GENETIC VARIABILITY, DIVERSITY FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza Sativa* L.)

THESIS

Submitted in partial fulfilment of the requirements for the Degree of

MASTER OF SCIENCE

IN

AGRICULTURE

(GENETICS AND PLANT BREEDING)

By

RAHUL TEJRAM GAHANE
(ADPM/21/2809)

DEPARTMENT OF AGRICULTURAL BOTANY
COLLEGE OF AGRICULTURE, DAPOLI

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Under the Guidance of

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DECLARATION OF STUDENT

I hereby declare that the experimental work and its interpretation of the Thesis entitled **"GENETIC VARIABILITY, DIVERSITY FOR YIELD AND QUALITY TRAITS IN RICE (*Oryza Sativa* L.)"** or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged and that no part of the thesis has been submitted for any other degree or diploma.

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CERTIFICATE

This is to certify that the thesis entitled, **"Genetic variability, diversity for yield and quality traits in rice (*Oryza sativa* L.)"** submitted for the degree of M.Sc. (Genetics and Plant Breeding), of the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, is a bonafide research work carried out by **Mr. Rahul Tejram Gahane (ADPM/21/2809)** under my supervision and that no part of this thesis has been submitted for any other degree. The student had completed all the Course and Research requirement as per the norms in regular mode.

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

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Head
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THESIS APPROVAL BY THE STUDENT'S ADVISORY COMMITTEE INCLUDING EXTERNAL EXAMINER

This is to certify that the thesis entitled, **"Genetic variability, diversity for yield and quality traits in rice (*Oryza sativa* L.)"** submitted by **Mr. Rahul Tejram Gahane (ADPM/21/2809)** to the College of Agriculture, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, in partial fulfillment of the requirements for the degree of M.Sc. (Genetics and Plant Breeding) in the subject having Plant Physiology as Minor subject of Department Agril. Botany has been approved by Student's Advisory Committee, Board of Studies of the Department and Evaluated by One External Examiner after an open Viva Voice examination in the presence of External Examiner on the same held on dated 11 / 06 / 2024

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Abbreviations used

%	:	Per cent
>	:	Greater than
<	:	Less than
/	:	Per
*	:	Significant at 5% level of significance
**	:	Significant at 1% level of significance
ANCOVA	:	Analysis of Covariance
ANOVA	:	Analysis of Variance
@	:	At the rate of
^{0}C	:	Degree Celsius
C.D.	:	Critical Difference
cm	:	Centimetre
mm	:	Millimetre
d.f.	:	Degree of Freedom
MIN	:	Minimum
MAX	:	Maximum
EMS	:	Error Mean Sum of Squares
MSS	:	Mean Sum of Squares
TSS	:	Treatment Sum of Squares
Err	:	Error
et al.,	:	And others
etc.	:	et cetera
kg	:	Kilogram (s)
m	:	Metre
g	:	Grams
µ	:	Micrometres
t	:	Tonnes
ppm	:	Parts per million
ml	:	Millilitre
nm	:	Nanometre
mg	:	Milligram
GCV	:	Genotypic coefficient of variance
PCV	:	Phenotypic coefficient of variance
ECV	:	Environmental coefficient of variance
ha	:	Hectare
h^2	:	Heritability
σ^2p	:	Phenotypical variance
σ^2g	:	Genotypical variance
σ^2e	:	Environmental variance

$\sigma^2 r$	:	Replication variance
σ	:	Standard deviation
i.e.,	:	That is
CV	:	Coefficient of Variation
S.E.	:	Standard Error
viz.,	:	Namely
GA	:	Genetic Advance
GAM	:	Genetic Advance as per percentage of Mean
RBD	:	Randomized Block Design
Fe	:	Iron
Zn	:	Zinc
Ca	:	Calcium
N	:	Nitrogen
FYM	:	Farm Yard Manure
AOAC	:	Association of Official Analytical Chemists

Glossary

Genetic Variability: Genetic variability is either the presence of, or the generation of genetic differences.

Heritability: Heritability is the amount of phenotypic (observable) variation in a population that is attributable to individual genetic differences.

Genotype: Genotype is the genetic makeup of an individual cell or organism that determines or contributes to its phenotype.

Genetic advance: Genetic advance is a measure of how much gain you may get from phenotypic selection for a trait.

Path analysis: Path analysis is a method to discern and assess the effects of a set of variables acting on a specified outcome via multiple causal pathways.

Genetic diversity: Genetic diversity is the biological variation that occurs within species.

Konkan: Konkan is the 700 km long rugged section of the western coast line of Arabian Sea which extends from Daman in the North to western side land of Maharashtra and Goa.

CHAPTER I : INTRODUCTION

I. Background Information

Rice (*Oryza sativa* L.) serves as a main food source for more than half of the world's population, especially in Asia and Africa. More than 100 countries cultivate this crop, in which Asia contribute majority in area and production. In tropics as well as parts of temperate regions of the world, rice is one of the most significant cereal crops. The United Nation designated year 2004 as the 'International Year of Rice' with the theme "Rice is life" to highlight the significance of the rice crop as a source of food, for trade, and the tight ties between rice-based systems and many cultures and people worldwide, especially in developing countries. After maize and sugarcane, rice is the agricultural product with the third-highest global production. For small-scale farmers in particular, rice is crucial as an income-producing crop because it offers a source of revenue.

Rice is an essential crop for food security and promoting rural development since it is an abundant supplier of carbohydrates, proteins, and other vital nutrients. Rice includes 87% carbohydrates, 7-8% proteins, and very little fat (Selvakumar *et al.*, (2014)). One-fifth of all calories consumed by humans worldwide, or 80% of calories consumed in Asia, come from rice. In comparison to other food crops, only rice is cooked and eaten as a whole grain, hence quality considerations are of the utmost importance (Hossain *et. al*., 2009). Poor people in some parts of Asia depend largely on rice.

De Candolle (1886) and Watt (1892) recognised south India as the origin of rice. Vavilov stated that the origin of rice cultivation should be attributed to India and Myanmar. The crop is grown in various agro-ecological zones, from irrigated highlands to rainfed lowlands. There are a total of 24 species in the genus *Oryza*, of which 22 are wild and two, *Oryza sativa* and *Oryza glaberrima*, are cultivated (Chatterjee, 1948). All rice-growing regions cultivate *Oryza sativa*, but only West Africa grows *Oryza glaberrima*. As a result, it suggests that West Africa and South-eastern Asia (India, Myanmar, and Thailand) may have served as the origins of modern cultivated rice. These days, *Oryza sativa indica* and *Oryza sativa japonica* are the two most popular rice species cultivated all over the world. The rice plant is a self-pollinating annual crop and a member of the Poaceae (ancient Gramineae) family. A cluster of spikelets in rice inflorescence is referred to as a panicle.

India is the world's second-largest producer and consumer of rice after China. Over the past few decades, as a result of the use of modern technology including irrigation, fertilizers, pesticides, and improved varieties there has been a tremendous increase in rice production. In the

year 2021 around the world, rice is grown over an area of 165.25 million hectares, with a total production of 787.29 million tonnes and yield of 4.76 tonnes per hectare (FAOSTAT, 2021).

The Indian economy places rice in a special position. In India, rice is raised on an area of 46.00 million ha with an annual yield of 130.84 million tonnes and a productivity of 2.607 tonnes/ha (Anonymous, 2023). However, productivity is poor because India has the largest rainfed lowland rice area (45%) in the world (Pradhan *et al.*, 2022).

Maharashtra covered rice crop over 14.65 lakh hectares of land with an annual production of 32.76 lakh tonnes and an average productivity of 2.180 t/ha, (Anonymous, 2023). Konkan region of Maharashtra is a significant rice-producing area with an area of about 3.69 lakh hectare producing yield of around 12.94 lakh tonnes and productivity of about 2.93 t/ha, (Anonymous, 2023). The Konkan region makes a significant contribution to Maharashtra's rice production. Due to the Konkan region's heavy rainfall, rice is usually grown during the *kharif* season (Meshram *et al.*, 2020).

Due to numerous factors like soil deterioration, pests, water scarcity, and climate change, rice farming has recently experienced significant difficulties. Due to these difficulties, agricultural yields and quality have declined, while production costs have risen up. As a result, farmers have suffered financial losses, and millions of people now face food insecurity. Numerous strategies have been developed to solve these issues, such as the application of contemporary crop management techniques, the development of high-yielding and stress-tolerant varieties, and the use of precision agriculture technologies. Additionally, research has been done to better understand the fundamental mechanisms of rice growth, development and developing novel crop improvement techniques.

A significant position is held by rice in Indian agriculture. It is challenging to increase the production using the current inbred varieties since the yield of high yielding varieties (HYVs) of rice is plateauing. Therefore, more rice production using high yielding varieties (HYVs) is necessary to maintain self-sufficiency in rice. Since the world's population is growing and dietary habits are changing, there is an expected further increase in the demand for rice, we will need to produce 40 % more rice by 2030. We require rice varieties with higher yield potential and improved production stability in order to address the challenge of growing more rice. Conventional hybridization and selection techniques, ideotype breeding, hybrid breeding, wide hybridization, and genetic engineering are some of the different methods now being used to increase the rice yield potential. To build long-lasting resistance to diseases and insects as well as tolerating abiotic stresses, a number of traditional and biotechnological approaches are being used.

Rice is an essential model crop for plant genetic research due to its small genome size, genetic tractability, and economic importance. For crop improvement, stress adaptability, and fulfilling the rising demand for food security, genetic diversity is crucial. Numerous elements, including the genetic make-up of particular cultivars, breeding practises, geographic origin, and selection pressure, affect the genetic diversity and variability of rice. New insights into the genetic diversity of rice have been made possible by technological advancements, including the detection of genetic variation, population structure, and traits distribution.

In India, there are several indigenous rice cultivars that are still cultivated by tribal people and small farmers in rural areas where modern farming methods, adequate food supplies, and healthcare systems are ideals. They have numerous native rice cultivars with medicinal and dietary benefits. Traditional farmers may cultivate indigenous rice varieties that have a significant genetic diversity that can be used to improve cultivated rice varieties genetically. Indigenous rice varieties have proven to be useful donors for sources of resistance or tolerance to many stressful situations as well as for imparting resistance to significant diseases and pests in rice varietal improvement programmes. In general, many landraces traditionally grown by farmers near centres of diversity and domestication of crops serve as major natural resources crucial for preserving future food security in the context of climate change. In context of these characteristics, the Department of Agricultural Botany, College of Agriculture, Dapoli has gathered a number of local germplasms. These germplasms have greater diversity of genetics, a high level of tolerance for both abiotic and biotic stresses, and a wide range of adaptation with significant nutritional quality.

II. Importance and need of the study:

Genetic diversity is the basis of plant breeding. Genetic diversity in the parent generation is assumed when yield is segregated for selective breeding by generation (or by qualities that contribute to yield). Estimating the genetic diversity in yield attributes is crucial for the policies that choose parents in crossing programmes (Khare *et al.,* 2014). The plant breeders tend to assess genetic diversity from morphological characters because this is inexpensive, rapid, and simple to score. The height of the plant and the number of tillers, for instance, are examples of the wide morphological variation in the vegetative traits of rice plants.

Grain yield is the combination of multiple factors leads to the complex traits (Singh *et al.*, 2015). Even though a wide range of genetic variability has been documented for yield traits in the past, there is still unexplored genetic variability in germplasms that is crucial for choosing the potential parents in order to maximise heterosis and produce superior recombinants (Rashmi *et al*. 2017). The degree to which the desired traits are heritable and the nature and amount of

variability inherent in the genetic stock both affect how well quantitative traits can be genetically improved (Namrata *et al.,* 2016). The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for an effective breeding programme (Nayak *et al.,* 2016). An effective breeding programme requires knowledge of the genetic variability of yield-contributing traits, how they interact, and how yield is related to these factors (Nayak *et al.,* 2016). Heritability knowledge helps plant breeders in making knowledgeable selections, predicting the characteristics of the next generation, and determining the extent of genetic improvement brought about by selection (Khatun *et al*., 2015). Furthermore, strong genetic progress combined with high heritability provides the most efficient condition for character selection (Larik and Rajput, 2000). To ascertain each character's contribution to yield, associations between them were important. Studies of correlation offer a chance to examine the strength and direction of relationships between various features and grain yield as well as the direct and indirect effects of those associations (Solanki *et al.,* 2017).

In the Indian medical system *Ayurveda*, coloured rice has been called *shastika* rice and claims that, it can restore imbalances in the human body. *Susruta* (400 BC), *Charaka* (700 BC), and *Vagbhata* (700 AD), the well-known *Vriddhatrayi* (Three elders) of *Ayurveda*, considered red rice the best among rice varieties, due to desirable property as they had the power to rectify the tridosha (*vata*, *pitta*, and *kapha*) whose imbalance in the body causes various types of diseases (Chakravorty 2020). Lots of work were done to collect, evaluate and characterize for morphological and agronomical traits, while very little efforts have been done on grain and nutritional properties of indigenous rice cultivars. Many traditional or local genotypes were lost without noted down much knowledge about grain and nutritional properties of these varieties. It is very much important to find out the grain quality and nutritional profile, before validating the medicinal properties. Besides yield improvement, quality enhancement of rice must be area of research after attaining sufficiency in food grain production in order to overcome the nutrient deficiency in rice consuming population. Hence the study conducted for grain quality assessment to identify superior cultivars for economically important grain characteristics and nutritional properties and to estimate the correlation coefficient among the different physiochemical characteristics.

Any crop improvement program's success is affected by the genetic diversity of the genotypes, which in turn affects genetic variability, heritability, genetic advance, character interaction, direct and indirect effects on yield, and its attributes (Rashmi *et al*., 2017; Adhikari *et al.,* 2018; Saha *et al*., 2019). For agricultural improvement, effective management, and the preservation of germplasm resources, appraisal and examination of genetic diversity are essential (Govindaraj *et al*., 2015; Bhandari *et al*., 2017). In order to boost the economic value of rice, a breeding programme was developed that emphasised high yield, insect resistance, and the

introduction of desired quality traits (Khan *et al*., 2015; Kaiser *et al*., 2020). In order to facilitate effective selection in a rice breeding programme, the study aimed to evaluate the diversity indices, variability, and heritability for important traits.

The aim of this research seeks to present a summary of our current understanding of genetic diversity and variability in rice. With an emphasis on rice breeding and crop development, the study will also examine the numerous strategies that have been created to comprehend and make use of the genetic makeup of rice. Genetic diversities effects on rice crop production, quality, and sustainability are examined in the project, along with the economic and social implications for farmers and other stakeholders. Overall, this study will add to our understanding of rice genetic diversity and provide insight into possibilities for rice breeding and crop improvement.

III. Objectives of study

Keeping in view, the above important aspects, the present investigation was carried out with following objectives –

1) To evaluate the genetic variability and diversity for yield in rice
2) To evaluate biochemical and nutritional content in rice

IV. Hypothesis

The knowledge about genetic variability, diversity and heritability will help in making an effective breeding programme. The identified superior genotypes having good biochemical and nutritional properties than others will be useful for breeding programmes. In order to secure food security, advance sustainable agriculture, and enhance the quality of life of small-scale farmers, the findings of this study will have a significant impact on policymakers, researchers, and farmers.

V. Scope and limitation of the study: -

Amongst the population, the superior genotypes can be identified and further breeding can help to develop the races having good variability and biochemical and nutritional properties. Increasing rice yield on existing land remains the primary strategy for increasing production, to meet the future demand for food, for increasing population. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations.

From the local rice genotypes, the identified superior genotypes having good nutritional properties will be used to make rice more nutritive and reduce the malnutrition in humans but the proper analysis and improvement is needed.

Limitations of the study: -

1. Delay in critical manual operations *viz*. transplanting, weeding, roughing, plant protection may limit the study.
2. Shortage of labour, equipment, irrigation water, chemicals for analysis may limit the study.
3. Low and imbalance use of manures and fertilizers, depletion of plant nutrients due to heavy rains in Konkan region.

CHAPTER II : REVIEW OF LITERATURE

Variability is a fundamental pre-requisite for any plant breeding program to be effective in enhancing the genetic potential of a product. The approximations of various genetic parameters are crucial for a better comprehension of the type and degree of genetic variability present in breeding material as well as the correlation between various yield and yield attributing characters.

Exploiting genetic diversity for crop development ought to be the final goal of genetic resource discovery and preservation. Plant genetic resources need to be properly protected in order to benefit future generations. For quality assessment and potential food industry applications, rice varieties must be screened for phytochemical traits. Very few studies were conducted regarding biochemical & nutritional traits in rice grains. Review of literature pertaining to the present investigation in rice is presented under the following headings:

2.1 Variability, Heritability and Genetic advance

2.2 Correlation coefficient and Path analysis

2.3 Genetic divergence

2.4 Biochemical & Nutritional traits

2.1 Variability, Heritability and Genetic advance

Any breeding program that aims to increase yields will find the relative values of variability and their heritability for yield and yield-contributing characteristics in the genotypes to be of enormous value. A quantitative traits phenotype is a composite of its genetics, environment and interactions. Therefore, the amount of genetic variability that can be used to enhance crops determines how successful any breeding effort will be. Hanson *et al.,* (1956) defined heritability in a broad sense as the ratio of genotypic variance to the total variance in the non-segregating populations. The proportion of heritable variance to measure variation will determine how consistently selection operates in subsequent generations. Planning any breeding scheme requires having a basic understanding of genetic variability and heritability. It should be simple to carry out efficient selection for the trait given the traits high heritability. The term "genetic advance" describes the increase in the mean genotypic value of the chosen plants relative to the basal group. According to Johnson *et al.,* (1955) the heritable figures do provide a helpful sign of the relative values of selection based on phenotypic expression. To reach a more trustworthy result, the genetic enhancement should also be taken into account. So, high heritability estimates coupled with high genetic advance could successfully be improved by

direct selection. Low genetic advance irrespective of high or low heritability leads to non-additive gene action (Panse and Sukhatme 1956) and improvement of that trait by simple selection may not be rewarding (Verma *et al.,* 1987).

Singh *et al.,* (2014) studied thirty-eight rice germplasm accessions during *kharif,* 2010 under rainfed condition in a Randomized Block Design with three replications and reported the magnitude of phenotypic coefficient of variation (PCV) was higher to corresponding genotypic coefficient of variation (GCV) for all the traits under study. The highest value of phenotypic and genotypic coefficient of variation was observed for total grains per panicle followed by grain yield per plot and test weight. High heritability associated with high genetic advance as percent of mean was found in the traits test weight and grain yield per plot. The genotypic correlation coefficient was found to be higher than phenotypic correlation coefficient indicating a strong inherent association for grain yield per plot and other traits.

Khatun *et al.,* (2015) evaluated 43 genotypes in a Randomized Complete Block Design with three replications. The highest phenotypic and genotypic coefficient of variation was recorded for the number of filled grains/panicles and yields/plant (g). The highest heritability was found in the number of filled grains/panicles and yields/plant (g). The first four principal components of 22 traits accounted for about 72% of the total variation and indicated a wide variation among the genotypes. The selected best trait of the number of filled grains/panicles and yields/plant (g), which showed high heritability and high genetic advance.

Nayak *et al.,* (2016) conducted experiment on twenty-five rice germplasm accessions to assess their genetic variability, heritability, genetic advance for grain yield and yield traits. The high estimate of genotypic and phenotypic coefficients of variation, heritability and genetic advance were observed for effective tillers per plant, filled grains per panicle, total grains per panicle and grain yield per plant. High heritability accompanied with high genetic advance were observed for days to maturity, plant height, filled grains per plant, test weight.

Srinivas *et al.,* (2016) evaluated eighteen rice genotypes for studying genetic parameters and genetic divergence for yield contributing characters. Heritability estimates and genetic advance values indicated that effective bearing tillers per plant, 1000-grain weight and number of grains per panicle were predominantly governed by additive genes, whereas non-additive genes played a dominant role in the inheritance of days to 50 per cent flowering, plant height and panicle length.

Khaire *et al.,* (2017) conducted an experiment with twenty-four rice genotypes collected from local areas of Maharashtra along with two check varieties in *Kharif,* 2015 in Randomized Block Design. The range of GCV and PCV was 5.76% to 24.79% and 2.62% to 24.34%

respectively. PCV and GCV were high for number of filled spikelets per panicle and number of spikelets per panicle. The broad sense heritability ranged from 20.37% to 97.78%. High estimates of broad sense heritability were observed for number of filled spikelets per panicle, number of spikelets per panicle, days to maturity and plant height. The genetic advance and genetic advance as percent of mean ranged from 1.00% to 71.22% and 2.18% to 68.60% respectively.

Rashid *et al.,* (2017) conducted an experiment with 10 genotypes in RBD to estimate genetic variability. Results of genetic analyses showed a higher phenotypic coefficient of variation compared to their corresponding genotypic coefficient of variation for all the traits measured, which indicates that the traits were influenced by environment. The higher estimates of PCV and GCV were observed for number of filled grains per panicle (27.53; 26.84), number of unfilled grains per panicle (26.76; 25.28) and plant height (23.14; 23.00), while days to 50 per cent flowering, days to maturity, panicle length, number of effective tillers per plant, fertility (%), 1000 Seed weight and yield per panicle showed low PCV and GCV values. High heritability values (>60%) along with high genetic advance as percentage of mean were found for all the traits.

Rashmi *et al.,* (2017) evaluated sixty-five rice genotypes and exhibited high estimates of PCV and GCV for panicle weight followed by filled grains per panicle. Characters like days to maturity, days to 50 per cent flowering and panicle weight showed high heritability coupled with moderate genetic advance as percent of mean, suggesting that selection for the improvement of these characters may be rewarding. Grain yield had high positive and significant association with panicle weight, filled grains per panicle, total grains per panicle and panicle length. Path coefficient analysis showed maximum direct contribution towards grain yield per plant with panicle weight followed by numbers of effective tillers per plant.

Srivastava *et al.,* (2017) studied twenty-two rice genotypes in a Randomized Complete Block Design and recorded highest phenotypic and genotypic coefficient of variation for the filled grains/panicle, spikelet per panicle and plant height. The highest heritability was found for filled grains/panicles, spikelets per panicle, plant height, test weight, flag leaf length and yields/plant (g). Cluster analysis based on 16 traits grouped the 22 rice genotypes into five clusters. Cluster I was the largest and consisted of 13 genotypes. The first five principal components of 16 traits accounted for about 83.71% of the total variation. The selected best trait number of filled grains/panicle and spikelet/panicle which showed high heritability and high genetic advance.

Adhikari *et al.,* (2018) conducted an experiment with 26 advanced rice genotypes to estimate genetic variability for yield and yield attributing traits. High phenotypic variation was

observed for grain yield (24.87%), number of grains/panicle (22.45%), number of panicles per square meter (20.95%) and straw yield (20.75%), whereas grain yield had medium (12.02%) and remaining traits showed low genotypic coefficient of variation (<10%) indicating environmental influence on the expression of traits. Grain yield and days to flowering showed medium and remaining traits showed low genotypic advance as percent of mean.

Chuchert *et al.,* (2018) evaluated twenty-two upland rice genotypes. High phenotypic and genetic coefficients of variation were observed for yield per plant, number of panicles per plant, and number of spikelets per panicle. High broad sense heritability and genetic advance were found for yield per plant. Cluster analysis grouped the twenty-two genotypes into cluster I, II, III and IV the clusters consisted of nine, five, six, and two genotypes respectively.

Lingaiah (2018) studied 31 elite mid early genotypes of rice. Phenotypic coefficients of variation (PCV) values were higher than genotypic coefficients of variation (GCV) for all the traits. High GCV were obtained for the traits number of grains per panicle and yield. The magnitude of PCV and GCV was moderate for the trait thousand grain weight. The high PCV observed for yield and number of grains per panicle. Heritability estimates were high for the characters thousand grain weight, panicle length, yield and number of grains per panicle. The characters number of grains per panicle, yield, test weight and plant height have high genetic advance as percent of mean along with high heritability.

Manjunatha *et al.,* (2018) conducted experiment with thirty-five advanced rice genotypes with two replications in Randomized Complete Block Design during *kharif,* 2018 and recorded higher PCV than GCV for all traits. The magnitude of PCV and GCV was moderate to high for the trait panicles per square meter and yield. The high PCV observed for yield/ha. The high GCV obtained for the number of panicles per square meter. Heritability estimates were high for all the characters. The traits like days to fifty percent flowering, yield and plant height exhibited high magnitude of genetic advance as percent of mean. The traits plant height, days to fifty percent flowering, panicles per square meter and yield have high heritability along with genetic advance as per cent of mean.

Pratap *et al.,* (2018) studied 38 rice genotypes to assess genetic variability for yield and yield contributing traits. He reported higher PCV than their corresponding GCV for all the trait studied. The highest PCV and GCV were recorded for grain yield per plant followed by filled grains per panicle and effective tillers per plant. Highest heritability was recorded for filled grain per panicle followed by spikelet fertility, days to maturity and test weight, whereas lowest heritability was recorded for panicle length. Genetic advance as percent of mean was recorded highest for grain yield per panicle followed by filled grains per panicle and effective tillers per plant, while lowest for panicle length followed by days to maturity and number of fertile

spikelets. High heritability coupled with high genetic advance as percent was recorded for filled grain per panicle, spikelet fertility percentage and test weight whereas high heritability coupled with low genetic advance as percent of mean were observed for grain yield per plant, effective tillers per plant.

Saha *et al.,* (2019) conducted an experiment on 40 landraces of rice for 13 yield and yield attributing traits. The higher value of phenotypic coefficient of variation (PCV) compared to the corresponding genotypic coefficient of variation (GCV) for all the studied traits indicated that there was an influence of the environment. Number of unfilled grains per panicle exhibited high estimates of PCV and GCV followed by number of filled grains per panicle, number of grains per panicle. High heritability coupled with high genetic advance was observed in number of grains per panicle and number of filled grains per panicle.

Tiwari *et al.,* (2019) evaluated 90 genotypes of rice in Randomized Block Design during *Kharif* 2018 and exhibited phenotypic coefficients of variation (PCV) slightly higher than the genotypic coefficient of variation (GCV) for all the traits. The analysis of variance showed that the genotypes differed significantly ($p<0.05$) for plant height and were highly significant ($p<0.01$) for days to flowering, days to maturity, thousand grain weight, grain yield, and tillers per square meter. The highest GCV of 12.86% was observed for grain yield followed by 5.24% and 4.28% GCV found in thousand grain weight and days to heading, respectively. Highest heritability of 94% was recorded from days to heading and lowest heritability of 16% was observed in plant height (cm). High heritability and genetic advance were observed in grain yield and days to heading and maturity.

Sudeepthi *et al.,* (2020) studied 107 elite rice genotypes to study the variability, heritability and genetic advance as per cent of mean for yield and yield component traits. The results revealed maximum range of variability for the trait total number of grains per panicle while minimum range was recorded for the number of ears bearing tillers per plant. Higher PCV, compared to GCV were recorded for all the traits studied. High phenotypic and genotypic coefficients of variation (>20%) were recorded for the number of ears bearing tillers per plant. High heritability coupled with high genetic advance as percent of mean was recorded for plant height, the number of ears bearing tillers per plant, the total number of grains per panicle, test weight and grain yield per plant.

Sadimantara *et al.,* (2021) conducted an experiment with eight new upland rice lines in Randomized Complete Block Design with three replications during *Kharif,* 2019. The phenotypic coefficient of variation (PCV) value was higher than the genotypic coefficient of variation (GCV), indicating a negligible environmental influence in the phenotypic expression of

traits. High heritability estimates coupled with high genetic advance were recorded for total grain per panicle and grain yield per hill.

Kumar *et al.,* (2022) conducted experiment during *Kharif,* 2021-22 to study the genetic variability in rice with 56 rice genotypes in Randomized Block Design (RBD) with three replications. Heritability was found to be maximum for plant height (96.12%) with genetic advance of 37.87, whereas PCV & GCV was recorded highest for number of unfilled grains/panicle (13.18 & 11.12 respectively).

Yadav *et al.,* (2022) studied 72 rice germplasms including three checks *viz* Shusk Samrat, NDR-359 and MTU-7029. The experiment was conducted in Augmented Block Design with three replications. The high estimates (>15%) of phenotypic (PCV) and genotypic (GCV) coefficients of variation were recorded in case of panicle bearing tillers per plant followed by biological yield per plant, seed yield per plant and plant height. The higher estimates of heritability coupled with moderate genetic advance for plant height, days of 50 per cent flowering, biological yield per plant, days to maturity, seed yield per plant, panicle length, 1000-grain weight, indicated that heritability of the trait is mainly due to additive effect and selection is effective for such traits.

2.2 Correlation and path coefficient

Basavaraja *et al.,* (2013) studied the associations among the yield components and direct and indirect influence of yield components on the grain yield of 100 local rice genotypes during *Kharif,* 2010. The correlation analysis indicated that grain yield was significantly associated with panicle length, test weight, number of tillers per plant, number of productive tillers per plant, number of spikelets per panicle, per cent spikelet fertility and amylase per cent. Path co-efficient analysis revealed that days to 50 per cent flowering, plant height, panicle length, panicle number, number of productive tillers per plant, spikelet fertility and amylose percent had positive direct effect on grain yield.

Singh *et al.,* (2015) evaluated hundred single plant progenies of rice along with their parents and the infector rows were evaluated for 13 quantitative traits. Positive and significant correlation were observed between grain yield per plant with days to 50 per cent flowering, plant height, panicle length, panicle weight, number of effective tillers per plant and test weight. Path-coefficients analysis showed that plant height, panicle length and test weight had high direct positive effect on grain yield.

Nayak *et al.,* (2016) evaluated twenty-five rice germplasm accessions to assess their characters association and path coefficient analysis for grain yield and yield traits. Positive and significant correlation were observed between grain yield per plant with days to 50 per cent

flowering, plant height, number effective tiller per plant, panicle length and test weight. Path coefficient analysis showed that panicle length, plant height, days to flowering and effective tiller per plant had a high direct positive effect on grain yield per plant.

Adhikari *et al.,* (2018) carried an experiment with 26 advanced rice genotypes to estimate genetic variability for yield and yield attributing traits. Panicle length (r = 0.230), days to flowering (r = 0.247), effective tillers (r = 0.488) and straw yield (r = 0.846) manifested significant positive association with grain yield.

Archana *et al.,* (2018) studied the character association and path coefficient analysis among grain yield, yield components and nutritional traits in 38 genotypes of rice. Analysis of variance revealed the existence of significant differences among genotypes for all the 17 characters studied. Grain yield per plant was positively and significantly associated with harvest index, panicle weight, number of productive tillers per plant, panicle length, number of filled spikelets per panicle and 1000-grain weight indicating that simultaneous improvement of all the characters is possible. Path coefficient analysis indicated that highest direct effects on grain yield in the traits *viz*., days to 50 per cent flowering, 1000-grain weight, number of filled spikelets per panicle, harvest index, plant height, iron and protein content.

Chuchert *et al.,* (2018) evaluated twenty-two upland rice genotypes and found positive significant correlations between number of panicles per plant and number of spikelets per panicle. The highest direct effects on yield were attributed to the number of spikelets per panicle and the number of panicles per plant.

Saha *et al.,* (2019) conducted an experiment on 40 landraces of rice for 13 yield and yield attributing traits. Grain yield per plant showed significant and positive correlation with days to 50 per cent flowering, days to maturity, number of total tillers per hill, number of effective tillers per hill, number of grains per panicle, number of filled grains per panicle.

Singh *et al.,* (2018) carried out investigation to study the correlation and path analysis in eighty-four (including Check) rice varieties. Biological yield per plant, harvest index, 1000-grain weight, panicle bearing tillers/plant and panicle length showed positive and significant correlation with grain yield per plant to emerge as most important associates of grain yield in rice. Path analysis identified biological yield per plant followed by harvest index as most important direct as well as indirect yield.

Sadimantara *et al.,* (2021) conducted an experiment with eight new upland rice lines in Randomized Complete Block Design with three replications during *Kharif,* 2019. Grain yield observed a highly significant positive correlation with panicle length (0.63), percentage of filled

grains (0.53), grain weight per panicle (0.54), and thousand-grain weight (0.52). It correlated negatively with days to 50 per cent flowering (-0.61) and days to maturity (-0.48).

Kumar *et al.,* (2022) carried an experiment during *Kharif,* 2021-22 to study correlation and path analysis in rice with 56 rice genotypes in Randomized Block Design (RBD) with three replications. Association of correlation was recorded significant and positive correlation of grain yield with plant height, tillers per meter square, 1000-grain weight, panicle length, number of filled grains /panicles, biological yield and harvest index. Path analysis revealed that the maximum direct effect was recorded for harvest index, biological yield and 1000-grain weight.

2.3 Genetic Divergence

Mahalanobis's D^2 statistics is an effective tool in quantifying the degree of genetic divergence at the genotypic level and provides a measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis's, 1936). Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding. Clustering by the D^2 statistic is helpful as it allows for the identification of the diverse genotypes for the purpose of hybridization programme. Less divergent genotypes are those that are clustered together than those that are clustered in other groups. When choosing genotypes for hybridization, there are three crucial considerations. 1. Selecting the specific cluster from which the genotypes will be derived as parents. 2. Picking specific genotypes from chosen clusters. 3. Characters' relative contributions to the overall divergence. Clusters separated by largest statistical distance (D^2) show maximum divergence (Singh and Chaudhary, 1977).

Bhati *et al.,* (2015) assessed genetic divergence using D^2 analysis in 52 rice genotypes for yield and quality attributes. All the genotypes were divided into 8 clusters with cluster IV containing a maximum of 14 cultivars among the characters: number of spikelets/panicles, plant height, grains per panicle and grain yield per plant accounted for maximum genetic divergence. Maximum inter-cluster distance was observed between cluster II and cluster VII displaying wide genetic diversity between cluster II and cluster VII displaying wide genetic diversity between the cluster which may be used in future breeding programmes for exploitation of transgressive segregants.

Khatun *et al.,* (2015) evaluated 43 genotypes in a Randomized Complete Block Design with three replications. Cluster analysis based on 22 traits grouped the 43 rice genotypes into five clusters. Cluster II was the largest and consisted of 20 genotypes mostly originating from the Philippines.

Toshimenla *et al.,* (2015) studied genetic divergence in a set of seventy-four genotypes of upland rice by using mahalanobis's D^2 statistics for yield and its contributing characters. The

genotypes under study were grouped into 15 clusters. The distribution pattern indicated that the maximum number of genotypes (35) were found in cluster I, followed by cluster II with 12 genotypes, whereas the minimum number of genotypes (1) had cluster XV. The inter-cluster distance was greater than intra-cluster distance indicating wide genetic divergence among genotypes. The highest intra-cluster distance was revealed in cluster XIV followed by cluster XIII and cluster XI. The maximum inter-cluster distance was observed between Cluster XIV and XV, followed by Cluster V and XV. The highest cluster mean was observed for yield/plant in cluster VII; however, contributing characters *viz*., panicle length, panicle weight, filled grains and 1000-seed weight were found in cluster XIV. Seed yield/plant was found to be a major contributing character towards the total genetic divergence.

Vennela *et al.,* (2015) conducted experiment to study genetic divergence with 50 genotypes of rice in *Kharif,* 2015 and reported that genetic divergence played a major role in identifying the genetically diverse parents for efficient and successful breeding programmes in order to achieve potential transgressive segregates. He grouped 50 genotypes into seven clusters, out of which cluster-III had a maximum of 18 genotypes followed by cluster-I with 14 genotypes. The maximum intra cluster distance was to be found in cluster-VI and minimum was found in cluster-V and VII and inter cluster distance was found to be maximum and minimum between cluster I and VII and cluster III and V.

Chandramohan *et al.,* (2016) revealed that 44 genotypes of rice were grouped into eleven clusters based on their D^2 values. Highest number of genotypes (10) were included in cluster III followed by cluster II (8 genotypes), Cluster I and IV (7 genotypes), cluster VIII (4 genotypes) and cluster X (3 genotypes), while the remaining clusters *viz*., cluster V, VI, VII, IX and XI were comprised of single genotype each. The intra cluster distances ranged from zero (Cluster V, VI, VII, IX and XI) to 4.32 (cluster X). Highest inter cluster distance (11.49) was observed between cluster IV and V followed by cluster V and IX (9.81), cluster V and VIII (9.73), cluster II and IV (9.56), cluster IV and VII (9.32) and cluster V and XI (8.93).

Kumari *et al.,* (2016) revealed that 24 rice genotypes were significantly different for all characters under study. 24 aerobic rice genotypes were grouped into 5 clusters following mahalanobis's D^2 analysis. Clustering pattern indicated that cluster I is the largest cluster comprising 9 out of 24 genotypes followed by cluster II, comprising 8 genotypes, cluster III comprised of 4 genotypes, whereas cluster IV comprised of 2 genotypes and cluster V comprised of 1 genotype. Highest intra cluster distance was observed for cluster III (854.58) followed by cluster II (511.13) and cluster I (486.62). The inter-cluster distances were higher than the intra-cluster distance reflecting wider genetic diversity among the genotypes of different groups. Maximum inter-cluster distance (9116.90) was found between cluster II and V.

Srinivas *et al.,* (2016) evaluated eighteen rice genotypes for studying genetic divergence for yield contributing characters. Mahalanobis's D^2 analysis distributed 18 genotypes into three clusters with cluster I containing maximum number of genotypes (14). Maximum inter-cluster distance (10.48) was observed between cluster II and cluster III indicating wider genetic diversity, hence. 1000 grain weight and days to 50% flowering were contributed maximum (75.16%) to the total divergence.

Umesh *et al.,* (2016) examined genetic divergence among 24 genotypes of basmati rice and placed them into five different clusters based on the interaction in genetic distances. The maximum intra cluster distance (D^2 values) was found in cluster V (1047.879) followed by cluster I (877.138). The highest mean genetic divergence was recorded between the cluster IV and V displaying wide diversity. Cluster I containing six cultivars was distinguished by lowest mean value for spikelet /panicle (103.18).

Imran *et al.,* (2017) evaluated thirty-seven genotypes of rice based on twelve major quantitative traits. All the genotypes were divided into seven clusters with cluster VI consisting of the 29 maximums of 9 cultivars followed by cluster III and IV each consisting of 7 genotypes. This indicated that the genotypes placed within a particular cluster are more or less genetically similar to each other. The maximum intra cluster distance was obtained for cluster V while lowest intra cluster distance was obtained for cluster III. Cluster VII produced the highest mean values for number of productive tillers per plant, panicle length, biological yield and grain yield per plant. Hence, on the basis of higher cluster mean for almost all major component traits, cluster VII has been identified as the most divergent cluster containing genotypes.

Devi *et al.,* (2019) assessed genetic divergence among 20 rice hybrids with 15 characters using mahalanobis's D^2 analysis. The 20 genotypes were grouped into 5 clusters using the Tocher method with a maximum number of 9 genotypes in cluster I. Cluster II is the second largest with 6 genotypes followed by cluster IV with 3 genotypes. The maximum intra cluster D^2 value was 95.18 for cluster IV followed by 90.27 for cluster II, 41.08 for cluster I, while it was zero for clusters III and V. The maximum inter cluster D^2 value was observed between cluster II and V (444.87) followed by cluster I and V (267.50). The cluster I is having highest mean value for panicle length; cluster II for number of total grains per panicle and grain yield per plant; cluster III for days to 50% flowering and days to maturity.

Mbe *et al.,* (2019) investigated genetic diversity among 76 rice genotypes, which were characterized for eight important quantitative traits. All the genotypes were grouped into thirteen clusters, thereby indicating the existence of a large amount of genetic diversity within the accessions. Among the clusters, cluster VIII was the largest with 26 genotypes followed by

cluster VII with 11 genotypes. Cluster III (48), VI and XII were unique with only a single genotype each. Cluster IV and XI had two genotypes each.

Singh *et al.,* (2019) evaluated genetic divergence of 50 rice genotypes for thirteen quantitative plant growth and yield related traits using mahalanobis' statistics (D^2) analysis. The genotypes were grouped into eight clusters using mahalanobis's D^2 analysis. Cluster VII constitutes 12 genotypes forming the largest cluster followed by cluster III (8 genotypes) cluster V and VI (7 genotypes) in each, cluster I and IV (6 genotypes) cluster VIII (3 genotypes) and cluster II (1 genotypes). Maximum intra cluster D^2 value (4122) was observed for cluster VI followed by cluster V (2737). The inter-cluster distance was maximum between cluster V and VIII (58955), followed by cluster II and Cluster III (45395) and between cluster III and VIII (44968) and cluster II and cluster VII (41743).

Singh *et al.,* (2020) evaluated 22 rice genotypes based on 16 quantitative traits for genetic diversity. Based on D^2 values, twenty-two genotypes were grouped into six clusters using Tocher's method. Cluster I had fifteen genotypes, Cluster II had three genotypes, whereas Cluster III, IV, V, and VI had a single genotype in each cluster. Range of an average intra-cluster D^2 value was 0 to 5.16. Cluster II had a maximum intra-cluster value (5.16), while cluster I showed a minimum intra-cluster distance (3.49). The minimum inter-cluster distance was recorded between cluster III and IV (5.12), followed by cluster V and VI (7.65), and cluster I and III (7.89). Cluster III recorded the highest mean values for the greatest number of traits *viz*., plant height (120.74), grains per panicle (164.45), spikelet fertility % (87.47), grain yield per plant (37.33) and zinc content (24.22).

Soundharya *et al.,* (2020) studied 21 rice genotypes to assess genetic diversity analysis. Based on D^2 analysis, twenty genotypes were grouped into four clusters. Cluster I was the largest cluster comprising fourteen genotypes followed by clusters II with three genotypes, cluster III with two genotypes, cluster IV was a monogenetic cluster. Inter-cluster distance was higher than intra-cluster distance, indicating wider genetic diversity among the genotypes. The data indicated that the cluster means for days to 50 percent flowering was highest in cluster VI (106.00) and the lowest in cluster I (82.38). Plant height was exhibited highest and lowest means in cluster I (122.03 cm) and IV (109.40 cm). Cluster I showed the highest test weight (25.44 g), while in cluster II it was low (15.26 g). Highest grain yield per plot was recorded in cluster II (9058 kg/ha) and lowest in cluster IV (7577.38 kg/ha).

2.4 Biochemical and Nutritional components: -

The genetics of the plant variety as well as environmental factors like the location and season of growth, the degree of milling, and storage conditions, all have a significant impact on

the chemical composition of rice grains. Rice is the main source of carbohydrates, proteins, fats and minerals (Deepa *et al.,* 2008). In rice, endosperm plays an important role in determining the nutritional value of rice through its component parts; starch, protein, lipids, fat and fiber (Kang *et al.,* 2006). It is one of the few crop species that is widely grown as a staple food source, rice has a significant nutritional value.

Dikshit *et al.,* (2016) evaluated sixty-eight landraces of rice germplasm of tripura for grain phenotypic traits and micronutrient content which revealed wide variation among genotypes in grain characteristics. The concentration of Zn ranged from 2.35 mg/100 g in Garumaruti to 5.04 mg/100 g in Hazar, while Fe concentration ranged from 2.80 mg/100 g in Chakchi badam to 47.68 mg/100 g in Hazar. Higher mineral content especially of Zn and Fe in the grains of local landrace germplasm like Hazar and Mai kasam.

Pathak *et al.,* (2016) assessed physicochemical properties of 22 pigmented glutinous rice varieties along with one non pigmented variety (Memon Bora) and reported that amylose content was lowest in Kmj Bora-61 (0.05 %) and highest in Kola Bora-5 (3.0 %), as compared to 0.4 % of non-pigmented-Memon Bora. Highest protein content was recorded in Narul Bora (10.17 %) and lowest in Til Bora-2 (8.32 %) against 9.7% of non-pigmented Memon Bora. Highest Zn content (4.42 mg/100 g) was found in Kmj Bora-50 and lowest in Pakhori Bora (3.14 mg/100 g), whereas non-pigmented Memon Bora contained 3.902 mg/100 g. Fat content values of rice grain ranged from 3.34 % (Pakhori Bora) to 3.76 % (Paro Chakuwa) with an average of 3.51 %, as compared to 2.82 % of non-pigmented-Memon Bora. The highest Fe content was recorded in Kmj Bora-21 (4.21 mg/ 100 g) and lowest in Narul Bora (3.12 mg/100 g) as against 2.70 mg/100 g of non-pigmented Memon Bora.

Pongjanta *et al.,* (2016) evaluated twelve pigmented rice varieties of rice grain with varying amylose content (low, medium and high). Amylose content among the three varieties of each pigmented rice flour ranged from 1.20 to 28.90 %.

Ritika *et al.,* (2016) evaluated some Indian rice varieties of basmati (Pusa Basmati-1, Pusa Basmati-1401, Pusa-2511, and Pusa Basmati-1509) and non-basmati (HKR-47, HKR-127) for physicochemical properties. Protein content of different cultivars ranged from 5.28 to 8.87 %. The order for the protein content of different cultivars was PP-1509>P-2511>PB1401>HKR-127>HKR-47>PB-1. The amylose content of different rice cultivars ranged from 5.19 to 23.10% and the basmati varieties showed significantly higher amylose content as compared to non-basmati varieties ($p \leq 0.05$). The highest amylose content was observed in PP-1509 (Basmati) and lowest in HKR-127 (non-Basmati) variety.

Abeysekera *et al.,* (2017) evaluated the physicochemical and nutritional properties of selected traditional 23 rice varieties of Sri Lanka. Out of 23 varieties tested, 20 varieties were red rice, while the rest were white rice. The mean crude protein and total carbohydrate contents of selected varieties varied from (10.59 ± 0.12) % to (13.27 ± 0.32) % and (81.42 ± 0.25) % to (85.66 ± 0.24) % respectively.

Kumari *et al.,* (2017) conducted experiment to evaluate the nutrient composition of rice bran. The mean content of Crude fat in rice bran is 18.90 %.

Lum *et al.,* (2017) evaluated five rice varieties (white, red, black, brown and aroma rice) for physicochemical characteristics. Study revealed that black rice showed the lowest 1000-grain weight, while white rice showed the highest 1000-grain weight and amylose content. Aromatic rice showed the highest amylose content. Amylose content of the rice varieties ranged between 10.83-14.93%.

Prasad *et al.,* (2017) evaluated chemical composition of popular Indian rice varieties namely Jaya, Lalat, NDR-97, PR-113, Shalivahana, Sasyasree, Savithri, Tellahamsa, Triguna, Varalu and one hybrid DRRH-3, having wide agronomical and grain morphological features were studied. The protein content ranged from 2.49% (Varalu) to 7.4% (Savithri). The Iron content ranged from 0.37 mg/100g (Triguna) to 1.21 mg/100g (Lalat). The Zn content ranged from Minimum level of 0.8 mg/100g (Salivahana) to maximum level of 2.31 mg/100g (Varalu).

Raghuvanshi *et al.,* (2017) conducted a study with two types of rice *viz*. indigenously grown raw red rice and white rice (Sarbati) to evaluate and compare the physical characteristics and nutritional quality. Of the thirteen physical quality parameters evaluated, red rice proved to be superior to white rice in all parameters barring seed length. Studies revealed that red rice had the highest 1000-kernel weight (18.3 g) than white rice. In all the parameters red rice proved to be superior to white rice, red rice had highest crude protein content (10.49%). Red rice was found to have a higher iron, calcium, and zinc content than white rice. White rice was found to have 7.6% crude protein and 78.34% carbohydrate. On the other hand, red rice was found to have 10.49% crude protein and 70.19% carbohydrate content. Red rice had 13.45 mg iron, 8.71 mg calcium, and 1.91 mg zinc while white rice was found to have 7.65 mg iron, 7.94 mg calcium and 1.49 mg zinc.

Verma and Srivastav (2017) analysed a total of six aromatic and two non-aromatic rice accessions for their nutritional quality attributes with three replications. Badshah Bhog exhibited the highest carbohydrate content (82.70%). Protein content ranged from 7.23% (kalanamak) to 9.51% (Khushboo). Among the minerals, the higher Ca (98.75 ppm), Zn (17.00 ppm) and Fe (31.50 ppm) were in Gopal Bhog. The identified aromatic rice accessions Gopal Bhog, Govind Bhog and Badshah Bhog and non-aromatic rice accession Sarbati were found nutritionally superior among all eight tested accessions.

Rathna Priya *et al.,* (2019) evaluated some South Indian varieties for nutritional and functional properties. Carbohydrate % ranged from 76.8–86.56 %. Protein % ranged from 5.8-9.72 %. Fat % of rice bran ranged from 15.0–19.7 %. Ca content ranged from 10-80 mg /kg. Fe content ranged from 8.6–43.0 ppm and Zn content ranged from 4.3–25.8 ppm.

Tripathy *et al.,* (2020) conducted an experiment on 92 diverse germplasm lines to explore high iron (Fe) and zinc (Zn) donors. Grain Fe content (8.3-52.15 ppm) and Zn content (3.0-52.7 ppm) revealed wide variation among the germplasm. The Fe and Zn dense genotypes identified above belong to the same distinct single cluster that showed high Fe and Zn content.

Pakuwal and Manandhar (2021) evaluated and compare the nutritional quality of different rice varieties (Taichung-176, Khumal-4 rice, and Black rice) with Jumli Marsi rice. The highest nutritional factors and phytochemical components were found in the Marsi rice (RR) and Black rice (BR). Amylose Content (%) ranged from 27.62 % (Taichung-176) to 5.28 (Black rice) and Carbohydrate content % ranged from 82.5% (Taichung-176) to 65.3% (Khumal-4 rice).

Kalita *et al.,* (2022) studied four indigenous rice varieties namely Kumol saaul, Kola Bora, Kola kunkuni Joha and Khamti Lahi have been selected for nutritional profiling and bioactive compounds screening. Macronutrient analysis revealed the highest carbohydrate content in Kumal Saul (48.3±0.34 g/100 g), The protein content was highest in Kola bora (8.9±0.02). Mineral content also showed significant differences in the four rice varieties. Iron and calcium content were found highest in Kola bora (1.21±0.01 mg/100g and 16.13±0.07 mg/100g respectively) whereas Zinc content was found highest in Khamti lahi (4.53±0.03 mg/100g).

Singh *et al.,* (2022) studied eleven (black, red and white) rice cultivars of NE India for antioxidant potentials, mineral and protein contents. Zn content ranged from 0.49 to 70.74 ppm. Fe content ranged from 1.24 to 252.62 ppm. Ca content ranged from 1.12 to 953.88 ppm among the studied cultivars. The total protein contents ranged from 3.62% to 11.06% with an average of 8.18%. Fe content in the present study was higher and Zn content was comparable (6–16 ppm Fe and 17–59 ppm Zn) with Thai brown rice varieties (Saenchai *et al.,* 2012). The averages of Zn, and Fe contents were higher (34.8 ppm Zn, 92.7 ppm Fe) than the previous study of local rice germplasm of Tripura, India (Dikshit *et al.,* 2016). Overall, Fe and Zn contents were also higher (0.25–34.8 ppm Fe and 0.85–195.3 ppm Zn) than rice varieties of West Bengal and adjoining areas of India (Roy and Sharma 2014).

Wisetkomolmat *et al.,* (2022) evaluated the proximate components and phytochemical profiles of 11 Thai rice bran varieties, 4 non-colored rice brans and 7 colored rice brans. Crude fat content ranged from 12.03% (KC CMU 107) to 18.68 % (BB 3 CMU).

CHAPTER III : MATERIAL AND METHODS

The field experiment of the present investigation entitled, **"Genetic variability, diversity for yield and quality traits in rice (*Oryza sativa* L.)"** were taken up in accordance with the objectives. The materials utilized and the methodologies adopted in the present study are described below.

3.1 EXPERIMENTAL DETAILS

3.1.1 Experimental site

The field experiment was conducted at Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri, Maharashtra state during *Kharif,* 2022. The selection of site was considered on the basis of suitability of the land and weather conditions for cultivation of rice.

The biochemical analysis i.e. Protein, fat, amylose, carbohydrate and calcium content was done at biochemistry laboratory, Regional Agricultural Research Station, Karjat, Dist. Raigad. Micronutrient analysis particularly Zinc and Iron content was carried out by using an atomic absorption flame spectrophotometer unit available at Department of Soil Science and Agricultural Chemistry, College of Agriculture, Dapoli.

3.1.2 Climate and weather condition

Geographically, Dapoli is a tropical region with 17º45'32" North latitude and 73º11'8" East longitude having elevation of 243.84 meters above the sea level with warm and humid conditions throughout the year and it falls under South Konkan Coastal Zone (MH-1) as per agro climatic zone (NARP). The mean annual precipitation is 3500 mm which is generally received during June to October at the location. The soil of the experimental site was lateritic soil.

3.1.3 Experimental material

The seed material used for the present investigation consisted of 25 genotypes of rice collected from the Research and Educational Farm, Department of Agril. Botany, College of Agriculture, Dapoli. The list of genotypes used in study is given in Table 3.1

3.1.4 Experimental design

The experiment was laid out in Randomized Block Design (RBD) with three replications. The experimental material comprised of 24 genotypes of rice along with one check, was sown on 10th June, 2022 separately in the nursery on raised beds. The seedlings were transplanted on 11th July, 2022 i.e., after 30 days of sowing. The experiment consisted of 25 treatments (genotypes)

of rice. Seedlings were transplanted with a spacing of 20 cm between rows and 15 cm between plants in a row. Net plot size was 3 m × 0.06 m. Each genotype consisted of three rows and each row with twenty plants. Sixty seedlings of each genotype per replication were maintained.

Table 3.1 Experimental material and their source

Sr. No.	Name of the genotype	Source
1	Ratnagiri-7 (check)	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
2	DPL-2	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
3	DPL-3	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
4	DPL-4	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
5	DPL-5	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
6	DPL-6	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
7	DPL-7	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
8	DPL-8	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
9	DPL-9	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
10	DPL-10	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
11	DPL-11	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
12	DPL-12	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
13	DPL-13	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
14	DPL-14	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
15	DPL-15	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
16	DPL-16	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
17	DPL-17	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
18	DPL-18	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
19	DPL-19	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
20	DPL-20	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
21	DPL-21	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
22	DPL-22	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
23	DPL-23	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
24	DPL-24	Research & Educational farm, Dept of Agril. Botany, COA Dapoli
25	DPL-25	Research & Educational farm, Dept of Agril. Botany, COA Dapoli

1. Season : *Kharif*, 2022
2. Date of sowing : 10/06/2022
3. Date of Transplanting : 11/07/2022
4. Design : Randomized Block Design (RBD)
5. No. of Replication : 03
6. No. of Treatments : 25
7. Spacing : 20 x 15 cm
8. Net plot size : 3.0 m×0.06 m.

3.1.5. Brief cultural practices

Recommended agronomic and plant protection measures were adopted to raise a healthy nursery during the entire period of investigation. Nursery beds were prepared by applying 15 kg N as urea, 20 kg P_2O_5 as single super phosphate and 2 kg K_2O in muriate of potash per 1000 m^2 of nursery bed, FYM @ 1 t/ha was also added. A basal dose of 7.5 t/ha FYM, 50 kg N, 50 kg P_2O_5 and 50 kg K_2O applied. 25 kg each of nitrogen was then applied at 30 days after transplanting and at 65 days after transplanting. The irrigation management was done as per requirement and the inter-culture operation was carried out time to time.

3.2 RECORDING OF OBSERVATIONS

From each genotype per replication, five competitive plants were chosen at random excluding border row to record observations on yield and yield attributing traits. Five panicles of chosen plants were observed for their panicle and grain characteristics. To record observations, tags were applied to the plants that were chosen at random. The steps taken to record observations on various characters are listed below:

1. Days to 50 per cent flowering

The number of days taken from the date of sowing to 50 per cent flowering was measured as days to 50 per cent flowering.

2. Days to maturity

The number of days from sowing to physiological maturity of plants in each plot of genotype taken as days to maturity. Turning 80% spikelets from green to golden yellow in the panicle is an indication of physiological maturity.

3. Plant height (cm)

Plant height was measured at the time of maturity from base of the plant to the tip of the panicle excluding awn if present and expressed in centimetres.

4. Numbers of productive tillers per plant

The total number of productive tillers per plant which produced healthy panicles was counted on each selected plant at the time of maturity.

5. Panicle length (cm)

It was measured in centimetres at the time of maturity from the base of the panicle to the tip of the last spikelet.

6. Number of filled grains per panicle

Total numbers of filled grains in the panicle were recorded from all the selected panicles.

7. Number of total spikelets per panicle

Number of filled and unfilled spikelets were counted from the selected panicles and recorded as the total number of spikelets per panicle.

8. Spikelet fertility (%)

It is estimated by dividing the number of filled grains per panicle to the number of total spikelets per panicle and multiplied by 100.

$$\text{SF (\%)} = \frac{\text{Number of filled grains per panicle}}{\text{Number of total spikelets per panicle}} \times 100$$

9. Test weight (g)

1000 dried and well filled grains were weighed from a random sample of each genotype in each replication and noted in grams using an electronic balance.

10. Grain yield per plant (g)

Mature panicles from each randomly selected plant were harvested, threshed, cleaned and dried separately. Total seed yield of each randomly selected plant was recorded in grams.

11. Straw yield per plant (g)

After threshing the total straw yield of each randomly selected plant was recorded in grams.

12. Harvest index (%)

The ratio of economic yield to biological yield is known as harvest index and it is expressed in percentage.

$$\text{HI (\%)} = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

13.Amylose (%)

The simplified procedure (auto analyzer and manual method) of Juliano (1971) is used for the amylose content analysis.

After estimating amylose content, the samples were classified as follows.

Table 3.2 Classification of Amylose (%) in different categories

Term	Amylose (%)	Characteristics when cooked
Waxy	1-2	On cooking it is sticky and soft
Very low	3-10	Absorbs little water and therefore has little volume expansion.
Low amylose	11-20	On cooking tends to be moist, sticky and glossy, split if over cooked.
Intermediate amylose	21-25	Cook fluffy, moist tender and do not become hard upon cooling and remain soft. (Most acceptable range for eating)
High amylose	> 25	Become hard when cool, Resist disintegration during boiling

(Source: - Juliano, 1971)

14. Protein (%)

The individual genotype grain sample was crushed into powder and nitrogen content in grain was recorded by micro Kjeldahl method (AOAC 1990). For recording protein content, total nitrogen in sample multiplied with 5.95 (multiplication factor).

Protein (g/100g) = Total nitrogen in sample x 5.95 (multiplication factor)

15. Carbohydrate (%)

The carbohydrate content was determined by using phenol sulphuric acid method Sadasivam, S. and Manickam, A. (2005)

16. Crude fat (%)

Crude fat was determined from an oven dried sample using a Soxhlet apparatus (AOAC 2000).

17. Zinc and Iron (ppm)

The rice grains were powdered using a clean pestle and mortar. 12.5 ml of 70% concentrated Nitric acid was added to 0.2 g powdered grain samples and the mixture was incubated overnight. Next day, 10 ml of di-acid mixture (Nitric acid: Per-chloric acid in the ratio of 2:1) was added to the incubated sample. The mixture was then placed on the electric hot plate, allowing evaporation of acid in the form of white fumes, until white precipitate was formed at the base of the flask. The digested sample was left to cool for an hour and the volume was made up to 50 ml using double distilled water. Calibration of an instrument for estimation of an element was done using five standard solutions with appropriate dilutions. A suitable blank was run simultaneously to account for contamination from the reagents. Zinc and iron concentrations in the grain samples of rice were estimated using Atomic Absorption Spectrophotometer (AAS) at 213.86 nm for zinc and 248.33 nm for iron and expressed as ppm of grain and data shown in ppm.

18. Calcium (ppm)

- ➢ Weigh 5 g of 2 mm sieved sample in 250 ml conical flask.
- ➢ Add extractant in proportion of 1:5 (Extractant = Neutral ammonium acetate 77.1 g in 1 litre distilled water and adjust pH to 7.0).
- ➢ Shake for 5 minutes.
- ➢ Filter it through Whatman paper No. 1.
- ➢ Collect the filtrate free from sediments and use it for estimation of Calcium.
- ➢ Pipette out 5 ml of extract in a porcelain dish or in 100 ml conical flask, add 5-10 ml distilled water, add 2-3 crystals of sodium Di thiocarbamate to avoid interference of heavy metals.
- ➢ Add 0.2 g ammonium purpurate to conical flask (red colour at this stage) by adding a few drops of 16% NAOH (buffer) and titrate against standard EDTA till colour changes from orange red to purple.

3.3 STATISTICAL ANALYSIS

For statistical analysis, mean values computed from the observations recorded on five selected plants for different characters were used and subjected to the following statistical analysis:

1. Analysis of variance
2. Genotypic and phenotypic coefficients of variation

3. Heritability and genetic advance
4. Estimation of Correlation
5. Path coefficient analysis
6. Genetic divergence analysis

3.3.1 Analysis of variance

Difference between 25 genotypes for different characters was tested for significance by using analysis of variance technique applicable to the Randomized Block Design on the basis of the model proposed by Panse and Sukhatme (1956). The significance was tested by referring to the values of the 'F' Table (Fisher and Yates, 1963). The analysis of variance was done as given below:

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

Where,

$\mathbf{Y_{ij}}$ = Phenotypic observation of i^{th} genotype and j^{th} replication

$\boldsymbol{\mu}$ = General mean

$\mathbf{g_i}$ = Effect of i^{th} genotype

$\mathbf{r_j}$ = Effect of j^{th} replication

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

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

Table 3.3 Analysis of variance for randomized block design

Source	Degrees of freedom	Mean sum of squares	Expected M.S.S.
Replications	(r-1)	RMS	$\sigma^2e + \sigma^2r$
Treatments	(t-1)	GMS	$\sigma^2e + \sigma^2g$
Error	(r-1) (t-1)	EMS	σ^2e
Total	(tr-1)		

Where,

r = Number of replications

g = Number of genotypes

MSS = Mean sum of squares

σ^2e = Environmental variance

σ^2g = Genotypic variance

σ^2r = Replication variance

The genotype mean sum of square (GMS) was tested against error mean sum of square (EMS) by 'F' test for n_1 = (g-1) and n_2 =(r-1) (g-1) degrees of freedom.

3.3.1.1 Estimation of mean and range

The mean value for each character was worked out by dividing the total by corresponding number of observations:

$$\bar{x} = \frac{\sum x_1}{n}$$

Where,

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

$\sum x_1$=Total of the character

n = Number of observations.

The lowest and highest value from the mean of each character was recorded as range.

$$\text{Coefficient of Variance (C.V.)} = \frac{\text{S.D.}}{\bar{x}} \times 100$$

Where,

$$\text{Standard Deviation (S.D.)} = \sqrt{\frac{1}{n}\Sigma(x - \bar{x})^2}$$

Classification of genotypes:

Genotypes were classified based on population mean and critical difference. The classification helps in identifying the superior as well as inferior genotypes. The classification was done as below;

Above average (>): Population mean ± C.D.

Medium : Population mean ± C.D.

Below average (<): Population mean ± C.D.

3.3.1.2 Estimation of components of variation

The phenotypic, genotypic and environmental variances were calculated as:

a) Environmental variance,

$$\sigma^2 e = EMS$$

b) Genotypic variance,

$$\sigma^2 g = \frac{GMS - EMS}{r}$$

c) Phenotypic variance,

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where,

GMS = Genotypic mean sum of squares

EMS = Error mean sum of squares

r = Number of replications

3.3.2 Estimation of coefficient of variation:

Burton and De Vane (1953) have given the formulae for calculation of phenotypic and genotypic coefficients of variation.

a) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{x}} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance.

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

b) Genotypic coefficient of variation

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{x}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

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

Categorization of range of variation as proposed by Siva Subramanian and Menon (1973):

i) Low: Less than 10 (%)

ii) Moderate: 10-20 (%)

iii) High: More than 20 (%)

3.3.3 Heritability and genetic advance

3.3.3.1 Estimation of heritability (h^2b):

Heritability in a broad sense was estimated for various characters by the formula.

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance.

As suggested by Johnson *et al.* (1955), heritability values are categorized as follows:

i) Low: Less than 30 (%)

ii) Moderate:30-60 (%)

iii) High: More than 60 (%)

3.3.3.2 Estimation of genetic advance (GA):

The genetic advance was calculated in per cent by the formula suggested by Johnson *et.al.* (1955).

a) $GA=\frac{\sigma^2 g}{\sigma^2 p} \times \sigma p \times K$

b) GA as percentage of mean (GAM)= $\frac{GA}{\bar{x}} \times 100$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

σp = Phenotypic standard deviation

K = Selection differential, at 5 per cent selection intensity (2.06)

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

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

i) Low: Less than 10 (%)

ii) Moderate: 10-20 (%)

iii) High: More than 20 (%)

3.3.3.3 Estimation of standard error, standard error of difference and critical difference.

a) Standard error of mean: SEM = $\sqrt{\frac{\sigma^2 g}{r}}$

b) Standard error of difference between two means was calculated as S.E. of difference of means:

S.E. of difference of means (SED) = SEM × $\sqrt{2}$

c) The critical difference between any two means was calculated as:

C.D. = 't' value at error degree of freedom × SEM

3.3.4 Correlation coefficient

Analysis of covariance was carried out by taking two characters at a time; plot error was used as environmental covariance. Thus, phenotypic and genotypic covariance was derived as below:

Table 3.4 Covariance analysis for randomized block design

Source	d.f.	Mean products
Replication	(r-1)	-
Varieties	(v-1)	GMP
Error	(r-1) (v-1)	EMP
Total	(rv-1)	-

Where,

r = Number of replications

v = Number of varieties

GMP = Genotypes sum of squares

EMP = Error sum of squares

The genotypic and phenotypic covariance was worked out as per formulae given by Singh and Chaudhary (1977).

a) Environmental covariance = (CoVe 1.2)

= EMP

b) Genotypic covariance = (CoVg 1.2)

$$= \frac{GMP - EMP}{r}$$

c) Phenotypic covariance = (CoVp 1.2)

= (CoVe 1.2) + (CoVg 1.2)

The appropriate variances and covariances were used for calculating phenotypic and genotypic correlation coefficients (Johnson *et al*. 1955)

A) Phenotypic correlation

Phenotypic correlation coefficient was derived as:

$$r_p\ 1.2 = \frac{CoVp\ 1.2}{\sqrt{(\sigma^2 p_1)\ (\sigma^2 p_2)}}$$

Where,

r_p 1.2 = Phenotypic correlation between characters 1 and 2.

CoVp 1.2 = Phenotypic covariance between characters 1 and 2.

$(\sigma^2 p_1)$ $(\sigma^2 p_2)$ = Phenotypic variance of characters, 1 and 2, respectively

B) Genotypic correlation

Genotypic correlation coefficient was obtained by the Formula:

$$r_g\ 1.2 = \frac{CoVg\ 1.2}{\sqrt{(\sigma^2 g_1)\ ((\sigma^2 g_2)}}$$

Where,

r_g 1.2 = Genotypic correlation between characters 1 and 2.

CoVg1.2 = Genotypic covariance between characters 1 and 2

$(\sigma^2 g_1)$ $(\sigma^2 g_2)$ = Genotypic variance of characters 1 and 2, respectively.

The significance of phenotypic and genotypic correlation coefficients can be tested by using 't' test.

$$t = r\sqrt{\frac{n-2}{1-r^2}}$$

Where,

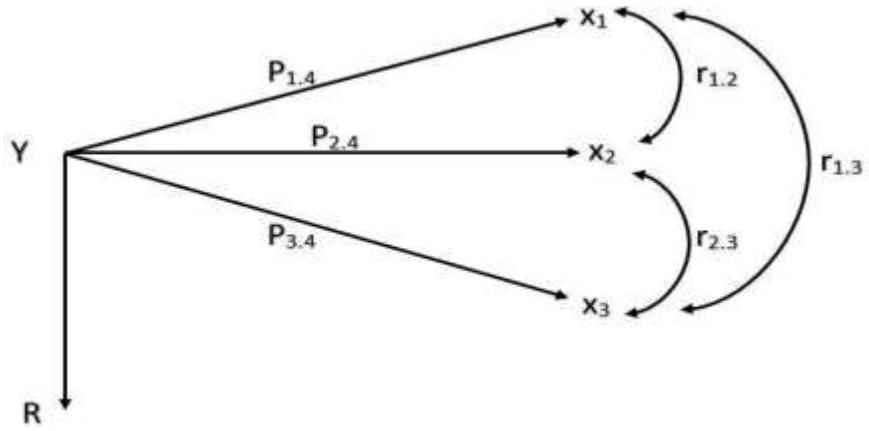
r = Correlation coefficients.

n = Total number of observations

The calculated 't' value is tested with Table 't' value for respective (n-2) degrees of freedom for significance.

3.3.5 Path coefficient analysis

Path coefficient analysis was done to establish a cause-and-effect relationship, the genotypic and phenotypic correlation coefficients were partitioned in direct and indirect effect by path analysis as suggested by Dewey and Lu (1959). The first step in path analysis is to prepare a path diagram based on cause-and-effect relationship.



Path coefficient analysis is simply a standardized partial regression coefficient which splits the correlation coefficient into the measures of direct and indirect effect. The concept behind this is that yield is the function of various components like x_1, x_2, x_3 then these components show following type of association with one another.

From the above figure, it is clear that yield is the result of x_1, x_2 and x_3 and some other undefined factors designated by 'R'. The double arrowed lines indicate mutual association as measured by correlation coefficients and the single arrowed line represented direct influence as measured by path coefficients P_{ij}.

Path coefficients were obtained by solving a set of simultaneous equation of the form,

$$r_{ny} = p_{ny} + r_{n2} + r_{n2}p_y + r_{n3} + \ldots\ldots$$

Where,

r_{ny} = represented correlation between one component and yield

p_{ny} = represented path coefficient between one component and the yield

r_{n2} = represented correlation between that character and each of the other yield components in turn

Matrix A

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{bmatrix}$$

Matrix B

$$\begin{bmatrix} 1 & r_{1.2} & r_{1.3}\text{.....} & r_{1n} \\ r_{2.1} & 1 & r_{2.3}\text{.....} & r_{2n} \\ r_{n1} & r_{n2} & r_{n3}\text{ .....} & 1 \end{bmatrix}$$

Where,

$r_{1.2} = r_{1.2}$ and so on.

r_{1y} = Correlation between one component character and yield

The 'B' matrix (P_{ij}) was obtained as –

$$(P_{ij}) = A \times (B^{-1})$$

The indirect effect of a particular character through other characters was obtained by multiplication of direct path and particular correlation coefficients between these characters separately.

Indirect effect = $r_{ij} \times P_{ij}$

Where,

i = 1 to n

j = 1 to n

$P_{ij} = P_1Y_1, P_2Y_2, \text{---} \text{------} P_nY_n$

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factor (s) were diagrammatically presented.

The residual factors i.e., variation in yield unaccounted for by these association was calculated from the following formula,

Residual factor (x) = $1 - R^2$

Where,

$R^2 = P_{1y}r_{1y} + P_{2y}r_{2y} + P_{3y}r_{3y}$ ..... ……+ $P_{ny}r_{ny}$

Where,

P_{1y}, P_{2y}..... P_{ny} = Path values

r_{1y}, r_{2y}.....r_{ny} = Correlation coefficients

The path coefficient is rated based on the scales given below: (Lenka and Mishra, 1973)

0.00 – 0.09 = Negligible

0.10 – 0.19 = Low

0.20 – 0.29 = Moderate

0.30 – 0.99 = High

>1.00 = Very high

3.3.6 Genetic divergence analysis

The genetic divergence in 25 genotypes for 19 characters was analyzed through Mahalanobis's D^2 statistical technique.

3.3.6.1 Mahalanobis's generalized distance (D^2)

Genetic diversity between genotypes can be well estimated by using D^2 analysis given by Mahalanobis's (1936).

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

$$\mathbf{D_{ij}^2 = P \sum t\text{-}1(Y_{it} - Y_{jt})}$$

Where,

$\mathbf{Y_{it}}$ = Uncorrected mean value of i^{th} genotype for t character.

$\mathbf{Y_{jt}}$ = Uncorrected mean value of j^{th} genotype for t character.

$\mathbf{D_{ij}^2}$ = D^2 value between i^{th} and j^{th} genotype

3.3.6.2 Test of significance

Variances were evaluated for all the characters and a test of significance was done. Analysis of covariance (ANCOVA) for the character pairs was estimated on the basis of mean value. From these estimates, a dispersion Table was prepared. After testing the differences between genotypes for each of the character a simultaneous test of significance of difference between the mean values of a number of correlated variables was done (Rao, 1952) by using 'V' Statistic, which in turn utilizes Wilk's criterion. The sum of products of error and error plus variety variance-covariance matrix were used for this purpose (Panse and Sukhatme, 1956).

The estimates of λ (Wilk's criterion) were done using the following formula:

$$\text{Wilk's criterion} = \frac{|E|}{|E+V|}$$

Where,

|E| = Determination of error matrix and

|E+V| = Determination of error + varieties matrix

The significance of λ was tested by

'V'stat = X^2pq = -mlog λ

Where,

m = n (p|q|) 1)/2 with pq degrees of freedom

n = degrees of freedom of error + varieties

p = number of characters

q = number of genotypes

At base of natural log λ = 2.3407 $\log_{10}$ λ

3.3.6.3 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation of differences in mean values of various characters of two genotypes i.e., $\sum di^2$. Therefore, transformation of correlated variables into standardized uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method in computation of D^2 values.

3.3.6.4 Testing the significance of D^2 values

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

3.3.6.5 Grouping of genotypes into various clusters

Grouping of the genotypes into various clusters was done by using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should at least on an average show a smaller D^2 values. The D^2 values of all the combinations in each genotype were arranged in the increasing order of their magnitude in the tabular form as described by Singh and Choudhary (1977). To start with, the two genotypes having a smallest distance from each other were considered, to which a third population having smaller D^2 values from the first genotype were added. Then comes the nearest fourth genotype and so it goes on. At certain stage it was felt that after adding a particular variety, there was a disrupt increase in the average D^2 value, then that variety was not considered

for inclusion in that cluster. Similarly, a second cluster was formed. This process was continued till all the genotypes were included into one or the other cluster.

3.3.6.6 Inter and inter cluster distances

A) Average intra-cluster distance

For the measurement of intra cluster distance, the formula used in $\sum Di^2/2$ where $\sum Di^2$ was the sum of distances between all possible combinations (n) of the genotypes included in a cluster.

B) Average inter-cluster distance

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

3.3.6.7 Cluster diagram

The clusters and their mutual relationship were presented diagrammatically. The square root of average D^2 which was an appropriate measure of divergence between groups, had been used to denote the distance.

3.3.6.8 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution toward divergence between two entries ($d_i = y_{it} - y_{jt}$).

Rank 1st was given to the highest mean difference and rank p to the lowest difference, where p is the total number of characters considered percentage contribution of each character towards genetic divergence was calculated using the formula:

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

Where,

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

M= All possible combinations of genotypes considered

CHAPTER IV : RESULT AND DISCUSSION

The present investigation, titled **"Genetic variability, diversity for yield and quality traits in rice (*Oryza Sativa* L.)"** had been carried out at Research and Educational farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri. Twenty-five rice genotypes were examined for nineteen characteristics in order to determine several genetic and biochemical parameters. The obtained experimental data was subjected to statistical analysis and the results from the statistical analysis are given and discussed under the following headings:

4.1 Genetic variability, heritability and genetic advance

4.2 Correlation coefficient

4.3 Path coefficient analysis

4.4 Genetic diversity

4.1 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

4.1.1 Analysis of variance (ANOVA)

The analysis of variance (ANOVA) findings, which are presented in Table 4.1, showed that the mean sum of squares among all the genotypes were significant for all the traits under study. It is reported that there was significant genetic variation present in each genotype for all the traits. Further estimations of genotypic and phenotypic variance were made using the calculated genotype and error mean sum of squares.

From ANOVA analysis, the mean sum of squares due to treatments were highly significant for all the characters under study. This suggested that the rice genotypes taken for study exhibit significant variation for the studied characters. Similar results were reported by Srinivas *et al.,* (2016), Rashid *et al.,* (2017), Adhikari *et al.,* (2018), Tiwari *et al.,* (2019) and Yadav *et al*., (2022)

4.1.2 Mean and range of variability

The mean performance, range, grand mean, standard error, critical difference and coefficient of variance obtained through statistical analysis in twenty-five rice genotypes for nineteen traits are given in Table 4.2

4.1.2.1 Days to 50 per cent flowering

Days to 50 percent flowering is one of the important characters which suggest whether the genotype is early or late and substantial variation was observed for this trait. The number of

days to 50 per cent flowering were recorded in a range of 76 days in DPL-2 to 123 days in DPL-3 with a general mean of 97 days. Among the 25 rice genotypes, 16 genotypes expressed early 50% flowering as compared to the general mean (97), while 9 genotypes recorded late 50 per cent flowering than the general mean (97). The genotypes DPL-2 (76) followed by DPL-21 (77), DPL-14 (84) and DPL-13 (85) were discovered to be the earliest, while the genotypes namely, DPL-3 (123), DPL-8 (119), DPL-5 (119), DPL-24 (112) and DPL-15 (107) were extremely late since they took a greater number of days to 50% flowering. Same kind of results were obtained by Srinivas *et al.,* (2016), Srivastava *et al.,* (2017), Adhikari *et al.,* (2018), Chuchert *et al.,* (2018), Tiwari *et al.,* (2019) and Yadav *et al.,* (2022) which support the present findings.

Table 4.1 Analysis of variance for yield contributing components in rice

Sr. No.	Source	Mean Sum of Squares (MSS)		
		Replication	**Treatment**	**Error**
	Degrees of freedom	2	24	48
1	Days to 50 per cent flowering	3.453	461.581**	1.398
2	Days to maturity	1.693	484.141**	2.054
3	Number of productive tillers per plant	0.257	4.534**	0.17
4	Panicle length (cm)	4.297	17.979**	1.995
5	Plant height (cm)	25.429	2023.653**	15.215
6	Grain yield per plant (g)	0.131	45.219**	2.547
7	Straw yield per plant (g)	0.113	43.589**	6.543
8	Harvest index (%)	0.279	36.608**	4.166
9	Test weight (g)	0.059	54.542**	0.221
10	Number of filled grains per panicle	27.012	2960.489**	12.806
11	Number of total spikelets per panicle	11.105	4397.669**	24.089
12	Spike fertility (%)	9.128	93.398**	5.437
13	Protein (%)	0.007	6.465**	0.058
14	Amylose (%)	0.059	5.572**	0.454
15	Carbohydrate (%)	3.007	51.011**	3.685
16	Fat content (%)	2.836	5.301**	1.429
17	Fe (ppm)	0.072	20.509**	0.908
18	Zn (ppm)	1.069	23.626**	0.678
19	Ca (ppm)	31.271	958.584**	44.366

*- Significant at 5 percent, ** -Significant at 1 percent

4.1.2.2 Days to maturity

Early maturity or late maturity is desirable for scheduling cropping patterns. The number of days to maturity were measured from 104 days (DPL-2) to 152 days (DPL-8)

with the average mean of 127 days. Among the 25 genotypes under study, 14 genotypes required less number of days to maturity, whereas 11 genotypes required relatively more number of days to maturity than general mean (127 days). The genotypes *viz*., DPL-2 (104), DPL-21 (109), DPL-13 (113), DPL-14 (113) and DPL-10 (114) were recorded earliest genotypes, while DPL-8 (152), DPL-3 (150), DPL-5 (148), DPL-24 (146) and DPL-15 (137) were recorded late genotypes as they took relatively more number of days to maturity. These results are in conformity with Srivastava *et al.,* (2017), Adhikari *et al.,* (2018), Chuchert *et al.,* (2018), Tiwari *et al.,* (2019) and Yadav *et al*., (2022).

4.1.2.3 Number of productive tillers per plant

Number of productive tillers per plant is an important character which is closely associated with grain yield and showed significant variation among studied cultivars. The number of productive tillers per plant varied from 4.13 (DPL-20) to 9.13 (DPL-23) with a general mean of 6.93. Out of the 25 genotypes under study, 13 genotypes exhibited less number of productive tillers per plant, whereas 12 genotypes shows more number of productive tillers per plant than general mean (6.93). The genotype DPL-20 (4.13) had the fewest productive tillers per plant, followed by DPL-5 (5.20), DPL-12 (5.47), DPL-22 (5.67) and DPL-7 (5.73), while DPL-23 (9.13) had the more number of productive tillers per plant, followed by DPL-14 (9.07), DPL-25 (8.47), DPL-2 (8.33) and DPL-18 (8.20). Thus, these genotypes can be used as donor parents in crop improvement programme. The results obtained for this character are in conformity with Srinivas *et al.,* (2016), Srivastava *et al.,* (2017), Chuchert *et al.,* (2018) and Yadav *et al*., (2022).

4.1.2.4 Panicle length (cm)

Panicle length is an important yield-related trait, strongly affects yield components, such as grain number, grain density and rice quality. The general mean of panicle length was recorded 23.53 cm with the lowest panicle length observed was 18.90 cm in DPL-21 and highest panicle length observed was 29.06 cm in DPL-17. Among all the genotypes under study, fourteen genotypes show less panicle length, while eleven genotypes show more panicle length than general mean (23.53 cm). The genotypes DPL-21 (18.90 cm), DPL-7 (20.50 cm), DPL-10 (21.10 cm), DPL-2 (21.50 cm) and DPL-25 (21.56 cm) measured lowest panicle length among twenty-five genotypes, while genotypes DPL-17 (29.06 cm), DPL-24 (28.43 cm), DPL-11 (26.97 cm), DPL-19 (26.90 cm) and DPL-23 (25.22 cm) measured highest panicle length. Same results were observed and supported by Srinivas *et al.,* (2016), Srivastava *et al.,* (2017) and Yadav *et al*., (2022).

Table 4.2 Mean performance of twenty-five rice genotypes for various yield contributing characters

Sr. No.	Genotypes	Days to fifty percent flowering	Days to maturity	Number of productive tillers per plant	Panicle length (cm)	Plant height (cm)	Grain yield per plant (g)	Straw yield per plant (g)	Harvest Index (%)	Test weight (g)	Number of filled grains per panicle
1	**DPL-1**	93	124	6.40	24.17	101	21.93	27.77	44.13	21.53	165
2	**DPL-2**	76	104	8.33	21.50	103	13.02	18.35	41.46	25.27	100
3	**DPL-3**	123	150	7.20	22.20	160	12.45	24.53	33.64	14.31	83
4	**DPL-4**	88	118	6.47	22.80	92	19.53	24.60	44.32	30.23	142
5	**DPL-5**	119	148	5.20	22.10	164	12.90	21.77	37.21	18.39	100
6	**DPL-6**	95	128	6.27	24.90	99	11.83	18.75	38.59	19.15	143
7	**DPL-7**	89	119	5.73	20.50	88	15.83	23.63	40.10	23.88	120
8	**DPL-8**	119	152	7.40	24.80	150	14.90	29.02	33.91	20.70	95
9	**DPL-9**	106	136	7.00	21.87	138	12.23	25.73	32.09	22.45	80
10	**DPL-10**	86	114	8.07	21.10	85	12.48	25.33	32.99	18.16	78
11	**DPL-11**	91	120	7.60	26.97	145	22.43	30.30	42.49	24.81	151
12	**DPL-12**	105	134	5.47	24.67	140	18.90	27.38	40.84	27.05	135
13	**DPL-13**	85	113	6.53	23.40	96	11.67	18.40	38.90	23.79	76
14	**DPL-14**	84	113	9.07	21.90	96	12.91	19.97	39.18	15.74	86
15	**DPL-15**	107	137	6.47	23.70	141	15.46	22.03	41.25	27.71	153
16	**DPL-16**	96	123	6.80	23.56	101	12.23	18.75	39.39	21.51	126
17	**DPL-17**	96	126	5.93	29.06	143	12.65	19.20	39.87	25.24	84
18	**DPL-18**	95	126	8.20	21.67	124	13.56	20.60	39.79	25.88	75
19	**DPL-19**	94	129	7.07	26.90	104	25.69	31.19	45.24	19.37	178
20	**DPL-20**	101	131	4.13	23.13	132	13.92	21.35	39.59	24.10	120
21	**DPL-21**	77	109	7.67	18.90	90	14.20	21.93	39.41	22.53	66
22	**DPL-22**	94	124	5.67	23.33	87	18.15	24.88	42.20	33.09	129
23	**DPL-23**	91	122	9.13	25.22	80	20.05	25.72	43.90	22.15	110
24	**DPL-24**	112	146	6.87	28.43	116	16.05	23.95	40.24	21.46	121
25	**DPL-25**	102	133	8.47	21.56	128	12.58	19.90	38.80	25.29	91
Mean		**97**	**127**	**6.93**	**23.53**	**116**	**15.5**	**23.4**	**39.58**	**22.95**	**112**
CV		1.22	1.13	5.96	6	3.36	10.29	10.93	5.16	2.05	3.19
SE m		0.68	0.83	0.24	0.82	2.25	0.92	1.48	1.18	0.27	2.07
CD at 5%		1.94	2.35	0.68	2.32	6.4	2.62	4.2	3.35	0.77	5.87
CD at 1%		2.59	3.14	0.9	3.09	8.54	3.49	5.6	4.47	1.03	7.84
Minimum		77	104	4.13	18.9	80	11.67	18.35	32.09	14.31	66
Maximum		123	152	9.13	29.06	164	25.69	31.19	45.24	33.09	178

Contd…

Sr. No.	Genotypes	Number of total spikelets per panicle	Spikelet fertility (%)	Protein (%)	Amylose (%)	Carbohydrate (%)	Fat (%)	Fe (ppm)	Zn (ppm)	Ca (ppm)
1	**DPL-1**	194	85.10	8.54	21.46	79.62	17.46	17.78	12.10	113.02
2	**DPL-2**	121	82.75	4.86	22.37	78.40	14.60	14.35	9.26	89.35
3	**DPL-3**	113	73.02	8.68	20.89	79.68	16.04	16.87	7.32	56.71
4	**DPL-4**	173	81.80	4.79	21.52	70.38	14.22	16.35	7.30	52.38
5	**DPL-5**	135	74.23	6.25	19.79	80.80	14.11	12.21	11.90	76.30
6	**DPL-6**	176	81.12	7.91	21.06	82.50	14.46	16.18	6.80	72.87
7	**DPL-7**	160	75.32	6.18	20.21	75.71	15.00	10.90	7.80	60.94
8	**DPL-8**	127	74.28	6.04	18.60	84.68	14.60	15.72	12.80	84.65
9	**DPL-9**	102	78.78	7.08	18.14	72.26	14.40	19.45	12.50	102.35
10	**DPL-10**	110	70.35	6.73	21.83	79.85	16.54	18.30	11.70	76.42
11	**DPL-11**	202	74.73	8.54	20.88	80.37	14.86	14.20	15.30	69.72
12	**DPL-12**	186	72.31	4.51	19.56	82.10	15.28	19.40	11.40	105.86
13	**DPL-13**	101	75.44	7.50	20.69	81.61	17.29	14.30	14.40	87.89
14	**DPL-14**	101	85.32	8.19	19.16	87.39	15.87	20.60	13.70	107.81
15	**DPL-15**	183	83.59	6.46	20.35	86.28	18.87	16.80	13.80	94.28
16	**DPL-16**	185	68.26	7.15	17.58	82.48	15.52	13.10	18.70	86.97
17	**DPL-17**	126	66.52	7.08	19.25	80.76	15.62	17.30	8.60	110.20
18	**DPL-18**	94	79.76	5.97	18.23	85.03	14.50	18.10	11.30	94.85
19	**DPL-19**	210	84.38	7.01	18.37	88.00	17.83	17.40	8.90	103.27
20	**DPL-20**	175	68.64	5.07	17.70	80.54	14.58	16.70	8.80	100.12
21	**DPL-21**	84	78.34	5.42	20.10	83.36	15.28	18.10	11.20	96.75
22	**DPL-22**	165	78.18	4.37	20.38	82.52	17.28	15.30	9.90	56.28
23	**DPL-23**	137	80.16	4.93	20.61	79.62	17.01	18.10	10.10	73.49
24	**DPL-24**	173	69.60	3.26	20.18	83.43	16.92	17.10	11.70	98.27
25	**DPL-25**	117	77.60	5.35	18.06	77.93	16.84	10.20	12.20	89.56
Mean		**146**	**76.78**	**6.31**	**19.88**	**81.01**	**15.8**	**16.19**	**11.18**	**86.41**
CV		3.36	3.04	3.82	3.39	2.37	7.57	5.88	7.37	7.71
SE m		2.83	1.35	0.14	0.39	1.11	0.69	0.55	0.48	3.85
CD at 5%		8.06	3.83	0.4	1.11	3.15	1.96	1.56	1.35	10.93
CD at 1%		10.75	5.11	0.53	1.48	4.2	2.62	2.09	1.8	14.59
Minimum		84	66.52	3.26	17.57	70.38	14.11	10.2	6.8	52.38
Maximum		210	85.32	8.68	22.37	88	18.87	20.6	18.7	113.02

4.1.2.5 Plant height (cm)

Plant height is an important agronomic trait for crop yield. The height of the plants ranged from 80 cm in DPL-23 to 164 cm in DPL-5 with a general mean height of 116 cm. Fourteen genotypes out of twenty-five genotypes measured plant height below the general mean, while eleven genotypes measured plant height above the general mean. Out of all twenty-five rice genotypes lowest plant height was measured in the genotypes namely, DPL-23 (80 cm), DPL-10 (85 cm), DPL-22 (87 cm) and DPL-7 (88 cm), while the highest plant height was measured by the genotypes DPL-5 (164 cm) followed by DPL-3 (160 cm), DPL-8 (150 cm) and DPL-11 (145 cm). Small heighted plant can be used for developing non-lodging varieties. Adhikari *et al.,* (2018) and Chuchert *et al.,* (2018) reported same kind of observations for plant height and support the current findings.

4.1.2.6 Grain yield per plant (g)

The grain yield per plant (g) differed significantly among all the twenty-five rice genotypes under investigation. The range of average grain yield per plant was from 11.67 g (DPL-13) to 25.69 g (DPL-19), with a general mean of 15.50 g. Out of twenty-five rice genotypes, sixteen genotypes exhibited less grain yield per plant, whereas nine genotypes exhibited more grain yield per plant than the average mean (15.50 g).

The genotype DPL-13 (11.67 g) had the lowest grain yield per plant, followed by DPL-6 (11.83 g), DPL-9 (12.23 g), DPL-16 (12.23 g) and DPL-3 (12.45 g), while the genotypes DPL-19 (25.69 g), DPL-11 (22.43 g), DPL-1 (21.93 g), DPL-23 (20.05 g) and DPL-4 (19.53 g) recorded highest grain yield per plant. Hence, these genotypes can be included in the crop improvement programme as a donor parents. Same results for grain yield per plant recorded by Srinivas *et al.*, (2016), Srivastava *et al.,* (2017) and Tiwari *et al.,* (2019).

4.1.2.7 Straw yield per plant (g)

Straw yield is an important trait in plant breeding, especially for crops like rice. Straw yield per plant (g) shows significant variation among studied varieties and varied from 18.35 g in DPL-2 to 31.19 g in DPL-19 with a general mean of 23.40 g. Out of 25 genotypes, 12 genotypes exhibited lower straw yield per plant, whereas 13 genotypes showed higher straw yield per plant than the average mean (23.40 g). The genotype DPL-2 (18.35g) observed the lowest straw yield per plant followed by DPL-13 (18.40 g), DPL-6 (18.75 g), DPL-16 (18.75 g) and DPL-17 (19.20 g), while the genotypes DPL-19 (31.19 g), DPL-11 (30.30 g), DPL-8 (29.02 g), DPL-1 (27.77 g) and DPL-12 (27.38 g) observed the highest straw yield per plant. Similar type of findings was observed by Srivastava *et al.,* (2017), Adhikari *et al.,* (2018) and Yadav *et al*., (2022).

4.1.2.8 Harvest index (%)

Harvest index is a measure of reproductive efficiency in plants. The general mean for the trait harvest index of all the twenty-five rice genotypes was recorded to be 39.58 % and mean values varied from 32.09 % (DPL-9) to 45.24 % (DPL-19). Eleven genotypes reported the lowest harvest index and the fourteen genotypes reported the highest harvest index than the general mean (39.58 %). The genotype DPL-9 (32.09 %) had the lowest harvest index, followed by DPL-10 (32.99 %), DPL-3 (33.64 %) and DPL-8 (33.91%), while the genotypes DPL-19 (45.24 %), DPL-4 (44.32 %), DPL-1 (44.13 %) and DPL-23 (43.90 %) recorded highest harvest index. Harvest index is used as a selection criterion to improve the yield potential of crops. Tiwari *et al.,* (2019) and Yadav *et al*., (2022) also observed similar results for harvest index and backup the current findings.

4.1.2.9 Test weight (g)

Test weight ranged from 14.31 g in DPL-3 to 33.09 g in DPL-22 with an average mean of 22.95 g. Out of 25 genotypes, 13 genotypes exhibited lower test weight, whereas 12 genotypes showed higher test weight than the average mean (22.95 g). The genotypes DPL-3 (14.31 g), DPL-14 (15.74 g), DPL-10 (18.16 g), DPL-5 (18.39 g) and DPL-6 (19.15 g) measured lowest test weight, while genotypes DPL-22 (33.09 g), DPL-4 (30.23 g), DPL-15 (27.71 g), DPL-12 (27.05 g) and DPL-18 (25.88 g) measured highest test weight. High test weight is associated with better grain quality and yield potential. The genotypes with high test weight can be used for higher profitability. Same findings were measured by Srinivas *et al.,* (2016), Tiwari *et al.,* (2019) and Yadav *et al*., (2022) which support the present results.

4.1.2.10 Number of filled grains per panicle

The number of filled grains per panicle is yield-related component and strongly affect the yield potential. It exhibited significant variation within studied cultivars and varied from 66 (DPL-21) to 178 (DPL-19) with a general mean of 112. The genotype with the fewest filled grains per panicle was DPL-21 (66) followed by DPL-18 (75), DPL-13 (76), DPL-10 (78) and DPL-9 (80), while the genotypes DPL-19 (178), DPL-1 (165), DPL-15 (153), DPL-11 (151) and DPL-6 (143) recorded the highest number of filled grains per panicle derived from 25 rice genotypes. Thirteen genotypes out of twenty-five genotypes recorded number of filled grains per panicle below the general mean (112.20), while Twelve genotypes recorded number of filled grains per panicle above the general mean. Srivastava *et al.,* (2017), Tiwari *et al.,* (2019) and Adhikari *et al.,* (2018) also recorded similar results for number of filled grains per panicle and support the current results.

4.1.2.11 Number of total spikelets per panicle

The number of spikelets per panicle among twenty-five rice genotypes ranged from 84 in DPL-21 to 210 in DPL-19, with a general mean value of 146. The genotype DPL-21 (84) recorded the lowest number of total spikelets per panicle followed by DPL-18 (94), DPL-14 (101), DPL-13 (101) and DPL-9 (102), whereas the genotypes DPL-19 (210), DPL-11 (202), DPL-1 (194), DPL-12 (186) and DPL-16 (185) recorded the highest number of total spikelets per panicle. These genotypes having more number of filled and total spikelets can be included in crop improvement programme. Similar findings were reported by Srinivas *et al.*, (2016), Sadimantara *et al.*, (2021) and Yadav *et al*., (2022).

4.1.2.12 Spikelet fertility (%)

Spikelet fertility is closely related trait to grain yield. The variation in spikelet fertility ranged from 66.52 % (DPL-17) to 85.32 % (DPL-14). This character's general mean was 76.78 %. Out of twenty-five rice genotypes, twelve genotypes exhibited lower spikelet fertility (%), whereas thirteen genotypes exhibited higher spikelet fertility (%) than the average mean (76.78 %). The lowest spikelet fertility reported in DPL-17 (66.52 %) followed by DPL-16 (68.26 %), DPL-20 (68.64 %), DPL-24 (69.60 %) and DPL-10 (70.35 %), whereas highest spikelet fertility observed in DPL-14 (85.32 %) followed by DPL-1 (85.10 %), DPL-19 (84.38 %), DPL-15 (83.59 %) and DPL-2 (82.75 %). Thus, these genotypes having high fertility % can be included in crop improvement programme since fertility % is positively associated with the yield. Tiwari *et al.,* (2019) and Sadimantara *et al.,* (2021) reported nearly same kind spikelet fertility percentage.

4.1.2.13 Protein (%)

Protein is a major nutrient in rice and ranged from 3.26 % in DPL-24 to 8.68 % in DPL-3 with a general mean of 6.31 %. Out of 25 genotypes, 13 genotypes recorded less protein content, while 12 genotypes recorded more protein content than general mean (6.31 %). The genotypes DPL-3 (8.68 %), DPL-11 (8.54 %), DPL-1 (8.54 %), DPL-14 (8.19 %) and DPL-6 (7.91 %) were having more protein content, while the genotypes DPL-24 (3.26 %), DPL-22 (4.37 %), DPL-12 (4.51 %), DPL-4 (4.79 %) and DPL-2 (4.86 %) were having less protein content. These high protein content genotypes can be used as donner plants to improve protein content. Ritika *et al.*, (2016), Raghuvanshi *et al*., (2017), Kalita *et al.,* (2022) and Singh *et al.*, (2022) also reported similar results for protein content and backup the present findings.

4.1.2.14 Amylose (%)

Amylose content plays an important role in determining the cooking and pasting properties of a rice. The cooking quality depends on the components of the rice such as proteins

and amylopectin. Amylose content of all the studied twenty-five rice genotypes, ranged from 17.58 % (DPL-16) to 22.37 % (DPL-2) with a general mean of 19.88 %. Eleven genotypes indicated lower level of amylose content, whereas fourteen genotypes reported higher levels of amylose content than the average mean (19.88 %). Among twenty-five genotypes, eleven genotypes had low and fourteen genotypes had moderate amylose content. Rice with a high amylose content (25-30%) tends to cook firm and dry, whereas rice with an intermediate amylose content (20-25%) tends to be softer and stickier and rice with a low amylose content (<20%) is generally quite soft and sticky. Same type of results for amylose content were reported by Ritika *et al.,* (2016), Pongjanta *et al.,* (2016) and Pakuwal and Manandhar (2021).

4.1.2.15 Carbohydrate (%)

The carbohydrate content of rice is mainly starch which is composed of amylose and amylopectin. The general mean for the trait carbohydrate content of all the twenty-five rice genotypes under investigation was recorded to be 81.01% and the mean values varied from 70.38 % in DPL-4 to 88 % in DPL-19. The genotypes DPL-4 (70.38 %), DPL-9 (72.26 %), DPL-7 (75.71 %), DPL-25 (77.93 %) and DPL-2 (78.40 %) reported the lowest carbohydrate content, and the genotypes DPL-19 (88.00 %), DPL-14 (87.39 %), DPL-15 (86.28 %), DPL-18 (85.03 %) and DPL-8 (84.68 %) reported the highest carbohydrate content. These results are in conformity with Verma and Srivastav (2017), Abeysekera *et al.,* (2017) and Raghuvanshi *et al.,* (2017) which support the present results.

4.1.2.16 Fat (%)

Fat (%) were significantly different among all the twenty-five rice genotypes and ranged from 14.11 % (DPL-5) to 18.87 % (DPL-15) with a general mean of 15.80 %. Fifteen genotypes out of twenty-five genotypes had the lowest fat content than the general mean (15.80%), whereas rest ten genotypes reported highest fat content. Genotypes DPL-5 (14.11 %), DPL-4 (14.22 %), DPL-9 (14.40 %), DPL-6 (14.46 %) and DPL-18 (14.50 %) reported lower levels of fat content, while the genotypes DPL-15 (18.87 %), DPL-19 (17.83 %), DPL-1 (17.46 %), DPL-13 (17.29 %) and DPL-22 (17.28 %) reported higher levels of fat content. Fat in rice is a good source of linoleic and other essential fatty acids but does not contain cholesterol (Eggum *et al.*, 1982). Fat content influences the taste of cooked rice because rice with high fat content tends to be tastier and have less starch (Hirokadzu *et al.,* 1979). Kumari *et al.,* (2017) and Rathna *et al.,* (2019) recorded same results for the fat content of rice bran.

4.1.2.17 Iron (Fe) (ppm)

Minerals are well-known essential nutrients and plays an important role in the effective body functioning. Iron is one of the two more important micronutrients for human body as

compare to others. Iron content values was varied from 10.20 ppm (DPL-25) to 20.60 ppm (DPL-14) with a general mean of 16.19 ppm. Maximum Fe content was reported in the genotype DPL-14 (20.60 ppm) followed by DPL-9 (19.45 ppm), DPL-12 (19.40 ppm), DPL-10 (18.30 ppm) and DPL-23 (18.10 ppm) whereas, the minimum Fe content was observed in DPL-25 (10.20 ppm), DPL-7 (10.90 ppm), DPL-5 (12.21 ppm) and DPL-16 (13.10 ppm). The genotypes having more Fe content can be used in crop improvement programme. For iron content same results were recorded by Verma and Srivastav (2017), Raghuvanshi *et al*., (2017) and Tripathy *et al.,* (2020) which backup the current results.

4.1.2.18 Zinc (Zn) (ppm)

Zinc plays vital role in various metabolic activities of the body as it is a part of many enzymes. Zn is also one of the two more important micronutrients for human body as compare to others. Its values for twenty-five genotypes were ranged from 6.80 ppm in DPL-6 to 18.70 ppm in DPL-16 with a general mean of 11.18 ppm. The genotypes DPL-16 (18.70 ppm), DPL-11 (15.30 ppm), DPL-13 (14.40 ppm) and DPL-15 (13.80 ppm) observed maximum zinc content whereas the genotypes DPL-6 (6.80 ppm), DPL-4 (7.30 ppm), DPL-3 (7.32 ppm) and DPL-7 (7.80 ppm) recorded minimum zinc content. Verma and Srivastav (2017), Raghuvanshi *et al*., (2017) and Tripathy *et al.,* (2020) reported similar results for zinc content.

4.1.2.19 Calcium (Ca) (ppm)

Calcium is an essential mineral that plays many roles in the human body, including bone health, muscle function, and nerve transmission. Its content ranges from 52.38 ppm (DPL-4) to 113.02 ppm (DPL-1) with a general mean of 86.41 ppm. The genotype DPL-1 (113.02 ppm) followed by DPL-17 (110.20 ppm), DPL-14 (107.81 ppm), DPL-12 (105.86 ppm) and DPL-19 (103.27 ppm) recorded maximum Ca content, whereas the minimum Fe content was observed in DPL-4 (52.38 ppm), DPL-22 (56.28 ppm), DPL-3 (56.71 ppm) and DPL-7 (60.94 ppm). Verma and Srivastav (2017) and Kalita *et al.,* (2022) observed similar results for calcium content and support the current results.

4.1.3 Components of variation

Phenotypic, genotypic and environmental variance constituted the entire populations variation. The estimations of these three variance components for nineteen characters provided in Table 4.3.

For various yield attributing traits, the phenotypic, genotypic, and environmental variations varied from 1.62 to 1481.95, 1.29 to 1457.86 and 0.17 to 44.37 respectively. Typically, phenotypic variations were higher in magnitude than genotypic and environmental variances. The phenotypic variance was higher for number of total spikelets per panicle

(1481.95) followed by number of filled grains per panicle (995.37), plant height (684.70), calcium (ppm) (349.11) and days to maturity (162.75). The genotypic variance was higher for number of total spikelets per panicle (1457.86) followed by number of filled grains per panicle (982.56), plant height (669.48), Ca content (304.74) and days to maturity (160.70). The environmental variance was maximum for Ca content (44.37) followed by number of total spikelets per panicle (24.09) followed by number of filled grains per panicle (12.81) and plant height (15.22). For each of the nineteen characters, the environmental variation was smaller than the genotypic variances. This showed that environmental variables compared to genotypic variables were more important for the expression of these traits. Khaire *et al.,* (2017), Rashid *et al., (*2017), Saha *et al.,* (2019) and Sadimantara *et al.,* (2021) recorded the similar type of results but Chuchert *et al.,* (2018) observed higher phenotypic and genotypic variance in yield per plant followed by number of total spikelets per panicle.

Table 4.3 Estimates of Components of variation for yield contributing components in rice.

Sr. No.	Characters	σ^2p	σ^2g	σ^2e
1	Days to fifty percent flowering	154.79	153.39	1.40
2	Days to maturity	162.75	160.70	2.05
3	Number of productive tillers per plant	1.63	1.45	0.17
4	Panicle length (cm)	7.32	5.33	2.00
5	Plant height (cm)	684.70	669.48	15.22
6	Grain yield per plant (g)	16.77	14.22	2.55
7	Straw yield per plant (g)	18.89	12.35	6.54
8	Harvest Index (%)	14.98	10.81	4.17
9	Test weight (g)	18.33	18.11	0.22
10	Number of filled grains per panicle	995.37	982.56	12.81
11	Number of total spikelets per panicle	1481.95	1457.86	24.09
12	Spikelet fertility (%)	34.76	29.32	5.44
13	Protein (%)	2.19	2.14	0.06
14	Amylose (%)	2.16	1.71	0.45
15	Carbohydrate (%)	19.46	15.78	3.69
16	Fat (%)	2.72	1.29	1.43
17	Fe (ppm)	7.44	6.53	0.91
18	Zn (ppm)	8.33	7.65	0.68
19	Ca (ppm)	349.11	304.74	44.37

4.1.4 Coefficient of variation

The estimates of the coefficient of variation at the phenotypic (PCV), genotypic (GCV), and environmental (ECV) levels are provided in Table 4.4

Normally, phenotypic coefficients of variation (PCV) were greater in magnitude than the corresponding genotypic coefficients of variation (GCV) and environmental coefficients of variation (ECV). The phenotypic coefficient of variation (PCV) was observed highest in the trait number of filled grains per panicle (28.12) followed by grain yield per plant (26.42), number of total spikelets per panicle (26.35), Zn content (25.81), protein content (23.46), plant height (22.53) and Ca content (21.62). whereas the characters carbohydrate content (5.45) recorded minimum phenotypic coefficient of variation followed by amylose content (7.39), spikelet fertility (7.68) and harvest index (9.78).

Genotypic coefficient of variation (GCV) is a quantitative measure of the level of genetic variation exists within a population. The genotypic coefficient of variation was observed highest in number of filled grains per panicle (27.94) followed by number of total spikelets per panicle (26.13), Zn content (24.74), grain yield per plant (24.33), protein content (23.14), plant height (22.28) and Ca content (20.20), while the characters carbohydrate content (4.90) recorded minimum genotypic coefficient of variation followed by amylose content (6.57), spikelet fertility (7.05), fat content (7.19) harvest index (8.31), panicle length (9.81) and days to maturity (9.97).

Similar type of findings for both phenotypic and genotypic coefficient of variation were observed by Khaire *et al.,* (2017), Srivastava *et al.,* (2017), Rashid *et al., (*2017) and Saha *et al.,* (2019) but in contrast Nayak *et al* (2016) reported higher PCV and GCV in number of productive tillers per plant followed by number of filled grains per panicle. Adhikari *et al.,* (2018), Chuchert *et al.,* (2018) and Yadav *et al*. (2022) observed higher PCV and GCV in grain yield per plant.

4.1.5 Heritability and Genetic advance

The estimates of broad sense heritability, genetic advance and genetic advance as percent of mean is given in Table 4.4

The heritability in a broad sense varied from 47.67 (fat %) to 99.10 (days to fifty percent flowering), indicate that the currently studied characters showed significant high heritability except for fat (%) which showed moderate heritability (47.67 %). Similar results were obtained by Rashid *et al.,* (2017) and Chuchert *et al.,* (2018). Sadimantara *et al.,* (2021) reported highest heritability in days to maturity followed by total spikelets per panicle. Khaire *et al.,* (2017) and Srivastava *et al.,* (2017) observed highest heritability in number of total spikelets per panicle followed by number of filled grains per panicle. Srinivas *et al.,* (2016) and Saha *et al.,* (2019) reported highest heritability in test weight.

The genetic advance was ranged from 1.61 for fat % to 78.01 for number of total spikelets per panicle. The magnitude of genetic advance was observed highest for the characters number of total spikelets per panicle (78.01), number of filled grains per panicle (64.16), plant

height (52.71), Ca content (33.60), days to maturity (25.95) and days to fifty percent flowering (25.40), while moderate magnitude of genetic advance was observed by the spikelet fertility (10.25) and rest characters recorded low estimates of genetic advance. Khaire *et al.,* (2017), Srivastava *et al.,* (2017) and Saha *et al.,* (2019) observed similar results which support the present results, but Chuchert *et al.,* (2018) recorded higher genetic advance in grain yield per plant.

Table 4.4 Estimates of coefficient of variation, heritability and genetic advance for yield contributing components in rice.

Sr. No.	Characters	ECV	GCV	PCV	h^2b	GA	GAM %
1	Days to fifty percent flowering	1.22	12.77	12.83	99.10	25.40	26.19
2	Days to maturity	1.13	9.97	10.03	98.74	25.95	20.41
3	Number of productive tillers per plant	5.96	17.41	18.41	89.51	2.35	33.94
4	Panicle length (cm)	6.00	9.81	11.50	72.76	4.06	17.24
5	Plant height (cm)	3.36	22.28	22.53	97.78	52.71	45.38
6	Grain yield per plant (g)	10.29	24.33	26.42	84.82	7.16	46.16
7	Straw yield per plant (g)	10.93	15.02	18.57	65.37	5.85	25.01
8	Harvest Index (%)	5.16	8.31	9.78	72.19	5.76	14.54
9	Test weight (g)	2.05	18.54	18.65	98.79	8.71	37.96
10	Number of filled grains per panicle	3.19	27.94	28.12	98.71	64.16	57.18
11	Number of total spikelets per panicle	3.36	26.13	26.35	98.38	78.01	53.39
12	Spikelet fertility (%)	3.04	7.05	7.68	84.36	10.25	13.34
13	Protein (%)	3.82	23.14	23.46	97.35	2.97	47.04
14	Amylose (%)	3.39	6.57	7.39	78.99	2.39	12.03
15	Carbohydrate (%)	2.37	4.90	5.45	81.06	7.37	9.09
16	Fat (%)	7.57	7.19	10.44	47.47	1.61	10.21
17	Fe (ppm)	5.89	15.79	16.85	87.80	4.93	30.47
18	Zn (ppm)	7.37	24.74	25.81	91.86	5.46	48.85
19	Ca (ppm)	7.71	20.20	21.62	87.29	33.60	38.88

The genetic advance as percent of mean was varied from 9.09 for the carbohydrate % to 57.18 for number of filled grains per panicle indicating low to high genetic advance as percent of mean for all the characters under study. The genetic advance as percent of mean was recorded low by carbohydrate content (9.09) and moderate by the characters fat content (10.21), amylose content (12.03), spikelet fertility (13.34), harvest index (14.54) and panicle length (17.24), while the rest characters show high genetic advance as per cent of mean. Same kind of results for

genetic advance as percent of mean were found by Rashid *et al.,* (2017), Srivastava *et al.,* (2017) and Saha *et al.,* (2019) which support the current results.

Broad sense heritability provides information on the portion of reported variability that can be linked to genetic variations. Heritability by itself cannot tell us how much of anything is inherited. In current study, high heritability coupled with high genetic advance were recorded for all the characters excepts for amylose %, spikelet fertility, harvest index, panicle length, fat % and carbohydrate %. Khaire *et al.,* (2017), Srivastava *et al.,* (2017), Sadimantara *et al.,* (2021) observed similar results which support the present results.

High heritability coupled with low genetic advance as percent of mean was reported for carbohydrate content (81.06 %, 9.09 % respectively) indicate the influence of non-additive gene action. Therefore, it is suggested to use suitable selection procedure for improvement of these characters since high heritability coupled with high genetic advance suggest the presence of less environmental influence and additive gene action in their expression.

4.2 CORRELATION COEFFICIENT

The relationship between the yield and yield-attributing characters must be studied since the grain yield is a complex trait that depends on numerous independent characters. All feasible combinations of the character's correlation coefficients were calculated in order to understand the relationship between the characters at the phenotypic and genotypic levels. The mutual connection among yield and its component features can be displayed using correlation analysis. Estimates of phenotypic and genotypic correlation give a useful tool for predicting selection response and finding suitable individuals in breeding populations. The phenotypic and genotypic correlation between the nineteen traits examined in the current investigation is presented in Table 4.5 and Table 4.6 and depicted in figure 4.2 and figure 4.3 respectively.

4.2.1 Phenotypic correlation coefficient

4.2.1.1. Correlation between grain yield and yield contributing components

The character grain yield per plant showed highly significant positive correlation with straw yield per plant (0.756), number of filled grains per panicle (0.699), harvest index (0.662) and number of total spikelets per panicle (0.633), and significant positive correlation with panicle length (0.364), spikelet fertility (0.301), fat content (0.267) and test weight (0.228). Grain yield per plant show positive but non-significant correlation with Fe content (0.1317), amylose content (0.1293) and carbohydrate content (0.0392), while this character exhibited negative non-significant correlation with plant height (-0.1520), days to fifty percent flowering (-0.1008), Zn content (-0.0922), protein content (-0.0561), days to maturity (-0.0393), number of productive tillers per plant (-0.0194) and Ca content (-0.0167).

Chuchert *et al.,* (2018) and Adhikari *et al.,* (2018) recorded similar results for grain yield per plant which supported the present findings, but Saha *et al.,* (2019) reported that grain yield per plant had highly significant and positive correlation with days to fifty per cent flowering, days to maturity and number of productive tillers per plant in addition.

4.2.1.2. Mutual association between different yield components

Days to fifty percent flowering exhibited highly significant positive correlation with days to maturity (0.981) and plant height (0.777) and significant positive correlation with panicle length (0.242), whereas positive but non-significant correlation with straw yield per plant (0.2112), number of total spikelets per panicle (0.1255), carbohydrate content (0.0734), number of filled grains per panicle (0.0331) and Zn content (0.0072). Days to fifty per cent flowering estimates highly significant negative correlation with harvest index (-0.386), while significant negative correlation with spikelet fertility (-0.330), amylose content (-0.317) and number of productive tillers per plant (-0.315). However, days to fifty per cent flowering exhibited negative but non-significant correlation with rest of the characters. Same kind of results were obtained by Chuchert *et al.,* (2018), while Sadimantara *et al.,* (2021) observed days to fifty percent flowering had negative highly significant correlation with grain yield per plant.

The character days to maturity displays highly significant positive correlation with the characters plant height (0.737) and significant positive correlation with panicle length (0.271) and straw yield per plant (0.244), while positive but non-significant association with number of total spikelets per panicle (0.1564), carbohydrate content (0.1095), number of filled grains per panicle (0.0778) and fat content (0.0005). This character shows significant negative correlation with harvest index (-0.329), amylose content (-0.326), number of productive tillers per plant (-0.301), spikelet fertility (-0.281) and test weight (-0.228), while negative but non-significant correlation with Fe content (-0.0520), protein content (-0.0466), grain yield per plant (-0.0393), Zn content (-0.0306), and Ca content (-0.0159). Similar findings were recorded by Adhikari *et al.,* (2018) which supported the current findings but Saha *et al.,* (2019) observed positive and highly significant correlation between grain yield per plant and days to maturity.

Number of productive tillers per plant exhibited significant and positive association with spikelet fertility (0.365), whereas positive but non-significant correlation with Zn content (0.2249), Fe content (0.1826), amylose content (0.1274), carbohydrate content (0.1119), protein content (0.1108), fat content (0.0840), straw yield per plant (0.0281) and Ca content (0.0205). This character show highly significant negative correlation with number of total spikelets per panicle (-0.453) and significant negative correlation with number of filled grains per panicle (-0.336), plant height (-0.283) and test weight (-0.266). Number of productive tillers per plant

Table 4.5 Estimates of phenotypic correlation coefficient between yield and yield contributing characters in rice genotypes

	DFF	DM	NPTPP	PL	PH	SYPP	HI	TW	NFGPP	NTSPP	SF	PC	AC	CC	FC	Fe	Zn	Ca	GYPP
DFF	1.0000	0.981**	-0.315*	0.242*	0.777**	0.2112	-0.386**	-0.2269	0.0331	0.1255	-0.330*	-0.0148	-0.317*	0.0734	-0.0132	-0.0806	0.0072	-0.0447	-0.1008
DM		1.0000	-0.301*	0.271*	0.737**	0.244*	-0.329*	-0.228*	0.0778	0.1564	-0.281*	-0.0466	-0.326*	0.1095	0.0005	-0.0520	-0.0306	-0.0159	-0.0393
NPTPP			1.0000	-0.1467	-0.283*	0.0281	-0.0723	-0.266*	-0.336*	-0.453**	0.365*	0.1108	0.1274	0.1119	0.0840	0.1826	0.2249	0.0205	-0.0194
PL				1.0000	0.2038	0.240*	0.270*	0.0442	0.419**	0.498**	-0.2236	0.0205	-0.0553	0.232*	0.230*	0.1441	0.0492	0.1984	0.364*
PH					1.0000	0.1094	-0.344*	-0.1258	-0.0763	0.0101	-0.313*	0.1651	-0.312*	0.0579	-0.1982	-0.0765	0.0939	0.1479	-0.1520
SYPP						1.0000	0.0193	-0.0229	0.395**	0.372*	0.1010	0.0428	0.0336	-0.0021	0.1501	0.2127	-0.0443	-0.0403	0.756**
HI							1.0000	0.425**	0.597**	0.531**	0.326*	-0.1952	0.1621	0.0522	0.2131	-0.0462	-0.0904	0.0138	0.662**
TW								1.0000	0.238*	0.239*	0.0570	-0.533**	0.0416	-0.245*	0.0475	-0.1711	-0.0466	-0.1233	0.228*
NFGPP									1.0000	0.956**	0.290*	0.0342	0.1153	0.0912	0.230*	-0.0666	-0.0564	-0.0412	0.699**
NTSPP										1.0000	0.0048	-0.0269	0.0379	0.0713	0.1739	-0.1267	-0.0031	-0.0482	0.633**
SF											1.0000	0.1489	0.2176	0.0924	0.1397	0.1895	-0.1096	0.0340	0.301*
PC												1.0000	0.0415	0.0951	0.0410	0.0628	0.2083	0.0643	-0.0561
AC													1.0000	-0.2257	0.0548	0.0286	-0.294*	-0.385**	0.1293
CC														1.0000	0.304*	0.2111	0.264*	0.350*	0.0392
FC															1.0000	0.1094	0.1834	0.1429	0.267*
Fe																1.0000	-0.0676	0.383**	0.1317
Zn																	1.0000	0.271*	-0.0922
Ca																		1.0000	-0.0167
GYPP																			1.0000

***Significant at 5% level (r = 0.2271) **Significant at 1% level (r = 0.3724)**

DFF- Days to 50% flowering, DM- Days to maturity, NPTPP- Number of productive tillers per plant, PL- Panicle length (cm), PH- Plant height (cm), NTSPP- Number of total of spikelets per panicle, NFGPP- Number of filled grains per panicle, SF – Spikelet fertility (%), TW- Test weight (g), SYPP- Straw yield per plant, HI- Harvest index (%), AC- Amylose content, PC- Protein content, CC- Carbohydrate content, FC- Fat content, Fe- Iron content, Zn- Zinc content, Ca- Calcium content & GYPP- Grain yield per plant.

displays negative but non-significant correlation with panicle length (-0.1467), harvest index (-0.0723) and grain yield per plant (-0.0194). Present results were supported by Chuchert *et al.*, (2018) and recorded similar results for number of productive tillers per plant.

Panicle length exhibited highly significant positive correlation with number of total spikelets per panicle (0.498) and number of filled grains per panicle (0.419) and significant positive correlation with grain yield per plant (0.364), harvest index (0.270), straw yield per plant (0.240), carbohydrate content (0.232) and fat content (0.230). This character shows non-significant positive correlation with plant height (0.2038), Ca content (0.1984), Fe content (0.1441), Zn content (0.0492), test weight (0.0442) and protein content (0.0205), while non-significant negative correlation with spikelet fertility (-0.2236) and amylose content (-0.0553). Same type of results was obtained by Adhikari *et al.,* (2018) which support present finding but Saha *et al.,* (2019) and Chuchert *et al.,* (2018) reported that panicle length had non-significant correlation with grain yield per plant.

The character plant height had non-significant but positive correlation with protein content (0.1651), calcium content (0.1479), straw yield per plant (0.1094), Zn content (0.0939), carbohydrate content (0.0579) and number of total spikelets per panicle (0.0101). Plant height had significant and negative association with harvest index (-0.344), spikelet fertility (-0.313) and amylose content (-0.312), whereas it shows negative non-significant correlation with fat content (-0.1982), grain yield per plant (-0.1520), test weight (-0.1258), Fe content (-0.0765) and number of filled grains per panicle (-0.0763). Adhikari *et al.,* (2018) and Sadimantara *et al.,* (2021) observed similar kind of results for the plant height and supported the current results.

Straw yield per plant showed positive and highly significant association with grain yield per plant (0.756) and number of filled grains per panicle (0.395), while positive significant association shown with number of total spikelets per panicle (0.375). This character had positive but non-significant correlation with Fe content (0.2127), fat content (0.1501), spikelet fertility (0.1010), protein content (0.0428), amylose content (0.0336) and harvest index (0.0193). Straw yield per plant shows the non-significant negative correlation with Zn content (-0.0443), Ca content (-0.0403), test weight (-0.0229) and carbohydrate content (-0.0021). Similar results for straw yield per plant were recorded by Adhikari *et al.,* (2018).

Harvest index exhibited highly significant and positive correlation with grain yield per plant (0.662), number of filled grains per panicle (0.597), number of total spikelets per panicle (0.531) and test weight (0.425) and significant positive correlation with spikelet fertility (0.326). Harvest index exhibited non-significant but positive correlation with fat content (0.2131), amylose content (0.1621), carbohydrate content (0.0522) and Ca content (0.0138), whereas negative non-significant correlation with protein content (-0.1952), Zn content (-0.0904) and Fe content (-0.0462). Saha *et al.,* (2019) reported same findings and support current results.

The character test weight had positive and significant correlation with number of total spikelets per panicle (0.239), number of filled grains per panicle (0.238) and grain yield per plant (0.228), while non-significant but positive correlation with spikelet fertility (0.057), fat content (0.0475) and amylose content (0.0416). Test weight shows highly significant negative correlation with protein content (-0.533), significant negative correlation with carbohydrate content (-0.245), whereas non-significant negative correlation with Fe content (-0.1711), Ca content (-0.1233) and Zn content (-0.0466). Nayak *et al.,* (2016) reported similar results, but Chuchert *et al.,* (2018) and Saha *et al.,* (2019) observed non-significant correlation between grain yield per plant and test weight.

The character number of filled grains per panicle exhibited highly significant and positive correlation with number of total spikelets per panicle (0.956) and grain yield per plant (0.699) and significant positive correlation with spikelet fertility (0.290) and fat content (0.230), whereas positive but non-significant correlation with amylose content (0.1153), carbohydrate content (0.0912) and protein content (0.0342). Number of filled grains per panicle displays negative non-significant correlation with Fe content (-0.0666), Zn content (-0.0564) and Ca content (-0.0412). Saha *et al.,* (2019) and Sadimantara *et al.,* (2021) reported similar findings, while Nayak *et al* (2016) and Adhikari *et al.,* (2018) observed non-significant correlation between number of filled grains per panicle and grain yield per plant.

Number of total spikelets per panicle reported highly significant and positive correlation with grain yield per plant (0.633) and positive but non-significant association with fat content (0.1739), carbohydrate content (0.0713), amylose content (0.0379) and spikelet fertility (0.0048). However, number of total spikelets per panicle shows negative non-significant association with Fe content (-0.1267), Ca content (-0.0482), protein content (-0.0269) and Zn content (-0.0031). Chuchert *et al.,* (2018) observed similar results for number of total spikelets per panicle. Sadimantara *et al.,* (2021) reported that number of total spikelets per panicle had non-significant correlation with grain yield per plant.

Spikelet fertility shows significant positive correlation with grain yield per plant (0.301) and positive but non-significant association with amylose content (0.2176), Fe content (0.1895), protein content (0.1489), fat content (0.1397), carbohydrate content (0.0924) and Ca content (0.0340), while negative non-significant association with Zn content (-0.1096). Nayak *et al.,* (2016) recorded spikelet fertility exhibited non-significant correlation with grain yield per plant.

The nutritional trait protein content exhibited non-significant but positive correlation with Zn content (0.2083), carbohydrate content (0.0951) and Ca content (0.0643), Fe content (0.0628), amylose content (0.0415) and fat content (0.0410), whereas non-significant negative correlation with grain yield per plant (-0.0561). Basavaraja *et al.,* (2013) recorded same results

but Archana *et al.,* (2018) reported protein content had significant and positive correlation with grain yield per plant.

The biochemical parameter amylose content had positive but non-significant association with grain yield per plant (0.1293), fat content (0.0548) and Fe content (0.0286). Amylose content exhibited highly significant negative correlation with Ca content (-0.385) and significant negative correlation with Zn content (-0.294), whereas non-significant negative correlation with carbohydrate content (-0.2257). According to Basavaraja *et al.,* (2013) amylose content exhibited positive and significant association with grain yield per plant.

The character carbohydrate content shows positive significant correlation with Ca content (0.350), fat content (0.304) and Zn content (0.264), while positive but non-significant correlation with Fe content (0.2111) and grain yield per plant (0.0392). Fat content exhibited significant positive correlation with grain yield per plant (0.267), while non-significant but positive correlation with Zn content (0.1834), Ca content (0.1429) and Fe content (0.1094).

The micronutrient parameter Iron content shows highly significant positive correlation with Ca content (0.383) and significant positive correlation with grain yield per plant (0.1317), whereas non-significant negative correlation with Zn content (-0.0676). Archana *et al.,* (2018) reported Fe content had non-significant but positive correlation with grain yield per plant.

Zinc content character had significant positive correlation with Ca content (0.271) and non-significant negative correlation with grain yield per plant (-0.0922). Archana *et al.,* (2018) reported Zn content had significant but negative correlation with grain yield per plant. The calcium content parameter exhibited non-significant negative correlation with grain yield per plant (-0.0167).

4.2.2 Genotypic correlation coefficient

4.2.2.1. Correlation between Grain yield and other yield factors

The estimates of genotypic correlation coefficient in the present study (Table 4.6) showed that grain yield per plant showed highly significant positive correlation with straw yield per plant (0.804), number of filled grains per panicle (0.776), harvest index (0.756), number of total spikelets per panicle (0.699), panicle length (0.462) and spikelet fertility (0.374) and significant positive correlation with fat content (0.353) and test weight (0.252). Grain yield per plant showed positive but non-significant correlation with amylose content (0.1631), Fe content (0.1489) and carbohydrate content (0.0899), while negative non-significant correlation with plant

height (-0.1641), days to fifty percent flowering (-0.1117), Zn content (-0.0949), protein content (-0.0732), days to maturity (-0.0583), number of productive tillers per plant (-0.0372) and Ca content (-0.0266).

Chuchert *et al.,* (2018) and Adhikari *et al.,* (2018) recorded similar results for grain yield per plant but Saha *et al.,* (2019) reported that grain yield per plant had highly significant and positive correlation with days to fifty percent flowering, days to maturity and number of productive tillers per plant in addition.

4.2.1.2. Mutual association between different yield components

Days to fifty percent flowering exhibited highly significant positive correlation with days to maturity (0.994) and plant height (0.788) and significant positive correlation with panicle length (0.274) and straw yield per plant (0.257), whereas positive but non-significant correlation with number of total spikelets per panicle (0.1252), carbohydrate content (0.0752), number of filled grains per panicle (0.0330) and Zn content (0.0056). This character had highly significant negative correlation with harvest index (-0.453) and significant negative correlation with spikelet fertility (-0.354), amylose content (-0.353), number of productive tillers per plant (-0.336) and test weight (-0.230), while negative but non-significant correlation with rest of the characters i.e., grain yield per plant (-0.1117), Fe content (-0.0792), Ca content (-0.0477), fat content (-0.0387) and protein content (-0.0152). Similar kind of results was obtained by Chuchert *et al.,* (2018), while, Sadimantara *et al.,* (2021) observed that days to fifty per cent flowering had negative highly significant correlation with grain yield per plant.

The character days to maturity displays highly significant positive correlation with the characters plant height (0.748) and significant positive correlation with panicle length (0.331) and straw yield per plant (0.299), while positive but non-significant association with number of total spikelets per panicle (0.1556), carbohydrate content (0.1259), number of filled grains per panicle (0.0766). These character showed highly significant negative correlation with harvest index (-0.412), amylose content (-0.375) and significant negative correlation with number of productive tillers per plant (-0.317), spikelet fertility (-0.306) and test weight (-0.232), while negative but non-significant correlation with grain yield per plant (-0.0583), Fe content (-0.0549), protein content (-0.0499), Zn content (-0.0309), Ca content (-0.0124) and fat content (-0.0096). Similar findings were recorded by Adhikari *et al.,* (2018) which supported the current findings but Saha *et al.,* (2019) observed positive and highly significant correlation between grain yield per plant and days to maturity.

Table 4.6 Estimates of genotypic correlation coefficient between yield and yield contributing characters in rice genotypes

	DFF	DM	NPTPP	PL	PH	SYPP	HI	TW	NFGPP	NTSPP	SF	PC	AC	CC	FC	Fe	Zn	Ca	GYPP
DFF	1.0000	0.994**	-0.336*	0.274*	0.788**	0.257*	-0.453**	-0.230*	0.0330	0.1252	-0.354*	-0.0152	-0.353*	0.0752	-0.0387	-0.0792	0.0056	-0.0477	-0.1117
DM		1.0000	-0.317*	0.331*	0.748**	0.299*	-0.412**	-0.232*	0.0766	0.1556	-0.306*	-0.0499	-0.375**	0.1259	-0.0096	-0.0549	-0.0309	-0.0124	-0.0583
NPTPP			1.0000	-0.1841	-0.281*	-0.0210	-0.0460	-0.283*	-0.357*	-0.480**	0.400**	0.1200	0.1123	0.1355	0.1931	0.1834	0.231*	0.0410	-0.0372
PL				1.0000	0.243*	0.347*	0.394**	0.0605	0.494**	0.578**	-0.255*	0.0191	-0.0588	0.280*	0.258*	0.1366	-0.0056	0.233*	0.462**
PH					1.0000	0.1416	-0.415**	-0.1294	-0.0815	0.0092	-0.352*	0.1671	-0.339*	0.0631	-0.286*	-0.0782	0.0995	0.1525	-0.1641
SYPP						1.0000	0.2225	-0.0278	0.503**	0.475**	0.1187	0.0463	0.0783	-0.0124	0.1506	0.267*	-0.0213	-0.1142	0.804**
HI							1.0000	0.505**	0.714**	0.628**	0.458**	-0.243*	0.1936	0.1664	0.399**	-0.0501	-0.1273	0.0726	0.756**
TW								1.0000	0.238*	0.241*	0.0560	-0.544**	0.0392	-0.258*	0.0583	-0.1816	-0.0449	-0.1416	0.252*
NFGPP									1.0000	0.960**	0.303*	0.0353	0.1358	0.1010	0.337*	-0.0712	-0.0624	-0.0427	0.776**
NTSPP										1.0000	0.0307	-0.0264	0.0433	0.0868	0.243*	-0.1322	-0.0038	-0.0542	0.699**
SF											1.0000	0.1611	0.283*	0.0783	0.302*	0.2010	-0.1347	0.0505	0.374**
PC												1.0000	0.0568	0.1219	0.0355	0.0694	0.2074	0.0552	-0.0732
AC													1.0000	-0.275*	0.1783	0.0193	-0.304*	-0.449**	0.1631
CC														1.0000	0.481**	0.265*	0.300*	0.428**	0.0899
FC															1.0000	0.0798	0.1977	0.2094	0.353*
Fe																1.0000	-0.1018	0.470**	0.1489
Zn																	1.0000	0.323*	-0.0949
Ca																		1.0000	-0.0266
GYPP																			1.0000

***Significant at 5% level (r = 0.2271) **Significant at 1% level (r = 0.3724)**

DFF- Days to 50% flowering, DM- Days to maturity, NPTPP- Number of productive tillers per plant, PL- Panicle length (cm), PH- Plant height (cm), NTSPP- Number pf total spikelets per panicle, NFGPP- Number of filled grains per panicle, SF – Spikelet fertility (%), TW- Test weight (g), SYPP- Straw yield per plant, HI- Harvest index (%), AC- Amylose content, PC- Protein content, CC- Carbohydrate content, FC- Fat content, Fe- Iron content, Zn- Zinc content, Ca- Calcium content & GYPP- Grain yield per plant

Number of productive tillers per plant exhibited highly significant and positive association with spikelet fertility (0.400) and significant and positive association with Zn content (0.231), whereas positive but non-significant correlation with fat content (0.1931), Fe content (0.1834), carbohydrate content (0.1355), protein content (0.1200), amylose content (0.1123) and Ca content (0.0410). This character show highly significant negative correlation with number of total spikelets per panicle (-0.480) and significant negative correlation with number of filled grains per panicle (-0.357), test weight (-0.283) and plant height (-0.281). Number of productive tillers per plant displays negative but non-significant correlation with panicle length (-0.1841), harvest index (-0.0460), grain yield per plant (-0.0372) and straw yield per plant (-0.0210). Present results were supported by Chuchert *et al.,* (2018).

Panicle length exhibited highly significant positive correlation with number of total spikelets per panicle (0.578), number of filled grains per panicle (0.494), grain yield per plant (0.462) and harvest index (0.394) and significant positive correlation with straw yield per plant (0.347), carbohydrate content (0.280), fat content (0.258), plant height (0.243) and Ca content (0.233), while non-significant positive correlation with Fe content (0.1366), test weight (0.0605) and protein content (0.0191). Panicle length shows significant negative correlation with spikelet fertility (-0.255), while it shows negative but non-significant association with amylose content (-0.0588) and Zn content (-0.0056). Similar type of result was obtained by Adhikari *et al.,* (2018) which support present finding but Saha *et al.,* (2019) and Chuchert *et al.,* (2018) reported that panicle length had non-significant correlation with grain yield per plant.

The character plant height had non-significant but positive correlation with protein content (0.1671), calcium content (0.1525), straw yield per plant (0.1416), Zn content (0.0995), carbohydrate content (0.0631) and number of total spikelets per panicle (0.0092). Plant height shows highly significant and negative association with harvest index (-0.415), then significant and negative association with spikelet fertility (-0.352), amylose content (-0.339) and fat content (-0.286), whereas it shows negative non-significant correlation with grain yield per plant (-0.1641), test weight (-0.1294), number of filled grains per panicle (-0.0815) and Fe content (-0.0782). Adhikari *et al.,* (2018) and Sadimantara *et al.,* (2021) were observed similar kind of results for the plant height.

Straw yield per plant showed positive and highly significant association with grain yield per plant (0.804), number of filled grains per panicle (0.503) and number of total spikelets per panicle (0.475), while positive significant association shown with Fe content (0.267). This character had positive but non-significant correlation with harvest index (0.2225), fat content (0.1506), spikelet fertility (0.1187), amylose content (0.0783) and protein content (0.0463). Straw yield per plant shows non-significant negative correlation with Ca content (-0.1142), test

weight (-0.0278), Zn content (-0.0213) and carbohydrate content (-0.0124). Similar results for straw yield per plant was recorded by Kumar *et al.,* (2022)

Harvest index reported highly significant and positive correlation with grain yield per plant (0.756), number of filled grains per panicle (0.714), number of total spikelets per panicle (0.628), test weight (0.505), spikelet fertility (0.458) and fat content (0.399). Harvest index exhibited non-significant but positive correlation with amylose content (0.1936), carbohydrate content (0.1664) and Ca content (0.0726). This character shows negative significant correlation with protein content (-0.243), while negative but non-significant association with Zn content (-0.1273) and Fe content (-0.0501). Kumar *et al.,* (2022) reported the similar type of results.

The character test weight had positive and significant correlation with grain yield per plant (0.252), number of total spikelets per panicle (0.241) and number of filled grains per panicle (0.238), while non-significant but positive correlation with fat content (0.0583), spikelet fertility (0.0560), and amylose content (0.0392). Test weight shows highly significant negative correlation with protein content (-0.544), and significant negative correlation with carbohydrate content (-0.258), whereas non-significant negative correlation with Fe content (-0.1816), Ca content (-0.1416) and Zn content (-0.0449). Nayak *et al* (2016) reported similar results, but Chuchert *et al.,* (2018) and Saha *et al.,* (2019) were observed non-significant correlation between grain yield per plant and test weight.

The character number of filled grains per panicle exhibited highly significant and positive correlation with number of total spikelets per panicle (0.960) and grain yield per plant (0.776) and significant positive correlation with fat content (0.337) and spikelet fertility (0.303), whereas positive but non-significant correlation with amylose content (0.1358), carbohydrate content (0.1010) and protein content (0.0353). Number of filled grains per panicle displays negative non-significant correlation with Fe content (-0.0712), Zn content (-0.0624) and Ca content (-0.0427). Saha *et al.,* (2019) and Sadimantara *et al.,* (2021) reported similar findings, while Nayak *et al* (2016) and Adhikari *et al.,* (2018) were observed non-significant correlation between number of filled grains per panicle and grain yield per plant.

Number of total spikelets per panicle reported highly significant and positive correlation with grain yield per plant (0.699) and positive significant association with fat content (0.243), while positive but non-significant association with carbohydrate content (0.0868), amylose content (0.0433) and spikelet fertility (0.0307). However, number of total spikelets per panicle shows negative non-significant association with Fe content (-0.1322), Ca content (-0.0542), protein content (-0.0264) and Zn content (-0.0038). Chuchert *et al.,* (2018) observed similar results for number of total spikelets per panicle. Sadimantara *et al.,* (2021) reported that number of total spikelets per panicle had non-significant correlation with grain yield per plant.

Spikelet fertility showed highly significant positive correlation with grain yield per plant (0.374) and positive significant association with fat content (0.302) and amylose content (0.283), whereas but non-significant association with Fe content (0.2010), protein content (0.1611), carbohydrate content (0.0783) and Ca content (0.0505), while negative non-significant association with Zn content (-0.1347). Nayak *et al.,* (2016) recorded spikelet fertility exhibited non-significant correlation with grain yield per plant.

The nutritional trait protein content exhibited non-significant but positive correlation with Zn content (0.2074), carbohydrate content (0.1219), Fe content (0.0694), amylose content (0.0568), Ca content (0.0552) and fat content (0.0355), whereas non-significant negative correlation with grain yield per plant (-0.0732). Basavaraja *et al.,* (2013) recorded similar results but Archana *et al.,* (2018) observed that protein content had significant and positive correlation with grain yield per plant.

The biochemical parameter amylose content had positive but non-significant association with fat content (0.1783), grain yield per plant (0.1631), and Fe content (0.0193). Amylose content exhibited highly significant negative correlation with Ca content (-0.449) and significant negative correlation with Zn content (-0.304), whereas non-significant negative correlation with carbohydrate content (-0.275). According to Basavaraja *et al.,* (2013) amylose content exhibited positive and significant association with grain yield per plant.

The character carbohydrate content showed positive highly significant correlation with fat content (0.481) and Ca content (0.428) and positive significant correlation with Zn content (0.300) and Fe content (0.265), while positive but non-significant correlation with and grain yield per plant (0.0899). Fat content exhibited significant positive correlation with grain yield per plant (0.353), while non-significant but positive correlation with Ca content (0.2094), Zn content (0.1977), and Fe content (0.0798).

The micronutrient parameter Iron content showed highly significant positive correlation with Ca content (0.470) and significant positive correlation with grain yield per plant (0.1489), whereas non-significant negative correlation with Zn content (-0.1018). Archana *et al.,* (2018) reported Fe content had non-significant but positive correlation with grain yield per plant.

Zinc content character had significant positive correlation with Ca content (0.323) and non-significant negative correlation with grain yield per plant (-0.0949). Archana *et al.,* (2018) reported Zn content had highly significant but negative correlation with grain yield per plant. The calcium content parameter exhibited non-significant negative correlation with grain yield per plant (-0.0266).

4.3 PATH COEFFICIENT ANALYSIS

The correlation coefficient of grain yield per plant with its nineteen components *viz*. days to 50 per cent flowering, days to maturity, plant height, number of tillers per plant, panicle length, number of filled grains per panicle, number of total spikelets per panicle, spikelet fertility, test weight, grain yield per plant, straw yield per plant, harvest index, protein content, fat content, carbohydrate content, amylose content, iron content, zinc content, calcium content was further split into respective direct and indirect effects, through path-coefficient analysis. The direct and indirect contribution of each character to the grain yield determined by path analysis are described under the following headings.

4.3.1 Phenotypic correlation coefficient partitioned for path coefficient analysis

The phenotypic correlation coefficients for path-coefficient analysis were splits into direct and indirect effects are presented in Table 4.7 and the cause-and-effect relationship is diagrammatically represented in figure 4.4

Days to fifty per cent flowering expressed positive and very low direct effect (0.0022) on grain yield per plant. Nayak *et al.,* (2016) reported similar results, but Chuchert *et al.,* (2018) observed days to fifty percent flowering expressed negative direct effect on grain yield. It had positive indirect effect *via* days to maturity (0.0021), plant height (0.0017), straw yield per plant (0.0005), panicle length (0.0005), carbohydrate content (0.0002), and number of filled grains per panicle (0.0001). It had negative indirect effect through harvest index (-0.0008), number of tillers per plant (-0.0007), spikelet fertility (-0.0007), amylose content (-0.0007) test weight (-0.0005), Fe content (-0.0002), Ca content (-0.0001), while it had no effect on protein content, fat content and Zn content. The resulting phenotypic correlation with grain yield per plant was non-significant negative correlation (-0.1008).

Days to maturity had low negative direct effect (-0.0336) on grain yield. Similar result was reported by Chuchert *et al.,* (2018), while Saha *et al.,* (2019) recorded negative direct effect of days to maturity on grain yield. This character showed positive indirect effect through harvest index (0.0110), amylose content (0.0109), number of tillers per plant (0.0101), spikelet fertility (0.0094), test weight (0.0077), Fe content (0.0017), protein content (0.0016), Zn content (0.0010) and Ca content (0.0005). It shows negative indirect effects via days to 50 per cent flowering (-0.0329), plant height (-0.0247), panicle length (-0.0091), straw yield per plant (0.0082), number of spikelets per panicle (-0.0052), carbohydrate content (-0.0037) and number of filled grains per panicle (-0.0026), while it had no effect on fat content. However, this character exhibited non-significant negative correlation with grain yield per plant (-0.0393).

Table 4.7 Path analysis for various characters at phenotypic level in rice genotypes.

	DFF	DM	NPTPP	PL	PH	SYPP	HI	TW	NFGPP	NTSPP	SF	PC	AC	CC	FC	Fe	Zn	Ca	GYPP
DFF	**0.0022**	0.0021	-0.0007	0.0005	0.0017	0.0005	-0.0008	-0.0005	0.0001	0.0003	-0.0007	0.0000	-0.0007	0.0002	0.0000	-0.0002	0.0000	-0.0001	-0.1008
DM	-0.0329	**-0.0336**	0.0101	-0.0091	-0.0247	-0.0082	0.0110	0.0077	-0.0026	-0.0052	0.0094	0.0016	0.0109	-0.0037	0.0000	0.0017	0.0010	0.0005	-0.0393
NPTPP	-0.0013	-0.0013	**0.0042**	-0.0006	-0.0012	0.0001	-0.0003	-0.0011	-0.0014	-0.0019	0.0015	0.0005	0.0005	0.0005	0.0004	0.0008	0.0010	0.0001	-0.0194
PL	0.0037	0.0042	-0.0023	**0.0154**	0.0031	0.0037	0.0042	0.0007	0.0065	0.0077	-0.0034	0.0003	-0.0009	0.0036	0.0036	0.0022	0.0008	0.0031	0.364*
PH	0.0020	0.0019	-0.0007	0.0005	**0.0025**	0.0003	-0.0009	-0.0003	-0.0002	0.0000	-0.0008	0.0004	-0.0008	0.0001	-0.0005	-0.0002	0.0002	0.0004	-0.1520
SYPP	0.1532	0.1772	0.0204	0.1741	0.0794	**0.7257**	0.0140	-0.0166	0.2867	0.2697	0.0733	0.0310	0.0244	-0.0015	0.1089	0.1544	-0.0322	-0.0292	0.756**
HI	-0.2414	-0.2058	-0.0452	0.1688	-0.2154	0.0121	**0.6262**	0.2663	0.3741	0.3324	0.2040	-0.1222	0.1015	0.0327	0.1335	-0.0289	-0.0566	0.0086	0.662**
TW	0.0079	0.0079	0.0092	-0.0015	0.0044	0.0008	-0.0148	**-0.0347**	-0.0082	-0.0083	-0.0020	0.0185	-0.0014	0.0085	-0.0016	0.0059	0.0016	0.0043	0.228*
NFGPP	0.0081	0.0191	-0.0822	0.1027	-0.0187	0.0968	0.1463	0.0582	**0.2449**	0.2341	0.0710	0.0084	0.0282	0.0223	0.0562	-0.0163	-0.0138	-0.0101	0.699**
NTSPP	-0.0246	-0.0307	0.0887	-0.0975	-0.0020	-0.0729	-0.1041	-0.0469	-0.1874	**-0.1960**	-0.0009	0.0053	-0.0074	-0.0140	-0.0341	0.0248	0.0006	0.0094	0.633**
SF	0.0158	0.0134	-0.0175	0.0107	0.0149	-0.0048	-0.0156	-0.0027	-0.0139	-0.0002	**-0.0478**	-0.0071	-0.0104	-0.0044	-0.0067	-0.0091	0.0052	-0.0016	0.301*
PC	-0.0002	-0.0005	0.0012	0.0002	0.0018	0.0005	-0.0021	-0.0057	0.0004	-0.0003	0.0016	**0.0107**	0.0004	0.0010	0.0004	0.0007	0.0022	0.0007	-0.0561
AC	0.0075	0.0077	-0.0030	0.0013	0.0073	-0.0008	-0.0038	-0.0010	-0.0027	-0.0009	-0.0051	-0.0010	**-0.0235**	0.0053	-0.0013	-0.0007	0.0069	0.0091	0.1293
CC	-0.0008	-0.0012	-0.0012	-0.0025	-0.0006	0.0000	-0.0006	0.0027	-0.0010	-0.0008	-0.0010	-0.0010	0.0025	**-0.0109**	-0.0033	-0.0023	-0.0029	-0.0038	0.0392
FC	-0.0002	0.0000	0.0011	0.0031	-0.0027	0.0020	0.0029	0.0006	0.0031	0.0023	0.0019	0.0006	0.0007	0.0041	**0.0135**	0.0015	0.0025	0.0019	0.267*
Fe	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	**0.0000**	0.0000	0.0000	0.1317
Zn	0.0000	0.0002	-0.0015	-0.0003	-0.0006	0.0003	0.0006	0.0003	0.0004	0.0000	0.0007	-0.0014	0.0020	-0.0018	-0.0012	0.0004	**-0.0066**	-0.0018	-0.0922
Ca	0.0004	0.0001	-0.0002	-0.0016	-0.0012	0.0003	-0.0001	0.0010	0.0003	0.0004	-0.0003	-0.0005	0.0031	-0.0029	-0.0012	-0.0031	-0.0022	**-0.0082**	-0.0167
GYPP	-0.1008	-0.0393	-0.0194	0.364*	-0.1520	0.756**	0.662**	0.228*	0.699**	0.633**	0.301*	-0.0561	0.1293	0.0392	0.267*	0.1317	-0.0922	-0.0167	**1.0000**

*** Significant at 5 % ** Significant at 1% Note: Bold figures indicate direct effects.**

DFF- Days to 50% flowering, DM- Days to maturity, NPTPP- Number of productive tillers per plant, PL- Panicle length (cm), PH- Plant height (cm), NTSPP- Number of total spikelets per panicle, NFGPP- Number of filled grains per panicle, SF – Spikelet fertility (%), TW- Test weight (g), SYPP- Straw yield per plant, HI- Harvest index (%), AC- Amylose content, PC- Protein content, CC- Carbohydrate content, FC- Fat content, Fe- Iron content, Zn- Zinc content, Ca- Calcium content & GYPP- Grain yield per plant.

The character number of productive tillers per plant showed positive and low direct effect (0.0042) on grain yield per plant. Similar findings were observed by Nayak *et al.,* (2016). However, it exhibited positive indirect effect *via* spikelet fertility (0.0015), Zn content (0.0010), Fe content (0.0008), amylose content (0.005), protein content (0.005), carbohydrate content (0.005), fat content (0.004), straw yield per plant (0.0001) and Ca content (0.0001). Number of productive tillers per plant exhibited negative indirect effect *via* number of total spikelets per panicle (-0.0019), number of filled grains per panicle (-0.0014), days to maturity (-0.0013), days to fifty per cent flowering (-0.0013), plant height (-0.0012), test weight (-0.0011), panicle length (-0.0006) and harvest index (-0.0003). The resulting phenotypic correlation with the grain yield per plant was negative and non-significant (-0.0194).

Panicle length had positive direct effect (0.0154) on grain yield per plant. Singh *et al.*, (2015) reported similar results. It had positive indirect effect *via* number of total spikelets per panicle (0.0077), number of filled grains per panicle (0.0065), harvest index (0.0042), days to maturity (0.0042), days to fifty percent flowering (0.0037), straw yield per plant (0.0037), carbohydrate content (0.0036), fat content (0.0036), Ca content (0.0031), plant height (0.0031), Fe content (0.0022), Zn content (0.0008), test weight (0.0007) and protein content (0.0003). Panicle length shows negative indirect effect through spikelet fertility (-0.0034), number of productive tillers per plant (-0.0023) and amylose content (-0.0009). The resulting phenotypic correlation with the grain yield per plant was positive and significant (0.364).

Plant height exhibited positive and negligible direct effect (0.0025) on grain yield per plant. For plant height similar results was observed by Singh *et al.,* (2015). It shows positive indirect effect *via* days to fifty per cent flowering (0.0020), days to maturity (0.0019), panicle length (0.0005), protein content (0.0004), Ca content (0.0004), straw yield per plant (0.0003), Zn content (0.0002) and carbohydrate content (0.0001). It had negative indirect effect through harvest index (-0.0009), spikelet fertility (-0.0008), amylose content (-0.0008), number of productive tillers per plant (-0.0007), fat content (-0.0005), test weight (-0.0003), Fe content (-0.0002) and number of filled grains per panicle (-0.0002). This character had no effect on grain yield via number of total spikelets per panicle and this character had non-significant negative correlation with grain yield per plant (-0.1520).

Straw yield per plant had positive high direct effect (0.7257) on the grain yield per plant. Kumar *et al.,* (2022) reported the similar findings. The straw yield per plant exhibited positive and significant indirect effect through number of filled grains per panicle (0.2867), number of total spikelets per panicle (0.2697), days to maturity (0.1772), panicle length (0.1741), Fe content (0.1544), days to fifty percent flowering (0.1532), fat content (0.1089), plant height (0.0794), spikelet fertility (0.733), protein content (0.0310), amylose content (0.244), number of

productive tillers per plant (0.0204) and harvest index (0.0140). However, it had negative indirect effect through Zn content (-0.032), Ca content (-0.0292), test weight (-0.0166) and carbohydrate content (-0.0015). The resulting phenotypic correlation with grain yield per plant was positive and highly significant (0.756).

Harvest index showed positive and direct effect (0.6262) with grain yield per plant. Singh *et al.,* (2018) reported the similar findings. The harvest index showed indirect effect *via* number of filled grains per panicle (0.3741), number of total spikelets per panicle (0.3324), test weight (0.2663), spikelet fertility (0.2040), panicle length (0.1688), fat content (0.1335), amylose content (0.1015), carbohydrate content (0.0327), straw yield per plant (0.0121) and Ca content (0.0086), Whereas, negative indirect effect *via* days to fifty per cent flowering (-0.2414), plant height (-0.2154), days to maturity (-0.2058), protein content (-0.1222), Zn content (-0.0566), number of productive tillers per plant (-0.0452) and Fe content (-0.0289). The resulting phenotypic correlation of harvest index with grain yield per plant was positive and highly significant (0.662).

The test weight exhibited negative direct effect (-0.0347) on the grain yield per plant. In contrast Chuchert *et al.,* (2018) and Saha *et al.,* (2019) reported test weight had positive direct effect on the grain yield per plant. The indirect effect is positive through protein content (0.0185), number of productive tillers per plant (0.0092), carbohydrate content (0.0085), days to fifty percent flowering (0.0079), days to maturity (0.0079), Fe content (0.0059), plant height (0.0044), Ca content (0.0043), Zn content (0.0016) and straw yield per plant (0.0008), whereas harvest index (-0.0148), number of total spikelets per panicle (-0.0083), number of filled grains per panicle (-0.0082), spikelet fertility (-0.0020), fat content (-0.0016), panicle length (-0.0015) and amylose content (-0.0014) shows negative and low indirect effect. This character significant positive correlation with grain yield per plant (0.228) at phenotypic level.

The direct effect of number of filled grains per panicle on the grain yield per plant was positive (0.2449). Similar findings was observed by Nayak *et al.,* (2016), while Saha *et al.,* (2019) reported that number of filled grains per panicle had negative direct effect on the grain yield per plant. The number of filled grains per panicle had positive indirect effect on the grain yield per plant *via* number of total spikelets per panicle (0.2341), harvest index (0.1463), panicle length (0.1027), straw yield per plant (0.0968), spikelet fertility (0.0710), test weight (0.0582), fat content (0.0562), amylose content (0.0282), carbohydrate content (0.0223), days to maturity (0.0191), protein content (0.0084) and days to fifty percent flowering (0.0081), while the characters number of productive tillers per plant (-0.0822), plant height (-0.0187), Fe content (-0.0163), Zn content (-0.0138) and Ca content (-0.0101) showed negative indirect effect on the grain yield per plant. The resulting phenotypic correlation of number of filled grains per panicle with the grain yield per plant was highly significant and positive (0.699).

The character number of total spikelets per panicle had negative direct effect (-0.1960) on grain yield per plant. Similar findings was observed by Nayak *et al.,* (2016), while Chuchert *et al.,* (2018) reported that number of total spikelets per panicle had positive direct effect on the grain yield per plant. Number of total spikelets per panicle had positive indirect effect through characters like number of productive tillers per plant (0.0887), Fe content (0.0248), Ca content (0.0094), Protein content (0.0053) and Zn content (0.0006). Number of total spikelets per panicle shows negative indirect effect on grain yield per plant through number of filled grains per panicle (-0.1874), harvest index (-0.1041), panicle length (-0.0975), straw yield per plant (-0.0729), test weight (-0.0469), fat content (-0.0341), days to maturity (-0.0307) and days to fifty percent flowering (-0.0246), carbohydrate content (-0.0140), amylose content (-0.0074), plant height (-0.0020) and spikelet fertility (-0.0009). The number of total spikelets per panicles phenotypic correlation with the grain yield per plant was positive and highly significant (0.633).

Spikelet fertility exhibited negative direct effect (-0.0478) with grain yield per plant. Nayak *et al.,* (2016) reported the same results. Spikelet fertility had positive indirect effect *via* characters days to fifty percent flowering (0.0158), plant height (0.0149), days to maturity (0.0134), panicle length (0.0107) and Zn content (0.0052), whereas negative indirect effect through number of productive tillers per plant (-0.0175), harvest index (-0.0156), number of filled grains per panicle (-0.0139), amylose content (-0.0104), Fe content (-0.0091), protein content (-0.0071), fat content (-0.0067), straw yield per plant (-0.0048), carbohydrate content (-0.0044), test weight (-0.0027), Ca content (-0.0016) and number of total spikelets per panicle (-0.0002). This characters phenotypic correlation with the grain yield per plant was positive and significant (0.301).

The direct effect of protein content on grain yield per plant was positive and low (0.0107). Archana *et al.,* (2018) is in conformity with these results. However, Basavaraja *et al.,* (2013) reported that the direct effect of protein content on grain yield per plant was negative and low. Protein content had positive indirect effect on grain yield per plant *via* Zn content (0.0022), plant height (0.0018), spikelet fertility (0.0016), number of productive tillers per plant (0.0012), carbohydrate content (0.0010), Fe content (0.0007), Ca content (0.0007), straw yield per plant (0.0005), number of filled grains per panicle (0.0004), amylose content (0.0004), fat content (0.0004) and panicle length (0.0002), whereas it had negative indirect effect through test weight (-0.0057), harvest index (-0.0021), days to maturity (-0.0005), number of total spikelets per panicle (-0.0003) and days to fifty percent flowering (-0.0002). The resulting phenotypic correlation of protein content with the grain yield per plant was negative and non-significant (-0.0561).

Amylose content had negative direct effect (-0.0235) on grain yield per plant. Basavaraja *et al.,* (2013) reported that the direct effect of amylose content on grain yield per plant was positive and low. Amylose content had positive indirect effect through characters Ca content (0.0091), days to maturity (0.0077), days to fifty per cent flowering (0.0075), plant height (0.0073), Zn content (0.0069), carbohydrate content (0.0053) and panicle length (0.0013). However, amylose content had negative indirect effect through spikelet fertility (-0.0051), harvest index (-0.0038), number of productive tillers per plant (-0.0030), number of filled grains per panicle (-0.0027), fat content (-0.0013), test weight (-0.0010), protein content (-0.0010), number of total spikelets per panicle (-0.0009), straw yield per plant (-0.0008) and Fe content (-0.0007). Amylose contents phenotypic correlation with the grain yield per plant was positive and non- significant (0.1293).

The direct effect of carbohydrate content on grain yield per plant was negative and low (-0.0109). Carbohydrate content had positive indirect effect on grain yield per plant *via* test weight (0.0027) and amylose content (0.0025), whereas it had negative indirect effect through Ca content (-0.0038), fat content (-0.0033), Zn content (-0.0029), panicle length (-0.0025), Fe content (-0.0023), number of productive tillers per plant (-0.0012), days to maturity (-0.0012), number of filled grains per panicle (-0.0010), spikelet fertility (-0.0010), protein content (-0.0010), number of total spikelets per panicle (-0.0008), days to fifty percent flowering (-0.0008), plant height (-0.0006), and harvest index (-0.0006). carbohydrate content had no any effect on grain yield per plant through straw yield per plant and resulting phenotypic correlation with the grain yield per plant was positive and non-significant (0.0392).

Fat content exhibited positive direct effect (0.0135) with grain yield per plant and positive indirect effect through carbohydrate content (0.0041), panicle length (0.0031), number of filled grains per panicle (0.0031), harvest index (0.0029), Zn content (0.0025), number of total spikelets per panicle (0.0023), straw yield per plant (0.0020), spikelet fertility (0.0019), Ca content (0.0019), Fe content (0.0015), number of productive tillers per plant (0.0011) amylose content (0.0007), protein content (0.0006) and test weight (0.0006), whereas negative indirect effect through plant height (-0.0027) and days to fifty percent flowering (-0.0002). Fat content had no any effect on grain yield per plant through days to maturity and phenotypic correlation with the grain yield per plant was positive and significant (0.267).

The micronutrient parameter iron content had no any direct or indirect effect with grain yield per plant through any character under study and phenotypic correlation with grain yield per plant was positive but non-significant (0.1317). Archana *et al.,* (2018) recorded direct effect of iron content on grain yield per plant is negative and low.

The direct effect of Zn content on grain yield per plant was negative and negligible (-0.0066). Archana *et al.,* (2018) recorded direct effect of zinc content on grain yield per plant is positive and low. Zinc content had positive indirect effect on grain yield per plant through characters amylose content (0.0020), spikelet fertility (0.0007), harvest index (0.0006), number of filled grains per panicle (0.0004), Fe content (0.0004), straw yield per plant (0.0003), test weight (0.0003) and days to maturity (0.0002), whereas it had negative indirect effect through carbohydrate content (-0.0018), Ca content (-0.0018), number of productive tillers per plant (-0.0015), protein content (-0.0014), fat content (-0.0012) plant height (-0.0006), panicle length (-0.0003). Zinc content exhibited no any direct and indirect effect on grain yield per plant through number of total spikelets per panicle and days to fifty percent flowering and resulting phenotypic correlation of Zn content with the grain yield per plant was negative and non-significant (-0.0922).

Ca content showed negative direct effect (-0.0082) with grain yield per plant and positive indirect effect through amylose content (0.0031), test weight (0.0010), days to fifty per cent flowering (0.0004), number of total spikelets per panicle (0.0004), straw yield per plant (0.0003), number of filled grains per panicle (0.0003), days to maturity (0.0001), whereas negative indirect effect through Fe content (-0.0031), carbohydrate content (-0.0029), Zn content (-0.0022), panicle length (-0.0016), Fat content (-0.0012), plant height (-0.0012), protein content (-0.0005), spikelet fertility (-0.0003), number of productive tillers per plant (-0.0002) and harvest index (-0.0001). The resulting phenotypic correlation with the grain yield per plant was negative and non-significant (-0.0167).

4.3.2 Genotypic correlation coefficient partitioned for path coefficient analysis

The genotypic correlation coefficients for path-coefficient analysis were splits into direct and indirect effects are presented in Table 4.8 and the cause-and-effect relationship is diagrammatically represented in figure 4.5

Days to fifty per cent flowering expressed negative direct effect (-0.2970) on grain yield per plant. Singh *et al.,* (2018) reported same results which support the present findings, while Saha *et al.,* (2019) reported days to fifty per cent flowering had positive direct effect on grain yield per plant. It had positive indirect effect *via* harvest index (0.1346), spikelet fertility (0.1052), amylose content (0.1048), number of productive tillers per plant (0.0997), test weight (0.0682), Fe content (0.0235), Ca content (0.0142), fat content (0.0115) and protein content (0.0045). It had negative indirect effect through days to maturity (-0.2951), plant height (-0.2341), panicle length (-0.0813), straw yield per plant (-0.0764), number of total spikelets per panicle (-0.0372), carbohydrate content (-0.0223), number of filled grains per panicle (-0.0098)

and Zn content (-0.0017). The resulting genotypic correlation with grain yield per plant was non-significant negative (-0.1117).

Days to maturity had positive direct effect (0.4950) on grain yield per plant. Same findings were observed by Singh *et al.,* (2018). In contrast negative direct effect on grain yield per plant was reported by Saha *et al.,* (2019). This character showed positive indirect effect through days to fifty per cent flowering (0.4917), plant height (0.3704), panicle length (0.1636), straw yield per plant (0.1480), number of total spikelets per panicle (0.0770), carbohydrate content (0.0623), number of filled grains per panicle (0.0379), while negative indirect effects *via* harvest index (-0.2037), amylose content (-0.1857), number of productive tillers per plant (-0.1569), spikelet fertility (-0.1516), test weight (-0.1147), Fe content (-0.0272), protein content (-0.0247), Zn content (-0.0153) Ca content (-0.0061) and fat content (-0.0048). However, this character exhibited non-significant negative genotypic correlation with grain yield per plant (-0.0583).

The number of productive tillers per plant showed positive direct effect (0.0500) on grain yield per plant. Similar kind of results were obtained by Singh *et al.,* (2018) and Saha *et al.,* (2019). It exhibited positive indirect effect through spikelet fertility (0.0200), Zn content (0.0115), fat content (0.0097), Fe content (0.0092), carbohydrate content (0.0068), protein content (0.0060), amylose content (0.0056) and Ca content (0.0020), whereas negative indirect effect *via* number of total spikelets per panicle (-0.0240), number of filled grains per panicle (-0.0178), days to fifty percent flowering (-0.0168), days to maturity (-0.0159), test weight (-0.0142), plant height (-0.0140), panicle length (-0.0092) harvest index (-0.0023) and straw yield per plant (-0.0001). The resulting genotypic correlation with the grain yield per plant was negative and non-significant (-0.0372).

Panicle length had negative direct effect (-0.0917) on grain yield per plant. Similar findings was observed by Singh *et al.*, (2018) In contrast positive direct effect on grain yield per plant reported by Saha *et al.,* (2019). It had positive indirect effect *via* spikelet fertility (0.0234), number of productive tillers per plant (0.0169), amylose content (0.0054) and Zn content (0.0005), whereas negative indirect effect through number of total spikelets per panicle (-0.0530), number of filled grains per panicle (-0.0452), harvest index (-0.0361), straw yield per plant (-0.0318), days to maturity (-0.0303), days to fifty per cent flowering (-0.0251), carbohydrate content (-0.0256), fat content (-0.0237), Ca content (-0.0214), plant height (-0.0223), Fe content (-0.0125), test weight (-0.0055) and protein content (-0.0018). The genotypic correlation of panicle length with the grain yield per plant was positive and highly significant (0.462).

Table 4.8 Path analysis for various characters at genotypic level in rice genotypes

	DFF	DM	NPTPP	PL	PH	SYPP	HI	TW	NFGPP	NTSPP	SF	PC	AC	CC	FC	Fe	Zn	Ca	GYPP
DFF	**-0.2970**	-0.2951	0.0997	-0.0813	-0.2341	-0.0764	0.1346	0.0682	-0.0098	-0.0372	0.1052	0.0045	0.1048	-0.0223	0.0115	0.0235	-0.0017	0.0142	-0.1117
DM	0.4917	**0.4950**	-0.1569	0.1636	0.3704	0.1480	-0.2037	-0.1147	0.0379	0.0770	-0.1516	-0.0247	-0.1857	0.0623	-0.0048	-0.0272	-0.0153	-0.0061	-0.0583
NPTPP	-0.0168	-0.0159	**0.0500**	-0.0092	-0.0140	-0.0010	-0.0023	-0.0142	-0.0178	-0.0240	0.0200	0.0060	0.0056	0.0068	0.0097	0.0092	0.0115	0.0020	-0.0372
PL	-0.0251	-0.0303	0.0169	**-0.0917**	-0.0223	-0.0318	-0.0361	-0.0055	-0.0452	-0.0530	0.0234	-0.0018	0.0054	-0.0256	-0.0237	-0.0125	0.0005	-0.0214	0.462**
PH	-0.1458	-0.1384	0.0519	-0.0449	**-0.1849**	-0.0262	0.0768	0.0239	0.0151	-0.0017	0.0651	-0.0309	0.0626	-0.0117	0.0529	0.0145	-0.0184	-0.0282	-0.1641
SYPP	0.2174	0.2527	-0.0177	0.2931	0.1196	**0.8452**	0.1881	-0.0235	0.4254	0.4012	0.1004	0.0391	0.0662	-0.0105	0.1272	0.2258	-0.0180	-0.0965	0.804**
HI	-0.2425	-0.2202	-0.0246	0.2105	-0.2223	0.1191	**0.5350**	0.2699	0.3818	0.3360	0.2448	-0.1298	0.1036	0.0890	0.2134	-0.0268	-0.0681	0.0388	0.756**
TW	-0.0453	-0.0457	-0.0558	0.0119	-0.0255	-0.0055	0.0994	**0.1970**	0.0468	0.0475	0.0110	-0.1072	0.0077	-0.0509	0.0115	-0.0358	-0.0089	-0.0279	0.252*
NFGPP	-0.1273	-0.2956	1.3765	-1.9051	0.3145	-1.9433	-2.7551	-0.9172	**-3.8606**	-3.7066	-1.1685	-0.1364	-0.5242	-0.3898	-1.2993	0.2748	0.2408	0.1647	0.776**
NTSPP	0.4513	0.5608	-1.7292	2.0843	0.0332	1.7113	2.2636	0.8698	3.4608	**3.6046**	0.1108	-0.0953	0.1561	0.3129	0.8751	-0.4766	-0.0138	-0.1953	0.699**
SF	-0.3188	-0.2756	0.3602	-0.2293	-0.3167	0.1068	0.4116	0.0504	0.2723	0.0276	**0.8997**	0.1450	0.2548	0.0705	0.2714	0.1808	-0.1212	0.0454	0.374**
PC	-0.0044	-0.0144	0.0346	0.0055	0.0482	0.0134	-0.0700	-0.1569	0.0102	-0.0076	0.0465	**0.2884**	0.0164	0.0352	0.0102	0.0200	0.0598	0.0159	-0.0732
AC	-0.0509	-0.0542	0.0162	-0.0085	-0.0489	0.0113	0.0279	0.0057	0.0196	0.0063	0.0409	0.0082	**0.1443**	-0.0397	0.0257	0.0028	-0.0439	-0.0648	0.1631
CC	0.0031	0.0051	0.0055	0.0113	0.0026	-0.0005	0.0068	-0.0105	0.0041	0.0035	0.0032	0.0049	-0.0112	**0.0406**	0.0195	0.0107	0.0122	0.0174	0.0899
FC	-0.0022	-0.0005	0.0109	0.0146	-0.0161	0.0085	0.0225	0.0033	0.0190	0.0137	0.0170	0.0020	0.0101	0.0271	**0.0564**	0.0045	0.0111	0.0118	0.353*
Fe	0.0147	0.0102	-0.0341	-0.0254	0.0145	-0.0496	0.0093	0.0337	0.0132	0.0246	-0.0373	-0.0129	-0.0036	-0.0492	-0.0148	**-0.1858**	0.0189	-0.0873	0.1489
Zn	-0.0013	0.0070	-0.0521	0.0013	-0.0225	0.0048	0.0287	0.0101	0.0141	0.0009	0.0304	-0.0468	0.0686	-0.0676	-0.0446	0.0230	**-0.2258**	-0.0729	-0.0949
Ca	-0.0126	-0.0033	0.0108	0.0614	0.0402	-0.0301	0.0191	-0.0373	-0.0112	-0.0143	0.0133	0.0145	-0.1183	0.1129	0.0552	0.1239	0.0851	**0.2636**	-0.0266
GYPP	-0.1117	-0.0583	-0.0372	0.462**	-0.1641	0.804**	0.756**	0.252*	0.776**	0.699**	0.374**	-0.0732	0.1631	0.0899	0.353*	0.1489	-0.0949	-0.0266	**1.0000**

*** Significant at 5 % ** Significant at 1% Note: Bold figures indicate direct effects.**

DFF- Days to 50% flowering, DM- Days to maturity, NPTPP- Number of productive tillers per plant, PL- Panicle length (cm), PH- Plant height (cm), NTSPP- Number of total spikelets per panicle, NFGPP- Number of filled grains per panicle, SF – Spikelet fertility (%), TW- Test weight (g), SYPP- Straw yield per plant, HI- Harvest index (%), AC- Amylose content, PC- Protein content, CC- Carbohydrate content, FC- Fat content, Fe- Iron content, Zn- Zinc content, Ca- Calcium content & GYPP- Grain yield per plant.

Plant height exhibited negative direct effect (-0.1849) on grain yield per plant. Similar results were recorded by Saha *et al.,* (2019), while Singh *et al.,* (2018) obtained positive direct effect on grain yield per plant. Plant height had positive indirect effect *via* harvest index (0.0768), spikelet fertility (0.0651), amylose content (0.0626), fat content (0.0529), number of productive tillers per plant (0.0519), test weight (0.0239), number of filled grains per panicle (0.0151) and Fe content (0.0145). It had negative indirect effect through days to fifty percent flowering (-0.1458), days to maturity (-0.1384), panicle length (-0.0449), protein content (-0.0309), Ca content (-0.0282), straw yield per plant (-0.0262), Zn content (-0.0184), carbohydrate content (-0.0117) and number of total spikelets per panicle (-0.0017) and this character had non-significant negative genotypic correlation with grain yield per plant (-0.1641).

The straw yield per plant had positive and high direct effect (0.8452) on the grain yield per plant. Same results were obtained by Singh *et al.,* (2018) and Kumar *et al.,* (2022) which support the current findings. straw yield per plant had positive indirect effect through number of filled grains per panicle (0.4254), number of total spikelets per panicle (0.4012), panicle length (0.2931), days to maturity (0.2527), Fe content (0.2258), days to fifty per cent flowering (0.2174), harvest index (0.1881), fat content (0.1272), plant height (0.1196), spikelet fertility (0.1004), protein content (0.0391), amylose content (0.0662), However, straw yield per plant had negative indirect effect through Ca content (-0.0965), test weight (-0.0235), Zn content (-0.0180), number of productive tillers per plant (-0.0177) and carbohydrate content (-0.0105). The resulting genotypic correlation of straw yield per plant with grain yield per plant was positive and highly significant (0.804).

Harvest index showed positive direct effect (0.5350) with grain yield per plant and this finding is supported by Kumar *et al.,* (2022). Harvest index had indirect effect through number of filled grains per panicle (0.3818), number of total spikelets per panicle (0.3360), test weight (0.2699), spikelet fertility (0.2448), fat content (0.2134), panicle length (0.2105), straw yield per plant (0.1191), amylose content (0.1036), carbohydrate content (0.0890), and Ca content (0.0388), Whereas, negative indirect effect *via* days to fifty per cent flowering (-0.2425), plant height (-0.2223), days to maturity (-0.2202), protein content (-0.1298), Zn content (-0.0681), Fe content (-0.0268) and number of productive tillers per plant (-0.0246). The resulting genotypic correlation of harvest index with grain yield per plant was positive and highly significant (0.756).

The test weight exhibited positive direct effect (0.1970) on the grain yield per plant. Similar results were obtained by Saha *et al.,* (2019). The positive indirect effect through harvest index (0.0994), number of total spikelets per panicle (0.0475), number of filled grains per panicle (0.0468), panicle length (0.0119), fat content (0.0115), spikelet fertility (0.0110), and amylose content (0.0077), whereas negative indirect effect through protein content (-0.1072), number of

productive tillers per plant (-0.0558), carbohydrate content (-0.0509), days to maturity (-0.0457), days to fifty per cent flowering (-0.0453), Fe content (-0.0358), Ca content (-0.0279), plant height (-0.0255), Zn content (-0.0089) and straw yield per plant (-0.0055). This character shows positive and significant correlation with grain yield per plant (0.252) at genotypic level.

The direct effect of number of filled grains per panicle on the grain yield per plant was negative (-3.8606) similar results reported by Saha *et al.,* (2019). The number of filled grains per panicle showed positive indirect effect with grain yield per plant *via* number of productive tillers per plant (1.3765), plant height (0.3145), Fe content (0.2748), Zn content (0.2408) and Ca content (0.1647), while negative indirect effect on grain yield per plant through number of total spikelets per panicle (-3.7066), harvest index (-2.7551), straw yield per plant (-1.9433), panicle length (-1.9051), spikelet fertility (-1.1685), fat content (-1.2993), test weight (-0.9172), amylose content (-0.5242), carbohydrate content (-0.3898), days to maturity (-0.2956), protein content (-0.1364) and days to fifty per cent flowering (-0.1273). The resulting genotypic correlation of number of filled grains per panicle with the grain yield per plant was highly significant and positive (0.776).

The number of total spikelets per panicle had positive and very high direct effect (3.6046) on grain yield per plant. Similar results were obtained by Saha *et al.,* (2019). Number of total spikelets per panicle exhibited positive indirect effect through characters like number of filled grains per panicle (3.4608), harvest index (2.2636), panicle length (2.0843), straw yield per plant (1.7113), fat content (0.8751), test weight (0.8698), days to maturity (0.5608), days to fifty per cent flowering (0.4513), carbohydrate content (0.3129), amylose content (0.1561), spikelet fertility (0.1108) and plant height (0.0332). This character shows negative indirect effect on grain yield per plant through number of productive tillers per plant (-1.7292), Fe content (-0.4766), Ca content (-0.1953), Protein content (-0.0953) and Zn content (-0.0138). The correlation between number of total spikelets per panicle and the grain yield per plant was positive and highly significant (0.699) at genotypic level.

Spikelet fertility exhibited positive direct effect (0.8997) with grain yield per plant and similar results reported by Singh *et al.,* (2018). Spikelet fertility had positive indirect effect *via* characters harvest index (0.4116), number of productive tillers per plant (0.3602), number of filled grains per panicle (0.2723), fat content (0.2714), amylose content (0.2548), Fe content (0.1808), protein content (0.1450), straw yield per plant (0.1068), carbohydrate content (0.0705), test weight (0.0504), Ca content (0.0454) and number of total spikelets per panicle (0.0276), whereas negative indirect effect through days to fifty percent flowering (-0.3188), plant height (-0.3167), days to maturity (-0.2756), panicle length (-0.2293) and Zn content (-0.1212). This characters genotypic correlation with the grain yield per plant was positive and highly significant (0.374).

The direct effect of protein content on grain yield per plant was positive (0.2884). Archana *et al.,* (2018) is in conformity with these results. However, Basavaraja *et al.,* (2013) reported that the direct effect of protein content on grain yield per plant was negative and low. Protein content had positive indirect effect on grain yield per plant *via* Zn content (0.0598), plant height (0.0482), spikelet fertility (0.0465), number of productive tillers per plant (0.0346), carbohydrate content (0.0352), Fe content (0.0200), amylose content (0.0164), Ca content (0.0159), straw yield per plant (0.0134), number of filled grains per panicle (0.0102), fat content (0.0102) and panicle length (0.0055), whereas negative indirect effect through test weight (-0.1569), harvest index (-0.0700), days to maturity (-0.0144), number of total spikelets per panicle (-0.0076) and days to fifty per cent flowering (-0.0044). The resulting genotypic correlation of protein content with the grain yield per plant was negative and non-significant (-0.0732).

Amylose content had positive direct effect (0.1443) on grain yield per plant. Basavaraja *et al.,* (2013) reported that the direct effect of amylose content on grain yield per plant was positive and low. Amylose content had positive indirect effect through characters spikelet fertility (0.0409), harvest index (0.0279), fat content (0.0257), number of filled grains per panicle (0.0196), number of productive tillers per plant (0.0162), straw yield per plant (0.0113), protein content (0.0082), number of total spikelets per panicle (0.0063), test weight (0.0057) and Fe content (0.0028). However, amylose content had negative indirect effect through Ca content (-0.0648), days to maturity (-0.0542), days to fifty per cent flowering (-0.0509), plant height (-0.0489), Zn content (-0.0439), carbohydrate content (-0.0397) and panicle length (-0.0085). Amylose contents genotypic correlation with the grain yield per plant was positive but non-significant (0.1631).

The direct effect of carbohydrate content on grain yield per plant was positive and low (0.0406). Carbohydrate content had positive indirect effect on grain yield per plant *via* fat content (0.0195), Ca content (0.0174), Zn content (0.0122), panicle length (0.0113), Fe content (0.0107), harvest index (0.0068), number of productive tillers per plant (0.0055), days to maturity (0.0051), protein content (0.0049), number of filled grains per panicle (0.0041), number of total spikelets per panicle (0.0035), spikelet fertility (0.0032), and days to fifty percent flowering (0.0031), plant height (0.0026), whereas negative indirect effect through amylose content (-0.0112), test weight (-0.0105) and straw yield per plant (-0.0005). The resulting genotypic correlation of carbohydrate content with grain yield per plant was positive and non-significant (0.0899).

Fat content exhibited positive direct effect (0.0564) on grain yield per plant and positive indirect effect through carbohydrate content (0.0271), harvest index (0.0225), number of filled

grains per panicle (0.0190) panicle length (0.0146), spikelet fertility (0.0170), number of total spikelets per panicle (0.0137), Ca content (0.0118), Zn content (0.0111), number of productive tillers per plant (0.0109), amylose content (0.0101) straw yield per plant (0.0085), Fe content (0.0045), test weight (0.0033) and protein content (0.0020), whereas negative indirect effect through plant height (-0.0161), days to fifty per cent flowering (-0.0022) and days to maturity (-0.0005). The genotypic correlation with the grain yield per plant was positive and significant (0.353).

The micronutrient parameter iron content had negative direct effect (-0.1858) on grain yield per plant. Archana *et al.,* (2018) recorded the direct effect of iron content on grain yield per plant is positive and high. Iron content had positive indirect effect through test weight (0.0337), number of total spikelets per panicle (0.0246), Zn content (0.0189), days to fifty per cent flowering (0.0147), plant height (0.0145), number of filled grains per panicle (0.0132), days to maturity (0.0102), harvest index (0.0093). Iron content had negative indirect effect via Ca content (-0.0873), straw yield per plant (-0.0496), carbohydrate content (-0.0492), spikelet fertility (-0.0373), number of productive tillers per plant (-0.0341), panicle length (-0.0254), fat content (-0.0148), protein content (-0.0129) and amylose content (-0.0036). The genotypic correlation of iron content with grain yield per plant was positive but non-significant (0.1489).

The direct effect of zinc content on grain yield per plant was negative (-0.2258). Archana *et al.,* (2018) recorded direct effect of zinc content on grain yield per plant is negative and high. Zinc content had positive indirect effect on grain yield per plant through characters amylose content (0.0686), spikelet fertility (0.0304), harvest index (0.0287), Fe content (0.0230), number of filled grains per panicle (0.0141), test weight (0.0101), days to maturity (0.0070), straw yield per plant (0.0048), panicle length (0.0013), number of total spikelets per panicle (0.0009), whereas negative indirect effect through carbohydrate content (-0.0676), Ca content (-0.0729), number of productive tillers per plant (-0.0521), protein content (-0.0468), fat content (-0.0446), plant height (-0.0225) and days to fifty per cent flowering (-0.0013). The genotypic correlation of Zn content with the grain yield per plant was negative and non-significant (-0.0949).

Calcium content showed positive direct effect (0.2636) on grain yield per plant and positive indirect effect through Fe content (0.1239), carbohydrate content (0.1129), Zn content (0.0851), panicle length (0.0614), Fat content (0.0552), plant height (0.0402), harvest index (0.0191), protein content (0.0145), spikelet fertility (0.0133) and number of productive tillers per plant (0.0108). Calcium content exhibited negative indirect effect through amylose content (-0.1183), test weight (-0.0373), straw yield per plant (-0.0301), number of total spikelets per panicle (-0.0143), days to fifty percent flowering (-0.0126), number of filled grains per panicle

(-0.0112), days to maturity (-0.0033). The genotypic correlation of Ca content with the grain yield per plant was negative and non-significant (-0.0266).

4.4 GENETIC DIVERGENCE (D^2 ANALYSIS)

Genetic divergence analysis and D^2 values were calculated with Mahalanobis's D^2 statistics among all the characters under study for twenty-five rice genotypes.

4.4.1 Clustering pattern of genotypes

Tocher method proposed by Rao (1952) is used to form the clusters. Table 4.9 showed the distribution of the twenty-five rice genotypes in the different clusters and figure 4.6 showed the clustering by tocher method.

Considering the magnitude of D^2 values, the twenty-five rice genotypes were grouped in 6 clusters. Among the 6 clusters, cluster II accommodated a greater number of genotypes (9 genotypes) followed by cluster III and cluster IV having same number of genotypes (5 genotypes each), cluster I (4 genotypes), cluster V (1 genotype) and cluster VI (1 genotype).

Table 4.9 Distribution of 25 genotypes into SIX different clusters

Cluster Group	No. of Genotypes
I	**4** (DPL-5, DPL-8, DPL-9 & DPL-24)
II	**9** (DPL-17, DPL-18, DPL-25, DPL-20, DPL-12, DPL-15, DPL-23, DPL-16 & DPL-7)
III	**5** (DPL-13, DPL-21, DPL-10, DPL-2 & DPL-14)
IV	**5** (DPL-1, DPL-19, DPL-6, DPL-11 & DPL-4)
V	**1** (DPL-22)
VI	**1** (DPL-3)

The genotypes having common genetic makeup may be grouped in similar cluster irrespective of their origin. Same results were confirmed by Chandramohan *et al.,* (2016) and Soundharya *et al*., (2020). Chandramohan *et al.,* (2016) grouped 44 rice genotypes into 11 clusters and Soundharya *et al*., (2020) grouped 20 genotypes into 4 cluster.

4.4.2 Average intra and inter cluster divergence

The average intra and inter cluster D^2 values are given in Table 4.10 and average intra and inter cluster distances (D) = ($\sqrt{D^2}$) are given in Table 4.11 and depicted in figure 4.7.

Table 4.10 Average intra and inter cluster values in six clusters (D^2) in rice

	I	II	III	IV	V	VI
I	167.05	473.83	921.17	898.94	1014.34	358.09
II		230.42	377.04	405.72	381.83	1013.13
III			171.85	469.26	610.21	1428.90
IV				315.33	506.41	1407.53
V					0.00	1964.48
VI						0.00

Table 4.11 Average intra and inter cluster distance in six clusters (D) = ($\sqrt{D^2}$) in rice

Clusters	I	II	III	IV	V	VI
I	12.92	21.77	30.35	29.98	31.85	18.92
II		15.18	19.42	20.14	19.54	31.83
III			13.11	21.66	24.70	37.80
IV				17.76	22.50	37.52
V					0.00	44.32
VI						0.00

The maximum intra-cluster D^2 value was observed for cluster IV (315.33) followed by cluster II (230.42), cluster III (171.85), cluster I (167.05), whereas both cluster V and cluster VI observed zero intra-cluster D^2 values. Devi *et al*., (2019) reported similar findings for maximum intra-cluster value in cluster IV.

The maximum inter-cluster D^2 value was observed between cluster V and cluster VI (1964.48), then between cluster III and cluster VI (1428.90), cluster IV and cluster VI (1407.53), cluster I and cluster V (1014.34) and cluster II and cluster VI (1013.13), whereas minimum inter-cluster D^2 values was recorded between cluster I and cluster VI (358.09) then between cluster II and cluster III (377.04), cluster II and cluster V (381.83), cluster II and cluster IV (405.72) and cluster III and cluster IV (469.26). Umesh *et al.,* (2016) recorded similar results with maximum inter-cluster D^2 value between cluster III and cluster IV.

The maximum inter-cluster distance was observed for cluster IV (17.76) followed by cluster II (15.18), cluster III (13.11), cluster I (12.92), whereas both cluster V and cluster VI observed zero intra-cluster distance. Similar findings reported by Devi *et al*. (2019) for maximum intra-cluster distance in cluster IV.

The maximum inter-cluster distance was observed between cluster V and cluster VI (44.32), then between cluster III and cluster VI (37.80), cluster IV and cluster VI (37.52), cluster I and cluster V (31.85) and cluster II and cluster VI (31.83), whereas minimum inter-cluster distance was recorded between cluster I and cluster VI (18.92) then between cluster II and cluster III (19.42), cluster II and cluster V (19.54), cluster II and cluster IV (20.14) and cluster III and

cluster IV (21.66). Umesh *et al.,* (2016) recorded similar results with maximum inter-cluster distance between cluster III and cluster IV. Chandramohan *et al.,* (2016) recorded maximum inter-cluster distance between cluster IV and cluster V. The genotypes which included in genetically diverse clusters may be use for further crop improvement programme in rice.

4.4.3 Cluster means for different characters

The cluster means for nineteen traits among all twenty-five rice genotypes are provided in Table 4.12

The cluster mean values for days to fifty percent flowering ranged from 81.53 in cluster III to 122.67 in cluster VI with a population mean of 100.48. For days to maturity cluster mean values varied from 110.73 (cluster III) to 150.00 (cluster VI) and population mean was 130.29. The least cluster mean value for number of productive tillers per plant was observed in cluster V (5.67), while largest mean value observed in cluster III (7.93) with a population mean of 6.81. The cluster mean values for panicle length (cm) ranged from 21.36 cm in cluster III to 25.15 cm cluster IV with a population mean of 23.34 cm. The values of cluster mean for the character plant height (cm) varied from 87.37 cm (cluster V) to 160.2 cm (cluster VI) and population mean 118.55 cm. For grain yield per plant cluster mean varied from 12.45 g in cluster VI to 20.28 g in cluster IV, while its population mean was 15.46 g. For the character straw yield per plant (g) less cluster mean value observed in cluster III (20.80 g), while the largest mean in cluster IV (26.52 g) with a population mean of 23.99 g. The cluster VI (33.64 %) had minimum cluster mean for character harvest index (%), whereas maximum in cluster VI (42.96 %) with population mean of 38.91 %. The cluster mean value for test weight varied from 14.31 g in cluster VI to 33.09 g in cluster V with a population mean of 22.84 g. A considerable amount of variation was observed for number of filled grains per panicle with maximum cluster mean value in cluster IV (155.54), while minimum cluster mean value in cluster III (81.19) and population mean was 109.99. The cluster mean values for number of total spikelets per panicle varied from 103.54 in cluster III to 191.06 in cluster IV and population mean of 143.12. Range of cluster mean values for spikelet fertility was from 73.02 % (cluster VI) to 81.42 % (cluster IV) with a population mean of 76.66 %.

A good amount of variation was observed for protein content with mean values varied from cluster V (4.37 %) to cluster VI (8.68 %) and population mean was 6.41 %. For the character amylose content cluster mean values varied from 19.06 % (cluster II) to 20.89 % (cluster VI) with population mean of 20.17 %. Range of cluster mean values for carbohydrate content was from 79.68 % (cluster VI) to 82.52 % (cluster V) with a population mean of 80.99 %. The least cluster mean value for fat content was observed in cluster I (15.01 %), while the largest mean value observed in cluster V (17.28 %) with a population mean of 15.99 %.

Table 4.12 Cluster mean performance of nineteen characters in rice genotypes

Sr. No.	Characters	Clusters						Population mean
		I	II	III	IV	V	VI	
1	Days to fifty percent flowering	114.08	98.04	81.53	92.20	94.33	122.67	100.48
2	Days to maturity	145.42	127.85	110.73	123.73	124.00	150.00	130.29
3	Number of productive tillers per plant	6.62	6.70	7.93	6.76	5.67	7.20	6.81
4	Panicle length (cm)	24.30	23.68	21.36	25.15	23.33	22.20	23.34
5	Plant height (cm)	141.97	119.76	93.72	108.29	87.37	160.2	118.55
6	Grain yield per plant (g)	14.02	15.02	12.85	20.28	18.15	12.45	15.46
7	Straw yield per plant (g)	25.12	22.06	20.80	26.52	24.88	24.53	23.99
8	Harvest Index (%)	35.86	40.39	38.39	42.96	42.20	33.64	38.91
9	Test weight (g)	20.75	24.76	21.10	23.02	33.09	14.31	22.84
10	Number of filled grains per panicle	99.05	112.62	81.19	155.54	128.99	82.53	109.99
11	Number of total spikelets per panicle	134.61	151.46	103.54	191.06	165.00	113.02	143.12
12	Spikelet fertility (%)	74.22	74.68	78.44	81.42	78.18	73.02	76.66
13	Protein (%)	5.66	5.85	6.54	7.36	4.37	8.68	6.41
14	Amylose (%)	19.18	19.06	20.83	20.66	20.38	20.89	20.17
15	Carbohydrate (%)	80.29	81.16	82.12	80.17	82.52	79.68	80.99
16	Fat (%)	15.01	15.91	15.91	15.77	17.28	16.04	15.99
17	Fe (ppm)	16.12	15.62	17.13	16.38	15.30	16.87	16.24
18	Zn (ppm)	12.22	11.41	12.05	10.08	9.90	7.32	10.50
19	Ca (ppm)	90.39	90.70	91.65	82.25	56.28	56.71	78.00

The cluster V (15.30 ppm) had minimum cluster mean for Fe content, whereas maximum in cluster III (17.13 ppm) with a population mean of 16.24 ppm. For the character Zn content cluster mean values varied from 7.32 ppm (cluster VI) to 12.22 ppm (cluster I) with population mean of 10.50 ppm. The cluster mean value for Ca content ranged from 56.28 ppm in cluster V to 90.70 ppm in cluster II with a population mean of 78.00 ppm.

4.4.4 Character contribution towards divergence

Number of times that each of the nineteen traits expressed in first rank and its corresponding percent contribution towards genetic divergence is given in Table 4.13. Figure 4.8 showed the pie chart of percent contribution towards genetic divergence. The contribution of grain yield per plant (15.77 %) was highest towards genetic divergence by taking 48 times ranking first followed by straw yield per plant (12.32 %) by 37 times, harvest index (8.5 %) by 26 times, test weight (8.22 %) by 25 times, number of total spikelets per panicle (7.88 %) by 24 times, number of filled grains per panicle (7.43 %) by 23 times, days to fifty percent flowering (4.34%) by 13 times, protein content (4.32 %) by 13 times, panicle length (3.88 %) by 12 times, days to maturity (3.76 %) by 11 times, number of productive tillers per plant (3.76 %) by 11 times respectively to the genetic divergence.

Table 4.13 Contribution of various characters towards divergence in rice genotypes

Sr. No.	Source	Contribution %	Times ranked 1st
1	Days to fifty percent flowering	4.34	13
2	Days to maturity	3.76	11
3	Number of productive tillers per plant	3.76	11
4	Panicle length (cm)	3.88	12
5	Plant height (cm)	2.65	8
6	Grain yield per plant (g)	15.77	48
7	Straw yield per plant (g)	12.32	37
8	Harvest Index (%)	8.5	26
9	Test weight (g)	8.22	25
10	Number of filled grains per panicle	7.43	23
11	Number of total spikelets per panicle	7.88	24
12	Spikelet fertility (%)	2.65	8
13	Protein (%)	4.32	13
14	Amylose (%)	2.33	7
15	Carbohydrate (%)	2.54	8
16	Fat (%)	3.44	10
17	Fe (ppm)	3.21	10
18	Zn (ppm)	1.67	5
19	Ca (ppm)	1.33	4

These findings were supported by Toshimenla *et al*., (2015) and recorded maximum contribution of grain yield per plant towards genetic divergence. Chandramohan *et al.,* (2016) recorded higher contribution of days to 50 per cent flowering and 1000-grain weight towards total divergence. Soundharya *et al*., (2020) reported higher contribution by number of filled grains per panicle followed by days to fifty per cent flowering.

The lowest contribution towards genetic divergence from the character Ca content (1.33 %) by taking 4 times ranking first, followed by Zn content (1.67 %) by 5 times, amylose content (2.33 %) by 7 times, carbohydrate content (2.54 %) by 8 times, plant height (2.65 %) by 8 times, spikelet fertility (2.65 %) by 8 times, Fe content (3.21 %) by 10 times, fat content (3.44 %) by 10 times respectively to the genetic divergence.

CHAPTER V : SUMMARY AND CONCLUSION

The present investigation entitled "**Genetic variability, diversity for yield and quality traits in rice (*Oryza sativa* L.)"**, was carried out at the Research and Educational farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri during *Kharif,* 2022. It was conducted with twenty-five rice genotypes in Randomized Block Design with three replications for yield and yield contributing traits under following objectives:

1. To study genetic variability and diversity for yield in rice

2. To evaluate biochemical and nutritional contents in rice

In this study, nature and magnitude of genetic variability, heritability in broad sense, genetic advance, correlation between grain yield and yield contributing traits, the direct and indirect effects of independent traits on dependent trait like grain yield and genetic diversity among the selected twenty-five genotypes was calculated**.** Five random plants of each genotype per replication were selected for recording observations. Days to 50 per cent flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, number of total spikelets per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), amylose (%), protein (%), carbohydrate (%), fat (%), iron (ppm), zinc (ppm) and calcium (ppm) were the nineteen traits studied in this experiment. All the genotypes recorded highly significant variation for all the characters under study suggesting the presence of considerable variation and thereby a great scope for selection of promising genotypes from present set of genotypes for crop improvement programme.

The genotypes DPL-2 followed by DPL-21, DPL-14, and DPL-13 were found earliest for days to fifty per cent flowering and days to maturity suggesting that these genotypes can be used as parents in hybridization programme for evolving early maturing rice varieties, whereas the genotypes DPL-8 followed by DPL-3, DPL-5, DPL-24 and DPL-15 were recorded extremely late genotypes for the character days to fifty per cent flowering and days to maturity indicating that these genotypes can be used for developing late maturing rice varieties.

The genotype DPL-23 had the greater number of productive tillers per plant, followed by DPL-14, DPL-25, DPL-2 and DPL-18. The genotypes DPL-17, DPL-24, DPL-11, DPL-19 and DPL-23 measured highest panicle length. Out of all twenty-five rice genotypes lowest plant height was measured by the genotypes DPL-23, DPL-10, DPL-22 and DPL-7, while the highest plant height was measured by the genotypes DPL-5, DPL-3, DPL-8 and DPL-11.

The highest number of filled grains per panicle recorded by the genotypes DPL-19, DPL-1, DPL-15, DPL-11 and DPL-6, whereas highest number of total spikelets per panicle observed in the genotypes DPL-19, DPL-11, DPL-1, DPL-12 and DPL-16. The genotypes DPL-14 followed by DPL-1, DPL-19, DPL-15 and DPL-2 reported highest spikelet fertility.

The genotypes DPL-22, DPL-4, DPL-15, DPL-12 and DPL-18 measured highest test weight. Grain yield per plant observed highest in the genotypes DPL-19, DPL-11, DPL-1, DPL-23 and DPL-4. The genotypes DPL-19, DPL-11, DPL-8, DPL-1 and DPL-12 observed the highest straw yield per plant. The genotypes DPL-19, DPL-4, DPL-1 and DPL-23 recorded highest harvest index.

Among the twenty-five genotypes, eleven genotypes had low and fourteen genotypes had moderate amylose (%). The genotypes DPL-3 followed by DPL-11, DPL-1, DPL-14 and DPL-6 were having more protein (%), while the higher levels of fat (%) reported by the genotypes DPL-15, DPL-19, DPL-1, DPL-13 and DPL-22. The genotypes DPL-19, DPL-14, DPL-15, DPL-18 and DPL-8 had the highest level of carbohydrate (%).

The maximum iron (ppm) was recorded in the genotypes DPL-14 followed by DPL-9, DPL-12, DPL-10 and DPL-23. The genotypes DPL-16, DPL-11, DPL-13 and DPL-15 observed maximum zinc (ppm), while the genotypes DPL-1 followed by DPL-17, DPL-14, DPL-12 and DPL-19 recorded maximum calcium (ppm).

In variance study, it is observed that the phenotypic variance was high in magnitude than genotypic and environmental variance for all the studied characters. The phenotypic and genotypic variance was very close to each other for majority of the characters thus, suggesting less significant role of environment in the expression of these characters. In general, phenotypic coefficients of variation (PCV) reported high magnitude than the corresponding genotypic coefficients of variation (GCV). High phenotypic and genotypic coefficient of variation was recorded for the characters number of filled grains per panicle followed by grain yield per plant, number of total spikelets per panicle, zinc (ppm), protein (%), plant height and calcium (ppm).

All the characters show the high heritability except fat content. Genetic advance was high in number of total spikelets per panicle, number of filled grains per panicle, plant height, calcium (ppm), days to maturity and days to fifty per cent flowering. All the characters exhibit higher estimates of genetic advance as per cent of mean except carbohydrate (%) which show low genetic advance as per cent of mean, fat (%), amylose (%), harvest index and panicle length.

The character correlation study observed that the genotypic correlation coefficient was higher in magnitude than corresponding phenotypic correlation coefficient. The genotypic and phenotypic correlation of grain yield per plant was recorded highly significant and positive

correlation with straw yield per plant, number of filled grains per panicle, harvest index, number of total spikelets per panicle. The genotypic and phenotypic correlation coefficient of grain yield per plant had significant positive correlation with fat (%) and test weight, while it had positive non-significant correlation with iron (ppm), amylose (%) and carbohydrate (%) at both phenotypic and genotypic level.

The path coefficient analysis shows that, the traits *viz*., number of productive tillers per plant, straw yield per plant, harvest index, protein (%) and fat (%) had positive direct effect on grain yield per plant at both phenotypic and genotypic levels, while zinc (ppm) had negative direct effect at both levels. The character days to fifty per cent flowering, panicle length, plant height and number of filled grains per panicle had positive direct effect on grain yield per plant at phenotypic level and negative direct effect at genotypic level. The character days to maturity, test weight, number of total spikelets per panicle, spikelet fertility, amylose (%), carbohydrate (%) and calcium (ppm) had negative direct effect on grain yield per plant at phenotypic level and positive direct effect at genotypic level. Iron (ppm) shows no direct effect on grain yield per plant at phenotypic level but negative direct at genotypic level.

Genetic divergence calculated by Mahalanobis's D^2 statistic grouped twenty-five genotypes into six clusters. Out of six clusters, cluster II was the largest (9 genotypes) followed by cluster III (5 genotypes), cluster IV (5 genotypes), cluster I (4 genotypes), while remaining two clusters had one genotype each. The high intra-cluster value was recorded in cluster IV (D^2 =315.33) followed by cluster II (D^2 = 230.42), cluster III (D^2 = 171.85), cluster I (D^2 = 167.05), cluster V (D^2 = 0.00) and cluster VI (D^2 = 0.00), thus indicating that the genotypes constituted in high intra-cluster value clusters might have different genetic constitution. The inter-cluster values were maximum in cluster V and VI (D^2 =1964.48) followed by cluster III and VI (D^2 =1428.90), cluster I and V (D^2 =1014.34), cluster II and VI (D^2 =1013.13) indicating significant difference between these clusters. Hence, the genotypes included in these clusters might be used in hybridization programme. In contrast, the lowest inter– cluster value between cluster I and VI followed by cluster II and III, cluster II and V indicated that the genetic constitution of genotypes included in these clusters were in close proximity. Among nineteen characters studied, grain yield per plant (15.77 %) recorded highest contribution towards genetic divergence followed by straw yield per plant (12.32 %), harvest index (8.5 %) and test weight (8.22 %). Hence, these characters may be taken into account during selection of genotypes for further crop improvement programmes.

Conclusion:

In conclusion, it is noted that the genotypes investigated for the various quantitative characteristics showed a significant range of variability. The results of the current research experiment show the wide range of variability for different traits, high heritability coupled with high genetic advance as percentage of mean for all yield contributing traits except carbohydrate (%), fat (%), amylose (%), spikelet fertility, harvest index and panicle length. Selections based on the traits which exhibit high heritability with high genetic advance as percentage of mean could directly increase productivity in rice.

Among nineteen characters studied, four characters *viz*., straw yield per plant, number of filled grains per panicle, harvest index and number of total spikelets per panicle exhibited highly significant and positive correlation with grain yield per plant at both phenotypic and genotypic level. The characters number of productive tillers per plant, straw yield per plant, harvest index, protein (%) and fat (%) had positive direct effect on grain yield per plant at both phenotypic and genotypic levels suggesting that yield can be improved by selecting the genotypes performing better grain for these characters. The study revealed that the genotypes included in cluster V and VI are most diverse to each other due to maximum inter-cluster value. Therefore, genotype included in these clusters *viz*., DPL-22 and DPL-3 have a broad-spectrum variability in segregating generations and may be used for hybridization programme.

- The genotype DPL-19 found superior for the characters grain yield per plant, straw yield per plant, harvest index, number of filled grains per panicle, number of total spikelets per panicle and carbohydrate per cent among all the studied genotypes.
- The highest protein per cent and lowest test weight was observed in DPL-3.
- DPL-15 showed the highest Fat per cent among all the studied genotypes.
- DPL-14, DPL-16 and DPL-1 observed superior for the parameters Fe content, Zn content and Ca content respectively.
- DPL-19, DPL-1, DPL-11, DPL-14, DPL-15, DPL-23, DPL-4, DPL-2, DPL-17, DPL-3, DPL-22 and DPL-16 were reported best for yield and yield contributing characters.
- Superior genotypes can be utilized as promising germplasms in future breeding programmes for development of higher yield and nutritional rich varieties in rice.

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APPENDICES

Appendix- I

Meteorological observation during the period of experiment *kharif*, 2022 at Dapoli

Meteorological period	MW	Tmax (^{0}C)	Tmin (^{0}C)	RH-I (%)	RH-II (%)	Wind speed (Kmph)	Rain (mm)	RD day	BSS (hrs.)
28.05 - 03.06	**22**	32.9	23.0	87	66	5.7	2.2	0	8.2
04.06 - 10.06	**23**	33.2	23.4	84	60	5.6	6.2	1	7.5
11.06 - 17.06	**24**	31.8	23.3	90	71	5.9	83.8	6	6.1
18.06 - 24.06	**25**	29.8	22.5	94	79	5.0	148.4	5	2.7
25.06 - 01.07	**26**	27.9	22.8	97	95	5.2	489.2	7	0.5
02.07 - 08.07	**27**	28.3	22.9	97	93	8.6	625.2	7	0.8
09.07 - 15.07	**28**	27.3	22.7	98	95	11.0	265.4	7	0.0
16.07 - 22.07	**29**	28.0	23.2	93	89	8.8	121.4	7	1.1
23.07 - 29.07	**30**	28.9	23.2	94	83	6.3	120.8	5	2.5
30.07 - 05.08	**31**	30.1	23.5	93	83	4.4	81.6	4	4.7
06.08 - 12.08	**32**	26.9	22.5	97	96	12.0	655.6	7	0.0
13.08 - 19.08	**33**	27.9	22.5	95	92	8.6	202.0	7	0.7
20.08 - 26.08	**34**	27.9	22.2	96	90	7.0	154.3	7	1.2
27.08 - 02.09	**35**	29.7	22.1	93	85	3.8	2.6	0	4.6
03.09 - 09.09	**36**	30.2	23.1	93	86	3.7	31.8	4	4.6
10.09 - 16.09	**37**	28.8	23.1	94	89	7.0	239.2	6	1.9
17.09 - 23.09	**38**	27.8	21.4	92	85	3.4	89.9	4	2.4
24.09 - 30.09	**39**	28.9	21.4	93	82	3.2	79.8	2	4.1
01.10 - 07.10	**40**	29.8	21.0	91	82	4.2	34.8	3	5.5
08.10 - 14.10	**41**	29.1	21.6	94	81	2.6	22.6	2	2.6
15.10 - 21.10	**42**	31.2	22.1	92	82	2.8	53.1	3	6.5
22.10 - 28.10	**43**	32.3	17.2	92	70	2.2	28.6	1	8.9
29.10 –04.11	**44**	31.9	15.2	88	62	5.5	0.0	0	10.2
05.11 –11.11	**45**	33.0	15.4	86	55	2.2	0.0	0	10.0
12.11 –18.11	**46**	32.8	15.0	91	50	2.2	0.0	0	9.9
19.11 –25.11	**47**	32.0	13.9	92	56	2.4	0.0	0	9.6
26.11 –02.12	**48**	32.9	16.6	93	52	2.4	0.0	0	8.5
03.12 –09.12	**49**	33.2	16.6	93	50	2.3	0.0	0	6.8
10.12 –16.12	**50**	32.1	17.7	92	53	2.5	0.0	0	5.5
17.12 –23.12	**51**	34.1	16.8	94	51	2.7	0.0	0	8.6
24.12 –31.12	**52**	32.2	14.4	92	55	2.7	0.0	0	8.4
							3559.5	**98**	

RD: Rainy days

BSS*: Bright Sun Shine hours

RH I: Morning Relative Humidity

RH II: Evening Relative Humidity

T max: Temperature Maximum

T min: Temperature Minimum

MW: Meteorological week

Appendix-II

❖ Determination of amylose content

Amylose content of milled rice samples was estimated by the method by Juliano (1971) involving the spectrophotometer.

Materials:

1. Balance (mg)
2. Water bath
3. Tri pod
4. Gas burner
5. Volumetric flasks (100 ml)
6. Pipettes (1 ml & 5 ml)
7. Absolute ethanol
8. Methanol
9. 1.0 N Sodium Hydroxide
10. 1.0 N Acetic acid
11. Stock Iodine solution (0.2% I2 + 2% KI)
12. Amylose (Purified Potato, Sigma)
13. 1 mm Sieve
14. Grinder
15. Spectrophotometer

Reagents:

1) 1.0 N Sodium Hydroxide: 40 gm of Anhydrous NaOH was dissolved in one litre distilled water

2) 1.0 Acetic acid: 57.75 ml of Glacial acetic acid was dissolved in one litre of distilled water.

3) Iodine solution: (0.2% I2 in 2% KI) 2 grams of Iodine and 20 grams of KI dissolved in one litre of distilled water.

4) Absolute alcohol: Above 95% alcohol (rectified spirit)

5) Standard Amylose solution: Take 40 mg of Amylose add 1 ml of absolute Alcohol and 1.0 Sodium Hydroxide, shake well and boil over water bath for 15 minutes and make solution to 100 ml volumetric flask.

Preparation of Amylose standard curve:

Protocol

H2O	6.0	4.8	3.6	2.4	1.2	0.0
Amylose solution	0.0	1.0	2.0	3.0	4.0	5.0
1.0 N. Acetic acid	0.0	0.2	0.4	0.6	0.8	1.0
I2-KI reagent	2.0	2.0	2.0	2.0	2.0	2.0

Mix the reagents in test tube and read at 620 nm (Absorbance) in Spectro photometer after 20 minutes.

Procedure for amylose standard solutions:

1. Take 40 mg amylose add 1 ml rectified spirit in a volumetric flask.
2. Then add 9 ml of 1.0 N Sodium Hydroxide.
3. Shake well and boil over water bath for 15 minutes and make the solution to 100 ml in a volumetric flask.
4. Pipette out 1 ml, 2 ml, 3 ml, 4 ml & 5 ml of the standard amylose into volumetric flasks in three replicates.
5. For 1 ml of standard amylose solution, add 0.2 ml of acetic acid and 2 ml I2+KI.
6. For 2 ml of standard amylose solution, add 0.4 ml of acetic acid and 2 ml I2+KI.
7. For 3 ml of standard amylose solution, add 0.6 ml of acetic acid and 2 ml I2+KI.
8. For 4 ml of standard amylose solution, add 0.8 ml of acetic acid and 2 ml I2+KI.
9. For 5 ml of standard amylose solution, add 1.0 ml of acetic acid and 2 ml I2+KI.
10. After adding I+KI solution, make up the solution to 100 ml and cover the flasks with a black cloth.
11. After 20 minutes take the reading in spectrophotometer at 620 nm.

Procedure for analysis of amylose content in rice:

1) Prepare standard rice samples:
   - Make sure that all samples to be used have been stored in same room for at least 2 days to ensure equal moisture content. In choosing standard samples include a range of rice representing the low, intermediate and high Amylose content.

- Grind each sample to fine powder in a Wig-L-Burg amalgamator or similar device for 40 seconds. A UD cyclone mill with 1 mm sieve may also be used for grinding.

2) Take 100 mg rice flour in test tube add 1 ml of rectified spirit and add 9 ml of 1.0 N Sodium Hydroxide.
3) Shake thoroughly and heat the test tubes on water bath for 15 minutes. Pour the samples after digestion in volumetric flask (100 ml) after rinsed with distilled water and then make up to sample to 100 ml.
4) Draw 5 ml solution in three replications into three 100 ml volumetric flasks
5) For each 5 ml solution add 1 ml of acetic acid and 2 ml of I2-KI reagent and make it to 100 ml in a volumetric flask.
6) Cover the all flasks with black clothes as I2-KI loses colour when exposed to light.
7) Adjust the spectrophotometer at 620 nm and take the readings.

After estimating amylose content, the samples were classified as follows.

Term	**Amylose (%)**	**Characteristics when cooked**
Waxy	1-2	On cooking it is sticky and soft
Very low	3-10	Absorbs little water and therefore has little volume expansion.
Low amylose	11-20	On cooking tends to be moist, sticky and glossy, split if over cooked.
Intermediate amylose	21-25	Cook fluffy, moist tender and do not become hard upon cooling and remain soft. (Most acceptable range for eating)
High amylose	> 25	Become hard when cool, Resist disintegration during boiling

(Source: - Juliano, 1979)

Appendix-III

❖ Determination of protein content

The protein content of was determined by estimating the nitrogen content as per the modified Kjeldhal method and multiplying the nitrogen content with a factor 5.95 and expressed on per cent basis for each genotype.

Methodology for the Determination of Protein by Kjeldhal Method

Principle:

The protein content is determined from the organic Nitrogen content by Kjeldahl method. The various nitrogenous compounds are converted into ammonium sulphate by boiling with concentrated sulphuric acid. The ammonium sulphate formed is decomposed with an alkali (NaOH) and the ammonia liberated is absorbed in excess of standard solution of acid and then back titrated with standard alkali.

Apparatus

a. Kjeldahl digestion flask - 500 or 800 ml

b. Kjeldahl distillation apparatus, - same digestion flask fitted with rubber stopper through which passes lower end of efficient rubber bulb or trap to prevent mechanical carryover of NaOH during distillation or apparatus as shown below:

c. Conical flask, 250 ml

d. Burette 50 ml.

Reagents

a. Concentrated Sulphuric acid – sp. gr. 1.84

b. Sodium Hydroxide solution - 45%. Dissolve 450 gm of Sodium Hydroxide In 1000 ml water

c. Standard Sulphuric acid solution – 0.1 N

d. Standard Sodium Hydroxide solution – 0.1 N

e. Methyl Red Indicator solution - Dissolve 0.5 gm methyl red in 100 ml of Alcohol

Procedure

Weigh quickly about 0.5 g of the sample and transfer to a 500 or 800 ml Kjeldahl flask taking care to see that no portion of the sample clings to the neck of the flask. Add 0.7 gm of Mercuric oxide, 15 gm of Potassium Sulphate and 40 ml of concentrated sulphuric acid. Add two to three glass beads. Place the flask in an inclined position on the stand in the digestion chamber

and digest. Heat the flask gently at low flame until the initial frothing ceases and the mixture boils steadily at a moderate rate.

During heating rotate the flask several times. Continue heating for about an hour or more until the colour of the digest is pale blue. Cool the digest and add slowly 200 ml of water. Cool, add a piece of granulated Zinc or anti bump granules and carefully pour down from the side of the flask sufficient Sodium Hydroxide solution (450gm/ litre) to make the contents strongly alkaline (about 110 ml) before mixing the acid and alkaline layer. Connect the flask to a distillation apparatus incorporating an efficient flash head and condenser. To the condenser fit a delivery tube which dips just below the surface of the pipette volume of standard acid contained in a conical flask receiver. Mix the contents of the digestion flask and boil until 150 ml have distilled into the receiver. Add 5 drops of methyl red indicator and titrate with 0.1 N Sodium hydroxide solutions. A blank was also run through all steps as above. Percent crude protein content of the sample was calculated by using the following formula:

% Crude Protein = 5.95* x %N (*. Correction factor)

$$\%N = \frac{(S - B) \times N \times 0.014 \times D \times 100}{\text{Wt.of the sample} \times V}$$

Where,

S = Sample titration reading

B = Blank titration reading

N = Normality of HCl

D = Dilution of sample after digestion

V = Volume taken for distillation

0.014 = Milli equivalent weight of Nitrogen

Appendix-IV

❖ Determination of Carbohydrate content

Estimation of total carbohydrate present in milled rice were observed using phenol sulphuric acid method.

Method

Equipment

- UV Spectrophotometer
- Vortex mixer
- Mantle heater/Water Bath.
- Test tube,
- Test tube stand,
- Pipettes, Beaker,
- Ice Test tube caps,
- Tissue paper,
- Wash bottle.

Reagents

- 5% Phenol
- 96% Sulphuric acid

Preparation of sample

(i) 100mg of flour from grains was taken in boiling tubes and to hydrolyse the sample 5ml of 2.5N HCL was added in it.

(ii) Boiling tubes was kept in water bath for 3hrs, and removed from water bath and cooled to room temperature.

(iii) After cooling it was neutralised by adding solid sodium carbonate until effervescence ceases.

(iv) Then whole volume was made 100ml by adding distilled water and centrifuged, supernatant is used as a sample.

Procedure

(i) A 0.2,0.4,0.6,0.8 and1ml of working standard (with 0.1mg/ml conc.) of glucose was taken in boiling tubes and the final volumes of each tube was made 1ml by adding distilled water.

(ii) 1ml of 5% Phenol and 5ml of 96% Sulphuric acid was added one by one in each tube and shook well so that the Phenol and Sulphuric acid get mixed thoroughly with working standard.

(iii) After 10 minutes all the tubes were placed in water bath at 25-30°C for 15 minutes.

(iv) Blank was set with 1ml of distilled water and O.D. of each tube was taken at 490nm with the help of spectrophotometer.

(v) Then the whole process following Phenol and Sulphuric acid method was repeated with 0.2ml of different samples of rice and the O.D.s of sample solutions were taken.

Table - 1: Absorbance at 490 nm with different concentration of working standard of glucose solution

Tube no.	Blank	1	2	3	4	5
Glucose sol. (in ml)	0	0.2	0.4	0.6	0.8	1
Distil water (in ml)	1	0.8	0.6	0.4	0.2	0
5% phenol sol. (in ml)	1	1	1	1	1	1
96% sulphuric acid sol. (in ml)	5	5	5	5	5	5
O. D	0	1.20	2.25	3.50	4.20	6
Conc. Of glucose mg/ml	0	0.020	0.040	0.060	0.080	0.10

Appendix-V

❖ Determination of fat content

Fat content of milled rice samples was estimated by the Soxhlet apparatus method.

Method

Equipment

- Analytical balance
- Electrical drying oven to be operated at 102ºC± 1ºC.
- Soxhlet extraction unit comprising:
  - Round bottom flask, 150 mL
  - Soxhlet extractor with 60 mL siphoning capacity and condenser.
  - Cellulose extraction thimbles (28 x 80 mm)
- Fume cupboard
- Heat source, either electric heating mantle, or steam bath 100 mL beaker
- Desiccator with silica gel desiccant
- Glass rod

Reagents

- Petroleum spirit boiling point 60-80ºC
- Cotton wool free of fat
- Acid washed sand

Procedure

1. Accurately weigh 5 g of sample into the thimble. Add 1 - 1.5 g of sand and mix the sand and sample with a glass rod. Wipe the glass rod with a piece of cotton wool and place cotton wool in the top of the thimble. (Addition of sand is not required for analysis of meat meal). Dry the sample in an oven at 102ºC for 5 hours. The drying step may be omitted in the analysis of meat meal.
2. Allow the sample to cool in a desiccator.
5. Take the piece of cotton wool from the bottom of the beaker and place it in the 3 top of the thimble.

6. Insert the thimble in a Soxhlet liquid/solid extractor (Figure 1).
7. Accurately weigh a clean, dry 150 mL round bottom flash and put about 90 mL of petroleum spirit into the flask.
8. Assemble the extraction unit over either an electric heating mantle or a water bath.
9. Heat the solvent in the flask until it boils. Adjust the heat source so that solvent drips from the condenser into the sample chamber at the rate of about 6 drops per second.
10. Continue the extraction for 6 hours. For sausage meat and other emulsified products, the extraction should be performed in stages: Extract for about 4 hours, then remove the heat source and drain the solvent from the extractor in the flask. Remove the thimble from the extractor and transfer the sample to a 100 mL beaker. Break up the sample with a glass rod. Return the sample to the thimble and replace the thimble in the extractor. Rinse the beaker with petroleum spirit and pour rinsings into the extract. Continue extraction for a further two hours.
11. Remove the extraction unit from the heat source and detach the extractor and condenser. Replace the flask on the heat source and evaporate off the solvent. (The solvent may be distilled and recovered).
12. Place the flask in an oven at 102ºC and dry the contents until a constant weight is reached (1-2 hours).
13. Cool the flask in a desiccator and weigh the flask and contents.

Weight of empty flask (g) = W1

Weight of flask and extracted fat (g) = W2

Weight of sample = S

$$\% \text{ Crude fat} = \frac{(W2 - W1)}{S} \times 100$$

THESIS ABSTRACT

a)	Title of the thesis	:	**Genetic variability, diversity for yield and quality traits in rice (*Oryza sativa* L.)**
b)	Full name of the student	:	Mr. Rahul Tejram Gahane
c)	Name and address of the major advisor	:	Dr. R. L. Kunkerkar Head Department of Agril. Botany, College of Agriculture, Dapoli.
d)	Degree to be awarded	:	M.Sc. (Agri.)
e)	Year of award of degree	:	2023
f)	Major subject	:	Genetics and Plant Breeding
g)	Total number of pages in the thesis	:	90
h)	Number of words in the abstract	:	330
i)	Signature of student	:	
j)	Signature, Name and address of forwarding authority	:	

THESIS ABSTRACT

The present investigation, entitled "Genetic Variability, Diversity for Yield and Quality Traits in Rice (*Oryza Sativa* L.)" was undertaken to study the genetic variability, correlation, path analysis and genetic divergence in twenty-five rice genotypes. The field experiment was conducted during *Kharif,* 2022 in a Randomized Block Design with three replications at Research and Educational farm, Department of Agriculture Botany, College of Agriculture, Dapoli. The biochemical analysis was done at biochemistry laboratory, Regional Agricultural Research Station, Karjat, Dist. Raigad.

In variance study, it is observed that the phenotypic variance was high in magnitude than genotypic and environmental variance for all the studied characters. All the characters show high heritability except fat (%). High heritability coupled with high genetic advance as percent of mean for all yield contributing traits except carbohydrate (%), fat (%), amylose (%), spikelet fertility harvest index and panicle length. The genotypic and phenotypic correlation of grain yield per plant

was recorded significant positive with straw yield per plant, number of filled grains per panicle, harvest index, number of total spikelets per panicle, fat (%) and test weight. The path analysis shows that, the traits *viz*., number of productive tillers per plant, straw yield per plant, harvest index, protein (%) and fat (%) had positive direct effect on grain yield per plant at both phenotypic and genotypic levels. Genetic divergence calculated by Mahalanobis's D^2 statistic grouped twenty-five rice genotypes into six clusters. Out of six clusters, cluster II was the largest (9 genotypes) followed by cluster III (5 genotypes), cluster IV (5 genotypes), cluster I (4 genotypes), while remaining two clusters had one genotype each. The high intra-cluster value was recorded in cluster IV, while inter-cluster values were maximum in cluster V and VI.

On the basis of results, it is concluded that the genotypes DPL-19, DPL-1, DPL-11, DPL-14, DPL-15, DPL-23, DPL-4, DPL-2, DPL-17, DPL-3, DPL-22 and DPL-16 were reported best for yield and yield contributing characters. These genotypes can be utilized as promising germplasms for future breeding programmes.

Key words: Genotype, Variability, heritability, Genetic advance, Genetic divergence *etc.*

VITA

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Genetic diversity studies for yield and quality traits in rice (*Oryza sativa* L.)

RT Gahane, RL Kunkerkar, TJ Bedse, MG Palshetkar, AV Mane and KM Lonare

Abstract
The experiment was conducted with Fifty-five rice genotypes during *Kharif* 2022 in a Randomized Block Design with three replications at Research and Educational farm, Department of Agriculture Botany, College of Agriculture, Dapoli to study the genetic divergence for yield and quality traits. Genetic divergence calculated by Mahalanobis's D^2 statistic grouped twenty-five rice genotypes into six clusters. Out of six clusters, cluster II was the largest (9 genotypes) followed by cluster III (5 genotypes), cluster IV (5 genotypes), cluster I (4 genotypes), while remaining two clusters had one genotype each. The high intra-cluster value was recorded in cluster IV followed by cluster II, cluster III, cluster I, thus indicating that the genotypes constituted in high intra-cluster value clusters might have different genetic constitution. The inter-cluster values were maximum in cluster V and VI followed by cluster III and VI, cluster I and V, cluster II and VI indicating significant difference between these clusters. Hence, the genotypes included in these clusters may be used in hybridization programmes.

Keywords: Genotype, hybridization, genetic divergence etc.

Introduction
Rice (*Oryza sativa* L.) serves as a main food source for more than half of the world's population, especially in Asia and Africa. More than 100 countries cultivate this crop, in which Asia contribute majority in area and production. The United Nation designated year 2004 as the 'International Year of Rice' with the theme "Rice is life" to highlight the significance of the rice crop as a source of food, for trade, and the tight ties between rice-based systems, many cultures and people worldwide, especially in developing countries.

In the year 2021 around the world, rice is grown over an area of 165.25 million hectares, with a total production of 787.29 million tonnes and yield of 4.76 t/ha (FAOSTAT, 2021). In India, rice is raised on an area of 46.00 million ha with an annual yield of 130.84 million tonnes and a productivity of 2.607 t/ha (Anonymous, 2023) [1]. Maharashtra covered rice crop over 14.65 lakh hectares of land with an annual production of 32.76 lakh tonnes and an average productivity of 2.180 t/ha, (Anonymous, 2023) [1]. Konkan region of Maharashtra is a significant rice-producing area with an area of about 3.69 lakh hectare producing yield of around 12.94 lakh tonnes and productivity of about 2.93 t/ha, (Anonymous, 2023) [1].

Any crop improvement program's success is affected by the genetic diversity of the genotypes. Estimating the genetic diversity in yield attributes is crucial for the policies that choose parents in crossing programmes. The plant breeders tend to assess genetic diversity from morphological characters because this is inexpensive, rapid, and simple to score. Genetic diversities effects on rice crop production, quality, and sustainability were examined in the project, along with the economic and social implications for farmers and other stakeholders. Overall, this study will add to our understanding of rice genetic diversity and provide insight into possibilities for rice breeding and crop improvement.

Materials and Methods
The field experiment was conducted at Research and Educational Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri, Maharashtra state during *Kharif* 2022. The experiment was laid out in Randomized Block Design (RBD) with three replications. The experimental material, 25 genotypes of rice was sown in the nursery on raised beds and seedlings were transplanted after 30 days of sowing with a spacing of 20 cm × 15 cm. From each genotypes per replication, five competitive plants were chosen at random

excluding border row to record observations on 19 yield and quality traits *viz.*, Days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, number of total spikelets per panicle, spikelet fertility (%), test weight (g), grain yield per plant (g), straw yield per plant (g), harvest index (%), amylose (%), protein (%), carbohydrate (%), fat (%), iron (ppm), zinc (ppm) and calcium (ppm). The mean of five plants was subjected to statistical analysis. Genetic divergence was analyzed through Mahalanobis's D^2 statistical technique and clustering of genotypes was done by using Tocher's method as described by Rao (1952) [7]. Wilk's criterion was used to test the significance.

Results and discussion

Genetic divergence analysis and D^2 values calculated with Mahalanobis's D^2 statistics distribute twenty-five rice genotypes into 6 clusters (Table 1) and depicted in Fig 1. Among the 6 clusters, cluster II accommodated a greater number of genotypes (9 genotypes) followed by cluster III and cluster IV having same number of genotypes (5 genotypes each), cluster I (4 genotypes), cluster V and cluster VI (1 genotype each). Same results were earlier confirmed by Chandramohan *et al.*, (2016) [2] and Soundharya *et al*., (2020) [8]. Chandramohan *et al.*, (2016) [2] grouped 44 rice genotypes into 11 clusters and Soundharya *et al*., (2020) [8] grouped 20 genotypes into 4 cluster.

Table 1: Distribution of 25 genotypes into SIX different clusters

Cluster Group	No. of Genotypes	List of Genotypes
I	4	DPL-5, DPL-8, DPL-9 & DPL-24
II	9	DPL-17, DPL-18, DPL-25, DPL-20, DPL-12, DPL-15, DPL-23, DPL-16 & DPL-7
III	5	DPL-13, DPL-21, DPL-10, DPL-2 & DPL-14
IV	5	DPL-1, DPL-19, DPL-6, DPL-11 & DPL-4
V	1	DPL-22
VI	1	DPL-3

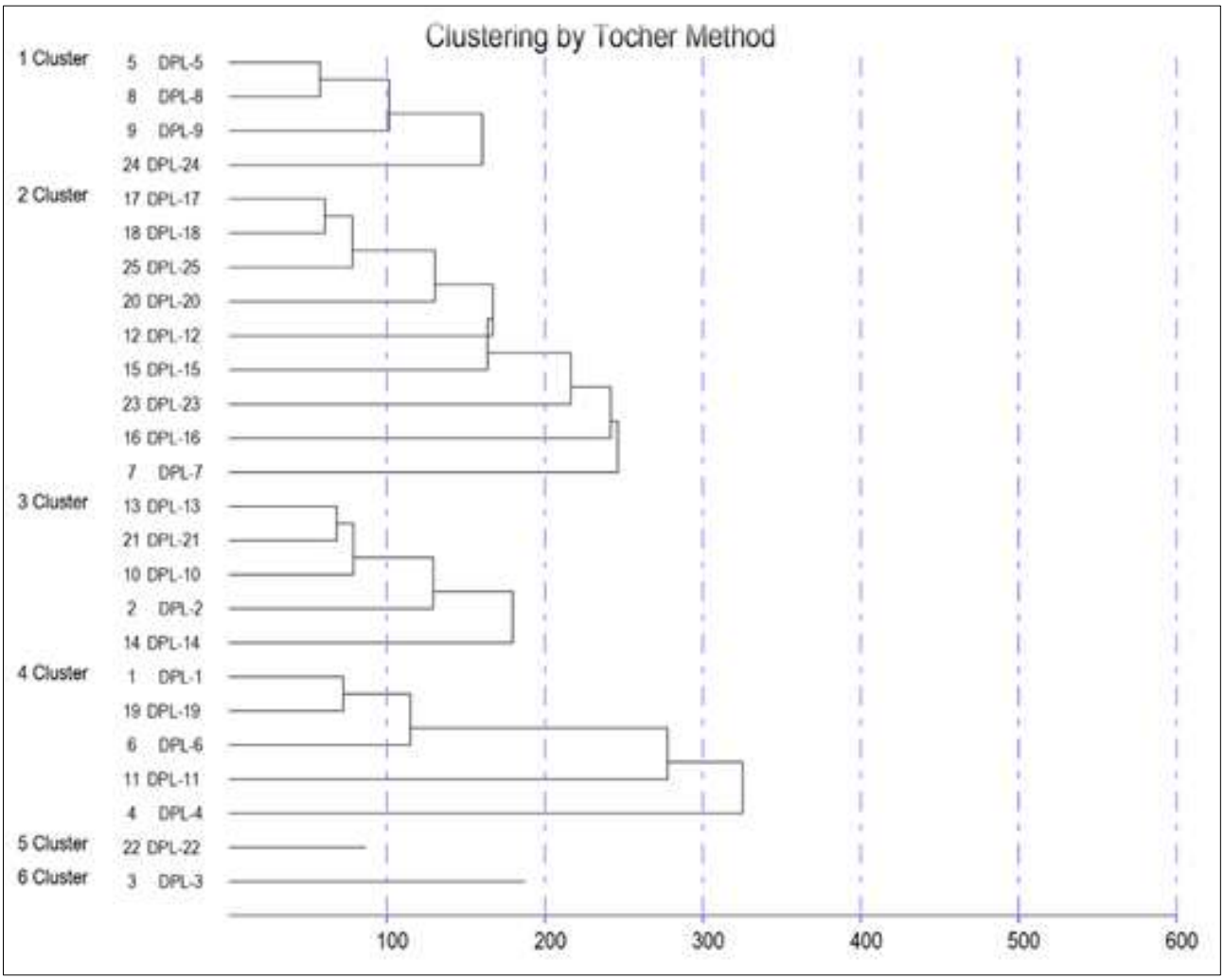

Fig 1: Clustering by tocher method

Intra and Inter cluster distances were given in Table 2 and depicted in Fig 2. The inter cluster distances were greater than intra cluster indicating wide genetic diversity among genotypes. The maximum intra-cluster D^2 value was observed for cluster IV (315.33) followed by cluster II (230.42), cluster III (171.85), cluster I (167.05), whereas both cluster V and cluster VI observed zero intra-cluster D^2 values. The high intra cluster values in cluster IV indicated the presence of wide genetic diversity among the genotypes. Devi *et al*., (2019) [3] reported similar findings.

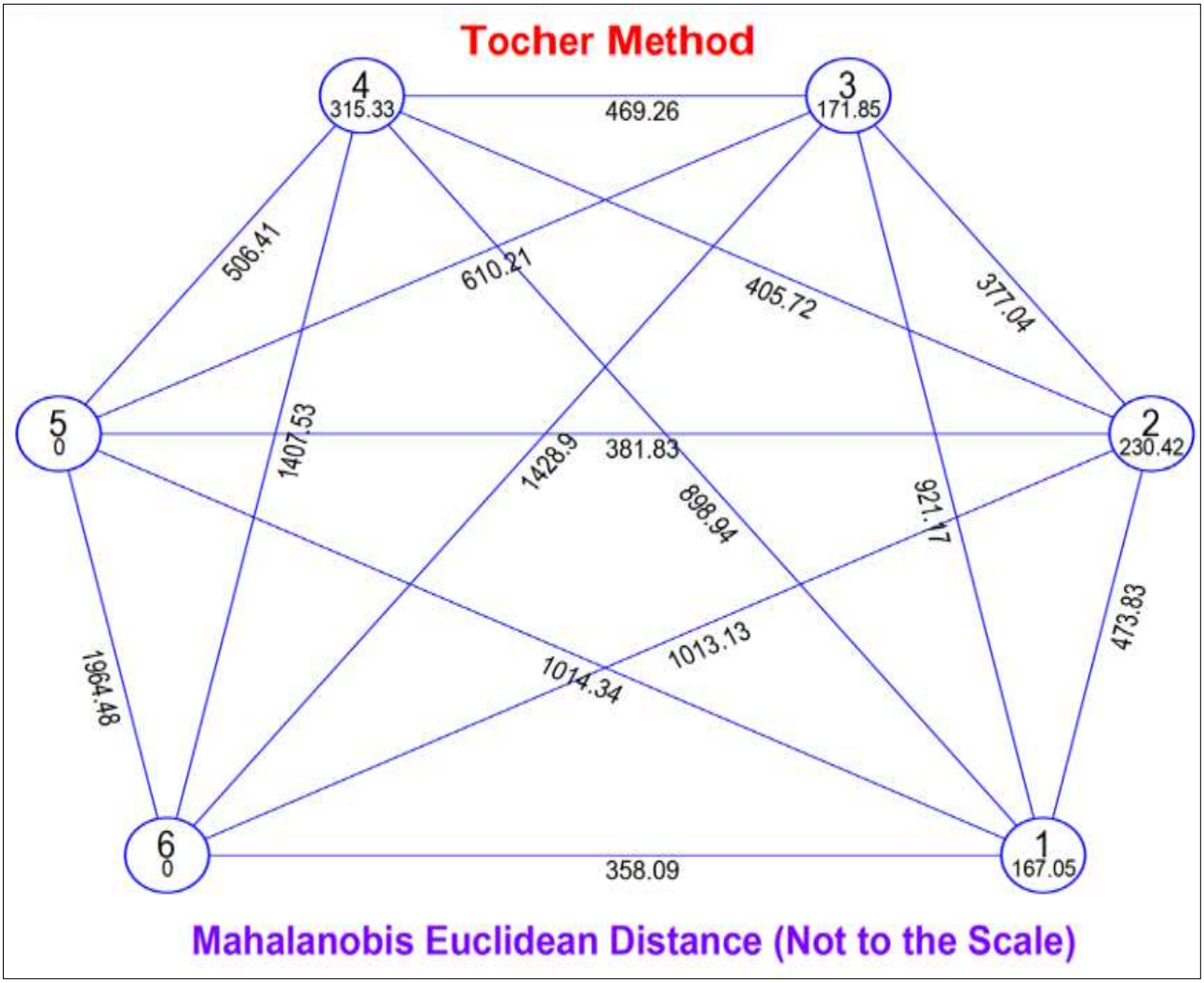

Fig 2: Cluster Diagram (Tocher Method)

Table 2: Average intra and inter cluster values in six clusters (D^2) in rice

	I	II	III	IV	V	VI
I	167.05	473.83	921.17	898.94	1014.34	358.09
II		230.42	377.04	405.72	381.83	1013.13
III			171.85	469.26	610.21	1428.90
IV				315.33	506.41	1407.53
V					0.00	1964.48
VI						0.00

The maximum inter-cluster D^2 value was observed between cluster V and cluster VI (1964.48), then between cluster III and cluster VI (1428.90), cluster IV and cluster VI (1407.53), cluster I and cluster V (1014.34) and cluster II and cluster VI (1013.13), whereas minimum inter-cluster D^2 values was recorded between cluster I and cluster VI (358.09) then between cluster II and cluster III (377.04), cluster II and cluster V (381.83), cluster II and cluster IV (405.72) and cluster III and cluster IV (469.26). Umesh *et al.*, (2016) [10] recorded similar results and support the current findings.

The cluster mean values for 19 traits are given in Table 3 and indicated a wide range of mean values between the traits. Percent contribution of various characters towards genetic divergence is also given in Table 3. The experimental finding displays that the contribution of grain yield per plant (15.77%) was highest towards genetic divergence followed by straw yield per plant (12.32%), harvest index (8.5%) test weight (8.22%), number of total spikelets per panicle (7.88%), number of filled grains per panicle (7.43%), days to fifty percent flowering (4.34%), protein content (4.32%), panicle length (3.88%), days to maturity (3.76%), number of productive tillers per plant (3.76%) respectively to the genetic divergence. These findings were supported by Toshimenla *et al*., (2015) and recorded maximum contribution of grain yield per plant towards genetic divergence. Chandramohan *et al.*, (2016) [2] recorded higher contribution of days to 50% flowering and 1000 grain weight towards total divergence. Soundharya *et al*., (2020) [8] reported higher contribution by number of filled grains per panicle followed by days to fifty percent flowering.

The lowest contribution towards genetic divergence from the character Ca content (1.33%), followed by Zn content (1.67%), amylose content (2.33%), carbohydrate content (2.54%), plant height (2.65%), spikelet fertility (2.65%), Fe content (3.21%), fat content (3.44%) respectively to the genetic divergence.

Table 3: Cluster mean performance and contribution towards divergence of nineteen characters in rice genotypes

Sr. No.	Characters	Clusters						Contribution%
		I	II	III	IV	V	VI	
1.	Days to fifty percent flowering	114.08	98.04	81.53	92.20	94.33	122.67	4.34
2.	Days to maturity	145.42	127.85	110.73	123.73	124.00	150.00	3.76
3.	Number of productive tillers per plant	6.62	6.70	7.93	6.76	5.67	7.20	3.76
4.	Panicle length (cm)	24.30	23.68	21.36	25.15	23.33	22.20	3.88
5.	Plant height (cm)	141.97	119.76	93.72	108.29	87.37	160.2	2.65
6.	Grain yield per plant (g)	14.02	15.02	12.85	20.28	18.15	12.45	15.77
7.	Straw yield per plant (g)	25.12	22.06	20.80	26.52	24.88	24.53	12.32
8.	Harvest Index (%)	35.86	40.39	38.39	42.96	42.20	33.64	8.5
9.	Test weight (g)	20.75	24.76	21.10	23.02	33.09	14.31	8.22
10.	Number of filled grains per panicle	99.05	112.62	81.19	155.54	128.99	82.53	7.43
11.	Number of total spikelets per panicle	134.61	151.46	103.54	191.06	165.00	113.02	7.88
12.	Spikelet fertility (%)	74.22	74.68	78.44	81.42	78.18	73.02	2.65
13.	Protein (%)	5.66	5.85	6.54	7.36	4.37	8.68	4.32
14.	Amylose (%)	19.18	19.06	20.83	20.66	20.38	20.89	2.33
15.	Carbohydrate (%)	80.29	81.16	82.12	80.17	82.52	79.68	2.54
16.	Fat (%)	15.01	15.91	15.91	15.77	17.28	16.04	3.44
17.	Fe (ppm)	16.12	15.62	17.13	16.38	15.30	16.87	3.21
18.	Zn (ppm)	12.22	11.41	12.05	10.08	9.90	7.32	1.67
19.	Ca (ppm)	90.39	90.70	91.65	82.25	56.28	56.71	1.33

Conclusion

The current study revealed that the genotypes included in cluster V and VI are most diverse to each other due to maximum inter-cluster value. Therefore, genotype included in these clusters *viz*., DPL-22 and DPL-3 have a broad-spectrum variability in segregating generations and may be used for hybridization programme. Among nineteen characters studied, grain yield per plant recorded highest contribution towards genetic divergence followed by straw yield per plant, harvest index and test weight. Hence, these characters may be taken into account during selection of genotypes for further crop improvement programmes.

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Similarity	40%
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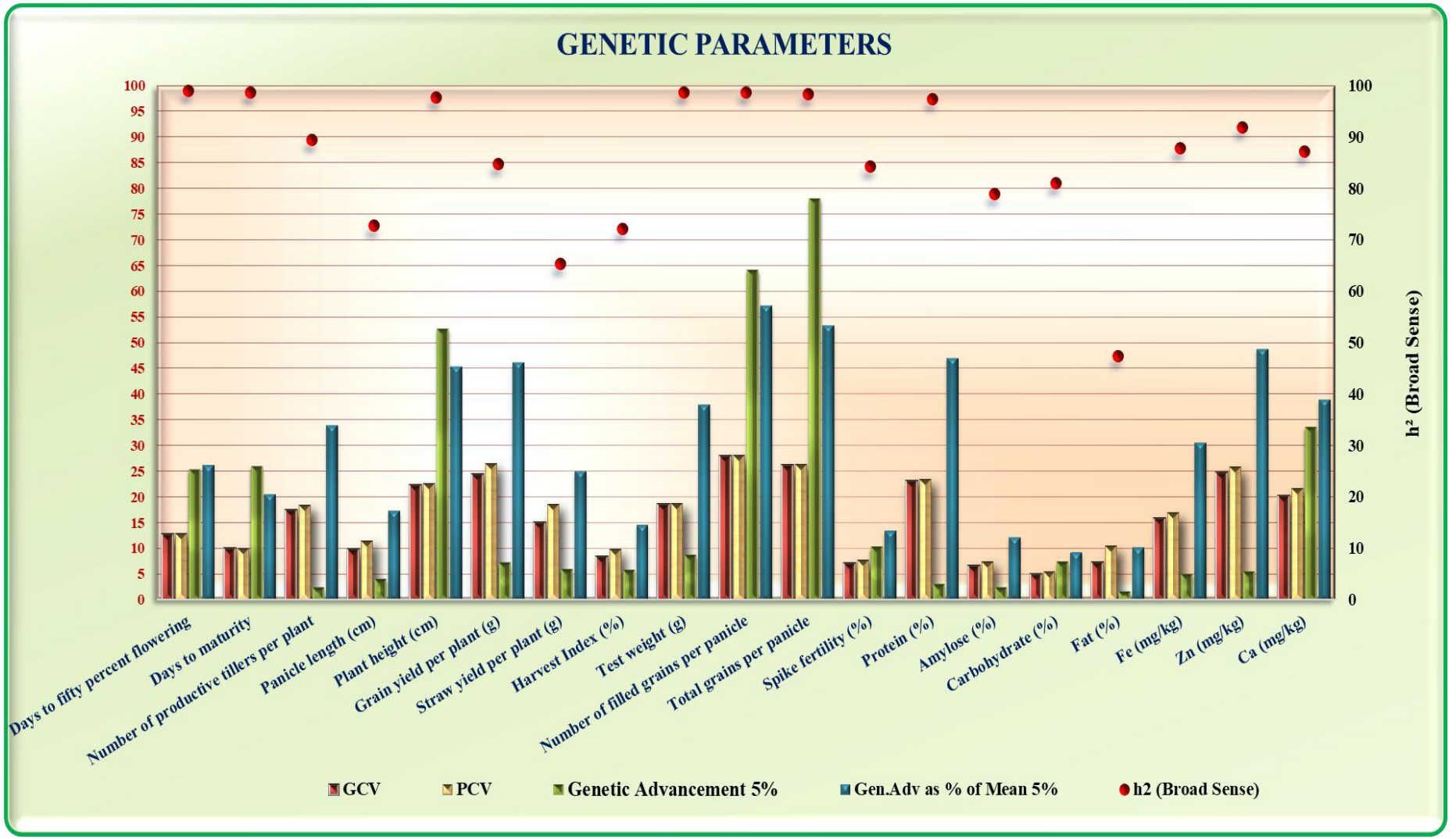

Fig.4.1: Graphical comparison of GCV, PCV, GA, h^2 (Board sense) and GAM as per centof mean for 19 characters in rice

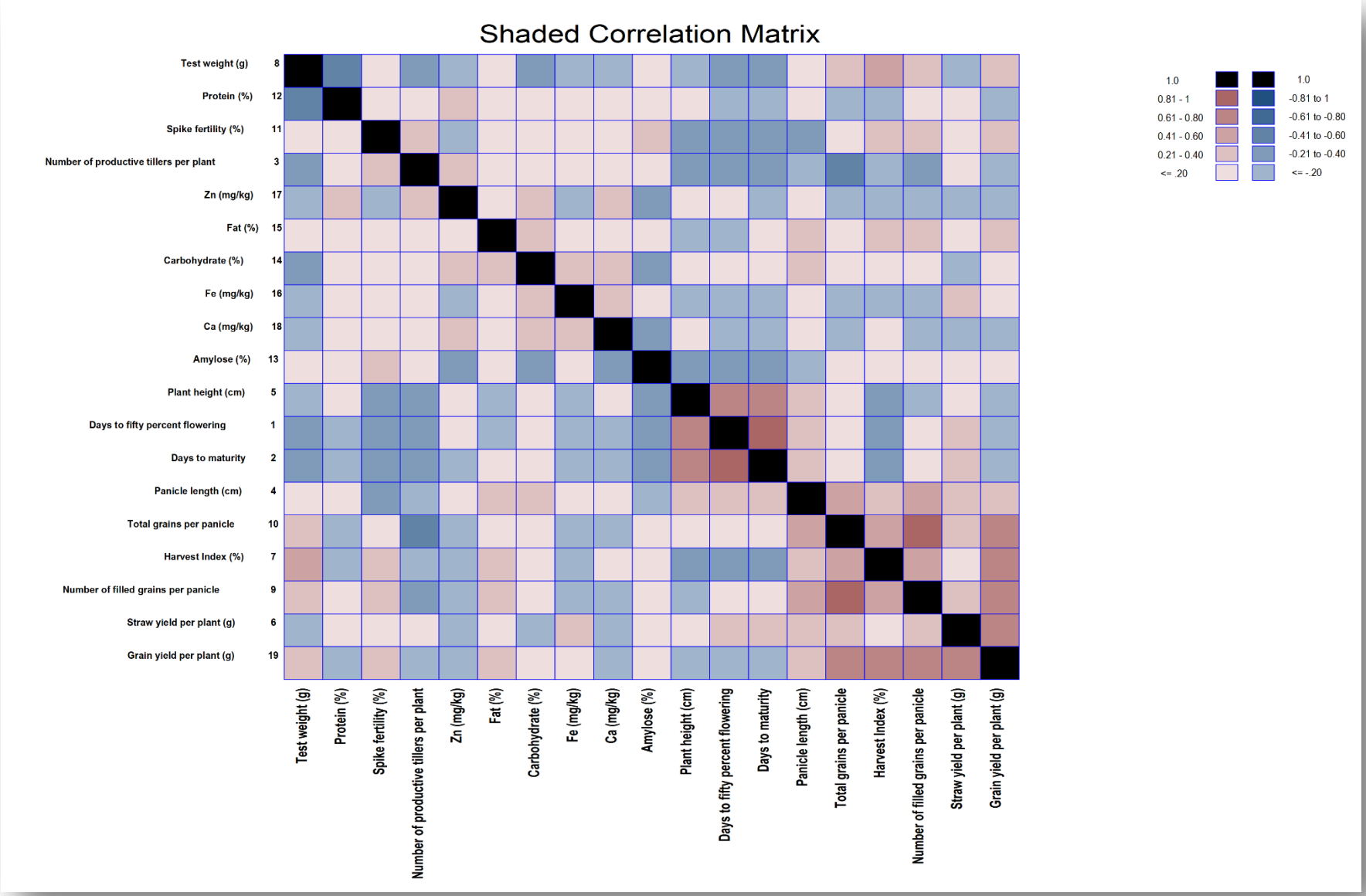

Fig. 4.2 : Shaded correlation matrix of phenotypic correlation of 19 characters of rice

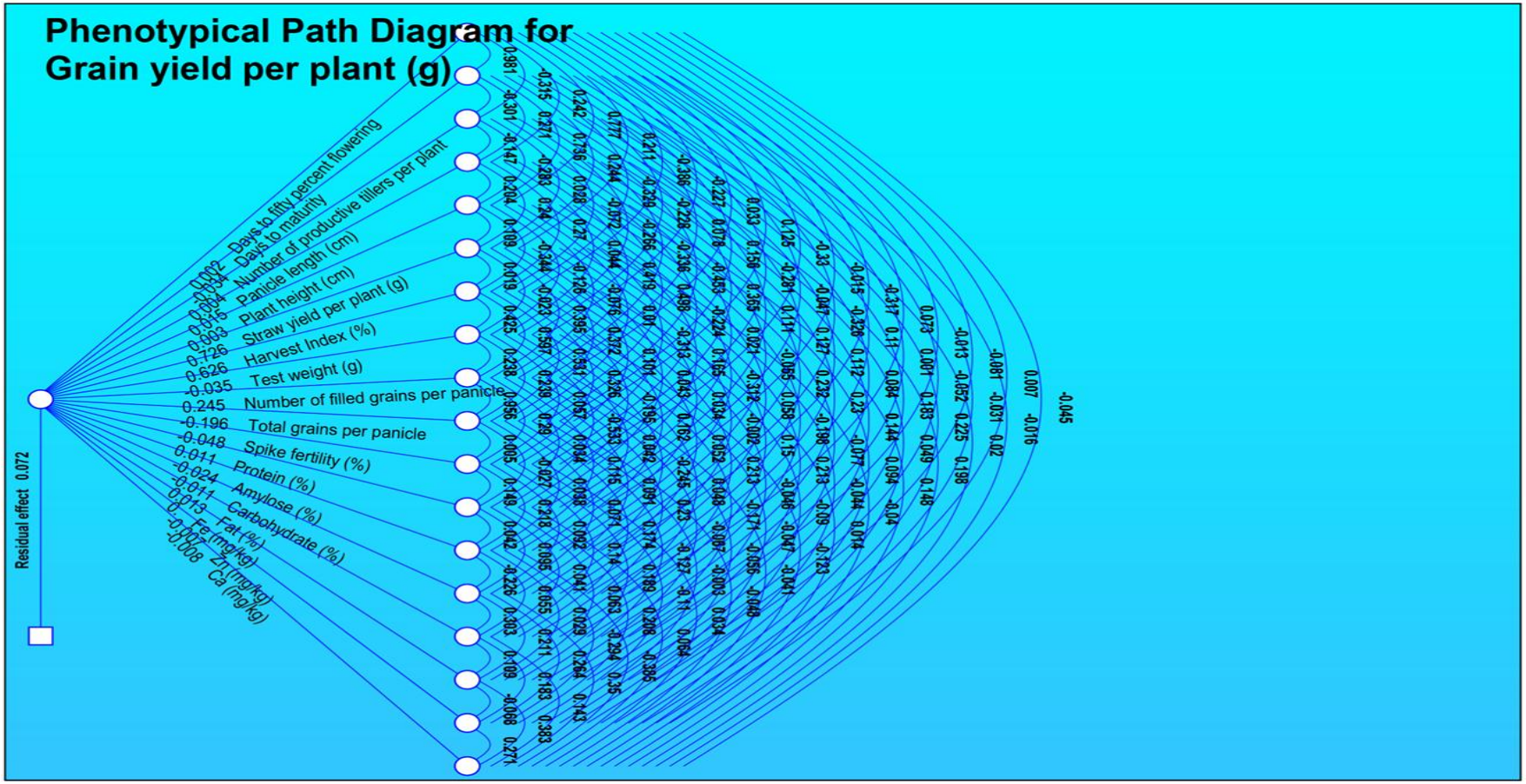

Fig. 4.4 : Phenotypical path diagram for grain yield per plant (g)

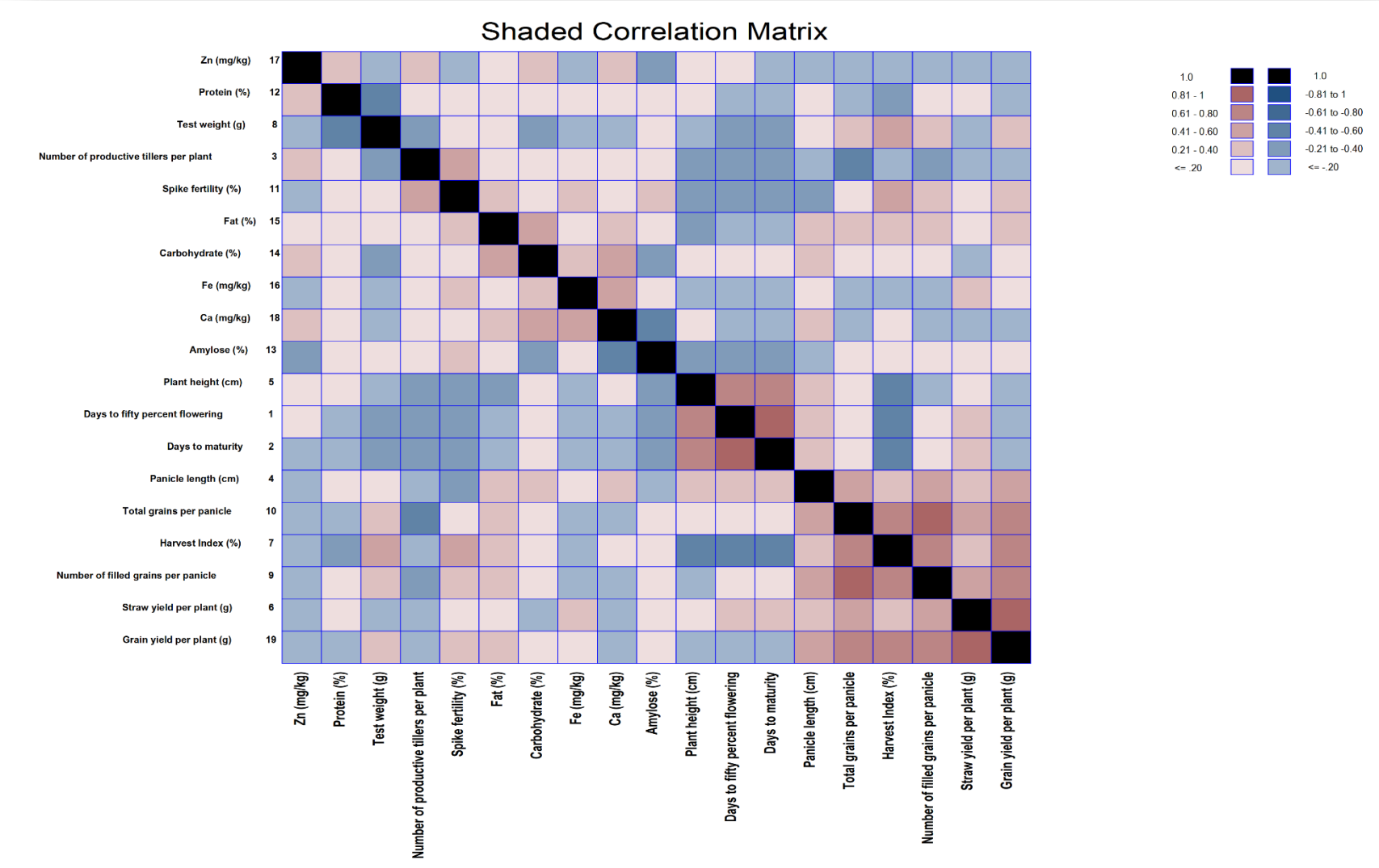

Fig. 4.3 : Shaded Correlation Matrix of Genotypic Correlation of 19 characters of rice

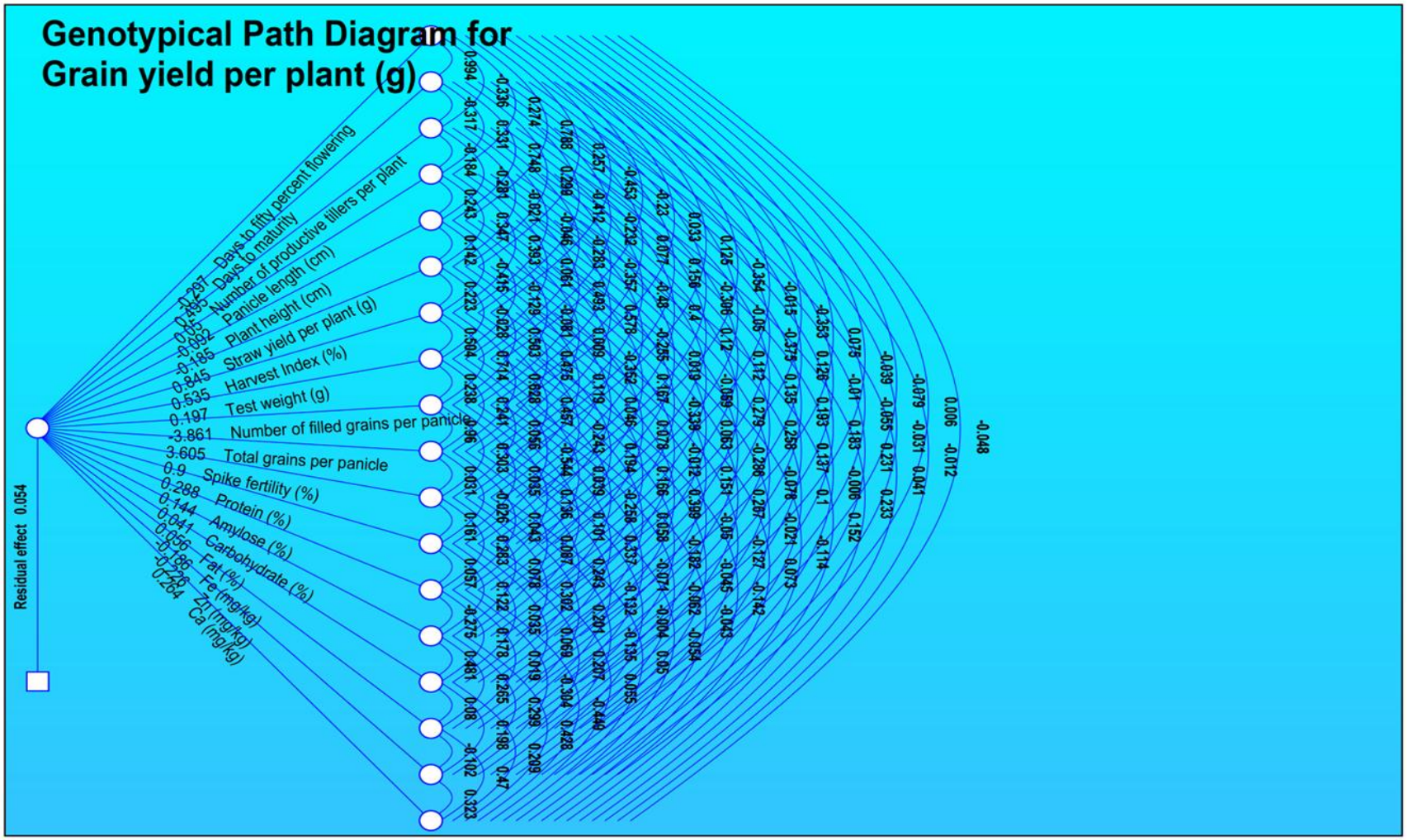

Fig. 4.5 : Genotypical path diagram for grain yield per plant (g)

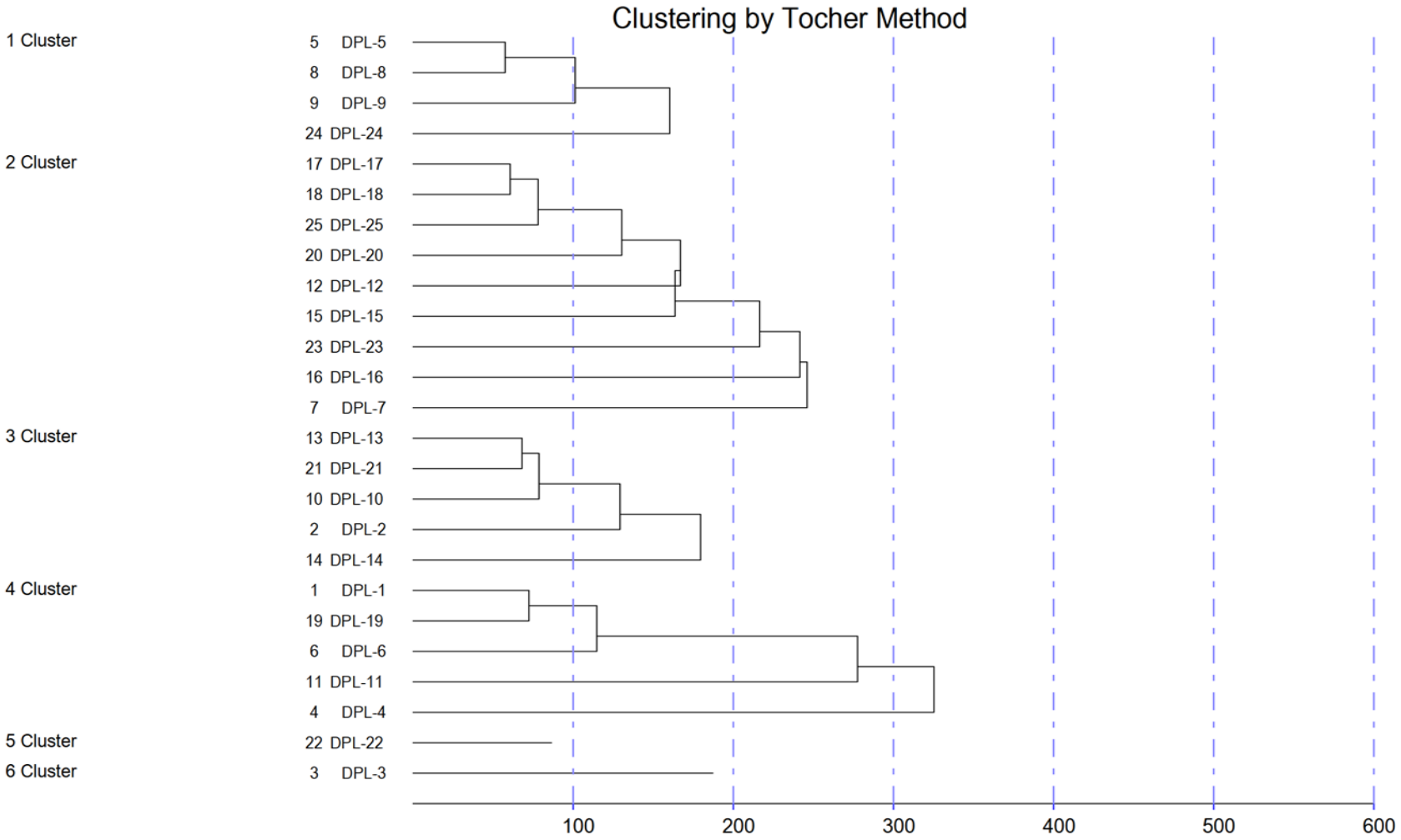

Fig. 4.6 : Clustering by Tocher method (Dendrogram)

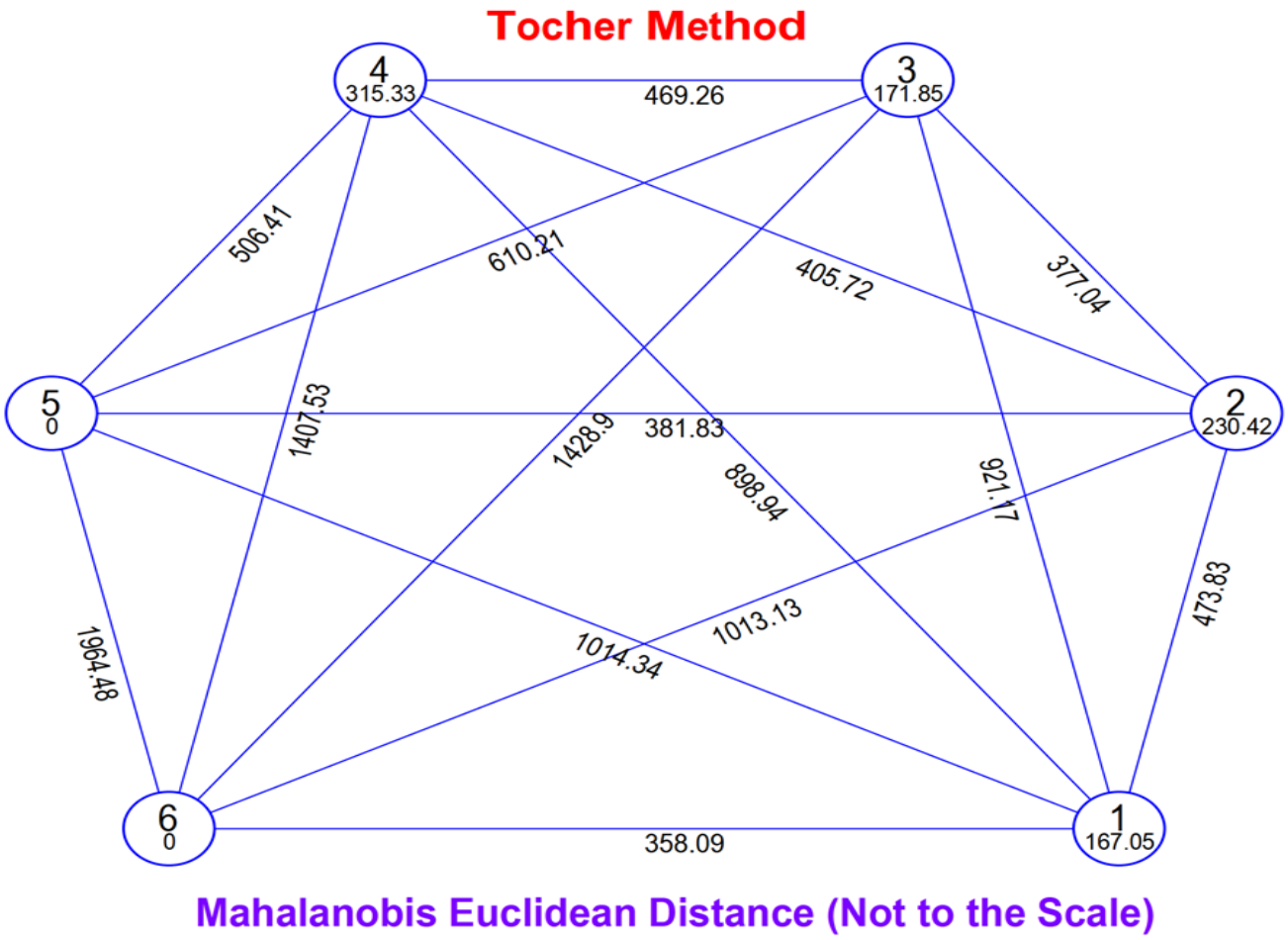

Fig. 4.7 : Cluster Diagram (Tocher Method)

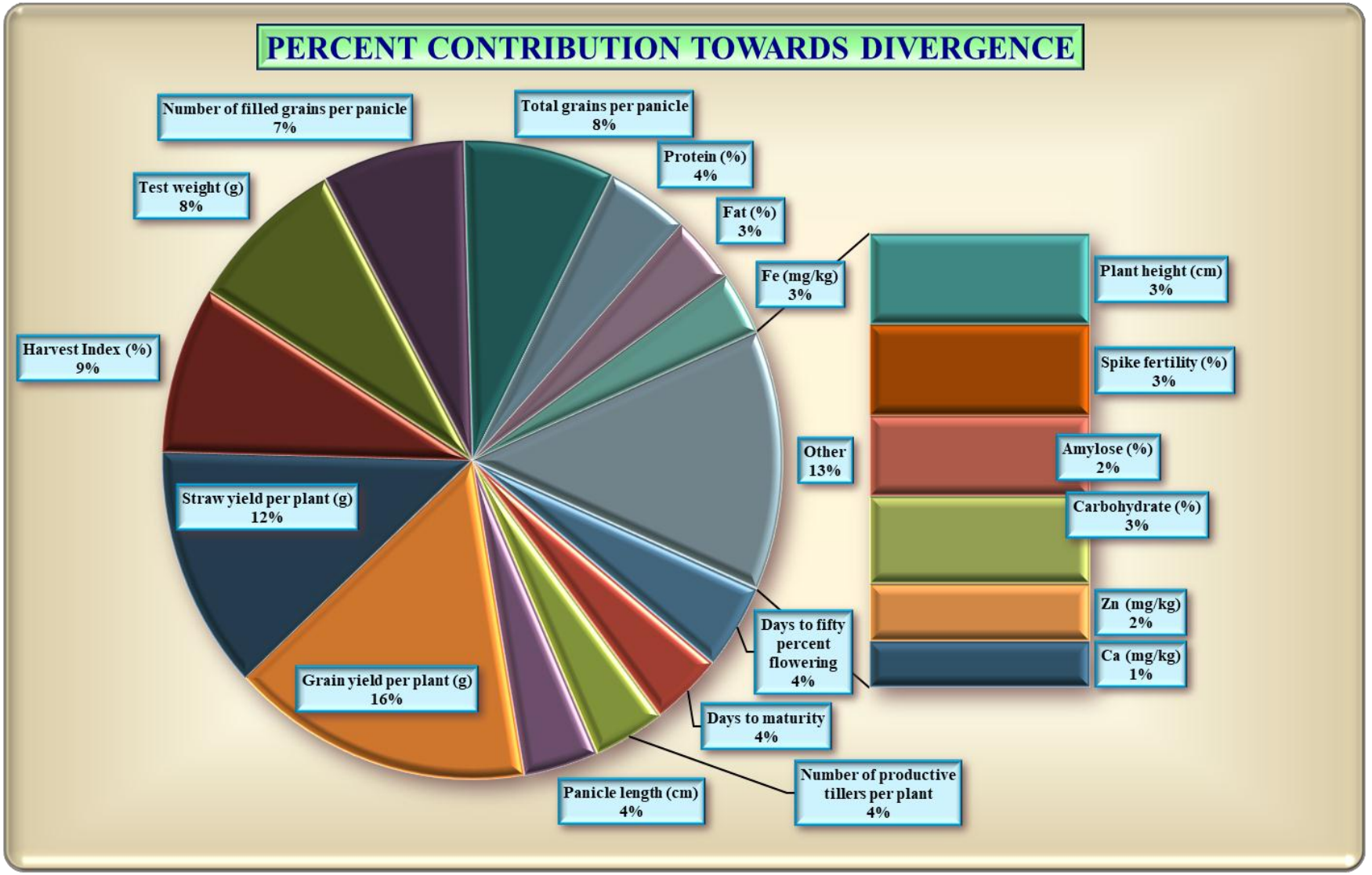

Fig. 4.8 : Per cent contribution of various 19 characters towards divergence

Plate IV : Variation in Panicle Length of 25 Rice Genotypes

Plate III : Variation in Grain Size and Colour of 25 Rice Genotypes after Milling

Plate II : Variation in Grain Size and Colour of 25 Rice Genotypes before Milling

Plate I : Overview of Research Plot During *Kharif* 2022