	14.30	26	168	21.71	20.42	5674.00
99.30	12.60	28	115	20.73	23.55	5374.00
99.00	9.60	29	104	20.88	16.14	5164.00
101.33	12.00	30	92	18.64	17.27	4508.00

Plant height	Productive tillers/plant	Panicle length	No. of		Grain		
			grains/pa nicle	1000 Gr. Wt	yield/plan t(g)	Gr.yield (kg/ha)	
80.16	9.00	25	127	21.56	10.42	1569.00	
80.83	9.60	21	105	18.62	9.76	1954.00	
75.00	10.60	21	120	18.28	7.73	1526.00	
131.66	10.00	24	208	18.79	13.36	7721.00	
128.00	9.60	26	218	15.08	14.37	6546.00	
133.66	10.60	25	196	15.19	18.64	6577.00	
89.33	8.00	26	94	18.56	9.15	4597.00	
90.16	10.00	26	100	19.93	8.48	4605.00	
93.00	11.30	27	90	16.38	7.18	4741.00	
82.66	12.00	24	116	24.07	9.04	2156.00	
81.30	9.00	23	122	24.10	8.51	1992.00	
76.30	8.30	21	114	26.64	7.94	2092.00	
96.00	10.30	28	95	23.72	13.41	4897.00	
93.16	9.00	26	110	25.14	13.67	3774.00	
95.83	10.00	27	122	28.09	13.19	4374.00	
79.00	11.00	25	85	19.07	12.12	2269.00	
77.73	11.60	22	80	18.19	10.20	2151.00	
75.66	10.00	21	77	16.15	7.58	2310.00	
178.33	7.60	31	109	9.90	10.73	1692.00	
180.00	7.30	31	85	10.46	12.16	1800.00	
173.00	9.30	29	120	9.80	14.16	1651.00	
155.31	11.00	31	205	9.56	8.61	1426.00	
158.60	8.30	33	220	9.11	12.14	1364.00	
155.60	10.60	33	255	9.66	8.41	1223.00	
93.30	11.60	25	88	19.92	8.11	1462.00	
81.30	9.60	20	76	19.06	5.33	1246.00	
80.30	9.60	22	69	15.30	6.37	1277.00	
170.33	13.00	31	197	9.94	6.62	1803.00	
171.60	9.30	31	180	8.51	9.36	1936.00	
170.30	12.30	30	196	10.43	8.06	1649.00	
161.30	9.00	32	95	11.76	8.30	1721.00	
164.60	11.60	33	105	12.54	10.72	2121.00	
167.60	10.00	30	125	11.76	8.87	1754.00	
115.30	13.30	25	195	11.30	8.13	2210.00	
116.70	11.00	28	210	9.58	10.69	1782.00	
112.00	12.30	24	215	11.70	11.48	1703.00	
171.00	11.00	31	100	11.63	7.91	1721.00	
172.00	13.60	32	148	12.51	8.56	1979.00	
168.00	9.00	31	120	11.32	8.93	1556.00	
157.30	9.60	26	72	10.51	8.63	1656.00	
160.50	11.00	27	69	11.37	9.20	1626.00	
154.60	10.60	25	85	12.20	8.15	1369.00	
161.60	12.00	27	102	9.10	9.67	3962.00	
167.30	12.60	27	105	8.56	12.00	4851.00	
161.30	11.00	26	118	8.28	8.61	3741.00	
100.00	11.00	19	110	26.01	10.35	4100.00	
87.30	11.30	18	125	11.03	12.81	3777.00	
88.00	12.00	18	117	15.69	10.53	3600.00	
104.50	10.60	22	110	20.22	14.48	6485.00	
105.60	12.00	25	120	25.39	18.03	5751.00	
102.33	10.60	25	125	23.80	14.81	5369.00	
89.60	10.30	26	100	27.17	15.66	5877.00	
89.50	12.00	25	120	27.92	18.54	6341.00	
85.60	10.00	23	128	26.52	16.38	6123.00	
94.80	11.30	18	146	13.55	10.24	3610.00	
93.60	11.30	21	140	12.64	10.25	3390.00	
95.00	13.60	21	170	12.28	9.18	4672.00	

Plant height	Productive tillers/plant	Panicle length	No. of		Grain		Gr.yield (kg/ha)
			grains/pa nicle	1000 Wt	yield/plan t(g)		
91.30	12.30	22	150	23.18	18.70	6256.00	
88.00	15.00	19	130	23.93	20.74	6056.00	
88.00	14.30	22	148	24.50	19.22	5049.00	
108.60	10.60	25	123	24.74	11.50	4621.00	
109.60	11.60	24	123	21.99	11.66	5121.00	
100.00	12.00	27	131	22.65	11.30	5221.00	
119.00	10.30	27	121	21.30	17.31	4905.00	
120.50	12.00	28	115	20.64	21.08	5726.00	
122.00	13.00	27	158	24.35	16.68	5792.00	
113.60	12.00	25	132	21.32	16.37	5736.00	
113.00	14.30	26	117	21.66	15.82	4659.00	
109.00	13.00	24	120	22.12	14.16	4303.00	
101.60	9.66	24	118	20.16	8.59	5256.00	
102.50	10.66	23	108	22.16	8.62	5038.00	
100.33	9.66	25	90	22.04	13.71	5092.00	
114.00	10.00	28	122	20.00	14.75	5549.00	
113.16	10.66	26	122	16.32	12.46	5015.00	
112.16	9.66	26	125	19.68	15.92	5956.00	
81.00	11.00	21	82	15.12	13.16	5323.00	
81.66	11.00	22	88	14.88	15.98	5041.00	
81.33	8.33	24	91	15.24	14.62	4654.00	
74.50	11.66	23	114	16.00	15.72	4426.00	
73.16	10.33	22	112	22.28	13.40	5167.00	
74.50	11.00	24	95	19.48	16.68	5297.00	
137.30	8.00	23	130	28.44	18.45	5369.00	
134.70	8.33	21	132	28.32	19.04	5526.00	
136.33	8.33	22	135	28.04	24.89	5297.00	
80.30	11.00	22	105	20.52	14.94	5410.00	
80.16	10.66	21	121	21.44	19.41	4913.00	
80.33	10.66	24	125	21.12	18.80	5003.00	
103.33	13.30	26	148	29.36	16.51	5605.00	
100.00	10.60	24	139	27.54	14.32	4790.00	
97.00	12.00	26	142	28.16	12.48	4618.00	
97.66	11.00	28	132	26.37	12.88	5790.00	
81.50	8.00	27	147	27.36	14.34	5469.00	
98.33	8.60	27	135	25.60	15.39	5510.00	
107.66	10.30	26	110	19.32	8.52	4085.00	
111.33	8.00	30	118	22.58	9.71	4782.00	
104.00	10.30	26	119	22.66	8.23	3531.00	
64.33	7.3	18	48	8.28	5.331	1213	
180	15	33	255	34.08	29.661	7721	

No of days to 50% flowering	Plant height	Productive tillers/plant	Panicle length	No. of grains/panicle	1000 Gr. Wt	Grain yield/plot(g)	Gr.yield (kg/ha)
83.3333	90.72	12.5	22	179	20.3173	24.64	4886.33
112.333	100	12.4	23.6667	169.667	20.5467	19.0927	6273.67
111.667	108.33	11.9667	26.3333	166.667	19.0707	13.5433	5883.67
95	101.22	11.1	27.3333	98	24.66	12.0567	3488
96.6667	90.3667	8.66667	25.6667	149.333	25.0933	13.913	2750.33
95.3333	134.277	10.5333	24.3333	159.667	22.94	23.7557	4844.33
98.3333	113.087	13.1667	28	142.667	21.0267	25.598	5508.67
99.3333	118.997	8.63333	26.3333	190.667	33.3547	27.091	5534.33
80.3333	76.22	11.9667	19	147.333	26.5133	15.0883	3193
81.3333	89.8867	10.4	20.6667	86.6667	24.4653	8.80333	3117.67
108.667	106.44	11.8667	22.6667	95.6667	27.9627	18.701	5679.67
106.333	112.22	10.5333	26	93.6667	21.6533	8.37133	3414
98	95.83	11.5	25	145.667	24.0493	22.0207	4773.67
80.3333	91.7733	13.9667	22.6667	88.3333	23.284	11.234	2031.67
98.3333	105.773	10.4333	24.3333	126.333	28.9333	18.349	4542
80.6667	99	10.5333	21.6667	128.333	32.1933	20.104	3386
93.3333	99.32	10.8667	22.6667	129.333	26.92	21.69	6576
106.667	106.667	11.7333	22.6667	113.333	23.6853	16.5113	5861.67
111.333	131.053	11.8667	25	173.667	17.0787	16.8773	6632.67

No of days to 50% flowering	Plant height	Productive tillers/plant	Panicle length	No. of grains/panicle	1000 Gr. Wt	Grain yield/plan t(g)	Gr.yield (kg/ha)
80.3333	142.163	11.3333	28.3333	109.333	22.2453	9.93333	2183
78.3333	123.63	12.3333	26.3333	48.6667	23.1253	7.933	2187.33
77.3333	80.83	10.4333	20.3333	91	27.784	11.962	2000
95.6667	110.383	9.5	30.6667	123.667	23.8347	12.442	4217.33
77.6667	113.887	10.8667	25.3333	74	20.7107	5.81473	1491.33
94.3333	90.72	12.9667	23.6667	126.333	19.5347	18.266	6287.33
100.333	124.987	11.3	22.6667	142.333	23.4907	23.8007	4161.33
81.6667	73.4433	11.0667	20.6667	75	21.3013	19.6903	5912
115.333	135.43	11.9667	26	146.333	14.4627	13.8593	5938.33
81.6667	105.997	11.5333	27.6667	126.667	14.5307	7.957	4871.67
97.3333	93.7	12.3333	26	73.6667	23.0613	7.011	2266
97.6667	76.72	10.5	24	75	25.892	7.154	2280.33
97.3333	66.33	11	23	110	16.2773	7.159	2274.33
104.667	87.3833	10.8333	24	203.333	13.0333	14.8997	5718
93.6667	77.11	10.7667	25	96	24.6307	11.5037	1951.33
83.6667	135.717	9.22	27.3333	145.667	20.7627	8.14	4547.67
97.6667	92.44	8.76667	25.3333	139.333	28.0213	17.0227	4886.33
98.3333	99.5533	12.2	27.6667	162.667	21.4973	20.1053	5527.33
94.6667	99.8767	11.4	29	103.667	20.0827	18.986	5015.33

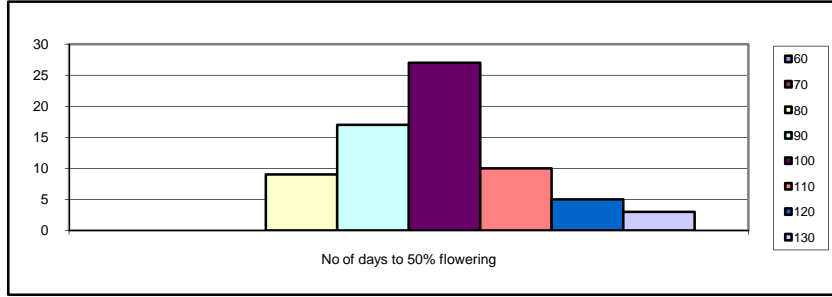
No of days to 50% flowering	Plant height	Productive tillers/plant	Panicle length	No. of grains/panicle	1000 Gr. Wt	Grain yield/pan (g)	Gr.yield (kg/ha)
78.3333	78.6633	9.73333	22.3333	117.333	19.488	9.302	1683
122	131.107	10.0667	25	207.333	16.352	15.4543	6948
119.333	90.83	9.76667	26.3333	94.6667	18.29	8.27	4647.67
78.3333	80.0867	9.76667	22.6667	117.333	24.9373	8.49733	2080
84.3333	94.9967	9.76667	27	109	25.652	13.424	4348.33
79.6667	77.4633	10.8667	22.6667	80.6667	17.8053	9.965	2243.33
86.3333	177.11	8.06667	30.3333	104.667	10.0547	12.3477	1714.33
79.6667	156.503	9.96667	32.3333	226.667	9.44267	9.71567	1337.67
79	84.9667	10.2667	22.3333	77.6667	18.0907	6.60233	1328.33
80.3333	170.743	11.5333	30.6667	191	9.62867	8.01267	1796
81	164.5	10.2	31.6667	108.333	12.0213	9.29747	1865.33
121	114.667	12.2	25.6667	206.667	10.86	10.0973	1898.33
123.667	170.333	11.2	31.3333	122.667	11.82	8.464	1752
90	157.467	10.4	26	75.3333	11.36	8.65933	1550.33
88.3333	163.4	11.8667	26.6667	108.333	8.64667	10.091	4184.67
106.333	91.7667	11.4333	18.3333	117.333	17.576	11.2303	3825.67
109.333	104.143	11.0667	24	118.333	23.1347	15.7733	5868.33
98.6667	88.2333	10.7667	24.6667	116	27.204	16.862	6113.67
97.6667	94.4667	12.0667	20	152	12.8227	9.88933	3890.67

No of days to 50% flowering	Plant height	Productive tillers/plant	Panicle length	No. of grains/panicle	1000 Gr. Wt	Grain yield/pan (g)	Gr.yield (kg/ha)
98.3333	89.1	13.8667	21	142.667	23.872	19.5517	5787
98.3333	106.067	11.4	25.3333	125.667	23.1267	11.4873	4987.67
80	120.5	11.7667	27.3333	131.333	22.096	18.3533	5474.33
99.6667	111.867	13.1	25	123	21.6987	15.4477	4899.33
95.3333	101.477	9.99333	24	105.333	21.4533	10.304	5128.67
100	113.107	10.1067	26.5667	123	18.668	14.3763	5506.67
97	81.33	10.11	22.1667	87	15.08	14.5893	5006
102.667	74.0533	10.9967	22.6667	107	19.2533	15.268	4963.33
101.667	136.11	8.22	22	132.333	28.2667	20.794	5397.33
97.3333	80.2633	10.7733	22	117	21.0267	17.7167	5108.67
85.6667	100.11	11.9667	25.3333	143	28.352	14.434	5004.33
96	92.4967	9.2	27.3333	138	26.4453	14.203	5589.67
84.3333	107.663	9.53333	27.3333	115.667	21.5187	8.819	4132.67

istribution of different variable

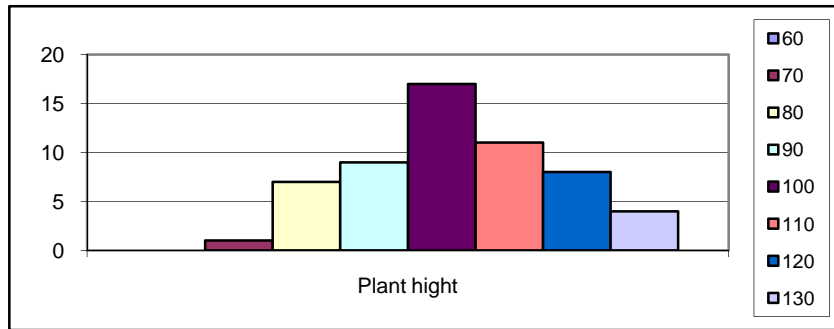
No of days to 50% flowering

Class	Frequency
60	0
70	0
80	9
90	17
100	27
110	10
120	5
130	3



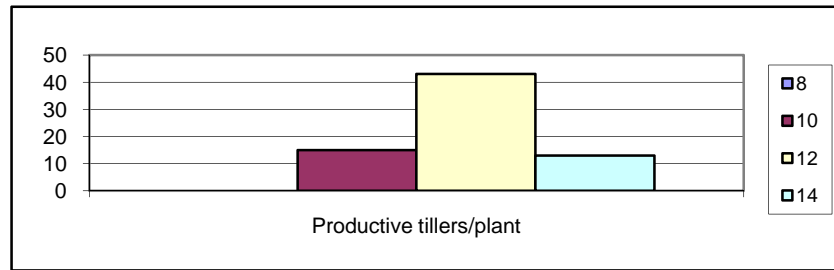
Plant hight

60	0
70	1
80	7
90	9
100	17
110	11
120	8
130	4



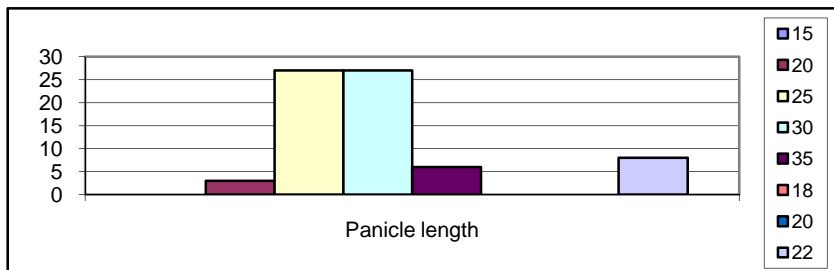
Productive tillers/plant

8	0
10	15
12	43
14	13
16	
18	
20	
22	



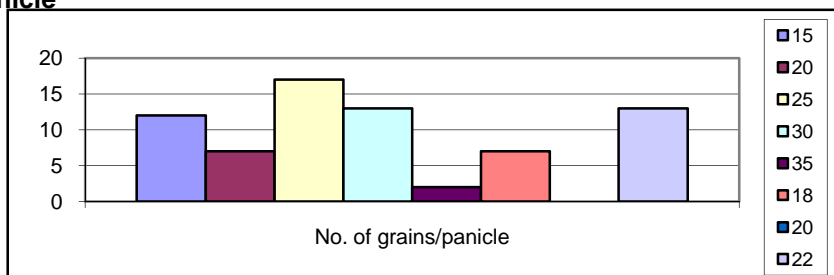
Panicle length

15	0
20	3
25	27
30	27
35	6
18	0
20	0
22	8



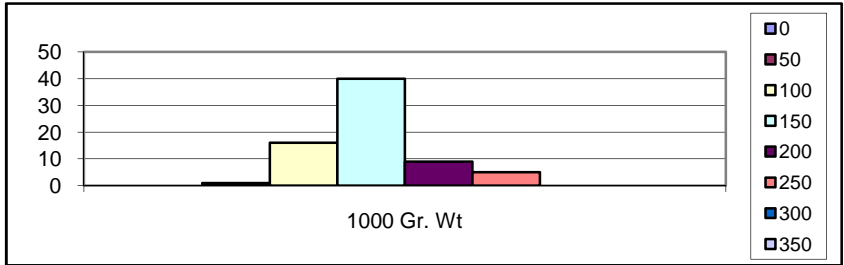
No. of grains/panicle

15	12
20	7
25	17
30	13
35	2
18	7
20	0
22	13



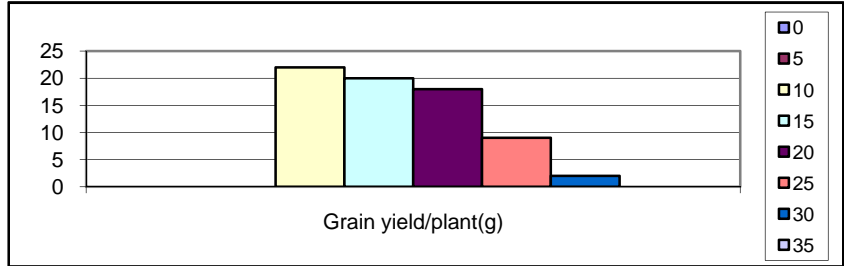
0
 50
 100
 150
 200
 250
 300
 350

1000 Gr. Wt



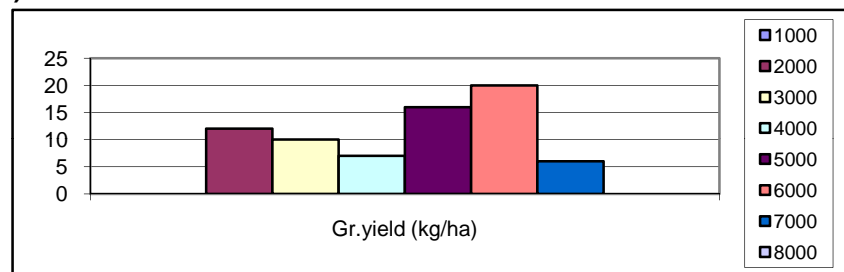
0
 5
 10
 15
 20
 25
 30
 35

Grain yield/plant(g)



1000
 2000
 3000
 4000
 5000
 6000
 7000
 8000

Gr.yield (kg/ha)



CHAPTER V

DISCUSSION

Breeding autogamous crop plants like rice needs right choice of parents for hybridization. Seed yield and grain quality characters are complex characters controlled by polygenes. Hence, exploiting heterosis and evolving desirable segregants to a large extent depends on the nature and degree of genetic divergence between parents selected for hybridization. Hence, the nature and extent of gene action controlling the inheritance of yield and quality characters is essential.

A critical analysis of genetic variability is a prerequisite for initiating any crop improvement programme and for adoption of appropriate selection techniques. However, mere study of variability does not ensure the improvement of complex characters. Hence, the study of association of various characters with yield along with direct and indirect relationship of yield related characters through correlations and path coefficients becomes essential.

The available information on various aspects of the investigation from 70 genotypes has been discussed under the following heads:

- 5.1 Variability, heritability and genetic advance
- 5.2 Genetic divergence
- 5.3 Character association
- 5.4 Path coefficient analysis

5.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

Success of plant breeding programmes largely depends on the amount of genetic variability present in a given crop species for the character under improvement. The genotypic coefficient of variation measures the range of variability available in the crop and also enables a breeder to compare the amount of variability present among different characters. The phenotypic expression of the character is the result of interaction between genotype and environment. Hence, the total variance should be partitioned into heritable and non-heritable components to assess the true breeding nature of the particular trait under study.

Heritability indicates the relative degree at which a character is transmitted from parent to off-spring. High heritability values indicate that the characters under study are less influenced by environment in their expression. The traits exhibiting high heritability could be improved by adopting simple selection methods. Further, the information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study (Table 4).

Yield contributing characters

5.1.1 Days to 50 per cent flowering

This trait showed significant genetic variability. The genotypic and phenotypic coefficients of variation were moderate. The small differences between the genotypic and phenotypic coefficients of variation indicate less influence of environment on this character. High heritability with high genetic advance indicates the influence of additive type of gene action in the inheritance of this trait. Hence, its

response to selection would be effective. The present findings are in conformity with the results of Manonmani *et al.* (1996), Chikkalingaiah (1999), Madhavalatha (2002) and Nayak *et al.* (2002).

5.1.2 Plant height

Plant height showed high genetic variability, while, the estimates of phenotypic and genotypic coefficients of variation were high. But, the differences between the estimates of PCV and GCV were low, indicating that the stability of the trait over environments. It had high heritability with high genetic advance indicating the influence of additive type of gene action in the inheritance of this trait. Hence, its response to selection would be effective. The present findings are in conformity with the results of Venkata Suresh (2001), Nayak *et al.* (2003), Patil *et al.* (2003), Suman (2003) and Sinha *et al.* (2004),

5.1.3 Number of productive tillers per plant

The genotypic and phenotypic coefficients of variation were low and the differences between GCV and PCV were low indicating less influence of environment on this character. Moderate heritability with low genetic advance indicated that the expression of this trait was mostly influenced by both non-additive and additive type of gene action in the inheritance of this trait. The present findings are similar with the results of Sahdev Singh *et al.* (1996), Niranjanamurthy *et al.* (1999), Tarasatyavathi *et al.* (2001) and Surender Raju (2002).

5.1.4 Panicle length

The genotypic and phenotypic coefficients of variation were moderate with small difference between these two estimates indicating less influence of environment on this character. The estimate of heritability was high with low genetic advance which indicates that the trait was influenced by non-additive type of gene action. High heritability is due to favourable influence of environment rather than genotype. These results are in accordance with the findings of Borbora and Hazarika (1998), Nagajyothi (2001), Nayak *et al.* (2002) and Suman (2003).

5.1.5 Number of grains per panicle

The wide range of variability was observed for this character. This trait showed high genotypic and phenotypic coefficients of variation. The little difference between the two estimates indicated less influence of environment on this character. High heritability with low genetic advance indicating that the trait is influenced by non-additive type of gene action. Similar results were observed by Satya Priya Lalitha and Sreedhar (1996), Debchoudhary and Das (1998), Nagajyothi (2001), Madhavilatha (2002) and Nayak *et al.* (2002).

5.1.6 1000-grain weight

High genotypic and phenotypic coefficient of variation for this trait observed. Narrow difference between GCV and PCV indicating the less influence of environment on this trait. High heritability with moderate genetic advance indicating the non-additive type of gene action. High heritability is due to favourable influence of environment. Hence, selection for this trait may not rewarding. These results are

in conformity with the findings of Reddy and De (1996), Mokate *et al.* (1998), Reddy *et al.* (1998), Kaw *et al.* (1999) and Sinha *et al.* (2004).

5.1.7 Grain yield per plant

This trait showed high genotypic and phenotypic coefficients of variation. The heritability estimate observed was high with low genetic advance indicating the non-additive type of gene action. High heritability and PCV greater than GCV indicating that this character is highly influenced by environment. Hence, response to direct selection may not be effective in improving this trait. Results are in unison with Balan *et al.* (1999), Nayak *et al.* (2002), Patil *et al.* (2003) and Suman (2003).

Grain quality parameters

5.1.8 Hulling percentage

Hulling percentage exhibited low genotypic and phenotypic coefficients of variation. Less environmental influence on this character was observed since difference between these two estimates was low. The heritability estimate for this character was high coupled with low genetic advance indicating the non-additive type of gene action in expression of this trait. This is in agreement with the findings of Surender Pathak and Sharma (1996), Raju (2000), Madhavalatha (2002) and Surender Raju (2002).

5.1.9 Milling percentage

Milling percentage recorded low GCV and PCV values. Narrow difference between PCV and GCV indicating the less influence of environment on this trait. The heritability estimate for this trait was high coupled with low genetic advance

indicating the non-additive type of gene action with more influence of environment. These results were in accordance with Nagajyothi (2001), Chaudhary *et al.* (2003) and Nayak *et al.* (2003).

5.1.10 Head rice recovery percentage

The GCV and PCV for this trait was moderate. The heritability estimates for this trait was high with moderate genetic advance indicating both additive and non-additive type of gene action with more influence of environment. These results were similar with Nayak *et al.* (2003) and Patil *et al.* (2003).

5.1.11 L/B ratio

L/B ratio recorded high GCV and PCV values. Narrow difference between PCV and GCV indicating the less influence of environment on this trait. The heritability estimate for this trait was high with low genetic advance indicating the influence of non-additive type of gene action. These results were in conformity with Ciridharan (1998), Sarwagi *et al.* (2000), Sakthivel (2001), Venkata Suresh (2001) and Madhavilatha (2002).

5.1.12 Kernel length after cooking

This trait exhibited moderate PCV and GCV values. High heritability estimate coupled with low genetic advance indicating the presence of non-additive type of gene action. These results were in accordance with Chaudhary *et al.* (2003), Nayak *et al.* (2003) and Patil *et al.* (2003).

5.1.13 Elongation ratio

Elongation ratio showed moderate GCV and PCV values. High heritability estimates coupled with low genetic advance indicating the non-additive type of gene action. These results were in conformity with Nayak *et al.* (2003) and Patil *et al.* (2003).

5.1.14 Volume expansion ratio

This trait recorded moderate GCV and PCV values. Narrow difference between PCV and GCV values indicating the less influence of environment on this trait. The high estimate of heritability with low value of genetic advance indicating the non-additive type of gene action. These observations were similar with Sarkar *et al.* (1994), Satya Priya Lalitha and Sreedhar (1999), Sakthivel (2001), Madhaviatha (2002), Surender Raju (2002) and Nayak *et al.* (2003).

5.1.15 Water uptake

The GCV and PCV values for this trait were found high. The high heritability estimate with high genetic advance indicating additive type of gene action. Hence, its response to selection would be effective. These findings are in conformity with the observations of Nayak *et al.* (2003).

5.1.16 Alkali spreading value

The GCV and PCV for this trait were moderate. The high estimate of heritability coupled with low genetic advance indicating non-additive type gene action. High heritability is due to favourable environment. Hence, direct selection

for this character is not rewarding. These results were in conformity with the observations of Sakthivel (2001), Nayak *et al.* (2003) and Patil *et al.* (2003).

5.1.17 Amylose content

The GCV and PCV values for this character were recorded low. The moderate estimate of heritability coupled with low genetic advance indicating the both additive and non-additive gene actions are involved. Hence, direct selection for this trait is not rewarding. These observations are in conformity with Chauhan *et al.* (1999), Nagajyothi (2001) and Patil *et al.* (2003).

5.1.18 Gel consistency

Moderate GCV and PCV values were observed for gel consistency. High heritability coupled with high genetic advance indicating the additive type gene action. Hence, direct selection may be effective for this trait. These findings are similar with the Chikkalingaiah (1999) and Nayak *et al.* (2003).

5.2 GENETIC DIVERGENCE

Genetic diversity has been considered as an important factor in discriminating the genotypes for genetically diverse parents for obtaining high yielding lines for efficient and successful hybridization programme. This will not only result in inducing genetic variability but also provide new recombinations of genes in the gene pool. Multivariate analysis using Mahalanobis's D^2 statistic has been found to be a potential biometrical tool in quantifying the degree of divergence in germplasm collections of crop plants. Genetic divergence analysis, therefore, was

attempted to identify suitable parents out of 70 rice genotypes belonging to different agro-climatic regions of the country.

5.2.1 Mahalanobis's D^2 analysis

Assessment of genetic diversity was made based on the data recorded for yield and quality characters in 70 genotypes using Mahalanobis's D^2 statistic analysis.

In the present study, the varietal composition of the clusters revealed that the genotypes did not follow their geographic distribution as varieties from diverse source were grouped into the same clusters *viz.*, cluster II, III and VIII. For example, in cluster II, the genotypes originating from Tamil Nadu, Chattisgadh and in cluster III genotypes included were from Haryana, West Bengal, Jammu and Kashmir, Andhra Pradesh and cluster VIII genotypes originating from Madhya Pradesh, Gujarat, Andhra Pradesh and Tamil Nadu.

On the contrary, the genotypes of common geographic region or same location also were grouped into different clusters as evidenced by the distribution of genotypes collected from Andhra Pradesh, Chattisgarh, Tamil Nadu and Punjab into different clusters indicating that geographic diversity though important may not necessarily be the only factor in determining the genetic diversity. These results were in accordance with the findings of Bhatt (1970) who suggested that genetic drift and artificial selection could cause greater diversity than the geographic distance.

This suggests that the genotypes originating at the same location might have different genetic architecture and could have undergone changes for different

characters under selection during the process of evolution. The clustering pattern failed to establish the fact that the genetic divergence is due to geographic distribution. However, in some cases, the influence of geographic origin on clustering was observed.

5.2.2 Intra and inter cluster D^2 values

Genotypes grouped to the same cluster diverge little from one another as the aggregate of characters measured. Statistical distances represent the index of genetic diversity among the clusters. Intra-cluster distance is minimum for cluster III (653.874) and maximum for cluster VIII (1365.297) while it is zero for cluster VII as it included only single genotype. The inter-cluster distance was minimum between cluster I and cluster VI (1382.263) indicating close relationship and similarly for most of the characters of the genotypes. The maximum inter-cluster distance was recorded between cluster VII and cluster VIII (3902.050). The inter-cluster distances were higher than intra-cluster distances which indicate the existence of substantial diversity among the genotypes. Based on the inter-cluster distances, cluster VII and VIII, VII and IX, II and VII and III and VII were found to be highly divergent from all others. The genotypes in these clusters may serve as potential parents and crossing between these genotypes may result in heterotic expression for yield components.

5.2.3 Cluster mean analysis

The cluster means for different characters indicated considerable differences between the clusters for all the characters (Table 11). Cluster II recorded maximum values for days to 50 per cent flowering, number of productive tillers per plant,

number of grains per panicle, hulling percentage, cluster III showed maximum values for number of grains per panicle, L/B ratio, alkali spreading value (ASV), gel consistency. Cluster V recorded maximum for 1000-grain weight, kernel length after cooking, elongation ratio, cluster VII recorded maximum values for water uptake, amylose content, whereas, gel consistency recorded maximum value in cluster VIII (92.28 mm). Plant height (156.55 cm), panicle length (29.17 cm) were maximum in cluster IX.

Based on cluster mean values, the following genotypes can be suggested as potential parents in hybridization programme. They are expected to create wide spectrum of variability for yield and grain quality characters in the segregating generations.

Cluster No.	Genotype	Character
I	MTU-3626	Head rice recovery percentage
II	White ponni	Number of productive tillers per plant Number of grains per panicle
III	Ranbir Basmati	L/B ratio
IV	PR-113, PR-114 Taroari Basmati	Alkali spreading value
V	Mahamaya	1000-grain weight
VII	ADT-36	Water uptake
VIII	Jaya	Gel consistency
IX	GR-104	Days to 50 per cent flowering Panicle length

The relative contribution of different plant characters to the total genetic divergence estimated by D^2 analysis indicated that water uptake contributed maximum to genetic divergence followed by gel consistency.

Apart from the high divergence, the performance of genotypes and the cluster with maximum contribution towards divergence should also be given due consideration which appear as desirable for inclusion for improvement of rice.

5.2.4 Canonical root analysis

Canonical analysis was used to confirm the clustering pattern obtained by D^2 statistic and to plot the 70 rice genotypes in two dimensional graph. The three vectors were responsible for 62.426 per cent of total variance of uncorrelated y variable, which indicated that the differentiation of these traits was nearly complete in three genotypes in three phases (Table 6). The relative distribution of genotypes reflected existence of broad parallelism between grouping obtained by D^2 analysis and vector analysis.

For getting a clear two-dimensional graph, the contribution by first three canonical roots should be more than 95 per cent. On contrary to the above, the three canonical vectors as a whole contributed only 62.426 per cent towards genetic divergence because of which discernible overlapping was observed in group constellations of canonical vectors.

The characters like water uptake in the first, second and sixth vector, gel consistency in the third vector, days to 50 per cent flowering in fourth vector, plant height in the fifth vector contributed maximum towards genetic divergence. The maximum contribution towards genetic divergence are water uptake, gel consistency, head rice recovery percentage.

5.3 CHARACTER ASSOCIATION

A thorough understanding of the association of plant characters with yield and among themselves is essential for successful crop improvement programme. It enables the breeders to manipulate the expression of these traits in crop improvement. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its components and among themselves. Correlation analysis provides information on the nature and magnitude of the association of different component characters with grain yield, which is regarded as highly complex trait in which the breeder is ultimately interested in. It also helps us to understand the nature of inter-relationship among the component traits themselves. Ultimately this kind of analysis could help the breeder to design his selection strategies to improve grain yield.

In the present investigation, a number of yield components were investigated and their relationship with yield as well as among themselves were examined using correlation analysis.

Genotypic correlations in general are high as compared to their phenotypic correlations indicated strong inherent association between the characters which might be due to masking or modifying effects of environment.

The correlation analysis indicated that grain yield was significantly associated with number of grains per panicle and 1000-grain weight. Similar kind of association was revealed by Reddy *et al.* (1997), Debchoudhury and Das (1998), Madhavalatha (2002) and Tarasatyavathi *et al.* (2002). Similar results of significance

for number of grains per panicle revealed by Sakthivel (2001), Kuldeep *et al.* (2004) and Sinha *et al.* (2004).

The grain yield per plant had non-significant positive association with days to 50 per cent flowering, number of productive tillers per plant. Similar kind of non-significant positive association revealed by Kumar *et al.* (1998), Rao and Srivastav (1999) and Vanga *et al.* (1999). Non-significant negative association with plant height and panicle length was revealed by Chauhan *et al.* (1993).

It indicated that grain yield can be increased whenever there is an increase in characters that showed positive and significant association with grain yield. Hence, these characters can be considered as criteria for selection for higher yield as these were mutually and directly associated with grain yield.

5.3.1 Days to 50 per cent flowering

Days to 50 per cent flowering had significant positive association with number of productive tillers per plant, number of grains per panicle. These results were in conformity with the earlier findings of Sawat *et al.* (1995) and Sakthivel (2001) for number of productive tillers per plant, Kavitha and Sree Rama Reddy (2001), Nayak *et al.* (2001) and Madhaviatha (2002) for number of grains per panicle.

5.3.2 Plant height (cm)

Plant height exhibited significantly positive association with panicle length, number of grains per panicle, 1000-grain weight. These results were in accordance with Janardhanam *et al.* (2001), Sakthivel (2001) and Surender Raju (2002) for

1000-grain weight. The results for the trait, panicle length were similar with the Tarasatyavathi *et al.* (2001), Madhavalatha (2002), Suman (2003) and Sinha *et al.* (2004). Positive significant association with plant height was in similar with Suman (2003).

5.3.3 Number of productive tillers per plant

Number of productive tillers per plant had non-significant positive association with number of grains per panicle. This was in conformity with Yolanda and Vijendra Das (1995) and Satya Priya Latha and Sreedhar (1996).

5.3.4 Number of grains per panicle

Number of grains per panicle had negative significant association with 1000-grain weight. Similar findings were revealed by Gupta *et al.* (1999) and Suman (2003).

5.3.5 1000-grain weight

1000-grain weight had positive significant association with grain yield. Similar findings were reported by Madhavalatha (2000), Sakthivel (2001), Tarasatyavathi *et al.* (2002), Kuldeep *et al.* (2004) and Sinha *et al.* (2004).

5.4 PATH COEFFICIENT ANALYSIS

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may some times be misleading, as it might be an over-estimate or under-estimate because of its

association with other characters are also associated with economic yield. Hence, indirect selection by correlated response may some times not be fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will help in formulating the basis of selection, more meaningful for breeding programme.

Based on the above considerations, the results obtained from the above investigation from the 70 rice genotypes on six quantitative characters with yield were subjected to path coefficient analysis and the estimates of direct and indirect contribution with yield are discussed hereunder for formulating sound selection programmes along with character associations.

5.4.1 Days to 50 per cent flowering

Days to 50 per cent flowering exhibited a positive direct effect on grain yield per plant. It had shown positive indirect effects on grain yield via plant height, productive tillers per plant, grains per panicle, while, it had shown negative indirect effect via panicle length, 1000-grain weight on grain yield per plant. Both direct effects and correlation coefficients are positive. Hence, direct selection of this character would be effective in improving grain yield. The results are in accordance with the findings of Gupta *et al.* (1998), Balan *et al.* (1999), Bala (2001), Nayak *et al.* (2001), Suman (2003) and Khedikar *et al.* (2004).

5.4.2 Plant height

The plant height exhibited positive direct effect on grain yield per plant but correlation coefficient was negative. It had shown moderate positive indirect effects on grain yield via number of grains per panicle, while, rest of the characters showed negligible positive as well as negative indirect effects. Hence, selection based on this character could not be effective in improving grain yield. These results are in consonance with Debchoudhury and Das (1998), Bala (2001), Janardhanam *et al.* (2001) and Madhaviatha (2002).

5.4.3 Number of productive tillers per plant

The direct contribution of this trait on grain yield per plant was observed. Its indirect effects were positive and manifested through days to 50 per cent flowering, panicle length and number of grains per panicle, while, rest of the characters expressed negligible indirect effects. The correlation coefficient estimate was also positive. Hence, simple selection would be effective in improving grain yield based on this trait. These results are in accordance with the findings of Gupta *et al.* (1998), Janardhanam *et al.* (2001), Nayak *et al.* (2001), Madhaviatha (2002), Satish *et al.* (2003) and Khedikar *et al.* (2004).

5.4.4 Panicle length

This character exhibited a negative direct effect on grain yield. It has a positive indirect effect on grain yield via plant height and number of grains per panicle while, correlation coefficients are negative with grain yield. Hence, simple selection would not be effective for improving grain yield based on this trait.

Similar results were also reported by Debchoudhury and Das (1998), Bala (2001), Nayak *et al.* (2001) and Madhavalatha (2002).

5.4.5 Number of grains per panicle

Number of grain per panicle showed high positive direct effect on grain yield per plant. It has a positive indirect effect on grain yield via plant height, days to 50 per cent flowering, number of productive tillers per plant. This trait exhibited significant positive correlations with grain yield. Hence, simple selection is more effective in improving grain yield based on this trait. These results are in agreement with the findings of Valarmathi and Leenakumari (1998), Nayak *et al.* (2001), Madhavalatha (2002) and Satish *et al.* (2003).

5.4.6 1000-grain weight

This trait showed high positive direct effect on grain yield per plant as well as correlation coefficients were also positive. It had positive indirect effects on grain yield via panicle length, rest of the characters exhibited negative indirect effects. This trait had significant positive correlation with grain yield per plant. Hence, simple selection would be effective for improving grain yield, if it is based on this trait. The results are in agreement with the findings of Reddy *et al.* (1997), Nagajyothi (2001) and Sakthivel (2001).

CHAPTER VI

SUMMARY

The present investigation aimed to study the magnitude of divergence, nature and amount of variability, the degree of association between yield and its component characters, direct and indirect effects of the different quantitative characters on grain yield and to understand grain quality variation of the genotypes which were collected from different agro-climatic zones. The following conclusions were drawn based on the results obtained.

Analysis of variance revealed that genotypes differ significantly among themselves for all the characters under study. The genotypes *viz.*, NDR-359, KRH-2, NLR-30491 and VRS-3 collected from different agro-climatic zones like upper gangetic plains, southern plateau and hills, west-coast plains and ghats and Gujarat plains and hills recorded high mean yield performance, respectively. Among the grain quality parameters, head rice recovery percentage observed more in the genotypes like VRS-3, NLR-30491, PR-116, Mandya Vijaya and ASG-4011, whereas this trait was low in the genotypes like Kasturi and Basmati-386; L/B ratio, kernel length after cooking were more in case of basmati varieties like Bas-370, Bas-386, Taroari basmati, Yamini, ADT-41 and ADT-43. The mean performance of the genotypes for other traits like amylose content, gel consistency and alkali spreading value were ranged between medium to high values.

The characters *viz.*, days to 50 per cent flowering, plant height, water uptake and gel consistency exhibited high heritability coupled with high genetic advance

indicating the predominance of additive gene action in controlling these characters and their suitability of selection for further improvement among the genotypes studied.

High heritability coupled with moderate genetic advance was observed for 1000-grain weight and head rice recovery percentage, indicating the involvement of both additive and non-additive gene actions. Hence, careful selection of these traits is necessary for further improvement. The characters *viz.* number of productive tillers per plant, panicle length, number of grains per panicle, grain yield per plant, hulling percentage, milling percentage, L/B ratio, kernel length after cooking, elongation ratio, volume expansion ratio, amylose content and alkali spreading value exhibited high heritability and low genetic advance which indicated the predominance of additive and non-additive gene action in controlling these traits.

The nature and magnitude of genetic diversity was assessed using Mahalanobis D^2 test in seventy rice genotypes representing different agro-climatic zones. It was observed that there was no association between the geographical distribution and genetic diversity. Based on genetic distance 70 genotypes were grouped into nine different clusters. Characters like water uptake, gel consistency and head rice recovery percentage were major contributing characters towards genetic divergence. The maximum inter cluster distance was observed between cluster VII and VIII. The genotypes from these clusters may be used as potential donors for future hybridization programmes to develop potential recombinants with high yield coupled with desirable grain quality.

In general, it was observed that genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients. It indicated that strong inherent association was somewhat masked at the phenotypic level due to environmental effect. Character association analysis revealed significantly positive association of grain yield per plant with number of grains per panicle and 1000-grain weight. Hence, selection for these traits can improve the yield.

Path coefficient analysis revealed that days to 50 per cent flowering, plant height, number of productive tillers per plant, number of grains per panicle and 1000-grain weight exhibited positive direct effect on grain yield. Among these characters, days to 50 per cent flowering, productive tillers per plant, number of grains per panicle and 1000-grain weight possessed both positive associations and high positive direct effects. Hence, selection for these traits could bring improvement in yield and yield attributes.

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