

EVALUATION OF LANDRACES OF RICE (*Oryza sativa* L.) FOR IRON, ZINC AND PROTEIN

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B.Sc (Ag.)

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(GENETICS AND PLANT BREEDING)**



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**EVALUATION OF LANDRACES OF RICE
(*Oryza sativa* L.) FOR IRON,
ZINC AND PROTEIN**

By

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B.Sc (Ag.)

**THESIS SUBMITTED TO THE PROFESSOR JAYASHANKAR
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2015

DECLARATION

I, **Mrs. R. NIROSHA** hereby declare that the thesis entitled “**EVALUATION OF LANDRACES OF RICE (*Oryza sativa* L.) FOR IRON, ZINC AND PROTEIN**” submitted to **PROFESSOR JAYASHAKAR TELANGANA STATE AGRICULTURAL UNIVERSITY** for the Degree of **MASTER OF SCIENCE IN AGRICULTURE** is a result of original research work done by me. It is further declared that no material contained in the thesis has been published earlier in any manner.

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This is to certify that the thesis entitled “**EVALUATION OF LANDRACES OF RICE (*Oryza sativa* L.) FOR IRON, ZINC AND PROTEIN**” submitted in partial fulfillment of the requirements for the degree of “**MASTER OF SCIENCE IN AGRICUTLURE**” of the **PROFESSOR JAYASHAKAR TELANGANA STATE AGRICULTURAL UNIVERSITY, Hyderabad**, is a record of the bonafide original research work carried out by **Mrs. R. NIROSHA**, under our guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee.

No part of the thesis has been submitted for any other degree or diploma. The published part has been fully acknowledged. All assistance and help received during the course of the investigation have been duly acknowledged by the author of the thesis.

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SYMBOLS AND ABBREVIATIONS

%	Per cent
σ_p^2	Phenotypic variance
σ_g^2	Genotypic variance
ANOVA	Analysis of variance
cm	Centimeter
CD	Critical difference
D^2	Genetic distance
<i>et al.</i>	And others
Fig.	Figure
g	Gram
GA	Genetic advance
GAM	Genetic advance as per cent of mean
GCV	Genotypic coefficient of variation
h^2	Heritability in broad sense
ha	Hectare
i.e.,	That is
ICRISAT	International Crops Research Institute for the Semi Arid-Tropics
IIRR	Indian Institute of Rice Research
M ha	Million hectare
mm	Millimeter
m.t	Million tones
No.	Number
PCV	Phenotypic coefficient of variation
RBD	Randomized Block Design
<i>viz.</i> ,	Namely

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ABSTRACT

In the present investigation, eighty five landraces of rice were evaluated to study the genetic diversity among them for selection of the diverse parents, to estimate the genetic parameters among the genotypes for yield and nutritional traits, and the extent of association between the yield and its component characters including the direct and indirect effects. The experiment was laid out in a randomized block design with two replications during *kharif* 2014 at Indian Institute of Rice Research (formally Directorate of Rice Research), Ramachandrapuram Farm, ICRISAT, Hyderabad.

Analysis of variance indicated the existence of significant genotypic differences among the genotypes for the yield, its components and grain quality traits. High GCV and PCV values were observed for grain yield per plant followed by number of grains per panicle, number of productive tillers per plant and days to fifty per cent flowering, 1000-grain weight, grain iron concentration.

High heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plant, number of grains per panicle, days to fifty per cent flowering, grain zinc concentration, grain iron concentration and 1000-grain weight, which indicated that these traits were controlled by additive type of gene action. The remaining traits were mostly under the influence of non-additive gene effects as they recorded low to moderate estimates of genetic advance.

Based on the relative magnitude of D^2 values, the genotypes were grouped into six clusters. Out of six clusters Cluster I was the largest one comprising of forty three landraces followed by cluster IV with sixteen landraces, cluster III with fourteen landraces, cluster II with ten landraces, cluster V and VI were monogenotypic clusters.

Based on the inter cluster distances, out of ten characters studied, five characters namely number of filled grains per panicle, grain zinc concentration, days to 50 per cent flowering, plant height and protein content contributed 97.23% towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations.

Maximum inter cluster distance was exhibited between clusters II and VI (100.30) followed by cluster IV and VI (78.61), cluster I and VI (77.77), cluster III and IV (77.45), cluster II and V (73.74), cluster III and VI (68.76), cluster IV and V (68.55).

The data on character means for six clusters indicated that, the cluster V has the highest mean value for panicle length, number of tillers per plant, 1000 grain weight and plant height. Cluster III for grain yield per plant is higher and cluster VI is higher for grain iron concentration and protein percentage. Such clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

The maximum contribution towards genetic divergence was observed in number of grains per panicle (42.91%), followed by grain zinc concentration (24.71%), days to 50% flowering (13.00%), grain protein content (8.99%), plant height (7.62%), grain iron concentration (2.04%), 1000 grain weight (0.53%), grain yield per plant (0.20%), and low divergence for number of tillers per plant and panicle length. Therefore, these diverse landraces useful in selection of parents during hybridization program.

Character association studies revealed that six characters (days to 50 per cent flowering, plant height, panicle length, number of tillers per plant, number of grains per panicle and 1000 grain weight) showed significant positive association with grain yield per plant. This indicated that simultaneous selection of all these characters is important for yield improvement.

A critical analysis of the results by path analysis revealed that 1000 grain weight exerted highest positive direct effect on grain yield followed by number of grains per panicle, days to 50 per cent flowering and plant height. Hence, these traits must be considered as important attributes in formulating selection criteria for achieving desired targets in future breeding programmes.

Chapter I

Introduction

Chapter I

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the agronomically and nutritionally important cereal crops. It is a major source of food for more than 2.7 billion people on a daily basis and is planted on about one-tenth of the earth's arable land. It is the single largest source of food energy to half of the humanity in the world, most of them in developing countries. Rice is the major food crop in India occupying nearly 43.97 million hectares with an annual production of 104.32 million tonnes and productivity of 2372 kg ha⁻¹ (Indiastat, 2012-2013). In the last two decades, new research findings generated by the nutritionists have brought to light the importance of micronutrients, vitamins and proteins in maintaining good health, adequate growth and even acceptable levels of cognitive ability apart from the problem of protein energy malnutrition.

Rice is grown in many different ecosystems. Iron and zinc deficiencies have been reported to be a food-related primary health problem affecting nearly two billion people worldwide. The brown and red rice genotypes have high grain iron and zinc content.

A detailed analysis of nutrient content of rice suggests that the nutrition value of rice varies based on a number of factors. It depends on the strain of rice, that is between white, brown, black, red and purple varieties of rice each prevalent in different parts of the world. It also depends on nutrient quality of the soil in which rice is grown in, whether and how the rice is polished or processed, the manner it is enriched, and how it is prepared before consumption.

Largest germplasm collections of rice is available in the world. This accessible collection of diverse varieties, landraces and related wild species has made great contributions to rice breeding. Landraces harbour a great deal of useful traits with genetic potential for rice improvement and they played a very important role in the local food security and sustainable development of agriculture, in addition to their significance as genetic resource for rice genetic improvement (Tang *et al.* 2002).

The landraces maintained by farmers are endowed with tremendous genetic variability, as they are not subjected to subtle selection over a long period of time. While most high yielding varieties in Asia are colourless with long and slender grains, local rice varieties often exhibit tremendous morphological diversity. This aids in the adaptation of landraces to wide agro-ecological conditions. This rich variability of complex quantitative

traits still remains unexploited. Land-races are also important genetic resources for resistance to pests and diseases; they provide “adaptability genes” for specific environmental conditions. Incorporation of adaptability genes from landraces could ensure optimum grain yield for the region (Vijayakumar *et al.* 2012)

Rice is a nutritional staple food which provides instant energy as its most important component is carbohydrate (starch). The endosperm (i.e. the inner part of the grain), contains mostly starch and around 6 to 10 per cent protein. The bran is more diverse in its composition and contains protein, lipids, fibres, vitamins and minerals. In husked rice, protein content ranges in between 7 and 12 per cent. Rice protein is of very high quality as compared to other food crops. Protein quality is determined by the amino acid composition and by its digestibility. Brown rice not only has a higher protein content, but also a higher proportion of lysine than milled rice. The human daily protein requirement is estimated at 0.8-1.2 grams per kilogram bodyweight, depending on age. The requirement is the highest for children and declines with advancing age. Consumption of the same amount of a high protein landrace (with fourteen per cent protein) contributes 28 grams of protein to the daily ration. The Grain Protein Content of rice is responsive to nitrogen fertilization, because nitrogen is required for the protein synthesis. Landraces tend to have high protein content although they are often cultivated without the use of fertilizer.

Iron deficiency is considered to be one of the most wide-spread micronutrient disorders in the world. Rice can only contribute significantly to the iron supply if it is eaten as brown rice. A different set of landraces from various Southeast Asian countries (unpublished data) demonstrated iron contents of up to 33 mg/kg. Generally, iron content tends to be higher in aromatic and colored (red and black) rice varieties than in colourless varieties. On the other hand inhibitory substances present in the grain, such as phytic acid or polyphenols can reduce the iron bioavailability (WHO 2002).

Zinc is believed to be low in the diets of around 2.5 billion people worldwide. It is involved in many enzymatic reactions in the body and is also essential for DNA synthesis. The requirement of zinc is increased during pregnancy as well as throughout childhood and adolescence. The clinical manifestations in severe cases of zinc deficiency include diarrhoea, weight loss, infections, and it is fatal if untreated. As with iron, most of the zinc present in the rice grain is located in the outer layers. The consumer’s preference for milled rice therefore substantially reduces the availability of zinc. Conversely, brown rice can contribute appreciable amounts of zinc to the diet. The variability in zinc content among

different rice varieties is quite pronounced. Values ranging from 14 to 59 mg/kg are given in scientific literature (Frei and Becker, 2005).

Biofortification is the idea of breeding crops to increase their nutritional value. This can be done either through conventional selective breeding or through genetic engineering. Biofortification differs from ordinary fortification because it focuses on making plant foods more nutritious as the plants are growing, rather than having nutrients added to the foods when they are being processed. In this context, breeders are now focusing on breeding for nutritional enhancement to overcome the problem of malnutrition. The range of iron and zinc concentration in brown rice is 6.3 to 24.4 µg/g and 13.5 to 28.4 µg/g, respectively. There is approximately a fourfold difference in iron and twofold difference in zinc concentration, suggesting that some genetic potential to increase the concentration of these micronutrients in rice grains (Graham *et al.* 1999).

Knowledge on the nature and magnitude of genetic variations governing the inheritance of quantitative characters like yield and its components is essential for genetic improvement. A critical analysis of genetic variability present in the germplasm of crop and its estimation is a pre-requisite for initiating any crop improvement programme as well as adopting appropriate selection techniques.

Heritability is the measure of transmission of characters from generation to generation and the estimates of heritability will be of immense help to the breeder in selecting superior individuals for a desired trait and successfully utilizing them in breeding programme. Genetic advance measures the difference between the mean genotypic values of selected population and the original population from which these were selected. Heritability estimated along with genetic advance is normally more helpful in predicting the genetic gain under selection than heritability estimates alone.

In addition to the above information, quantification of the degree of divergence in a given experimental materials of immense value in the identification of divergent genotypes for further use in hybridization to create new variability. Mahalanobis D² statistic has been proven to be powerful tool for quantifying genetic divergence in a given population. Divergent genotypes could be obtained by collection from different eco-geographical regions or it could be induced by combination breeding.

Yield is the end product of multiplicative interaction between various yield components and this necessitates a thorough understanding of character association and

direct and indirect effects contributed by each character on grain yield before launching any breeding programme. Correlation is the measure of the mutual relationship between two variables. It is a measure of the degree of closeness and the linear relationship between two variables. The study of correlations may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters.

Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable upon the other. Direct selection for yield is not a reliable approach since it is influenced by the environment. Therefore, it is essential to identify the component characters through which yield can be improved. Selection would be more effective for the trait, which has got high genetic advance and high correlation with grain yield.

Keeping in view the importance of aforesaid aspects, the present investigation was undertaken with the following objectives

1. To study the composition of iron, zinc and protein in available land races.
2. To study the variability, heritability and genetic advance for yield and yield components.
3. To study the extent of association between the yield and nutritional characters.

Chapter II

Review of Literature

Chapter II

REVIEW OF LITERATURE

The high nutritional quality of rice landraces can form a solid basis for changing priorities in rice breeding, putting more emphasis on the grain nutritional value. Modern conventional breeding techniques, including molecular marker-assisted selection, may be very useful in accelerating the development of more nutritious rice varieties. Combining high yields and high grain nutritional value thus appears to be possible without any genetic manipulation.

Rice biofortification program aims at biological and genetic enrichment of food products with vital nutrients, vitamins and proteins. Ideally, once rice is biofortified with vital nutrients, the farmer can grow the variety indefinitely without any additional input to produce nutrient packed rice grains in a sustainable way so that the produce reaches the malnourished population in rural India.

Variability is the basic requirement for a successful plant breeding programme to improve genetic potential in any crop. The estimates of different genetic parameters are important for better understanding of the nature and magnitude of genetic variability available in the breeding material along with the association of different yield and quality attributing characters.

The pertinent literature is cited here in the following sections as per the objectives of the experiment.

2.1 Nutritional Aspects.

2.2 Genetic Variability, Heritability and Genetic Advance

2.3 Genetic Divergence

2.4 Character Association

2.5 Path Coefficient Analysis

2.1 NUTRITIONAL ASPECTS

High yield along with more nutrients is important for present day healthy diet. Qui *et al.* (1995) reported a higher variability in mineral contents in some rice cultivars and the

level of iron content varied from 15.41 mg kg⁻¹ to 162.37 mg kg⁻¹ and zinc content ranged from 23.92 mg/kg to 145.78 mg/kg.

Wang *et al.* (1997) reported the range for zinc content in grains of rice ranged from 0.79 - 5.89 mg/100 g with an average of 3.34 mg/100 g in a study done among 57 rice varieties. The largest zinc value was found in Ganjay Roozy, a variety grown at IRRI while the lowest zinc value recorded was in long grain fragrant rice.

Ahmed *et al.* (1998) reported that scented rice varieties of Assam had amylose content varying from 18.9 to 23.2 per cent and iron content that ranged from 1.5 to 5.0 mg 100 g⁻¹ with an average value of 3.2 mg/100 g. Graham *et al.* (2001) reported trait for high iron and zinc has been linked to aromatic varieties such as jasmine and basmati.

Welch and Graham (2004) found 4-fold differences in mineral levels of iron and zinc concentration among rice genotypes, which suggests that there is a potential to increase the concentration of these micronutrients in rice grain with genetic technology.

Bhattacharjee (2006) observed 0.136 to 11.4 per cent of amylose content in glutinous rice cultivars of Assam. Nine genotypes of rice were evaluated for iron and zinc content in rice grain at IRRI by found a range of 8.8 to 21.0 ppm, 14.0 to 40.0 ppm for iron, and zinc respectively (Martinez *et al.* 2006). Zozali *et al.* (2006) reported grain oiZn concentration is substantially higher in certain landraces of Southeast Asia than in commonly grown high yielding rice varieties.

Yet another potential of wild relatives of rice, which involves the improvement of seed protein content was reported by Ahmed *et al.* (2008). A significant increase in seed protein content was observed in an interspecific hybrid between *Oryza sativa ssp. indica* and the wild species *Oryza nivara*. The hybrid showed a protein content of 12.4%, which was 28 and 18.2% higher than those of the parents *O. nivara* and IR 64, respectively.

Devi *et al.* (2008) reported significant variation among cultivars for total starch content from 73.77% to 85.33% of carbohydrate content while studying fifteen indigenous rice and 100 upland rice cultivars respectively. Chakraborty *et al.* (2009) noticed bold grained rice genotypes had starch content varied from 65.60 to 79.88 per cent.

A breeding program to develop Zn rich genotypes can be initiated by screening of available germplasm accessions to identify the genetic variation for the trait that could

serve as donors. Then high zinc containing genotypes can be crossed with high yield potential, tolerance to biotic and abiotic stresses, and good grain quality genotypes (Martinez *et al.* 2010).

Mallikarjuna Swamy *et al.* (2011) studied 126 accessions/varieties of rice germplasm including wild relatives *O. rufipogon* and *O. nivara*. The Fe concentration in brown rice ranged from 6 ppm (Athira) to 72 ppm (*O. nivara*). Zn concentration ranged from 27 ppm (Jyothi) to 67 ppm (*O. rufipogon*). Iron and zinc concentration varies between brown rice and polished rice. Also, when whole rice grains and broken rice grains were compared, there was variation in iron concentration but not in zinc concentration.

Anuradha *et al.* (2012) analyzed 126 accessions of brown rice genotype including 7 accessions of two wild species for Fe and Zn concentration and reported that iron concentration ranged from 6.2 ppm to 71.6 ppm and zinc from 26.2 ppm to 67.3 ppm. Zn concentration and grain elongation (-0.25) were significantly correlated. The wild accessions had the highest Fe and Zn.

Devi *et al.* (2012) observed a range of 70% to 89.25% of total carbohydrate content studying eighteen indigenous cultivars of North-Eastern hill regions of India. 79% carbohydrate content is recommended by USDA Nutritional database, U.S.

Jahan *et al.* (2013) used fifty two local landraces, showed the highest Fe content. In this experiment, ANOVA table revealed that significant variation was found among the genotypes for the iron concentration. This suggested that there were inherent genetic differences among the genotypes.

Ravindra Babu (2013) reported genotypic differences in grain quality including protein, micronutrient concentrations and few of the yield attributing parameters of twenty one popular rice hybrids. The data revealed huge variations in grain quality among the hybrids. Mean micronutrient iron concentration of hybrids (68.4 ppm) was found to be 1.83 times that of zinc (37.3 ppm). Two hybrids with both high iron and zinc concentration (DRRH-2 with 125.8 ppm and 43.8 ppm; and Sahyadri-4 with 104.8 and 43.0 ppm) were identified.

Roja *et al.* (2013) observed high iron and zinc concentration in BC₄F₄ derived back cross between an indica cultivar Sambamahsuri and wild rice. The iron and zinc content in these lines were measured by adsorption spectroscopy and reported that the iron concentration ranges from 6.4 to 106.6 $\mu\text{g g}^{-1}$ where as zinc concentration ranged from

15.5 to 52.05 $\mu\text{g g}^{-1}$. They also concluded that the lines that had high iron concentration are also has higher zinc concentration levels, but the lines with higher zinc concentration levels did not have high iron levels.

Edwina *et al.* (2014) studied ten pigmented landraces of rice were analyzed for chemical composition and antioxidant properties. The results of proximate composition and calcium, iron, zinc content showed intra variability among landraces. The amylose, total anthocyanin (TAC) and phytate contents were found to be in the range of 22.01 - 44.38%, 28.73 - 193.36 mg cyanidin-3-glucoside/100 g and 1.16 - 24.49 mg Fe/100 g.

2.2 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The nature and extent of variability forms the basis for all crop improvement programs. 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.

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

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

Madhaviatha *et al.* (2005a) revealed high variability, heritability and genetic advance for number of grains per panicle, grain yield per plant, harvest index and kernel L/B ratio, while days to maturity, fertility per centage, hulling recovery and kernel elongation ratio had high heritability coupled with low genetic advance.

Saxena *et al.* (2005) observed high PCV and GCV values for number of unfilled spikelets, seed yield per plant, biological yield per plant, number of filled spikelets, total number of spikelets, and length:breadth ratio of rough rice. Broad-sense heritability was also very high for number of filled spikelets, 100-seed weight, plant height, total number of spikelets and panicle length, indicating the possibility of improving such traits through selection. Seed yield per plant and number of unfilled spikelets showed high genetic advance.

Shukla *et al.* (2005) revealed high co-efficients of variation as well as high values of heritability coupled with expected genetic advance for grain yield per plant, harvest index and biological yield per plant.

Singh *et al.* (2006) recorded a wide range of variation for all the traits studied. The highest genotypic and phenotypic coefficients of variation were recorded for grain yield. High heritability and high genetic advance were recorded for plant height, indicating the predominance of additive gene action for this trait.

Kibanda and Luzi-kihupi (2007) reported absence of environmental influence on grain length and grain size (length/width) but observed higher genetic variance for these traits.

Mustafa and Elsheikh (2007) observed a wide range of genetic variability among the genotypes for most of the characters. The highest genotypic coefficient of variation was recorded for grain yield, per cent unfilled grains per panicle, number of grains per panicle and number of filled grains per panicle.

El-Malky *et al.* (2008) observed high broad sense heritability estimate of 98.89 % for days to maturity, 75.20 % for the number of tillers per plant, 41.74% for the number of panicles per plant, 98.97 % for 1000 grain weight.

Anbanandan *et al.* (2009) observed high PCV and GCV values for grain yield per plant for cross 1 followed by cross 2 in both F₃ and F₄ generations. Also, cross 1 and cross 2 recorded high heritability and genetic advance for number of productive tillers per plant, 1000-grain weight and grain yield per plant in both F₃ and F₄ generations.

Bisne *et al.* (2009) reported high genotypic and phenotypic coefficient of variations for harvest index and 100 grain weight; high heritability coupled with high

genetic advance for harvest index, grain yield per plant from a trial with four CMS lines, eight testers and thirty-two hybrids evaluated.

Chakraborty *et al.* (2009) reported high heritability with low genetic advance for total starch content. Chandra *et al.* (2009) observed high PCV and GCV values for number of productive tillers per plant, number of grains per panicle, 1000-grain weight and grain yield per plant. High heritability along with high genetic advance was observed for plant height, number of grains/panicle and 1000-grain weight.

Susanto (2009) in IRRI reported that broad sense heritability of iron and zinc content in polished rice grains were 57.28 % and 76.36 % in population obtained from IR75862-206-2-8-3-B-B-B/IR64 parents.

Nagarathna *et al.* (2010) reported the presence of wide genetic variability in rice Zn content from 0.84 to 5.00 mg/100g dry weight. Thongbam *et al.* (2010) reported low GCV and PCV, moderate heritability and low genetic advance while studying thirteen indigenous medicinally used cultivars of Manipur.

Abarshahr *et al.* (2011) observed broad-sense heritability varied from 0.05 for brown grain width to 0.99 for plant height and number of spikelets per panicle under optimum irrigation and from 0.1 for brown grain width to 0.99 for plant height. The lowest and highest phenotypic CV values were observed for panicle fertility per centage and paddy yield and genotypic CV was related to brown grain width and plant height, respectively.

Akinwale *et al.* (2011) observed high to medium broad sense heritability for days to flowering, plant height, and low broad sense heritability for days to maturity, the number of tillers per plant and 1000 grain weight and also high heritability and genetic advance were recorded for grain yield per plant in rice.

Low GCV, moderate PCV, moderate heritability and moderate genetic advance as percentage of mean for protein content was reported by Samak *et al.* (2011).

Singh and Pandey (2011) reported high heritability and high genetic advance for the traits plant height, effective tillers per plant, spikelets per panicle, filled grains per panicle, grain weight per panicle, specific leaf weight, test weight, kernel length cooked kernel length, leaf area index, grain length, L/B ratio and gelatinization temperature.

Subbaiah *et al.* (2011) reported high GCV and PCV, high heritability and high genetic advance as percentage of mean for amylose content.

Yadav *et al.* (2011) reported high PCV and GCV values for seed yield, harvest index, biological yield, number of spikelets per panicle, flag leaf length, plant height and number of tillers. High heritability coupled with high genetic advance as per cent of mean was registered for seed yield, harvest index, number of spikelets per panicle, biological yield and flag leaf length.

Chakravorty *et al.* (2012) evaluated forty four lowland traditional rice genotypes during kharif season. The GCV was less than PCV for all the characters indicating considerable influence of the environment on their expression. High significant and positive genotypic and phenotypic association revealed between number of secondary branches panicle⁻¹ and number of spikelet panicle⁻¹, number of spikelets on secondary branches panicle⁻¹ and number of grains on secondary branches panicle⁻¹.

Chakravorty and Ghosh (2012) evaluated fifty one landraces of rice for the estimation of genetic variation among the agro morphological characters. Heritability estimates were higher for morphological traits ranging from 45.8 to 99.9. Correlation analysis indicated that plant height had positive and significant association with panicle length, and grain weight.

Devi *et al.* (2012) observed low GCV and PCV, high heritability, moderate genetic advance as percentage of mean studying eighteen indigenous rice cultivars of Tripura for the trait total carbohydrate content.

Hosseini *et al.* (2012) were used 18 diverse rice genotypes which are exposed to 3 salt stress treatments in three. High heritability estimates associated with high genetic advance were obtained in height (x_1), root dry weight (x_6) and shoot length (x_2) characters.

Estimates of variability, heritability, genetic advance, correlation and path analysis in rice for fifteen characters by Satheesh kumar and Saravanan (2012). High heritability was observed for all the characters, except kernel breadth. High genetic advance as per cent of mean were observed for all the characters except spikelet fertility and kernel breadth.

Aditya and Anuradha (2013) studied fifteen quantitative traits in eighteen rice genotypes under rainfed ecosystem and reported the estimate of GCV and PCV be highest for grain yield per plot followed by fertile grains per panicle and grains per panicle. The broad sense heritability was highest for plant height and fertile grains per panicle (98.14%) followed by grains per panicle (97.74%), days to 50 per cent flowering (95.18) and days to maturity (94.71). The estimate of genetic advance was found to be highest for grains per panicle and fertile grains per panicle.

Awaneet and Senapati (2013) evaluated thirty three lines of F₅ progenies obtained from Sabita/Sambamahsuri derivatives along with parents and three check varieties for 19 characters. High estimates of PCV and GCV were recorded for grain yield per plant, panicle weight, number of panicles per plant, number of secondary branches per panicle, number of grains per panicle, 1000 grain weight and florets number per panicle. High heritability was observed for most of the characters viz. plant height, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, days to 50 per cent flowering, fertility %, days to maturity, 1000 grain weight and kernel L/B ratio. High genetic advance was observed for florets number per panicle, plant height and number of grains per panicle. Genetic advance as per centage of mean was highest for grain yield per plant where as lowest was for days to maturity. High heritability coupled with high GA was recorded for plant height, days to 50% flowering, fertility %, days to maturity and 1000 grain weight. High heritability with low genetic advance was observed for grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth and kernel L/B ratio.

The maximum genotypic co-efficient of variability and phenotypic co-efficient of variability were observed for test weight, number of productive tillers per plant, number of spikelet per panicle, amylase per cent and grain yield/plant (g) in 100 genotypes of local rice studied by Basavaraja *et al.* (2013). High heritability coupled with high genetic advance as per cent of mean were observed for days to 50 per cent flowering, test weight, number of spikelet per panicle, per cent of spikelet fertility, protein per cent and grain yield/plant (g) will be useful for further breeding program.

Genetic parameters of variability and heritability of 13 characters were studied in 100 genotypes of local rice by Basavaraja *et al.* (2013). High heritability coupled with high genetic advance as per cent of mean were observed for days to 50 per cent flowering, test weight, number of spikelet per panicle, per cent of spikelet fertility, protein per cent and grain yield/plant (g) will be useful for further breeding programme.

Berhanu *et al.* (2013) conducted a study to evaluate genetic variability parameters, correlations that exist for grain Zn concentration and yield related traits and identification of SSR markers linked to these traits in rice. Grain yield per plant and grain zinc concentration showed higher phenotypic and genotypic co-efficient of variation.

Higher values of genotypic and phenotypic coefficient of variability was observed for plant height, number of tillers per plant, number of productive tillers per plant, panicle weight, grain length, test weight, iron and zinc content and grain yield per plant (Gangashetty *et al.*, 2013). The moderate genotypic and phenotypic coefficients of variance were recorded for panicle length, grain breadth and L/B ratio. The days to 50 per cent flowering had recorded lower values of genotypic and phenotypic variance. High heritability with high genetic advance was observed for all traits except days to 50 per cent flowering.

Analysis of variance revealed high significant variation for grain yield per plant and grain zinc content. High GCV, PCV (103.06, 109.16) was observed for grain yield per plant and moderate GCV, PCV (17.02, 18.39) was observed for grain zinc content (Naveen *et al.*, 2013).

Fourteen red rice ecotypes from temperate regions and correlation and path coefficients were also studied for fifteen agro-morphological characters by Sanghera *et al.* (2013). Genotypic and phenotypic coefficients of variation were high for grain yield, secondary branches per panicle and panicle weight; moderate for grain number per panicle, grain length: breadth (L:B) ratio and panicle density. High heritability accompanied by high to moderate genetic advance for panicle density, days to 50% flowering, plant height, grain number indicated the predominance of additive gene action for the expression of these characters.

Shiva Prasad *et al.* (2013) studied one hundred and fifty genotypes including five check varieties of rice. The estimates of genotypic and phenotypic coefficients of variation (GCV and PCV) were high for all the characters except days to 50% flowering and panicle length. Heritability and genetic advance were high for all the traits except yield/ plant and fertile grains per panicle and radical length which had a moderate magnitude of genetic advance, which had moderate genetic advance along with high heritability indicating the involvement of additive type of gene action in controlling these characters.

Singh *et al.* (2013) conducted studies with 11 genotypes of upland rice during *Kharif*. Maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed only for number of spikelets per panicle, while plant height, flag leaf length, flag leaf width, panicle length, harvest index and grain yield per plant showed moderate GCV and PCV. High estimates of heritability coupled with high genetic advance as per cent of mean was observed for plant height, flag leaf length, flag leaf width, number of spike lets per panicle and grain yield per plant.

Toshimenla and Changkija (2013) evaluated seventy four upland rice accessions for 13 quantitative traits. All the genotypes differed significantly with respect to all the quantitative characters. High estimates of heritability coupled with moderate or high value of genetic advance as percentage of means was observed for yield per plant, 100 seed weight, leaf length, days to 80% flowering, leaf width, number of unfilled grains, days to maturity and panicle weight.

Correlation coefficient and estimates of broad sense heritability of the 15 characters associated with grain yield for the combined data showed wide significant genetic variability ($p < 0.0001$) amongst the genotypes in 15 rice breeding lines (Ukaoma *et al.*, 2013). Alam *et al.* (2014) evaluated the agronomic performance of 76 rice genotypes and to learn the variability, heritability and genetic advance of yield and its components. The genotypes differed significantly for all the characters viz., days to 50% flowering, days of maturity, number of tillers plant⁻¹, number of effective tillers plant⁻¹, plant height, panicle length, number of filled grain panicle⁻¹, number of unfilled grain panicle⁻¹, 1000-seed weight and yield plant⁻¹. The phenotypic co-efficient of variation (PCV) were higher than genotypic co-efficient of variation (GCV) for all the characters studied indicating that they all interacted with the environment to some extent. All the characters studied in the present investigation expressed high heritability estimates ranging from 78.38 to 99.14 per cent.

Chouhan *et al.* (2014) evaluated thirty five rice accessions to assess their genetic variability for grain yield and yield attributing traits. The magnitude of phenotypic coefficient of variation was higher to corresponding genotypic coefficient of variation. High heritability coupled with high genetic advance as per cent of mean was found in the trait fertile spikelet per panicle, total number of grains per panicle and grain yield per plant. The genotypic correlation coefficient was found to be higher than phenotypic correlation coefficient

Ganapati *et al.* (2014) evaluated twenty five genotypes for yield and yield contributing characters to observe their variability. Grain panicle⁻¹ and filled grain panicle⁻¹ had high genotypic variance, high heritability, high genetic advance and high genotypic coefficient of variation.

Gokulakrishnan *et al.* (2014) studied twenty three genotypes of rice with high degree of variation for all characters. Panicle weight, number of grains per panicle, grain L/B ratio, plant height, 1000 grain weight and grain breadth were recorded moderate phenotypic and genotypic coefficients of variation. High heritability coupled with high genetic advance as per cent of mean was observed for grain breadth, grain L/B ratio, and plant height, number of grains per panicle and grain yield per plant indicating that the characters were controlled by additive gene action.

Jambhulkar *et al.* (2014) found traits like plant height, ear bearing tiller and yield has high genotypic coefficient of variance, phenotypic coefficient of variance and genetic advance. Bornare *et al.* (2014) observed high coefficients of phenotypic and genotypic variability for effective tillers/plant followed by grain yield/plant, plant height and angle of floret. High heritability accompanied with high genetic advance indicated predominance of additive gene action for the traits viz., 1,000 seed weight, plant height, anther breadth, anther length, effective tillers/plant and angle of floret opening.

Thirty three lines of F₅ progenies obtained from Sabita/Sambamahsuri derivatives were evaluated along with parents and three check varieties for 19 characters by Kumar and Senapati (2014). High heritability was observed for most of the characters viz. plant height, grain length, grain breadth, grain L/B ratio, kernel length, kernel breadth, days to 50 per cent flowering, fertility %, days to maturity, 1000 grain weight and kernel L/B ratio. High genetic advance was observed for florets number per panicle, plant height and number of grains per panicle. Genetic advance as percentage of mean was highest for grain yield per plant where as lowest was for days to maturity.

Majumder *et al.* (2014) studied ten aromatic restorer lines of hybrid rice to assess genetic variability for out crossing traits in rice. Minimum differences of genotypic and phenotypic variances and coefficient of variation as well as high heritability coupled with high genetic advance were observed for anther breadth, pollen fertility and grain yield of restorer lines.

Neha *et al.* (2014) investigated 45 upland rice germplasms. Highly significant variation was obtained for number of spikelets per panicle, plant height, harvest index, biological yield, days to 50% flowering and days to maturity. Seed yield per plant, number of spikelets per panicle, biological yield, flag leaf length and number of tiller per plant showed relatively high GCV and PCV estimates. High heritability was obtained for number of spikelets per panicle (100%), flag leaf width (96%), plant height (93%), biological yield (88%), days to maturity (87%) and days to 50% flowering (84%) which indicates high heritable portion of variation.

Osekita *et al.* (2014) studied genetic variability and environmental effect on the agronomic performance of yield component traits in four upland rice genotypes *Oryza sativa*. Number of tiller per hill had the highest estimate of phenotypic coefficient of variation (PCV) 24.74 due to the influence of the environmental component of phenotypic expression; the genotypic coefficient of variation (GCV) was 15.31. This was closely followed by grain width with PCV 23.38 and very low GCV value 2.45 then plant height had PCV 19.04 with little environmental effect when compared with its corresponding GCV values 15.31. Heritability was highest for four characters as seen in grain length 51.2%, number of tiller per hill 39.2%, 1000 grain weight 27.9% and panicle length 23.7%.

Patel *et al.* (2014) estimated analysis of variance of 44 diverse genotypes and observed significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes for various traits. Results of correlation studies also indicated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for most of the traits.

Rafii *et al.* (2014) evaluated 17 rice genotypes consisting of 12 F₁ progenies and five parental lines for performance of grain qualities, yield and yield components and vegetative traits. Except grain length, all other grain quality characters, yield components and vegetative traits varied significantly among the genotypes, the highest heritability value was observed in plant height with 99.75% followed by panicle length having 96.90% and grain shape with 56.70% which could be successfully inherited to the next generations. The rest of the traits had low heritability values and ranged from 20.24 to 35.88%.

Rahman *et al.* (2014) assessed twenty one rice varieties for thirteen morphological characters. Analysis of variance revealed significant differences among the varieties for all the traits. Plant height, number of effective tillers per square meter, number of spikelets per panicle, number of effective spikelets per panicle, number of ineffective spikelets per panicle, 1000 grains weight, straw yield and grain yield exhibited that they were controlled by additive gene action and selection for the improvement of these traits would be rewarding.

Ramanjaneyulu *et al.* (2014) evaluated ten popular low land rice genotypes for variability, genetic divergence, stability and suitability under aerobic conditions on Alfisols. Results showed low variability in some of the growth and yield attributes like plant height, tillers/plant, spikelet length and harvest index, whereas high heritability (broad sense) estimates were observed for quantitative characters such as 1000-grain weight and grain yield.

Rathor *et al.* (2014) selected forty rice accessions including eleven local land races. Highest Phenotypic Coefficient of Variation (%) and Genotypic Coefficient of Variation (%) were observed in grain yield per hill (g) and number of spikelet's per panicle whereas, lowest in days to maturity, test weight (g) and days to 50% flowering. However, lowest difference between GCV and PCV was observed in most of the traits studies. Highest of heritability were observed for number of spikelets per panicle and test weight and high genetic advance were observed for number of spikelet's per panicle and plant height (cm).

Sandhya *et al.* (2014a) investigated the genetic variability. Genotypic coefficient of variation played a major role for the expression of the traits and ranged from 4.15 (days to maturity) to 27.58 (grain yield per plant). Heritability is ranged from 18.00 (flag leaf length) to 92.17 (number of spikelets per panicle). High genetic advance was observed for the trait, number of spikelets per panicle (99.83) coupled with high heritability (92.17), indicating the preponderance of the non-additive gene action.

Shahriar *et al.* (2014) analyzed thirty advanced T-aman rice (*Oryza sativa* L.) breeding lines along with four checks. Phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the traits studied indicating that the measured traits interacted with the environment to some extent. All the traits expressed moderate to high heritability estimates. High heritability along with high genetic advance was noticed for the following traits: number of filled grain per panicle, number of

unfilled grain per panicle and plant height. Data suggests a few promising breeding lines might be potential as short duration and high yielding T-aman variety.

Thirumala Rao *et al.* (2014) studied genetic variability between yield and its contributing traits in 49 Rice cultures. The magnitude of PCV and GCV was moderate to high for number of grains per panicle, test weight and grain yield. High heritability coupled with high genetic advance as per cent of mean was observed for test weight and grain yield indicating the role of additive gene in expressing these traits.

Pradhan *et al.* (2015) evaluated thirty elite low land rice cultivars along with ten checks under both normal and submerged situations to study the genetic basis of yield variations in low land rice and to identify the best performing genotypes. Majority of traits exhibited higher magnitude of both GCV and PCV under sub-merged conditions except for panicle length and plot yield.

2.3 GENETIC DIVERGENCE

Estimation of degree of divergence between populations and contribution of different characters to total divergence can be done by Mahalanobis D^2 statistics, which is more reliable method in selection of parents for hybridization programme.

Genetic diversity determines the inherent potential of a cross for heterosis and frequency of desirable recombinants in advanced generations. For or the same, genetic distance plays a vital role, as the parental diversity in optimum magnitude is required to obtain superior genotypes in segregating population. Some of the important reports regarding this have been cited below:

Kumary and Rangasamy (1997) estimated genetic divergence by using Mahalanobis's D^2 statistics in 62 early rice genotypes and grouped them into six clusters. They found that there was no relationship between geographical distribution and genetic diversity. Characters like grain yield per plant, panicle exertion and plant height made largest contribution to total divergence.

Rahaman *et al.* (1997) estimated the nature and magnitude of genetic divergence in 52 low land rice collections. The cultivars were grouped into eight clusters, among which cluster VII and VIII were identified as genetically most divergent. Cluster V exhibited high mean for spikelets panicle⁻¹ and grain yield plant⁻¹, while cluster VI scored highest value for productive tillers plant⁻¹ and panicle length.

Shanthi and Singh (2001) studied the genetic divergence by using Mahalanobis's D^2 statistic by Tocher's method and grouped them into four clusters. The first cluster contained nine genotypes, the second containing six while third (MM-72) and fourth (MM-71) clusters were monogenic. The genotypes belonging to clusters II and III having greater cluster distance were recommended for inclusion in a hybridization programme as they were expected to produce good segregates.

Chauhan and Singh (2003) studied genetic divergence in 45 genotypes and grouped into 11 clusters. Cluster II was the largest and consisted of 10 genotypes followed by cluster I with 9 genotypes. Clusters III and V had 7 genotypes each, similarly clusters VI and VII contained 3 genotypes each. Clusters VIII to XI were monogenetic. Hybridization among genotypes included in the diverse clusters (I, IV, VIII, X and XI) and the clusters having high means for quality traits such as high elongation (cluster IV), intermediate alkali value (cluster VIII and IX) and high milling recovery (cluster IX and X) would give high heterotic combinations and produce large variability, better segregants in the segregating generations.

Mani (2003) assessed the degree and nature of genetic divergence among a set of 61 elite basmati rice genotypes and grouped into 4 clusters. Maximum number of genotypes (43) was included in cluster I, followed by cluster II (13), cluster III (4) and cluster IV (1). Cluster III showed the maximum genetic distance from cluster IV, while cluster II and III had the minimum genetic distance. Plant height contributed the maximum towards genetic divergence followed by days to 50% flowering and grain yield per plant.

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

Awasthi *et al.* (2005) studied the genetic divergence of 21 Indian aromatic rice genotypes and grouped into 6 clusters for different characters. The inter-cluster distance ranged from 0.00 for clusters IV, V and VI to 40.21 for cluster III. The inter-cluster distance was observed to be highest between clusters II and III, indicating that the genotypes of these 2 clusters were genetically more diverse. The number of grains per

panicle, grain yield per plant, days to 50% flowering, leaf length and leaf width showed high per cent contribution towards total genetic divergence.

Bose and Pradhan (2005) assessed the nature and magnitude of genetic divergence among 35 deep water rice genotypes and grouped them into 10 clusters showing fair degree of relationship between geographic distribution and genetic divergence. Traits such as plant yield, days to 50% flowering, and plant height were the major contributors to genetic divergence.

Chand *et al.* (2005) studied 19 genotypes of Aman rice for their genetic divergence by using Mahalanobis D^2 statistics and grouped them into six clusters. Cluster I was the largest with eight genotypes followed by cluster II with four genotypes. The maximum inter-cluster distance was found between these groups.

Chaturvedi and Maurya (2005) studied genetic divergence analysis in 26 rice genotypes which were grouped into 8 clusters. The maximum inter-cluster D^2 value was obtained between cluster III and VI and III and VIII. It is suggested that for developing better cultivar, the genotypes of cluster III could be utilized in hybridization programme with the genotypes of cluster VI and VIII.

Kandamoorthy and Govindarasu (2005) studied genetic diversity in 30 extra-early rice genotypes. Results revealed that Cluster I had the highest number of genotypes. The highest inter-cluster distance was observed between cluster I and III followed by cluster II in direct sown condition. Under transplanted condition, cluster II showed the highest inter-cluster distance with cluster V followed by cluster II and IV. Plant height and days to flowering contributed to genetic diversity in transplanted conditions.

Madhavalatha *et al.* (2005) studied the genetic diversity in 44 elite rice germplasm lines classified them into nine clusters based on Mahalanobis D^2 statistic. Results on inter-cluster distances revealed maximum diversity between genotypes of clusters IV and VIII. Intra-cluster distance was maximum for cluster V, indicating the existence of variability within the cluster. Plant height and days to 50% flowering accounted for 82.04% of the total genetic divergence, indicating their importance in the choice of parents for hybridization programmes.

Suman *et al.* (2005) grouped 114 rice genotypes into 10 clusters by using Mahalanobis D^2 statistic. The maximum inter-cluster distance was observed between clusters V and X. Harvest index gave the highest contribution towards divergence followed

by seed density and total number of tillers per plant. Geographical diversity did not relate to genetic diversity.

Naik *et al.* (2006) studied genetic divergence to estimate the nature and magnitude of diversity in 50 aromatic rice accessions and grouped them into 7 clusters. The cluster VI had the highest mean for grain yield per plant and for biological yield per plant. Inter-cluster distance was recorded highest between cluster 3 and cluster 4. The conclusion drawn by the cluster analysis is that in the studied population high variability observed between the genotypes in different clusters for different characters.

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

Mundhe *et al.* (2006) studied genetic diversity in 39 rice genotypes and grouped them into 7 clusters. Intra-cluster distance was maximum in cluster III followed by cluster II and cluster I. Inter-cluster distance was maximum between cluster V and VII followed by cluster III and V, and cluster II and V.

Ravinder *et al.* (2006) studied genetic divergence in 50 unscented rice genotypes for yield and grouped them in 3 and 4 clusters in normal and late-sown conditions, respectively. There was no relationship between clustering pattern and geographical distribution. Based on the high cluster mean and wide genetic distance, hybridization between superior genotypes of clusters Individuals (IR 36, Palman 579, BR 827, HKR 117, HKR 126, HKR 86-105, IR 64 and RP 2151-21-22) and cluster III (Govind and NDR 84) had been advocated to achieve high heterosis and high yielding segregants.

Reddy *et al.* (2006) assessed the genetic divergence in 64 early rice genotypes and the genotypes were grouped into 13 clusters. There was no relationship observed between geographical distribution and genetic diversity. Per cent contribution of characters, i.e. 1000-grain weight, plant height, grain yield per plant and number of spikelets per panicle was highest towards genetic divergence indicating that due consideration should be given to these characters while selecting parents from distant clusters for hybridization.

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

Singh *et al.* (2006) studied the genetic divergence in 52 traditional lowland rice genotypes by using Mahalanobis D^2 statistics and grouped into six clusters. Clusters II, III, and IV exhibited high values for most of the characters. Plant height, followed by leaf angle and leaf area, highly contributed to the formation of clusters. Clusters II, IV, and V showed maximum inter-cluster distances and high values of plant height, days to 50% flowering, panicle length, grain yield/plant and milling per cent, may be used for initiating a hybridization programme.

Chandra *et al.* (2007) assessed the nature and magnitude of genetic divergence in 57 upland rice genotypes for and grouped them into five clusters. The most divergent clusters were III and IV ($D^2=3387.9$) followed by III and V ($D^2=2808.2$) and clusters II and III ($D^2=1908.7$). The clustering patterns of the genotypes were quite at random indicating that the geographical origin and genetic diversity were not related. The characters contributing more towards the genetic divergence were 1000-grain weight, grain yield and biological yield.

Sarawgi and Bisne (2007) studied genetic divergence in 81 scented rice genotypes. Based on D^2 statistics genotypes were grouped into nine clusters. The genotypes from cluster II having desired mean for characters like hulling %, milling % and head rice recovery and panicle length; cluster VII having high value for kernel length and L/B ratio and cluster V low value for days to 50% flowering but highest value for grain yield Kgha⁻¹.

Kumar *et al.* (2008) estimated genetic divergence in 30 genetically diverse genotypes of rice by using Mahalanobis D^2 statistic and grouped them into eight clusters. The inter-cluster distance was highest between clusters V and VI. This indicates that the genotypes could be used in hybridization programme and are likely to exhibit high heterosis and possibility of throwing transgressive segregants in subsequent generations.

Ramya and Kumar (2008) studied the genetic divergence in 50 genotypes of rice and formed them 11 clusters. Cluster I was the largest with 35 genotypes. The inter cluster distances were greater than intra cluster distances. The inter cluster distance between clusters IV and VIII recorded maximum distance (37.58), which indicates that the divergence among these clusters was the highest. Number of grains per panicle, number of productive tillers per plant and grain yield per plant showed high per cent contribution towards genetic divergence.

Sabesan *et al.* (2009a) studied the genetic diversity in rice genotypes by using Mahalanobis D² statistic and grouped them into 13 clusters. Cluster I with seven genotypes was the largest cluster followed by Cluster V with four genotypes. Clusters IV, VII, VIII, X, XI, XII and XIII were mono genotypic clusters. The maximum inter cluster distance ($D^2 = 8235.56$) was recorded between clusters II and III. Cluster XII recorded highest mean value for grain yield per plant and lowest mean value for days to first flower. Number of grains per panicle (42.71%) followed by days to first flower (25.62%) contributed maximum to total divergence.

Shahidullah *et al.* (2009) assessed the genetic divergence in 40 aromatic rice for grain quality and nutrition aspects. Genotypes were grouped into six clusters in multivariate analysis. The inter-cluster D² value was maximum (26.53) between I and VI followed by 21.28 (between I and V). Majority of the local aromatic rice varieties with smaller kernels were included in the cluster I. The cluster III contains Elai, sarwati and sugandha-1 with long-slender kernel and 'very good' appearance. Thus, these varieties can be used in breeding programme for improvement of germplasm.

Raut *et al.* (2009) grouped 40 rice genotypes into 3 clusters by using Mahalanobis D² statistic. Cluster I emerged as the largest with 36 genotypes. Cluster II had 3 genotypes while cluster III was mono genotypic. Investigation revealed the independence of the genetic diversity from the eco geographic distribution of the genotypes. Length to breadth ratio of grain followed by number of grains per panicle, length of grain and seed yield per plant exhibited the greater contribution to the genetic divergence among genotypes.

Rouf *et al.* (2009) used D² analysis to measure the genetic distance in 75 genotypes and grouped them into 11 clusters. Cluster VI, IX and X among themselves showed greater genetic separation. Though Cluster II and Cluster I had more strength which would help in achieving high genetic gain.

Banumathy *et al.* (2010) evaluated 53 rice genotypes for yield and yield attributing characters using D^2 analysis, based on the analysis the genotype were grouped into 11 clusters. Among the eight traits studied, grain yield, days to 50 per cent flowering, total grains per panicle and plant height together contribute 86.62% towards total divergence. Therefore, these characters may be given importance during hybridization programme.

Pandey and Anurag (2010) assessed the nature and magnitude of genetic divergence in 40 rice genotypes by using Mahalanobis D^2 -statistics and grouped them into seven clusters. Cluster VI was the largest one containing 11 genotypes followed by cluster III with 9 genotypes. Plant height, biological yield and test weight contributed considerably, accounting for 86.16% of total divergence. The highest inter-cluster distance was observed between cluster II and VII.

Mohanty *et al.* (2010) studied 40 rice genotypes using Mahalanobis D^2 analysis and grouped them into five clusters. The pattern of distribution of genotypes revealed that geographical diversity and genetic diversity were not related. The characters viz., leaf area at 90 DAS, number of grains panicle⁻¹ and days to 50% flowering contributed maximum towards genetic divergence.

Padmaja *et al.* (2010) analysed the genetic divergence in 150 genotypes of rice by using Mahalanobis D^2 statistics revealed the existence of considerable diversity among the genotypes. On the basis of D^2 values, the genotypes were categorized into 13 clusters. Cluster XI was the largest consisting of 28 genotypes, while cluster I contained only two genotypes. Cluster I showed maximum inter-cluster distance with cluster IX indicating that the genotypes from these clusters may be used as potential donors in hybridization programme to obtain desirable recombinants.

Reddy *et al.* (2010) estimated the genetic divergence in 50 rice genotypes and grouped into 11 clusters. Cluster IV was emerged as largest cluster with 12 genotypes. The highest inter-cluster distance was observed between clusters VIII and XI. The genotypes UPR-1840, PAU-3042-3-3-4, UPR-2554-9-1 and NDR-2062 were identified as genetically diverse parents, which can be used further as parents in hybridization programme.

Chaturvedi *et al.* (2011) assessed the nature and magnitude of genetic divergence in 35 rice genotypes by using Mahalanobis D^2 and grouped them

into eight clusters. The panicle weight followed by effective tillers per plant and yield per plant contributed maximum towards divergence.

Pandey *et al.* (2011) studied fifty rice genotypes using Mahalanobis's D^2 statistics into six clusters and revealed no correlation between genetic diversity and geographical diversity. The characters days to 50 per cent flowering, plant height and 100-seed weight contributed maximum to the genetic diversity.

Sharma *et al.* (2011) studied the genetic divergence using D^2 statistic in 63 rice genotypes and grouped them into 8 different clusters, in which, cluster VII was the largest having 16 genotypes. Based on mean performance, genetic distances and clustering pattern, the genotypes; Pusa Basmati-1 and Taraori Basmati of cluster II, Sarju-52, Narendra Usar-3 and Narendra-80 of cluster IV, Badshah Bhog, MTU-7029 and BPT-5204 of cluster VI and Malviya-36, Kanakjeer and Super Basmati of cluster VIII proved to be promising for use in hybridization programme.

Hassan *et al.* (2012) used 8 (SSR) primers for assessing fifty nine rice genotypes. By the DNA profiling, a total of 114 alleles were detected. Allele number per/locus ranged from 9 to 27, with an average of 14.25. Average polymorphism information content (PIC) value was 0.857 with lowest 0.767 to highest 0.857. Mean gene diversity over all SSR loci was 0.870 with a range from 0.792 to 0.948.

Jahani *et al.* (2013) studied 100 genotypes of rice for average grain length, width and thickness (length/ width ratio). Results showed that morphological diversity analysis produced three clusters of rice genotypes considering three grain size characters.

Kar *et al.* (2013) evaluated 65 indigenous aromatic rice genotypes through divergence analysis. The genotypes were grouped into thirteen clusters. Based on clustering pattern, maximum genetic distance among genotypes existed between clusters IV and V and clusters IV and XI.

Genotypes of basmati rice representing different regions of India on the basis of yield and quality characteristics utilizing Mahalanobis D^2 analysis. Based on the genetic distance (D^2 values), the rice genotypes were grouped into six clusters. Of the six clusters formed cluster VI consisted of maximum eight genotypes followed by cluster V accommodating six genotypes, cluster I with four genotypes, cluster III and IV with three genotypes each and cluster II with one genotype (Allam *et al.*, 2014).

Ramanjaneyulu *et al.* (2014) evaluated ten popular low land rice genotypes for variability, genetic divergence, stability and suitability under aerobic conditions on Alfisols. Pattern of constellations into 4 clusters indicated the existence of a significant amount of variability. The maximum intra-cluster distance (D: 0.773) was observed in cluster III and selection with this cluster may thus be useful.

Rathor *et al.* (2014) selected and studied 40 rice accessions including eleven local land races. Wards minimum cluster diagram and principal component analysis was used to estimation the pattern of variation in the population. First four PC scored 78.6% variation and cluster diagram represent five different clusters. Cluster I contained 12 accessions, cluster II contained 1 accession, Cluster III contained 3 accessions, Cluster IV contained 10 and Cluster V contained 14.

Samal *et al.* (2014) studied 78 genotypes of aromatic rice including International check varieties, traditional Basumati and evolved Basumati on the basis of morphological, biochemical and genetical variations. The plant height among the genotypes ranged from 85.91cm to 159.67 cm whereas the panicles/plant ranged from 6.06 to 16.22 with the mean value of 9.56.

Sandhya *et al.* (2014b) carried out diversity studies with 32 elite rice genotypes to identify diverse genotypes. On the basis of D^2 values the genotypes were grouped into six clusters. Cluster I and VI was the largest containing 8 genotypes followed by cluster IV with 6 genotypes. The mode of distribution of genotypes from different eco-regions into various clusters was at random indicating that geographical diversity and genetic diversity were not related. The maximum intercluster distance was recorded between clusters V and VI and the maximum intra-cluster distance was found in cluster IV followed by I. The characters like number of number of spikelets per panicle, biological yield per plant, test weight, harvest index and days to 50 per cent flowering contributed maximum towards genetic diversity.

Shamim *et al.* (2014) evaluated genetic diversity in eighteen rice varieties on the basis of sixteen quantitative characters using numerical taxonomic approach. Eighteen varieties were grouped into nine different clusters revealing sufficient amount of variability among the varieties.

Sajid *et al.* (2015) studied 32 different agro-morphological traits (15 qualitative and 17 quantitative). The rice germplasm exhibited sufficient genetic variation for most of

the qualitative and quantitative traits. Rice accession 6531 took minimum days to 50% flowering while accession 6512 showed superiority for panicle length. Accession 6536 showed superiority for biological yield. Rice accession 6547 showed excellent performance for grain yield while accession 6537 showed the maximum value for 1000-grain yield.

2.4 CHARACTER ASSOCIATION

Study of character association helps the breeder in fixing a selection criterion 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. 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 here under:

Yield and nutrient uptake by rice is affected by moisture regimes, puddling and time of application of organic matter (Das and Mandal, 1986). Prasad *et al.* 2002 reported that Plant height has significant correlation with grain yield. Mohammad *et al.* 2002 observed significant variation among the studied cultivars for the trait plant height.

Agahi *et al.* (2007) observed that grain yield was significantly correlated with days to heading ($r_p=0.403^{**}$, $r_g=0.525^{**}$), total tillers ($r_p=0.585^{**}$, $r_g=0.524^{**}$) number of productive tillers ($r_p=0.604^{**}$, $r_g=0.570^{**}$), days to maturity ($r_p=0.296$ by Kumar and Senapati (2014) $r_g=0.424^{**}$), number of grain per panicle ($r_p=0.349^*$, $r_g=0.339^*$), flag leaf length ($r_p=0.350^*$, $r_g=0.301^*$), flag leaf width ($r_p=0.279^*$, $r_g=0.093^{ns}$) and plant height ($r_p=-0.220^{ns}$, $r_g=-0.300^*$).

Karad and Pol (2008) reported the grain yield was positively correlated with almost all the characters except 1000-grain weight at both genotypic and phenotypic levels. Genotypic correlation estimates were higher than phenotypic correlation with grain yield plot^{-1} .

Kole *et al.* (2008) reported positive and significant correlation of grain yield with plant height, panicle number per plant, straw weight and harvest index but negative and significant correlation with days to 50% flowering at both genotypic and phenotypic levels. Plant height was significantly and positively correlated with panicle length.

Khan *et al.* (2009) reported positive and significant association of plant height with panicle length.

Sabesan *et al.* (2009b) reported positive significant association of grain yield per plant with panicle length and productive tillers per plant at both genotypic and phenotypic levels. The 100 grain weight was positively significantly correlated with plant height, grains per panicle and grain breadth. Days to 50% flowering was positively significantly correlated with number of productive tillers per while plant height was positively and significantly correlated with panicle length and kernel breadth. Satish Chandra *et al.* (2009) revealed significant positive association of grain yield per plant with number of productive tillers per plant, 1000-grain weight, panicle length and number of grains per panicle.

Saravanan and Sabesan (2009) revealed that grain yield per plant had significant positive association with total number of tillers per plant, number of productive tillers per plant and grain breadth. Chakraborty *et al.* (2010) revealed significant positive genotypic correlation of yield/plant with plant height (0.21), panicles/plant (0.53), panicle length (0.53), effective grains/panicle (0.57) and harvest index (0.86). The panicle length was positively and significantly correlated with number of filled grains per panicle. Rajesh *et al.* 2010 reported a range of 78.80 cm to 217.80 cm.

Yield potential of 16 rice genotypes including 12 hybrids, 3 inbreds, and 1 new plant type (NPT), were studied by Islam *et al.* (2010). Yield and yield components were determined at maturity. Hybrid produced higher spikelets/panicle and 1000-grain weight than inbred rice. Spikelet filling per cent was higher in inbred than hybrid rice.

The correlation studies revealed strong positive association of yield with days to 50 per cent flowering, plant height, number of grains per panicle, number of spikelets per panicle and spikelet fertility in thirty three genotypes evaluated by Nandan *et al.* (2010) for identifying their efficiency with respect to 20 yield and quality traits.

Pankaj *et al.* (2010) carried out experiment using 48 genotypes of rice for grain yield its components and quality characters, revealed that grain yield exhibited significant

positive correlation with grains/panicle, spikelets/panicle and effective tillers/plant at maturity at both phenotypic and genotypic levels. Total tillers/plant had correlation with grain yield/plant at phenotypic level only. Significant negative genotypic correlation with days to 50 per cent flowering and grain yield revealed that early maturing genotypes yielded high under Palampur condition.

Rathi *et al.* (2010) and Chakraborty *et al.* (2010) observed that genotypic correlation coefficients were of higher in magnitude than the corresponding phenotypic correlation coefficients. According to Dewey and Lu (1959), very close values for genotypic and phenotypic correlations might be due to reduction in error (environmental) variance to minor proportions.

Yang *et al.* (2010) studied correlation analysis for grain quality traits, namely, grain length (GL), grain width (GW), grain length/width ratio (LWR) and chalkiness degree (CD). CD was significantly and negatively correlated with GL ($R=-0.5628^{**}$) and LWR ($R=-0.7498^{**}$), but positively correlated with GW ($R=0.7539^{**}$).

Akhtar *et al.* (2011) reported negative non-significant association of plant height and positive significant correlation of 1000-grain weight with paddy yield at both phenotypic and genetic levels.

Babu *et al.* (2011) reported characters like number of tillers/hill, number of spikelets/panicle and number of panicles/hill showed positive significant correlation with grain yield/hill at both genotypic and phenotypic levels.

Bagheri *et al.* (2011) revealed panicle length ($r=0.818$), the total number of spikelet per panicle ($r=0.617$), the number of filled grains per panicle ($r=0.790$) and the panicle number per plant ($r=0.498$) correlated significantly with grain yield. Fiyaz *et al.* (2011) reported number of productive tillers, total spikelet per panicle, total biomass, days to 50 per cent flowering and plant height had significant positive association with grain yield.

Gyanendra *et al.* (2011) reported positive and significant correlation of grain yield with test weight and L/B ratio. Singh *et al.* (2011) reported grain yield/plant was positively and significantly associated with panicle bearing tillers/plant, harvest-index, biological yield/plant, L/B ratio and significant positive correlation with 1000-grain weight in all environments and pooled level.

Yadav *et al.* (2011) studied the extent of genetic association between yield and its components. Grain yield was significantly and positively associated with harvest index, number of tillers per hill, number of panicles per plant, panicle length, number of spikelets per panicle and test weight at both genotypic and phenotypic levels and negative correlation with days to 50% flowering and plant height.

Parikh *et al.* (2012) characterized seventy-one aromatic rice germplasm. The genetic parameters for the ten agronomic traits indicated that the selection of genotypes may be done for fertile spikelets per panicle, spikelet density, spikelet sterility percentage, and hundred seed weight.

Rangare *et al.* (2012) revealed grain yield was significantly and positively associated with biological yield per plant, number of fertile tillers per plant, number of spikelets per panicle, test weight, panicle length and days to maturity but non significantly associated with days to 50% flowering, days to initial flowering, harvest index and plant height.

Ravindra Babu *et al.* (2012) revealed positive association of grain yield per plant with number of productive tillers per plant, negative significant correlation with days to 50% flowering. Plant height was significantly and positively correlated with panicle length and negatively with productive tillers per hill.

Seyoum *et al.* (2012) reported days to 50% flowering, days to 85% maturity, plant height and 1000-grain weight had negative and non-significant correlation with grain yield both at genotypic and phenotypic levels.

Aditya and Anuradha (2013) studied eighteen rice genotypes under rainfed ecosystem for fifteen quantitative traits. The phenotypic correlation coefficient among fifteen traits showed that grain yield was significantly and positively correlated with plant height, days to 50 per cent flowering, days to maturity, flag leaf length, flag leaf width, panicle length, grains per panicle, fertile grains per panicle, kernel length and L/B ratio.

Berhanu *et al.* (2013) conducted a study to evaluate correlations for grain Zn concentration and yield related traits and identification of SSR markers linked to these traits in rice. Significant positive correlation was observed for grain yield per plant with number of productive tillers per plant ($r=0.5$) and number of tillers per plant

($r=0.4$). Grain zinc concentration showed negative correlation with grain yield per plant ($r=-0.27$).

Chakravorty *et al.* (2013) evaluated fifty-one landraces of rice evaluated for 18 agro-morphological traits. All the traits except ligule length, culm length, number of grains panicle-1 and number of primary branches panicle-1 exhibited positive and significant correlation coefficients with kernel weight. Leaf length was positively and significantly correlated with leaf breadth ($r=0.760$), plant height ($r=0.309$) culm length ($r=0.352$); plant height showed similar association with flag leaf angle ($r = 0.337$), culm diameter ($r=0.688$), culm number ($r=0.706$) and panicle length ($r=0.654$).

Singh *et al.* (2013) conducted with 11 genotypes of upland rice during *Kharif*. Grain yield showed positive and significant correlation with plant height and panicle length at both genotypic level and phenotypic level.

Forty-one aromatic rice germplasm of diverse sources were used to assess the character association and contribution of characters towards grain yield by Dilruba *et al.* (2014). Analysis of phenotypic and genotypic correlation co-efficient of quantitative characters and partitioning of genotypic correlation to grain revealed that the correlation coefficients of grain yield per hill with 1000-grain weight and harvest index were positive and highly significant. Spikelet sterility showed highly significant negative correlation with grain yield at genotypic level only.

Dutta *et al.* (2013) estimated variability and genetic parameters of sixty-eight rice genotypes for twelve agronomically important characters. Characters were under the influence of additive gene action and a satisfactory selection programme for agronomic improvement on the basis of these characters is possible.

Singh *et al.* (2013) studied 11 genotypes of upland rice during *Kharif*. Grain yield showed positive and significant correlation with plant height and panicle length at both genotypic level and phenotypic level.

Nagesh *et al.* (2013) studied 14 genotypes to estimate phenotypic and genotypic association among grain iron, zinc, yield attributes and grain yield and reported a positive correlation between iron and zinc content was observed while a negative correlation between grain iron content and grain yield was recorded.

Naveen *et al.* (2013) reported high significant variation for grain yield per plant and grain zinc content. Grain zinc content showed negative correlation (-0.379, -0.221) with grain yield per plant.

Sanghera *et al.* (2013) evaluated fourteen red rice ecotypes from temperate regions and correlation and path coefficients were also studied for fifteen agro-morphological characters. Grain yield was found to be positively and significantly correlated with number of tiller per plant, panicle density m⁻² and number of grain per panicle at both genotypic and phenotypic levels indicating the importance of these characters for yield improvement in this material.

Ukaoma *et al.* (2013) characterized 15 rice breeding lines using 15 agronomic traits. Correlation coefficient and estimates of broad sense heritability of the 15 characters associated with grain yield for the combined data showed wide significant genetic variability ($p < 0.0001$) amongst the genotypes. Of all the characters evaluated, only number of grains per plant had the highest and significant correlation with grain yield ($r = 0.7643$). Days to booting and days to 50% heading had negative but high correlation.

Bornare *et al.* (2014) Selections can be effective on the basis of correlation and path analysis for characters like effective tillers/plant, spikelet density, angle of floret opening, duration of floret opening, panicle length, 1,000 seed weight and days to 50 per cent flowering.

A field experiment was conducted for two consecutive years to evaluate the forty four low land traditional rice cultivars for twenty three panicle yield and its attributing traits (Chakravorty *et al.*, 2014). Among the panicle yield attributing traits, number of primary branches per panicle, number of grains on primary branches panicle-1, number of spikelets on primary branches panicle-1, grain length, grain breadth, grain thickness, kernel breadth, kernel thickness, 100 grain weight, 100 kernel weight correlated significantly and positively with panicle yield both at the genotypic and phenotypic levels. Direct selection of the above said traits might be rewarding for panicle yield improvement since they revealed a true relationship with the panicle yield.

Chouhan *et al.* (2014) Evaluated the thirty five rice accessions to assess their character association and path analysis for grain yield and yield attributing traits. Leaf width, plant height, panicle length, fertile spikelet per panicle, total grains per panicle,

spikelet fertility, test weight, kernel length and kernel breadth showed positive and significant association with grain yield per plant at genotypic and phenotypic levels.

Hosseini *et al.* (2014) evaluated eighteen rice genotypes to determine relations among main quantitative traits and the contribution of each trait to the total dry weight production in three salt stress levels (3, 6 and 8 dS/m levels) through correlation coefficient and path analysis. At 3 dS/m level, the values of the correlation coefficient with total dry weight were ordered as $x_6 > x_5 > x_7 > x_2$ with 0.945, 0.828, 0.823 and 0.634, respectively. The results of correlation coefficient at 6 dS/m level exhibited that root dry weight was again positively correlated with total dry weight ($P < 0.01$). At 8 dS/m salinity level, shoot dry weight was positively correlated with total dry weight ($P < 0.01$).

Jambhulkar *et al.* (2014) conducted with twenty two upland genotypes. Plant height, ear bearing tiller, panicle length, panicle weight and length were positively and significantly correlated with yield.

Forty-one aromatic rice germplasm of diverse sources were used to assess the character association and contribution of characters towards grain yield by Karim *et al.* (2014). Analysis of phenotypic and genotypic correlation co-efficient of quantitative characters and partitioning of genotypic correlation to grain revealed that the correlation coefficients of grain yield per hill with 1000-grain weight and harvest index were positive and highly significant.

Lingaiah *et al.* (2014) carried out a study on correlation and path analysis for yield and yield contributing characters in sixty four mid early group genotypes of rice. Yield exhibited positive association with effective tillers per plant, panicle length and test weight. And negative association with days to 50% flowering and plant height.

Madakemohekar *et al.* (2014) investigation was carried out to study the genetic parameters for quality and nutritional characters in 60 recombinant inbred lines (RIL's) of rice. Analysis of variance revealed significant differences for all the traits. It was observed that grain yield per plant was positively significant associated with seed width, milling per cent, gelatinization temperature, amylose content and kernel breadth before cooking. Kernel length after cooking, seed width, milling per cent, amylose content and gelatinization temperature had positive direct effect on grain yield.

Ten aromatic restorer lines of hybrid rice were studied to assess genetic variability, mean performance, character association and path coefficient analysis for out crossing traits in rice by Majumder *et al.* (2014). Another breadth, pollen fertility and grain yield/hill showed a high degree of positive correlation with grain yield/hill for the lines.

Naseem *et al.* (2014) studied twenty genotypes of rice (*Oryza sativa* L.) for genetic variability and correlation. Flag leaf area, number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and 1000 grain weight had a highly positive significant genotypic correlation with grain yield per plant. Same results were obtained for the phenotypic correlation.

Norain *et al.* (2014) investigated the relationships between agronomic characters and grain yield for high yielding rice varieties. Grain yield per plant was positively associated with plant height ($r=0.296$ $p<0.01$), number of tiller per plant ($r=0.765$ $p<0.01$), panicle number per plant ($r=0.767$ $p<0.01$), flag leaf width ($r=0.370$ $p<0.01$), flag leaf length ($r=0.415$ $p<0.01$), number of grains per panicle ($r=0.750$ $p<0.01$), 1000-grain per weight ($r=0.278$ $p<0.01$), and grain length ($r=0.248$ $p<0.01$) indicating that simultaneous selection for these characters would result in improvement of yield.

Patel *et al.* (2014) carried out a study on forty four diverse genotypes. Correlation studies indicated that genotypic correlation coefficients were higher in magnitude than their corresponding phenotypic correlation coefficients for most of the traits. Grain yield per plant was found positively and significantly associated with plant height, panicle length, number of total tillers per plant, number of effective tillers per plant, number of grains per panicle, harvest index and 1000-grain weight at both genotypic and phenotypic levels indicating that these traits were main yield attributing traits.

Grain yield/plant of newly developed advanced fine rice lines and check showed positive association in respect of number of effective tillers/hill (0.308), number of filled spikelets/panicle (0.110) and weight of 1000-grains (0.109), whereas significant negative association with panicle length (-0.609), number of unfilled spikelets/panicle(-0.542) and non significant negative association with plant height (-0.136) and number of ineffective tillers/hill (-0.304) (Rahman *et al.*, 2014).

Ranawake and Amarasinghe (2014) correlated the grain yield with number of fertile spikelets/panicle ($r=0.765$), panicle weight ($r=0.727$), number of spikelets/panicle

($r=0.638$), filled grain percentage ($r=0.620$), number of fertile tillers/plant ($r = 0.611$), number of tillers/plant ($r=0.575$). Hundred grain weight ($r=0.336$) and plant height ($r=0.278$) were also correlated with at 1% significant level. None of the studied trait was negatively correlated with the yield.

Rathor *et al.* (2014) selected 40 rice accessions including eleven local land races. The estimates of phenotypic coefficient between pairs of characters revealed that seed yield has a strong positive significant association tillers/ hill, panicles/ hill, panicle length (cm), biological yield (gm), harvest Index (%), spikelet's/ panicle, test weight (gm). Hence, main focused should be given on these traits during selection to improve lines.

Sandhya *et al.* (2014a) studied association among the yield component traits, their direct and indirect effects on the yield. Biological yield per plant (0.78, 0.72), harvest index (0.57, 0.58) and number of spikelets per panicle (0.18, 0.18) were positively associated with grain yield at both genotypic and phenotypic levels respectively, indicating improvement in these traits will increase the grain yield.

Thirumala Rao *et al.* (2014) studied character association and path analysis between yield and its contributing traits in 49 Rice cultures. Grain yield was significant positively correlated with number of grains per panicle, panicle length and test weight.

Venkata Lakshmi *et al.* (2014) evaluated seventy genotypes of rice (*Oryza sativa* L.) during *Kharif* to study the nature and extent of correlation among yield and yield attributing characters, days to 50 per cent flowering, days to maturity, number of effective tillers per plant, plant height, panicle length, number of grains per panicle, 1000-grain weight, grain yield per plant, kernel length, kernel breadth and L/B ratio. The results revealed that grain yield per plant to be positively and significantly associated with days to maturity, number of productive tillers per plant, plant height and kernel length indicating importance of these traits as selection criteria in yield improvement programmes.

Venkanna *et al.* (2014) studied the association between yield traits in F_2 generation in 36 crosses of rice. Seed yield had highly significant positive correlations with total biomass both phenotypically and genotypically and 1000 weight genotypically. The study revealed that genetic improvement of grain yield in rice is admissible by selecting character having high positive correlation and positive direct effect.

2.5 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) 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 here under in

Gomathinayagam *et al.* (1988) reported highest direct effect of plant height on grain yield in rice. While, Qamar *et al.* (2005) stated that productive tillers per hill, days to maturity and days to 50% flowering may be considered important for the improvement of grain yield in the non-aromatic group whereas productive tillers per hill, spikelets per panicle, fertility %age and plant height may be considered as the selection criteria for the direct improvement of grain yield in the aromatic group.

Deepa *et al.* (2006) reported that correlated traits except panicle length exhibited high positive direct effects towards single plant yield.

Chaturvedi *et al.* (2008) reported positive direct effect of 1000-grain weight on grain yield at both genotypic and phenotypic levels. Karad and Pol (2008) reported length of panicle had the highest positive direct effect followed by number of panicles, number of tillers plant⁻¹ and number of mature panicles whereas the characters plant height, number of immature panicles and 1000 grain weight had the negative direct effect via indirect effect on grain yield plot⁻¹.

Kole *et al.* (2008) revealed that panicle number had the highest positive direct effect followed by grain number, test weight, plant height, days to flower and straw weight on grain yield. Panicle length had negative direct effect on grain yield.

Rokonuzzman *et al.* (2008) reported positive direct effect of number of productive tillers per hill on grain yield.

Krishnappa *et al.* (2009) observed poor direct effect (0.224) of plant height. Tillers per plant showed negative direct effects (-0.1492), panicle length showed high direct effects (0.4124), grain number per panicle showed direct effect (0.0788) and 100-grain weight showed positive low direct effects (0.0355) on grain yield.

Khan *et al.* (2009) reported highest positive direct effect of number of filled grains per panicle and negative direct effect of number of productive tillers per plant on grain yield.

Saravanan and Sabesan (2009) revealed that grain breadth, grain L/B ratio and total number of tillers per plant had the highest direct effect on grain yield per plant, suggesting that the improvement in grain yield could be efficient if the selection is based on these component traits.

Satish Chandra *et al.* (2009) revealed that number of grains per panicle, days to 50% flowering, 1000-grain weight and number of productive tillers per plant have shown high positive direct effects and panicle length had negative direct effect on grain yield. Chakraborty *et al.* (2010) reported positive direct effect of plant height, 1000-grain weight and panicle length on grain yield.

Nandan *et al.* (2010) evaluated thirty three genotypes for identifying their efficiency with respect to 20 yield and quality traits. Path analysis indicated that the number of grains per panicle had maximum direct effect on grain yield per plant followed by kernel length after cooking (KLAC), days to 50 per cent flowering, hulling percentage, plant height, harvest index and kernel breadth after cooking (KBAC).

Direct positive effect of tillers/plant at maturity, grains/panicle, protein content, plant height at maturity, amylose content and days to maturity at genotypic level was observed in 48 genotypes of rice for grain yield (Pankaj *et al.*, 2010), whereas length: breadth ratio had a negative direct effect.

Rajeswari *et al.* (2010) conducted path analysis for 10 grain quality characters of 30 pre- released cultures and high yielding varieties and revealed that head rice recovery had highly significant positive association ($r=0.86$) with milling per centage and significant negative association with elongation ratio (-0.39).

Yadav *et al.* (2010) revealed that harvest index, biological yield, number of tillers per hill, panicle length, number of spikelets per panicle, plant height and test weight had

direct positive effect on seed yield per hill, whereas days to 50% flowering had negative direct effect on grain yield.

Akinwale *et al.* (2011) reported significant positive correlation of grain yield with the number of tillers per plant ($r=0.58^{**}$), panicle weight ($r=0.60^{*}$) and number of grains per panicle ($r=0.52^{*}$). Therefore, the results suggest that these traits can be used for grain yield selection.

Babu *et al.* (2011) reported number of tillers/hill and number of spikelets/panicle had maximum direct effect on grain yield/hill at both genotypic and phenotypic levels.

Bagheri *et al.* (2011) revealed that panicle length had the highest positive direct effect. Ashfaq *et al.* (2012) evaluated forty rice genotypes on the basis of various morphological traits in a field experiment and reported a significant variation for all the traits studied among the genotypes. The results indicated that the highest genetic variability was observed in plant height, spikelets per panicle, panicle length, days to heading and days to maturity. Significant correlation with yield was also noticed for Panicle length ($r=0.265^{**}$), seeds per panicle ($r=0.266^{**}$) and seed weight per panicle ($r=0.339^{**}$) showed significant positive correlation with grain yield.

Haider *et al.* (2012) reported positive direct effect of 1000-grain weight and its positive significant genetic correlation with grain yield per plant. Rangare *et al.* (2012) reported that biological yield per plant (1.0284 and 1.0216), harvest index (0.6381 and 0.6291), number of fertile tiller per plant (0.1058 and 0.1048), days to 50% flowering (0.0806 and 0.0756), test weight (0.0353 and 0.0338), days to maturity (0.0022 and 0.0076) and panicle length (0.0007 and 0.0002) had high direct effect on grain yield per plant while days to initial flowering (-0.0644 and -0.0676), number of spikelets per panicle (-0.0483 and -0.0359), plant height (-0.0106 and -0.0170) had negative direct effect on grain yield per plant on genotypic and phenotypic level.

Aditya and Anuradha (2013) studied eighteen rice genotypes under rain fed ecosystem for fifteen quantitative traits. The estimates of direct and indirect effect revealed that L/B ratio had the highest positive direct effect on grain yield followed by kernel width, grains per panicle, and tillers per plant.

Berhanu *et al.* (2013) conducted a study to evaluate genetic variability parameters, correlations that exist for grain Zn concentration and yield related traits and identification

of SSR markers linked to these traits in rice. The path-coefficient analysis indicated the positive direct effect of number of productive tillers /plant on grain yield / plant.

Krishna Veni *et al.* (2013) assessed seventy rice (*Oryza sativa* L.) genotypes for genetic variability and correlations between yield and yield components and quality parameters. The relative contribution of characters towards variability and results of correlation and path coefficient indicated the importance of days to 50 per cent flowering, ear bearing tillers and panicle length.

Nagesh *et al.* (2013) studied 14 genotypes to estimate phenotypic and genotypic association among grain iron, zinc, yield attributes and grain yield. Path analysis revealed the highest direct effect of test weight on grain yield followed by number of productive tillers per plant and iron content.

Naveen *et al.* (2013) identified transgressant lines for high zinc content from 160 RILs derived from IRRI38 X Jeerigesanna grown under aerobic condition using augment design. Path coefficient analysis has shown high positive and negative direct effect of number of productive tillers (0.748) and number of tillers (-0.532) respectively on grain yield. Among RILs grain zinc content was ranged from 16.1 ppm to 35.5 ppm. Eight transgressant lines were identified based on high grain zinc content (31.2 ppm to 35.5 ppm).

Sanghera *et al.* (2013) assesses 14 red rice ecotypes from temperate regions and correlation and path coefficients were also studied for fifteen agro-morphological characters. Genotypic path analysis revealed that panicle density had the highest positive direct effect followed by plant height and days to flower.

Awaneet and Senapati (2014) evaluated thirty three lines of F₅ progenies obtained from Sabita/Sambamahsuri derivatives along with parents and three check varieties for 19 characters. Kernel length imparted the highest positive direct effect on grain yield followed by grain L/B ratio, grain breadth and fertility %.

Chouhan *et al.* (2014) evaluated the thirty five rice accessions to assess their genetic variability, character association and path analysis for grain yield and yield attributing traits. The path analysis with grain yield as dependent variable indicated that the highest positive direct effects were observed by effective tillers per plant followed by panicle length, fertile spikelet per panicle and test weight.

The parameter 1000-grain weight showed the highest positive direct effect on grain yield in the experiment of Dilruba *et al.* (2014) in forty-one aromatic rice germplasm of diverse sources. Panicle length and spikelet sterility showed negative negligible direct effect. The highest positive indirect effect was observed for 1000-grain weight via plant height and the highest negative indirect effect for 1000-grain weight via number of filled grains per panicle.

Ganapati *et al.* (2014) evaluated twenty five genotypes for yield and yield contributing characters to observe their variability, associations and direct and indirect effect on yield. Path coefficient analysis also revealed that, tiller hill⁻¹, thousand grain weight and grain panicle⁻¹ had higher direct effects on yield.

Hosseini *et al.* (2014) used eighteen rice genotypes to determine relations among main quantitative traits and the contribution of each trait to the total dry weight production in three salt stress levels (3, 6 and 8 dS/m levels) through correlation coefficient and path analysis. Result based on direct and summation of indirect effects exhibited that direct effect of root dry weight was higher than indirect effect at 3 and 6 dS/m salt stress levels. But, at 8 dS/m salt stress level, shoot, root and leaf dry weight direct effects with 0.499, 0.429 and 0.329 were higher than indirect effects.

Jambhulkar *et al.* (2014) conducted research with twenty two upland genotypes. Plant height and grain per panicle, 50% flowering, thousand grain weight and ear bearing tiller has high direct effect on yield.

Karim *et al.* (2014) used forty-one aromatic rice germplasm of diverse sources to assess the character association and contribution of characters towards grain yield. Path coefficient analyses were carried out for selected genotypes and to find out the direct and indirect effect of component characters on grain yield.

Majumder *et al.* (2014) studied ten aromatic restorer lines of hybrid rice to assess genetic variability, mean performance, character association and path coefficient analysis for out crossing traits in rice. High positive direct effect regarding anther breadth and pollen fertility of restorer lines showed the highest positive direct effect on grain yield/hill. These characters had the major contribution towards the grain yield/hill.

Lingaiah *et al.* (2014) studied correlation and path analysis studies for yield and yield contributing characters in sixty four mid early group genotypes of rice. Path analysis indicated that panicle length, effective tillers per plant and test weight exhibited direct

positive effect on yield indicating the importance of these traits during selections for improvement of yield in rice.

Naseem *et al.* (2014) evaluated twenty genotypes of rice (*Oryza sativa* L.) for genetic variability and correlation. Path analysis for yield related traits revealed that number of productive tillers per plant, number of spikelets per panicle, number of grains per panicle and days to maturity had positive direct effect on grain yield per plant.

Neha *et al.* (2014) investigated 45 upland rice germplasms. Number of spikelets per panicle had maximum direct effect and highly significant genotypic correlation coefficient with grain yield.

Patel *et al.* (2014) carried out study on forty four diverse genotypes. Path analysis revealed that straw yield per plant had the highest positive direct effect on grain yield followed by grain length, harvest index, days to maturity, protein content, number of total tillers per plant and number of grain per panicle.

Rahman *et al.* (2014) studied seven newly developed lines viz. S-1, S-2, S-5, AL-33(II), AL-36, AL-42(II), AL-44(I) and chinigura path analysis revealed that plant height had positive direct effect (0.154), number of effective tillers/hill had positive direct effect (0.065), number of ineffective tillers/hill had negative direct effect (-0.114), panicle length had positive direct effect (0.163), number of filled spikelets/panicle had positive direct effect (0.285), number of unfilled spikelets/panicle had negative direct effect (-0.154), weight of 1000-grains had positive direct effect (0.234) on grain yield/plant.

Saikumar *et al.* (2014) evaluated a backcross inbred population derived from ‘Swarna’ and ‘WAB450-I-B-P-157-2-1’ (*Oryza sativa* L. x *O. glaberrima*) under both irrigated and lowland drought stresses for yield and yield related traits Harvest index exhibited maximum positive direct effect on grain yield under both the conditions; in addition, filled grains per panicle, spikelet fertility and biomass had positive direct effect on grain yield under both irrigated and lowland drought stresses state.

Sandhya *et al.* (2014a) studied association among the yield component traits, their direct and indirect effects on the yield. Number of panicle per plant (4.33, 0.08), biological index per plant (1.04, 0.80), harvest index (0.90, 0.67), panicle length (0.23, 0.03) and test weight (0.02, 0.03) had positive direct effect on yield at both genotypic and phenotypic levels respectively.

Thirumala Rao *et al.* (2014) studied genetic variability, character association and path analysis between yield and its contributing traits in 49 Rice cultures. Path coefficient analysis indicated that number of grains per panicle, test weight and productive tillers per square meter were essential traits to be considered for realizing the improvement in yield.

Venkanna *et al.* (2014) observed the association between yield traits in F₂ generation in 36 crosses of rice. Number of filled grains per panicle showed highly positive indirect effect through panicle density, total biomass and days to 50% flowering on grain yield.

Chapter III

Material and Methods

Chapter III

MATERIAL AND METHODS

The present experiment to study the evaluation of Iron, Zinc and Protein among the land races of rice was carried out during *Kharif* 2014-2015 at Indian Institute of Rice Research (formally DRR) Farm, ICRISAT campus, Patancheru, Hyderabad, India. The material used, experimental design adopted, the mode of data collection and the statistical procedures followed in present the study are outlined below.

3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of eighty five landraces of rice obtained from the plant breeding division, crop improvement section, Indian Institute of Rice Research (formally, Directorate of Rice Research), Rajendranagar, Hyderabad. The eighty five landraces of rice were furnished in Table 3.1 and the photograph of the experimental plot is shown in Plate 3.1.

3.2 METHODS

All the genotypes were sown on 3rd July, 2014 separately in the nursery on raised beds. Twenty five days old seedlings of each genotype were transplanted in 2 rows of 3 m length by adopting a spacing of 20 cm between and 15 cm between in a Randomized Block Design replicated twice. Recommended agronomic and plant protection measures for raising a healthy nursery and main crop were taken up during the experiment.

3.3 RECORDING OF OBSERVATIONS

Five plants of each genotype in each replication selected randomly were used to record data. Ten characteristics, which include seven quantitative characters and three nutritional traits, were recorded. The observations recorded and the techniques adopted to record each of them are furnished below.

3.3.1 Yield Characters

3.3.1.1 Days to Fifty per cent Flowering

The total number of days taken from the date of sowing to fifty per cent of the total plants in the net plot.

3.3.1.2 Plant Height (cm)

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

Table 3.1 Details of landraces rice used in the study

S. No	CODES	NBPGR IC NO
1	GP-9006	67626
2	GP-9007	67630
3	GP-9019	67856
4	GP-9022	67935
5	GP-9024	67949
6	GP-9025	67958
7	GP-9028	70804
8	GP-9036	70879
9	GP-9043	85717
10	GP-9047	85719
11	GP-9048	85720
12	GP-9051	85722
13	GP-9053	85724
14	GP-9055	85726
15	GP-9064	85746
16	GP-9070	85751
17	GP-9111	86010
18	GP-9119	86026
19	GP-9152	86070

20	GP-9153	86071
21	GP-9157	86079
22	GP-9166	86093
23	GP-9187	86121
24	GP-9192	86125
25	GP-9195	86127
26	GP-9200	86176
27	GP-9200	86176
28	GP-9202	86137
29	GP-9207	86141
30	GP-9210	86144
31	GP-9212	86150
32	GP-9223	86234
33	GP-9244	86276
34	GP-9255	89184
35	GP-9390	99113
36	GP-9555	137415
37	GP-9623	145630
38	GP-9634	145643
39	GP-9703	145852
40	GP-9725	146124
41	GP-9729	146146
42	GP-9788	203389

43	GP-9790	203404
44	GP-9797	203416
45	GP-9801	203423
46	GP-9807	203437
47	GP-9811	203453
48	GP-9812	203454
49	GP-9814	203455
50	GP-9817	203461
51	GP-9820	203467
52	GP-9825	203497
53	GP-9835	203531
54	GP-9846	203563
55	GP-9847	203567
56	GP-9848	203568
57	GP-9850	203570
58	GP-9855	205836
59	GP-9856	205837
60	GP-9859	205841
61	GP-9861	205860
62	GP-9863	205862
63	GP-9865	205864
64	GP-9867	205866
65	GP-9868	205867

66	GP-9901	205994
67	GP-9913	206018
68	GP-9916	206021
69	GP-9917	206022
70	GP-9920	206027
71	GP-9926	206033
72	G3P-9927	206034
73	GP-9928	206035
74	GP-9929	206036
75	GP-9932	206041
76	GP-9933	206042
77	GP-9937	206046
78	GP-9949	207998
79	GP-9957	208021
80	GP-9986	208150
81	GP-10038	211233
82	GP-10047	211242
83	GP-10048	211243
84	GP-10056	211250
85	GP-10122	248020



**Plate 3.1 General view of the experimental plot at IIRR (DRR) farm,
ICRISAT Campus, Patancheru.**

3.3.1.3 Total Number of Tillers per Plant

Number of ear bearing tillers per plant was counted at the time of harvest.

3.3.1.4 Panicle Length (cm)

It was measured in centimeters at the time of plant maturity from the base of panicle (neck node) to the tip of last spikelet prior to harvesting.

3.3.1.5 Total Number of Filled Grains per Panicle

Number of filled grains was counted from five panicles in each selected plant and the mean was taken.

3.3.1.6 1000-Grain Weight (g)

One thousand well filled grains were counted at random from each genotype per replication and weighed after thorough drying to 15 per cent moisture content and was 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 required moisture content.

3.3.2 Nutritional Characters

3.3.2.1 Grain Iron Concentration and Zinc Concentrations

Grain iron and zinc concentrations were determined by X-Ray Fluorescence Spectrometry. In XRF the preselected wavelength of incident X-rays expel an electron from the innermost orbit followed by the transfer of one of the electrons from the outermost orbit to the innermost orbit leading to the release of specific wavelength of X-rays. The energy of the emitted radiation is specific for a particular atom. Therefore, it is simultaneously identified and quantified by the detector. This instrument is quite useful in non-destructive determination of relative iron and zinc concentrations in rice samples with more ease.

Ten dust free rice sample sachets were arranged in a row. Nearly 5 grams of each sample was weighed and poured into pre-identified aluminum cup which was properly

loaded with disposable inner XRF film and they were arranged in sample tray. The tray was carefully tapped along with aluminum cups by holding the ends of tray with both hands in order to spread the grain uniformly in all the aluminum cups and each cup was placed into a sample sleeve XRF machine without disturbing the grain starting from 1 to 10. X-ray lamp key was inserted into machine and turned it on. Then the name of each sample was entered using keyboard, the entries were checked once again, the suitable method was selected and start button was selected to start analysis. At the end of analysis time, iron and zinc concentration values appeared in a new window on the screen and the values were noted down and then accept button was clicked.

3.3.2.2 Grain Protein Content (%)

Protein/Nitrogen Determination by Combustion Method by using instrument protein analyzer. The basic principle was Nitrogen freed by combustion at high temperature in pure oxygen is measured by thermal conductivity detection and converted to equivalent protein by appropriate numerical factor.

Turn furnaces on (or take off standby). Turn gas regulators to desired flow rate. Wait until furnaces have stabilized at desired temperature. Enter sample number on console, other parameters as required by computer software. Enter appropriate N content of pure primary standard. Include two blanks and three dried or dessicated pure primary standards at the beginning of each run to calculate the calibration factor for determining N. Weigh samples and transfer to auto-sampler tray. Weigh a second subsample to determine laboratory dry matter and run the samples.

Calculation: Per cent Nitrogen (N)

$$\% \text{ N (DM basis)} = \% \text{ N (from analyzer output) Lab DM/100}$$

Calculation: Per cent Crude Protein (CP)

$$\text{CP (DM basis)} = \% \text{ N (DM basis)} \times \text{F}$$

$$\text{Multiplication factor (F)} = 6.25 \text{ for rice}$$

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 Distance D^2
5. Estimation of Extent of Association
6. 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, 1985). The significance was tested by referring to the values of 'F' table (Fisher and Yates, 1963).

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

Where ,

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

μ = General mean

g_i = True effect of ' i^{th} ' genotype

r_j = True effect of ' j^{th} ' replication

e_{ij} = Random error association with ' i^{th} ' genotype and ' j^{th} ' replication.

Analysis of variance:

Source	Degrees of freedom	Mean sum of squares	F-ratio
Replication	$(r-1)$	$M'r$	$M'r / M'e$
Treatment	$(t-1)$	$M't$	$M't / M'e$
Error(e)	$(r-1)(t-1)$	$M'e$	
Total	$(tr-1)$	TMSS	

Where,

r and t = Number of replications and treatments, respectively.

$M'r$, $M't$ and $M'e$ = Mean sum of squares due to replications, treatments and error respectively.

Variance

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

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

$$\text{Phenotypic variance } (\sigma_p^2) = (\sigma_g^2) + (\sigma_e^2)$$

Where, (σ_e^2) = error variance

3.4.2 Genotypic and Phenotypic Coefficients of Variance

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

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

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

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

<10% : Low

10-20% : Moderate

>20% : High

3.4.3 Heritability and Genotypic 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).

$$h^2 (bs) = \frac{\sigma_g^2}{\sigma_p^2}$$

Where

$h^2 (bs)$ = heritability in broad sense

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance (σ_g^2) + (σ_e^2)

σ_e^2 = environmental variance

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

Low : 0-30%

Medium : 30-60%

High : above 60%

3.4.3.2 Genetic Advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting 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% selection intensity

σ_p = phenotypic standard deviation

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

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

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

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)

Genetic diversity between genotypes can be better estimated using D^2 statistics given by Mahalanobis (1936).

3.4.4.1 Test of Significance

Variances were calculated for all the 9 characters studied and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1985). After testing the difference between genotypes for each of the character, a simultaneous test of significance for differences in the mean values for a number of correlated variables with regard to pooled effect of 9 characters was carried out using 'V' statistic, which in turn utilizes Wilk's Criterion. The sum of squares and sum of products of error and error + variety variance – covariance matrix were used

for this purpose. The estimation of 'V' (Wilk's criterion) was done by using the following relationship.

$$'V' = W/S$$

Where,

'V' = Wilk's criterion

W = Determinant of error matrix and

S = Determinant of error + variety matrix

The significance of 'V' was tested by V (stat):

$$\chi^2_{pq} = V(stat) = -m \log_e 'V' = \left[n - \frac{P+Q+1}{2} \right] \log_e 'V'$$

Where,

$$m = n - \frac{P+Q+1}{2}$$

P = number of characters (or) variable observations

Q = number of genotypes-1 (or) degrees of freedom for population

n = degrees of freedom for error + genotypes at base of

natural log = 2.7183

V (stat) can be approximately considered to be distributed as χ^2_{pq} and if the calculated 'V' value from the formulae exceeds $\chi^2_{pq}(K)$, the hypothesis is rejected at 'K' level of significance; otherwise not.

3.4.4.2 Transformation of Correlated Variables

Transformation was done by using pivotal condensation method. Transformation of correlated variables into standardized uncorrelated ones was done before working out the D² values because of computation of D² values was reduced to simple enumeration of differences in mean values of various characters of the two genotypes i.e., $\sum d_i^2$.

3.4.4.3 Computation of D^2 values

The D^2 value between i^{th} and j^{th} genotypes for 'p' character was calculated as:

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

Where,

$\bar{Y}_{it}$ = uncorrelated mean value of the i^{th} genotype for t character

$\bar{Y}_{jt}$ = uncorrelated mean value of the j^{th} genotype for t character

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

3.4.4.4 Testing the Significance of D^2 Values

The D^2 value obtained for a pair of genotypes was taken as the calculated value of χ^2 and tested against tabulated χ^2 at p degrees of freedom where, 'p' is the number of characters considered.

3. 4.4.5 Grouping of Genotypes into Various Clusters

Grouping of genotypes into different clusters was done by using Tocher's method. The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should have a smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all the combinations for each genotype were arranged in the increasing order of their magnitude (Singh and Chaudhary, 1985). To start with two genotypes having the smallest distance from each other was considered first to which third population having the smallest average D^2 value from the first two genotypes was considered and so on. At certain stage when it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that genotype was not considered for inclusion in that cluster. Similarly, a second cluster was formed. The process was continued till all the genotypes were included in one or the other clusters.

3.4.4.6 Intra and Inter Cluster Distance

3.4.4.6.1 Average Intra Cluster Distance

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

Where,

$\sum D_i^2$ = Sum of distance between all possible combinations and

‘ n ’ = Number of genotypes included in a cluster.

3.4.4.6.2 Average Inter Cluster Distance

Clusters were taken one by one and their distances from other clusters were calculated. The distance between the two clusters as the sum of D^2 value between the number one cluster to each of the members 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 ‘ D ’ 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.

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

Where n_1 and n_2 are number of genotypes of two clusters

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

3.4.4.7 Cluster Diagram

The clusters and their mutual relationship were presented diagrammatically by using D^2 values.

3.4.4.8 Contribution of Individual Characters towards Divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = y_{it} - y_{jt}$). Rank I was given to the highest mean difference and rank 'p' to the lowest difference; p is the total number of characters considered. Percentage contribution of each character (X) towards genetic divergence was calculated using the following formula:

$$\text{Percent contribution of character (X)} = \frac{N \times 100}{M}$$

Where,

X = Per cent contribution of character

N = Number of genotype combinations where the characters ranked first.

M = All possible combinations of genotypes considered.

3.4.5 Estimation of Character Association

Correlation coefficients were calculated to determine the degree of association of yield and also among themselves.

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

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

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 levels were estimated by taking seed yield as dependant variable, using path coefficient analysis as 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.

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

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

$$\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot$$

$$: \quad : \quad : \quad : \quad :$$

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

Where;

1, 2 n = Independent variables

y = Dependant variable

$r_{1y}, r_{2y}, \dots, r_{ny}$ = Coefficient of correlation between casual factors '1' to 'n' on dependent character 1

$P_{1y}, P_{2y}, \dots, P_{ny} =$ Direct effect of character '1' to 'n' on character

The above equations can be written in matrix form as:

$$\begin{matrix} A & C & B \\ \begin{pmatrix} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ \cdot \\ r_{ny} \end{pmatrix} & \begin{pmatrix} 1 & r_{12} & r_{13} & \cdot & \cdot & r_{1n} \\ r_{21} & 1 & r_{23} & \cdot & \cdot & r_{2n} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ r_{n1} & r_{n2} & r_{n3} & \cdot & \cdot & 1 \end{pmatrix} & \begin{pmatrix} P_{1y} \\ P_{2y} \\ \cdot \\ \cdot \\ \cdot \\ P_{ny} \end{pmatrix} \end{matrix}$$

Then $B = (C)^{-1} A$ where

$$C^{-1} = \begin{pmatrix} c_{11} & c_{12} & c_{13} & \cdot & \cdot & c_{1n} \\ c_{21} & c_{22} & c_{23} & \cdot & \cdot & c_{2n} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ c_{n1} & c_{n2} & c_{n3} & \cdot & \cdot & c_{nn} \end{pmatrix}$$

Direct effects were as follows:

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

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

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

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

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

Where,

p_{ny} = Direct effect of x_n on Y

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

Chapter IV

Results and Discussion

Chapter IV

RESULTS AND DISCUSSION

The present investigation is intended to evaluate eighty five landraces of rice using nutritional and quantitative traits in order to reveal the amount of variability and genetic diversity present in the experimental material and also to work out the correlation between yield, its contributing characters and grain quality parameters. The experimental findings obtained from the present study are furnished under the following heads and the available information on various aspects of the investigation has discussed subsequently.

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

4.1 ANALYSIS OF VARIANCE

The numerical data collected on seven quantitative characters and three grain nutritional characters were statistically analysed and the analysis of variance Table 4.1 showed significant differences among the landraces of rice under study for all the eleven traits viz., Days to 50 per cent flowering, plant height (cm), Number of tillers per hill, Panicle length (cm), Number of filled grains per panicle (g), Grain yield per plant (g), 1000-grain weight(g), Grain Iron concentration, Grain Zinc concentration and Protein percentage, indicating the presence of considerable genetic variability among the experimental material under study.

Analysis of variance showed significant differences for all the characters studied in the present investigation. The results of analysis of variance are presented in Table 4.1.

4.2 MEAN PERFORMANCE

The mean performance of eighty five landraces of rice is presented in Table 4.2 and genotypic and phenotypic coefficient of variation, heritability, genetic advance as per cent of mean were calculated for yield and its contributing traits and grain quality parameters. The details of the results obtained in this regard are furnished below

Table 4.1: ANOVA for yield and yield contributing characters in different landraces of Rice

S. No.	Character	Mean sum of squares		
		Replications (d.f.=1)	Treatments (d.f.=84)	Error (d.f.=84)
1	Days to 50 per cent flowering	93.388**	555.59**	1.019
2	Plant height (cm)	10.876*	669.30**	1.617
3	Panicle length (cm)	28.087**	12.10**	0.876
4	Number of tillers/ plant	15.24**	14.24**	1.027
5	Number of grains per panicle	4.288	4733.79**	3.407
6	1000 grain weight (g)	3.551**	35.69**	0.487
7	Grain yield per plant (g)	0.447	205.17**	3.373
8	Grain iron concentration (mg/kg)	0.004	5.60**	0.03
9	Grain zinc concentration (mg/kg)	0.124*	20.43**	0.021
10	Grain Protein Content (per cent)	1.022**	2.11**	0.013
** Significant at 1% level * Significant at 5% level				

4.2.1 Quantitative Characters

4.2.1.1 Days to 50 per cent Flowering

The number of days to 50 per cent flowering ranged from 54 days to 107 days with a general mean of 79.82 days. Among all the genotype GP-9244 was earliest (54.50 days) while (GP-9212) was found to be late (107.00 days).

4.2.1.2 Plant Height (cm)

Plant height ranged from 73.00 cm to 142.10 cm with a general mean of 112.70 cm. The shortest genotype (GP 9859) had 73.00cm while the tallest genotype (GP 9200) had 142.10 cm.

4.2.1.3 Panicle Length (cm)

The panicle length ranged from 16.10 to 27.40 cm with a general mean of 22.25 cm. The genotype GP 9867 had shorter panicle value (16.10 cm) and the genotype GP 10047 exhibited highest value (27.40 cm).

4.2.1.4 Number of Tillers per plant

The mean productive tillers per plant ranged from 5.25 tillers (GP 9867) to 15.66 tillers (GP 9043) with a general mean of 10.90 tillers per plant.

4.2.1.5 Number of Filled Grains per Panicle

The mean values for number of filled grains per panicle ranged from 47.50 (GP 10048) to 241.00 (GP 9210) with general mean of 113.90.

4.2.1.6 1000-grain Weight (g)

The mean of 1000-grain weight was 22.97g and the mean values ranged from 10.30 g (GP 9928) to 34.54 g. Among the genotypes GP 9064(34.54g) recorded the highest grain weight and GP 9928 (10.30g) recorded the lowest grain weight.

4.2.1.7 Grain Yield per Plant (g)

The mean for grain yield per plant was 22.44g and the mean value ranged from 2.90g (GP 9865) to 49.25g (GP 9623). The genotype GP 9865 recorded lowest grain yield were the genotype GP 9623 exhibited highest grain weight.

4.2.2 GRAIN QUALITY CHARACTERS

4.2.2.1 Grain Iron Concentration

The mean for grain iron concentration was 9.55 mg and the mean value ranged from 6.95 mg (GP 9043, GP 9867) to 13.25 mg (GP 9064).

Table 4.2: Mean performance of 85 landraces of rice for yield and yield contributing characters.

S.No	Accession No.	Days to 50 per cent flowering	Plant height (cm)	Panicle length (cm)	No.tillers /plant	Number of filled grains per panicle	1000 grain weight (g)	Grain yield per plant (g)	Grain iron concentr tion (mg/kg)	Grain zinc concentra tion (mg/kg)	Grain Protein Content %
1	GP-9006	61.50	129.70	24.00	11.85	73.55	27.44	13.96	10.05	18.15	7.16
2	GP-9007	62.50	120.90	21.33	11.60	101.00	26.43	29.65	7.95	16.55	8.55
3	GP-9019	62.50	115.33	23.90	14.15	135.00	23.45	35.06	9.60	16.32	7.81
4	GP-9022	61.50	114.10	21.89	13.30	99.00	25.76	30.50	11.25	16.10	8.59
5	GP-9024	61.50	103.55	21.33	12.33	52.00	23.98	19.88	9.95	17.60	7.48
6	GP-9025	61.50	138.55	25.55	14.15	122.55	23.82	26.44	8.20	19.10	7.14
7	GP-9028	93.00	141.77	26.10	11.10	141.23	26.00	30.71	7.50	19.25	6.10
8	GP-9036	81.00	92.10	21.30	12.88	198.55	22.75	17.83	8.55	18.55	7.11
9	GP-9043	91.00	128.83	23.89	15.65	122.55	28.32	30.71	6.95	18.70	6.59
10	GP-9047	86.50	113.33	22.00	12.00	85.50	25.57	17.8	11.2	18.55	6.45
11	GP-9048	84.50	123.20	24.00	12.90	91.00	22.86	8.995	8.35	15.35	6.39
12	GP-9051	88.00	83.33	19.33	9.65	88.55	24.78	20.76	8.33	17.95	9.12
13	GP-9053	81.00	89.12	21.15	13.68	103.00	26.75	29.13	8.12	15.25	8.08
14	GP-9055	80.00	121.60	23.95	15.55	83.54	22.80	9.78	8.33	19.05	8.42
15	GP-9064	79.00	119.11	23.60	11.25	110.00	34.54	44.97	13.25	24.25	8.39
16	GP-9070	91.00	139.80	24.10	10.85	217.00	19.05	25.93	8.30	21.65	7.53
17	GP-9111	83.00	131.80	24.90	9.55	169.00	28.05	26.03	9.90	20.25	6.80
18	GP-9119	95.00	129.33	23.55	10.75	117.50	26.95	31.39	8.30	18.75	6.75
19	GP-9152	76.50	121.55	21.30	13.55	61.54	29.05	35.83	12.85	18.85	8.78

Table 4.2 (contd...).

S.No	Accession No.	Days to 50 per cent flowering	Plant height (cm)	Panicle length (cm)	No.tillers /plant	Number of filled grains per panicle	1000 grain weight (g)	Grain yield per plant (g)	Grain iron concentr ation (mg/kg)	Grain zinc concentra tion (mg/kg)	Grain Protein Content %
20	GP-9153	76.00	105.00	20.50	11.35	67.34	26.45	20.03	11.60	21.75	7.39
21	GP-9157	95.00	129.80	24.30	10.90	119.89	22.25	31.51	9.45	21.30	7.38
22	GP-9166	76.50	123.40	20.80	13.10	81.66	21.90	10.92	11.33	18.15	7.81
23	GP-9187	106.50	123.87	23.50	11.70	159.98	23.73	40.63	10.05	18.10	7.28
24	GP-9192	103.50	132.10	23.80	11.70	141.50	24.26	39.94	7.45	17.10	7.18
25	GP-9195	91.50	130.90	24.30	11.90	151.0	24.05	30.66	7.15	12.95	6.39
26	GP-9200	89.00	142.10	26.00	10.88	154.50	23.36	33.35	8.95	14.95	7.14
27	GP-9195	86.00	127.40	24.20	11.68	119.66	26.25	39.89	10.55	19.65	7.32
28	GP-9202	86.50	125.33	23.30	12.50	185.56	22.19	26.03	10.75	15.45	6.59
29	GP-9207	84.50	131.30	26.10	11.80	219.60	27.05	30.50	8.55	14.45	6.67
30	GP-9210	87.00	129.20	22.80	11.55	241.00	27.05	36.22	7.05	11.65	5.9
31	GP-9212	107.00	136.20	22.00	11.33	129.34	24.00	32.12	7.55	13.35	5.69
32	GP-9223	106.00	130.20	25.45	13.90	50.23	22.90	4.995	9.10	26.75	8.04
33	GP-9244	54.00	140.10	26.55	12.75	211.23	23.61	19.32	11.55	19.05	9.40
34	GP-9255	55.00	137.33	26.69	13.40	101.00	23.00	25.68	7.75	16.35	6.98
35	GP-9390	86.50	121.20	19.74	17.40	179.23	23.95	29.51	12.55	18.30	9.10
36	GP-9555	59.00	139.98	25.90	14.90	106.55	26.25	29.56	10.50	25.20	8.50
37	GP-9623	81.00	133.58	23.18	15.50	109.50	33.45	49.25	7.95	17.55	7.39
38	GP-9634	101.00	115.78	21.98	12.70	201.00	19.60	16.85	11.95	25.35	9.90

Table 4.2 (contd...).

S.No	Accession No.	Days to 50 per cent flowering	Plant height (cm)	Panicle length (cm)	No.tillers /plant	Number of filled grains per panicle	1000 grain weight (g)	Grain yield per plant (g)	Grain iron concentr tion (mg/kg)	Grain zinc concentra tion (mg/kg)	Grain Protein Content %
39	GP-9703	57.50	129.60	19.70	11.20	99.00	28.25	25.79	10.25	21.75	9.60
40	GP-9725	58.50	129.33	25.80	11.70	114.00	25.20	17.91	12.90	19.65	8.54
41	GP-9729	89.00	125.30	23.60	12.43	95.00	25.00	29.57	10.70	19.15	8.45
42	GP-9788	89.00	124.20	22.55	14.44	79.00	23.94	29.34	9.30	20.25	8.56
43	GP-9790	89.00	123.50	22.60	15.25	162.00	17.80	20.89	9.10	17.05	7.65
44	GP-9797	58.50	127.00	21.90	11.90	111.00	24.20	27.06	9.55	16.55	7.80
45	GP-9801	91.50	119.70	21.60	11.80	149.00	23.32	19.96	10.10	16.55	7.85
46	GP-9807	89.00	110.40	21.10	10.45	113.23	25.25	25.3	10.45	13.85	6.74
47	GP-9811	89.50	123.90	22.30	13.35	131.66	24.20	25.74	9.35	14.45	6.07
48	GP-9812	85.50	127.40	25.20	10.25	159.45	21.82	27.88	9.55	14.40	6.28
49	GP-9814	89.00	116.50	22.10	11.80	59.90	26.90	33.90	10.25	15.15	6.70
50	GP-9817	55.00	91.60	17.75	10.90	49.54	26.17	32.89	12.25	20.55	7.46
51	GP-9820	54.50	105.33	20.68	11.30	100.00	25.00	16.63	7.70	14.95	5.69
52	GP-9825	91.50	126.40	24.45	10.90	126.50	23.05	27.85	8.05	14.75	7.08
53	GP-9835	55.00	87.25	20.05	7.30	57.00	21.57	8.52	12.95	19.85	8.66
54	GP-9846	95.50	109.60	21.90	8.10	261.00	19.05	19.45	13.05	16.55	7.75
55	GP-9847	56.50	99.70	23.20	10.40	100.50	22.50	20.07	8.70	20.10	6.99
56	GP-9848	96.00	123.45	21.50	10.50	159.23	11.55	9.07	9.10	13.95	6.90
57	GP-9850	97.00	113.30	23.30	11.90	91.45	25.90	22.25	9.00	18.85	6.25

Table 4.2 (contd...).

S.No	Accession No.	Days to 50 per cent flowering	Plant height (cm)	Panicle length (cm)	No.tillers /plant	Number of filled grains per panicle	1000 grain weight (g)	Grain yield per plant (g)	Grain iron concentr tion (mg/kg)	Grain zinc concentra tion (mg/kg)	Grain Protein Content %
58	GP-9855	55.50	105.50	22.00	11.65	131.00	27.65	32.97	9.45	13.45	6.48
59	GP-9856	56.00	99.30	20.20	6.85	82.00	22.05	21.70	9.10	13.65	6.06
60	GP-9859	54.50	73.00	17.20	13.33	59.45	19.63	8.91	9.55	14.55	6.34
61	GP-9861	57.50	81.70	19.65	7.55	79.50	16.95	5.06	11.05	18.60	7.81
62	GP-9863	90.50	87.40	18.80	6.40	55.00	18.62	8.33	12.95	18.45	8.58
63	GP-9865	56.50	91.50	17.70	10.55	19.00	11.90	2.90	11.15	20.30	8.70
64	GP-9867	55.50	78.00	16.10	5.25	61.00	14.10	6.255	6.95	15.50	7.26
65	GP-9868	89.00	91.10	19.70	6.45	139.00	19.35	31.31	7.65	14.70	6.58
67	GP-9901	91.50	103.20	22.25	6.75	95.00	22.55	17.45	10.15	16.35	7.48
68	GP-9913	93.50	103.50	25.30	8.54	98.00	19.10	15.08	7.25	15.75	6.94
69	GP-9916	101.00	110.20	22.20	6.95	94.00	26.95	19.49	10.55	17.30	7.34
70	GP-9917	89.00	89.90	19.75	5.84	101.00	18.45	10.32	7.65	14.50	6.65
71	GP-9920	87.00	102.00	20.40	7.45	94.33	20.75	23.99	8.35	13.45	7.01
72	GP-9926	89.50	97.60	19.30	7.45	101.23	23.44	26.59	7.10	13.85	5.66
73	GP-9927	86.50	83.40	19.60	6.85	61.93	25.60	28.44	9.25	17.40	6.99
74	GP-9928	99.50	100.40	20.10	5.80	97.23	10.30	10.19	11.10	19.95	7.85
75	GP-9929	100.50	95.70	20.40	7.50	92.00	19.30	8.40	10.00	14.75	6.9
76	GP-9932	89.00	97.50	19.60	10.33	101.45	20.55	13.08	9.60	11.85	7.58
77	GP-9933	88.00	109.55	20.90	6.55	178.50	21.95	12.00	10.15	17.45	7.25

Table 4.2 (contd...).

S.No	ACCESSION NO	Days to 50 per cent flowering	Plant height (cm)	Panicle length (cm)	No.tillers /plant	Number of filled grains per panicle	1000 grain weight (g)	Grain yield per plant (g)	Grain iron concentration (mg/kg)	Grain zinc concentration (mg/kg)	Grain Protein Content %
78	GP-9937	99.50	80.00	17.85	8.23	69.55	18.05	9.85	8.15	15.15	6.70
79	GP-9949	56.00	90.10	19.55	8.15	159.00	19.99	7.30	8.60	14.30	6.64
80	GP-9957	99.50	100.90	20.85	9.20	169.00	17.47	22.15	7.60	17.30	5.67
81	GP-9986	87.00	88.20	25.65	10.55	82.00	19.33	15.85	11.05	24.40	8.16
82	GP-10038	88.00	113.12	25.5	11.10	95.00	22.35	19.29	8.55	19.35	5.65
83	GP-10047	57.00	119.30	27.40	9.90	71.00	23.90	16.08	8.25	23.20	7.02
84	GP-10048	62.50	79.40	23.20	11.20	47.50	13.70	14.90	12.10	22.45	9.16
85	GP-10056	63.00	89.60	23.20	13.50	122.00	20.70	19.27	8.30	22.20	6.22
	Mean	79.82	112.70	22.25	10.90	113.90	22.97	22.44	9.55	17.70	7.37
	C.V.	1.26	1.12	4.20	9.29	1.62	3.03	8.181	1.82	0.81	1.54
	F ratio	545.13	414.20	13.82	13.87	1389.32	73.24	60.83	184.74	989.08	163.01
	S.E.	0.71	0.89	0.66	0.71	1.30	0.49	1.29	0.12	0.10	0.08
	C.D. 5%	2.00	2.52	1.86	2.01	3.67	1.38	3.65	0.34	0.28	0.22
	C.D. 1%	2.66	3.35	2.46	2.67	4.86	1.84	4.84	0.45	0.37	0.30

4.2.2.2 Grain Zinc Concentration

The mean for zinc concentration was 17.70 mg per kg and the mean value ranged from 11.65 mg (GP 9210) to 26.75 mg (GP 9223).

4.2.2.3 Grain Protein Content (Per cent)

The mean for grain protein content was 7.37% and the mean value ranged from 5.65% (GP 10038) to 9.90% (GP 9634).

4.3 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The presence of adequate genetic variability and critical analysis of genetic variability are needed for initiating any crop improvement programme and for adopting of appropriate selection techniques. Greater variability in the initial breeding material ensures better chances of producing a desired form of a crop plant.

The genotypic coefficient of variation indicates the range of heritable variation present in the genotypes, while the phenotypic coefficient of variation measures the role of environment on the genotypes, 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. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement programmes.

It is very difficult to judge whether observed variability is heritable or not. Heritable estimates provide authentic information about a particular genetic attribute which will be transmitted to the successive generations.

Again the heritable portion of the total variation might not be always due to additive gene action. Thus estimates of heritability alone will not give clear indication of the associating genetic progress that would result from selecting the best plants. Thus a character possessing high heritability along with high genetic advance will be valuable in the selection programme.

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for 85 genotypes. Results are furnished in Table 4.3 and Fig 4.1 for PCV, GCV and heritability, genetic advance, genetic advance as per cent of mean respectively. The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values.

4.3.1 QUANTITATIVE CHARACTERS

4.3.1.1 Days to 50 per cent Flowering

The genotypic and phenotypic coefficients of variation were moderate i.e., 20.89 and 20.86, respectively. The observed heritability estimate for this trait was higher (99.61) along with high genetic advance as per cent of mean (42.89). The result is conformity with Aditya and Anuradha (2013) for high heritability and Seyoum, *et al.* (2012) for genetic advance as per cent of mean.

4.3.1.2 Plant Height (cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were moderate i.e., 16.25 and 16.21, respectively. The observed heritability estimates for this character was high (99.50) with high genetic advance as per cent of mean (33.32). The similar result reported by Karad and Pol (2008) for high genetic advance as per cent of mean **and** Umadevi *et al.* (2009), Aditya and Anuradha (2013) for high heritability coupled with high genetic advance as per cent of mean for plant height.

4.3.1.3 Panicle Length (cm)

The genotypic and phenotypic coefficients of variation for this trait were low i.e., 11.45 and 10.65 respectively. The observed heritability estimate was low (86.56) and with high genetic advance as per cent of mean (20.40). Similar result was reported by Singh *et al.* (2013) and Shiva Prasad *et al.* (2013) for maximum GCV and PCV.

4.3.1.4 Number of Tillers per Plant

The GCV and PCV for this trait were moderate i.e., 25.33 and 23.57, respectively. The heritability observed for this trait was low (86.61). This character recorded high genetic advance as per cent of mean (45.17). Similar results were observed by Ravindra Babu *et al.* (2011) and Akinwale *et al.* (2011) for high heritability and Tiwari *et al.* (2011) and Bornare *et al.* (2014) for moderate genetic advance per cent of mean.

4.3.1.5 Number of Filled Grains per Panicle

A high GCV (42.72) and PCV (42.69) were observed for this trait. The heritability estimate for this trait was very high (99.95) with high genetic advance as per cent of mean (87.89). Similar result was observed by Pankaj *et al.* (2010) and Seyoum *et al.* (2012) for high GCV and PCV, Pankaj *et al.* (2010) for high heritability and whereas Umadevi *et al.* (2009) for high genetic advance per cent of mean.

4.3.1.6 1000-Grain Weight (g)

Moderate genotypic (18.51) and phenotypic (18.26) coefficients of variation were recorded for this trait with high heritability estimate of 97.31 and the genetic advance as per cent of mean was high (37.10). Similar result were found by Tiwari *et al.* (2011) for moderate GCV and PCV and Pankaj *et al.* (2010) for high heritability coupled with high genetic advance per cent of mean.

4.3.1.7 Grain Yield per Plant (g)

A high genotypic coefficient of variation (45.49) and phenotypic coefficient of variation (44.75) were observed for this trait. A high heritability estimate (96.84) coupled with high genetic advance as per cent of mean (90.68). The results are conformity with Pankaj *et al.* (2010) and Seyoum *et al.* (2012) for high GCV and PCV and Pankaj *et al.* (2010) for heritability coupled with high genetic advance as per cent of mean.

4.3.2 Grain Quality Characters

4.3.2.1 Grain Iron Concentration

A moderate genotypic coefficient of variation (17.56) and phenotypic coefficient of variation (17.47) were observed for this trait. A high heritability estimate (98.90) coupled with high genetic advance as per cent of mean (35.79). The results are in conformity with Gangashetty *et al.* (2013) for high heritability and high genetic advance as per cent of mean.

4.3.2.2 Grain Zinc Concentrations

A moderate genotypic coefficient of variation (18.06) and phenotypic coefficient of variation (18.05) were observed for this trait. A high heritability estimate (99.80) coupled with high genetic advance as per cent of mean (37.14). The results are in conformity with Gangashetty *et al.* (2013) for high heritability and high genetic advance as per cent of mean. Naveen *et al.* (2013) for high GCV and PCV.

4.3.2.3 Grain Protein Content

A low genotypic coefficient of variation (13.99) and phenotypic coefficient of variation (13.90) were observed for this trait. A high heritability estimate (98.80) with moderate genetic advance as per cent of mean (28.46). The results are in conformity with Samak *et al.* (2011) for heritability, moderate genetic advance, Basavaraja *et al.* (2013) for high heritability and genetic advance.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are

important selection parameters. Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.* 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for days to 50% flowering, plant height, No of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight, grain yield per plant, grain iron concentration, grain zinc concentration, grain protein content indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits. The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character.

High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection. All quality characters also exhibited high degree of broad-sense heritability, which revealed that these characters are less influenced by environment and there could be greater correspondence between phenotypic and breeding values.

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

4.4 GENETIC DIVERSITY

Genetic improvement of any crop mainly depends upon the amount of genetic variability present in the population. In order to generate variability, hybridization between genotypes of diverse origin is suggested to unlock new recombinations. Genetic divergence has been used as an indirect parameter of moderate effectiveness in selecting parents to produce high yielding progenies.

Table 4.3: Estimates of variability, heritability and genetic advance in 85 landraces of rice

S.No	Characters	Phenotypic Variance	Genotypic Variance	PCV(%)	GCV(%)	Heritability in broad sense(h ₂)(%)	GA	G.A as per cent of Mean(at 5%)
1	Days to 50% Flowering	278.30	277.28	20.89	20.86	99.61	34.24	42.89
2	Plant Height (cm)	335.45	333.84	16.25	16.21	99.50	37.54	33.32
3	Panicle Length(cm)	6.49	5.61	11.45	10.65	86.56	4.54	20.40
4	No. of tillers/ plant	7.63	6.60	25.33	23.57	86.61	4.92	45.17
5	Number of grains/ panicle	2368.60	2365.19	42.72	42.69	99.95	100.11	87.89
6	1000 grain weight(g)	18.09	17.60	18.51	18.26	97.31	8.52	37.10
7	Grain yield/ plant (g)	104.27	100.90	45.49	44.75	96.84	20.35	90.68
8	Grain iron concentration (mg/kg)	2.81	2.78	17.56	17.47	98.90	3.41	35.79
9	Grain zinc concentration (mg/kg)	10.22	10.20	18.06	18.05	99.80	6.57	37.14
10	Grain Protein Content(per cent)	1.067	1.05	13.99	13.90	98.80	2.10	28.46

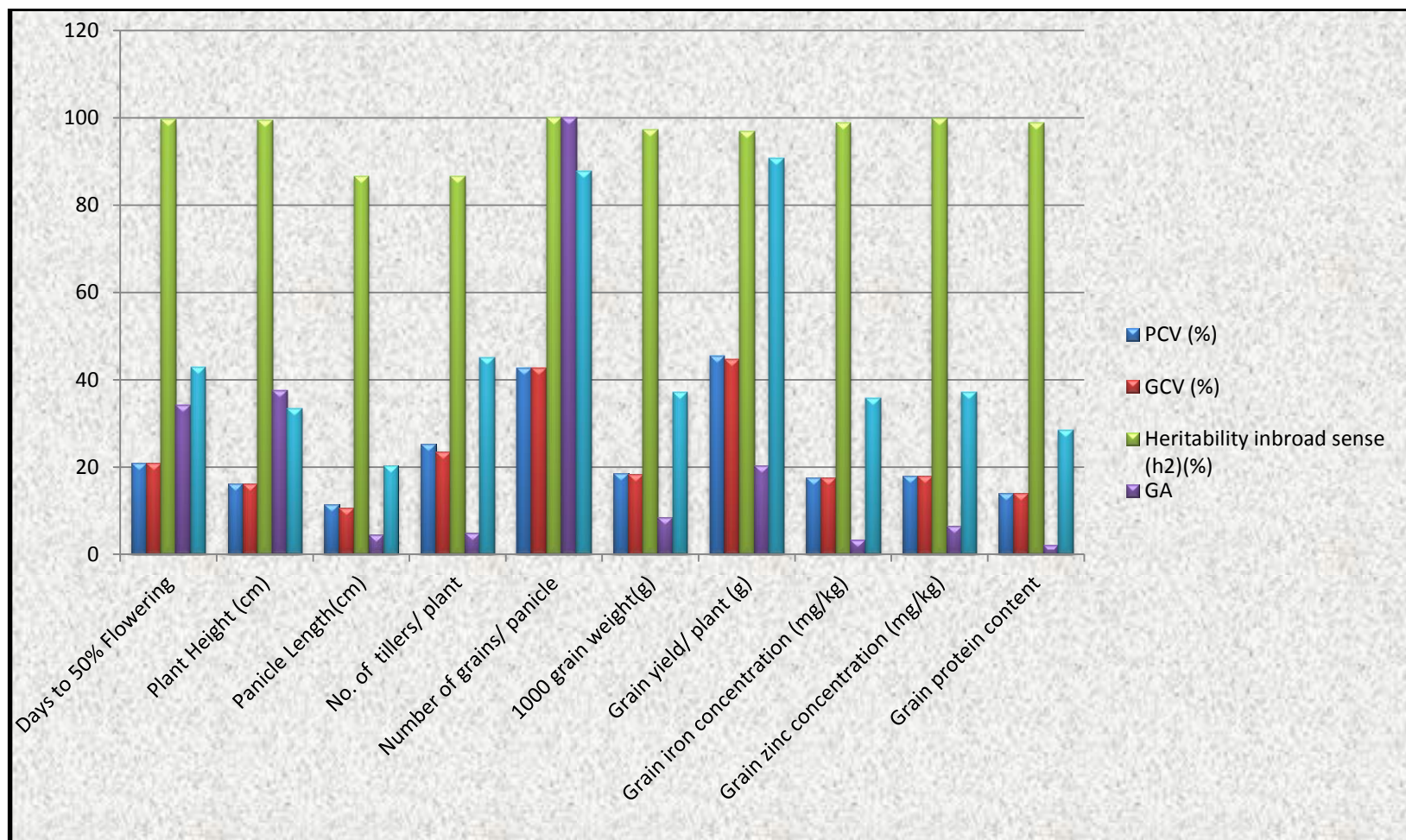


Figure 4.1: Graphical representation of phenotypic and Genotypic coefficients of variation, Heritability (broad sense), Genetic advance, Genetic advance as per mean (5%) for various characters in landraces of rice.

Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology and plant breeding. Information on genetic diversity within and among closely related crop germplasm is essential for rational use of genetic resources. Parents selected on the basis of such study would help in obtaining higher amount of heterotic expression in F_{1s} and broad spectrum of variability in subsequent segregating generations for various quantitative characters and to study the genetic diversity among them so as to utilize them in the hybridization programme for the development of new lines with improved grain yield, quality and tolerance to stress conditions. The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for 85 rice genotypes and the results obtained from the study are presented below.

4.4.1 Wilk's 'V' Criterion Test

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by % at 840 degrees of freedom. The 'V' statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of 85 land races of rice in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.4.2 Mahalanobis's Generalized Distance D^2 Values

In order to assess the genetic diversity among 85 landraces of rice, D^2 statistic was used following the procedure given by Rao (1952). Since the entire 10 yield component characters were correlated, they were transformed into uncorrelated linear combination through pivotal condensation method.

4.4.3 Grouping of Genotypes into Various Clusters

All landraces of rice under study were distributed into six clusters based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belonging to different clusters. The distribution of genotypes into various clusters is presented in Table 4.4 and Figure 4.2. Out of six clusters, cluster I was the largest comprising of forty three landraces, followed by cluster IV with sixteen, cluster III with fourteen, cluster II with ten and cluster V and cluster VI were monogenotypic clusters, suggesting the existence of high degree of heterogeneity among the genotypes.

Clustering pattern showed that the landraces originating from similar geographical regions were classified into different clusters, indicating that geographical diversity and genetic diversity were not related due to differences in adaption, selection criteria, selection pressure and environmental conditions.

4.4.4 Average Inter and Intra Cluster Distances

D² analysis is considered as the most effective method to measure the forces of differentiation at two levels namely, intra cluster and inter cluster levels.

The average intra and inter cluster D² values are presented in Table 4.5 and statistical distance among 85 genotypes. Intra cluster D² values ranged from zero (cluster V, VI) to 39.77 (cluster IV). Maximum intra cluster distance was observed in cluster IV (39.77), followed by cluster III (38.98), cluster II (35.36), cluster and cluster I (32.93), indicating that some genetic divergence still existed among the genotypes. Selection within such clusters might be executed based on maximum mean value for the desirable characters. This could be made use of in the yield improvement through recombination breeding.

From the inter cluster D² values of the six clusters, the inter cluster distance was higher than intra cluster distance indicating the presence of wide genetic diversity among the landraces under study. It can be seen that the highest divergence occurred between cluster II and VI (100.30) followed by cluster IV and VI (78.61), cluster I and VI (77.77), cluster III and IV (77.45), cluster II and V (73.74), cluster III and VI (68.76), cluster IV and V (68.55) suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination in order to get high heterotic recombinants. While the lowest was noticed between cluster I and II (43.83), followed by cluster I and III (50.79), cluster III and V (52.33), cluster II and IV (54.34), cluster V and VI (59.93) cluster I and II (59.10).

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. But for a plant breeder, the objective is not only high heterosis but other quality characters also. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that hybridization between the genotypes of cluster II and cluster VI, cluster IV and cluster VI, cluster I with cluster VI, cluster III and IV would produce encouraging results. The genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

Table 4.4: Clustering pattern among 85 landraces of rice (Tocher's method)

Cluster No	Number of land races	Name of the land races
I	43	GP-9043, GP-9119,GP-9034, GP-9192, GP-9200, GP-9157, GP-9623, GP-9850, GP-10047,GP-9729 ,GP-9917, GP-9047 ,GP-9913, GP-9055, GP-9788, GP-9166, GP-9007, GP-9025, GP-9048 ,GP-9019, GP-9797, GP-9825, GP-9916, GP-9801, GP-9022, GP-9053, GP-9807, GP-9811, GP-9814, GP-9932, GP-9926, GP-9920, GP-9051, GP-9929, GP-9790, GP-9868, GP-9200, GP-9255, GP-9006 ,GP-9928, GP-9847, GP-9927, GP-9812
II	10	GP-9820, GP-9856, GP-9855, GP-9957, GP-9859, GP-9867, GP-9024, GP-9861, GP-9949, GP-9933
III	14	GP-9195, GP-9255, GP-9848, GP-9202, GP-9986,GP-9937,GP-9207, GP-9202, GP-9036, GP-9111,GP-9390 GP-9070, GP-9210, GP-9846
IV	16	GP-9817, GP-9835, GP-9865, GP-10056, GP-9901 GP-9153,GP-9152, GP-9863, GP-10122, GP-9703, GP-10038, GP-9725, GP-9064 ,GP-9555, GP-9223
V	1	GP-9244
VI	1	GP-9634

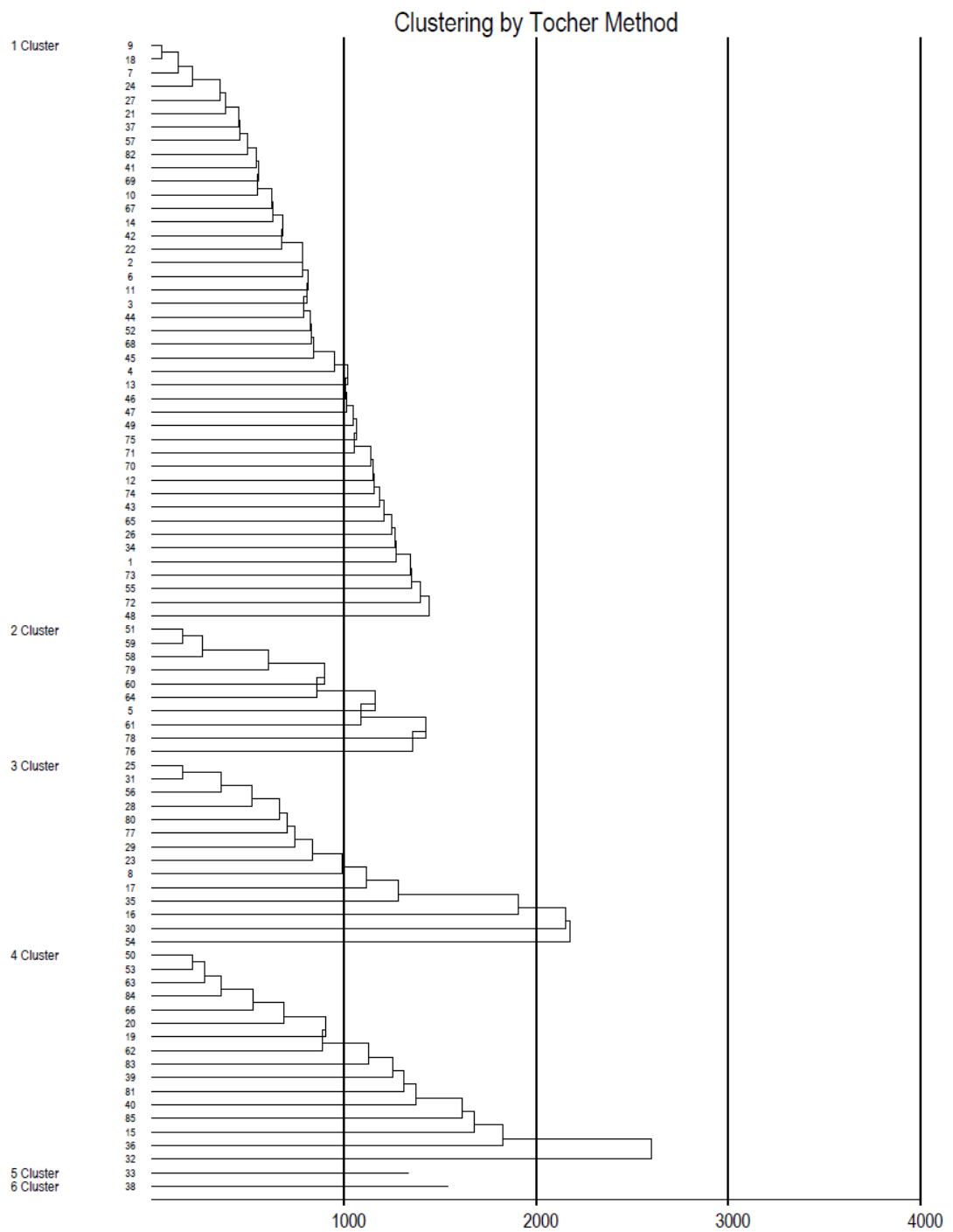


Figure 4.2: Clustering pattern by Tocher's Method

Table 4.5: Intra (diagonal) and inter-cluster average of D^2 values of 85 landraces of rice

CLUSTER	I	II	III	IV	V	VI
I	32.93	43.83	50.79	52.33	60.34	77.77
II		35.36	66.44	59.10	73.74	100.30
III			38.98	77.45	54.34	68.76
IV				39.77	68.55	78.61
V					0.00	59.93
VI						0.00

4.4.5 Cluster Means of the Characters

The cluster means for each of the ten characters are presented in Table 4.6. From the data it can be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for days to 50 per cent flowering was highest in cluster VI (101.00) and the lowest in cluster V (41.00). Plant height was highest in cluster V (140.10 cm) and lowest in cluster II (91.39cm). Cluster V recorded the highest panicle length (26.50) and the lowest number in cluster II (19.34). Cluster V and cluster VI recorded the highest number of tillers per plant (12.70cm) and the lowest was recorded in cluster II (9.46 cm). The number of grains per panicle was highest in cluster V (211.00) and the lowest in cluster IV (70.56). Highest 1000 grain weight was recorded in cluster I (23.63 g) and the lowest in cluster VI (19.60g). Cluster III recorded the highest grain yield per plant (25.58 g) while in cluster II it was low (14.17 g). Cluster II recorded low Grain iron concentration (9.00) whereas it was high in cluster VI (11.95). High grain zinc concentration was recorded in cluster VI (25.35) while it was low in cluster II (6.81). cluster VI recorded high grain protein content (9.90) where it was lowest in cluster II (6.81). The result indicated that selection of landraces having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

The cluster V is having highest mean value for panicle length, number of tillers per plant, 1000 grain weight and plant height. Cluster III for grain yield per plant is higher and cluster VI is higher for grain iron concentration and protein percentage from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

4.4.6 Relative Contribution of Characters towards Genetic Divergence

The number of times that each of the 10 characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.7. The results showed that the contribution of No. of grains per panicle was highest towards genetic divergence (42.91%) by taking 1532 times ranking first, followed by grain zinc concentration (24.71%) by 882 times, Days to 50% flowering (13.00%) by 464 times,

Table 4.6: Cluster means for 10 characters in 85 landraces of rice (cluster analysis).

Cluster No	Days to 50% flowering	Plant height(cm)	Panicle Length (cm)	No. of tillers/plant	Number of grains/panicle	1000 grain weight(g)	Grain yield/plant (g)	Grain iron concentration(mg/kg)	Grain zinc concentration (mg/kg)	Grain Protein Content %
Cluster I	84.29	116.31	22.73	11.15	107.71	23.63	24.79	9.05	17.03	7.21
Cluster II	63.95	91.39	19.34	9.46	89.35	20.77	14.17	9.55	14.96	6.81
Cluster III	91.68	121.79	22.65	11.11	186.82	22.27	25.58	9.35	16.41	6.90
Cluster IV	68.47	106.32	22.21	10.88	70.56	23.45	19.14	11.28	21.78	8.33
Cluster V	41.00	140.15	26.50	12.75	211.00	23.62	19.33	11.55	19.05	9.41
Cluster VI	101.00	115.70	21.95	12.75	201.00	19.65	16.86	11.95	25.35	9.90

grain protein content (8.99%) by 321 times, plant height (7.62%) by 272 times, grain iron concentration (2.04%) by 73 times, 1000 grain weight (0.53%) by 19 times, grain--yield per plant (0.20%) by 7 times, number of tillers per plant and panicle length each by zero times, respectively to the genetic divergence in decreasing order. Similar results were in conformity with Ramya and Kumar (2008) for number of filled grains per panicle, number of productive tillers per plant and grain yield per plant; Banumathy *et al.* (2010) for grain yield, days to 50 per cent flowering, total grains per panicle and plant height; Padmaja *et al.* (2010) reported major contribution to diversity through total number of grains/panicle; Mohanty *et al.* (2010) for number of grains per panicle and days to 50 per cent flowering, Sandhya *et al.* (2014b) also reported characters like number of spikelets per panicle, biological yield per plant, test weight, harvest index and days to 50 per cent flowering contributed maximum towards genetic diversity.

Out of ten characters studied, five characters namely total number of filled grains per panicle, grain zinc concentration, days to fifty per cent flowering, plant height and protein content contributed 97.23 per cent towards total divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations. Using this particular set of landraces, so far not utilized in breeding programmes, which have potential for use in future rice improvement programmes aiming at the development of rice varieties or hybrid with high yield and better grain quality.

4.5 CHARACTER ASSOCIATION

The primary importance of character association studies is to know the suitability of various characters for selection, because selection of a particular trait may induce desirable or undesirable changes in the associated characters. Generally, direct selection for yield was not aimed at, as it is not a most complex trait, the result of the interaction of a number of components and highly influenced by environment.

Crop yield is the end product of the interaction of a number of other, often interrelated attributes. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character.

Table 4.7: Relative contribution of different characters to genetic diversity in 85 landraces of rice.

S.No	Characters	Times Ranked 1st	Contribution %
1	Days to 50% Flowering	464	13.00%
2	Plant Height (cm)	272	7.62%
3	Panicle Length (cm)	0	0.00%
4	No. of tillers/plant	0	0.00%
5	Number of grains/ panicle	1532	42.91%
6	1000 grain weight (g)	19	0.53%
7	Grain yield/ plant (g)	7	0.20%
8	Grain iron concentration (mg/kg)	73	2.04%
9	Grain zinc concentration (mg/kg)	882	24.71%
10	Grain Protein Content	321	8.99%

Phenotypic and genotypic correlations were worked out on yield and yield contributing characters in 85 genotypes. In general, genotypic correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between characters studies, its expression is lessened due to influence of environment and considering the importance of phenotypic correlation it was discussed in the results which were presented in table 4.8.

4.5.1 Yield Characters

4.5.1.1 Days to 50 per cent Flowering

The days to 50 per cent flowering recorded a significant positive phenotypic and genotypic correlation with Number of filled grains/panicle (0.2902^{**}/0.2917^{**}) and plant height (0.1802^{*}/0.1809^{*}), grain yield per plant (0.1658^{*}/0.1689^{*}). Positive non significant correlation to panicle length (0.1016/0.1082), Negative and significant with grain protein content(-0.2494^{**}/-0.2498^{**}) and at genotypic level of grain iron concentration(-0.1735^{*}) The characters, No of tillers/plant (-0.0793/-0.0824), 1000 grain weight (-0.0722/-0.0727) at phenotypic level of grain iron concentration showed negative and non-significant association. Similar results were reported by Nandan et al. (2010) for plant height and 1000 grain weight, Pankaj *et al.* (2010) for plant height, grain yield per plant, 1000 grain weight, kernel breadth, Fiyaz *et al.* (2011) for panicle length, 1000 grain weight Basavaraja *et al.* (2011) and Ravindra Babu *et al.* (2012) for number of productive tillers per plant, Padmaja *et al.* (2010) for 1000 grain weight. Deepa *et al.* (2006), Singh *et al.* (2006) for plant height, Sabesan *et al.* (2009b) and Laxuman *et al.* (2011) for number of tillers per plant.

4.5.1.2 Plant Height (cm)

The plant height registered a significant positive phenotypic and genotypic correlation with grain yield per plant (0.5113^{**}/0.5224^{**}), number of tillers per plant (0.5252^{**}/0.5623^{**}), panicle length (0.6998^{**}/0.7479^{**}), number of grains per panicle (0.4376^{**}/0.4393^{**}) and 1000 grain weight (0.4437^{**}/0.4495^{**}). Where positive and non-significant correlation with grain zinc concentration (0.0960/0.0964). It had negative and non-significant correlation with grain iron concentration (-0.0966/-0.0970) and grain protein content (-0.0328/-0.0320). Similar result were reported by Chakraborty *et al.* (2010) for yield/plant, Padmaja *et al.* (2010) for 1000 grain weight, Pankaj *et al.* (2010) for panicle length, 1000 grain weight, kernel length and L/B ratio, Nandan *et al.* (2010) for number of grains per panicle and Ravindra Babu *et al.* (2012) for panicle length and number of grains per panicle.

Table 4.8: Phenotypic (P) and Genotypic (G) correlation coefficient analysis of yield and yield contributing characters in rice

Character		Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No of tillers/ plant	No of grains per panicle	1000 grain weight (g)	Grain iron concentration (mg/kg)	Grain zinc concentration (mg/kg)	Grain Protein Content%	Grain yield per plant (g)
Days to 50% flowering	P	1.0000	0.1802*	0.1016	-0.0793	0.2902**	-0.0722	-0.01712	-0.1107	-0.2494**	0.1658*
	G	1.0000	0.1809*	0.1082	-0.0824	0.2917**	-0.0727	-0.1735*	-0.1113	-0.2498**	0.1689*
Plant Height (cm)	P		1.0000	0.6998**	0.5252**	0.4376**	0.4437**	-0.0966	0.0960	-0.0328	0.5113**
	G		1.0000	0.7479**	0.5623**	0.4393**	0.4495**	-0.0970	0.0964	-0.0320	0.5224**
Panicle Length (cm)	P			1.0000	0.3924**	0.3181**	0.3026**	-0.1138	0.2727**	-0.0814	0.3276**
	G			1.0000	0.4717**	0.3418**	0.3290**	-0.1224	0.2921**	-0.0866	0.3740**
Number of tillers / plant	P				1.0000	0.1553*	0.3839**	0.0157	0.2165**	0.1262	0.3739**
	G				1.0000	0.1681*	0.4179**	0.0161	0.2289**	0.1483	0.4056**
Number of grains/panicle	P					1.0000	0.0291	-0.1233	-0.2027**	-0.1850*	0.3164**
	G					1.0000	0.0286	-0.1235	-0.2029**	-0.1871*	0.3208**
1000 Grain Weight (g)	P						1.0000	0.0075	0.0695	-0.0058	0.6539**
	G						1.0000	0.0057	0.0696	-0.0021	0.6701**
Grain iron concentration (mg/kg)	P							1.0000	0.4129**	0.5816**	-0.1106
	G							1.0000	0.4149**	0.5907**	-0.1138
Grain zinc concentration (mg/kg)	P								1.0000	0.5181**	-0.0688
	G								1.0000	0.5239**	-0.0695
Grain Protein Content	P									1.0000	-0.1198
	G									1.0000	-0.1243
* Significant at 5 per cent level; ** Significant at 1 per cent level											

4.5.1.3 Panicle Length (cm)

The panicle length registered a significant positive phenotypic and genotypic correlation with Number of tillers per plant ($0.3924^{**}/0.4717^{**}$), number of grains per panicle ($0.3181^{**}/0.3418^{**}$), 1000 grain weight ($0.3026^{**}/0.3290^{**}$), grain zinc concentration ($0.2727^{**}/0.2921^{**}$) and grain yield per plant ($0.3276^{**}/0.3740^{**}$). The character grain iron concentration ($-0.1138/-0.1224$) and Grain Protein Content ($-0.0814/-0.0866$) showed negative non-significant correlation.

Similar results were reported by Panwar and Mashiat (2007) for panicle length, grain yield per plant and number of grains per panicle. Bagheri *et al.* (2011) revealed panicle length ($r=0.818$), the total number of spikelet per panicle ($r=0.617$), the number of filled grains per panicle ($r=0.790$) and the panicle number per plant ($r=0.498$) correlated significantly with grain yield. Padmaja *et al.* (2010) and Ravindra babu *et al.* (2012) for grain yield per plant.

4.5.1.4 Number of Tillers per Plant

Panicle length registered significant positive phenotypic and genotypic correlation with number of grain per panicle ($0.1553^{*}/0.1681^{*}$), 1000 grain weight ($0.3839^{**}/0.3839^{**}$), grain zinc concentration ($0.2165^{**}/0.2289^{**}$) and grain yield per plant ($0.3740^{**}/0.4056^{**}$). Positive and non significant correlation with grain concentration ($0.0157/0.0161$) and Grain Protein Content ($0.1262/0.1483$).

Similar results were reported by Nandan *et al.* (2010) for 1000 grain weight, kernel length and L/B ratio, Padmaja *et al.* (2010) for 1000 grain weight and number of grain per panicle, Ravindra Babu *et al.* (2012) for 1000 grain weight. Fiyaz *et al.* (2011) and for grain yield. Sabesan *et al.* (2009b), Saravanan and Sabesan (2009), Laxuman *et al.* (2011), Sadeghi (2011).

4.5.1.5 Number of Grains per Panicle

Number of filled grains per panicle exhibited a significant positive phenotypic and genotypic correlation with grain yield per plant ($0.3164^{**}/0.3208^{**}$) positive and non significant correlation with 1000 grain weight ($0.0291/0.286$) whereas negative and significant correlation with grain zinc concentration ($-0.2027^{**}/-0.2029^{**}$) and Grain Protein Content ($-0.1850^{*}/-0.1871^{*}$). Negative and non significant correlation with grain iron content ($-0.1233/-0.1235$) is observed.

Similar results were reported by Nandan *et al.* (2010) for 1000 grain weight, kernel length, Panwar and Mashiat (2007) for 1000 grain weight and grain yield per plant, Padmaja *et al.* (2010) for grain yield per plant, Bagheri *et al.* (2011) and Aditya and Anuradha (2013) for grain yield per plant.

4.5.1.6 1000-Grain Weight (g)

1000 grain weight showed a significant positive phenotypic and genotypic correlation with grain yield per plant (0.6539**/0.6701**), positive and non significant correlation with grain iron concentration (0.0075/0.0057) and grain zinc concentration (0.0695/0.0696). It had negative non significant correlation with grain protein content (-0.0058/-0.0021). Similar results were reported by Singh *et al.* (2011) and Rangare *et al.* (2012) and Dilruba *et al.* (2014) for grain yield per plant.

4.5.1.7 Grain Yield per Plant

Phenotypic and genotypic correlations revealed that grain yield per plant had significant positive association with 1000 grain weight (0.6539**/0.6701**), Plant height (0.5113**/0.5224**), number of tillers per plant (0.3740**/0.4056**), number of grains per panicle (0.3164**/0.3208**) and days to fifty per cent flowering (0.1658*/0.1689*). The trait recorded a non significant negative association with grain iron concentration (-0.1106/-0.0688) and grain zinc concentration (-0.0688/-0.0695). Grain protein content (-0.1198/-0.1243) showed negative non significant correlation.

Grain yield per plant showed positive significant association with plant height, number of tillers per plant, 1000 grain weight, number of filled grains per panicle. This indicated that all these characters were important for yield improvement. Similar kind of association was revealed by Fiyaz *et al.* (2011) for plant height, Ravindra Babu *et al.* (2012) for number of productive tillers per plant and Pankaj *et al.* (2010) for number of filled grains per panicle. Hence, these characters could be considered as criteria for selection for higher yield as these were mutually and directly associated with grain yield.

4.5.2 Grain Quality Characters

4.5.2.1 Grain Iron Concentrations

Phenotypic and genotypic correlations of grain iron concentration revealed that positive and significant correlation with grain zinc concentration (0.4129**/0.4149**) and grain protein content (0.5816**/0.5907**). Grain yield per plant (-0.1106/-0.1138) had non-significant and negative association. Similar kind of association was revealed by Nagesh *et al.* (2013), Tiwari *et al.* (2011) for grain quality attributes and grain yield.

4.5.2.2 Grain Zinc Concentrations

Grain zinc concentration of phenotypic and genotypic correlations revealed that positive and significant correlation with grain protein content (0.5181**/0.5239**) and character with grain yield per plant showed negative and non-significant correlation (-0.0688/-0.0695). These results are in agreement with Nagesh *et al.* (2013) for yield

attributes and grain yield and Naveen *et al.* (2013) and Tiwari *et al.* (2011) for grain yield per plant.

4.5.2.3 Grain Protein Content.

Grain protein content of phenotypic and genotypic correlations revealed that this character with grain yield per plant (-0.1198/-0.1243) showed negative and non significant correlation. Similar results were earlier reported by Nagesh *et al.* (2013).

4.6 PATH COEFFICIENT ANALYSIS

The genetic architecture of grain yield is based on the balance or overall net effect produced by various yield components interacting with one another. 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 its component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. If relationship is due to multiple effects of gene(s) it is difficult to separate these effects by selecting a particular character. Hence indirect selection by correlated response may not be sometimes fruitful. Correlation gives only the relation between two variables whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921). Hence, this objective was undertaken in the present investigation. If the correlation coefficient between causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and direct selection of this trait will be effective. The correlation coefficient is positive and the direct effects are negative or negligible, the indirect effects seem to be the cause of correlation. In such situations the other factors influencing the trait have to be considered simultaneously. Correlation coefficients may be negative but the direct effect may be positive and high. Under these conditions a restricted simultaneous selection model is to be followed i.e., restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effects.

Based on the data recorded on the genotypes in the present investigation, the genotypic and phenotypic correlations were estimated to determine direct and indirect effects of yield and yield contributing characters.

As discussed in character association based on the importance of phenotypic effects the present results of phenotypic path coefficient of yield and yield contributing characters discussed here under which were presented in table 4.9 and Fig 4.3 and 4.4.

4.6.1.1 Days to 50 per cent Flowering

The days to 50 per cent flowering had positive direct effect (0.1274/0.1326) at both genotypic and phenotypic levels on grain yield and the correlation between days to 50 per cent flowering and grain yield per plant (0.1658/0.1689) was significant and positive at genotypic and phenotypic levels respectively. The correlation was positive and significant mainly due to positive indirect effect through plant height (0.023/0.024), panicle length (0.0129/0.0143), No. of grains per panicle (0.0370/0.0387).

The trait exhibited negative indirect effects on number of tillers/plant (-0.0101/-0.0109), 1000 grain weight (-0.0092/-0.0096), grain iron concentration (-0.0218/-0.0230), grain zinc concentration (-0.0141/-0.0147), grain protein content (-0.0318/-0.0331).

It clearly indicated that direct selection of this trait would be effective in improving grain yield per plant. Satish Chandra *et al.* (2009) and Rangare *et al.* (2012) revealed that number of grains per panicle, days to 50% flowering, 1000-grain weight and number of productive tillers per plant has shown high positive direct effects.

4.6.1.2 Plant Height

Plant height had positive direct effect on grain yield per plant (0.1252/0.1023) at both genotypic and phenotypic levels where as the correlation of plant height with grain yield (0.5113/0.5224) was significant and positive. This is in agreement with findings of Gomathinayagam *et al.* (1988), who reported the highest direct effect of plant height is with grain yield in rice. Similarly, Kole *et al.* (2008), Madhavalatha *et al.* (2005a), Chakraborty *et al.* (2010), Yadav *et al.* (2010), Sadeghi (2011), Yadav *et al.* (2011) and Jambhulkar *et al.* (2014) were reported positive direct effect of plant height on grain yield per plant.

The correlation between plant height and grain yield was significant and positive mainly due to positive indirect effect contribution through days to 50 per cent flowering (0.0226/0.0185), panicle length (0.0876/0.0765) number of tillers per plant (0.0658/0.0575), number of grains per panicle (0.0548/0.0449), 1000 grain weight (0.0556/0.0460) and grain zinc concentration (0.0120/0.0099). The trait exhibited negative indirect effects on grain iron concentration (-0.0121/-0.0099) and grain protein content (-0.0041/0.0033).

Table 4.9: Phenotypic (P) and Genotypic (G) Path coefficient analysis of yield and yield contributing characters in rice

Character		Days to 50% flowering	Plant height(cm)	Panicle length(cm)	No of productive tillers/plant	No of filled grains per panicle	1000 grain weight (g)	Grain iron concentration (mg/kg)	Grain zinc concentration (mg/kg)	Grain Protein Content%	Grain yield per plant(g)
Days to 50% flowering	P	0.1274	0.023	0.0129	-0.0101	0.0370	-0.0092	-0.0218	-0.0141	-0.0318	0.1658
	G	0.1326	0.024	0.0143	-0.0109	0.0387	-0.0096	-0.023	-0.0147	-0.0331	0.1689
Plant Height (cm)	P	0.0226	0.1252	0.0876	0.0658	0.0548	0.0556	-0.0121	0.012	-0.0041	0.5113
	G	0.0185	0.1023	0.0765	0.0575	0.0449	0.046	-0.0099	0.0099	-0.0033	0.5224
Panicle length(cm)	P	-0.0032	-0.0218	-0.0312	-0.0122	-0.0099	-0.0094	0.0036	-0.0085	0.0025	0.3276
	G	-0.0008	-0.0054	-0.0072	-0.0034	-0.0025	-0.0024	0.0009	-0.0021	0.0006	0.374
Number of tillers / plant	P	-0.0075	0.0498	0.0372	0.0948	0.0147	0.0364	0.0015	0.0205	0.012	0.3739
	G	-0.0084	0.0576	0.0483	0.1024	0.0172	0.0428	0.0016	0.0234	0.0152	0.4056
Number of filled grains/panicle	P	0.0535	0.0807	0.0586	0.0286	0.1844	0.0054	-0.0227	-0.0374	-0.0341	0.3164
	G	0.054	0.0813	0.0632	0.0311	0.185	0.0053	-0.0229	-0.0375	-0.0346	0.3208
1000 Grain Weight (g)	P	-0.0418	0.2573	0.1755	0.2226	0.0169	0.5798	0.0044	0.0403	-0.0034	0.6539
	G	-0.0431	0.2666	0.1952	0.2479	0.017	0.5932	0.0034	0.0413	-0.0012	0.6701
Grain iron concentration(mg/kg)	P	0.0054	0.003	0.0036	-0.0005	0.0039	-0.0002	-0.0314	-0.013	-0.0183	-0.1106
	G	0.0044	0.0024	0.0031	-0.0004	0.0031	-0.0001	-0.0252	-0.0104	-0.0149	-0.1138
Grain zinc concentration (mg/kg)	P	0.007	-0.0061	-0.0174	-0.0138	0.0129	-0.0044	-0.0263	-0.0637	-0.033	-0.0688
	G	0.0079	-0.0068	-0.0207	-0.0162	0.0144	-0.0049	-0.0294	-0.0709	-0.0371	-0.0695
Grain Protein Content	P	0.0024	0.0003	0.0008	-0.0012	0.0018	0.0001	-0.0057	-0.005	-0.0097	-0.1198
	G	0.004	0.0005	0.0014	-0.0023	0.003	0	-0.0093	-0.0083	-0.0158	-0.1243
Phenotypic residual effect = 0.6657; Genotypic residual effect = 0.6471; BOLD values are direct effects											

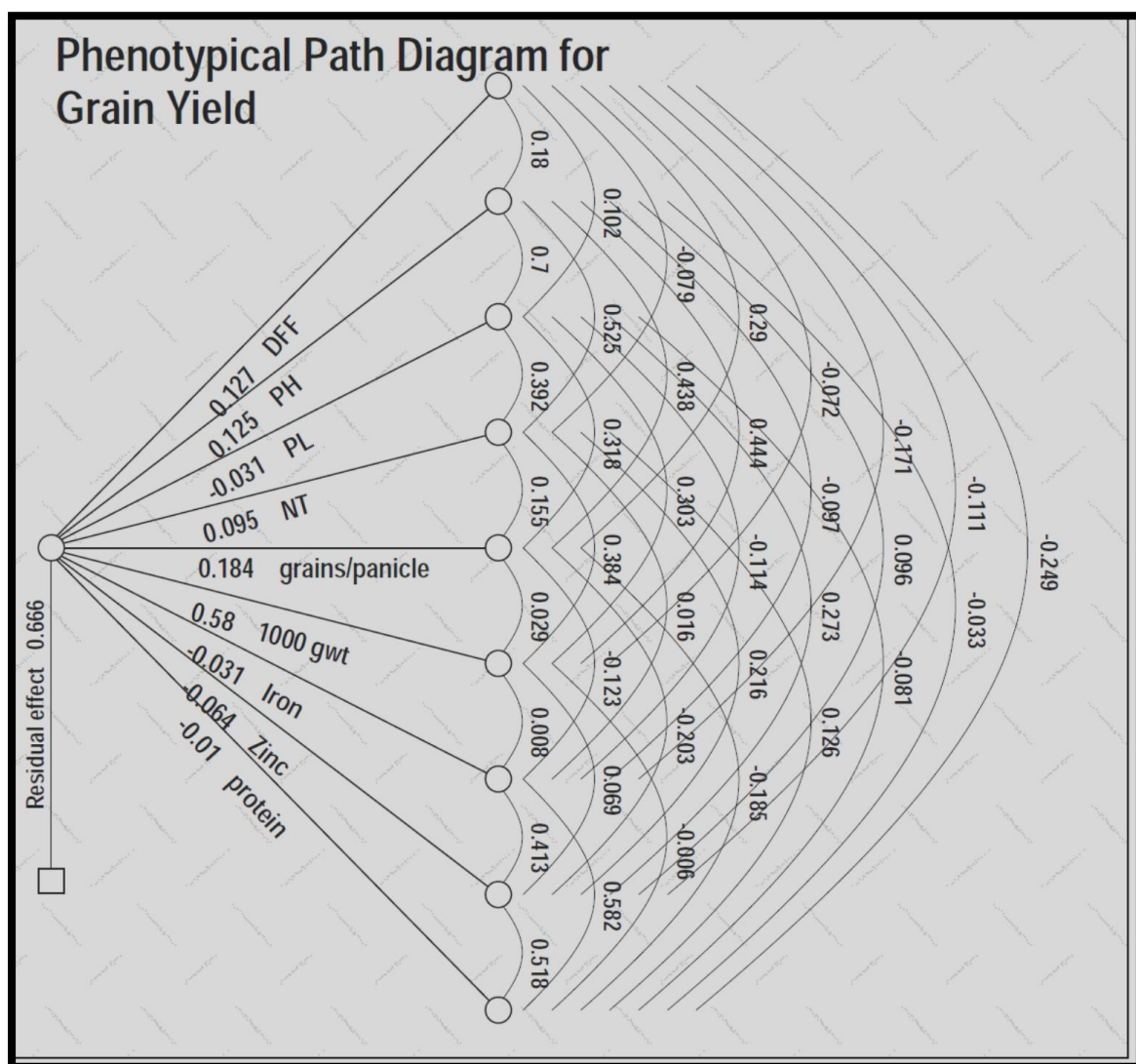


Figure 4.3: Phenotypical Path Diagram for grain yield

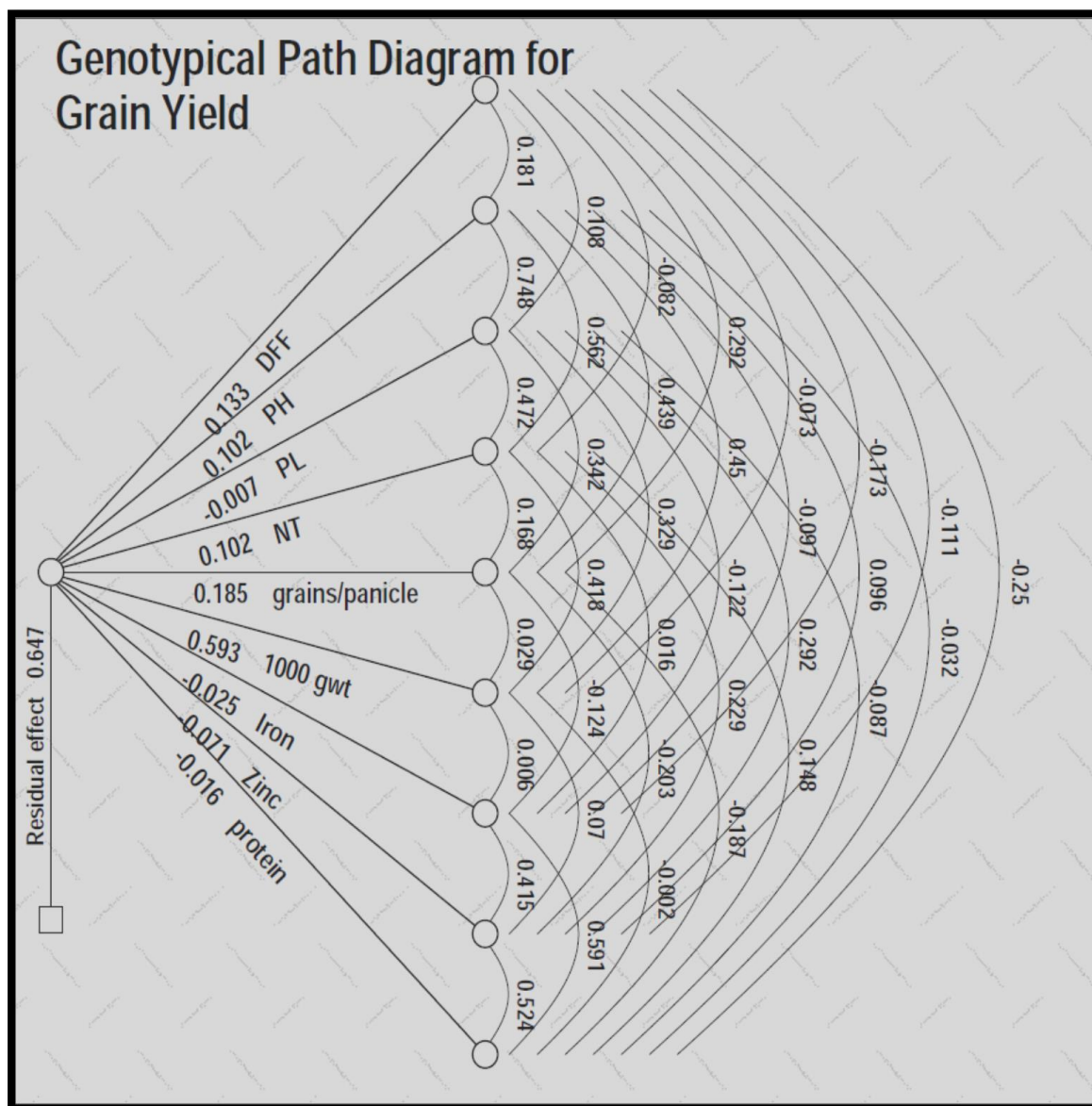


Figure 4.4: Genotypical Path Diagram for grain yield

4.6.1.3 Panicle Length (cm)

Panicle length had direct negative effect (-0.0312/-0.0072) on grain yield per plant at both genotypic and phenotypic levels. The positive indirect contribution through grain iron concentration (0.0036/0.0009) and Grain Protein Content (0.0025/0.0006). Days to 50% flowering (-0.0032/-0.0008), plant height (-0.0218/-0.0054), number of tillers per plant (-0.0122/-0.0034), number of grains per panicle (-0.0099/-0.0025) and 1000 grain weight (-0.0094/-0.0024) and grain zinc concentration (-0.0085/-0.0021) showed negative indirect effects. However correlation of panicle length with grain yield per plant (0.3276/0.3740) was positive and significant.

Similar results were reported by Kole *et al.* (2008), Satish Chandra *et al.* (2009), Ganga shetty *et al.* (2013), Padmaja *et al.* (2010), Rahman *et al.* (2014), which indicates negative direct effect of Panicle length on grain yield per plant.

4.6.1.4 Number of tillers per plant

Productive tillers per plant which exhibited a positive direct effect on grain yield per plant (0.0948/0.1024) both genotypic and phenotypic levels, while the correlation with grain yield per plant (0.3739/0.4056) was also significant and positive. The correlation was positive and significant mainly due to positive indirect effect contribution through plant height (0.0498/0.0576), panicle length (0.0372/0.0483), number of filled grain per panicle (0.0147/0.0172), 1000 grain weight (0.0364/0.0428), grain iron concentration (0.0015/0.0016), grain zinc concentration (0.0205/0.0234) and grain protein content (0.0120/0.0152). This trait exhibited negative indirect effect on days to 50 per cent flowering (-0.0075/-0.0084).

Similar results were reported by Basavaraja *et al.* (2011), Fiyaz *et al.* (2011), Padmaja *et al.* (2010), Ravindra Babu *et al.* (2012), Thirumala Rao *et al.* (2014) and Patel *et al.* (2014), observed positive direct effect of number of productive tillers per plant on grain yield per plant.

4.6.1.5 Number of Filled Grains per Panicle

Number of filled grains per panicle had direct positive effect (0.1844/0.1850) on grain yield per plant both genotypic and phenotypic levels. Its correlation with grain yield per plant (0.3164/0.3208) was also significant and positive. The correlation between number of filled grains per panicle and grain yield per plant was positive and significant mainly due to positive indirect effect contribution through days to 50 per cent flowering (0.0535/0.0540), plant height (0.0807/0.0813), number of tillers per plant (0.0286/0.0311) and 1000 grain weight (0.0054/0.0053).

This trait showed negative indirect effects on grain iron concentration, (-0.0227/-0.0229) and grain zinc concentration (-0.0374/-0.0375) and grain protein concentration (-0.0341/-0.0346).

Similar positive direct effect of number of filled grains per panicle on grain yield per plant was also reported by Nandan *et al.* (2010), Zahid *et al.* (2006), Mustafa and Elsheikh (2007), Kole *et al.* (2008), Hairmansis *et al.* (2010), Bagheri *et al.* (2011), Padmaja *et al.* (2010) and Aditya and Anuradha (2013).

4.6.1.6 1000-Grain Weight (g)

Thousand grain weight had direct positive effect on grain yield per plant (0.5798/0.5932) at both genotypic and phenotypic levels. While its correlation with grain yield per plant (0.6539/0.6701) was significant and positive mainly due to positive indirect effect influence through plant height (0.2573/0.2666), panicle length (0.1755/0.1952), number of tillers per plant (0.2226/0.2479), number of grains per panicle (0.0169/0.0170), grain iron concentration (0.0044/0.0034), and grain zinc concentration (0.0403/0.0413) on grain yield per plant. Days to fifty per cent flowering (-0.0418/-0.0431) and protein content (-0.0034/-0.0012) showed negative indirect effect. Similar result was reported by Chaturvedi *et al.* (2008), Kole *et al.* (2008), Satish Chandra *et al.* (2009), Chakraborty *et al.* (2010), Yadav *et al.* (2010), Gyanendra *et al.* (2011), Sadeghi (2011), Yadav *et al.* (2011), Haider *et al.* (2012) and Dilruba *et al.* (2014).

4.6.2. Grain Quality Characters

4.6.2.1 Grain Iron Concentration

Grain iron concentration has direct negative effect on grain yield per plant (-0.0314/-0.0254) at both genotypic and phenotypic levels. While its correlation with grain yield per plant (-0.1106/-0.1138) was negative and non-significant. The correlation between grain iron concentration and grain yield per plant was negative, which is mainly due to negative indirect effect influence through number of tillers per plant (-0.0005/-0.0004), 1000 grain weight (-0.0002/-0.0001), grain zinc concentration (-0.0130/-0.0104), and grain protein content (-0.0183/0.0149) on grain yield per plant. This trait exhibited positive indirect effect on days to fifty per cent flowering (0.0054/0.0044), plant height (0.0030/0.0024), panicle length (0.0036/0.0031) and number of filled grains/panicle (0.0039/0.0031). Similar result was reported by Nagesh *et al.* (2013) and Naveen *et al.* (2013).

4.6.2.2 Grain Zinc Concentration

Grain zinc concentration had direct negative effect on grain yield per plant (-0.0637/-0.0709) at both genotypic and phenotypic levels. While its correlation with grain

yield per plant (-0.0688/-0.1138) was negative and non-significant. The correlation between grain iron concentration and grain yield per plant was negative, which is mainly due to negative indirect effect influence through plant height (-0.0061/-0.0068), panicle length (-0.0174/-0.0207), number of tillers per plant (-0.0138/-0.0162), 1000 grain weight (-0.0044/-0.0049), grain zinc concentration (-0.0263/-0.0294) and grain protein content (-0.0330/-0.0371) on grain yield per plant. This trait exhibited positive indirect effect on days to fifty per cent flowering (0.0070/0.0079), number of filled grains/panicle (0.0129/0.0144), which is in accordance with findings of Nagesh *et al.* (2013), Naveen *et al.* (2013), Tiwari *et al.* (2009) and Nagarathna *et al.* (2010), reported negative effect with grain yield/plant.

4.6.2.3 Grain Protein Content.

Grain protein content had direct negative effect on grain yield per plant (-0.0097/-0.0158) at both genotypic and phenotypic levels. While its correlation with grain yield per plant (-0.1198/-0.1243) was negative and non-significant which is accordance with findings of Ravindra Babu (2013) and Jahan *et al.* (2013). The correlation between grain protein content and grain yield per plant was negative, mainly due to negative indirect effect influence through number of tillers per plant (-0.0012/-0.0023), grain iron concentration (-0.0057/-0.0093), grain zinc concentration (-0.0050/-0.0083) and on grain yield per plant. This trait exhibited positive indirect effect on days to fifty per cent flowering (0.0024/0.0040), plant height (0.0003/-0.0005), panicle length (0.0008/0.0014) and 1000 grain weight (0.001/0).

A critical analysis of the results by path analysis revealed that 1000 grain weight exerted highest positive direct effect on grain yield followed by number of grains per panicle, days to 50% flowering and plant height were directly influencing the grain yield per plant indicating that selection for these characters was likely to bring about an overall improvement in grain yield per plant directly. A critical analysis of correlation and direct and indirect effects indicated that emphasis should be directed towards selection of parents having high 1000 grain weight exerted highest positive direct effect on grain yield. As the yield component of 1000 grain weight is in turn dependent on plant height, panicle length, number of tillers/ plant, number of grains per panicle, grain iron concentration and grain zinc concentration were influencing the grain yield per plant, which would be more desirable for selection to realize higher yield with good quality traits.

Chapter V

Summary and conclusions

Chapter V

SUMMARY AND CONCLUSIONS

Among cereals, rice is undoubtedly the most important cereal of the world, which is the staple food for more than half of the world's population. It has shaped the cultures, diets and economics of billions of people living in Asia where it has a long history of cultivation and is deeply ingrained in the daily lives of Asian people. Land races of rice harbor a great deal of useful traits and played a very important role in the local food security and sustainable development of agriculture, in addition to their significance resource for the improvement of rice cultivars

The research work entitled "Evaluation of Landraces of Rice (*Oryza sativa* L.) for Iron, Zinc and Protein" was conducted with eighty five landraces of rice obtained from Indian Institute of Rice Research (formerly Directorate of Rice Research), Rajendranagar, Hyderabad. The objectives of the investigation were to study the genetic diversity present in the experimental material for selection of the diverse parents, nutritional traits, identifying the promising genotypes possessing desirable traits and the extent of association between the yield, grain quality and its component characters including the direct and indirect effects.

The experiment was carried out in a Randomized block design, with two replications during *Kharif* 2014. Observations were recorded on five randomly selected plants per genotype in each replication for ten characters viz., days to 50 per cent flowering, plant height, panicle length, number of tillers per plant, number of grains per panicle, 1000-grain weight, grain yield per plant, grain iron concentration, grain zinc concentration, grain protein content.

Analysis of variance indicated high significant differences among the genotypes for all the traits under study for all ten characters viz., days to 50 per cent flowering, plant height, panicle length, number of tillers per plant, number of grains per panicle, 1000-grain weight, grain yield per plant, grain iron concentration, grain zinc concentration, grain protein content indicating the presence of considerable genetic variation in the experimental material.

A perusal of genetic parameters viz., that phenotypic and genotypic coefficient of variation revealed less influence of environment on the characters under study therefore, response to direct selection may be effective in improving these traits. Among all the characters under study, grain yield per plant exhibited highest GCV and PCV followed by number of grains per panicle, number of productive tillers per plant and days to fifty per

cent flowering, 1000-grain weight and grain iron concentration. The values of genotypic and phenotypic coefficients of variation were low for four traits (panicle length, grain protein content, plant height and grain zinc concentration).

All the characters under study except panicle length exhibited high heritability coupled with high genetic advance as per cent of mean was observed for grain yield per plant, number of grains per panicle, days to fifty per cent flowering, grain zinc concentration, grain iron concentration and 1000-grain weight, which indicated the preponderance by additive gene action in controlling these traits. These characters can be further improved by following simple selection procedure. The high estimates of heritability coupled with moderate and low genetic advance as per cent of mean for plant height, number of tillers per plant and grain protein content indicated the presence of non-additive gene effects, in addition to influence of environment to some extent.

Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The diversity was more for number of filled grains per panicle, grain iron concentration, days to 50 per cent flowering, grain iron concentration and plant height indicating their importance in contribution towards genetic diversity.

The 85 landraces of rice under study were distributed into six clusters based on D^2 values using Tocher's method such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. Out of six clusters Cluster I was the largest one comprising of forty three landraces followed by cluster IV with sixteen landraces, cluster III with fourteen landraces, cluster II with ten landraces, cluster V and VI were monogenotypic clusters suggesting the pattern of group constellations indicated significant variability among the genotypes.

Maximum intra cluster distance was observed in cluster IV (39.77), followed by cluster III (38.98), cluster II (35.36), cluster and cluster I (32.93), indicating that some genetic divergence still existed among the landraces. From the inter cluster D^2 values of the six clusters, the inter cluster distance was higher than intra cluster distance indicating the presence of wide genetic diversity among the landraces under study. It can be seen that the highest divergence occurred between cluster II and VI (100.30) followed by cluster IV and VI (78.61), cluster I and VI (77.77), cluster III and IV (77.45), cluster II and V (73.74), cluster III and VI (68.76), cluster IV and V (68.55) is suggested to generate promising segregants for grain yield and quality traits would produce encouraging results.

The cluster V is having highest mean value for panicle length, number of tillers per plant, 1000 grain weight and plant height. Cluster III for grain yield per plant is higher and cluster VI is higher for grain iron concentration and protein percentage from these clusters having high mean values may be directly used for adaptation or may be used as parents in future hybridization programme.

The maximum genetic divergence was observed in number of grains per panicle was highest towards genetic divergence (42.91%) by taking 1532 times ranking first, followed by grain zinc concentration (24.71%) by 882 times, Days to 50% flowering (13.00%) by 464 times, Grain Protein Content (8.99%) by 321 times, plant height (7.62%) by 272 times, grain iron concentration (2.04%) by 73 times, 1000 grain weight (0.53%) by 19 times, grain yield per plant (0.20%) by 7 times, number of tillers per plant and panicle length each had no divergence. Therefore, these characters should be given importance during hybridization and selection of segregating populations.

Character association studies revealed that the genotypic coefficients were higher than phenotypic correlation coefficients indicating strong inherent association between the characters. Grain yield per plant registered significant positive association with days to 50 per cent flowering, plant height, panicle length, number of tillers per plant, number of grains per panicle, 1000 grain weight. This indicated that simultaneous selection of all these characters was important for improving yield. Non-significant and negative association of grain yield was observed with grain iron concentration, grain zinc concentration and grain protein content.

A critical analysis of the results by path analysis revealed that 1000 grain weight exerted the highest positive direct effect on grain yield followed by number of grains per panicle, days to 50 per cent flowering and plant height, which directly influences the grain yield per plant indicating that selection for these characters was likely to bring about an overall improvement in grain yield per plant directly.

A critical analysis of correlation and direct and indirect effects indicated that emphasis should be directed towards selection of parents having high 1000 grain weight exerted the highest positive direct effect on grain yield. As a yield component, 1000 grain weight is in turn dependent on plant height, panicle length, number of tillers per plant, number of grains per panicle, grain iron concentration and grain zinc concentration influenced the grain yield per plant of would be more desirable for selection to realize higher yield with good quality traits.

Future line of work:

The immense genetic diversity in rice landraces is similarly reflected by their multiplicity of nutritional characteristics. Appropriate rice varieties exist for enhancing the supply of various nutrients, including protein, essential lipids, certain minerals, and to some extent also β -carotene. The high nutritional quality of rice landraces can form a solid basis for changing priorities in rice breeding by putting more emphasis on the grain nutritional value. Modern conventional breeding techniques, including molecular marker-assisted selection, may be very useful in accelerating the development of more nutritious rice varieties.

The current prevalence of milled rice on the market reduces the rice's nutritional value and essentially turns it into a simple carbohydrate food. Therefore, in addition to developing more nutritious varieties, awareness of the benefits of eating brown rice should be raised among rice consumers. Such a combined approach would ultimately result in a sustainable enhancement of the essential nutrient supply in rice-based diets.

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