"GENETIC DIVERSITY AND PATH ANALYSIS STUDIES IN RICE (*Oryza sativa* L.)"

A thesis submitted to the

MAHATMA PHULE KRISHI VIDYAPEETH,
RAHURI-413722,
DIST.-AHMEDNAGAR,
MAHARASHTRA STATE (INDIA)

by

MISS KOMAL RAMCHANDRA RAUT

in partial fulfilment of the requirements for the degree of

MASTER OF SCIENCE (AGRICULTURE)

In

AGRICULTURAL BOTANY
(CYTOGENETICS AND PLANT BREEDING)

DEPARTMENT OF AGRICULTURAL BOTANY
MAHATMA PHULE KRISHI VIDYAPEETH
COLLEGE OF AGRICULTURE
PUNE - 411005
MAHARASHTRA, INDIA

2007

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CANDIDATE'S DECLARATION

I hereby declare that this thesis entitled **"Genetic diversity and path analysis studies in Rice (*Oryza sativa* L.)"** or part there of has not been submitted by me or any other person to any other University or Institute for Degree or Diploma.

Place : Pune

Dated : 19 / 5 / 2007

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This is to certify that the thesis entitled **"Genetic diversity and path analysis studies in Rice (*Oryza sativa* L.)"** submitted to the Faculty of Agriculture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar for the award of degree of **MASTER OF SCIENCE (Agriculture)** in Agricultural Botany (Cytogenetics and Plant Breeding), embodies the results of a piece of *bona fide* research work carried out by **Miss Raut Komal Ramchandra** under my guidance and supervision, and that no part of the thesis has been submitted for any other Degree or Diploma.

The assistance and the help received during the course of this investigation have been duly acknowledged.

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CERTIFICATE

This is to certify that the thesis entitled **"Genetic diversity and path analysis studies in Rice (*Oryza sativa* L.) "** in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (Agriculture)** in Agricultural Botany (Cytogenetics and Plant Breeding), embodies the results of a piece of *bona fide* research work carried out by **Miss Komal Ramchandra Raut** under the guidance and supervision of Dr. P. N. Harer, Professor of Agricultural Botany, Botany section, College of Agriculture, Pune - 5 and that no part of the thesis has been submitted for any other Degree or Diploma.

Place : Pune
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With the modest salutation to Lord Shiva .... !

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Although far from here, my work owes completely to my parents, whose love, affection , support and guidance will serve me lifelong......!

Place : Pune
Date : 19/5/2007

(Komal Ramchandra Raut)

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ABBREVIATIONS

–	:	minus
%	:	Percentage
σ^2_e	:	Environmental variance
σ^2_g	:	Genotypic variance
σ^2_p	:	Phenotypic variance
/	:	Per
+	:	Plus
<	:	Less than
=	:	Equal to
>	:	Greater than
ARS	:	Agricultural Research Station
C.D.	:	Critical difference
C.V.	:	Coefficient of variance
cm	:	Centimeters
D	:	Divergence
DC	:	Divergence classes
DC1	:	Divergence class 1
DC2	:	Divergence class 2
DC3	:	Divergence class 3
DC4	:	Divergence class 4
DRR	:	Directorate of Rice Research
et al.	:	et all (and others)
F_2	:	Second filial generation
g	:	Gram
GA	:	Genetic advance
GCV	:	Genotypic coefficient of variation
$h^2_{(b.s.)}$	:	Heritability in broad sense

i.e.	:	That is
IARI	:	Indian Agricultural Research Institute
IRRI	:	International Rice Research Institute
L:B	:	Length to Breadth ratio
M_2	:	Second mutagenic generation
mm	:	millimeters
NARP	:	National Agricultural Research Project
No.	:	Number
PCV	:	Phenotypic coefficient of variation
Per se	:	Actual
R	:	Residual effect
RDN	:	Radhanagari
S.E.	:	Standard error
U.P.	:	Uttar Pradesh
via	:	through
viz.,	:	Videlicent (namely)
$\overline{X}$	:	General mean
x	:	Multiplication
Y	:	Yield

ABSTRACT

"GENETIC DIVERSITY AND PATH ANALYSIS STUDIES IN RICE (*Oryza sativa* L.)".

by

MISS. RAUT KOMAL RAMCHANDRA

A candidate for the degree

of

Master of Science (Agriculture)

in

Cytogenetics and Plant Breeding

(Agricultural Botany)

Research Guide : Dr. P.N. Harer
Professor of Agril. Botany,
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Discipline : Agricultural Botany

Major Field : Cytogenetics and Plant Breeding

The present investigation was carried out with the objectives to know the extent of variability for 13 characters in 40 rice genotypes, to estimate broad sense heritability and genetic advance, to study the association among different characters and find out direct and indirect effects of various characters on seed yield, to measure the genetic divergence between different genotypes and group them into suitable clusters. The studies involved 40 genotypes of rice from 11 diverse origins, laid in a randomized block design with three replications during

kharif 2006, at Botany Farm, College of Agriculture, Pune. Observations were recorded on 13 characters, *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), effective tillers per plant, panicle length (cm), number of secondary branches and grains per panicle, length of grain (mm), breadth of grain, length : breadth ratio of grain, 1000 grain weight (g), protein content (%) and seed yield per plant (g).

Appreciable amount of variability among the genotypes for all the characters was observed. Genotypic as well as phenotypic coefficient of variation was highest for seed yield per plant (49.703 and 50.887, respectively), followed by 1000 grain weight and grains per panicle. Genotypic coefficients for other characters ranged from 7.944 (days to maturity) to 29.535 (protein content). Heritability in broad sense was very high for all the traits and ranged between 74.67 per cent (panicle length) and 98.48 per cent (number of grains per panicle). Genetic advance was highest for number of grains per panicle (91.973), followed by plant height (33.589).

Correlation study revealed that seed yield was significantly and positively associated with secondary branches per panicle (0.684), number of days to 50 per cent flowering (0.567), 1000 grain weight (0.444), grains per panicle (0.491), plant height (0.436), panicle length (0.428), effective tillers per plant (0.390) and days to maturity (0.332). Two traits, protein content (-0.297) and L:B ratio of grain (-0.020) exhibited negative but non significant correlation with seed yield. Path analysis revealed that number of days to maturity was the most important component in determining the seed yield, which had highest direct as well as final contribution towards yield, thus can be considered as reliable yield indicator in rice.

Divergence analysis following Mahalanobis's (1936) D^2 analysis has revealed presence of substantial amount of genetic diversity among

the genotypes. D^2 values ranged from 294.569 to 11574.290. Clustering of genotypes based on the D^2 values, following Tocher's method as described by Rao (1952), led into grouping of genotypes into only 3 clusters, of which one was monogenotypic, while most of the genotypes (36) were grouped into cluster I. Intercluster distance (D^2) ranged between 2526.216 (cluster I and II) and 11574.290 (cluster II and II).

Grouping pattern of the genotypes suggested no parallelism between genetic divergence and geographical distribution of the genotypes. Variance of cluster means revealed that length to breadth ratio of grain and number of grains per panicle had maximum contribution towards divergence in the present material. A tentative crossing programme between clusters, separated by moderate genetic distance is also suggested.

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INTRODUCTION

CHAPTER 1

INTRODUCTION

Rice (*Oryza sativa* L.) is the premier food of the world. It is world's most important food crop after wheat. China, India, Japan, Korea, South Eastern Asia and the adjacent islands of the Pacific account for about 90 per cent of the world's rice production. Globally, rice is produced on 150 million hectares area with production of 573 million tonnes and average productivity is 3.83 tonnes per hectare (Anonymous, 2006a). In terms of area and production it is second to wheat. Maximum area under rice is in Asia.

Rice occupies pivotal place in Indian agriculture as it is the staple food of India. It provides 43 per cent of calorie requirement for more than 70 per cent of Indian population. The area grown under rice in India is about 42.80 million hectares is, the largest among all the rice growing countries. India ranks second in production with 129.20 million tonnes annual production, having an average productivity of 3.00 tonnes per hectare (Anonymous, 2006b).

Rice is grown in almost all the states in India. Kerala, Bihar, Uttar Pradesh, Madhya Pradesh and West Bengal lead in the area, while West Bengal and Tamil Nadu have the highest rice production. Punjab has highest productivity of rice. As far as Maharashtra state is concerned the area under the rice cultivation is about 1.50 million hectares with an annual production of about 2.52 million tonnes and average productivity of 1.68 tonnes per hectare (Anonymous, 2007).

The introduction of the semi dwarf high yielding varieties like TN-1, IR-8 and Taichung-65 during 1965-68 contributed a great deal towards 'green revolution' in India. The new ideas in plant breeding were also attempted by Indian scientists and Jaya followed by Padma were released three years later. Subsequently, large number of varieties have been released from various research institutes.

However, to meet the demand of increasing population and maintaining self sufficiency, the present production level of around 90 million tonnes need to be increased upto 100 million tonnes by the year 2010 and in 2025, the demand will be 140 million tonnes (Anonymous, 2004). This increase in production has to be achieved in the backdrop of declining and deteriorating resource base such as land, water, labour and other inputs and without adversely affecting the quality of environment. Hence, plant breeders still have to perform enormous role in understanding and utilizing the genetic background of the available gene bank.

Germplasm constitutes the foundation of any genetic improvement programme of crop. The pace and magnitude of genetic improvement generally depends on the amount of genetic variability present in a population. Majority of the economically important characters including grain yield and it's components are amenable for genetic improvement through *inter se* breeding among genetically diverse parents.

Before starting breeding programme, it is necessary to assess the existing variability in initial parental material. The efficiency of selection depends upon the magnitudes of genetic components of variability. The extent of the genetic and non-genetic components of variation formulates proper breeding programme to reach the goal. Higher mean accompanied by higher genetic variability affords a scope for selection.

The D^2 statistics is a tool which helps in the identification of genetically divergent parents for their exploitation in hybridization programmes as hybrids between lines of diverse origin display a greater heterosis than those between closely related strains. Murthy and Arunachalam (1966) stated that multivariate analysis with "Mahalanobis

D^2 statistics" is a powerful tool to know the clustering pattern to establish the relationship between genetic and geographic divergence and to determine the role of different quantitative characters towards the maximum divergence.

Yield is governed by many characters. Therefore, for designing effective breeding programme, adequate knowledge about the degree and direction of association between yield and its component traits, is of great significance to the breeders when they have to exercise selection for simultaneous improvement of more than one character. However, simple correlations don't take into consideration the complex relationship among various characters, which are related to dependent variable. In such a situation, path coefficient analysis suggested by Dewey and Lu (1959) proves helpful in partitioning the correlation coefficient into the measure of direct and indirect effects for set of independent variables on dependent variable.

Robinson *et al.*(1949) emphasized that heritability of the characters is the main concern to the breeder, since it indicates the possibility and extent to which improvement is possible through selection. It has been suggested that heritability together with genetic advance will bring out the genetic gain expected from selection (Johnson *et al.,* 1955).

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

1. To know the extent of variability for different characters and to estimate broad sense heritability and genetic advance.
2. To study association between different characters and find out the direct and indirect effects of various characters on grain yield.
3. To measure the genetic divergence between different genotypes under study and group different genotypes into suitable clusters and suggest crossing programme based on the parental divergence.

REVIEW OF LITERATURE

CHAPTER 2

REVIEW OF LITERATURE

Improvement of both qualitative and quantitative characters of a crop is the main aim of any breeding programme. The information on genetic architecture of various quantitative traits contributing to yield and quality is useful in planning the breeding programmes. Various biometrical techniques have been developed for studying the genetics of quantitative traits. This information can be used for developing more sophisticated and efficient approach to select the parents.

The present investigation aimed at finding out the statistical parameters, namely genetic variability, correlation coefficient, path analysis and genetic diversity in forty genotypes of rice. Hence, the literature on these aspects has been reviewed and presented in this chapter.

2.1 Genetic variability

Since, many of the quantitative plant characters, which are of economic value are highly influenced by environmental conditions, the progress of breeding in such a population is primarily conditioned by the magnitude, nature and interaction of genotypic and non-genotypic variation in the various plant characters.

Johannsen (1909) in his famous 'Pure line theory' suggested that both heritable and non heritable changes affect the somatic variation and that the variation in a pure line is entirely due to environment.

Nilson Ehle (1909) and East (1916) proposed the need to partition the phenotypic variability into it's genetic and non-genetic components, because of environmental influence.

The observable variation in the population is the result of interaction of genotypic and the environmental factors. The effects due to these two factors are found to be blended together and hence, can not be resolved directly. Fisher (1930) first presented the method to separate these effects due to the above two factors. The extent of genotypic variability was presented by him with appropriate statistical method and the value was expressed as a genotypic coefficient of variation. He also considered it as very useful to know how much genetic variation is heritable.

Charles and Smith (1939) and Power *et al.* (1950) separated genetic variance from total variance by use of estimates of environmental variance from the non segregating population. Genotypic coefficient of variation indicates the relative magnitude of genetic diversity present in the material and helps to compare the genetic variability present for different characters.

Burton (1952) has suggested genetic coefficient of variation as a measure of the extent of genetic variability present in a population for a particular character. Whereas, phenotypic coefficient of variation measures the extent of total or phenotypic variability.

The variability studies in rice were carried out by various research workers as described below.

Chauhan and Tandon (1984) reported that the genotypic coefficient of variation was high for grain yield, plant height, ear bearing tillers and number of grains per panicle and low for days to flower, days to maturity, length of panicle and per cent spikelet fertility.

Amirthadevarathinam (1990) found that the range of variation for different characters indicated wide differences among the genotypes in *indicas* and also *japonicas*. The maximum range of variation was observed for grains per panicle followed by culm length, days to 50 per cent flowering, seedling height, plant yield, tiller number and panicle length.

In the study of 8 yield related traits on 20 rice varieties , Choubey and Singh (1994) noticed higher PCV than GCV.

Reddy *et al.* (1995) found significant genotypic variations in all the yield attributing characters like number of tillers, number of productive tillers, number of grains per panicle, 1000 grain weight and yield.

Sawant and Patil (1995a) reported wide range of variations for all the measured characters . Higher coefficient of variation was observed for grains per panicle, grain yield per plant and plant height.

Reddy and De (1996) observed significant differences among the genotypes for all the 12 characters studied. Among all the characters, grain yield per hill, number of grains per panicle and panicle weight showed higher estimates of GCV and PCV indicating the importance of these traits in selection.

Singh and Choudhary (1996) recorded higher PCV than GCV for all the characters studied indicating that they all interact with the environment to some degree. Estimates of GCV and PCV were highest for biological yield, followed by number of panicles per plant, number of grains per panicle, grain yield per plant, 1000 grain weight and harvest index.

Marekar and Siddiqui (1997) recorded high genotypic and phenotypic coefficients of variation for grain length and length : breadth (L/B) ratio in the study of 73 rice varieties.

Borbora and Hazarika (1998) recorded highly significant variation among 30 genotypes of rice. The differences between genotypic and phenotypic coefficients of variation were relatively low for almost all the characters except grain yield per plant.

Rather *et al.* (1998) recorded high genotypic coefficient of variability coupled with moderate heritability and genetic advance for spikelet sterility and grains per panicle. Significant differences were observed for all the characters among the genotypes.

Jha *et al.* (1999) derived information on mean, range, genotypic and phenotypic coefficients of variability, heritability and genetic advance from data on 16 quantitative traits in 14 populations of *Oryza nivara*, 50 of *O. sativa f. spontanea* and one of *O. rufipogon*. The phenotypic coefficient of variability was higher than the genotypic coefficient of variability.

In twenty semi-deep water rice varieties, Tripathi *et al.* (1999) noticed high genotypic and phenotypic variation for plant height and panicle length. However, high genotypic coefficient of variation, heritability and genetic advance were observed for grain yield.

Vange *et al.* (1999) observed significant variation for most of the traits in the study of 10 rice genotypes. Grain yield ranged from 2.0 to 4.2 t/ha, 1000 grain weight ranged from 22.4 to 30.9 g, grains per panicle ranged from 116 to 155, panicles/m^2 ranged from 140 to 233. Genotypes showed consistent significant ($P \leq 0.01$) differences for grain yield.

Kumar *et al.* (2001) studied population of 42 progenies derived from seven rice crosses in segregating generations for 10 quantitative characters. The phenotypic coefficient of variation was comparatively higher than the corresponding genotypic coefficient of variation for all characters.

Roy *et al.* (2001) observed high phenotypic and genotypic variances for grain yield followed by number of filled grains per panicle.

Naik *et al.* (2002) reported significant differences among 200 scented rice genotypes including one non scented check, Ratna, from the analysis variance for all the characters studied. The GCV and PCV values were high for panicle number, number of filled grains per panicle and grain yield per plant. Medium to low values of GCV and PCV were observed for plant height, panicle length, 1000 grain weight, grain length, length/breadth ratio and days to 50 per cent flowering.

Pandey and Awasthi (2002) observed significant genetic variability among 21 genotypes of aromatic rice for yield attributing traits, *viz.,* plant height, days to 50 per cent flowering, total number of tillers per plant, panicle length, number of grains per panicle, test weight, grain length, grain breadth and grain yield per plant. From this study, they concluded that all the yield attributing traits played major role in enhancement of production of grain yield.

Kumari *et al.* (2003) evaluated 55 rice cultivars and their 42 crosses for phenotypic variation in yield and yield components, *viz.,* days to 50 per cent flowering, plant height, tiller number, panicle length, boot leaf length, boot leaf breadth, number of grains per panicle, spikelet fertility and 100-grain weight. Tiller number, number of grains per panicle and boot leaf length exhibited high phenotypic and genotypic coefficients of variation.

Mall *et al.* (2005) recorded a wide range of variation for mean values of plant height, days to panicle initiation, days to 50 per cent flowering, number of tillers per plant, number of panicles per plant, number of spikelets per panicle, panicle length and flag leaf length and width.

Patil and Sarawgi (2005) recorded high genetic and phenotypic coefficient of variation for number of unfilled grains per panicle, unfilled grain percentage, grain yield per plant, 1000 grain weight, number of ear bearing tillers per plant and number of filled grains per panicle.

Vaithiyalingan and Nadarajan (2006) observed significant differences between the F_2 populations of different inter sub-specific crosses for all the characters studied, i.e. days to 50 per cent flowering, pollen fertility, plant height, productive tillers per plant, panicle length, grains per panicle, spikelet fertility, test weight and grain yield. Grain yield showed high genotypic coefficient of variation followed by spikelet fertility, productive tillers per plant and number of grains per panicle.

2.2 Heritability and genetic advance

Heritability is an index to transmissibility of a character from parents to their offsprings. The concept of heritability is important in determining whether the phenotypic differences among the individual are genetical or the result of environmental factors. Genetic advance measures the expected gain from the selection applied in a population. Heritability along with genetic advance gives the best picture of the efficiency of selection.

Lush (1940, 1949) classified heritability into broad sense and narrow sense. Broad sense heritability means the ratio of genotypic variance to the phenotypic variance and in narrow sense it is a ratio of additive variance to the phenotypic variance.

Robinson *et al.* (1949) defined heritability as the additive genetic variance in percentage of total variance. According to them additive genetic variance indicates the degree to which the progenies are likely to resemble the parents.

Johnson *et al.* (1955) suggested that heritability in conjunction with genetic advance was more effective and reliable in predicting the resultant effect of selection. Genetic advance is a measure of expected genetic progress based on which selection procedure can be evaluated.

Robinson (1966) classified heritability estimates in three categories, *viz.,* low heritability (5-10%), medium heritability (10-30%) and high heritability above 30 per cent.

The heritability values are most important to plant breeders because they indicate that the selection of parents bearing particular, measurements will produce offsprings of similar phenotypes. Thus, the improvement in valuable traits depends upon a fairly accurate evaluation of the heritability. Further, genotype x environment interaction are those in which the relative performance of different genotypes vary with environments in which the genotypes are placed. The genotypic variances as a cause for phenotypic differences may arise from a variety of sources, like additive factors, dominant effects, epistasis or interaction effects (Strickberger, 1968).

Sawant and Patil (1995b) recorded high values of heritability coupled with high expected genetic advance for the characters, grains per panicle, plant height, grain yield per plant and 1000 grain weight.

Reddy and De (1996) estimated the range of heritability from 43.63 per cent for number of ear bearing tillers per hill to 94.96 per cent for grain length. Higher values of heritability were observed for grain length followed by 1000 grain weight, grain breadth, plant height, panicle weight, grain yield and number of grains per panicle.

Vanniarajan *et al.* (1996) drew the information on 9 characters in F_6 generation of 3 crosses, MS37A x IR50, Zehen Zhan 97A x IR50 and Erjiunan1A x IR50. Filled grains per panicle showed high heritability coupled with genetic advance in cross MS37A x IR50. Heritability and genetic advance were high for grain yield in Erjiunan1A x IR50.

High heritability estimates were observed for plant height (99.15%) followed by days to 50 per cent flowering (98.20%) and productive tillers per plant (98.19%) by Saravanan and Senthil (1997) in the study of 3 male sterile lines and their F_1 hybrids.

Borbora and Hazarika (1998) observed high heritability and genetic advance for number of chaffy and filled grains per panicle, 1000 grain weight, grain yield per panicle and number of secondary branches per panicle, indicating the effectiveness of selection for these characters.

Shanthakumar *et al.* (1998) recorded high heritability and genetic advance together with significant genotypic coefficient of variability for plant height, total tillers per hill, flag leaf length and grain yield per hectare in 34 rice genotypes.

In nine rice genotypes, developed through F_2 derived anther culture, Pattanayak and Gupta (1999) recorded high heritability estimates for days to flowering, maturity, plant height, yield per plant and grain yield. Genetic advance as percentage of mean was highest for yield per plant followed by grain yield.

Thakur *et al.* (1999) estimated high heritability coupled with high genetic advance for biological yield, panicle weight, branches per panicle and grains per panicle among F_2 populations of Anupama x IR 36 cross.

Venkataramana and Hittalmani (1999) recorded high values of heritability coupled with genetic advance for grain yield per plant, productive tillers per plant, panicle excertion and epicuticular wax content per leaf in F_2 segregates of rice.

Ali *et al.* (2000) observed that the heritability estimates were maximum for plant height, 100-seed weight, number of tillers per plant, spikelet density and panicle length, but maximum genetic gain relative to the mean was expected for number of tillers per plant, plant height and spikelet density.

Thakur *et al.* (2000) drew the information on range, genotypic and phenotypic coefficients of variation, heritability and genetic advance for nine yield related traits in the parents and F_2 progeny of the cross Anupama x IR-50. Biological yield and panicle weight showed high heritability coupled with high genetic advance and were positively associated with grain yield.

Verma *et al.* (2000) recorded high to moderate genotypic coefficient of variation and high narrow sense heritability coupled with high genetic advance for plant height, days to flowering and 100 grain weight.

Yadav (2000) observed appreciable amount of genotypic coefficient of variation, heritability and genetic advance for total grains per panicle, total grains per plant and grain yield per plant in the study of 15 rice genotypes.

Roy *et al.* (2001) found range of heritability from 50 per cent (grain yield per hill) to 90 per cent (grain breadth) in 25 rice genotypes. Genetic advance as a percentage of mean was highest for number of filled grains per panicle (70.34) followed by grain yield (68.72). Number of filled grains per panicle, 1000-grain weight, grain length and breadth exhibited less environmental effect and high heritability coupled with moderate to high genetic advance.

Kumar *et al.* (2001) noticed higher heritability for days to 50 per cent flowering, plant height and 1000 grain weight, while studying population of 42 progenies derived from 7 rice crosses in segregating generations. Characters like plant height, grain L/B ratio and 1000 grain weight showed moderate genetic advance.

Naik *et al.* (2002) reported high heritability estimates for all the characters studied in the evaluation of 200 scented rice genotypes including one non-scented check, Ratna. The heritability values ranged from 71.4 per cent (panicle number per plant) to 99.5 per cent (days to 50 per cent flowering). The genetic advance expressed in percentage of mean was high for number of grains per panicle, number of sipkelets per panicle and grain yield per plant.

Kumari *et al.* (2003) reported high heritability and genetic advance for the characters, tiller number, number of grains per panicle and boot leaf length. Plant height, panicle length and 100-grain weight showed high heritability coupled with moderate genetic advance, indicating the role of non-additive gene effects in the inheritance of these traits.

Mall *et al.* (2005) reported high heritability coupled with high genetic advance for plant height, number of tillers per plant, number of panicles per plant, number of spikelets per panicle and flag leaf length.

2.3 Correlation and path analysis

The information on nature and extent of association between character pair would strengthen the selection programme, aiming at the improvement in grain yield as yield is a complex character and is governed by polygenic system. Moreover, it is highly influenced by environmental fluctuations.

Genotypic correlation coefficient provides a measure of genotypic association between characters and gives an indication of more useful characters. They provide a basic information to breeder in understanding the nature of the species with which they work. They also help to identify characters that have little or no importance in the selection programme.

Correlation studies give the amount of association between any pair of character. The direct and indirect effect of the components of yield are however, not revealed by this study. Especially, when more and more varieties are included in the study, the indirect contribution becomes more complex and paramixing. However, path coefficient analysis developed by Wright (1921) helps in partitioning the correlation coefficient into direct and indirect effects, thereby providing relative importance of each of the causal factors. Dewey and Lu (1959) used this technique first time for plant selection in crested wheat grass.

A number of workers have studied the relationship between yield and other characters and carried out path analysis in rice. A brief review of it is given below.

Moeljopawiro (1986) observed that the grain width and 100-grain weight were positively associated with each other, but negatively correlated with other characters. Grain length was also negatively associated with grain width.

Reddy and Ramachandraiah (1990) reported highly significant positive correlations between grain yield per plant and eight of the yield components, *viz.*, plant height, panicle length, flag leaf area, number of effective tillers per plant, number of fertile grains per panicle, number of primary branches per panicle, number of secondary branches per panicle and 1000 grain weight. Path analysis revealed the highest direct contribution to grain yield per plant from number of secondary branches per panicle.

Anand Kumar (1992) noticed significant positive association of yield with tiller number, panicle length and boot leaf breadth. He also reported negative association between plant height, panicle length and boot leaf breadth with yield.

Saimuraliraj (1992) recorded positive and significant association between grain yield and panicle weight, number of productive tillers per plant and harvest index both at phenotypic and genotypic levels.

Deosarkar and Nerkar (1994) worked out simple correlations and path coefficients in the F_2 populations of two crosses namely, Prabhavati x IET 8573 and Prabhavati x Basmati 370. They observed maximum direct effect of L : B ratio on kernel elongation in cross Prabhavati x Basmati 370.

Mehetre *et al.* (1996) revealed the largest positive direct effects of days to 50 % flowering and days to maturity on grain yield in induced mutant varieties.

Cheema *et al.* (1998) observed highly significant correlations of grain yield per plant with number of spikelets per panicle, number of primary and secondary branches per panicle and panicle length. Number of secondary branches per panicle showed highly significant positive correlations with number of primary branches per panicle, spikelets per panicle and panicle length. Number of primary branches per panicle and panicle length were also significantly correlated. Path coefficient analysis showed that the number of secondary branches per panicle was more important than panicle length and number of primary branches in the determination of yield.

Choudhary and Das (1998) noticed positive correlations for days to 50% flowering, days to maturity, plant height, grains per panicle and panicle length with yield.

Gupta *et al.* (1998) recorded positive correlation of grain yield with 1000 grain weight. Panicle length, panicle density and sterility percentage were the main component characters affecting yield directly. Indirect effects were contributed by 1000 grain weight and days to flowering through grains per panicle and panicle length, respectively.

High positive correlation for grain yield with plant height, panicle length, spikelet fertility and 1000 grain weight in 34 rice genotypes was noticed by Kumar *et al.* (1998). Path analysis revealed the direct effect of spikelet fertility and moderate direct effects of plant height, panicle length and 1000 grain weight to yield.

Selvarani and Rangasamy (1998) noticed that days to flowering, leaf area index, number of productive tillers, dry matter production and harvest index were significantly and positively correlated with grain yield in F_2 population of the cross IR 50 x TNAU 801793.

Singh *et al.* (1998) reported positive and significant genotypic correlations for test weight with grain density, amylose content, grain length, grain width with volume expansion in 45 indigenous genotypes of rice.

Thakur *et al.* (1998) recorded positive correlation of grain yield with biological yield, number of tillers per plant, harvest index, plant height and panicle weight in the F_2 population.

Verma and Mani (1998) evaluated 280 F_3 progenies and recorded that grain yield per plant was positively and significantly associated with tillers per plant, grains per panicle and 1000 grain weight at phenotypic level.

In the study of 114 homozygous lines, Bagali *et al.* (1999) reported significant correlation coefficient of grain yield with panicle density, number of filled grains per panicle, panicle weight, harvest index and fertility (%) at genotypic level. Panicle weight followed by number of grains per panicle and harvest index had the greatest positive direct effects on grains yield per plant at the phenotypic level. Panicle weight showed high positive indirect effects through harvest index and number of grains.

Govindarasu *et al.* (1999) studied correlations and observed that spikelets, grains, high density grains per panicle, secondary branches per panicle were the important yield contributing characters.

Gupta *et al.* (1999) recorded positive association of grain yield with panicles per plant, panicle length, grains per panicle and panicle weight. Negative correlations were observed for panicles per plant with grains per panicle and grains per panicle with 100 grain weight. Path analysis revealed that panicles per plant, grains per panicle and panicle weight were the most important component characters of grain yield and need greater selection emphasis.

Rao and Shrivastav (1999) revealed the positive association of days to flowering with days to maturity and number of fertile spikelets per panicle, fertile spikelets per panicle with fertility of spikelets and grain yield, harvest index with grain yield in the study of 18 divergent rice genotypes.

Sathya *et al.* (1999) observed that productive tillers per plant was the principal character responsible for grain yield per plant, followed by 100 grain weight, days to 50 per cent flowering, plant height and harvest index as they had positive and significant association with yield in hybrid rice.

Sinha *et al.* (1999) recorded the high association between the number of secondary branches and number of spikelets per panicle in 36 gora rice varieties. Grains per secondary branch was the next most important character due to its high indirect contribution through number of secondary branches per primary branch and kernel breadth. Grain length, breadth and weight had negative effects on number of spikelets per panicle, grains per primary branch and number of high density grains had almost negligible direct and indirect effects on number of spikelets per panicle.

Vange *et al.* (1999) found that the genotypic correlation were slightly higher than the phenotypic correlation. Genotypic correlation of yield with grain weight per panicle, grains per panicle, panicle weight, branches per panicle, panicles per m^2 and flag leaf area were more than 0.50 but lower for 1000 grain weight, panicle length and 50 per cent heading.

Verma and Mani (1999) observed that correlated response to selection for the characters, namely tillers per plant, panicle length, grains per panicle and 1000 grain weight in 280 F_3 progenies of the cross UPR 8334 x Sita .

Balan *et al.* (2000) recorded the significant positive association of number of panicles/m^2 with grain yield. Path coefficient analysis showed high positive direct effects of number of panicles /m^2 on grain yield. Days to 50% flowering exerted a high positive indirect effect on grain yield through number of panicles/m^2.

Cristo *et al.* (2000) reported the highest correlation between the final height, panicle length, full grains per panicle and yield in the study of rice hybrids and cultivars.

Bastian *et al.* (2000) found that grain yield was positively correlated with number of grains per panicle, single panicle weight and number of primary rachis, in the study carried out on 16 rice cultivars.

Manonmani *et al.* (2000) revealed the significant and positive correlation of the earliness with most of the characters by analyzing 20 crosses among lines of *indica* rice. Correlation studies revealed that the selection for very early types obviously resulted in reduction in panicle length , number of grains and 100 grain weight, which in turn reduced the yield.

Shivani and Reddy (2000) found that the genotypic correlation coefficients were in general higher than the corresponding phenotypic ones. Grain yield showed positive significant correlation with plant height, days to 50 per cent flowering and leaf area at genotypic level. He revealed the negative direct effect of plant height on grain yield per plant, while days to 50 % flowering contributed maximum positive direct effect on grain yield.

Venkataramana and Hittalmani (2000) recorded highest positive direct and indirect effect via productive tillers per plant and harvest index on grain yield. Highest negative direct effect was recorded by plant height. Selection based on number of grains per panicle with maximum productive tillers will be efficient.

Ganesan (2001) studied the direct and indirect effects of yield component characters of 48 rice hybrids. Filled grains per panicle had the highest significant positive direct effect (0.895) on yield per plant followed by number of tillers per plant (0.688), panicle exsertion (0.172), panicle length (0.167) and plant height (0.149). Plant height, days to flowering, number of tillers per plant and productive tillers per plant had positive and negative indirect effects on yield.

Nayak *et al.* (2001) recorded positive correlation of grain yield per plant with plant height, panicle number per plant, panicle length, total number of spikelets per panicle and total number of grains per panicle at both genotypic and phenotypic levels. Path coefficient analysis revealed that panicle number per plant, total number of grains per panicle and 1000 grain weight contributed to the grain yield of the plant. Days to 50 per cent flowering and panicle length had negative direct effect on yield.

Shanthi and Singh (2001) in their studies on six quantitative characters found that plant height was positively and significantly associated with panicle length, number of grains per panicle and grain yield per plant at both genotypic and phenotypic levels. The number of grains per panicle affected the panicle length. It was concluded that the yielding ability in rice would be improved by selecting taller plants with longer panicles coupled with a higher number of grains per panicle.

Oad *et al.* (2002) observed positive correlation of grain yield with plant height, ratoon rating, 1000-grain weight, number of panicles, panicle length, seed length and tillers at harvest among 30 rice ratoon cultivars and advance lines. Total tillers at harvest, panicles per plant, panicle length and ratoon rating contributed maximum to the determination of yield.

Surek and Beser (2003) observed highest positive direct effects of biological yield and harvest index on grain yield in the study of 80 breeding lines derived from 11 different cross populations in F_2 generations.

Patil and Sarawgi (2005) revealed the positive direct effect of 1000 grain weight on grain yield, followed by number of ear bearing tillers per plant, number of filled grains per panicle and number of days to 50 per cent flowering. However, 1000 grain weight showed indirect effect on grain yield per plant through the number of filled grains per panicle and plant height.

Manonmani and Ranganathan (2006) analyzed four lines and five testers along with twenty crosses of rice. Number of productive tillers per plant had high positive direct effect on yield followed by days to 50 per cent flowering, plant height, grains per panicle and 100- grain weight.

Swain and Reddy (2006) noticed positive correlation of number of panicles per plant and single panicle weight with grain yield under normal planting. Path analysis further revealed that single panicle weight was the most important character under these situations.

2.4 Genetic divergence

One important object of obtaining biometric measurements is to study the possibilities of classifying different groups of individuals in the form of a significant pattern.

This is possible with a generalized distance between any two pairs of groups as suggested by Mahalanobis (1936). With the concept realized by many research workers that geographical isolation may not be the only reason for genetic divergence, Mahalanobis D^2 became an useful statistical tool to measure it. Analysis of divergence has been used by plant breeders and it has helped them to classify their breeding material into useful groups.

Rao (1948) suggested more flexible method which would replace the measurements on a large number of characters, all of which contribute in some degree or other towards discrimination by relatively few measurements.

Allard (1961) described relationship between genetic diversity and consistency of performance in different environments by using three distinct levels of genetic diversity and productivity were completely related and further stated that many factors determined the productivity of mixed population, while genetic diversity and stability appeared more simply related irrespective of number of characteristics of the components involved.

Murthy and Arunachalam (1966) while assessing the nature of divergence in relation to breeding systems, reported that geographical distribution and genetic diversity could not be directly related in any of the crops examined. They suggested that genetic drift and selection in different environments could cause greater diversity than geographical distance. They observed that the D^2 analysis, canonical vectors and the size of canonical roots had revealed parallel features in the mechanism of genetic diversity, in all the crops examined in spite of their contrasting breeding systems. They also stated that in general, height, flowering time, tiller number and number of seeds were the largest contributors to genetic diversity in the crops Brassica, linseed, wheat, Nicotiana and sorghum.

Bhatt (1970) carried out multivariate analysis to select parents for hybridization aiming at yield improvement in self-pollinated crops and observed that the genotypes from different origins were clustered together. He suggested that,it would be logical to effect crosses between genotypes belonging to the clusters separated by high estimated statistical distance. The relative contribution of each character to the total divergence showed that yield *per se* had a low contribution (3.2 %).

Kumari and Rangasamy (1997) grouped 62 early rice genotypes into 6 clusters based on eight important yield contributing characters. There was no relationship between geographical distribution and genetic diversity. Characters like grain yield per plant, panicle exertion and plant height made the largest contribution to total divergence.

Hanamaratti *et al.* (1998) grouped 50 rice genotypes into 18 and 17 clusters under low and upland conditions, respectively, independent of their geographical origin.

Grouping of 25 rice genotypes into 5 clusters was done by Mokate *et al.* (1998). They observed that the genotypes belonging to these clusters form ideal pairs for planning a hybridization programme.

Eighty five indigenous rice varieties were grouped into 12 clusters by Ahmed and Borah (1999). Tiller number, panicles per hill, grains per panicle, grain fertility and grain yield accounted for the major portion of divergence.

Bansal *et al.* (1999) identified the intervarietal crosses which may be useful in creating wider variability for early maturity, dwarf and high yielding segregants based on mean performance, genetic distance and clustering pattern by studying 15 clusters formed among 34 rice genotypes.

Kandhola and Panwar (1999) clustered 52 indigenous and exotic genotypes of rice into 11 clusters. There was no association between genetic and geographic diversity. They concluded that hybridization among genotypes drawn from widely divergent clusters with high yield potential is likely to produce heterotic combinations and wide variability in segregating generations.

Fifty rice genotypes were grouped into 6 clusters by Pandey *et al.* (1999). The characters contributing the most to total divergence were days to 50 per cent flowering, plant height, primary branches per panicle and 100 seed weight (27.9, 24.7, 16.4 and 10.4, respectively). Genetic diversity was not correlated with geographical diversity.

Kole (2000) clustered 20 genotypes of aromatic rice into 4 clusters. Grain length, panicle number, 500 grain weight, flag leaf area and days to flower were the major characters contributing towards divergence.

Thirty eight rice varieties were classified into four clusters by Shanmugasundaram *et al.* (2000) using Mahalanobis D^2 statistic based on ten morphological traits. It was reported that genotypes within a cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance with regard to yield.

Bhardwaj *et al.* (2001) concluded that length : breadth ratio contributed maximum towards the genetic divergence followed by 100-grain weight and grain yield per plant accounting to 87 per cent of total divergence in 50 genotypes of rice.

Rather *et al.* (2001) divided 50 diverse rice cultivars into 8 clusters. Geographical origin was not found to be the good parameter of genetic divergence. The 100 grain weight and length : breadth ratio of grain were important components of divergence.

Roy *et al.* (2002) noticed that the pattern of distribution of genotypes within various clusters was random and independent of geographical origin or region of adaptation by studying 10 clusters formed from 50 high yielding varieties and traditional germplasm of rice. Days to 50 per cent flowering, grain length, kernel breadth and grain yield per plant were found to be the major component characters, contributing towards genetic diversity.

Babu *et al.* (2003) grouped 33 rice cultivars into 10 clusters based on genetic distance. High order of divergence recorded between clusters could be used as promising parents for hybridization to obtain high heterotic response.

Jadhav *et al.* (2003) grouped 49 rice cultivars into 9 clusters based on genetic distance. The cultivars from clusters, IV, V, VIII and IX were found to have potential as parents for the development of hybrids with high yield and quality.

Manna *et al.* (2003) studied genetic divergence for yield and yield components in 60 rice cultivars. Kernel characteristics and 100 embryo weight showed the greatest contribution towards genetic divergence.

Shiv Datt and Mani (2003) recorded greater genetic variability among basmati genotypes which were clustered into 4 groups. Plant height contributed the maximum genetic divergence (52.24 %) followed by days to 50 per cent flowering (22.56 %) and grain yield per plant (8.63 %).

Based on D^2 values, Senapati and Sarkar (2005) clustered 40 tall indica rice genotypes into 5 clusters using Mahalanobis's D^2 statistic. Panicle number per hill, panicle length, sterility percentage, yield per plot and 1000 grain weight were the chief contributors towards genetic divergence.

Singh *et al.* (2005) concluded that the cultivars included in diverse groups can be used as promising parents for hybridization programme for obtaining high heterotic response. They clustered 17 induced mutants of Basmati rice into 5 clusters using Mahalanobis D^2 statistic.

Gahalain (2006) grouped 55 rice genotypes into twelve clusters by using Mahalanobis's D^2 statistic. The highest contribution towards total divergence was rendered by total grains per panicle (22.6 %), followed by fertile grains per panicle (22.6 %), panicle weight (10.1 %), days to 50 per cent flowering (7.6 %) and shoot height (7.2 %).

Naik *et al.* (2006) noted the presence of appreciable amount of genetic diversity in D^2 analysis of 50 aromatic rice accessions. Seven clusters were formed such that high variability is observed between the genotypes in different clusters for different characters.

Shukla *et al.* (2006) classified thirty nine "new plant type" tropical *japonica* lines and three improved cultivars into 14 clusters using Mahalanobis D^2 statistic. Harvest index contributed maximum (45.99 %) to the total divergence, while maximum inter cluster distance (1328.30) was recorded between cluster VI and VII.

MATERIAL AND METHODS

CHAPTER 3

MATERIAL AND METHODS

The present investigation "Genetic diversity and path analysis studies in rice (*Oryza sativa* L.)" was conducted at the Botany Farm, College of Agriculture, Pune -5 during *Kharif* 2006. The details of the material used and procedures followed during the course of this investigation are given below.

3.1 Material

For the present study forty genotypes of rice originating from different geographic regions and showing phenotypic variability for different agronomic and yield characters were obtained from the germplasm maintained by Agricultural Research Station, Radhanagari.

3. 2 Methods

3.2.1 Raising of the experimental material

The forty genotypes of rice were sown on 26th June, 2006 in a completely randomized block design with three replications. Each entry was represented by a single row of 3 m length with a spacing of 22.5 cm between and 10 cm within the row. One border row was sown on both the sides of blocks to reduce the border effects. Two seeds were dibbled per hill to ensure better crop stand and a single seedling was kept per hill after thinning.

Table 3.1. The genotypes, their pedigree and origin

Sr. No.	Accession No. (ARS number)	Identity / Pedigree	Origin
1	RDN 1	Bishnubhog	Orissa
2	RDN 3	Lalu	Orissa
3	RDN 4	Lectimachi	Orissa
4	RDN 6	Shrabanmasi	Orissa
5	RDN 7	Sheetalkani	Orissa
6	RDN 8	Tulsiganthi	Orissa
7	RDN 9	Tulsikanthi	Orissa
8	RDN 11	R.K. 1019 (Sel. From Krishnabhog)	Chhattisgarh
9	RDN 12	R.D. 1008 (Sel. From Dubraj)	Chhattisgarh
10	RDN 13	R.R. 399 (Sel. From Rajabhog)	Chhattisgarh
11	RDN 14	R.D. 1214 (Sel. From Dubraj)	Chhattisgarh
12	RDN 15	R.D. 934 (Sel. From Dubraj)	Chhattisgarh
13	RDN 18	R.B. 2258 [Sel. From Dubraj, (Dadhwa)]	Chhattisgarh
14	RDN 19	R.C. 781 (Sel. from Chinoor)	Chhattisgarh
15	RDN 20	R.T. 206 (Sel. From Til kasturi)	Chhattisgarh
16	RDN 21	R.T. 150 (Sel. From Tendu Phool)	Chhattisgarh
17	RDN 23	R.B. 287 [Sel. from Dubraj (Bandi)]	Chhattisgarh
18	RDN 24	R.B. 122 (Sel. From Bhanta Phool)	Chhattisgarh
19	RDN 26	R.M. 1A ||| (Sel. from Muni Bhog)	Chhattisgarh
20	RDN 27	R.J. 293 || (Sel. From Jira)	Chhattisgarh
21	RDN 29	Adan Chini B	U.P.

Sr. No.	Accession No. (ARS number)	Identity / Pedigree	Origin
22	RDN 30	Kanak Jeer B	U.P.
23	RDN 32	Loung Choosi A	U.P.
24	RDN 37	Bhanta Phool A	U.P.
25	RDN 42	Champaran Basmati -4	Bihar
26	RDN 43	Kanak Jeera	Bihar
27	RDN 44	Maricha	Bihar
28	RDN 45	Type – 3 (Sel. Form Deharadoon Basmati)	Uttarkhand
29	RDN 46	Basmati 370 (Pure line selection from local lines form Punjab, Now in Pakistan)	Pakistan
30	RDN 47	Bhura Rata 4 – 10 x Pakistan Basmati	DRR, Hyderabad
31	RDN 48	Taroari Bamati (Sel. form Karnal Local)	Haryana
32	RDN 49	Pusa Basmati-1 (Pusa 150 x Karnal local)	IARI, New Delhi
33	RDN 50	Vasumati (PR 109 x Pakistan Basmati)	DRR Hyderabad
34	RDN 51	Sugandhamati (Pusa Basmati – 1 x IET 12603)	DRR, Hyderabad
35	RDN 52	Kalanamak (Bordpur)	Uttarkhand
36	RDN 54	Ambemohar – 157	Maharashtra
37	RDN 57	Diwani	U.P.
38	RDN 58	RTN 105-1-2-1-1	Maharashtra
39	RDN 59	KJT 17-6-8-15-27	Maharashtra
40	RDN 60	BR 827-35-3-1-1-1 (Sel. form BR 827)	IRRI, Phillipines

3.2.2 Cultural practices

Thinning and gap filling were carried out to ensure individual plant per hill. All recommended agronomic practices were carried out as and when required. Total dose of fertilizers applied during crop duration was 75 kg N, 30 kg P_2O_5, 30 kg K_2O per hectare. Nitrogen was applied in three split doses of 15, 30 and 30 kg N/ha at land preparation, 35-40 days after sowing and panicle initiation stage, respectively. Total dose of P_2O_5 and K_20 was applied at sowing.

3.3 Observations

Observations on following 12 quantitative characters and one qualitative character was recorded on five randomly selected plants from each plot in each replication. These plants were tagged before flowering.

3.3.1 Days to 50 per cent flowering (No.)

The total number of days taken by each entry from sowing to opening of first flowers in 50 per cent of the plants in each plot was recorded.

3.3.2 Days to maturity (No.)

The total number of days taken by each entry from sowing to maturity on plot basis were counted and recorded.

3.3.3 Plant height (cm)

Height of the plant at maturity from the base of the plant to the tip of the main panicle excluding awns if any, was measured.

3.3.4 Effective tillers per plant (No.)

The number of tillers bearing the panicles per plant were recorded.

3.3.5 Panicle length (cm)

The total length of the panicle from its base to the tip excluding awns if any, was measured.

3.3.6 Secondary branches per panicle (No.)

The total number of the branches of the panicle bearing grains were recorded.

3.3.7 Grains per panicle (No.)

The total number of filled grains for all the panicles per plant was counted and averaged to obtain the number of grains per panicle.

3.3.8 Grain length (mm)

The average length of ten dehulled grains form each entry in each replication was measured and averaged.

3.3.9 Grain breadth (mm)

Ten dehulled grains (used for measuring length) of each accession were arranged breadth wise, for the cumulative measurement of breadth in centimeters. The average breadth of these dehulled grains from each entry in each replication was measured and averaged.

3.3.10 Length : Breadth (L:B) ratio

Average of the ratio of length to the breadth of the same ten dehulled grains used for recording grain length and breadth was calculated and recorded.

3.3.11 1000 grain weight (g)

Weight of one thousand randomly selected filled grains was recorded in gram for each genotype in each replication.

3.3.12 Protein content (%)

The total protein content of the grain was estimated by following Micro-Kjeldahls distillation method for estimation of nitrogen and multiplied by factor 5.95 to obtain percentage of protein (Singh and Singh, 1994).

3.3.13 Seed yield per plant (g)

The total weight all the filled grains per plant was measured in grams.

3.4 Statistical analysis

The analysis of variance for each character, covariance for each character pair, D^2 analysis as a measure of diversity and path analysis for knowing direct and indirect effects of different characters on yield were carried out by subjecting the mean data for computer analysis.

3.4.1 Analysis of variance for treatment differences

The analysis of variance to test the hypothesis that there are no genotypic differences for the characters studied,was done according to Panse and Sukhatme (1985) in the following form.

Source of variation	D.F.	M.S.S.	Expected mean square
Replication	(r-1)	MSr	$\sigma^2_e + t\sigma^2_r$
Treatment	(t-1)	MSt	$\sigma^2_e + r\sigma^2_t$
Error	(r-1) (t-1)	MSe	σ^2_e
Total	(rt-1)		

Where,

r = Number of replications

t = Number of treatments

3.4.2 Genotypic coefficient of variation (G.C.V.)

Genotypic coefficient of variation (G.C.V.) was estimated by the formula suggested by Burton (1952).

$$GCV\ \% = \sqrt{\sigma^2_g} \ / \ \bar{x} \times 100$$

Where,

$$\sigma^2_g = \frac{\text{Mean sum of squares due to genotypes} - \text{Mean sum of squares due to error}}{r}$$

Here,

$\sigma^2_g = V_g$ = Genotypic variance

$\bar{x}$ = General mean of the character

r = Number of replications

3.4.3 Phenotypic coefficient of variation (P.C.V.)

Phenotypic coefficient of variation (P.C.V.) was also estimated by the formula suggested by Burton (1952).

$$PCV\ \% = \sqrt{\sigma^2_p} \;/\; \bar{x} \times 100$$

Where,

σ^2_p = Genotypic variance + Mean sum of squares due to error

Here,

$\sigma^2_p = V_p$ = Phenotypic variance

3.4.4 Heritability ($h^2_{b.s.}$)

Heritability estimates in broad sense (H) were computed by the formula suggested by Burton (1952).

$$h^2\,(b.s.) = Vg/Vp \times 100$$

Where,

h^2 = Heritability percentage in broad sense

V_g = Genotypic Variance and

V_p = Phenotypic Variance

3.4.5 Genetic Advance :

The extent of genetic advance expected through selection for each character was calculated as per the formula suggested by Johnson *et al.* (1955).

$$G A = K \times (V_g / V_p) \times \sigma_p \qquad \text{or}$$

$$= K \times h^2 \times \sigma_p$$

Where,

h^2 = Heritability percentage in broad sense

V_g = Genotypic Variance and

V_p = Phenotypic Variance

K = Selection differential which is 2.06 at 5 per cent selection intensity (Lush, 1949).

σ_p = Phenotypic standard deviation

Genetic advance as per cent of mean

$$\text{G.A. as per cent mean} = \text{G.A.} / \bar{x} \times 100$$

Where,

G.A. = Genetic advance

$\bar{x}$ = Mean of the character

3.4.6 Association analysis

The correlation coefficients were calculated to determine the degree of association of the characters with yield and yield attributes.

For that genotypic and phenotypic correlation coefficients were worked out by adopting method described by Singh and Chaudhary (1977).

$$r_p = \text{Covariance } X,Y._{(p)} / \sqrt{\text{Variance } X_{(p)}. \text{ Variance } Y_{(p)}}$$

Where,

r_p = Phenotypic correlation between character X and Y

p = Phenotypic

and

$$r_g = \text{Covariance } X,Y_{(g)} / \sqrt{\text{Variance } X_{(g)} . \text{Variance } Y_{(g)}}$$

Where,

$r_{g.}$ = Genotypic correlation between character X and Y

g = Genotypic

Significance of correlation coefficients was tested against 'r' values at (n-2) degrees of freedom as given by Fisher and Yates (1938) both at 0.05 and 0.01 probability levels of their significance.

3.4.7 Path coefficient analysis

Path coefficient analysis was carried out using both phenotypic and genotypic correlation coefficients to ascertain the direct and indirect effects of the yield component on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

If 'Y' is the effect and 'X_1' is the cause, the path coefficient for the path from cause X_1 to the effect is$\sigma X_1/\sigma Y$. Direct and indirect effects were worked out by using genotypic correlations as below:

Direct effect of X_1 on Y = $P_{X1,Y}$

Where,

P_{X1Y} = Path coefficient of X_1 on Y.

Similarly, direct effects of other attributes on yield were worked out.

Indirect effects of X_1 via X_2 on Y = $P_{X2\,Y} r_{X1,\,X2}$

Where,

$P_{X2.Y}$ = Path coefficient of the component character X_2 on Y.

$r_{X1.X2}$ = Genotypic correlation between X_1 and X_2

Similarly, indirect effect on all possible combinations were calculated for all component characters.

The residual effect (R) was calculated as below

$R = [1 - (P_{X1Y}.\, r_{X1Y}) - (P_{X2Y}.r_{X2Y}) \ldots\ldots (P_{XnY}.\, r_{XnY})]^{1/2}$

Where,

P_{X1Y}, P_{X2Y}, ------, P_{XnY} = Direct effects of respective character on seed yield.

R_{X1Y}, r_{X2Y}, --------, r_{XnY} = Correlation coefficient between respective characters and yield.

3.4.8 D^2 analysis

The generalized distance between two population is defined by Mahalanobis (1936) as $D^2 = \Sigma\, \Sigma\, \lambda ij.\ \delta i.\ \delta j$.

Where,

λij = Reciprocal matrix to the common dispersion matrix

δi = difference between the mean values of two populations for i^{th} character

δj = difference between the mean values of two populations for j^{th} character

Estimation of D^2 values from the above formula is very complicated in the present study. Since, it requires the inversion of a eleventh order determinant and then the evaluation of 11(11+1)/2 terms whose sum is D^2. It was found convenient to work with a set of uncorrelated characters constructed from the original measurements. D^2 with such transformed variables reduced to the evaluation of simple sum of squares. Transformation was done by using pivotal condensation method (Singh and Chaudhary, 1977). The coefficient for the transformation were obtained by dividing the first row of the reduced matrix by the square root of the corresponding pivotal condensation elements.

3.4.9 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as the calculated value of x^2 and is tested against the tabulated values x^2 for 'p' degrees of freedoms where p is the number of characters considered (Singh and Chaudhary, 1977).

3.4.10 Determination of gene constellations

Tocher's method as described by Rao (1952) was followed for cluster formation. No formal rules can be laid down for finding the clusters because a cluster is not a well defined term. The only criteria appears to be that any two groups belonging to the same cluster should at least on an average show a smaller D^2 than those belonging to the two different clusters. A simple device suggested by K.D. Tocher is to start with the two closely associated groups and find a third group which has the smallest D^2 from the two. Similarly, the fourth is chosen to have the smallest D^2 from the first three and so on. If at any stage the average D^2 of a group from those already listed appears to be high, then this group does not fit in the former groups and is therefore, taken outside the former cluster. The group of first cluster are then omitted and the rest are treated similarly. It is also useful to calculate the change in average D^2 within a cluster due to inclusion of an additional group. If the changes are appreciable, then the newly added group has to be considered as outside the cluster.

3.4.11 Average intra and inter cluster D^2 and D Values

i) Average intra cluster $D^2 = \Sigma Di^2 / n$

Where,

ΣD_i^2 is sum of distances between all possible combinations (n) of the population included in a cluster

ii) Average inter cluster D^2

$$D^2 = \frac{\Sigma \text{ of distances between the population of cluster i and j}}{n_i . n_j}$$

Where,

n_i = Number of populations in the cluster i

n_j = Number of populations in the cluster j

iii) Average intra and inter cluster distance

$D = \sqrt{D^2}$

3..4.12 Cluster means

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in that cluster.

RESULTS

CHAPTER 4

EXPERIMENTAL RESULTS

The present investigation was carried out to assess the variability among 40 rice genotypes for 13 characters, correlation with interdependent characters and direct and indirect effects of independent variables on yield.

The experimental data obtained was subjected to statistical analysis and the findings are presented in this section.

4.1 Mean performance of genotypes

The mean performance of 40 genotypes is presented in Table 4.1.

4.1.1 Days to 50 per cent flowering (No.)

The genotype RDN-57 flowered in 69 days and was the earliest among all genotypes, followed by RDN-3 (71.67 days) and RDN-29 (78.33 days). Maximum days for flowering were required by the genotypes RDN-11 (116 days), followed by RDN-8 (115.67 days), RDN-30 (115.33 days) and RDN-14 and RDN-23 (115.00 days). The general mean for this character was 104.28 days within the range of 69 to 116 days.

4.1.2 Days to maturity (No.)

This character showed a wide range from 99.67 to 145.67 days with a general mean of 132.83 days. RDN-57 (99.67 days) was the earliest to mature, followed by RDN-29 (105.67 days) and RDN-3 (106.33 days). RDN-8 required maximum number of days (145.67 days) to mature, followed by RDN-30 (144.67 days) and RDN-24 (143.33 days).

4.1.3 Plant height (cm)

RDN-54 was the tallest (148.07 cm) among all genotypes, followed by RDN - 37 (144.40 cm) and RDN - 14 (141.90 cm). The dwarfest

Table 4.1. Mean performance of 40 genotypes of rice for 13 characters

Sr. No.	Genotypes (ARS numbers)	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Effective tillers per plant (No.)	Panicle length (cm)	Secondary branches per panicle (No.)	Grains per panicle (No.)	Length of grain (mm)	Breadth of grain (mm)	Length: breadth ratio of grain	1000 grain weight (g)	Protein content (%)	Seed yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	RDN.1	107.33	140.67	127.47	6.67	19.33	10.13	197.67	4.32	2.20	1.97	13.33	5.55	12.66
2	RDN.3	71.67	106.33	76.80	4.33	15.67	5.80	72.73	4.01	2.23	1.81	10.57	6.11	6.35
3	RDN.4	108.67	141.67	134.80	4.93	20.07	8.53	134.80	4.09	2.21	1.85	9.63	8.88	7.17
4	RDN.6	92.00	124.67	130.67	4.73	20.10	7.67	177.47	4.00	2.09	1.92	9.53	5.83	6.33
5	RDN.7	109.00	138.67	107.07	5.73	19.30	11.30	196.60	4.03	2.47	1.63	16.43	6.38	16.07
6	RDN.8	115.67	145.67	108.00	4.73	18.00	6.80	104.93	4.26	2.31	1.84	11.10	8.88	6.22
7	RDN.9	109.67	140.00	113.53	4.93	24.83	7.87	171.13	4.04	2.26	1.79	11.23	6.38	9.59
8	RDN.11	116.00	141.33	133.00	5.87	20.50	10.33	151.00	7.94	2.32	3.42	27.50	6.38	25.84
9	RDN.12	114.33	140.33	104.73	6.47	17.53	10.33	137.33	5.93	2.28	2.60	20.27	8.05	16.55
10	RDN.13	113.00	138.00	109.73	2.73	17.67	8.33	150.53	5.76	1.98	2.91	17.27	6.11	7.43
11	RDN.14	115.00	141.33	141.90	5.20	20.90	10.67	148.27	6.30	2.40	2.62	23.17	6.61	18.40
12	RDN.15	111.33	141.67	123.27	3.97	18.47	9.60	124.13	6.02	1.99	3.03	18.33	5.55	7.98
13	RDN.18	115.00	141.33	126.07	4.93	19.37	9.73	126.33	6.38	2.34	2.72	26.23	6.94	15.67
14	RDN.19	105.67	136.67	139.27	4.73	21.03	10.47	136.20	6.99	2.61	2.68	32.17	6.66	14.87
15	RDN.20	103.00	131.67	137.57	4.20	26.23	11.07	150.83	6.56	2.69	2.44	28.13	6.11	11.62
16	RDN.21	110.33	139.67	132.07	5.13	19.73	8.80	129.13	4.40	2.30	1.91	15.60	10.55	12.53
17	RDN.23	115.00	140.67	119.20	6.27	19.27	9.67	95.60	5.69	1.98	2.88	17.43	5.83	13.65
18	RDN.24	113.0	143.33	105.73	4.80	17.60	11.33	139.13	6.37	2.04	3.12	18.37	8.88	13.17
19	RDN.26	114.33	114.33	125.43	6.47	22.60	9.33	104.20	5.82	1.99	2.92	19.70	6.94	24.64
20	RDN.27	113.00	140.00	121.93	6.00	19.83	10.13	92.07	5.94	1.99	2.98	18.33	5.83	16.63
21	RDN.29	78.33	105.67	73.60	5.37	15.47	8.50	72.47	5.07	1.98	2.57	8.27	6.09	5.80
22	RDN.30	115.33	144.67	114.93	4.80	18.73	9.80	192.67	4.17	1.99	2.10	9.27	5.83	12.30

Sr. No.	Genotypes (ARS numbers)	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Effective tillers per plant (No.)	Panicle length (cm)	Secondary branches per panicle (No.)	Grains per panicle (No.)	Length of grain (mm)	Breadth of grain (mm)	Length: breadth ratio of grain	1000 grain weight (g)	Protein content (%)	Seed yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
23	RDN.32	107.00	136.00	139.73	6.13	20.80	10.20	134.53	5.66	2.17	2.61	3.33	5.55	14.19
24	RDN.37	104.67	138.67	144.40	5.40	22.37	8.53	132.07	5.32	2.32	2.30	12.17	8.05	6.89
25	RDN.42	105.67	137.33	140.60	10.07	20.93	9.87	111.00	5.86	2.30	2.55	16.30	5.83	12.38
26	RDN.43	113.67	141.67	115.80	4.87	19.53	7.40	94.53	4.43	2.14	2.07	10.30	8.88	5.76
27	RDN.44	100.33	128.33	123.07	5.60	18.53	8.07	74.67	4.35	2.50	1.74	19.40	6.66	8.12
28	RDN.45	94.33	126.00	110.73	5.47	17.87	9.20	79.67	6.35	2.25	2.82	10.10	13.05	7.02
29	RDN.46	92.00	124.00	120.73	5.07	20.13	6.20	43.53	6.53	2.00	3.28	6.30	11.38	5.83
30	RDN.47	94.67	123.00	103.00	5.53	18.40	5.73	28.47	7.68	1.75	4.40	13.40	9.71	5.85
31	RDN.48	94.67	123.67	111.07	4.40	18.07	6.07	43.53	7.65	1.87	4.10	6.20	13.05	5.94
32	RDN.49	95.00	126.33	102.27	6.57	18.07	8.47	60.20	7.50	2.01	3.72	28.10	11.66	8.77
33	RDN.50	97.67	127.67	94.93	4.00	17.27	8.20	48.13	7.72	1.98	3.89	4.53	9.71	5.99
34	RDN.51	96.67	127.00	87.73	6.87	16.87	8.27	70.20	6.55	1.82	3.60	10.23	9.16	6.47
35	RDN.52	108.33	137.00	130.47	5.47	20.73	9.67	100.67	6.16	2.19	2.81	18.13	10.55	9.94
36	RDN.54	108.67	138.67	148.07	6.13	20.27	9.67	92.60	4.81	2.45	1.96	14.20	12.77	6.35
37	RDN.57	69.00	99.67	70.13	2.00	15.67	5.13	51.07	6.62	2.02	3.31	16.60	5.55	4.74
38	RDN.58	108.00	136.67	116.80	2.27	16.40	9.00	88.73	7.13	2.51	2.84	27.30	9.16	5.88
39	RDN.59	100.67	133.00	99.47	7.00	17.00	6.53	51.33	6.41	2.39	2.69	18.20	5.27	7.45
40	RDN.60	111.00	130.00	84.67	2.87	17.87	8.47	80.53	6.30	2.74	2.30	27.20	5.55	6.23
Mean		104.28	132.83	116.26	5.22	19.22	8.77	109.82	5.78	2.20	2.67	16.10	7.85	10.38
S.E. (m) ±		4.486	4.780	8.775	0.555	1.023	0.537	4.558	0.178	0.543	0.105	1.496	0.343	0.925
C.D. at 5%		8.792	9.368	17.199	1.088	2.005	1.053	8.934	0.348	0.106	0.207	2.933	0.672	1.813
C.D. at 1%		12.31	11.56	22.61	1.43	2.64	1.38	11.74	0.46	0.13	0.27	3.85	0.88	2.38
C.V. (%)		5.269	4.407	9.244	13.032	6.517	7.504	5.084	3.765	3.019	4.839	11.386	5.350	10.911

genotype was RDN-57 (70.13 cm), followed by RDN-29 (73.60 cm). The mean plant height for 40 genotypes was 116.26 cm. Nineteen genotypes exceeded the mean height.

4.1.4 Effective tillers per plant (No.)

Number of effective tillers per plant varied from 2.00 to 10.07 with the average of 5.22. RDN-42 had the highest number (10.07) of effective tillers per plant, followed by RDN-59 (7.00) and RDN-51 (6.87). The minimum number of effective tillers per plant were observed for RDN-57 (2.00), followed by RDN-58 (2.27) and RDN-13 (2.73). Eighteen genotypes exceeded the average number of effective tillers per plant.

4.1.5 Panicle length (cm)

With the mean of 19.22 cm, the panicle length varied in the range of 15.47 to 26.23 cm. The minimum panicle length was exhibited by RDN-29 (15.47 cm), followed by RDN 3 (15.67 cm). The highest panicle length was shown by RDN-20 (26.23 cm), followed by RDN-9 (24.33 cm) and RDN-26 (22.60 cm). Twenty one genotypes had the higher panicle length than the average.

4.1.6 Secondary branches per panicle (No.)

RDN-24 had the highest number of secondary branches per panicle (11.33), followed by the genotypes RDN-7 (11.30) and RDN-20 (11.07). The genotype RDN-57 exhibited the lowest number of secondary branches per panicle (5.13), followed by RDN-3 (5.80) and RDN-48 (6.07). The character varied between 5.13 to 11.33 secondary branches per panicle. Twenty one genotypes had higher number of secondary branches per panicle than the average (8.77).

4.1.7 Grains per panicle (No.)

The mean performance of genotypes was 109.82 grains per panicle with the range of 28.47 to 197.67 grains per panicle. The minimum number of grains per panicle (28.47) were exhibited by RDN-47, followed by RDN-46 and RDN-48 (43.53) and RDN-50 (48.13). RDN-1 had the highest number of grains per panicle(197.67), followed by RDN-7 (196.60) and RDN-30 (192.67). Nineteen genotypes exhibited more number of grains per panicle than average.

4.1.8 Length of grain (mm)

The length of grain ranged between 4.00 and 7.94 mm. RDN-6 had the shortest (4.00 mm) grain, followed by RDN-3 (4.01 mm) and RDN-7 (4.03mm). The longest grain size of 7.94 mm was exhibited by RDN-11, followed by RDN-50 (7.72 mm), RDN-47 (7.68 mm) and RDN-48 (7.65 mm), Twenty three genotypes had longer grains than the average (5.78 mm).

4.1.9 Breadth of grain (mm)

The mean breadth of grain for 40 genotypes was 2.20 mm, which varied in the range of 1.75 to 2.74 mm. RDN-60 had the thick (2.74 mm) grains, followed by RDN-20 (2.69 mm) and RDN-58 (2.51mm). The lowest breadth of 1.75 mm was of RDN-47, followed by RDN-51 (1.82 mm) and RDN-48 (1.87 mm). Twenty one genotypes had the breadth above average.

4.1.10 Length : Breadth ratio of grain

Length : Breadth ratio of grain was within the range of 1.74 to 4.40. Twenty genotypes exhibited above average (2.67) length : breadth ratio of grain. Maximum ratio (4.40) was exhibited by RDN-47, followed by RDN-50 (3.89) and RDN-49 (3.72). RDN-44 had the minimum (1.74) length : breadth ratio of grain, followed by RDN-9 (1.79), RDN-3 (1.81) and RDN-8 (1.84).

4.1.11 1000 grain weight (g)

Maximum 1000 grain weight was exhibited by RDN-19 (32.17 g), followed by RDN-20 (28.13 g) and RDN-49 (28.10 g). RDN-32 had the minimum (3.33 g) 1000 grain weight, followed by RDN-50 (4.53 g) and

RDN-48 (6.20 g). Twenty one genotypes had the higher 1000 grain weight over the mean (16.10 g) of all genotypes.

4.1.12 Protein content (%)

The protein content ranged between 5.27 and 13.05 per cent among 40 genotypes with an average of 7.85 per cent proteins. RDN-45 and RDN-48 exhibited high protein percentage (13.05%), followed by RDN-54 (12.77%) and RDN-49 (11.66%). The genotypes with low proteins were RDN-59 (5.27%), followed by RDN-1, RDN-15, RDN-57, RDN-32 and RDN-60 (5.55%). Eighteen genotypes had higher protein percentage than average (7.85%).

4.1.13 Seed yield per plant (g)

RDN-11 yielded high (25.84 g), followed by RDN-26 (24.64 g) and RDN-7 (16.07 g). Whereas, lowest yield was shown by RDN-57 (4.74 g), followed by RDN-43 (5.76 g) and RDN-29 (5.80 g). The mean yield of 40 genotypes was 10.38 g distributed in the range of 16.07 g to 25.80 g. Sixteen genotypes exhibited above average yield.

4.2 Analysis of variance

The analysis of variance for thirteen characters is presented in Table 4.2. It revealed that there were highly significant differences among the genotypes for all the characters under study. It indicated the presence of appreciable amount of diversity among genotypes.

4.3 Parameters of genetic variability

Range of variability, estimates of genotypic and phenotypic coefficients of variation, heritability percentage in broad sense, genetic advance and genetic advance expressed as percentage of mean is presented in the Table 4.3.

Table 4.2. Analysis of variance for 13 characters in rice

Source of variation	Degrees of freedom	Mean sum of squares												
		Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Effective tillers per plant (No.)	Panicle length (cm)	Secondary branches per panicle (No.)	Grains per panicle (No.)	Length of grain (mm)	Breadth of grain (mm)	Length/ breadth ratio of grain	1000 grain weight (g)	Protein content (%)	Seed yield per plant (g)
Replication	2	66.188	96.125	102.875	1.055	2.568	0.240	61.75	0.060	0.0001	0.015	2.449	0.055	2.900
Treatment	39	411.981**	368.263**	1174.170**	6.053**	15.455**	7.833**	6103.273**	4.324**	0.167**	1.424**	157.541**	16.296**	81.160**
Error	78	30.183	34.269	115.5111	0.462	1.570	0.433	31.168	0.047	0.004	0.017	3.359	0.176	1.283

*,** - Significant at 5 and 1 per cent, respectively

Table 4.3. Variability in 40 genotypes of rice

Sr. No.	Character	Range	Mean	G.C.V.	P.C.V.	Heritability % (B.S.)	Genetic advance	G.A. as % of mean
1.	**Days to 50% flowering (No.)**	69.00-116.00	104.28	10.819	12.033	80.83	20.894	20.037
2.	**Days to maturity (No.)**	99.67-145.67	132.83	7.944	9.085	76.46	19.007	14.309
3.	**Plant height (cm)**	70.13-148.07	116.26	16.158	18.616	75.34	33.589	28.891
4.	**Effective tillers per plant (No.)**	2.00-10.07	5.22	26.165	29.231	80.12	2.517	48.247
5.	**Panicle length (cm)**	15.47-26.23	19.23	11.190	12.950	74.67	3.830	19.920
6.	**Secondary branches per panicle (No.)**	5.13-11.33	8.77	17.905	19.414	85.06	2.984	34.017
7.	**Grains per panicle (No.)**	28.47-197.67	109.82	40.967	41.282	98.48	91.973	83.750
8.	**Length of grain (mm)**	4.00-7.94	5.78	20.663	21.003	96.79	2.420	41.876
9.	**Breadth of grain (mm)**	1.75-2.74	2.20	10.570	10.994	92.45	0.461	20.945
10.	**Length : breadth ratio of grain**	1.74- 4.40	2.67	25.671	26.123	96.57	1.386	51.967
11.	**1000 grain weight (g)**	3.33-28.13	16.10	44.537	45.969	93.86	14.308	88.887
12.	**Protein content (g)**	5.27-13.05	7.85	29.535	30.016	96.82	4.699	59.868
13.	**Seed yield per plant (g)**	4.74-25.84	10.38	49.703	50.887	95.40	10.382	100.000

G.C.V. – Genotypic coefficient of variation
P.C.V. – Phenotypic coefficient of variation

4.3.1 Coefficients of variation

It was observed that the estimates for genotypic coefficients of variation (G.C.V.) were lower than the phenotypic coefficients of variation (P.C.V.) for all the characters.

The number of days to maturity exhibited the lowest G.C.V. (7.944) as well as P.C.V. (9.085). Whereas, the seed yield per plant had the highest G.C.V. and P.C.V. (49.703 and 50.887, respectively). It was followed by 1000 grain weight, number of grains per panicle, protein content, number of effective tillers per plant, length : breadth ratio of grain, length of grain, number of secondary branches per panicle, plant height, panicle length, number of days to 50 per cent flowering and breadth of grain. The highest difference between G.C.V. and P.C.V. values was observed for number of effective tillers per plant (3.066) followed by plant height (2.458). Number of grains and secondary branches per panicle had the lowest difference between GCV and PCV estimates (0.315).

4.3.2 Heritability (b.s.) percentage

According to Robinson's (1966) classification, heritabilities obtained in the present investigation for all the characters could be classified as very high heritabilities. The lowest heritability (b.s.) was observed for panicle length (74.67 %), followed by plant height (75.34%) and number of days to maturity (76.46 %). Number of grains per panicle showed the highest broad sense heritability (98.48 %) and it was followed by protein content (96.82 %) and length of grain (96.79 %). Heritabilities for other characters ranged between 80.12 (number of effective tillers per plant) and 96.57 per cent (length : breadth ratio of grain).

4.3.3 Genetic advance

The character, number of grains per panicle showed the highest genetic advance (91.973), followed by plant height (33.589) and number of days to 50 per cent flowering (20.894). The lowest genetic advance was observed for breadth of grain (0.461), followed by length : breadth ratio of grain (1.386) and length of grain (2.420). The genetic advance for seed yield was low (10.382), however, when expressed as the percentage of mean value, it was 100 per cent. Other characters, *viz.*, 1000 grain weight (88.887), number of grains per panicle (83.750), protein content (59.868) and the length : breadth ratio of grain (51.967) showed high genetic advance as percentage of mean.

4.4 Correlations

The phenotypic and genotypic correlation coefficients between yield and its related components in all possible comparisons are presented in Table 4.4.

The phenotypic and genotypic correlations among different characters were mostly comparable in magnitude. However, genotypic correlations, in general, were higher than the corresponding phenotypic correlations except between the characters length : breadth of grain and the seed yield per plant.

Only genotypic correlations will be referred to and presented throughout the text henceforth.

The perusal of the Table 4.4 revealed that seed yield per plant showed highly significant positive relationship with the number of secondary branches per panicle (0.684) followed by the number of days to 50 per cent flowering (0.567), number of grains per panicle (0.491), 1000 grain weight (0.444), plant height (0.436) and panicle length (0.428). The number of days to maturity and effective tillers per plant also exhibited significant positive correlation with the seed yield per plant (0.332 and 0.390, respectively). The association of yield with the length and breadth of grain was positive but non significant. The traits, L : B

Table 4.4. Genotypic (above diagonal) and phenotypic (below diagonal) correlations of 13 characters in 40 genotypes of rice

Character	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Effective tillers per plant (No.)	Panicle length (cm)	Secondary branches per panicle (No.)	Grains per panicle (No.)	Length of grain (mm)	Breadth of grain (mm)	Length : breadth ratio of grain	1000 grain weight (g)	Protein content (%)	Seed yield per plant (g)
Days to 50% flowering (No.)	1	0.967**	0.611**	0.197	0.464**	0.683**	0.548**	-0.089	0.264	-0.213	0.337*	-0.068	0.567**
Days to maturity (No.)	0.759**	1	0.686**	0.203	0.416**	0.620**	-0.600**	-0.172	-0.290	-0.291	0.205	0.001	0.332*
Plant height (cm)	0.517**	0.491**	1	0.359*	0.802**	0.565**	0.500**	-0.117	0.342*	-0.271	0.183	0.095	0.436**
Effective tillers per plant (No.)	0.144	0.171	0.263	1	0.269	0.306	0.060	-0.088	-0.089	-0.037	-0.101	0.012	0.390*
Panicle length (cm)	0.353*	0.278	0.623**	0.183	1	0.401**	0.499**	-0.134	0.336*	-0.265	0.182	-0.096	0.428**
Secondary branches per panicle (No.)	0.556**	0.508**	0.446**	0.243	0.393*	1	0.670**	-0.018	0.365*	-0.213	0.440**	-0.189	0.684**
Grains per panicle (No.)	0.492**	0.513**	0.431**	0.048	0.426**	0.609**	1	-0.499**	0.301	-0.578**	0.139	-0.422**	0.491**
Length of grain (mm)	-0.075	-0.147	-0.094	-0.083	-0.119	-0.018	-0.487**	1	-0.157	0.895**	0.377*	0.278	0.101
Breadth of grain (mm)	0.234	0.278	0.281	-0.074	0.284	0.343*	0.289	-0.146	1	-0.570**	0.56**	-0.174	0.154
Length : breadth ratio of grain	-0.188	-0.265	-0.223	-0.038	-0.231	-0.202	-0.564**	0.887**	-0.573**	1	0.051	0.330*	-0.020
1000 grain weight (g)	0.286	0.178	0.149	-0.073	0.143	0.387*	0.138	0.361*	0.530**	0.046	1	-0.207	0.444**
Protein content (g)	-0.067	-0.010	0.075	0.005	-0.072	0.166	-0.414**	0.271	-0.162	0.321*	-0.196	1	-0.297
Seed yield per plant (g)	0.497**	0.279	0.364*	0.324*	0.382*	0.632**	0.471**	0.106	0.139	-0.010	0.418**	-0.282	1

*,** - Significant at 5 and 1 per cent level, respectively .

ratio of grain and protein content exhibited non significant negative correlation with seed yield.

Other important genotypic correlations observed in the present study were as below.

The highest value of correlation (0.967) was observed for the association between number of days to 50 per cent flowering and days to maturity. Days to 50 per cent flowering also showed positive and significant correlation with the number of secondary branches per panicle (0.683), plant height (0.611), grain yield per plant (0.567), number of grains per panicle (0.548), panicle length (0.464) and 1000 grain weight (0.337) and with other characters, it exhibited non significant negative or positive correlation. The number of days to maturity had the significant positive correlation with the plant height (0.686), number of secondary branches per panicle (0.620), panicle length (0.416) and seed yield per plant (0.332). It was negatively and significantly associated with grains per panicle (-0.600). The characters, length : breadth ratio of grain (-0.291), breadth of grain (-0.290), length of grain (-0.172) and protein content (-0.001) showed negative non significant correlation with days to maturity.

Plant height exhibited the significant and positive association with panicle length (0.802), followed by the number of secondary branches per panicle (0.565), number of grains per panicle (0.500), seed yield per plant (0.436), number of effective tillers per plant (0.359) and breadth of grain (0.342). Plant height was negatively correlated with two characters, *viz.*, length : breadth ratio of grain (-0.271) and length of grain (-0.117) and with other characters, it's association was non significant and positive.

None of the characters showed significantly positive association with effective tillers per plant except seed yield per plant (0.390) and plant height (0.359). This trait was negatively but non significantly correlated with 1000 grain weight (-0.101), breadth of grain (-0.089), length of grain (-0.088) and length : breadth ratio of grain (-0.037).

Panicle length had significant positive correlation with number of grains per panicle (0.499), seed yield per plant (0.428), number of secondary branches per panicle (0.401) and breadth of grain (0.336). It showed negative but non significant correlation with the length : breadth ratio of grain (-0.265), length of grain (-0.134) and protein content (-0.096).

Number of secondary branches per panicle had the significantly positive correlation with the seed yield per plant (0.684), number of grains per panicle (0.670), 1000 grain weight (0.440) and breadth of grain (0.365). It was negatively correlated with the length : breadth ratio of grain (-0.213), protein content (-0.189) and length of grain (-0.018).

Number of grains per panicle showed significantly positive correlation with the seed yield per plant (0.491). It was negatively and significantly correlated with the length : breadth ratio of grain (-0.578), length of grain (-0.499) and protein content (-0.422).

Length of grain had the significant positive correlation with the length : breadth ratio of grain (0.895) and 1000 grain weight (0.377). This trait exhibited negative correlation with the breadth of grain (-0.157) but was non-significant.

Breadth of grain had the significantly positive correlation with the 1000 grain weight (0.560). It had negative significant correlation with the length : breadth ratio (-0.570).

Length : breadth ratio of grain had the positive significant correlation with the protein content (0.330). However, it was negatively correlated with the seed yield per plant (-0.020).

The 1000 grain weight was significantly and positively correlated with seed yield per plant (0.444). It had negative but non significant correlation with protein content (-0.207). The negative correlation was observed between protein content and seed yield per plant (-0.297).

4.5 Path analysis

The inter relationship of the characters as revealed by the path coefficient analysis using genotypic correlations are presented in Table 4.5.

It is evident from Table 4.5 that seed yield per plant was the result mainly of days to 50 per cent flowering, days to maturity, plant height, effective tillers per plant, panicle length, secondary branches per panicle, grains per panicle and 1000 grain weight as they were significantly correlated with it. These variables were related inter se, so that each factor influenced the seed yield by a direct contribution and by indirect contributions through other variables with which it was correlated.

The highest and positive direct effect (2.678) on seed yield was exhibited by the trait number of days to maturity. This trait also influenced the yield indirectly *via* length : breadth ratio of grain (0.869), secondary branches per panicle (0.773) and panicle length (0.638). However, its relatively low correlation (0.332) with seed yield might be due to its indirect negative contribution through traits, days to 50 per cent flowering, plant height, grains per panicle, length and breadth of grain. It didn't influence on seed yield *via* protein content.

Highest direct effect on seed yield in negative direction was exhibited by length : breadth ratio of grain (-2.981). However, it's correlation with seed yield though negative (-0.020), was of less magnitude. It would be due to it's highly positive indirect effects on seed yield *via* length of grain (1.830), breadth of grain (1.140), grains per panicle (0.551), days to 50 per cent flowering (0.509) and plant height (0.387).

Days to 50 per cent flowering exhibited second highest negative direct effect (- 2.385) on seed yield. It also had high negative indirect

Table 4.5. Direct (diagonal) and indirect effects using genotypic correlation of different characters towards yield in rice

Character	Days to 50% flowering (No.)	Days to maturity (No.)	Plant height (cm)	Effective tillers per plant (No.)	Panicle length (cm)	Secondary branches per panicle (No.)	Grains per panicle (No.)	Length of grain (mm)	Breadth of grain (mm)	Length/ breadth ratio of grain	1000 grain weight (g)	Protein content (%)	Seed yield per plant (g)
Days tot50% flowering (No.)	-2.385	2.589	-0.874	0.011	0.711	0.853	-0.522	-0.184	-0.529	0.636	0.251	0.008	0.567**
Days to maturity (No.)	-2.307	2.678	-0.981	0.012	0.638	0.773	-0.571	-0.352	-0.580	0.869	0.153	0.000	0.332**
Plant height (cm)	-1.458	1.837	-1.429	0.021	1.228	0.704	-0.476	-0.240	-0.684	0.807	0.137	-0.011	0.436**
Effective tillers per plant (No.)	-0.469	0.545	-0.514	0.058	0.412	0.381	-0.057	-0.180	0.179	0.111	-0.075	-0.001	0.390*
Panicle length (cm)	-1.106	1.114	-1.149	0.016	1.532	0.501	-0.475	-0.273	-0.671	0.789	0.136	0.011	0.428**
Secondary branches per panicle (No.)	-1.630	1.660	-0.807	0.018	0.614	1.248	-0.638	-0.038	-0.729	0.635	0.328	0.022	0.684**
Grains per panicle (No.)	-1.307	1.607	-0.714	0.004	0.764	0.835	-0.952	-1.019	-0.602	1.724	0.104	0.049	0.491**
Length of grain (mm)	0.213	-0.461	0.168	-0.005	-0.205	-0.023	0.475	2.045	0.313	-2.668	0.282	-0.033	0.101
Breadth of grain (mm)	-0.631	0.777	-0.489	-0.005	0.514	0.455	-0.287	-0.320	-1.999	1.700	0.418	0.021	0.154
Length : breadth ratio of grain	0.509	-0.781	0.387	-0.002	-0.406	-0.266	0.551	1.830	1.140	-2.981	0.038	-0.039	-0.020
1000 grain weight (g)	-0.803	0.548	-0.261	-0.006	0.279	0.549	-0.132	0.771	-1.120	-0.152	0.747	0.024	0.444**
Protein content (%)	-0.161	-0.002	-0.135	0.001	-0.147	-0.236	0.402	0.568	0.347	-0.984	-0.154	-0.118	-0.29

Residual effect = 0.1836213

effect through plant height (-0.874), breadth of grain (-0.529) and grains per panicle (-0.522). But its highly positive significant correlation with seed yield (0.567) might be due to the indirect influence through days to maturity (2.589), followed by secondary branches per panicle (0.853), panicle length (0.711) and Length : breadth ratio of grain (0.636).

Plant height though had high negative direct effect (-1.429) on seed yield, it had highly significant correlation (0.436) with seed yield *via* positive indirect effect through days to maturity (1.837), panicle length (1.228), length : breadth ratio of grain (0.807) and secondary branches per panicle (0.704). It had high negative indirect effect on seed yield through days to 50 per cent flowering (-1.458), breadth of grain (-0.684) and grains per panicle (-0.240).

Number of effective tillers per plant which showed significant positive correlation (0.390) with seed yield per plant, had negligible (0.058) direct effect on seed yield per plant. It might be due to its high positive indirect effect on seed yield through the characters, days to maturity (0.545), panicle length (0.412) and secondary branches per panicle (0.381). This trait also had the high negative indirect effect through traits plant height (-0.514) and days to 50 per cent flowering (-0.469).

Panicle length had the greater direct effect (1.532) on seed yield and negative indirect effects through plant height (-1.149), days to 50 per cent flowering (-1.106), breadth of grain (-0.671) and grains per panicle (-0.475), while it had positive indirect effects through days to maturity (1.114), length : breadth ratio of grain (0.789) and secondary branches per panicle (0.501).

The trait, secondary branches per panicle which had the highest positive correlation with seed yield exhibited high positive direct effect (1.248) on seed yield. It also exerted it's influence on seed yield *via* high positive indirect effects of the characters, days to maturity (1.660), panicle length (0.614), L : B ratio of grain (0.635) and 1000 grain weight (0.328). However, it also had negative indirect contribution to yield through the traits mainly days to 50 per cent flowering (-1.630), plant height (-0.807), grain breadth (-0.729) and grains per panicle (-0.638).

Grains per panicle had negative direct effect (-0.952) on seed yield though it had significant positive correlation with seed yield (0.491). This was due to high positive indirect effects through length : breadth ratio of grain (1.724), days to maturity (1.607), secondary branches per panicle (0.835), panicle length (0.764) in positive direction. It exerted negative influence through days to 50 per cent flowering (-1.307), length of grain (-1.019), plant height (-0.714) and breadth of grain (-0.602).

Length of grain had the high positive direct effect (2.045) on seed yield, while its correlation with seed yield (0.101) was non significant. It's positive direct effect might have negated through its high negative indirect effect on seed yield *via* length to breadth ratio of grain (-2.668).

Breadth of grain had positive but non significant correlation with seed yield (0.154) instead of its highly negative direct effect (-1.999) on seed yield. It had high positive indirect effects through length : breadth ratio of grain (1.700), days to maturity (0.777), panicle length (0.514) and secondary branches per panicle (0.455).

The trait, 1000 grain weight had highly significant correlation (0.444) with seed yield and also had positive direct effect (0.747) on it. It's contribution through breadth of grain (-1.120) and days to 50 per cent flowering (-0.803) was negative.

Protein content exhibited relatively low negative direct effect (-0.118) on seed yield per plant which also had negative correlation (-0.297) with it. It had negative contribution to seed yield per plant mainly through L :B ratio of grain (-0.984). However, it exerted positive effects on seed yield indirectly *via* grain length (0.568) and grains per panicle (0.402).

4.6 Divergence

Genetic divergence in 40 genotypes of rice was measured following Mahalanobis's (1936) D^2 statistic. The D^2 values corresponding to the pair of comparison between these genotypes ranged from 23.82 (RDN.21 and RDN.27) to 12905.85 (RDN.42 and RDN.57). These 40 genotypes were grouped into 3 clusters following Tocher's method as described by Rao (1952). These clusters along with genotypes included under them are presented in Table 4.6.

Table 4.6. Distribution of 40 rice genotypes into different clusters

Clusters	Total No. of genotypes included	Accession No. (Genotypes)		
I	36	RDN.1, RDN.6, RDN.9, RDN.12, RDN.19, RDN.23, RDN.27, RDN.30, RDN.59, RDN.45, RDN.48, RDN.51,	RDN.3, RDN.7, RDN.13, RDN.14, RDN.20, RDN.24, RDN.15, RDN.32, RDN.43, RDN.46, RDN.49, RDN.52,	RDN.4, RDN.8, RDN.11, RDN.18, RDN.21, RDN.26, RDN.29, RDN.37, RDN.44, RDN.47, RDN.50, RDN.54
II	3	RDN.57,	RDN.58,	RDN.60,
III	1	RDN.42,		

Table 4.6 revealed that cluster I alone contained maximum i.e. 36 genotypes. While only 3 genotypes were grouped together forming cluster II. The cluster III was monogenotypic.

4.6.1 Intra and inter cluster distances

Intra and inter cluster D^2 and D values were worked out using D^2 values from divergence analysis. These are presented in Table 4.7.

Table 4.7. Average intra and inter cluster D^2 and D (in parenthesis) values of 3 clusters formed from 40 genotypes of rice

	I	**II**	**III**
I	767.648 (D=27.706)	2526.216 (D=50.261)	4457.125 (D=66.762)
II		294.569 (D=17.163)	11574.290 (D=107.584)
III			0.000 (D=0.000)

The minimum intra-cluster distance was found in cluster II (D^2 = 294.569) followed by cluster I (D^2 = 767.648). The cluster III being monogenotypic, had intra-cluster D^2 equal to 0.00.

The maximum inter-cluster distance was observed between cluster II and III (D^2 = 11574.29). The former cluster had three genotypes *viz.*, RDN-57, RDN-58 and RDN-60, which were early to flower and mature, dwarf, having long bold (LB) grains and lesser protein content. Cluster III was monogenotypic having genotype RDN-42, which was late to flower and mature, tall, having medium slender (MS) grains and higher protein content. This maximum inter-cluster D^2 value was followed by 4457.125 (cluster I and III).

The minimum inter-cluster distance was observed between cluster I and II (D^2 = 2526.216) indicating proximity with each other. The former cluster comprised 36 genotypes. Whereas, latter comprised 3 genotypes (Table 4.6).

Cluster I was more distant from the cluster III (D = 66.76), than cluster II (D= 50.261).

Cluster II showed the highest distance from cluster III (D = 107.584).

4.6.2 Cluster means

Cluster means for thirteen characters are presented in Table 4.8. It revealed wide range of variability among the clusters for the characters days to 50 per cent flowering, plant height, effective tillers per plant, panicle length, grains per panicle, length of grain, 1000 grain weight and seed yield per plant.

Cluster means for days to 50 per cent flowering were ranged between 96 days (cluster II) and 104.93 days (cluster I). Cluster III was close (104.28 days) to cluster I.

For days to maturity, range of cluster means was observed between 122.11 days (cluster II) and 133.59 days (cluster I). Here also, mean performance of cluster III (132.83 days) was close to that of the cluster I.

Plant height showed the range of cluster means from 90.53cm (cluster II) to 117.73 cm (cluster I). Cluster mean for cluster III (116.26 cm) was close to that of the cluster I.

Number of effective tillers per plant ranged for their cluster means between 2.38 (cluster II) and 5.32 (cluster I). Whereas, mean performance of cluster III was 5.22 for effective tillers per plant.

Mean panicle length of clusters ranged between 16.64 (cluster II) and 19.39 cm (cluster I).

Table 4.8. Mean performance of clusters in rice

Character	Clusters		
	I	II	III
Days to 50% flowering (No.)	104.93	96.00	104.28
Days to maturity (No.)	133.59	122.11	132.83
Plant height (cm)	117.73	90.53	116.26
Effective tillers per plant (No.)	5.32	2.38	5.22
Panicle length (cm)	19.39	16.64	19.23
Secondary branches per panicle (No.)	8.84	7.53	8.77
Grains per panicle (No.)	112.82	73.44	109.82
Length of grain (mm)	5.70	6.69	5.78
Breadth of grain (mm)	2.18	2.42	2.20
Length :breadth ratio of grain	2.66	2.82	2.67
1000 grain weight (g)	15.46	23.70	16.10
Protein content (%)	8.00	6.75	7.85
Seed yield per plant (g)	10.72	5.62	10.38

Number of secondary branches per panicle varied for their cluster means from 7.53 (cluster II) to 8.84 (cluster I), while cluster III had on an average 8.77 secondary branches per panicle.

Number of grains per panicle differed in the range of cluster means between 73.44 (cluster II) and 112.82 (cluster I). Cluster III had on an average 109.82 grains per panicle.

Grain length ranged for its cluster mean between 5.70 mm (cluster I) and 6.69 mm (cluster II). Performance of cluster III (5.78 mm) was near to that of the cluster I.

Breadth of grain varied from 2.18 mm (cluster I) to 2.42 mm (cluster II) for its cluster mean. Cluster III had the mean breadth of 2.20 mm.

Length : breadth ratio of grain showed the range of cluster means between 2.66 (cluster I) and 2.82 (cluster II). Mean performance of cluster III for this trait (2.67) was nearer to the cluster I.

The trait, 1000 grain weight exhibited wide range of variation for cluster means between 15.46 g (cluster I) and 23.70 g (cluster II). Whereas, cluster III had the mean 1000 grain weight of 16.10 g.

Protein content varied among clusters between 6.75% (cluster II) and 8.00 % (cluster I). The average protein content for cluster III was 7.85 %.

Seed yield per plant varied from 5.62 g (cluster II) to 10.72 g (cluster I) among the clusters. Mean seed yield per plant for cluster II was 10.38 g.

4.6.3 Per cent contribution of various characters for divergence

The per cent contribution of the 13 characters studied, towards total divergence is presented in Table 4.9. It was observed that length : breadth ratio of grain contributed highest (33.333%) for divergence, followed by number of grains per panicle (32.051%), length of grain (11.154%) and seed yield per plant (10.385%). Days to 50 per cent flowering, days to maturity, plant height, effective tillers per plant contributed least (0.128 %) to the divergence, followed by panicle length (0.256 %), secondary branches per panicle (0.385 %), 1000 grain weight (1.282 %), breadth of grain (3.077) and protein content (7.564 %).

Table 4.9. Per cent contribution of 13 characters for divergence in rice

Sr. No.	Character	No. of times appearing I in ranking	Per cent contribution
1.	**Days to 50% flowering (No.)**	1	0.128
2.	**Days to maturity (No.)**	1	0.128
3.	**Plant height (cm)**	1	0.128
4.	**Effective tillers per plant (No.)**	1	0.128
5.	**Panicle length (cm)**	2	0.256
6.	**Secondary branches per panicle (No.)**	3	0.385
7.	**Grains per panicle (No.)**	250	32.051
8.	**Length of grain (mm)**	87	11.154
9.	**Breadth of grain (mm)**	24	3.077
10.	**Length :breadth ratio of grain**	260	33.333
11.	**1000 grain weight (g.)**	10	1.282
12.	**Protein content (%)**	59	7.564
13.	**Seed yield per plant (g)**	81	10.385
	Total	780	100.000

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DISCUSSION

CHAPTER 5

DISCUSSION

Improvement through breeding programme in any crop depends on the presence of genetic variability in the material available. The utility of such material in the germplasm could be judged on the basis of knowledge of the extent of variability, character association and direct and indirect effect of different characters (path analysis) available in the material. In the present investigation, 40 genotypes of rice were evaluated to assess the variability parameters, character association and interaction effects for 13 characters. The information obtained on variability parameters, character association, path coefficient and divergence studies is discussed under the following sub headings:

1. Variability, heritability and genetic advance
2. Correlation
3. Path analysis
4. Genetic divergence

5.1 Variability, heritability and genetic advance

The analysis of variance revealed highly significant differences for all the 13 characters studied (Table 4.2). Reddy and De (1996) and Naik *et al.* (2002) also noticed significant differences among genotypes for different traits.

In present investigation, for all the characters condiderable amount of variation was observed (Table 4.3). In plant breeding programmes, wide range of variation among the genotypes paves the way to bring a desirable improvement in the crops. The present material therefore, could serve a pool for selection of suitable material in breeding programmes.

RDN. 19

RDN. 20

RDN. 9

RDN. 37

RDN. 30

RDN. 43

Plate I. A. Variability for seed size, shape and colour among rice genotypes.

RDN. 42

RDN. 44

RDN. 54

RDN. 29

RDN. 18

RDN. 12

Plate I. B. Variability for seed size, shape and colour among rice genotypes.

RDN. 1

RDN. 7

RDN. 14

RDN. 23

RDN. 11

RDN. 49

Plate I. C. Variability for seed size, shape and colour among rice genotypes.

Similar results were obtained by Sawant and Patil (1995a), Vange *et al.* (1999) and Amirthadevarathinam (1990).

The estimation of genetic (heritable) and environmental (non-heritable) components of the total variability is required as these help us in the choice of desired breeding technique. Johanssen (1909), Nilson Ehle (1909) and East (1916) separated genetic variance from total variance by using environmental variance. Now, it is an accepted pattern in all the biometrical studies as it helps in arriving at precise conclusions about the true breeding value of a genotype. Thus, in the present study, the components of variation such as phenotypic and genotypic coefficient of variability, heritability and predicted genetic advance and genetic advance as percentage of mean were computed in respect of both the yield and it's component characters together with few physical grain quality parameters.

Seed yield per plant exhibited the highest GCV and PCV, followed by 1000 grain weight, grains per panicle and effective tillers per plant indicating the importance of these traits in selection. This was in the conformity with the results of Reddy *et al.* (1995) and Singh and Choudhary (1996). Lowest GCV and PCV were recorded for days to maturity, followed by days to 50 per cent flowering. Chauhan and Tandon (1984) also reported similar results.

The magnitudes of PCV were higher than the GCV for all corresponding characters. This revealed the importance of environmental variance in expression of different traits in rice crop. Choubey and Singh (1994), Jha *et al.* (1999) and Kumar *et al.* (2001) also observed higher PCV than GCV. However, all characters showed very low difference between PCV and GCV which indicated the low level of environmental factors operating and there is good correspondance between genotypic and phenotypic expression of the traits. It was maximum for effective

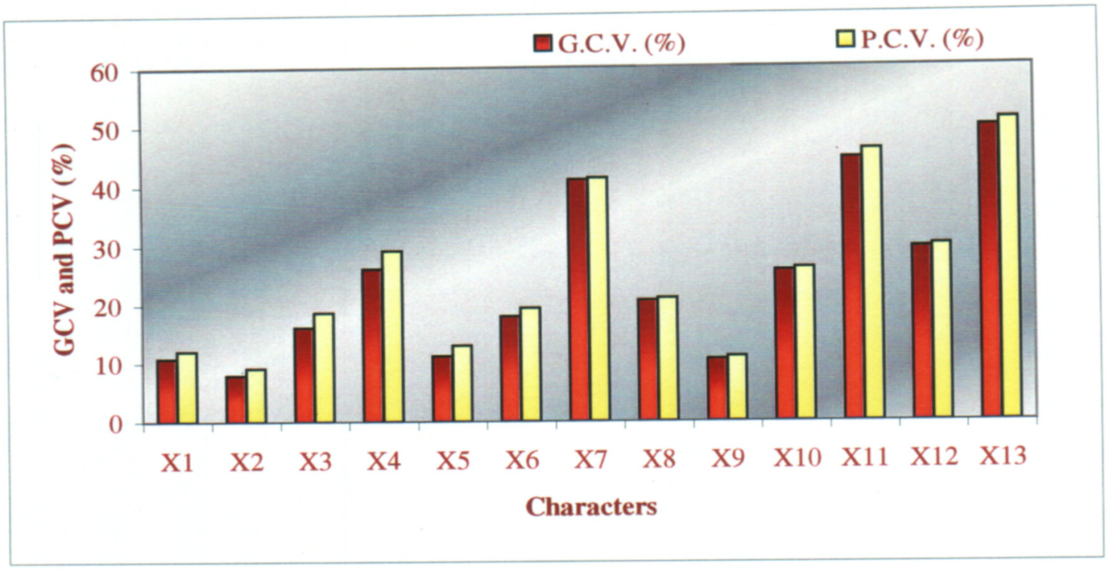

Fig. 1. Genotypic and phenotypic cofficient of variation for 13 characters in rice

X1 : Days to 50% flowering (No.)

X2 : Days to maturity (No.)

X3 : Plant height (cm)

X4 : Effective tillers per plant (No.)

X5 : Panicle length (cm)

X6 : Secondary branches per panicle (No.)

X7 : Grains per panicle (No.)

X8 : Length of grain (mm)

X9 : Breadth of grain (mm)

X10 : Length : breadth ratio of grain

X11 : 1000 grain weight (g)

X12 : Protein content (g)

X13 : Seed yield per plant (g)

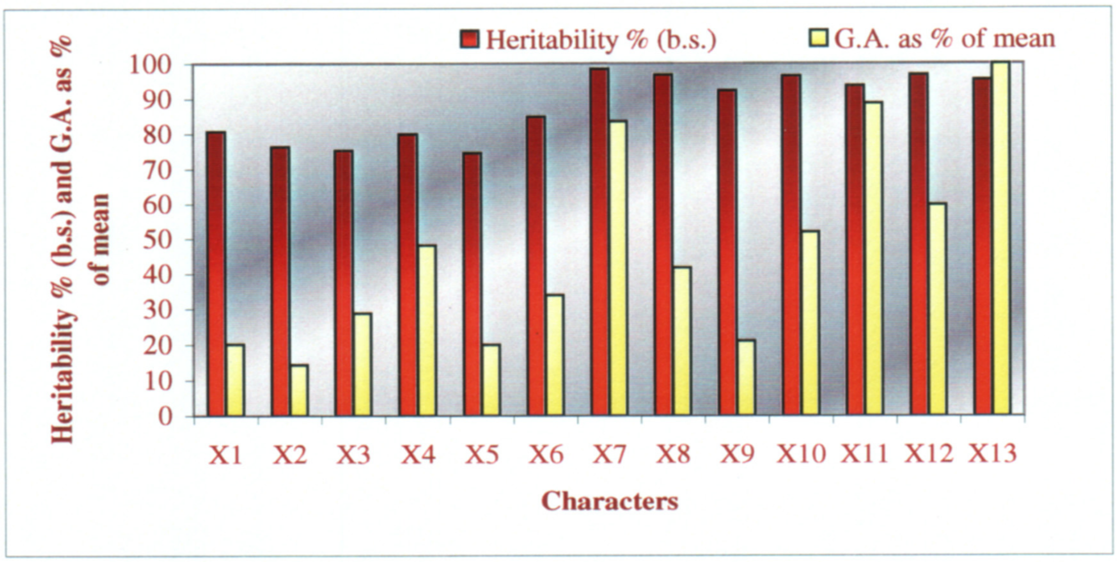

Fig. 2. Heritability % (b.s.) and G.A. as percentage of mean for different characters in rice

RDN. 7

RDN. 29

RDN. 44

RDN. 58

RDN. 49

RDN. 37

RDN. 42

RDN. 43

Plate II. Variability for grain size and shape among rice genotypes

tillers per plant (3.066), followed by plant height (2.458) and panicle length (1.760). Borbora and Hazarika (1998) also reported similar results with an exception of grain yield per plant.

The coefficient of variation reveals the extent of variability present for different characters and it does not indicate the heritable portion. To obtain the knowledge of heritable portion of the variability, it is essential to know the heritability estimates of the different attributes.

In the present investigation, all characters showed high heritability (b.s.) ranging from 74.67 (panicle length) to 98.48 per cent (grains per panicle), indicating the scope for selection of these traits. Naik *et al.* (2002) also recorded high heritability for all the traits under study. Highest heritability for grains per panicle was also obtained by Sawant and Patil (1995b), Vanniarajan *et al.* (1996) and Yadav (2000).

Heritability estimates in broad sense do not serve as true indicator of the genetic potentiality of the genotypes, since, their scope is restricted by their interaction with the environment. The heritability estimates separate the environmental influence from the total variability and indicates the accuracy with which a genotype can be identified by it's phenotypic performance, thus making the selection more effective. As such as heritability in broad sense includes both additive and non additive gene effects (Hanson *et al.* 1956).

It is advisable to consider the predicted genetic advance along with heritability estimates as a tool in the selection programme for still better efficiency in selection. In the present study, grains per panicle exhibited highest heritability (98.48 %) coupled with highest genetic advance (91.973). It was followed by plant height, days to maturity and 1000 grain weight. Selection based on these traits in rice would be effective for increasing the yield. The variability in the characters with high heritability and genetic advance might be due to additive gene interaction.

Genetic advance for yield was low, but when expressed as percentage of mean, it was fairly high.

From the studies on genetic parameters, it seems that grains per panicle is the character which needs due attention in the selection programme because it had higher PCV and GCV with minimum difference between them, very high heritability coupled with high genetic advance and highest range of variability to be exploited in the rice improvement programme.

5.2 Correlation

The phenotype of a plant is the result of interaction of a large number of factors. Therefore, the final yield, a polygenically controlled character, is the sum total of all the effects of several component characters. The influence of these characters can be known through the correlation studies. Genetic correlation between various plant characters arises because of linkage or pleiotropy. To assess the extent and nature of association between yield and yield contributing components, knowledge of interaction of characters among themselves and with environment is very essential. In the present investigation, both genotypic and phenotypic correlations were worked out for yield and yield contributing characters.

The phenotypic and genotypic correlations among different characters were mostly comparable in magnitude. However, genotypic correlations, in general, were higher than the corresponding phenotypic correlations excepting for the characters, length : breadth ratio of grain and seed yield per plant. Earlier workers, Vange *et al.* (1999) and Shivani and Reddy (2000) recorded higher genotypic correlation coefficients than the corresponding phenotypic ones.

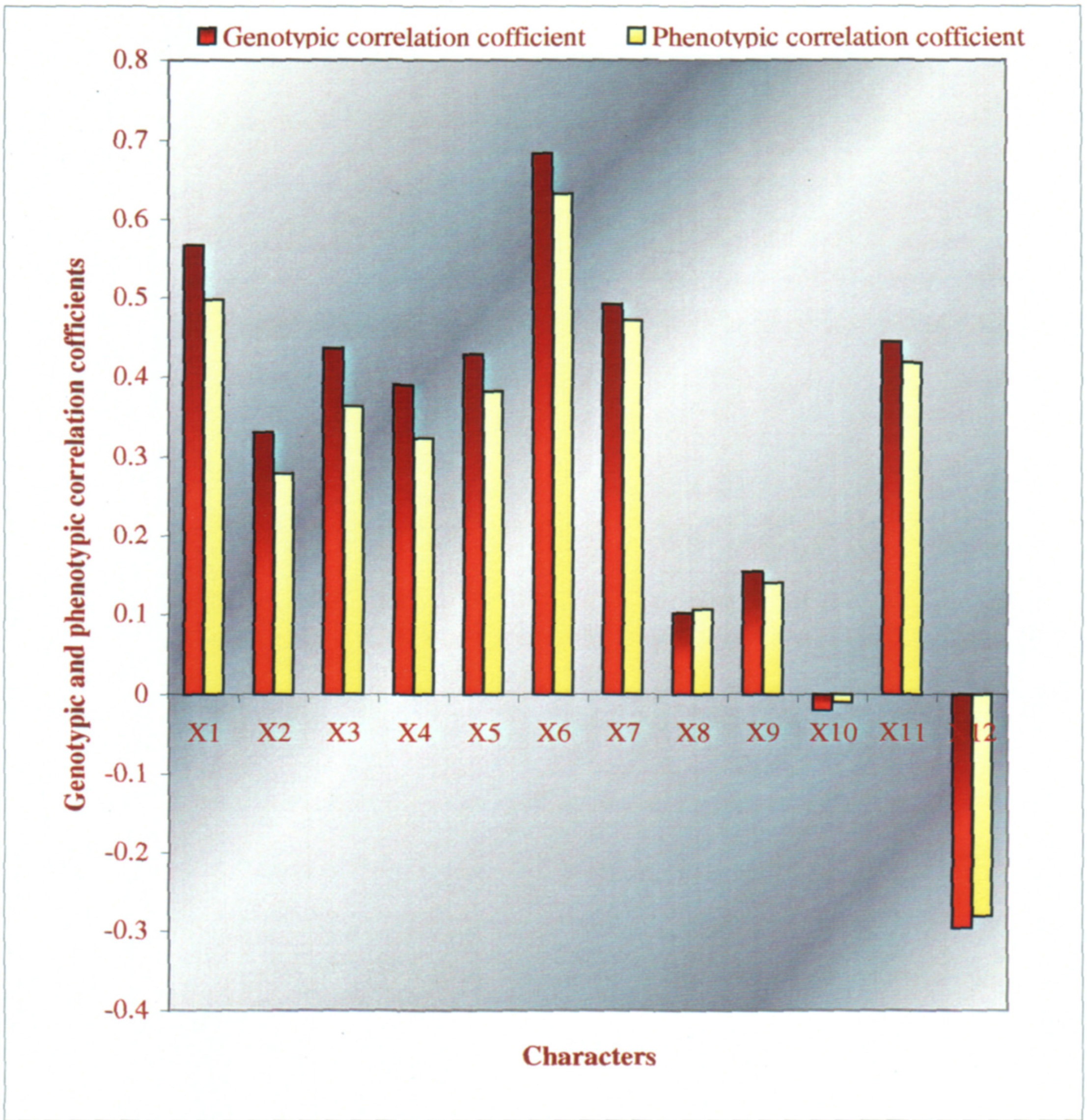

Fig. 3. Genotypic and phenotypic correlation cofficients of 12 characters with seed yield in rice

X1 : Days to 50% flowering

X2 : Days to maturity (No.)

X3 : Plant height

X4 : Effective tillers per plant

X5 : Panicle length (cm)

X6 : Secondary branches per panicle (No.)

X7 : Grains per panicle (No.)

X8 : Length of grain (mm)

X9 : Breadth of grain (mm)

X10 : Length : breadth ratio of grain

X11 : 1000 grain weight (g)

X12 : Protein content (g)

In the present study, the characters days to 50 per cent flowering, plant height, effective tillers per plant, panicle length, secondary branches per panicle, grains per panicle and 1000 grain weight exhibited significant positive association with grain yield at both phenotypic and genotypic levels indicating their importance in the selection. Whereas, days to maturity showed significant positive association with seed yield only at genotypic level. These results were in general comparable to those of Reddy and Ramchandraiah (1990), Choudhary and Das (1998), and Verma and Mani (1999) and Cristo *et al.* (2000). Two traits, *viz.*, length : breadth ratio of grain and protein content were negatively correlated with the seed yield in the present investigation.

Among all characters, secondary branches per panicle showed highest positive correlation with seed yield as also reported by Cheema *et al.* (1998) and Sinha *et al.* (1999). It was followed by days to 50 per cent flowering, grains per panicle, plant height and effective tillers per plant. Thus, from the relationships of different characters with seed yield in the present study and in those, observed by earlier workers, it is seen that a late maturing tall variety with more number of effective tillers per plant having more number of secondary branches and grains per panicle can be selected as these attributes are considered as yield indicators.

Among other correlations, the most striking was association between days to 50 per cent flowering and days to maturity. As the correlation coefficient was almost equal to unity (0.967), selection for days to maturity and vice versa will give the similar results. Rao and Shrivastav (1999) also revealed the positive association between these traits.

Days to maturity were significantly and negatively associated with grains per panicle but has significant positive correlations with plant height, panicle length and secondary branches per panicle.

Plant height showed significant positive correlation with panicle length, followed by secondary branches per panicle, grains per panicle and effective tillers per plant. Panicle length was significantly and positively correlated with secondary branches and grains per panicle. Verma and Mani (1998) and Gupta *et al.* (1999) also revealed similar correlations. The trait, effective tillers per plant didn't show desirable correlations with any other trait except seed yield per plant.

Highly significant positive correlation between number of secondary branches and grains per panicle observed under this investigation were also reported by Sinha *et al.* (1999). This trait also exhibited highly significant positive correlation with 1000 grain weight.

Grains per panicle had positive but non significant association with grain breadth at both the levels, however, it possessed highly significant negative association with grain length and L:B ratio suggesting that increased length of grain may result in lesser number of grains per unit length of panicle.

Grain length and L:B ratio were found to be associated strongly with each other in positive direction. But, it also exhibited negative association with the trait, grain breadth. From these results, it is clear that selection for better grain length would result in increased L : B ratio and in turn decreased economic yield as L:B ratio had negative though non significant association with seed yield per plant. It has also been observed that selection for more grain length would surely reduce the grain breadth. This falls in line with the results of Saimuraliraj (1992) and Deosarkar and Nerkar (1994).

Highly negative association was observed between the traits, grain breadth and L : B ratio at both phenotypic and genotypic levels. The association indicated that selection for smaller grain breadth would result in increased L : B ratio and hence, economic yield per plant would be reduced. This was in accordance with the result of Moeljopawiro (1986).

The trait, 1000 grain weight exhibited positive association with breadth of grain, secondary branches per panicle, length of grain and days to 50 per cent flowering at both the levels suggesting that longer and thicker grains increase the grain weight, which in turn increases the grain yield per plant. Gupta *et al.* (1998) also observed close positive association of 1000 grain weight with seed yield per plant.

Protein content had highly significant and non significant negative association with grains per panicle and seed yield per plant, respectively, indicating selection of high yielding genotypes would have adverse effect on protein content or vice versa.

Above correlations revealed that high seed yield in rice, in present investigation was mainly subscribed by secondary branches per panicle, days to 50 per cent flowering, grains per panicle and 1000 grain weight.

5.3 Path coefficient analysis

The estimation of correlation coefficients does not consider the dependence of one variable on another independent variable. Path coefficient analysis first suggested by Wright (1921) and later by Dewey and Lu (1959) being a statistical tool provides an effective measure of direct and indirect influence of association and depicts the relative importance of each factor involved in contributing to the final product i.e. grain yield per plant. In order to obtain the development relations, the cause and effect relationship between yield *per se* and 12 characters at

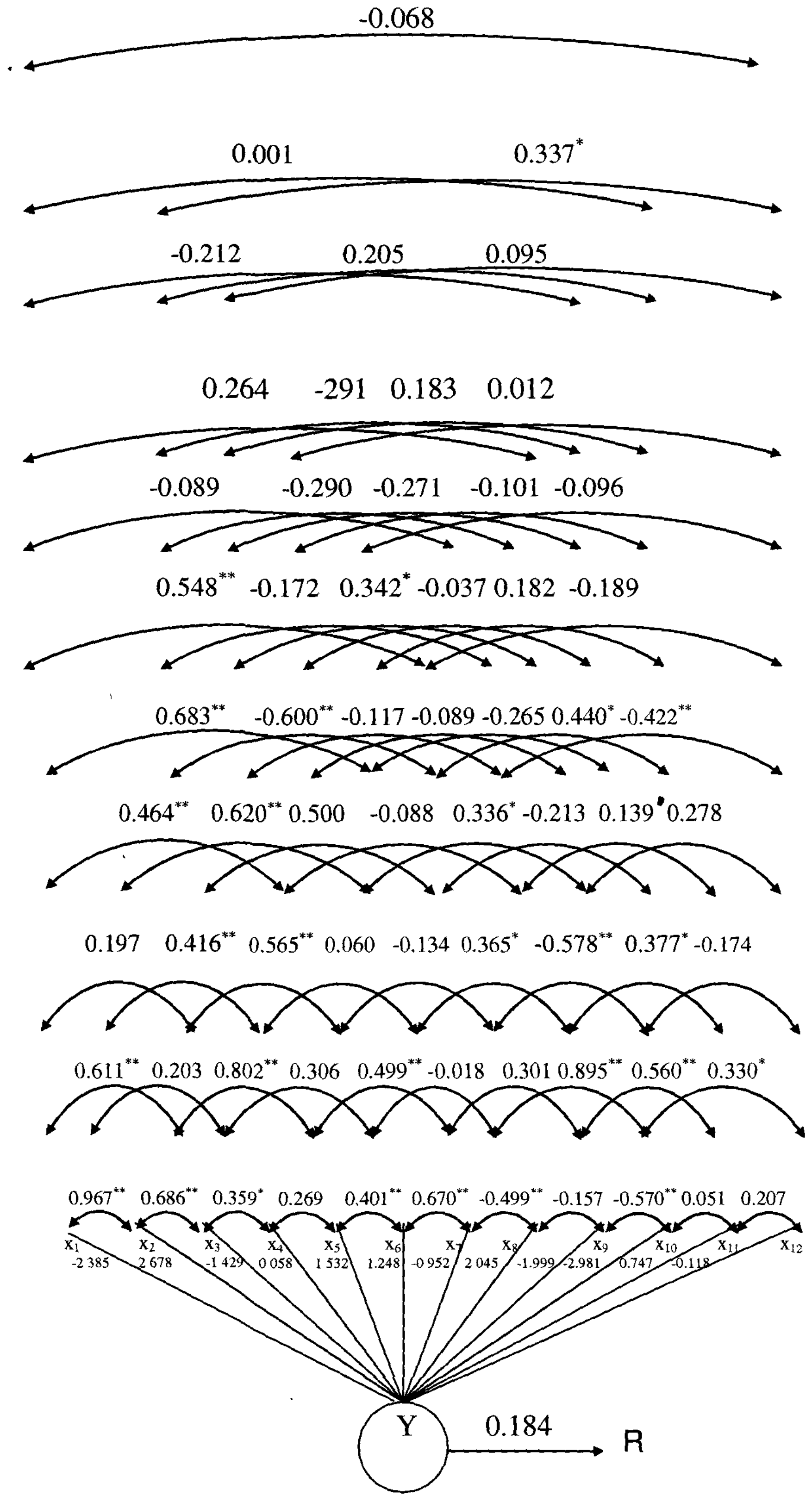

Fig. 5.1. Path diagram and genotypic coefficient of factors influencing seed yield in rice (*Oryza sativa* L.)

X_1 : Days to 50 per cent flowering	X_7 : Grains per panicle (No.)
X_2 : Days to maturity	X_8 : Length of grain (mm)
X_3 : Plant height (cm)	X_9 : Breadth of grain (mm)
X_4 : Effective tillers per plant (No.)	X_{10} : Length : breadth ratio of grain
X_5 : Panicle length (cm)	X_{11} : 1000 grain weight (g)
X_6 : Secondary branches per panicle (No.)	X_{12} : Protein content (%)
Y : Seed yield per plant (g)	R : Residual Effect

genotypic level were studied in rice through path coefficient analysis and the results are discussed below.

The direct and indirect effects of different characters in the present investigation are presented in Table 4.5 and path diagram is presented in Fig. 5.1. It revealed that in the present study, yield was subscribed mainly by days to 50 per cent flowering, days to maturity, plant height, effective tillers per plant, panicle length, secondary branches per panicle, grains per panicle and 1000 grain weight which was evident from their strong positive correlations with seed yield. Similar reports were forwarded by Reddy and Ramchandraiah (1990).

The characters, days to maturity, grain length, panicle length, secondary branches per panicle and 1000 grain weight influenced the seed yield per plant by their positive direct effect on it. These traits also had significantly positive correlation with seed yield except grain length. This indicated that selection for these traits would help to develop high yielding rice genotype. The desirable contribution of days to maturity for seed yield was also reported by Mehetre *et al.* (1996).

Four traits, *viz.*, days to 50 per cent flowering, plant height, grains per panicle and grain breadth though had significant positive correlations (except the latter) with seed yield, their direct effects were negative. However, these traits, influenced the yield through the positive indirect effects mainly *via* length and breadth of grain. Nayak *et al.* (2001) also reported the highest negative direct effect of days to 50 per cent flowering and plant height, respectively, on seed yield. However, Selvarani and Rangasamy (1998) and Shivani and Reddy (2000) reported positive direct effect of days to 50 per cent flowering.

The length : breadth ratio and protein content of grain showed the negative effect on seed yield with a non significant negative correlation. However, it influenced the yield positively through other characters namely, length and breadth of grain, grains per panicle and days to 50 per cent flowering (except for protein content).

The importance of 1000 grain weight in determining the seed yield of rice was also advocated by Gupta *et al.* (1998), Kumar *et al.* (1998), Verma and Mani (1998) and Sathya *et al.* (1999).

The residual effect determines how best the causal factors account for the variability of the dependent factors, the seed yield, in this case. In the present study, residual effect was quite low (0.1836) indicating that the characters considered account for 81.64 per cent of the variability in seed yield in rice.

5.4 Genetic divergence

Configuration of several groups of genotypes or to be more precise, of the group's characteristics may admit a description in terms of a few group constellations and their interrelationships. Mahalanobis's (1936) distance statistic (D^2) is an useful tool for this and is now well established and widely used in plant breeding for classifying the genetic stocks, on the basis of genetic divergence between populations.

5.4.1 Clusters, their distances and mean performances

In the present study, D^2 values between all possible 780 pairs of 40 genotypes ranged between 23.82 (RDN-13 and RDN-27) to 12905.85 (RDN-42 and RDN-57). This high range for D^2 values indicated the presence of a great amount of diversity in genotypes of rice under study.

Clustering of genotypes following the Tocher's method as described by Rao (1952) led to formation of 3 clusters in the present study. The distribution of genotypes into different clusters is presented in Table 4.6. The cluster I comprised most of the genotypes i.e. 36, while cluster II had 3 genotypes and cluster III was monogenotypic. Grouping of genotypes into 3 clusters suggested the presence of relatively low

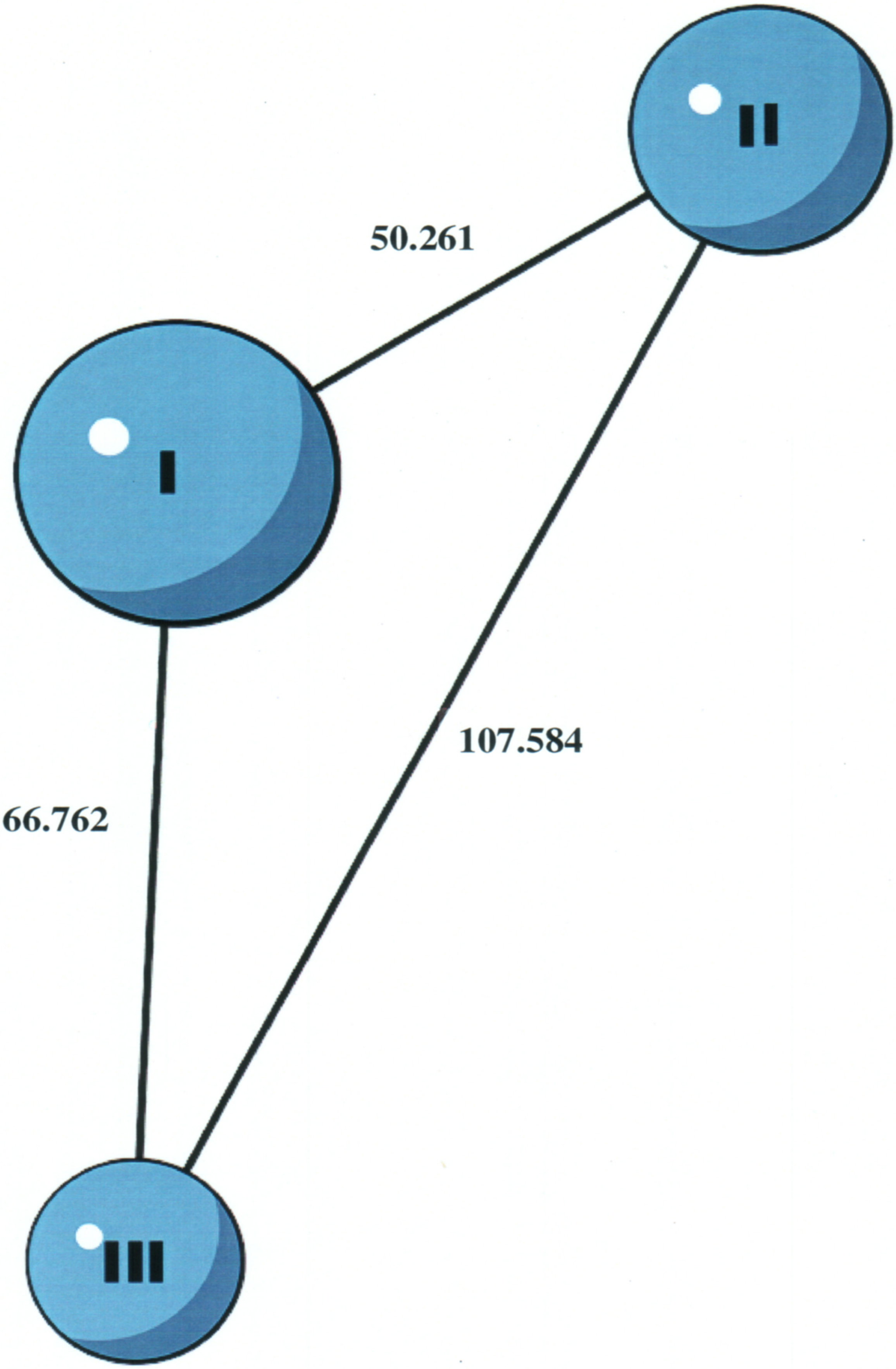

Fig 5. Cluster Diagram – Clusters and Their interrelationships

amount of genetic diversity in the material under investigation. The genotype RDN-42 forming cluster III indicated wide diversity from rest of the genotypes forming cluster I and cluster II. This genotype may have entirely different architecture from the others.

Perusal of Table 4.7 and Fig. 5.2 revealed that maximum inter-cluster distance was observed between cluster II and III (D=107.584) suggesting that genotypes included in cluster II might have entirely different genetical architecture from the genotypes included in the cluster III. Cluster III being monogenotypic, the inter-cluster distance between cluster I and III was 66.762 i.e. second largest in present investigation, though their mean performances were nearly similar for all the traits under study. The lower value of D (50.261) between cluster I and II suggested that the genetic constitution of the genotypes in cluster I is in close proximity with the genotypes in cluster II.

The D^2 values indicated that the cluster II and III had maximum divergence (D^2 = 11574.290) from the rest of the clusters as well as from each other.

Based on the mean performances of the clusters for 13 characters (Table 4.8), cluster II was found to be the least yielder. It comprised of 3 genotypes, *viz.,* RDN-57, RDN-58 and RDN-60 having earliness, less height, long bold grains, higher 1000 grain weight as compared to other genotypes belonging to other clusters. Low yield by these genotypes can be attributed to lower number of effective tillers per plant (2.88), grains per panicle (73.44) and lesser panicle length (16.64 cm).

Cluster I and cluster III exhibited nearly comparable yields(10.72 g and 10.38 g, respectively). Both possessed taller genotypes, longer panicles, more number of secondary branches and grains per panicle, medium 1000 grain weight with medium slender to long slender grains.

Cluster I, the most important cluster, which possessed 36 genotypes, in general included the most productive late maturing genotypes with medium to tall height, more number of effective tillers per plant and secondary branches and grains per panicle and fairly good protein content (8.00%). Mean seed yield per plant of this cluster was 10.72 g.

5.4.2 Genetic divergence in relation with geographical origin

The material used in the present study comprised of 40 genotypes from different eco-geographical origins (Table 3.1). Nearly all i.e. 39 genotypes were indigenous from ten different origins, *viz.*, Orissa, Chhattisgarh, U.P., Maharashtra, IARI.,New Delhi, Bihar, Uttarkhand, Pakistan (pureline selection from local lines from Punjab), DRR. Hydrabad and Haryana. One genotype i.e. RDN-60 was from IRRI. Phillipines i.e. selection from BR 827.

Clustering pattern of the genotypes from these different (diverse) origins revealed no parallelism between genetic divergence and geographical distribution of the genotypes (Table 5.1). This was revealed by the fact that genotypes from different origins were grouped in the same cluster, as they had low genetic distance (D value) from each other. This was evident from cluster II, which had low intra-cluster distance (D value = 17.163), followed by cluster I (D value = 27.706). Cluster III being monogenotypic, had intra cluster D equal to zero. The cluster I (the largest with 36 genotypes) comprised genotypes from nine different sources (all indigenous). Whereas, cluster II comprised 3 genotypes, one each from U.P., Maharashtra and IRRI, Phillipines. Cluster III comprised one genotype from Bihar.

In the present study, the genotypes belonging to the same geographical region or same location fell into different clusters, separated by high genetical distances. The genotypes from U.P. and Maharashtra were found to be distributed in two clusters, I and II, while that of from Bihar in cluster I and III. Out of these clusters, II and III were the more distant (D=107.584) from each other followed by cluster I and III (D=66.762) and cluster I and II (D=50.261). One genotype (RDN-60) from IRRI, Phillipines fell in cluster II.

Table 5.1. Clusters in relation to Eco-geographical origin of the genotypes

Clusters	Geographical origin of the genotypes included
I	Orissa (1, 2, 3, 4, 5, 6 and 7), Chhattisgarh (8, 9, 10, 11, 12,13,14, 15, 16, 17, 18, 19 and 20) U.P. (21, 22, 23 and 24), Maharashtra (36 and 39), Bihar (26 and 27), Uttarkhand (28 and 35), Pakistan (29), DRR Hyderabad (30, 33 and 34), Haryana (31), IARI, New Delhi (32)
II	U.P. (37), Maharashtra (38), IRRI, Phillipines (40)
III	Bihar (25)

N.B. Figures in parenthesis indicate the serial number of the genotypes given in Table 3.1

Though, above pattern of clustering confirmed the existence of relatively low amount of genetic diversity in the material from each of the locations mentioned above, it revealed the independence of genetic divergence from geographical distribution of genotypes. Kandhola and Panwar (1999) suggested this pattern of grouping of genotypes together from distant places indicated that the nature of selection process operating under any eco geographical region does not seem to be very dissimilar to that of other regions. Hanamaratti *et al.* (1998) also reported that the disposition of rice genotypes from various sources into different constellations did not follow any consistent pattern, in relation to geographic diversity. These results also confirmed the earlier findings of Murthy and Arunachalam (1966) and Bhatt (1970), who stated that the genetic drift and selection in different environments may cause greater diversity among varieties than their geographical distances. Bhatt (1970) also suggested that such findings tend to show that the D^2 technique was a sensitive tool for measuring divergence among genotypes.

Similar results were also obtained by Kumari and Rangasamy (1997), Mokate *et al.* (1998), Bansal *et al.* (1999), Kandhola and Panwar (1999), Jadhav *et al.* (2003) and Singh *et al.* (2005), who suggested that quantitative measure of genetic divergence was a better criterion for choosing diverse parental lines for hybridization than on the basis of pedigree relationship. Pandey *et al.* (1999), Rather *et al.* (2001) and Roy *et al.* (2002) also reported similar observations.

5.4.3 Relative contribution of characters towards divergence

The variance of cluster means provides information on relative importance of characters towards the divergence. The perusal of Table 4.9 indicated that the variance of cluster means was much higher for length : breadth ratio of grain, followed by number of grains per panicle, length of grain and seed yield per plant. Such type of trend was also reported by Kole *et al.* (2000), Rather *et al.* (2001) and Roy *et al.* (2002). Bhardwaj *et al.* (2001) observed the importance of length : breadth ratio of grain. Whereas, Pandey *et al.* (1999) showed that days to 50 per cent flowering, plant height, primary branches per panicle and 100 seed weight were important for genetic divergence in rice. Ahmed and Borah (1999) found that, the tiller number, panicles per hill, grains per panicle, grain fertility and grain yield accounted major portion of the divergence. In the present investigation, number of days to 50 per cent flowering and maturity, plant height, effective tillers per plant, panicle length, number of secondary branches per panicle had relatively much low contribution towards divergence. Thus, some discrepancies in the characters contributing to divergence were observed in the present investigation and results of the previous workers. Such discrepancies in the results might be due to the different sets of material and also due to the role of environmental variability as suggested by Hanamaratti *et al.* (1998), who formed different number of clusters i.e. 18 and 17 under lowland and upland conditions, respectively, for the same set of 50 genotypes.

5.4.4 Genetic divergence and selection of potent parents

The success of any crop improvement programme involves selection of the best parents having high potential for the economically important characters. Among the different approaches of selecting parents, selection based on diversity has its own significance as diversity is the basic need of crop improvement. In the present study, studies on diversity among different genotypes yielded valuable information, that could be useful in suggesting potent parents for crossing. Shanmugasundaram *et al.* (2000) has also advocated the use of multivariate analysis for the selection of parents. According to them, the genotypes within a cluster with high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance with regard to yield. Bhatt (1970) suggested that it would be logical to effect crosses between genotypes belonging to the clusters separated by high estimated statistical distances.

Arunachalam and Bandyopadhyay (1984) devised a method to delineate parental divergence into four divergence classes (DC). To take into account the variable magnitude of variation in parental divergence, the mean (m) and standard deviation (s) of the values of intra and inter cluster divergence (D) were calculated. They defined divergence classes as below :

DC 1 : $D \geq (m+s)$

DC 2 : $D < (m+s)$ and $\geq m$

DC 3 : $D \leq (m-s)$ and $< m$

DC 4 : $D < (m-s)$

Experiment by them (two in groundnut and one in rapeseed) showed that the chances for the occurrence of a high frequency of heterotic crosses with high values of heterosis were more, when the parents were chosen to have their divergence in the interval, m – s and m + s, compared to the crosses between parent, whose divergence fall outside this interval, i.e. those fall in DC 1 and DC 4.

In the present study, an attempt was made to classify the cluster combinations into four divergence classes, following the above procedure suggested by Arunachalam and Bandyopadhyay (1984). The statistical distance (D) given in Table 4.7 represents the index of genetic diversity among clusters. The mean of 3 inter cluster and 2 intra cluster (as monogenotypic cluster III had no intra cluster distance) was 53.895 and standard deviation was 31.926. the minimum (X) and maximum (Y) values among these distances were 17.163 and 107.584, respectively. Thus, the divergence classes were as presented in Table 5.2.

Table 5.2. Distribution of different cluster combinations into four divergence classes based on D values between them

CLUSTER COMBINATIONS	
	Y (107.584)
DC 1	(II, III)
	m + s (85.821)
DC 2	(I, III)
	m (53.895)
DC 3	(I, II), (I, I)
	m – s (21.969)
DC 4	(II, II)
	X (17.163)

DC 4		DC 3		DC 2		DC 1	
X		m –s		m		m + s	Y
17.163		21.969		53.895		85.821	107.584

Grouping of the cluster pairs into these divergence classes have presented in Table 5.2. On the light of the above discussion, initial choice of the parents should be made from the cluster combinations falling in the divergence classes DC 2 and DC 3. As cluster combination (I, III) fall in the DC 2, crosses of the genotypes grouped into cluster I can be formulated with the genotypes grouped into cluster III.

However, while choosing among the genotypes of a cluster, the *per se* performance of genotypes for different traits such as yield, disease reaction, quality, lodging index etc. should be taken into account, so that desirable segregates would be obtained after hybridization.

Keeping in view all the above aspects, the following, genotypes in the present studies, deserve to be considered as potent parents for crossing.

1) RDN – 1	7) RDN – 9
2) RDN – 7	8) RDN – 26
3) RDN – 11	9) RDN – 27
4) RDN – 12	10) RDN – 30
5) RDN – 14	11) RDN – 58
6) RDN - 18	12) RDN – 42

Kandhola and Panwar (1999) studied the genetic divergence among indigenous and exotic genotypes of rice and concluded that widely divergent clusters with high yield potential is likely to produce heterotic combinations and still wider variability in segregating generations.

SUMMARY AND CONCLUSIONS

CHAPTER 6

SUMMARY AND CONCLUSION

The present investigation "Genetic diversity and path analysis studies in Rice (*Oryza sativa* L.)" was undertaken to assess the extent of variability for different characters in rice to know their heritabilites and genetic advances, correlations among themselves and their direct and indirect contributions towards yield and to measure the genetic divergence. The material involved 40 genotypes of rice from 11 different eco-geographical origins, out of which 39 were indigenous from 10 different origins and only one was exotic. The experiment was laid down in a randomized block design with three replications during *kharif* 2006. Observations were recorded on 13 characters, *viz.,* days to 50 per cent flowering, days to maturity, plant height (cm), effective tillers per plant, panicle length (cm), secondary branches per panicle, grains per panicle, length of grain (mm), breadth of grain (mm), length : breadth ratio of grain, 1000 grain weight (g), protein content (%) and seed yield per plant (g).

Wide range of variation was observed for all the 13 characters considered for the study. The analysis of variance exhibited significant differences among the genotypes for all the characters indicating the presence of substantial degree of variability. Phenotypic coefficient of variation (PCV) was found to be more than the genotypic coefficient of variation (GCV) for all the characters, indicating the role of environment for expression of the traits. Seed yield per plant exhibited the high GCV as well as PCV (49.703 and 50.887, respectively). It was followed by 1000 grain weight and grains per panicle. The number of days to maturity exhibited the least GCV and PCV (7.944 and 9.085, respectively). Among the traits, difference between GCV and PCV values was high for number of effective tillers per plant (3.066) and low for the number of grains and secondary branches per panicle. (0.315).

Heritability (b.s.) of all the characters in the present study, was categorized to be very high. It was lowest for panicle length (74.67%) and highest for number of grains per panicle (98.48%), followed by protein content (98.82%) and length of grain (96.79 %). Very high heritability coupled with high genetic advance observed for grains per panicle and plant height advocated high genetic progress for them.

In the present study, genotypic correlations in general were higher than the corresponding phenotypic correlations. Seed yield per plant was significantly and positively correlated with number of secondary branches per panicle (0.684), days to 50 per cent flowering (0.567), number of grains per panicle (0.491), 1000 grain weight (0.444), plant height (0.436), panicle length (0.428), effective tillers per plant (0.390) and days to maturity (0.332). However, it had negative but non significant correlation with protein content (-0.297) and length : breadth ratio of grain (-0.020).

The characters, days to maturity, grain length, panicle length, secondary branches per panicle and 1000 grain weight influenced the seed yield per plant by their positive direct effect on it. These traits also had significantly positive correlation with seed yield except grain length. This indicated that selection for these traits would help to develop high yielding rice genotype.

Four traits, *viz.,* days to 50 per cent flowering, plant height, grains per panicle and grain breadth though had significant positive correlations (except the latter) with seed yield, their direct effects were negative. However, these traits, influenced the yield through the positive indirect effects mainly *via* length and breadth of grain.

Correlation among the characters and path analysis revealed days to maturity and secondary branches per panicle as the most important and reliable yield indicators in rice. The interrelationships in the present study also demonstrated that a late maturing dwarf variety having longer panicles with more number of secondary branches and grains per panicle will be high yielding in rice. However, to obtain a high yielding genotype with higher protein content seems to be difficult as they were negatively correlated.

In the present investigation, D^2 values between all possible pairs of 40 genotypes ranged between 2526.216 and 11574.290. The genotypes were grouped into only 3 clusters. Cluster I contained maximum number of genotypes (36), while that of cluster II contained only 3 genotypes and cluster III was monogenotypic. Intra-cluster D^2 values ranged between 294.269 (cluster II) and 767.648 (cluster I). The maximum inter cluster distance was observed between cluster II and III (D^2 = 11574.290), followed by cluster I and III (4457.125) and cluster I and II (2526.216).

The present study revealed no parallelism between genetic divergence and geographical distribution of the genotypes, which was demonstrated by the grouping of genotypes from same origin into different clusters, separated by high genetic distances. This suggested that, genetic drift and selection in different environments may cause geographical distances. Variance of cluster means revealed L : B ratio of grain and grains per panicle as the main characters contributing to the genetic divergence in the present material.

On the basis of divergence classes (DC), crosses of genotypes from cluster I can be formulated with genotype grouped in cluster III. This was on the ground that crosses between parent separated by moderate genetic distance would yield heterotic F_1 and transgressive segregants in advanced generations.

LITERATURE CITED

CHAPTER 7

LITERATURE CITED

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VITA

CHAPTER 8

VITA

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MASTER OF SCIENCE (AGRICULTURE)

in

AGRICULTURAL BOTANY
(CYTOGENETICS AND PLANT BREEDING)

2007

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